

生物物理

S E I B U T S U B U T S U R I

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Vol.65

第63回年会予稿集

主催 一般社団法人 日本生物物理学会



会期 2025年
9月24日(水) - 26日(金)

会場 奈良県
コンベンションセンター

年会長 高田 彰二
(京都大学理学研究科生物物理教室)

第 63 回日本生物物理学会年会



The 63rd Annual Meeting of the Biophysical Society of Japan

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開催概要 / General Information

第63回日本生物物理学会年会（2025年度）

The 63rd Annual Meeting of the Biophysical Society of Japan

会期 / Date

2025年9月24日（水）－26日（金）

September 24(Wed) – 26(Fri), 2025

会場 / Venue

奈良県コンベンションセンター

Nara Prefectural Convention Center

年会長・実行委員長 / Chair of the Organizing Committee

高田 彰二（京都大学大学院理学研究科生物物理学教室）

Shoji Takada (Dept. Biophysics, Grad. Sch. of Science, Kyoto University)

キャッチフレーズ / Catchphrase

『古の都・奈良にて、生物物理の現在と未来を繋ぐ』

～ At the ancient capital Nara, moving from the present biophysics to the future ～

年会ウェブサイト / Website of the Annual Meeting

<https://www2.aeplan.co.jp/bsj2025>

年会長挨拶

第63回年会 年会長・実行委員長

高田 彰二

京都大学大学院理学研究科生物物理学教室



日本生物物理学会の第63 回年会を、2025 年9 月24 日（水）より26日（金）までの3 日間、奈良県コンベンションセンター（奈良市）で開催します。世界遺産に囲まれる古都・奈良での年会は、当学会として初めてとなります。京都大学、奈良先端科学技術大学、および近郊の学会員からなる年会実行委員会により運営いたします。

生物物理学は、生物が示すさまざまな活動を、物理、化学、生物学、情報科学などを基礎として解明しようとする学問です。ヘテロな研究者の集まりである日本生物物理学会にとって、年会は最新の研究成果を発表・議論し、研究者同士の交流を深めるためのもっとも大切なイベントです。新型コロナ禍を乗り越え、IUPAB2024との合同年会の大成功を踏まえて、ますます熱気のある、楽しい奈良年会にすべく、実行委員一同、準備を進めています。

奈良年会では、例年の年会の伝統を引き継ぎながらも、新しい試みもいくつか計画しています。年会一日目夕方の時間帯には、ウェルカムレセプションとイブニングセッションを計画しています。食事や飲み物をとりながら、ゆったり議論を楽しむ機会になればと考えています。また、生物物理若手の会が中心となって、年会の前日に研究発表と交流を行う企画も計画されています。生物物理学会の熱気は、ひとえに次世代を担う若手研究者によっています。是非、盛りあがってほしいと思います。現在の研究をけん引するシニアな研究者と未来を担う若手研究者が、一体となって盛りあがる奈良年会になることを願って、『古都・奈良にて、生物物理の現在と未来を繋ぐ』をキャッチフレーズに決定しました。

奈良年会の会場で、多くの皆さまとお会いできることを心待ちにしております。

年会実行委員会

Organizing Committee

年会長・実行委員長

高田 彰二 (京都大学)

Chair

Shoji Takada (Kyoto Univ.)

副実行委員長

寺川 剛 (京都大学)

Vice Chair

Tsuyoshi Terakawa (Kyoto Univ.)

会場

今元 泰 (京都大学)

山下 高廣 (京都大学)

水野 操 (京都大学)

Venue

Yasushi Imamoto (Kyoto Univ.)

Takahiro Yamashita (Kyoto Univ.)

Misao Mizuno (Kyoto Univ.)

プログラム

菅瀬 謙治 (京都大学)

古川 亜矢子 (京都大学)

深井 周也 (京都大学)

中曽根 祐介 (京都大学)

櫻井 一正 (近畿大学)

青木 一洋 (京都大学)

安達 泰治 (京都大学)

井上 康博 (京都大学)

今井 啓雄 (京都大学)

岩田 想 (京都大学)

角五 彰 (京都大学)

片平 正人 (京都大学)

加藤 稔 (立命館大学)

北原 亮 (立命館大学)

剣持 貴弘 (同志社大学)

杉山 正明 (京都大学)

高橋 卓也 (立命館大学)

竹田 一旗 (京都大学)

谷口 雄一 (京都大学)

塚崎 智也 (奈良先端科学技術大学院大学)

津下 英明 (京都産業大学)

永田 崇 (京都大学)

藤原 敬宏 (京都大学)

宮下 尚之 (近畿大学)

望月 敦史 (京都大学)

横山 謙 (京都産業大学)

米澤 康滋 (近畿大学)

Program

Kenji Sugase (Kyoto Univ.)

Ayako Furukawa (Kyoto Univ.)

Shuya Fukai (Kyoto Univ.)

Yusuke Nakasone (Kyoto Univ.)

Kazumasa Sakurai (Kindai Univ.)

Kazuhiro Aoki (Kyoto Univ.)

Taiji Adachi (Kyoto Univ.)

Yasuhiro Inoue (Kyoto Univ.)

Hiroo Imai (Kyoto Univ.)

So Iwata (Kyoto Univ.)

Akira Kakugo (Kyoto Univ.)

Masato Katahira (Kyoto Univ.)

Minoru Kato (Ritsumeikan Univ.)

Ryo Kitahara (Ritsumeikan Univ.)

Takahiro Kenmotsu (Doshisha Univ.)

Masaaki Sugiyama (Kyoto Univ.)

Takuya Takahashi (Ritsumeikan Univ.)

Kazuki Takeda (Kyoto Univ.)

Yuichi Taniguchi (Kyoto Univ.)

Tomoya Tsukazaki (NAIST)

Hideaki Tsuge (Kyoto Sangyo Univ.)

Takashi Nagata (Kyoto Univ.)

Takahiro Fujiwara (Kyoto Univ.)

Naoyuki Miyashita (Kindai Univ.)

Atsushi Mochizuki (Kyoto Univ.)

Ken Yokoyama (Kyoto Sangyo Univ.)

Yasushige Yonezawa (Kindai Univ.)

若林 憲一 (京都産業大学)

原田 慶恵 (大阪大学)

財務

高田 彰二 (京都大学)

HP

寺川 剛 (京都大学)

Giovanni Brandani (京都大学)

山置 佑大 (京都大学)

富樫 祐一 (立命館大学)

牧 功一郎 (京都大学)

庶務

栃尾 豪人 (京都大学)

関山 直孝 (京都大学)

星野 大 (京都大学)

山置 佑大 (京都大学)

西山 雅祥 (近畿大学)

懇親会

林 重彦 (京都大学)

水野 操 (京都大学)

加藤 博章 (京都大学)

大友 章裕 (京都大学)

高校生・高専生発表

上久保 裕生 (奈良先端科学技術大学院大学)

安原 主馬 (奈良先端科学技術大学院大学)

末次 志郎 (奈良先端科学技術大学院大学)

作村 諭一 (奈良先端科学技術大学院大学)

ウエルカムレセプション

木下 慶美 (京都大学)

清水 将裕 (京都大学)

宗 正智 (京都大学)

前夜祭

小島 慧一 (岡山大学)

片山 耕大 (名古屋工業大学)

Ken-ichi Wakabayashi (Kyoto Sangyo Univ.)

Yoshie Harada (Osaka Univ.)

Finance

Shoji Takada (Kyoto Univ.)

Website

Takeshi Terakawa (Kyoto Univ.)

Giovanni Brandani (Kyoto Univ.)

Yudai Yamaoki (Kyoto Univ.)

Yuichi Togashi (Ritsumeikan Univ.)

Koichiro Maki (Kyoto Univ.)

General Affairs

Hidehito Tochio (Kyoto Univ.)

Naotaka Sekiyama (Kyoto Univ.)

Masaru Hoshino (Kyoto Univ.)

Yudai Yamaoki (Kyoto Univ.)

Masayoshi Nishiyama (Kindai Univ.)

Banquet

Shigehiko Hayashi (Kyoto Univ.)

Misao Mizuno (Kyoto Univ.)

Hiroaki Kato (Kyoto Univ.)

Akihiro Ohtomo (Kyoto Univ.)

High School & KOSEN Students

Hiroaki Kamikubo (NAIST)

Kazuma Yasuhara (NAIST)

Shiro Suetsugu (NAIST)

Yuichi Sakumura (NAIST)

Welcome Reception

Yoshimi Kinoshita (Kyoto Univ.)

Masahiro Shimizu (Kyoto Univ.)

Masatomo So (Kyoto Univ.)

Eve Fest

Keiichi Kojima (Okayama Univ.)

Kota Katayama (Nagoya Inst. Tech.)

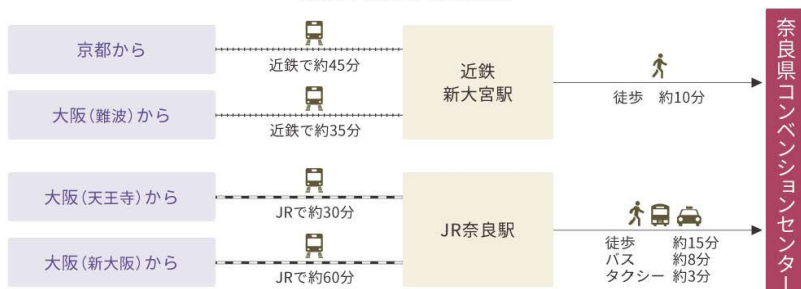
アクセス



飛行機をご利用の方



鉄道をご利用の方

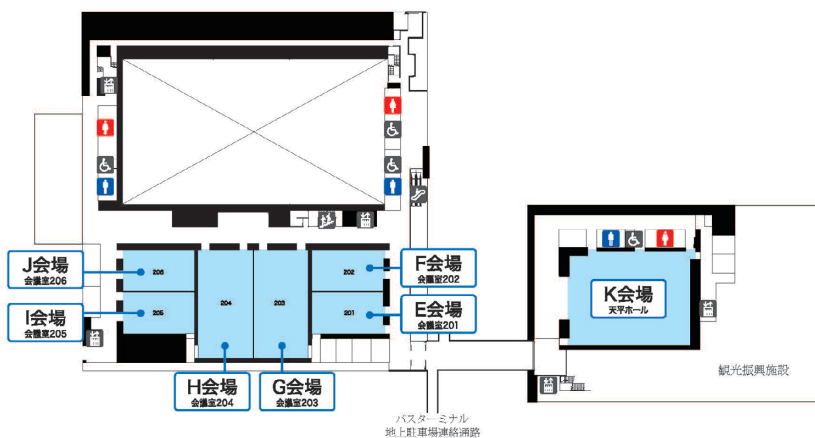


会場図

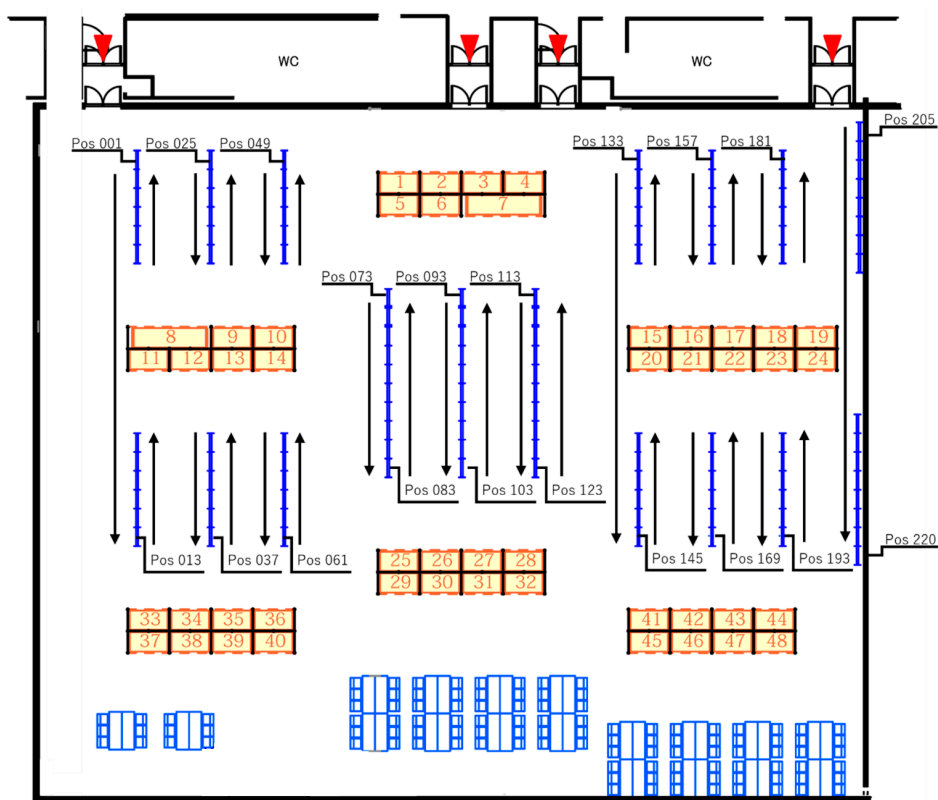
1F



2F



ポスター・企業展示会場（コンベンションホールA+B）



出展企業一覧

1. 横河電機(株)	31. (株)Visualix
2. タイテック(株)	32. 正晃テック(株)
3. ブルカー・ジャパン(株)	33. ナニオンテクノロジーズジャパン(株)
4. 浜松ホトニクス(株)	34. デル・テクノロジーズ(株)
5. (株) 島津製作所	35. (株)東京インスツルメンツ
6. シグマ光機(株)	36. (株)NanoAndMoreジャパン
7. ソーラボジャパン(株)	37. キコーテック(株)
8. (株)エビデント	38. セイコーフューチャークリエーション(株)
9. (株)堀場製作所	39. 日本電気(株)
10. SGサイエンス(合)	40. トプティカフオトニクス(株)
11. (株)ブラスト	41. ピンポイントフォトニックス(株)
12. 東京応化工業(株)	42. (株)セルフリーサイエンス
13. ティー・エイ・インスツルメント・ジャパン(株)	43. フィジオマキナ(株)
14. (株)トッケン	44. (株) 生体分子計測研究所
15. オックスフォード・インスツルメンツ(株)	45. (株)ナックイメーজテクノロジー
16. (株)フォトロン	46. エムエステクノシステムズ
17. (株)モルシス	47. 1NA Technologies B.V.
18. 2026年第64回日本生物物理学会年会 (釜山年会)	48. 日本カンタム・デザイン(株)
19. (一財)高度情報科学技術研究機構	
20. (株)エマージングテクノロジーズ	
21. (株)ニコンソリューションズ	
22. (公財)高輝度光科学研究センター	(2025年8月4日 現在)
23. クロマテクノロジー・ジャパン(合)	
24. (株)アグロデザイン・スタジオ	
25. (株)オプトサイエンス	
26. プネウム(株)	
27. (株)イーシーフロンティア	
28. (株)オプトライン	
29. (公財)中谷財団	
30. (株)日本レーザー	

■ 2025年 9 月 23 日 (火・祝)

	部屋名	会場	8	9	10	11	12	13
2 階	会議室201	E会場						
	会議室203	G会場						

■ 2025年 9 月 24 日 (水)

	部屋名	会場	8	9	10	11	12	13
1 階	会議室 101+102	A会場		1SAA 実験・分子シミュレーション・情報 科学の融合による分子動態可視化 (笠口 友隆、井上 倫太郎)			理事会	若手奨励賞 選考委員会
	会議室 103+104	B会場		1SBA AIや機械学習を活用した生物 物理・シミュレーション研究の探究 (宮下 尚之、米澤 康滋)				BPPB編集 委員会
	会議室 105+106	C会場	デル・テクノ ジーズ	1SCA 光の螺旋性が拓くキラル物質科学の変革： 超螺旋光を用いた生物物理学への新たな挑戦 (細川 千絵、尾松 孝茂)				
	会議室 107+108	D会場		1SDA 動的・高次構造の生物物理学： 計測から制御まで (大出 真央、戸田 浩史)				
	会議室 201	E会場		1SEA クロマチンの物性とその制御 (前島 一博、西山 朋子)				
	会議室 202	F会場		1SFA 細胞外小胞を基軸とした生命の 理解と操作ツール開発 (末次 志郎、鈴木 健一)		BPセミナー1 浜松ホトニクス (株)		
	会議室 203	G会場		1SGA タンパク質の量子ー古典プロセス研究と生成 的デザインによる新規機能性タンパク質開発 (井上 圭一、久保 稔)		キャリア支援 説明会		
	会議室 204	H会場		1SHA 細胞の膜系と骨格系のメソスケール協同的 組織化と機能：先端顕微鏡技術による解明 (楠見 明弘、山城 佐和子)				
	会議室 205	I会場		1SIA 発生、老化、病態における細胞骨 格のダイナミクス (島本 勇太、宮崎 牧人)		BPセミナー2 (株) 島津製 作所		
	会議室 206	J会場		1SJA タンパク質凝集体の構造、病理、 計算をつなぐ研究の新展開 (田中 元雅、中山 隆宏)		BPセミナー3 ライカマイクロス テムス(株)		
2 階	天平ホール	K会場		1YK 若手招待講演シンポジウム				
	コンベンション ホール A+B	ポスター会 場	貼付	ポスター掲示				ポスター発表 (演題番号奇数)
1 階		企業展示 会場		機器・試薬展示				

※「企業展示ブース訪問推奨時間」は、特に企業展示ブースの訪問を積極的に行っていただきたい時間帯です。
年會運営には企業等からの支援をいただいております。
これ以外の時間帯にも積極的に企業ブース等へ訪問いただき、製品情報等のご収集にお役立てください。

14	15	16	17	18	19	20
サブグループ研究会						
前夜祭（若手の会）						

14	15	16	17	18	19	20
	口頭発表（学生発表賞） 1GA タンパク質：構造、機能				イブニングセッション 1EA 核酸：結合タンパク質、 ナノテクノロジー	
	口頭発表（学生発表賞） 1GB タンパク質：物性、天然変性				イブニングセッション 1EB バイオイメージング、計測	
	口頭発表（学生発表賞） 1GC タンパク質：計測、タンパク質工学、 膜タンパク質、バイオエンジニアリング				イブニングセッション 1EC 細胞生物学的課題、 分子モーター、非平衡	
	口頭発表（学生発表賞） 1GD 細胞生物学的課題、神経・感覚				イブニングセッション 1ED 生体膜、合成生物学、理 論生物学	
	口頭発表（学生発表賞） 1GE 分子モーター、核酸：結合タンパク質、 ナノテクノロジー				イブニングセッション 1EE 計算生物学：分子シミュ レーション、モデリング	
	口頭発表（学生発表賞） 1GF 生体膜・人工膜：構造、物性、ダイナミクス、 情報伝達				1MSF ベシカルダイナミクスの最前 線：先端イメージング、AI、 メディカル応用 (Seohyun Lee、樋口 秀男)	
	口頭発表（学生発表賞） 1GG 生命の起源・進化、理論生物学、 バイオイメージング				1MSG 若手の会が紡いだ 生物物理学のフロンティア (柴垣 光希、藤井 真子)	
	口頭発表（学生発表賞） 1GH 計算生物学：分子シミュレーション、モデリング				1MSH 日本のタンパク質水素可 視化最近の動き (田中 伊知朗、栗原 和夫)	
	口頭発表（学生発表賞） 1GI 光生物学：光受容、光合成、生態／環境				1MSI タンパク質デザインへの 誘い (小杉 貴洋、新津 藍)	
	口頭発表（学生発表賞） 1GJ 合成生物学・人工細胞、計測、その他				1MSJ ゲノム構造の原理を紐解 く：理論と実験の融合 (Giovanni Brandani、河野 秀俊)	
	BPPB論文賞講演					
ポスター発表 (演題番号偶 数)	ポスター掲示				ポスター掲示（任意）	撤 去
機器・試薬展示				ウエルカムレセプション		

■ 2025年 9 月 25 日 (木)

			8		9		10		11		12		13		
部屋名			会場												
1階	会議室 101+102	A会場			2SAA 計算科学と情報科学の融合による実験 データからの生体分子複合体の 構造推定 (森 貴治、Florence Tama)										
	会議室 103+104	B会場			2SBA 膜タンパク質を介したシグナル伝達 (Phuoc Duy Tran、堂浦 智裕)										
	会議室 105+106	C会場			2SCA 予知合成科学：実験と計算を 融合する生合成研究の新たな展開 (森脇 由隆、佐藤 玄)										
	会議室 107+108	D会場			2SDA 化学による細胞と異世界の マリアージュ～界面の概念拡張による 生命世界の拡大 (岸村 顕広、金原 数)										
2階	会議室 201	E会場			2SEA 区画・領域依存的生命現象と その可視化 (田上 俊輔、大友 康平)		企業 展 示 ブ ー ス 訪 問 推 奨 時 間		BPセミナー4 横河電機 (株)						
	会議室 202	F会場			2SFA 力学が生みだす生体秩序 (吉村 成弘、柴田 達夫)				BPセミナー5 カルツァイス (株)						
	会議室 203	G会場			2SGA 情報科学とイメージングで迫る バイオリジカルクラスターの実態 (北村 朗、立川 正志)										
	会議室 204	H会場			2SHA 鏡像生命の創成：創れるのか、 創ってよいのか、創ってどうするのか？ (藤原 慶、青木 航)				分野別専門 委員会						
	会議室 205	I会場			2SIA 蛋白質液-液相分離の設計と 制御 (池田 恵介、鎌形 清人)				BPセミナー6 理化学研究所 BDR						
	会議室 206	J会場			2SJA 古くて新しいロドプシン研究最前線 (片山 耕大、加藤 英明)										
	天平ホール	K会場			2SKA 日韓二国間シンポジウム： 拡大 する日韓生物物理研究のフロンティア (高橋 聡、Young-Ho Lee)								会員総会・ 総会シンポジウム		
1階	コンベンション ホール A+B+C	ポスター会場		貼付	ポスター掲示										
		企業展示 会場				機器・試薬展示									
		懇親会場													

※「企業展示ブース訪問推奨時間」は、特に企業展示ブースの訪問を積極的に行っていただきたい時間帯です。
 年會運営には企業等からの支援をいただいております。
 これ以外の時間帯にも積極的に企業ブース等へ訪問いただき、製品情報等のご収集にお役立てください。

14	15	16	17	18	19	20
	キコテック（株）	25AP エピゲノブリッジ：クロマチン構造形成におけるエピゲノムの役割とその複製機構の分子・細胞スケールに渡る理解 （角南 智子、寺川 剛）				
		25BP 動的溶液環境の観点から紐解く生体分子凝縮体 （関山 直孝、中村 秀樹）				
		25CP 重力場における生命の適応進化戦略「細胞骨格ダイナミクス」ホメオスタシスから超高齢社会のQOLを考える～自己組織化・分子シャペロン・Hippo経路：可視化と意識的活動 （跡見 順子、井上 大介）				
		25DP 多細胞生物の解明に向けて：組織内で細胞の特徴を捉えるための多彩なアプローチ （北條 望、神谷 真子）				
		25EP 生物物理からのアクティブマターへのアプローチ （川又 生吹、早川 雅之）				
		25FP スーパーコンピュータ「富岳」による創薬と医療の促進 （荒木 望嗣、寺山 慧）				
		25GP あらゆる地球環境で光合成を可能とする超分子構造制御 （斉藤 圭亮、白井 剛）				
		25HP メゾ複雑体の機能解明に向けた計算科学と実験科学の統合的アプローチ （西田 紀貴、笠原 健人）				
		25IP 複雑な細胞機能を解き明かす：メカニズム解明と技術革新 （出口 真次、木戸秋 悟）				
		25JP 日豪台三国間シンポジウム：量子生命科学による最先端生体計測の新展開 （国際量子科学技術年記念シンポジウム） （石綿 整、David Simpson）				
		25KP 人工細胞そして生命～非生命の境界 （野地 博行、市橋 伯一）				
ポスター発表 （演題番号奇数）	ポスター発表 （演題番号偶数）	ポスター掲示		ポスター掲示（任意）		撤去
機器・試薬展示				懇親会		

■ 2025年 9 月 26 日 (金)

			8		9		10		11		12		13	
部屋名			会場											
1 階	会議室 101+102	A会場	3SAA ノルウェー・日本の二国間 シンポジウム (古池 美彦)				企業 展 示 ブ ー ス 訪 問 推 奨 時 間							
	会議室 103+104	B会場	3SBA 生物発光における合成・定量計 測・理論計算の融合研究 (樋山 みやび、山本 典史)											
	会議室 105+106	C会場			9:40-11:00 企業との意見交換会									
	会議室 107+108	D会場	高校生・高専生 発表											
2 階	会議室 201	E会場	3SEA NMRの方法論開発と複雑な 生体分子系への応用の新展開 (石井 佳彦、松木 陽)						BPセミナー7 ツイストバイオ サイエンス					
	会議室 202	F会場	3SFA 学際研究で迫る生物物理的視点 からの生命の起源研究 (Tony Z. Jia、車 愈澈)						11:40-13:10 男女共同参画・若手支援 委員会 企画シンポジウム					
	会議室 203	G会場	3SGA 計測科学 x 情報科学が切り開く 生物学の地平線 (小松崎 民樹)						11:40-12:40 科研費説明会					
	会議室 204	H会場	3SHA 生命の高次元システムを予測と検 証により合理的に理解する (望月 敦史、今吉 格)											
	会議室 205	I会場	3SIA 人工細胞膜をつくる・つかう 分子テクノロジー (安原 主馬、森垣 憲一)						BPセミナー8 日本蛋白質 構造データ バンク					
	会議室 206	J会場	3SJA 時間タンパク質学: 生命現象の時 間をタンパク質から理解する (大出 晃士、原田 慶恵)											
	天平ホール	K会場												
1 階	コンベンション ホール A+B	ポスター会 場		貼付	ポスター掲示								ポスター発表 (演題番号奇数)	
		企業展示 会場					機器・試薬展示							

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参加者へのご案内

1. 開催方式

年会は対面開催で行います。ただし、会員総会・総会シンポジウム、若手招待講演シンポジウムなど一部のシンポジウムを学会員限定でオンライン配信する予定です。詳しくは年会WEBサイト等案内します。

2. 参加登録

◇事前参加登録

事前参加登録期間内に参加登録をされた方には参加証と領収証を事前送付いたします。同時に懇親会への参加登録をされた方の参加証には「懇親会」と印字されております。また、申込時に参加証へのQRコードの印字に同意いただいた方の参加証には、氏名・所属・E-mailアドレス・参加受付番号の情報を含むQRコードが印刷されております。QRコードは、展示会でのスタンプラリーやBPセミナーに参加される際に必要となります。

参加証ホルダーは、参加受付付近で配布いたします。会場では必ず参加証をご着用ください。

◇当日登録

事前参加登録がお済でない方は、当日登録を行ってください。なお、お支払いは現金のみとなります。

場 所：奈良県コンベンションセンター 1F ロビー

日 時：9月24日（水）－ 25日（木）8:15-17:00

9月26日（金）8:15-13:30

◇学会デスク

参加受付に学会デスクを設けております。新入会や年度会費の支払いを受け付けております。

3. プログラム集 / 予稿集

プログラム集は、日本生物物理学会会員および事前登録された非会員に事前に送付します。なお、予稿本文（PDF版）は、年会WEBサイトに9月上旬ごろ掲載いたしますので、ダウンロードしてご覧ください。

予稿集（PDF版）：

<https://www2.aeplan.co.jp/bsj2025/about/proceedings.html>

ダウンロードID: 63ambsj

Password: nara2025

※ プログラムと予稿集は、年会終了後に日本生物物理学会ウェブサイトの年会の記録およびJ-STAGEの「生物物理誌」において、パスワードなしで公開されます。

※ 本年会では、Confit Web版（オンライン予稿集）は作成しておりません。

4. 年会当日のご案内

◇使用言語

使用言語は原則英語です。ただし、高校生・高専生発表、男女共同参画・若手支援委員会企画シンポジウム、会員総会シンポジウム、キャリア支援説明会、科研費説明会、BPセミナー（一部）などの企画は日本語で実施します。

◇インターネット（Wi-Fi）接続

全館Wi-Fi（無料）接続が可能です。SSID、パスワードについては当日会場内に掲示いたします。

◇会員総会・総会シンポジウム

一般社団法人日本生物物理学会会員総会・総会シンポジウムを9月25日（木）12:45-13:55にK会場（天平ホール）で開催いたしますのでご出席ください。

◇若手招待講演シンポジウム

第21回若手奨励賞の選考会である若手招待講演シンポジウムを9月24日（水）9:00-11:30にK会場（天平ホール）で開催いたします。授賞式は、翌日の懇親会で行います。

◇クローク

貴重品、コンピュータなどについては、紛失、破損などの責任を負いかねますのでお預かりできません。また、傘もお預かりできません。

場 所：奈良県コンベンションセンター 1F ホワイエ

日 時：9月24日（水）8:15-20:45

9月25日（木）8:15-20:45（懇親会終了まで）

9月26日（金）8:15-16:30

◇昼食

企業共催バイオフィジックスセミナー（9月24日（水）-26日（金））、キャリア支援説明会（9月24日（水））、男女共同参画・若手支援シンポジウム、科研費説明会（9月26日（金））については、お弁当とお茶が無料で提供されます。なお、参加するには当日配布する整理券が必要となります。整理券は下記の通り発行いたします。

時 間：各日 8:15～11:00

場 所：奈良県コンベンションセンター 1F ロビー 参加受付 付近

※整理券は当日開催される分のみ配布いたします。枚数がなくなり次第終了となります。

※開始時間までにご来場されない場合、整理券は無効となりお弁当はチケットをお持ちでない参加者に提供されますことをご了承ください。

※バイオフィジックスセミナーは企業、団体等の支援による共催セミナーです。参加される場合は**最後まで聴講いただくとともに、共催企業・団体のアンケート等には必ず所属・氏名・メールアドレスを記入**して回答するよう、ご協力をお願いいたします。

※お弁当の数に限りがあるため、コンベンションセンター脇の観光振興施設内にあるレストランやコンビニエンスストアなどご利用ください。

◇機器・試薬等附設展示会

コンベンションホール（A+B）で、機器・試薬等の附設展示会を行います。なお、「企業展示ブース訪問推奨時間」も設けておりますので、積極的に企業展示ブースにお立ち寄りください。また、当日はスタンプラリーを実施いたします。スタンプラリーの詳細は年会のWebサイトでお知らせします。

◇駐車場

会場には有料駐車場がありますが、原則として公共交通機関をご利用ください。

◇託児所

託児所を設置いたします。詳しくは年会WEBサイトをご覧ください。

◇前夜祭

会期前日に若手の会主催の前夜祭を開催いたします。詳細については、年会WEBサイトをご覧ください。

正式名称：生物物理学会年會前夜祭2025

日時：9月23日（火）13:30-

会場：会議室203、204

◇ウェルカムレセプション

ウェルカムレセプションを下記の通り開催いたします。

日時：9月24日（水）18:20-20:30

会場：奈良県コンベンションセンター 1F コンベンションホール（A+B）

奈良の地酒を楽しみながら議論を深めていただければ嬉しいです。おつまみや、夜のセッション参加のための軽食も用意いたします。ミニシンポジウム、イブニングセッションの会場に軽食を持参することもできます。ぜひお立ち寄りください。

※協賛企業、奈良県ビジターズビューローの支援により飲料、食事を提供しています。

◇懇親会

懇親会を下記の通り開催いたします。

日時：9月25日（木）19:00-20:30

会場：奈良県コンベンションセンター 1F コンベンションホール（A+B+C）

当日参加も受け付けておりますが、数に限りがあるため参加を希望されている方は、お早めに参加登録受付でご登録ください。

◇閉会式

26日のポスター発表終了後、ポスター・企業展示会場（コンベンションホール（A+B））で閉会式を開催いたします。閉会式では学生発表賞受賞者の発表やスタンプラリーの抽選を行います。ぜひ、皆様ご参加ください。

5. 禁止事項

- 1）予稿集ダウンロード用のログインIDやパスワードを第三者に伝えることを禁止します。
- 2）会場内及び講演画面のカメラ、ビデオ、携帯電話などによる撮影や講演音声の録音などを禁止します。

オーガナイザー、座長、発表者へのご案内

◇発表言語

発表言語は、高校生・高専生発表を除きすべて英語です。

◇発表方法（シンポジウム（ミニシンポジウムを含む）、口頭発表（学生発表賞、イブニングセッション、高校生・高専生発表））

ご自身のノートPCによる発表となります。発表データの作成や発表の際は下記の点についてご注意ください。

- 1）パワーポイントの画面比率は16:9（ワイド画面）で作成してください。
- 2）プロジェクトとの接続はHDMIのみとなります。端子の形状が異なる場合は変換コネクタをご持参ください。
- 3）バッテリー切れに備え、電源アダプターをお持ちください。
- 4）発表中にスクリーンセーバーや省電力モードにならないよう、あらかじめ設定しておいてください。

◇シンポジウム（ミニシンポジウムを含む）オーガナイザーの皆様へ

受付：セッション開始の15分前までに各会場の「座長席」にお越しの上、係の者に来場された旨をお伝えください。

進行：一任いたしますので、発表者の発表時間を厳守し、円滑な運営にご協力ください。発表時間をお知らせするベルを鳴らすタイミングについては、計時係にご指示いただきますようお願いいたします。

◇シンポジウム（ミニシンポジウムを含む）発表者の皆様へ

受付：セッション開始の15分前までに発表用のご自身のノートPCをお持ちになり、各会場の「PC接続席」にお越しください。係の者が来場を確認したのち、プロジェクトとの接続確認をお願いいたします。

発表時間：シンポジウムの時間配分はオーガナイザーに一任しております。若手招待講演シンポジウムの発表時間は、発表10分、討論3分、パソコン交換2分です。

◇口頭発表（学生発表賞、イブニングセッション、高校生・高専生発表）座長の皆様へ

受付：セッション開始の15分前までに各会場の「座長席」にお越しの上、係の者に来場された旨をお伝えください。

進行：発表者の発表時間を厳守し、円滑な運営にご協力ください。

◇口頭発表（学生発表賞、イブニングセッション、高校生・高専生発表）発表者の皆様へ

受付：セッション開始の15分前までに発表用のご自身のノートPCをお持ちになり、各会場の「PC接続席」にお越しください。PC接続補助係の者が来場を確認したのち、プロジェクトとの接続確認をお願いいたします。

発表時間：発表時間は、発表10分、討論3分、パソコン交換2分です。

◇ポスター（一般発表）発表者の方へ

発表要項：

- 1) ポスターは英語で作成してください。ただし、タイトル、所属、著者名は、可能であれば日本語の併記もお願いいたします。発表者の氏名には○印を付けてください。
- 2) ポスターパネルは幅900mm x 高さ2,100mmです。貼り付けに必要なピンは年会事務局で用意いたします。なお、演題番号（A5判）をパネルの左上に張り付けてあります。
- 3) ポスターは毎日張り替えになりますので、発表当日の朝（8:30-9:00）に貼り付けていただき、ポスターセッション終了後は速やかに撤去してください。撤去されていないポスターは、年会事務局にて破棄いたしますので、ご了承ください。
- 4) ウェルカムレセプション（9/24）および懇親会（9/25）の時間帯のポスター掲示は任意いたします。飲食中にポスター前で議論を続けることができます。

ポスター発表タイムテーブル：

		9月24日（水）	9月25日（木）	9月26日（金）
貼付		8:30-9:00	8:30-9:00	8:30-9:00
説明・討論	奇数番号	15:10-16:10	14:00-15:00	13:10-14:10
	偶数番号	16:10-17:10	15:00-16:00	14:10-15:10
撤去		18:10-20:40	18:45-20:40	15:10-15:30

謝 辞

本年会の開催・運営にあたり、以下の団体よりご協力・ご援助いただきました。関係者一同より御礼を申し上げます。

第63回日本生物物理学会年会
年会長・実行委員長
高田 彰二

助成

一般財団法人 奈良県デジタルズビューロー

共催

JST CREST「革新的計測解析」（社会課題解決を志向した革新的計測・解析システムの創出）

JST CREST「ゲノム合成」（ゲノムスケールのDNA設計・合成による細胞制御技術の創出）

JST CREST「細胞を遊ぶ」（細胞操作）

JST CREST「予測数学基盤」（予測・制御のための数理科学的基盤の創出）

JST さきがけ「高次構造体」（細胞の動的な高次構造体）

学術変革領域研究（A）「キラル光物質科学」（光の螺旋性が拓くキラル物質科学の変革）

学術変革領域研究（A）「クラスター細胞学」（バイオロジカルクラスター：細胞内における超分子複合体の形成機構と機能特性）

学術変革領域研究（A）「クロススケール新生物学」（細胞内構造生命科学の技術革新と新たな概念の創出）

学術変革領域研究（A）「ゲノムモダリティ」（DNAの物性から理解するゲノムモダリティ）

学術変革領域研究（A）「光合成ユビキティ」（あらゆる地球環境で光合成を可能とする超分子構造制御）

学術変革領域研究（A）「時間タンパク質学」（多様な「時」を生み出すタンパク質マシナリー）

学術変革領域研究（A）「生体秩序力学」（「力」が制御する生体秩序の創発）

学術変革領域研究（A）「蛋白質新機能生成」（タンパク質機能のポテンシャルを開放する生成的デザイン）／文部科学省・学際領域展開ハブ形成プログラム「マルチスケール量子－古典生命インターフェース究コンソーシアム」

学術変革領域研究（A）「予知合成科学」（生体反応の集積・予知・創出を基盤としたシステム生物合成科学）

学術変革領域研究（B）「エピゲノブリッジ」（エピゲノム継承への分子・細胞スケールブリッジアプローチ）

「富岳」成果創出加速プログラム「生体分子シミュレータを基にした大規模推論システムの開発と応用」

「富岳」成果創出加速プログラム「富岳」で目指すシミュレーション・AI駆動型次世代医療・創薬」

細胞膜研究フォーラム

石井・石橋基金 慶應義塾大学若手研究者育成ものづくり特別事業「鏡像世界の構築から広がるマルチバーズ創成」

Greetings

The 63rd Annual Meeting of the Biophysics Society of Japan

Chair of the Organizing Committee

Shoji Takada

Dept. Biophysics, Grad. Sch. of Science, Kyoto University



The 63rd Annual Meeting of the Biophysical Society of Japan will be held at the Nara Convention Center (Nara City) for three days from September 24 (Wed.) to 26 (Fri.), 2025. This will be the first time for the society to hold its annual meeting in Nara, an ancient capital surrounded by World Heritage sites. The annual meeting will be managed by the Executive Committee consisting of members from Kyoto University, Nara Institute of Science and Technology, and other nearby academic societies.

Biophysics is the study of the various activities exhibited by living organisms on the basis of physics, chemistry, biology, and information science. For the Biophysical Society of Japan, a heterogeneous group of researchers, the annual meeting is the most important event to present and discuss the latest research results and to deepen exchanges among researchers. After overcoming the new corona disaster and based on the great success of the joint annual meeting with IUPAB2024, the organizing committee is now preparing to make the Nara Annual Meeting even more enthusiastic and enjoyable.

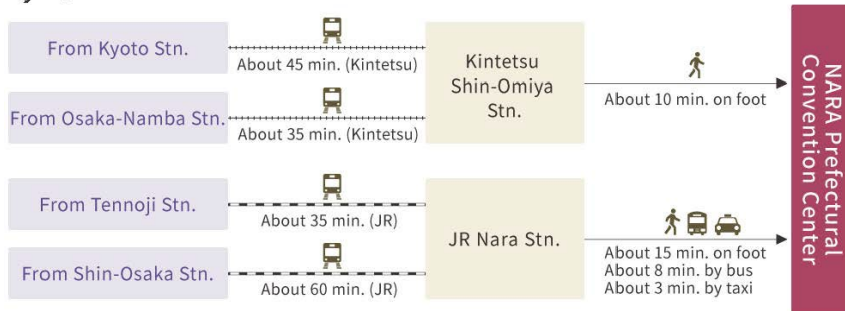
While continuing the traditions of previous years' meetings, we are also planning several new challenges for the Nara Annual Meeting. In the evening of the first day of the Annual Meeting, we are planning a welcome reception and evening sessions. We hope this will be an opportunity to enjoy a relaxed discussion over food and drinks. Also planned is a research presentation and social event on the day before the annual meeting, led by the Young Biophysicists' Group. The enthusiasm of the Biophysical Society of Japan is generated by the young researchers who will lead the next generation. I hope that the event will be a great success. The catchphrase for the meeting is "At the ancient capital Nara, moving from the present biophysics to the future" in the hope that senior researchers who are leading the current research and young researchers who will lead the future will be united and excited.

We are looking forward to seeing many of you at the Nara Annual Meeting.

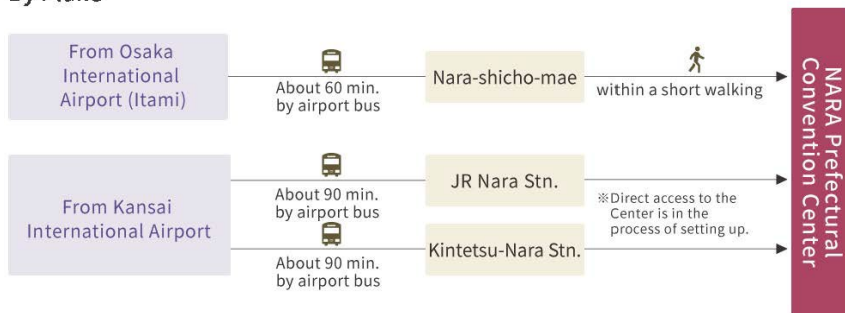
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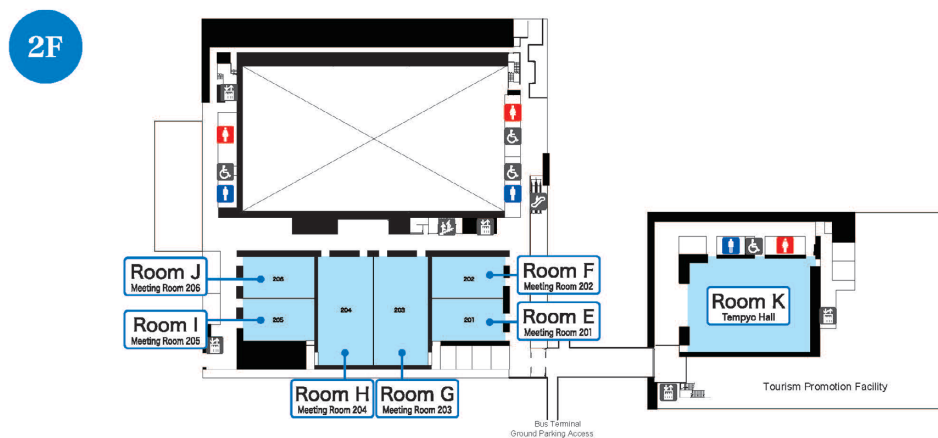
By Train



By Plane



Floor Map



■ September 23(Tue.), 2025

	Room	Venue	8	9	10	11	12	13
2F	Meeting Room 201	Room E						
	Meeting Room 203	Room G						

■ September 24(Wed.), 2025

	Room	Venue	8		9	10	11	12	13			
1F	Meeting Room 101 + 102	Room A	DELL Technologie		1SAA Molecular motions visualized by integration of experiments, simulation, and informatics (Tomotaka Oroguchi, Rintaro Inoue)	Recommended Time to Visit Exhibition Booths	Board Meeting		Recommended Time to Visit Exhibition Booths	Early Career Awards Selection Meeting		
	Meeting Room 103+104	Room B			1SBA Exploring Biophysics and Simulation Research Using AI and Machine Learning (Naoyuki Miyashita, Yasushige Yonezawa)			BPPB Committee				
	Meeting Room 105+106	Room C			1SCA Revolution of Chiral Materials Science using Helical Light Fields: New Challenges in Biophysics using Helical Light Fields (Chie Hosokawa, Takashige Omatsu)							
	Meeting Room 107+108	Room D			1SDA Biophysics of dynamic supramolecular assemblies: measurement, investigation, and design (Mao Oide, Hirofumi Toda)							
2F	Meeting Room 201	Room E			1SEA Chromatin structure: physical properties and regulation (Kazuhiro Maeshima, Tomoko Nishiyama)		Recommended Time to Visit Exhibition Booths				Recommended Time to Visit Exhibition Booths	
	Meeting Room 202	Room F			1SFA Unveiling life by the function and modification of extracellular vesicles (Shiro Suetsugu, Ken-ichi GN Suzuki)			BP Seminar 1 Hamamatsu Photonics				
	Meeting Room 203	Room G			1SGA Integration of Quantum-Classical Mechanisms and Generative Design for the Development of Novel Functional Proteins (Keiichi Inoue, Minoru Kubo)			Career Support Events				
	Meeting Room 204	Room H			1SHA Mesoscale cooperative formation and function of cellular membranes and cytoskeleton revealed by advanced microscopy (Akihiro Kusumi, Sawako Yamashiro)							
	Meeting Room 205	Room I			1SIA Cytoskeletal dynamics in development, aging and disease (Yuta Shimamoto, Makito Miyazaki)	BP Seminar 2 Shimadzu						
	Meeting Room 206	Room J			1SJA New frontiers in research linking structure, pathology, and computation of protein aggregates (Motomasa Tanaka, Takahiro Nakayama)	BP Seminar 3 Leica Microsystems						
	Tempyo Hall	Room K			1YK Early Career Award in Biophysics Candidate Presentations							
1F	Convention Hall A+B	Poster		Set up	Poster Display					Poster Presentation Odd num.		
		Exhibition				Exhibition						

*[Recommended Time to Visit Exhibition Booths] is a time when you are especially encouraged to visit exhibition booths. The Annual Meeting is supported by companies and other organizations. Please visit exhibition booths even outside of the recommended times to obtain product and other information.

14	15	16	17	18	19	20
Subgroup Research Seminar						
Eve Fest (The Society of Young Scientists in Biophysics)						

14	15	16	17	18	19	20
	Student Presentation Award 1GA Protein: Structure, Function				Evening Session 1EA Nucleic acid: binding protein, nanotechnology	
	Student Presentation Award 1GB Protein: Property, Intrinsic disorder				Evening Session 1EB Bioimaging, Measurement	
	Student Presentation Award 1GC Protein: Measurement, Engineering, Membrane proteins, Bioengineering				Evening Session 1EC Cell biology, Molecular motor, Nonequilibrium	
	Student Presentation Award 1GD Cell biology, Neuroscience & Sensory systems				Evening Session 1ED Biological membrane, Synthetic biology, Theoretical biology	
	Student Presentation Award 1GE Molecular motor, Nucleic acid: binding protein, nanotechnology				Evening Session 1EE Computational biology: Molecular simulation and modeling	
	Student Presentation Award 1GF Biological & Artificial membrane: Structure, Property, Dynamics, Signal transduction				1MSF Unlocking Vesicle Dynamics: Advanced Imaging, AI, and Biomedical Applications (Seohyun Lee, Hideo Higuchi)	
	Student Presentation Award 1GG Origin of life & Evolution, Theoretical biology, Bioimaging				1MSG Frontiers in Biophysics Spun by the Society of Young Scientists (Mitsuki Shibagaki, Masako Fujii)	
	Student Presentation Award 1GH Computational biology: Molecular simulation, Modeling				1MSH Recent developments in protein hydrogen visualization in Japan (Ichiro Tanaka, Kazuo Kurihara)	
	Student Presentation Award 1GI Photobiology: Photoreception, Photosynthesis, Ecology & Environment				1MSI Invitation to Protein Design (Takahiro Kosugi, Ai Niitsu)	
	Student Presentation Award 1GJ Synthetic biology & Artificial cells, Measurements, Miscellaneous topics				1MSJ Elucidating the Principles of Genome Organization: Bringing Together Theory and Experiments (Giovanni Brandani, Hidetoshi Kono)	
	Award Seminar of Outstanding Biophysics and Physicobiology Paper					
Poster Presentation Even num.	Poster Display			Poster Display (optional)		Removal
Exhibition				Welcome Reception		

■ September 25(Thu.), 2025

September 22 (Sat.) / 2013														
Room		Venue	8		9		10		11		12		13	
1F	Meeting Room 101+102	Room A			2SAA Inferring Biomolecular Complex Structures Using Experimental Data (Takaharu Mori, Florence Tama)									
	Meeting Room 103+104	Room B			2SBA Signal transduction through membrane proteins (Phuoc-Duy Tran, Tomohiro Doura)									
	Meeting Room 105+106	Room C			2SCA Forecasting Biosynthesis: A New Frontier in Biosynthesis Research that Integrates Experiment and Computation (Yoshitaka Moriwaki, Hajime Sato)									
	Meeting Room 107+108	Room D			2SDA A marriage of cells with "another world" produced by chemistry ~ Augmentation of the world of life through the innovative concept of interface (Akihiro Kishimura, Kazushi Kinbara)									
2F	Meeting Room 201	Room E			2SEA Compartment- and Region-Dependent Biological Phenomena and Visualization (Shunsuke Tagami, Kohei Otomo)				BP Seminar 4 YOKOGAWA					
	Meeting Room 202	Room F			2SFA Self-transformation of living systems induced by mechanical forces (Shige H. Yoshimura, Tatsuo Shibata)				BP Seminar 5 Carl Zeiss					
	Meeting Room 203	Room G			2SGA Exploring the reality of biological clusters through information science and advanced imaging (Akira Kitamura, Masashi Tachikawa)									
	Meeting Room 204	Room H			2SHA Mirror-Life Synthesis: Its Possibility, Potential, and Problems (Kei Fujiwara, Wataru Aoki)				Sectoral Specialties Committee Meeting					
	Meeting Room 205	Room I			2SIA Design and control of liquid-liquid phase separation of proteins~ (Keisuke Ikeda, Kiyoto Kamagata)				BP Seminar 6 RIKE BDR					
	Meeting Room 206	Room J			2SJA Cutting Edge of Rhodopsin Research ~Where Tradition Meets Innovation~ (Kota Katayama, Hideaki Kato)									
	Tempyo Hall	Room K			2SKA Korea-Japan Bilateral Symposium: Expanding Frontiers of Biophysics in Two Countries (Satoshi Takahashi, Young-Ho Lee)								General Assembly Symposium	
1F	Convention Hall A+B+C	Poster		Set up	Poster Display									
		Exhibition				Exhibition								
		Banquet												

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14	15	16	17	18	19	20
	Kiko Tech	25AP EpigenoBridge: Toward Understanding the Epigenome's Role in Chromatin Structure Formation and Replication Mechanisms from the Molecular to the Cellular Scale				
		25BP Understanding Biomolecular Condensation from the Perspective of Dynamic Solution Environments (Naotaka Sekiyama, Hideki Nakamura)				
		25CP Adaptive Evolutionary Strategy of Life in a Gravitational Field "Cytoskeletal Dynamics", "Mechanical Homeostasis" for Quality of Life in a Super-aging Society - Self-organization, Molecular Chaperones, Hippo Pathway, Visualization and Conscious Activity (Yoriko Atomi, Daisuke Inoue)				
		25DP Towards the elucidation of multicellular organisms: Diverse approaches to capturing the characteristics of cells within tissues (Nozomi Hojo, Mako Kamiya)				
		25EP Approaching Active Matter from Biophysics Perspective (Ibuki Kawamata, Masayuki Hayakawa)				
		25FP Advancing drug discovery and healthcare through supercomputer Fugaku (Mitsugu Araki, Kei Terayama)				
		25GP Supramolecular Complexes and Their Regulations to Enable Photosynthesis All Around the Globe (Keisuke Saito, Tsuyoshi Shirai)				
		25HP Towards the Elucidation of Structure of Meso-entangled Bodies through the Integration of Computational and Experimental Approaches (Noritaka Nishida, Kento Kasahara)				
		25IP Deciphering complex cellular functions: Mechanistic insights and technological innovations (Shinji Deguchi, Satoru Kidoaki)				
		25JP Japan-Australia-Taiwan Trilateral Symposium: New Frontiers in Biological Measurement Enabled by Quantum Life Science (International Quantum Science and Technology Year Commemorative Symposium) (Hitoshi Ishiwata, David Simpson)				
		25KP Artificial cell and boundary between living and non-living matters (Hiroyuki Noji, Norikazu Ichihashi)				
Poster Presentation Odd num.	Poster Presentation Even num.	Poster Display			Poster Display (optional)	Removal
Exhibition				Banquet		

■ September 26(Fri.), 2025

September 26 (Fri), 2020

	Room	Venue	8	9	10	11	12	13	
1F	Meeting Room 101+102	Room A	3SAA Norway-Japan Bi-lateral Symposium (Yoshihiko Furuike)				Recommended Time to Visit Exhibition Booths		
	Meeting Room 103+104	Room B	3SBA Bioluminescence Interdisciplinary Collaboration between Experimental and Theoretical Approach (Miyabi Hiyama, Norifumi Yamamoto)						
	Meeting Room 105+106	Room C		9:40-11:00 Opinion meeting with companies					
	Meeting Room 107+108	Room D	High School & KOSEN Students presentation						
2F	Meeting Room 201	Room E	3SEA Advances in NMR Methodologies and Applications to Complex Biological Systems/Landscapes (Yoshitaka Ishii, Yoh Matsuki)				BP Seminar 7 Twist Bioscience		
	Meeting Room 202	Room F	3SFA Interdisciplinary investigations into the biophysics of the origins of life (Tony Z. Jia, Yutetsu Kuruma)					11:40-13:10 Japanese Session Gender Equality and Young Researchers Support Symposium	
	Meeting Room 203	Room G	3SGA Integrating Measurement and Information Science: Unlocking New Frontiers in Biology (Tamiki Komatsuzaki)				11:40-12:40 KAKENHI Guide Meeting		
	Meeting Room 204	Room H	3SHA Understanding the high-dimensional biological systems rationally through prediction and verification (Atsushi Mochizuki, Itaru Imayoshi)						
	Meeting Room 205	Room I	3SIA Molecular technologies for creating and utilizing artificial cell membranes (Kazuma Yasuhara, Kenichi Morigaki)				BP Seminar 8 PDBj		
	Meeting Room 206	Room J	3SJA Chronoproteinology: protein-driven understanding of biological time (Koji Ode, Yoshie Harada)						
	Tempyo Hall	Room K							
1F	Convention Hall A+B	Poster	Set up	Poster Display					Poster Presentation Odd num.
		Exhibition			Exhibition				

*[Recommended Time to Visit Exhibition Booths] is a time when you are especially encouraged to visit exhibition booths. The Annual Meeting is supported by companies and other organizations. Please visit exhibition booths even outside of the recommended times to obtain product and other information.

14		15		16		17		18		19		20	
	Poster Presentation Even num.	Removal	Closing ceremony										
	Exhibition												

Information for Participants

1. Format

The annual meeting will be held in-person format. However, some events, such as the General Assembly, the General Assembly Symposium, and the Early Career Award in Biophysics Candidate Presentations, are planned to be streamed online exclusively for society members. Further details will be provided on the annual meeting website.

2. Registration

◇Early bird registration

For those who have registered during the "early bird registration" period: A name badge and a receipt will be sent in advance, and "Banquet" is printed on the name badge for those who have registered for the banquet. Also, a QR code containing the information about your name, affiliation, Registration ID, and e-mail address is printed on the name badge if you agreed to it when you registered. This QR code will be required for participating in the stamp rally at the exhibition and for attending BP seminars.

Name badge holders will be distributed near the registration desk. Please be sure to wear your name badge at the venue.

◇On-site registration

On-site registration is available at the registration desk for those who have not completed early bird registration. Only cash payment is accepted.

Location: Foyer, 1F, Nara Prefectural Convention Center

Open hours: September 14 & 15: 8:15-17:00 / September 16: 8:15-13:30

◇The Biophysical Society of Japan desk

Application for membership and payment of the annual membership fee can be made at the Biophysical Society of Japan desk located at the registration area.

3. Program booklet / Proceedings

A program booklet has been sent in advance to members of the Biophysical Society of Japan and non-members who have registered during the early registration period.

Proceedings (PDF) will be posted on the meeting website (scheduled in Early September), please download it.

Proceedings (PDF):

<https://www2.aeplan.co.jp/bsj2025/en/about/proceedings.html>

Download ID: 63ambsj

Password: nara2025

*Program and proceedings will be made available without password on the website of the Biophysical Society of Japan and in "Seibutsu Butsuri" on J-STAGE after the annual meeting.

*The Confit web version (online abstract collection) is not available for this year's annual meeting.

4. On the day of the annual meeting

◇Language

As a general rule, English is the language used. However, High school & KOSEN students presentation, Gender equality promotion and young researchers support symposium, General Assembly Symposium, Career support event, KAKENHI guide meeting, and BP seminars (in part) will be held in Japanese.

◇Internet access (Wi-Fi)

Free Wi-Fi is available throughout the entire building. The SSID and password will be posted at the venue on the day of the annual meeting.

◇General assembly / Assembly symposium

Please join the general assembly / assembly symposium of the Biophysical Society of Japan which will be held in Room K (Tempyo Hall) on September 25 from 12:45 to 13:55.

◇Early Career Award in Biophysics Candidate Presentation Symposium

Early Career Award in Biophysics Candidate Presentation Symposium, which is the selection for the 21st early career award, will be held in Room K (Tempyo Hall) on September 24 from 9:00 to 11:30. The award ceremony will be held in the banquet on the next day.

◇Cloakroom

Please be advised that valuables, computers etc. are not accepted as we are not responsible for any loss or damage. Umbrellas are also not accepted.

Location: Foyer, 1F, Nara Prefectural Convention Center

Open hours: September 24: 8:15-20:45

September 25: 8:15-20:45 (until the banquet ends)

September 26: 8:15-16:30

◇Lunch

Free box lunch and tea will be provided at Biophysics seminars (September 24-26), Career support event (September 24), Gender equality promotion and young researchers support symposium (September 26), and KAKENHI guide meeting (September 26). To receive it, a numbered ticket which is to be distributed on the day is required. Numbered tickets will be distributed as follows.

Location : Near the Registration Desk, Foyer, 1F, Nara Prefectural Convention Center

Open hours: 8:15~11:00 each day

*Numbered tickets will only be distributed for the sessions that will be held on the same day. Ticket distribution will be closed when all the tickets are distributed.

*Please note that the tickets will become invalid when you do not arrive before the start time and lunches will be served to those who attend without the ticket.

*Biophysics seminars are co-sponsored seminars supported by companies and organizations. If you attend the seminars, please stay until the end and be sure to answer a questionnaire with your name and affiliation. We kindly ask for your cooperation.

*As the number of box lunches is limited, please also consider using restaurants and convenience stores located in the tourism promotion facility next to the convention center.

◇ **Exhibition**

An exhibition of equipment, reagents, and other related items will be held in the Convention Hall (A+B). We have also designated specific "Recommended Times for Visiting Exhibition Booths," so we encourage all participants to actively visit the company booths. In addition, a stamp rally will be held on the day of the event. Details of the stamp rally will be announced on the official website.

◇ **Parking**

Paid parking is available at the venue, but please use public transportation as a general rule.

◇ **Child care**

Day care service will be available. Please visit the annual meeting website for more information.

◇ **Welcome Reception**

The welcome reception will be held as follows:

Date & Time: September 24(Wed.), 18:20~20:30

Venue: Convention Hall (A+B), 1F, Nara Prefectural Convention Center

We hope you will take this opportunity to enjoy local sake from Nara and engage in meaningful discussions. Light snacks and refreshments will also be provided for those participating in the night sessions. You may bring light snacks to the venues for the Mini Symposium and Evening Session. Please feel free to drop by.

◇ **Banquet**

Date & Time: September 25(Thu.) 19:00-20:30

Venue: Convention Hall (A+B+C), 1F, Nara Prefectural Convention Center

*On-site registration will be available, but please register early as it is limited.

◇ **Closing ceremony**

A closing ceremony will be held in the poster/exhibition hall (Convention Hall A+B) after the poster presentations on September 26. The winners of the student presentation award will be also announced at the ceremony. We look forward to your participation.

5. Prohibitions

- 1) Giving login ID and password to a third party is prohibited.
- 2) Photography and audio/video recordings with any devices are prohibited in the lecture rooms and other areas of the venue.

Information for Organizers, Chairpersons, and Presenters

◇ **Language**

All presentations are in English, except for those by high school and KOSEN students.

◇ **Presentation (Symposium(including Mini-Symposium), Oral presentations (Student presentation award, Evening session, and High school & KOSEN students presentations)**

Presentations are delivered using your own laptop. Please note the following points regarding preparation of presentation data and presentation.

1. Please create a PowerPoint file with a 16:9 (widescreen) aspect ratio.
2. Only HDMI is available for connection to the projector. If your connector is a different type, please bring a conversion connector.
3. Please bring your AC adaptor in case the battery runs out.
4. Please deactivate screen-saver and power saving mode in advance.

◇ **For symposium(including Mini-Symposium) organizers**

Arrival:

Please come to the organizers' desk at each room and let the staff know of your arrival at least 15 minutes before the session.

Process:

Please start and finish all presentations as scheduled for smooth operation. Regarding the timing of the chime signaling presentation time, please instruct the timekeeper accordingly.

◇ **For symposium(including Mini-Symposium) speakers**

Arrival:

Please come to the PC desk at each room with your own laptop at least 15 minutes before the session.

Presentation time:

Time allocation is left to the organizers.

[Early Career Award in Biophysics Candidate Presentation Symposium]

10 min. for presentation / 3 min. for discussion / 2 min. for laptop exchange

◇ **For chairpersons of oral presentation (Student Presentation Award, Evening session and High School & KOSEN Students Presentation)**

Arrival:

Please come to the Chairpersons' desk at each room and let the staff know of your arrival at least 15 minutes before the session.

Process:

Please start and finish all presentations as scheduled for smooth operation.

◇ **For presenters of oral Presentations (Student presentation award, High school & KOSEN students presentations and Evening Session)**

Arrival:

Please come to the PC desk at each room with your own laptop at least 15 minutes before the session.

Presentation time:

10 min. for presentation / 3 min. for discussion / 2 min. for laptop exchange

◇ **For poster presenters (General presentations)**

- 1) Posters should be prepared in English. If possible, please write title, affiliations, and authors' names in Japanese as well. Also, please put a circle for the presenting author's name.
- 2) The size of poster panel is 900mm wide x 2,100mm high. Pushpins will be provided at the venue. Please note that the presentation number (A5 size) has been affixed to the upper left corner of the panel.
- 3) Posters will be changed every day. Please put up your poster in the morning (8:30-9:00) on the day of your presentation and remove it immediately after the poster session. Please note that posters remaining after the removal time will be discarded by the secretariat.
- 4) Poster display during the Welcome Reception (September 24) and the Banquet (September 25) is optional. You may continue discussions in front of the posters while eating and drinking.

Timetable for poster presentation:

		Sep. 24	Sep. 25	Sep. 26
Set up		8:30-9:00	8:30-9:00	8:30-9:00
Presentation & Discussion	Odd numbers	15:10-16:10	14:00-15:00	13:10-14:10
	Even numbers	16:10-17:10	15:00-16:00	14:10-15:10
Removal		18:10-20:40	18:45-20:40	15:10-15:30

第 11 回会員総会シンポジウム：生命とは何か？死とは何か？：生物物理学からの考察

オーガナイザー：日本生物物理学会 理事会

日 時：9 月 25 日（木）12:45 ～ 13:55

場 所：2 階 K 会場（天平ホール）

演 者：水野大介（九大）、姫岡優介（東大）、宮田真人（大阪公立大）

モデレーター：小松崎民樹（北大）

司 会：永井健治（阪大）

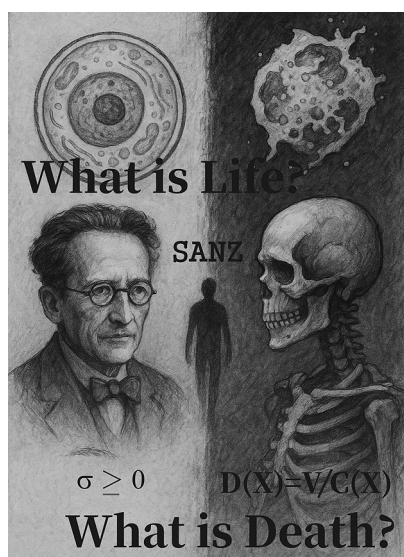
※このイベントは日本語で開催します。

* This event will be presented in Japanese language.

概 要：1944 年、物理学者エルヴィン・シュレーディンガー氏は『生命とは何か？（What is Life?）』の中で、生命を「秩序を秩序で維持する存在」、すなわち熱力学的な乱雑さ（エントロピー）に抗い、構造と情報を保つシステムとして捉え直した。この視点は現代の分子生物学の礎を築くとともに、生命の物理的本質に迫る問いを投げかけた。さらに 2003 年、金子邦彦氏は著書『生命とは何か』において、生命を単なる物質の集合ではなく、「多階層的な自己組織化と情報継承の動的過程」として理論的に定式化した。生命の自己複製・分化・進化を統一的に理解する枠組みが、そこで提案された。しかし、生命とは本当にそのように定義できるのか。逆に「死」とは何か、その境界はどこにあるのか。さらに、近年の合成生物学の発展に

より、人工的に「生きた細胞」をつくる試みが加速する中で、生命と死の概念そのものが揺らぎつつある。

そこで本シンポジウムでは、生物物理学、数理モデル、合成生物学といった異なる視点から「生命」「死」の本質に迫る。九州大学の水野大介氏が非平衡物理の視点から、生命の創発性を支える揺らぎと物性を、東京大学の姫岡優介氏が「死の相空間（SANZ）」という概念を通じて死の定量的理解を提示する。さらに、大阪公立大学の宮田真人氏が合成生物学の最前線から、人工生命の構築を通じた生命・死の再定義に挑む。これらの話題提供を起点に、北海道大学の小松崎民樹氏のファシリテートのもと、生命とは何か、死とは何か、そしてその境界をいかに捉えるべきかを多角的に議論する。生命の定義を再考し、次世代の生物物理学の可能性を切り拓く討論の場として、本シンポジウムを開催する。



一般社団法人日本生物物理学会 第 13 回 Biophysics and Physicobiology 論文賞受賞講演会
The 13th Award Seminar for outstanding Biophysics and Physicobiology paper

オーガナイザー：日本生物物理学会 Biophysics and Physicobiology 論文賞選考委員会

Organizers: Award committee for outstanding Biophysics and Physicobiology paper

日 時：9 月 24 日（水）15:10 ～ 18:10

場 所：2 階 K 会場（天平ホール）

形 式：講演会

第 13 回 Biophysics and Physicobiology 論文賞受賞者

小島 慧一

Keiichi Kojima

岡山大・学術研究院医歯薬

Fac. Med. Dent. Pharm. Sci. Okayama Univ.

アニオンチャネルロドプシンの分子理解と改変

Molecular characterization and engineering of anion channelrhodopsins

Microbial rhodopsins are a family of photoreceptive proteins containing retinal as a chromophore and play crucial roles in the photoreception of microorganisms. Recently, they have become essential tools in optogenetics to regulate biological phenomena by light. In this symposium, we will introduce recent studies on the molecular diversity and structure–function relationships of rhodopsins, including anion channelrhodopsins, based on experimental and theoretical approaches, and discuss future perspectives.

辻村 真樹

Masaki Tsujimura

理化学研究所 開拓研究所

Pioneering Research Institute, RIKEN

アニオンチャネルロドプシンの分子機構の理論解析

Theoretical insights into the molecular mechanism of anion channelrhodopsins

塚本 卓

Takashi Tsukamoto

北海道大学大学院先端生命科学研究院（北大院・先端生命）

Faculty of Advanced Life Science, Hokkaido University (Fac. Adv. Sci., Hokkaido Univ.)

アニオンチャネルロドプシンの実験的研究からわかった思いがけないこと

Unexpected Insights Gained from Experimental Studies of Anion Channelrhodopsins

一般社団法人日本生物物理学会 第 14 回 Biophysics and Physicobiology 論文賞受賞講演会
The 14th Award Seminar for outstanding Biophysics and Physicobiology paper

オーガナイザー：日本生物物理学会 Biophysics and Physicobiology 論文賞選考委員会

Organizers: Award committee for outstanding Biophysics and Physicobiology paper

日 時：9 月 24 日（水）15:10 ～ 18:10

場 所：2 階 K 会場（天平ホール）

形 式：講演会

第 14 回 Biophysics and Physicobiology 論文賞受賞者

関口武治

Takeharu Sekiguchi

東京科学大学 工学院 電気電子系

Dept. of EEE, Sch. of Eng., Inst. of Sci. Tokyo

蛍光ナノダイヤモンドを用いた細胞内部温度センサ

Fluorescent nanodiamonds as a robust temperature sensor inside a single cell

Diamond quantum sensors have been attracting great attention worldwide due to their potential sensitivity and their wide range of applications. Nitrogen-vacancy centers are fluorescent paramagnetic defects in diamond and serve as spin-based sensors to detect tiny signals such as temperature and magnetic field. The sensing is based on monitoring the fluorescence intensity from the diamond while applying microwave to cause electron paramagnetic resonance. Among a variety of applications, we have reported in 2018 a temperature sensing inside a single cell by using fluorescent nanodiamonds (FNDs). A single FND inside a single cell allowed temperature sensing with 1°C accuracy with robustness against various cellular environmental factors such as pH and viscosity. In the session, we'd also like to review further developments of diamond quantum sensors in particular as a high-sensitivity magnetometer for medical and other applications by using millimeter-scale diamonds. This work was supported by JSPS KAKEHNI 26220602, by MEXT KAKENHI 15H05931, by JSPS Grant-in-Aid for JSPS Research Fellow A18J002870, and by MEXT Q-LEAP JPMXS0118067395.

波多野雄治

Yuji Hatano

東京科学大学 工学院 電気電子系

Dept. of EEE, Sch. of Eng., Inst. of Sci. Tokyo

ミリメートルスケールダイヤモンド量子センサの応用

Applications of millimeter-scale diamond quantum sensor

男女共同参画・若手支援委員会企画シンポジウム 自分推しキャリアを作ろう！アカデミアと企業で未来を描く

オーガナイザー：日本生物物理学会 男女共同参画・若手支援委員会

Organizers: Promotion of Gender Equality and Young Researchers Committee

日時：9月26日（金）11:40～13:10

会場：2階F会場

言語：日本語

昼食：お弁当とお茶を無料で提供いたします。ただし、数に限りがあります。

形式：パネルディスカッション

司会：藤原郁子（長岡技術科学大学）

発表者：石谷隆一郎（東京科学大学）、酒井崇匡（東京大学）、篠崎幹彦（三菱UFJキャピタル株式会社）、寺川まゆ（京都大学総合研究推進本部）

概要：近年、アカデミア（学術研究）と企業（産業界）の関係性は大きく変化しています。多くの大学ではURA（リサーチ・アドミニストレーター）の体制が整備され、産学連携による共同研究の促進や、大学発ベンチャー企業の増加といった動きが見られるようになりました。さらに、企業における博士号取得者の採用は増加傾向にあり、大学研究者を客員研究員や技術アドバイザーとして受け入れる企業も増えています。このように、研究・資金・人材といった多様な側面でアカデミアと企業の垣根が低くなる中で、双方の流動性が高まり、多様なキャリアパスの可能性が広がってきています。そこで本シンポジウムでは、アカデミアと企業の双方の視点と経験を共有することで、参加者の皆さまが自身のキャリアを振り返り、将来のキャリアアップを考える契機となる場を提供したいと考えています。

本シンポジウムでは、大学や企業での研究、ベンチャーキャピタル、URAなど多様なキャリアを歩まれた、様々な世代・性別の登壇者の皆さまに情報を提供していただき、パネルディスカッションを行います。それぞれの立場での経験や苦労、感じたメリット・デメリットなどをざっくばらんに語っていただきながら、これらの知見を融合し、アカデミアと企業の垣根を越えた未来のキャリア形成について考えていきたいと思っています。具体的には、以下の3つの観点を中心に議論を展開する予定です。

[1] 研究するならどっち？ 若手研究者への羅針盤：アカデミア vs 企業

[2] 大学研究者でも起業できる！ 大学発ベンチャー企業の実情

[3] アカデミア×企業の未来図 これから求められるものとは？

本シンポジウムでは、上記の3つの観点を軸に、パネルディスカッション形式で皆さまと共に議論を深めていきたいと考えています。アカデミアや企業の発展に貢献したいとお考えの研究者の方々はもちろん、今後のキャリア形成について考え始めている学生や若手研究者の皆さまのご参加も心より歓迎いたします。アカデミアと企業の特徴を活かしながら、自分推しのキャリア形成を一緒に考えていきましょう。

キャリア支援説明会

オーガナイザー：日本生物物理学会 男女共同参画・若手支援委員会

日 時：9月24日（水）11:50～12:40

会 場：2階G会場

形 式：ランチョンセミナーと個別キャリア相談会

※このイベントは日本語で開催します。

* This event will be presented in Japanese language.

概 要：若手研究者や学生の今後のキャリア構築の一助となるように、今年度も「キャリア支援説明会」を開催します。昨年の反響を受けて本年会は、(株)アカリクから講師を迎えて大学院生やポストドクター向けの就職支援活動セミナーを実施します。また、昨年度と同様に今年度も個別キャリア相談会を実施いたしますので、是非ご活用ください。博士課程出身のアカリク社員が何でも質問に答えます！

講師プロフィール

神中 俊明（かみなか としあき）

東京理科大学大学院理学研究科物理学専攻で博士（理学）を取得後、博士研究員を経て2018年10月より株式会社アカリクに所属しています。博士課程2年秋に所属研究室が解散した経験や博士研究員としての活動を元に現在、大学院生を始めとする研究に接する人のキャリア支援、キャリアガイダンス、ワークショップを行っています。研究を志すキャリアの見通しを良くし、研究環境をより良くすることが目標です。

アカリクについて

株式会社アカリクは「知恵の流通の最適化」を目指している企業です。大学院を経て企業へ就職を希望される方、ポストドクをはじめとするアカデミアの研究者の方のキャリア支援や、転職をされる方のサポートをしています。また、Cloud LaTeXの開発運営や、ジョブ型研究インターンシップの運営、キャリアガイダンス、FDセミナー等を通じて大学院生を始めとする研究者のキャリアがより良いものとなることを目指し、各種事業を展開しております。事業を通して研究者、大学院の環境、企業との関係をより良いものにしていきたいと考えています。

プログラム:理系大学院生や研究者の就活・転職について、「専門外就職」や「博士人材向け」の情報も交えてお話しいたします。

【Part 1】 11:50 ～ 12:15 理系大学院生（修士課程，博士課程）の就職活動スケジュール
最近の就職市場の変化は著しく，大学院生も例外ではありません。ここでは現在の産業界・アカデミアの就活スケジュール，博士課程の就活の特徴と注意点についてご説明します。また，アカリクで毎月実施しているアンケート調査を元に，現代の大学院生の就活進捗についてご紹介します。

【Part 2】 12:15 ～ 12:30 PD 以降の方の為の民間企業転職の手引き

博士人材は企業の採用対象として存在感を増してきています。一方でPD以降の方の民間企業転職事情はあまり知られていません。本節では，転職活動の適切なタイミング，アカデミアから民間企業への転職事例をご紹介します。

【Part 3】 12:30 ～ 12:40 トランスファラブルスキルと「専門外就職」を知る

アカデミアで身につけた技術や高度な専門知識が，民間で100%活かせることは多くはありません。アカデミアでの活動をトランスファラブルスキルの形で棚卸しすることで，様々な分野での活躍可能性が見えてきます。本節では，研究生活で培われるトランスファラブルスキル，実際の専門外就職事例等についてお話しいたします。

個別キャリア相談会

就職活動・キャリアに関する悩みや不安を気軽にご相談ください。本大会では，現地（ポスター・企業展示会場）での相談会を開催いたします。就活ノウハウや企業での待遇面など，分からないことがあれば遠慮なくお尋ねください。

【ブースオープン時間】

9/24（水）10:00–18:00

9/25（木）10:00–18:00

9/26（金）10:00–15:00

※直接ブースにお越し下さい。空いている場合はすぐご案内できますが，混み合っている場合は，お手数ですが時間を空けて再度お越し下さい。

科学研究費助成事業について

Reorganization of KAKENHI: Current Activities of JSPS

世話人：秋山修志（自然科学研究機構 分子科学研究所，日本学術振興会学術システム研究センター専門研究員）

Organizer：Shuji Akiyama (Institute for Molecular Science, NINS; Program Officer, Research Center for Science Systems, JSPS)

日 時：9 月 26 日（金）11:40 ～ 12:40

会 場：2 階 G 会場

形 式：プレゼンテーション

※このイベントは日本語で開催します。

* This event will be presented in Japanese language.

概 要：今，日本が将来にわたって卓越した研究成果を持続的に生み出し続け，世界の中で存在感を保持できるかが問われています。こうした中，科学技術・学術審議会において，学術研究への現代的要請として，「挑戦性・総合性・融合性・国際性」の四つを挙げ，科研費制度の抜本的改革が提言されました。これを踏まえ，文部科学省では「科研費改革の実施方針」を策定し，科研費の研究種目・枠組みの見直しや審査システムの見直し（「審査システム改革 2018」）が行われ，平成 30 年度科研費（平成 29 年 9 月公募）において，新たな審査システムによる審査を実施しました。今回は，科研費制度の最近の主な変更点を中心に，制度の改善や充実を図った点等について，ご説明をいただきます。

1 日目 (9 月 24 日 (水)) / Day 1 (Sep. 24 Wed.)

9:00~11:30

K 会場 (天平ホール / Room K (Tempyo Hall))

1YK 日本生物物理学会若手奨励賞選考会

Early Research in Biophysics Award Candidate Presentations

オーガナイザー：男女共同参画・若手支援委員会

Organizer: Promotion of Gender Equality and Young Researchers Committee

Biophysical Society of Japan (BSJ) grants “Early Career Award in Biophysics” and “Early Career Presentation Award” to young BSJ members for their excellent presentations that show great potential to contribute to the progress of biophysics. In this 21th year, we received 44 highly qualified applications. After the first round of competitive screening based on submitted documents, the following ten applicants were selected as candidates for Early Career Award in Biophysics. In this symposium, each speaker will give a 10-minute presentation followed by a 3-minute discussion as the second round of screening. Up to five awardees of the Early Career Award in Biophysics will be selected. The best presenter will also be awarded IUPAB award from International Union of Pure and Applied Biophysics. The Early Career Presentation Award will be given to the rest of the excellent invited speakers. We welcome all the BSJ members to attend this symposium to foresee the future of biophysics in Japan through the speakers and their research.

09:00 Subhan Hadi Kusuma [2Pos144](#)

1YK0900 Autonomous Multicolor Bioluminescence Imaging in Bacteria, Mammalian, and Plant Hosts
Subhan Hadi Kusuma (*SANKEN, The University of Osaka*)

09:15 Yusuke Himeoka [2Pos192](#)

1YK0915 「細胞死」の理論

Theoretical Basis for Cell Death

○姫岡 優介¹, 堀口 修平^{2,3}, 小林 徹也^{1,3} (¹ 東京大学大学院理学系研究科生物普遍性研究機構,
² 金沢大学ナノ生命科学研究所, ³ 東京大学 生産技術研究所)

Yusuke Himeoka¹, Shuhei A. Horiguchi^{2,3}, Tetsuya J. Kobayashi^{1,3} (¹*Universal Biology Institute, The University of Tokyo*, ²*Nano Life Science Institute, Kanazawa University*, ³*Institute of Industrial Science, The University of Tokyo*)

09:30 Yoshiko Nakagawa [1Pos214](#)

1YK0930 一分子蛍光イメージングを用いた分子シャペロンによるアミロイド脱凝集過程のメカニズムの解明
Amyloid conformation-dependent disaggregation of chaperone revealed by single molecule fluorescent imaging

○中川 幸姫¹, 玉井 真悟¹, 野村 高志¹, 中山 隆宏², 田中 元雅¹ (¹ 理研・脳神経科学研究センター, ² 金沢大学 ナノ生命科学研究所)

Yoshiko Nakagawa¹, Shingo Tamai¹, Takashi Nomura¹, Takahiro Nakayama², Motomasa Tanaka¹
(¹*RIKEN, CBS*, ²*WPI Nano Life Science Institute, Kanazawa University*)

- 09:45 Katsuhiko Minami [2Pos062](#)
 1YK0945 複製依存的ヒストン標識 (Repli-Histo 標識) を用いて明らかにする, ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい
 Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells
 ○南 克彦^{1,2}, 仲里 佳子^{1,2}, 井手 聖^{1,2}, 海津 一成^{3,4}, 東 光一^{2,5}, 田村 佐知子¹, 豊田 敦⁶, 高橋 恒一³, 黒川 顕^{2,5}, 前島 一博^{1,2} (¹ 遺伝研・ゲノムダイナミクス研究室, ² 総研大・先端学術院, ³ 理研 BDR・バイオコンピュータリング研究チーム, ⁴ 生命創成研究センター・細胞シミュレーション研究グループ, ⁵ 遺伝研・ゲノム進化研究室, ⁶ 遺伝研・先端ゲノミクス支援センター)
Katsuhiko Minami^{1,2}, Kako Nakazato^{1,2}, Satoru Ide^{1,2}, Kazunari Kaizu^{3,4}, Koichi Higashi^{2,5}, Sachiko Tamura¹, Atsushi Toyoda⁶, Koichi Takahashi³, Ken Kurokawa^{2,5}, Kazuhiro Maeshima^{1,2}
 (¹*Genome Dynamics Laboratory, NIG*, ²*SOKENDAI*, ³*Laboratory for Biologically Inspired Computing, RIKEN BDR*, ⁴*Cell Modeling and Simulation Group, ExCELLS*, ⁵*Genome Evolution Laboratory, NIG*, ⁶*Comparative Genomics Laboratory, NIG*)
- 10:00 Takuya Ohmura [1Pos201](#)
 1YK1000 機械学習画像解析を活用した 3 次元バクテリアバイオフィルムの In vivo マイクロレオロジー計測
 In vivo microrheological measurement for 3D bacterial biofilm with machine learning image analysis
Takuya Ohmura¹, Dominic J. Skinner², Konstantin Neuhaus^{3,4}, Gary P.T. Choi⁵, Jörn Dunkel⁶, Knut Drescher³ (¹*RIES, Hokkaido Univ.*, ²*Cent. Comput. Biol., Flatiron Instit.*, ³*Biozentrum, Univ. of Basel*, ⁴*Dept. Phys., Univ. of Marburg*, ⁵*Dept. Math., Chinese Univ. of Hong Kong*, ⁶*Dept. Math., MIT*)
- 10:15 Tomohiro Nobeyama [2Pos214](#)
 1YK1015 黄金の蝶々型ナノ粒子を用いた液液相分離液滴の生成消滅制御テクノロジー
 Regulatory nanotechnology of liquid-liquid phase separated condensates formation/deformation dynamics by using gold nano-butterflies
 ○延山 知弘¹, 高田 耕児³, 村上 達也³, 山田 洋一², 白木 賢太郎² (¹ 京都大学高等研究院, ² 筑波大学数理物質系理工学域, ³ 富山県立大学大学院工学研究科)
Tomohiro Nobeyama¹, Koji Takata³, Tatsuya Murakami³, Yoichi Yamada², Kentaro Shiraki² (¹*Institute for Advanced Study iCeMS, Kyoto University*, ²*Pure and Applied Physics, University of Tsukuba*, ³*Graduate School of Engineering, Toyama Prefectural University*)
- 10:30 Naito Ishimoto [2Pos005](#)
 1YK1030 性纖毛 H-Pilus の構造が明らかにした TrhA pilin の環状化
 Structural basis of the conjugation H-pilus reveals the cyclic nature of the TrhA pilin
 ○石本 直偉士^{1,2,3}, Wong Joshua², Heb Shan², Shriranc Sally⁴, Paramio Olivia², Seddon Chloe^{2,3}, Singha Nanki^{2,3}, Balsalobred Carlos⁵, Sonanie Ravi⁶, Clements Abigail³, Egelman Edward⁶, Frankel Gad², Beis Konstantinos^{2,3} (¹ 横浜市大・院生命医科, ² インベリアル・カレッジ・ロンドン生命科学部, ³ ハーヴェルリサーチコンプレックス ラザフォードアップルトン研究所, ⁴ セント・アンドリューズ大学 バイオメディカル・サイエンス・リサーチ・コンプレックス・マスマスベクトロメトリー&プロテオミクス, ⁵ バルセロナ大学 遺伝学部, ⁶ バージニア大学生化学生物学・分子遺伝学部)
Naito Ishimoto^{1,2,3}, Joshua Wong², Shan Heb², Sally Shriranc⁴, Olivia Paramio², Chloe Seddon^{2,3}, Nanki Singha^{2,3}, Carlos Balsalobred⁵, Ravi Sonanie⁶, Abigail Clements³, Edward Egelman⁶, Gad Frankel², Konstantinos Beis^{2,3} (¹*Grad. Sch. Life Sci., Yokohama City Univ.*, ²*Department of Life Sciences, Imperial College London*, ³*Rutherford Appleton Laboratory, Research Complex at Harwell*, ⁴*Biomedical Sciences Research Complex Mass Spectrometry & Proteomics Facility, University of St Andrews*, ⁵*Department de Genètica, Universitat de Barcelona*, ⁶*Department of Biochemistry and Molecular Genetics, University of Virginia*)

- 10:45 Rieko Sumiyoshi [1Pos077](#)
 1YK1045 テザーの改変によるキネシン-1 モータードメインの基本的運動機構の解明
 Tether-dependent regulation reveals core motility mechanism of the kinesin-1 motor domain
 ○住吉 里英子¹, 山岸 雅彦^{1,2}, 矢島 潤一郎^{1,2,3} (¹ 東大・総合文化, ² 東大・先進科学研, ³ 東大・生物普遍研)
Rieko Sumiyoshi¹, Masahiko Yamagishi^{1,2}, Junichiro Yajima^{1,2,3} (¹*Grad. Arts & Sci., Univ. Tokyo*, ²*Komaba Inst. Sci., Univ. Tokyo*, ³*RCCSB, UBI, Univ. Tokyo*)
- 11:00 Masahito Tanaka [1Pos094](#)
 1YK1100 初期胚における一過的な核の物性変化と転写のバーストの促進
 Changes in the physical properties of early embryonic nuclei promote a transcriptional burst
 ○田中 真仁¹, 坂上 凜², 鷹巣 篤志², 宮川 靖基³, 渡邊 直子¹, Chen Yu-Chia⁴, Suzuki Aussie⁴, 宮本 圭^{2,3}, 島本 勇太^{1,5} (¹ 国立遺伝学研究所 物理細胞生物学研究室, ² 近畿大学 生物理工学部, ³ 九州大学 農学部, ⁴ ウィスコンシン大学マディソン校, ⁵ 総研大, 遺伝学コース)
Masahito Tanaka¹, Rin Sakanoue², Atsushi Takasu², Yasuki Miyagawa³, Naoko Watanabe¹, Yu-Chia Chen⁴, Aussie Suzuki⁴, Kei Miyamoto^{2,3}, Yuta Shimamoto^{1,5} (¹*Laboratory of Physics and Cell Biology, National Institute of Genetics.*, ²*Graduate School of Biology-Oriented Science and Technology, Kindai University*, ³*Faculty of Agriculture, Kyushu University*, ⁴*McArdle Laboratory for Cancer Research, Department of Oncology, University of Wisconsin-Madison*, ⁵*Department of Genetics, Sokenkai University*)
- 11:15 Yuhei Hosokawa [2Pos133](#)
 1YK1115 幅広い時間スケールでの時分割結晶構造解析により明らかになったクリプトクロムのシグナル伝達機構
 Cryptochrome signal transduction mechanism revealed by time-resolved crystallography across broad timescales
Yuhei Hosokawa^{1,2,3,4}, Po-Hsun Wang^{2,5}, Nicolas Caramello⁶, Mai Nakamura³, Sylvain Engilberge⁶, Antoine Royant⁶, Lars-Oliver Essen⁵, Ming-Daw Tsai², Junpei Yamamoto³, Manuel Maestre-Reyna^{1,2} (¹*Dept. Chem., National Taiwan Univ.*, ²*Inst. Biol. Chem., Academia Sinica*, ³*Grad. Sch. Eng. Sci., Osaka Univ.*, ⁴*PRI, RIKEN*, ⁵*Dept. Chem., Philipps Univ. Marburg*, ⁶*ESRF*)

1日目 (9月24日(水)) / Day 1 (Sep. 24 Wed.)

1SAA 実験・分子シミュレーション・情報科学の融合による分子動態可視化
Molecular motions visualized by integration of experiments, simulation, and informatics

オーガナイザー：苮口 友隆 (慶應義塾大学), 井上 倫太郎 (京都大学)

Organizers: Tomotaka Oroguchi (Keio Univ.), Rintaro Inoue (Kyoto Univ.)

09:00~11:30

A会場 (会議室 101+102) / Room A (Meeting Room 101+102)

Many molecules, including proteins, utilize molecular motions to express their functions, hence visualization of such motions is essential for understanding the mechanisms underlying their functionality. While integrating experimental data with molecular simulations offers a promising approach for such visualization, a gap remains: the difficulty of reproducing experimental data through simulations. This gap reduces the effectiveness of such integration. To address this issue, informatics approaches are gaining traction as powerful tools for bridging the gap. In this symposium, we present various integration strategies leveraging informatics, such as information geometry and machine learning, and discuss their potential for visualizing molecular motions.

はじめに

Opening Remarks

1SAA-1 Visualization of domain motion in multi-domain protein as studied by neutron scattering and molecular dynamics simulation

Rintaro Inoue (*Institute for Integrated Radiation and Nuclear Science, Kyoto University*)

1SAA-2 情報幾何学による実験データと MD の統合: 蛋白質構造アンサンブル可視化への適用
Visualization of protein conformational ensembles by integrating experiments and MD via information geometry

○苮口 友隆 (慶應大・理工・物理)

Tomotaka Oroguchi (*Dept. Phys., Keio Univ.*)

1SAA-3 高速原子間力顕微鏡データと分子シミュレーションの融合による生体分子の構造ダイナミクスのデータ同化解析

Data assimilation analysis of structural dynamics of biomolecules by combining HS-AFM data and molecular simulations

○測上 壮太郎¹, 新稲 亮², 加藤 傑², 松永 康佑³, 高田 彰二⁴ (¹ 静岡県大・薬, ² 理研・BDR, ³ 埼玉大院・理工, ⁴ 京大院・理)

Sotaro Fuchigami¹, Toru Niina², Suguru Kato², Yasuhiro Matsunaga³, Shoji Takada⁴ (¹*Sch. Pharm. Sci., Univ. Shizuoka*, ²*RIKEN BDR*, ³*Grad. Sch. Sci. & Eng., Saitama Univ.*, ⁴*Grad. Sch. Sci., Kyoto Univ.*)

1SAA-4 クライオ電子顕微鏡単粒子画像からの3Dモデル直接推定によるタンパク質マルチコンフォメーション状態の解明

Uncovering Multiple Conformational States of Protein via Direct 3D Models Estimation from CryoEM single-particle images

○徳久 淳師 (理研 計算科学研究センター)

Atsushi Tokuhisa (*RIKEN Center for Computational Science*)

[1SAA-5](#) SAXS/SANS と MD シミュレーションを用いた分子複合体の統合的構造モデリング
Integrative structural modeling of macromolecular complexes using SAXS/SANS and MD simulations
○松本 淳 (量子科学技術研究開発機構・量子生命科学研究所)
Atsushi Matsumoto (*iQLS, QST*)

おわりに
Closing Remarks

1SBA AI や機械学習を活用した生物物理・シミュレーション研究の探究
Exploring Biophysics and Simulation Research Using AI and Machine Learning
オーガナイザー：宮下 尚之 (近畿大学), 米澤 康滋 (近畿大学)
Organizers: Naoyuki Miyashita (Kindai Univ.), **Yasushige Yonezawa** (Kindai Univ.)

09:00~11:30

B 会場 (会議室 103+104) / Room B (Meeting Room 103+104)

Recently, the application of AI and machine learning to life sciences has advanced significantly, with examples such as AlphaFold. This symposium will discuss the use of AI and machine learning in addressing various issues in biophysics, as well as their application to analytical simulation techniques and the development of new methodologies. In particular, the symposium will focus on how AI and machine learning can be utilized to analyze and understand the dynamics of bimolecular simulations.

[1SBA-1](#) タンパク質構造変化の AI ベースモーフィングと構造ダイナミクスの Transformer 解析
AI-based Morphing of Protein Structural Changes and Transformer-based Analysis of Conformational Dynamics
○宮下 尚之^{1,2}, 樫山 佳広², 平澤 理音¹, 下河内 翔太², 塩田 優真², 清岡 亮太² (¹ 近畿大・生物理工, ² 近畿大・院・生物理工)
Naoyuki Miyashita^{1,2}, Yoshihiro Kashiama², Rin Hirasawa¹, Shota Shimogochi², Yuma Shiota², Ryota Kiyooka² (¹*BOST, KINDAI Univ.*, ²*Grad. Sch. BOST, KINDAI Univ.*)

[1SBA-2](#) CGBack：拡散モデルを用いたバックマッピングによる粗視化タンパク質シミュレーションからの原子レベル構造の大規模再構築
CGBack: Large Scale Reconstruction of Atomistic Detail from Coarse-Grained Protein Structures with a Diffusion Model
○ウガルテ ラトレ ディエゴ レナト¹, 杉田 有治^{1,2} (¹RIKEN R-CCS, ²RIKEN PRI)
Diego Renato Ugarte La Torre¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS*, ²*RIKEN PRI*)

[1SBA-3](#) Deciphering allosteric regulation in disease-associated proteins with MD simulation and deep learning
Yuko Tsuchiya (*AIRC, AIST*)

[1SBA-4](#) 機械学習を用いたタンパク質ダイナミクスや細胞ダイナミクスの次元縮約とデータ生成
Machine Learning-Based Dimensionality Reduction and Data Generation for Protein and Cellular Dynamics
○藤崎 弘士 (日医大)
Hiroshi Fujisaki (*Nippon Med. Sch.*)

- 1SBA-5** 蛋白質 MD シミュレーションデータの動的特徴量とその時間依存性を精密に同時抽出する新規機械学習法
A novel machine learning method for the simultaneous and accurate extraction of dynamic features and time dependence from MD simulations
○米澤 康滋 (近畿大学 先端技術総合研究所)
Yasushige Yonezawa (*Kindai University Institute of Advanced Technology*)
- 1SBA-6** 機械学習手法を用いたヘムタンパク質における配列構造機能相関の解析
Analysis of sequence-structure-function relationships in heme proteins by using machine learning methods
○近藤 寛子 (北見工大)
Hiroko X. Kondo (*Kitami Inst. Tech.*)
- 1SBA-7** 大規模分子動力学計算・動的モンテカルロ法・機械学習を統合した不均一系における物質輸送の研究手法
Integration of large-scale MD calculation, dynamic MC method, and machine learning to study mass transport in heterogeneous systems
○永井 哲郎¹, 吉川 信明², 陣内 亮典², 木村 将之³, 岡崎 進⁴ (¹福岡大学理学部化学科, ²株式会社豊田中央研究所, ³トヨタ自動車株式会社, ⁴横浜市立大学生命ナノシステム科学研究科)
Tetsuro Nagai¹, Nobuaki Kikkawa², Ryosuke Jinnouchi², Masayuki Kimura³, Susumu Okazaki⁴
(¹Department of Chemistry, Faculty of Science, Fukuoka University, ²Toyota Central R&D Labs., Inc., ³Toyota Motor Corporation, ⁴Graduate School of Nanobioscience, Yokohama City University)
- 1SBA-8** 疾患の複雑性を解読する：難病創薬のためのデータ駆動的アプローチ
Decoding Disease Complexity: Integrative Data-Driven Approaches for Rare Disease Drug Discovery
○夏目 やよい^{1,2} (¹医薬基盤・健康・栄養研究所, ²徳島大学 先端酵素学研究所)
Yayoi Natsume-Kitatani^{1,2} (¹National Institutes of Biomedical Innovation, Health and Nutrition, ²Institute of Advanced Medical Sciences, Tokushima University)
- おわりに
Closing Remarks

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- 1SCA** 光の螺旋性が拓くキラル物質科学の変革：超螺旋光を用いた生物物理学への新たな挑戦
Revolution of Chiral Materials Science using Helical Light Fields: New Challenges in Biophysics using Helical Light Fields

共催 学術変革領域研究 (A) 「キラル光物質科学」

オーガナイザー：細川 千絵 (大阪公立大学), 尾松 孝茂 (千葉大学)

Organizers: Chie Hosokawa (Osaka Metro. Univ.), Takashige Omatsu (Chiba Univ.)

09:00~11:30

C 会場 (会議室 105+106) / Room C (Meeting Room 105+106)

Chirality, in which objects cannot be superimposed on their mirror images, is very universal in biological sciences: for instance, the homochirality of biomolecules and cell chirality. Helical light fields, such as optical vortices possessing a helical wavefront, have demonstrated chiral crystallizations, and microfabrication of chiral materials through wavefront-sensitive light matter interactions. These demonstrations will offer potentially a new avenue in biophysics towards advanced tissue engineering with multiple helical fibers and light-induced chiral swarming of active matters. In this symposium, researchers in optics, materials science, and biophysics discuss the prospects of new challenges using helical light fields in biophysics.

はじめに
Opening Remarks

- [1SCA-1](#) 生物物理学のための Structured Light
Structured light for biophysics
○尾松 孝茂 (千葉大学)
Takashige Omatsu (*Chiba University*)
- [1SCA-2](#) らせんの組織工学の創製
Development of Helical Tissue Engineering
○松崎 典弥 (大阪大学・大学院工学研究科)
Michiya Matsusaki (*The University of Osaka*)
- [1SCA-3](#) 細胞内温度計測：蛍光性ナノ材料を用いた細胞機能の探索
Intracellular thermometry: Probing cell function with fluorescent nanomaterials
○原田 慶恵 (大阪大学ヒューマン・メタバース疾患研究拠点)
Yoshie Harada (*PRIME, The University of Osaka*)
- [1SCA-4](#) 光渦/高速 AFM 複合機で光の螺旋性を可視化する
High-speed AFM combined with optical vortex visualizes optical helicity
○馬越 貴之 (阪大院工)
Takayuki Umakoshi (*Dept. Appl. Phys., Univ. Osaka*)
- [1SCA-5](#) 液滴およびアミロイド線維形成に至るタンパク質の光捕捉ダイナミクス
Optical trapping dynamics of protein assembly into condensates and amyloid fibrils
○茶谷 絵理¹, 柚 佳祐^{1,2}, Chien Yi-Sian², 増原 宏² (¹神戸大・院理, ²台湾国立陽明交通大・理学院)
Eri Chatani¹, Keisuke Yuzu^{1,2}, Yi-Sian Chien², Hiroshi Masuhara² (¹*Grad. Sch. Sci., Kobe Univ.*, ²*Dept. Appl. Chem., National Yang Ming Chiao Tung Univ.*)
- [1SCA-6](#) 紫外域における放射光キラル分光と生体分子の構造観測
Synchrotron radiation chiral spectroscopy in ultraviolet region and structural characterization of biomolecules
○松尾 光一 (放射光・広島大学)
Koichi Matsuo (*Res. Inst. Synchrotron Rad. Sci., Hiroshima Univ.*)
- [1SCA-7](#) 集光フェムト秒光渦レーザーによる単一神経細胞の刺激
Single-neuron stimulation with a focused femtosecond optical vortex laser
○細川 千絵 (阪公大・院理)
Chie Hosokawa (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)
- [1SCA-8](#) マウスノード不動繊毛は変形の向きを感知して左右軸を決定する
Immotile cilia mechanically sense the direction of fluid flow for left-right determination
○加藤 孝信 (東大・院医)
Takanobu Katoh (*Grad. Sch. Med., The Univ. of Tokyo*)

おわりに
Closing Remarks

1SDA 動的高次構造の生物物理学: 計測から制御まで

Biophysics of dynamic supramolecular assemblies: measurement, investigation, and design

共催 JST さきがけ 「細胞の動的な高次構造体」

オーガナイザー: 大出 真央 (大阪大学), 戸田 浩史 (筑波大学)

Organizers: Mao Oide (The Univ. of Osaka), Hirofumi Toda (Univ. of Tsukuba)

09:00~11:30

D 会場 (会議室 107+108) / Room D (Meeting Room 107+108)

Cells are composed of multiscale assemblies such as protein complexes, RNA-protein complexes, liquid droplets, and organelles. Tons of biomolecules orchestrate these structured components, dynamic supramolecular assemblies, to regulate pivotal functions in diverse biological processes. To understand the rich behaviors of cells based on the spatiotemporal dynamics of each supramolecular assembly, not only investigating such assemblies, but it is also important to develop measurement techniques and/or to design controllable systems. In this symposium, we will invite talented researchers from various relevant research fields and discuss cutting-edge research approaching to the dynamic function of supramolecular assemblies.

はじめに

Opening Remarks

[1SDA-1](#)

微細加工温度センサが導く単一細胞の独特な熱挙動

Unique thermal behaviors of single cells revealed by microfabricated thermometer

○猪股 直生 (東北大学)

Naoki Inomata (*Tohoku University*)

[1SDA-2](#)

天然変性タンパク質の凝集を決定する配列ルールの解読

Decoding Sequence Rules for Condensation of Disordered Proteins

○足立 景亮^{1,2}, 川口 喬吾^{2,3} (¹理研 iTHEMS, ²理研 PRI, ³東京大 理学系研究科 知の物理学研究センター)

Kyosuke Adachi^{1,2}, Kyogo Kawaguchi^{2,3} (¹RIKEN iTHEMS, ²RIKEN PRI, ³IPI, Grad. Sch. Sci., Univ. Tokyo)

[1SDA-3](#)

The cellular basis of long-term memory: L-LTP-dependent extension of endoplasmic reticulum into spines via septin 3

Natsumi Ageta-Ishihara (*Fac. Sci., Toho Univ.*)

[1SDA-4](#)

How does the nucleus move within 'super crowded' plant cells?

Hiroto Takatsuka^{1,2}, Toshiki Amari³ (¹Dept. Biol. Sci., NWU, ²JST・Presto, ³Div. Biol. Sci. Tech., Kanazawa Univ.)

[1SDA-5](#)

TIGR-Tas(タイガー・タス): Nop ドメインタンパク質群によるモジュラーな RNA 誘導性システム

TIGR-Tas: Modular RNA-guided systems with Nop domain-containing proteins

○齋藤 諒 (理研・開拓研究所 生命現象エンジニアリング理研 ECL 研究チーム)

Makoto Saito (*RIKEN PRI Biophenomena Engineering RIKEN ECL Research Team*)

[1SDA-6](#)

リボソーム液滴を標的とする新規抗菌ペプチド

A Novel Antimicrobial Peptide that Targets Liquid Ribosomal Condensates

○戸田 浩史 (筑波大学 国際統合睡眠医科学研究機構)

Hirofumi Toda (*IIIS, University of Tsukuba*)

おわりに

Closing Remarks

1SEA クロマチンの物性とその制御
Chromatin structure: physical properties and regulation

共催 学術変革領域研究 (A) 「ゲノムモダリティ」

オーガナイザー：前島 一博 (国立遺伝学研究所), 西山 朋子 (京都大学)

Organizers: Kazuhiro Maeshima (NIG), Tomoko Nishiyama (Kyoto Univ.)

09:00~11:30

E 会場 (会議室 201) / Room E (Meeting Room 201)

Recent technology developments in imaging and genome sequencing have uncovered higher-order chromatin structures in the cell. However, their physical properties and regulation remain unclear. This symposium will explore the chromatin structure, its dynamics and regulations with cellular functions and diseases. It will also provide an interdisciplinary discussion of the chromatin structure from multiple viewpoints, including mathematics, biochemistry, cell biology, and bioinformatics.

はじめに

Opening Remarks

[1SEA-1](#) コヒーシオン HEAT サブユニット IDR のクロマチン高次構造形成における重要性
Impact of IDR in the HEAT repeat protein STAG in building higher-order chromatin structure
○西山 朋子 (京大・院理学)
Tomoko Nishiyama (*Grad. Sch. Sci., Kyoto Univ.*)

[1SEA-2](#) Repli-Histo 標識によって明らかにする生細胞におけるユークロマチンとヘテロクロマチンの物性
Replication-dependent histone labeling dissects the physical properties of euchromatin and heterochromatin in living human cells
○前島 一博^{1,2} (¹国立遺伝学研究所, ²総研大)
Kazuhiro Maeshima^{1,2} (¹National Institute of Genetics, ²SOKENDAI)

[1SEA-3](#) Physical modeling of chromatin dynamics
Soya Shinkai (*RIKEN BDR*)

[1SEA-4](#) 精子クロマチン凝縮過程の追跡
Tracking the Process of Sperm Chromatin Condensation
○岡田 由紀¹, 羽田 政司¹, 牧野 吉倫^{1,2}, 兼子 智^{1,3} (¹東京大学 定量生命科学研究所, ²札幌厚生病院, ³エスセットクリニック)
Yuki Okada¹, Masashi Hada¹, Yoshinori Makino^{1,2}, Satoru Kaneko^{1,3} (¹Institute for Quantitative Biosciences, The University of Tokyo, ²Sapporo Kosei Hospital, ³SSET clinic)

[1SEA-5](#) Target-DNA searching process of a light-regulated transcription factor, Photozipper, observed by high-speed atomic force microscopy
Akihiro Tsuji¹, Hayato Yamashita¹, Osamu Hisatomi², Masayuki Abe¹ (¹Grad. Sch. Eng. Sci., UOsaka, ²Grad. Sch. Sci., UOsaka)

[1SEA-6](#) 核小体における DNA 二重らせん構造の力学的制御メカニズム
Mechano-regulation of DNA duplex structure in a nucleolus
○牧 功一郎^{1,2,3,4}, 福手 淳平^{1,3}, 安達 泰治^{1,2,3,4} (¹京都大学・医生物学研究所, ²京都大学・院工学, ³京都大学・院生命科学, ⁴京都大学・院医学)
Koichiro Maki^{1,2,3,4}, Junpei Fukute^{1,3}, Taiji Adachi^{1,2,3,4} (¹Institute for Life and Medical Sciences, Kyoto University, ²Grad. Sch. Eng., Kyoto University, ³Grad. Sch. Biostudies, Kyoto University, ⁴Grad. Sch. Med., Kyoto University)

1SFA 細胞外小胞を基軸とした生命の理解と操作ツール開発
Unveiling life by the function and modification of extracellular vesicles

共催 JST CREST 「細胞を遊ぶ」

オーガナイザー：末次 志郎（奈良先端科学技術大学院大学）、
鈴木 健一（岐阜大学／国立がん研究センター）

Organizers: Shiro Suetsugu (NAIST), Ken-ichi GN Suzuki (Gifu Univ./NCC)

09:00～11:30

F 会場（会議室 202）／Room F（Meeting Room 202）

Extracellular vesicles (EVs) are abundantly secreted from almost all types of cells. However, the role and function of EVs have not been clarified yet. There are two major sources of EVs: the plasma membrane and the endosomes. The tiny and long plasma membrane protrusions are the direct source of the EVs. The intraluminal vesicles of the endosomes are also the source of the EVs. With the modification and engineering of these EVs, as well as artificial nanoparticles, a new concept of understanding life is emerging.

はじめに
Opening Remarks

[1SFA-1](#) 細胞膜由来の細胞外小胞を介した効率的タンパク質伝達
Efficient protein transfer through the protrusion-derived extracellular vesicles

○西村 珠子, 末次 志郎（奈良先端大・バイオ）

Tamako Nishimura, Shiro Suetsugu (NAIST)

[1SFA-2](#) 1 粒子追跡と超解像顕微鏡観察による細胞外小胞の結合・取り込み機構の解明
Mechanisms of extracellular vesicle binding and internalization uncovered by single-particle tracking and super-resolution microscopy

○鈴木 健一^{1,2} (¹ 岐阜大・糖鎖生命コア研, ² 国立がん研セ)

Kenichi G. N. Suzuki^{1,2} (¹ Gifu Univ.・iGCORE, ² NCCRI)

[1SFA-3](#) 大腸菌生細胞からのメンブレンベシクル創発：バイオポリマー合成が"引き金"
Controllable secretion of membrane vesicles (MVs) from viable *Escherichia coli* triggered by intracellular polymer accumulation

○高 相晃, 田口 精一（信州大・ARG 機構）

Sangho Koh, Seiichi Taguchi (Inst. ARG, Shinshu Univ.)

[1SFA-4](#) 細胞外小胞の物質送達機構の解明と薬物送達への応用
Analysis of intracellular trafficking of extracellular vesicles for drug delivery applications

○曽宮 正晴（大阪大学 産業科学研究所）

Masaharu Somiya (SANKEN, The University of Osaka)

[1SFA-5](#) 生物材料ナノマシーンによるゲノム編集送達
Genome Editing Delivery by Biomaterial Nanomachines

○堀田 秋津（京大・CiRA）

Akitsu Hotta (CiRA, Kyoto University)

[1SFA-6](#) バーコード化細胞外小胞を活用した細胞外小胞研究の新展開
Barcoded Extracellular Vesicles for Next-generation Extracellular-vesicle Research
○小嶋 良輔 (東京大学 大学院医学系研究科)
Ryosuke Kojima (*Graduate School of Medicine, The University of Tokyo*)

おわりに
Closing Remarks

1SGA タンパク質の量子―古典プロセス研究と生成的デザインによる新規機能性タンパク質開発
Integration of Quantum–Classical Mechanisms and Generative Design for the Development of
Novel Functional Proteins

共催 学術変革領域研究 (A)「蛋白質新機能生成」／文部科学省・学際領域展開ハブ形成プログラム
「マルチスケール量子―古典生命インターフェース研究コンソーシアム」

オーガナイザー：井上 圭一 (東京大学), 久保 稔 (兵庫県立大学)
Organizers: Keiichi Inoue (*The Univ. of Tokyo*), **Minoru Kubo** (*Univ. of Hyogo*)

09:00～11:30
G 会場 (会議室 203) / Room G (Meeting Room 203)

Proteins have a wide range of highly efficient biological functions. However, their molecular mechanisms remain poorly understood, which makes the artificial design of new functional molecular tools challenging. In this symposium, cutting-edge research addressing this difficulty will be highlighted. A particular focus will be the fundamental studies on the functional mechanisms of photoreceptive proteins to understand the interface between the quantum mechanical light-associated events and the classical, macroscopic functional processes, paving the way for advancements in next-generation optogenetics. Additionally, innovative generative design approaches for creating novel functional molecular tools will be presented.

はじめに
Opening Remarks

[1SGA-1](#) 人工設計したタンパク質構造に機能を埋め込む試み
Embedding Functional Sites in De Novo Designed Protein Structures
○古賀 信康 ^{1,2} (¹ 阪大・蛋白研, ²ExCELLS, 自然科学研究機構)
Nobuyasu Koga^{1,2} (¹ASPiRE, IPR, *Univ. Osaka*, ²ExCELLS, NINS)

[1SGA-2](#) Toward generative design of circadian clock modulators: Chemical and structural analyses of
mammalian CRY
Tsuyoshi Hirota (*ITbM, Nagoya Univ.*)

[1SGA-3](#) DNA の光修復：分子進化とメカニズム進化
Light-Driven DNA Repair: Mechanistic Insights and Molecular Evolution
○久保 稔 (兵庫県立大学・院理)
Minoru Kubo (*Grad. Sch. Sci., Univ. Hyogo*)

[1SGA-4](#) 新奇イオン輸送型微生物ロドプシンを用いた光遺伝学ツールの探索と開発
Exploration and development of optogenetic tools based on novel ion-transporting microbial
rhodopsins
○井上 圭一 (東京大学物性研究所)
Keiichi Inoue (*ISSP, Univ. Tokyo*)

- [1SGA-5](#) 高精度量子化学が解き明かす光生物学の分子メカニズム
Exploring Photobiology via High-Precision Quantum Chemistry
○藤本 和宏 (名大・ITbM)
Kazuhiro Fujimoto (*ITbM, Nagoya Univ.*)
- [1SGA-6](#) チャネルロドプシンの光感度に対する電気生理学的アプローチ
A new model of light sensitivity in Channelrhodopsins
○細島 頌子^{1,2} (¹名古屋工業大学大学院 工学研究科, ²オプトバイオテクノロジー研究センター)
Shoko Hososhima^{1,2} (¹*Graduate School of Engineering, Nagoya Institute of Technology*, ²*Opto Bio Technology Research Center, Nagoya Institute of Technology*)
- [1SGA-7](#) タンパク質の古典的機能動態を高速 AFM でとらえる
Visualizing Classical Functional Dynamics of Proteins by High-Speed AFM
○内橋 貴之 (名古屋大学)
Takayuki Uchihashi (*Nagoya University*)
- おわりに
Closing Remarks
-

1SHA 細胞の膜系と骨格系のメソスケール協同的組織化と機能：先端顕微鏡技術による解明
Mesoscale cooperative formation and function of cellular membranes and cytoskeleton revealed by advanced microscopy

共催 細胞膜研究フォーラム

オーガナイザー：楠見 明弘 (沖縄科学技術大学院大学), 山城 佐和子 (京都大学)

Organizers: Akihiro Kusumi (OIST), Sawako Yamashiro (Kyoto Univ.)

09:00~11:30

H 会場 (会議室 204) / Room H (Meeting Room 204)

Recently, various mesoscale (30–300 nm) structures in cellular membranes and the cytoskeleton have been identified as functional units. These mesoscale structures often cooperatively form and play essential roles in integrating diverse cellular functions and delicately tuning cell behavior. For example, neuronal synapses likely comprise distinct mesoscale subdomains that are cooperatively formed through liquid–liquid phase separation of multiple constituent proteins, interfacing with both the cytoskeleton and various membrane systems. Advanced biophysical microscopy techniques have immensely contributed to unveiling such mesoscale structures and their functions. This symposium will highlight the latest advances in this emerging field and discuss future perspectives.

- [1SHA-1](#) Force Transmission and Mechanical Memory at Integrin-Based Adhesions Revealed by Live-Cell Single-Molecule Imaging
Sawako Yamashiro^{1,2}, Ying Liu¹, David Rutkowski³, Dimitrios Vavylonis³, Naoki Watanabe^{1,2} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*Grad. Sch. Medicine, Kyoto Univ.*, ³*Dept. Physics, Lehigh Univ.*)
- [1SHA-2](#) Kindlin converts the talin•integrin slip bond under mechanical load to an ideal bond
Reinhard Faessler (*Max Planck Institute, Martinsried, Germany*)
- [1SHA-3](#) Deciphering the mechano-sensitive properties of the membrane periodic skeleton in neurons
Gregory Giannone¹, Zhou Xuesi¹, Théo Dudon¹, Jean-Baptiste Trebbia², Anna Brachet¹, Brahim Lounis² (¹*University Bordeaux, CNRS, Interdisciplinary Institute for Neuroscience, UMR 5297, Bordeaux, France*, ²*Laboratoire Photonique Numérique et Nanosciences (LP2N), Institut d'Optique Graduate School and CNRS, UMR 5298, Talence, France*)

[1SHA-4](#) SuperPAINT ライブラリー：1 分子超解像観察のために系統的にデザインしたタグタンパク質と蛍光リガンドのペア
SuperPAINT Library: Systematically designed pairs of tag proteins and fluorescent ligands for single-molecule super-resolution imaging
○唐 博¹, 角山 貴昭¹, 王 茂基¹, Shinozaki Ryuto¹, Aladag Amine¹, 藤原 敬宏², 楠見 明弘¹ (¹ 沖縄科学技術大学院大学, ² 高等研究院 物質－細胞統合システム拠点 京都大学)
Bo Tang¹, Taka A. Tsunoyama¹, Maoji Wang¹, Ryuto Shinozaki¹, Amine Aladag¹, Takahiro K. Fujiwara², Akihiro Kusumi¹ (¹*Okinawa Institute of Science and Technology*, ²*Institute for Advanced Study, Institute for Integrated Cell-Material Sciences, Kyoto University*)

[1SHA-5](#) 細胞膜上で形成分解を繰り返す準安定ナノ液状シグナル統合プラットフォーム：iTRVZ によるガン増殖の促進
Metastable nano-liquid signal integration hub on the plasma membrane, iTRVZ, which enhances cancer development
○楠見 明弘 (沖縄科学技術大学院大学)
Akihiro Kusumi (*Okinawa Institute of Science and Technology Graduate University (OIST)*)

1SIA 発生, 老化, 病態における細胞骨格のダイナミクス
Cytoskeletal dynamics in development, aging and disease
オーガナイザー：島本 勇太 (国立遺伝学研究所), 宮崎 牧人 (理化学研究所)
Organizers: Yuta Shimamoto (NIG), Makito Miyazaki (RIKEN)

09:00~11:30

I 会場 (会議室 205) / Room I (Meeting Room 205)

The cytoskeleton, a dynamic network of protein filaments, mediates diverse intracellular motility and plays essential roles in cell physiology and genome stability. Cytoskeletal malfunctions are associated with diseases, congenital disorders and aging, with mechanisms that remain to be fully understood. This symposium highlights the frontiers of cytoskeletal research by bringing together leading experts in cell and developmental biology. Through interactions with biophysics, we aim to foster new ideas and explore novel approaches. We also encourage students and postdocs to present their work and engage with the forefront of this ever-evolving field.

はじめに
Opening Remarks

[1SIA-1](#) Lamins regulating nuclear stiffness, genome dynamics and early embryonic development
Yuta Shimamoto (*Nat'l Inst Genetics*)

[1SIA-2](#) 脳皮質発生におけるニューロン隘路遊走の細胞機構
The cellular mechanism and lifelong impact of neuronal migration in confined brain tissue
○見學 美根子^{1,2}, 中澤 直高¹, 張 喆菁², Greci Gianluca³, Canela Andres⁴ (¹ 京都大・アイセムス, ² 京都大・院生命科学, ³ シンガポール大・MBI, ⁴ 京都大・放生研)
Mineko Kengaku^{1,2}, Naotaka Nakazawa¹, Zhejing Zhang², Gianluca Greci³, Andres Canela⁴ (¹*WPI-iCeMS, Kyoto Univ.*, ²*Grad. Sch. Biostudies, Kyoto Univ.*, ³*Mechanobiol. Inst., Natl. Univ. Singapore*, ⁴*Rad. Biol. Cent., Kyoto Univ.*)

- 1SIA-3** 微小管によるメカノケミカルクロストークが細胞移動の方向性を制御する
 Mechano-chemical crosstalk induced by microtubules in directed cell migration
 ○西村 有香子¹, 近藤 龍樹¹, 折井 良太², 神原 丈敏³, 繁富 (栗林) 香織⁴, 岡田 康志^{3,5,6}, 谷本 博一², 茂木 文夫¹ (¹北大・遺制研, ²横浜市立大・理, ³理研・BDR, ⁴北大・大機構, ⁵東大・理, ⁶東大・医)
Yukako Nishimura¹, Tatsuki Kondo¹, Ryota Orii², Taketoshi Kambara³, Kaori Kuribayashi-Shigetomi⁴, Yasushi Okada^{3,5,6}, Hirokazu Tanimoto², Fumio Motegi¹ (¹*Inst. Gen. Med., Hokkaido Univ.*, ²*Dept. Sci., Yokohama City Univ.*, ³*BDR, Riken*, ⁴*Inst. Adv. Grad. Edu., Hokkaido Univ.*, ⁵*Grad. Sch. Sci., Tokyo Univ.*, ⁶*Grad. Sch. Med., Tokyo Univ.*)
- 1SIA-4** 加齢にともなう卵子の染色体数異常の細胞生物学的な原因
 Cell biological mechanisms of age-associated egg aneuploidy
 ○北島 智也 (理化学研究所生命機能科学研究センター)
Tomoya Kitajima (*RIKEN Biosystems Dynamics Research*)
- 1SIA-5** マウス Metaphase II 卵の紡錘体局在を細胞質流動から守るアクチン構造
 Cytoplasmic Flow-Resistant Spindle Positioning by Actin Structures in Mouse Metaphase II Oocytes
 ○大杉 美穂, 寺井 康徳 (東大・理・生物科学専攻)
Miho Ohsugi, Kotoku Terai (*Dept. Biol. Sci., Grad. Sch. Sci., Univ. of Tokyo*)
- 1SIA-6** 細胞骨格のエネルギー動態：アクチン線維構造から細胞分裂へ
 Energetics of the Cytoskeleton: From F-actin Architecture to Cell Division
 ○坂本 遼太^{1,2}, マレル マイケル^{2,3} (¹中央研究院・物理研, ²イエール大・生体医工, ³イエール大・物理)
Ryota Sakamoto^{1,2}, Michael Murrell^{2,3} (¹*Inst. Phys., Academia Sinica*, ²*Dept. Biomed. Engr., Yale Univ.*, ³*Dept. Phys., Yale Univ.*)
- 1SIA-7** アクチン重合の光操作で探る密度依存的な細胞骨格の機能制御
 Optogenetic control of actin network assembly reveals density-dependent functions of actin binding proteins
 ○宮崎 牧人^{1,2,3} (¹理研・IMS, ²理研・BDR, ³信州大・院総合医理工学)
Makito Miyazaki^{1,2,3} (¹*RIKEN IMS*, ²*RIKEN BDR*, ³*Grad. Sch. Med., Sci., & Tech., Shinshu Univ.*)

1SJA タンパク質凝集体の構造, 病理, 計算をつなぐ研究の新展開
 New frontiers in research linking structure, pathology, and computation of protein aggregates
 オーガナイザー：田中 元雅 (理化学研究所), 中山 隆宏 (金沢大学)
Organizers: Motomasa Tanaka (RIKEN), Takahiro Nakayama (Kanazawa Univ.)

09:00~11:30

J 会場 (会議室 206) / Room J (Meeting Room 206)

Protein aggregates are involved in the pathogenesis of various human diseases, including Alzheimer's disease. Therefore, it is necessary to integrate structural, pathological, and computational analyses of protein aggregates to gain a deeper understanding of the nature of protein aggregates. In this symposium, we will have talks by leading researchers who are working to understand the structure, pathology, and computation of protein aggregates individually while also linking these findings. This research is expected to lead to the development of novel biophysical technologies and understanding of a wide range of biological phenomena.

はじめに
Opening Remarks

- [1SJA-1](#) 小胞体関連分解におけるタンパク質の逆行輸送を促進する膜上ナノクラスター構造
A nanocluster mesh on ER membranes facilitates protein retrotranslocation in ERAD
○持田 啓佑^{1,2}, 梅田 健一³, 中戸川 仁¹, 古寺 哲幸³, 田中 元雅² (¹東京科学大・総合研究院, ²理研・脳神経科学, ³金沢大・ナノ生命科学)
Keisuke Mochida^{1,2}, Kenichi Umeda³, Hitoshi Nakatogawa¹, Noriyuki Kodera³, Motomasa Tanaka²
(¹IIR, Science Tokyo, ²CBS, Riken, ³NanoLSI, Kanazawa Univ.)
- [1SJA-2](#) 高速 AFM によるアミロイドタンパク質の構造動態と凝集機構の解明
High-speed AFM visualization of structural dynamics and aggregation mechanisms in amyloidogenic proteins
○中山 隆宏 (金沢大学ナノ生命科学研究所)
Takahiro Watanabe-Nakayama (WPI-Nano Life Science Institute, Kanazawa University)
- [1SJA-3](#) α シヌクレイノパチーの病理とバイオマーカー (seed amplification assay)
Pathology and Biomarkers of Alpha-Synucleinopathies: Focus on Seed Amplification Assays
○奥住 文美 (順天堂大学神経学講座)
Ayami Okuzumi (Juntendo University, Department of Neurology)
- [1SJA-4](#) アミロイド繊維形成とアミノ酸残基レベルの自由エネルギーとの相関
Amyloid Fibril Formation Correlates with Residue-Level Free Energy Profiles
○藤浪 大輔¹, 林 成一郎², 伊藤 杏¹, 伊藤 創平¹, 神田 大輔³ (¹静岡県大・薬食生命, ²分子研, ³九大・生医研)
Daisuke Fujinami¹, Seiichiro Hayashi², An Ito¹, Sohei Ito¹, Daisuke Kohda³ (¹Grad. Sch. Integr. Pharm. Nutr. Sci., Univ. of Shizuoka, ²NINS, Institute for Molecular Science, ³MIB, Kyushu Univ.)
- [1SJA-5](#) Unveiling Protein Dynamics through Data Integration Simulations
Osamu Miyashita (RIKEN Center for Computational Science)
- [1SJA-6](#) プリオン株多様性の構造および分子基盤の解明
Structural and mechanistic basis for prion strain diversity
○田中 元雅 (国立研究開発法人理化学研究所 脳神経科学研究センター)
Motomasa Tanaka (RIKEN Center for Brain Science)

2 日目 (9 月 25 日 (木)) / Day 2 (Sep. 25 Thu.)

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- 2SAA 計算科学と情報科学の融合による実験データからの生体分子複合体の構造推定
Inferring Biomolecular Complex Structures Using Experimental Data

共催 富岳成果創出加速プログラム 「生体分子シミュレータを基にした大規模推論システムの開発と応用」

オーガナイザー：森 貴治 (東京理科大学), Tama Florence (名古屋大学)
Organizers: Takaharu Mori (Tokyo Univ. of Science), Florence Tama (Nagoya Univ.)

09:00~11:30

A 会場 (会議室 101+102) / Room A (Meeting Room 101+102)

This symposium focuses on cutting-edge methods for predicting the three-dimensional structures of biomolecular complexes using experimental data, including cryo-EM, high-speed AFM, and other advanced techniques. It aims to address challenges in integrating diverse datasets to develop accurate and reliable structural models. Researchers will present progress in computational approaches and their applications in understanding biomolecular mechanisms, fostering collaboration between experimental and computational fields. By bridging these disciplines, the symposium seeks to accelerate advancements in structural biology and contribute to a deeper understanding of complex biological systems, paving the way for novel scientific discoveries.

はじめに

Opening Remarks

[2SAA-1](#) Integrative Structure Modeling of Protein Complexes Using Experimental Data with Errors and Noise

Takaharu Mori (*Tokyo University of Science*)

[2SAA-2](#) ゲノム分子モデリングにおける統合的多階層手法

An Integrative Multi-Scale Approach to Genome Molecular Modeling

Giovanni Bruno Brandani (*Department of Biophysics, Graduate School of Science, Kyoto University*)

[2SAA-3](#) Investigation of conformational landscape from single-particle cryoEM data via reference based approach

Mao Oide¹, Yuji Sugita^{2,3} (¹*IPR, Osaka Univ.*, ²*CPR, RIKEN*, ³*R-CCS, RIKEN*)

[2SAA-4](#) 生体分子の機能推定のための高速原子間力顕微鏡動画に基づく理論的考察

Theoretical considerations based on high-speed atomic force microscopy movies to estimate biomolecular functions

○炭竈 享司^{1,2} (¹京大・生命科学研究科, ²金沢大・ナノ生命科学研究所)

Takashi Sumikama^{1,2} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*Nano Life Sci. Inst., Kanazawa Univ.*)

[2SAA-5](#) AFM 画像セグメンテーション誘導フレキシブルフィッティングによるオートファジー関連天然変性蛋白質構造の推論

Inferring autophagy-related intrinsically disordered protein structures using AFM image segmentation guided flexible fitting

○唐澤 直之¹, 石曾根 毅², 本間 さくら¹, 前島 遼太³, 古寺 哲幸⁴, 中村 和幸⁵, 松永 康佑^{1,6} (¹埼玉大・院理工, ²明大・研究知財, ³明大・院先端数理, ⁴金大・WPI-NanoLSI, ⁵明大・総合数理, ⁶理研・R-CCS)

Naoyuki Karasawa¹, Tsuyoshi Ishizone², Sakura Homma¹, Ryota Maejima³, Noriyuki Kodera⁴, Kazuyuki Nakamura⁵, Yasuhiro Matsunaga^{1,6} (¹*Grad. Sch. Sci. Eng., Saitama Univ.*, ²*Organ. Strateg. Coord. Res. Intellect. Prop., Meiji Univ.*, ³*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, ⁴*WPI-NanoLSI, Kanazawa Univ.*, ⁵*Sch. Interdiscip. Math. Sci., Meiji Univ.*, ⁶*R-CCS, RIKEN*)

[2SAA-6](#) Development of high performance coarse-grained molecular dynamics for large-scale biomolecular simulations

Jaewoon Jung^{1,2}, Cheng Tan¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS*, ²*RIKEN PRI*)

[2SAA-7](#) Integrative modeling approaches to characterize the dynamics of biomolecules

Florence Tama^{1,2} (¹*Grad. Sch. Sci., Nagoya University*, ²*RIKEN Center for Computational Science*)

おわりに

Closing Remarks

2SBA 膜タンパク質を介したシグナル伝達
Signal transduction through membrane proteins

オーガナイザー：Tran Duy Phuoc (東京科学大学), 堂浦 智裕 (名古屋大学)

Organizers: Duy Phuoc Tran (Science Tokyo), Tomohiro Doura (Nagoya Univ.)

09:00~11:30

B 会場 (会議室 103+104) / Room B (Meeting Room 103+104)

Signal transduction through membrane proteins is a cornerstone of cellular communication, playing a critical role in regulating physiological processes across all living organisms. This symposium aims to explore the intricate mechanisms by which membrane proteins sense, transmit, and amplify signals in response to environmental or intracellular cues. Bringing together experts from structural biology, biochemistry, and computational modeling, we will discuss recent breakthroughs in understanding receptor activation, ion channel dynamics, and downstream signaling pathways. Emphasis will also be placed on emerging experimental techniques and advanced simulations, highlighting their impact on drug discovery and therapeutic interventions targeting membrane proteins.

はじめに

Opening Remarks

[2SBA-1](#) Understanding Activation Mechanisms in GPCRs - 1) Biophysical studies 2) Computational Validation, and 3) Drug discovery strategies

Robert Scott Prosser¹, Akio Kitao², Duy Phuoc Tran², Adnan Sljoka³, David Young⁴ (¹*Chemistry & Biochemistry Departments, University of Toronto, Toronto, Ontario, Canada*, ²*School of Life Science and Technology, Tokyo Institute of Technology, Tokyo, Japan*, ³*RIKEN Center for Advanced Intelligence Project, Tokyo, Japan*, ⁴*KisoJi Biotechnology, Canada*)

[2SBA-2](#) プロテアーゼ活性化受容体の活性化機構と G タンパク質結合の構造的基盤
Structural Basis of Activation Mechanism and G Protein Coupling in Protease-Activated Receptors

○浅田 秀基, 林 到炫, 足立 誠 (京都大学 大学院医学研究科)

Hidetsugu Asada, Dohyun Im, Makoto Adachi (*Kyoto University Graduate school of Medicine*)

[2SBA-3](#) 活性化時の構造変化に基づく GPCR の化学遺伝学的制御
Chemogenetic regulation of GPCRs based on structural changes upon activation

○堂浦 智裕 (名大・院工)

Tomohiro Doura (*Grad. Sch. Eng., Nagoya Uni.*)

[2SBA-4](#) G タンパク質バイアスリガンドによるヒト GPR84 のシグナル伝達機構
Mechanism of human GPR84 signaling by G-protein biased ligands

Shota Suzuki¹, Duy Phuoc Tran², Koki Nishikawa³, Akio Kitao², Yoshinori Fujiyoshi¹ (¹*Adv. Res. Init., Science Tokyo*, ²*Sch. of Life Sci. and Tech., Science Tokyo*, ³*Joint Res. Csr. Adv. Biomol. Character., TUAC*)

[2SBA-5](#) G タンパク質共役型受容体活性化・不活性化メカニズムのインシリコ研究
In silico investigation of the activation and inactivation mechanisms of G protein-coupled receptors

○北尾 彰朗 (東京科学大生命理工)

Akio Kitao (*Sch. Life Sci. Tech, Science Tokyo*)

[2SBA-6](#) Probing Allosteric and biased signaling with rigidity theory, NMR, and geometric Monte-Carlo simulations in GPCRs

Adnan Sljoka (*RIKEN*)

2SCA 予知生合成科学：実験と計算を融合する生合成研究の新たな展開

Forecasting Biosynthesis: A New Frontier in Biosynthesis Research that Integrates Experiment and Computation

共催 学術変革領域研究 (A) 「予知生合成科学」

オーガナイザー：森脇 由隆（東京科学大学），佐藤 玄（東京大学）

Organizers: Yoshitaka Moriwaki (Science Tokyo), Hajime Sato (The Univ. of Tokyo)

09:00~11:30

C 会場（会議室 105+106）／Room C（Meeting Room 105+106）

Recent advances in computational technology have made it possible not only to predict the function of biosynthetic genes, which serve as the blueprint for natural product chemistry, but also to artificially create them. In this session, we will report the latest research on extracting unknown useful information from the continuously accumulating genomic data and creating new substances using biosynthesis and chemical synthesis methods by integrating experiment and computation. We will also discuss the new developments in the relationship between recent advances in bioinformatics and biosynthesis research.

はじめに

Opening Remarks

[2SCA-1](#)

3次元立体構造を用いた酵素機能の予測：FUJISANの開発と応用

Predicting enzyme functions using 3D Structures: Development and application of FUJISAN

○藤田 卓, 寺田 透（東大・院農）

Suguru Fujita, Tohru Terada (*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

[2SCA-2](#)

非生物学的化学反応を指向した酵素データベースの探索

Database Mining-driven Enzyme Discovery for Abiotic Chemical Transformations

○加藤 俊介（阪大・院工）

Shunsuke Kato (*Grad. Sch. Eng., UOsaka*)

[2SCA-3](#)

機械学習モデルによる新規酸素反応性 PLP 依存性酵素の発見

Machine learning-guided discovery of novel oxygen and PLP-dependent enzymes

○野口 智弘^{1,2}, 淡川 孝義¹, 齋藤 裕² (¹北里大院・未来工学, ²理研・環境資源科学研究センター)

Tomohiro Noguchi^{1,2}, Takayoshi Awakawa¹, Yutaka Saito² (¹*Graduate School of Frontier Engineering, Kitasato Univ.*, ²*CSRS, RIKEN*)

[2SCA-4](#)

Transformer 言語モデルを用いた天然化合物生合成遺伝子クラスターの予測と設計に向けて

A transformer-based platform for the prediction and design of biosynthetic gene clusters

○梅村 舞子（京工繊大・院）

Maiko Umemura (*Appl. Biol., Kyoto Inst. Tech.*)

[2SCA-5](#)

人工設計タンパク質を利用した新規酵素機能改変戦略

Engineering by Proxy: A Novel Strategy for Enzyme Function Redesign Using Synthetic Designer Proteins

○田中 俊一（京都府立大学・院生命環境科学）

Shun-ichi Tanaka (*Grad. Sch. Life and Environ. Sci., Kyoto Pref. Univ.*)

[2SCA-6](#)

酵素反応の理論的予測と改良

Computational prediction and improvement of enzymatic reactions

○新井 宗仁^{1,2} (¹ 東大・総合文化・生命環境, ² 東大・理・物理)

Munchito Arai^{1,2} (¹*Dept. Life Sci., Univ. Tokyo*, ²*Dept. Phys., Univ. Tokyo*)

おわりに

Closing Remarks

2SDA

化学による細胞と異世界のマリアージュ～界面の概念拡張による生命世界の拡大

A marriage of cells with “another world” produced by chemistry – Augmentation of the world of life through the innovative concept of interface

オーガナイザー：岸村 顕広（九州大学），金原 数（東京科学大学）

Organizers: Akihiro Kishimura (Kyushu Univ.), Kazushi Kinbara (Science Tokyo)

09:00～11:30

D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

To pioneer the next generation of biophysics, it is essential to expand our concept of the world of life. Therefore, in this symposium, we will focus on the cellular-level world and discuss the possibility of augmenting the world surrounding cells through innovative technologies based on chemistry and materials science. We invite up-and-coming chemists and material scientists who are developing innovative interfaces, particularly to measure and manipulate living cells, to propose new concepts of artificial cells, and to develop new approaches using synthetic molecules. We hope everyone will join the discussion, using their imagination to consider how cells might behave in ‘another world.’

はじめに

Opening Remarks

[2SDA-1](#)

液体足場：細胞の未知との遭遇

Fluid Scaffolds: An Encounter with the Unknown for Cells

○中西 淳（物質・材料研究機構）

Jun Nakanishi (NIMS)

[2SDA-2](#)

Design of non-sticking microdroplets toward single cell analysis

Mizuki Tenjimbayashi (*National Institute for Materials Science*)

[2SDA-3](#)

生体分子集合体の階層構造が導く非球形凝縮体の創生

Supramolecular Hierarchical Assembly Involving Peptides and Oligonucleotides Forming Non-Spherical Biomolecular Condensates

○菅井 祥加（東京科学大・総合研究院）

Hiroka Sugai (*IIR, Science Tokyo*)

[2SDA-4](#)

低分子コアセルベートの形成と内部環境や機能化に対する化学構造の影響

Impact of Molecular Structure on Low-Molecular-Weight Coacervates: Formation, Internal Environments, and Functionalization

○東 小百合^{1,2,3}, 藤本 竜太郎⁴, 廣澤 幸一朗^{5,6}, 金丸 恒太^{7,8}, 吉田 紀生⁷, 鈴木 健一^{5,6}, 池田 将^{2,3,4,5} (¹岐阜大・高等研究院,²岐阜大・院連創薬,³岐阜大・COMIT,⁴岐阜大・院自然科学技術,⁵岐阜大・iGCORE,⁶国立がん研・バイオイメージング,⁷名古屋大・院情報学,⁸京大・福井セ)

Sayuri Higashi^{1,2,3}, Ryutaro Fujimoto⁴, Koichiro Hirosawa^{5,6}, Kodai Kanemaru^{7,8}, Norio Yoshida⁷, Kenichi Suzuki^{5,6}, Masato Ikeda^{2,3,4,5} (¹*Inst. Adv. Study, Gifu Univ.*, ²*Grad. Sch. Drug Disc. & Med. Info. Sci., Gifu Univ.*, ³*COMIT, Gifu Univ.*, ⁴*Dept. Life Sci. & Chem., Grad. Sch. Nat. Sci. & Technol., Gifu Univ.*, ⁵*iGCORE, Gifu Univ.*, ⁶*Div. Adv. Bioimaging, NCCRI*, ⁷*Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.*, ⁸*FIFC, Kyoto Univ.*)

[2SDA-5](#)

コアセルベートによる革新的生体高分子送達

Innovative Delivery of Biomacromolecules via Coacervates

○川口 祥正 (京大化研)

Yoshimasa Kawaguchi (*Inst. Chem. Res*)

おわりに

Closing Remarks

2SEA

区画・領域依存的な生命現象とその可視化

Compartment- and Region-Dependent Biological Phenomena and Visualization

オーガナイザー：田上 俊輔 (理化学研究所), 大友 康平 (順天堂大学)

Organizers: Shunsuke Tagami (RIKEN), Kohei Otomo (Juntendo Univ.)

09:00~11:30

E 会場 (会議室 201) / Room E (Meeting Room 201)

This symposium will explore the spatial organization of biological systems and the visualization techniques that reveal their complexity. Topics will include molecular assemblies, organelles, membrane fusion, multicellular pattern formation, and large-scale imaging techniques for live and fixed samples. By integrating insights from biophysics, cell biology, and imaging technologies, we aim to uncover the fundamental principles governing compartmentalized biological processes. The symposium will provide a platform for discussing the latest advancements and future directions in understanding how spatial organization influences cellular and tissue functions.

はじめに

Opening Remarks

[2SEA-1](#)

生命の起源：ペプチド集合体・区画による RNA 合成の活性化

The origin of life: Enhancement of RNA synthesis by peptide aggregates and compartments

○田上 俊輔 (理化学研究所 IMS)

Shunsuke Tagami (*RIKEN IMS*)

[2SEA-2](#)

RNA が導く膜のない細胞内区画の形成：その機構と分子論的理解

RNA-Guided Formation of Membraneless Intracellular Compartments: Mechanisms and Molecular Insights

○山崎 智弘 (阪大・院生命機能)

Tomohiro Yamazaki (*Front. Biosci., The University of Osaka*)

- [2SEA-3](#) 人工細胞回路による多細胞パターンデザイン
Programming multicellular patterns with synthetic cell-cell communication
○戸田 聡 (大阪大・蛋白研)
Satoshi Toda (*IPR, Univ. Osaka*)
- [2SEA-4](#) 植物に寄生するシストセンチュウは破壊者か？建築家か？
Cyst nematodes: Destroyers or Architects? ~Insights from the 3D structure of host plant tissues~
○大津 美奈 (奈良先端大・バイオ)
Mina Ohtsu (*NAIST, Bio.*)
- [2SEA-5](#) ライブイメージングのための透明化試薬の開発
Minimally invasive optical clearing media for live cell imaging ex vivo and in vivo
○稲垣 成矩 (九州大学 医学研究院)
Shigenori Inagaki (*Grad. Sch. Med. Sci., Kyushu Univ*)
- [2SEA-6](#) 区画・領域依存的な生命現象を可視化する 3D 蛍光顕微鏡法の開発
Novel 3D Fluorescence Microscopy to Visualize Compartment- and Region-Dependent Biological Phenomena
○大友 康平^{1,2,3} (¹順天堂大・医, ²自然科学研究機構・生理研, ³自然科学研究機構・ExCELLS)
Kohei Otomo^{1,2,3} (¹*Sch. Med., Juntendo Univ.*, ²*NIPS, NINS*, ³*ExCELLS, NINS*)
- おわりに
Closing Remarks

2SFA 力学が生みだす生体秩序
Self-transformation of living systems induced by mechanical forces
共催 学術変革領域研究 (A) 「生体秩序力学」
オーガナイザー：吉村 成弘 (京都大学), 柴田 達夫 (理化学研究所)
Organizers: Shige H. Yoshimura (Kyoto Univ.), Tatsuo Shibata (RIKEN)

09:00~11:30
F 会場 (会議室 202) / Room F (Meeting Room 202)

An embryo produces cells with specific fates, forms, and functions during development. These cells are self-organized into an ordered pattern through collective interactions of biomolecules and mechanical forces at various spatio-temporal scales. We aim at developing new paradigms of the fundamental design principles of biological systems through holistic understanding of how mechanical forces elicit self-organizing feedback leading to progressive self-tuning transformation of multicellular systems. In this symposium, recent advances in this field, as well as cutting-edge technologies needed to interrogate the mechanical processes and establish a unique model for multi-disciplinary research that harnesses expertise from biomedical sciences, engineering, mathematics, physics, and chemistry will be introduced.

はじめに
Opening Remarks

- [2SFA-1](#) In vitro における微小管の機械的適応
Mechanical adaptation of in vitro microtubules
○井上 大介 (九大院・芸工)
Daisuke Inoue (*Fac. Des., Kyushu Univ.*)

- [2SFA-2](#) CD44 を介した細胞集団内の力学ネットワーク感知と集団運動
CD44-Mediated Mechanical Network Sensing within Cell Populations and Collective Cell Migration
○柴田 桂太郎¹, 浅野 千帆莉¹, 石田 紘基², 堀井 拓登², 米村 重信¹ (¹徳島大・院医歯薬学,²徳島大・医学部)
Keitaro Shibata¹, Chihori Asano¹, Koki Ishida², Takuto Horii², Shigenobu Yonemura¹ (¹*Grad. Sch. Biomed. Sci., Tokushima Univ.*, ²*Med. Faculty, Tokushima Univ.*)
- [2SFA-3](#) カルマンフィルタで上皮組織の力の時間変化を推定する
Kalman force inference for epithelial deformation: a force inference method for time-lapse movies
○荻田 豪士¹, 三好 建正², 柴田 達夫¹ (¹理研・BDR,²理研・R-CCS)
Goshi Ogita¹, Takemasa Miyoshi², Tatsuo Shibata¹ (¹*BDR, RIKEN*, ²*R-CCS, RIKEN*)
- [2SFA-4](#) Mechanical Instability Induces Transition in Epithelial Layer Structure via Nucleation and Growth
Shuya Fukamachi¹, Datta Razib¹, Makiko Arai¹, Rei Yagasaki², Shuhei Horiguchi², Satoru Okuda²
(¹*Grad. Sch. NanoLS., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*)
- [2SFA-5](#) 変形可能細胞の数理モデルから迫る, 高密度細胞集団動態
Modeling Collective Dynamics in Densely Packed Deformable Cells
○斉藤 稔 (広島大・統合生命)
Nen Saito (*Grad. Sch. Integr. Sci. Life, Hiroshima Univ.*)
- [2SFA-6](#) メカノ勾配による Wnt モルフォゲンノイズ除去システムは組織パターン形成の頑強性を支える
“Mechano-gradients” drive morphogen-noise correction to ensure robust patterning
○青木 佳南, 石谷 太 (大阪大・微研・生体統御)
Kana Aoki, Tohru Ishitani (*Dept. of Homeostatic regulation, RIMD, Univ. Osaka*)
- [2SFA-7](#) 軟骨細胞のカラム形成を介して骨形態形成を制御する力学場
Mechanical stress field regulating bone morphogenesis through chondrocyte column formation
○横山 優花¹, 亀尾 佳貴², 須長 純子³, 牧 功一郎^{3,4}, 安達 泰治^{3,4} (¹東京科学大・難治研,²芝浦工大・工学,³京大・医歯研,⁴京大・工学)
Yuka Yokoyama¹, Yoshitaka Kameo², Junko Sunaga³, Koichiro Maki^{3,4}, Taiji Adachi^{3,4} (¹*Med. Res. Lab., Science Tokyo*, ²*Col. Eng., Shibaura Inst. Tech.*, ³*Inst. Life Med. Sci., Kyoto Univ.*, ⁴*Grad. Sch. Eng., Kyoto Univ.*)

2SGA 情報科学とイメージングで迫るバイオリジカルクラスターの実態
Exploring the reality of biological clusters through information science and advanced imaging

共催 学術変革領域研究 (A) 「クラスター細胞学」

オーガナイザー：北村 朗 (北海道大学), 立川 正志 (横浜市立大学)

Organizers: Akira Kitamura (Hokkaido Univ.), Masashi Tachikawa (Yokohama City Univ.)

09:00~11:30

G 会場 (会議室 203) / Room G (Meeting Room 203)

Complex structures formed by the high-order assembly of multiple biomolecules play a role in biological functions. Although these protein complexes are traditionally called ‘aggregates’ or ‘phase-separated biomolecular condensates’, highly ordered and non-phase-separated supramolecular complexes are involved in various biological functions and show different biophysical properties from those of aggregates and condensates: we call the supramolecular complexes with biological significance in cells as ‘biological cluster’. However, the formation of biophysical characteristics of biological clusters remains elusive. In this symposium, we discuss cutting-edge information science and advanced imaging techniques to clarify their formation and functional characteristics.

はじめに

Opening Remarks

[2SGA-1](#)

走査型蛍光相関分光法により明らかとなったタンパク質凝集体内における低移動性 TDP-25
Scanning fluorescence correlation spectroscopy reveals slowly mobile TDP-25 within protein aggregates

○濱田 悠太¹, 北村 朗² (¹ 北大・院生命科学, ² 北大・院先端生命)

Yuta Hamada¹, Akira Kitamura² (¹*Grad. Sch. Sci. of Life Sci., Hokkaido Univ.*, ²*Fac. of Adv. Life Sci., Hokkaido Univ.*)

[2SGA-2](#)

平衡および非平衡条件におけるアミロイドβ凝集の分子動力学シミュレーション

Molecular dynamics simulation of amyloid-β aggregation under equilibrium and nonequilibrium conditions

○奥村 久士^{1,2,3} (¹ 生命創成探究センター, ² 分子科学研究所, ³ 総合研究大学院大学)

Hisashi Okumura^{1,2,3} (¹*Exploratory Research Center on Life and Living Systems*, ²*Institute for Molecular Science*, ³*SOKENDAI*)

[2SGA-3](#)

興奮性シナプス形成の開始誘導：ナノモラー濃度での SynGAP 液状凝縮体形成とそれが誘導する PSD95 と受容体のアセンブリー

Initiation of excitatory synapse formation: SynGAP LLPS at nanomolar concentrations induces PSD95 and receptor oligomer recruitment

Saahil Acharya¹, Taka A. Tsunoyama¹, Christian Hoffmann², Perez Gerard Aguilar², Irina Meshcheryakova¹, Aya Nakamura-Norimoto¹, Tara Mastro³, Ward G. Walkup IV³, Takahiro Fujiwara⁴, Mary B. Kennedy³, Dragomir Milovanovic², Akihiro Kusumi^{1,4} (¹*Membrane Cooperativity Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan*, ²*Laboratory of Molecular Neuroscience, German Center for Neurodegenerative Diseases (DZNE), Berlin, Germany*, ³*Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, California, U.S.A.*, ⁴*Institute for Integrated Cell-Material Sciences (WPI-iCeMS), Kyoto University, Kyoto, Japan*.)

2SGA-4

トランスクリプトームおよび画像解析による枯草菌の遊走コロニーの時空間プロファイリング Multimodal Spatiotemporal Profiling of *Bacillus subtilis* Swarm Development via Integrated Transcriptomics and Microscopy

○納庄 一樹^{1,2,3}, Jeckel Hannah³, Neuhaus Konstantin³, Hastewell Alasdair⁴, Skinner Dominic⁴, Saha Dibya³, Netter Niklas³, Paczia Nicole⁵, Dunkel Jörn⁴, Drescher Knut³ (¹ 東京大学 大学院農学生命科学研究科 応用生命工学専攻, ² 東京大学 微生物科学イノベーション連携研究機構, ³ パーゼル大学 バイオセンター, ⁴ マサチューセッツ工科大学 数学科, ⁵ マックスプランク陸生微生物学研究所)

Kazuki Noshio^{1,2,3}, Hannah Jeckel³, Konstantin Neuhaus³, Alasdair Hastewell⁴, Dominic Skinner⁴, Dibya Saha³, Niklas Netter³, Nicole Paczia⁵, Jörn Dunkel⁴, Knut Drescher³ (¹ *Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo*, ² *Collaborative Research Institute for Innovative Microbiology, The University of Tokyo*, ³ *Biozentrum, University of Basel*, ⁴ *Department of Mathematics, Massachusetts Institute of Technology*, ⁵ *Max Planck Institute for Terrestrial Microbiology*)

2SGA-5

上皮の細胞間接着形成過程におけるダイナミクス

Dynamic processes of cell-cell adhesion in epithelial cells

○小田 裕香子 (京都大学)

Yukako Oda (*Kyoto University*)

2SGA-6

クライオ光電子相関顕微鏡の開発と現在の状況

Development and Current Status of Cryogenic Correlative Light and Electron Microscopy

○藤芳 暁 (Science Tokyo 物理)

Satoru Fujiyoshi (*Dept. Phys., Science Tokyo*)

おわりに

Closing Remarks

2SHA 鏡像生命の創成：創れるのか、創ってよいのか、創ってどうするのか？

Mirror-Life Synthesis: Its Possibility, Potential, and Problems

共催 石井石橋基金 慶應義塾大学若手研究者育成ものづくり特別事業「鏡像世界の構築から広がるマルチベース創成」

オーガナイザー：藤原 慶 (慶應義塾大学), 青木 航 (大阪大学)

Organizers: Kei Fujiwara (Keio Univ.), Wataru Aoki (The Univ. of Osaka)

09:00~11:30

H 会場 (会議室 204) / Room H (Meeting Room 204)

Recent technological advances in synthetic biology and enantiomeric synthesis of biomolecules (L-DNA/RNA, and D-proteins) have paved the way for the synthesis of mirror-image life that will be self-replicated entirely using enantiomer of the molecules in present living organisms. However, the ethical implications of such research have become increasingly prominent, as claimed by a recent opinion article in *Science* that warns the potential threats by the synthesis of mirror-life. This symposium brings together experts in synthetic biology, bioengineering, evolutionary biology, chiral biopolymer synthesis, ethics, and policy to discuss the feasibility, advantages, and evolutionary potential of creating mirror-image life.

はじめに
Opening Remarks

[2SHA-1](#) 試験管内自律的セントラルドグマへの挑戦と鏡像生命に向けた展望
Challenges to realizing in vitro autonomous central dogma and prospects for mirror life
○青木 航 (大阪大学)
Wataru Aoki (*The University of Osaka*)

[2SHA-2](#) 翻訳システムから考える鏡像生命創成への展望
Toward Mirror-Image Life: Insights from Translation Systems
○清水 義宏 (理研 BDR)
Yoshihiro Shimizu (*RIKEN, BDR*)

[2SHA-3](#) タンパク質化学合成と In vitro セレクションによる鏡像抗体ミメティックの創成
Mirror-image Antibody Mimetic Generated via Chemical Protein Synthesis and mRNA Display
○林 剛介 (名大・院工)
Gosuke Hayashi (*Grad. Sch. Eng., Nagoya Univ.*)

[2SHA-4](#) Perspective on the Evolution of Mirror-Life Based on Microbial Experimental Evolution
Chikara Furusawa^{1,2} (¹BDR, *RIKEN*, ²Univ. Biol. Inst., *Univ. Tokyo*)

[2SHA-5](#) 新興技術における「責任ある研究イノベーション (RRI)」のあり方を考える
Navigating the Future of Emerging Technologies: Responsible Research and Innovation (RRI)
○松尾 真紀子 (東大・公共政策)
Makiko Matsuo (*Grad. Sch. Public Policy, Univ. Tokyo*)

おわりに
Closing Remarks

2SIA 蛋白質-液相分離の設計と制御
Design and control of liquid-liquid phase separation of proteins
オーガナイザー：池田 恵介 (富山大学), 鎌形 清人 (岐阜大学)
Organizers: Keisuke Ikeda (*Univ. of Toyama*), **Kiyoto Kamagata** (*Gifu Univ.*)

09:00~11:30

I 会場 (会議室 205) / Room I (Meeting Room 205)

Intracellular proteins form condensed droplets by liquid-liquid phase separation via intermolecular interactions. It has become clear that these droplet formations play an important role in diverse biological processes as well as in diseases involving protein aggregation and amyloid formation. Therefore, exploring molecules that promote or inhibit protein phase separation, designing artificial systems that form phase-separated droplets, and developing technologies that control the droplets are required not only for elucidation of the mechanisms underlying the phase separation phenomenon, but also for drug discovery targeting droplet formation and protein aggregation. In the proposed symposium, five researchers working on the above issues will give lectures.

[2SIA-1](#) 人工液-液相分離ペプチドのデザインと物性制御
Design and control of physicochemical properties of artificial liquid-liquid phase-separating peptides
○池田 恵介 (富山大・薬)
Keisuke Ikeda (*Fac. Pharm. Sci., Univ. Toyama*)

- 2SIA-2** ペプチドによる α -シヌクレインの液-液相分離誘導と物性制御
Peptide-Mediated Modulation of α -Synuclein Liquid-Liquid Phase Separation and Its Biophysical Properties
○池之上 達哉 (大阪大・蛋白研)
Tatsuya Ikenoue (*IPR, Univ. Osaka*)
- 2SIA-3** 酵母プリオン Sup35 配列由来のデザインタンパク質を用いた液-液相分離に影響を及ぼすアミノ酸の解析
Analysis of amino acids affecting liquid-liquid phase separation using a design protein based on the yeast prion Sup35 sequence
○大橋 祐美子¹, 高島 晴², 田口 英樹^{1,2} (¹ 科学大・研究院・細胞センター, ² 科学大・生命理工)
Yumiko Ohhashi¹, Haru Takabatake², Hideki Taguchi^{1,2} (¹*CBC, IIR, Science Tokyo*, ²*Sch. of Life Sci. Tech, Science Tokyo*)
- 2SIA-4** ALS 関連 FUS 変異体の相挙動に対する圧力・温度および低分子の影響
Effects of pressure, temperature, and small molecules on phase behavior of amyotrophic lateral sclerosis-linked FUS variants
○北原 亮^{1,2} (¹ 立命館大・薬, ² 立命館大・院薬)
Ryo Kitahara^{1,2} (¹*Coll. Pharm. Sci., Ritsumeikan Univ.*, ²*Grad. Sch. Pharm., Ritsumeikan Univ.*)
- 2SIA-5** タンパク質液滴を測り、操り、創る
Watching, manipulating, and creating protein droplets
○鎌形 清人 (岐阜大・工・化学生命工)
Kiyoto Kamagata (*Fac. Eng. & Grad. Sch. Eng., Gifu Univ.*)

2SJA 古くて新しいロドプシン研究最前線
Cutting Edge of Rhodopsin Research ~Where Tradition Meets Innovation~
オーガナイザー：片山 耕大 (名古屋工業大学), 加藤 英明 (東京大学)
Organizers: Kota Katayama (Nagoya Inst. of Tech.), Hideaki Kato (The Univ. of Tokyo)

09:00~11:30

J 会場 (会議室 206) / Room J (Meeting Room 206)

Optogenetics, a revolutionary technique using light to control cellular and physiological functions, has become a vital tool in neuroscience and cell biology. At its core is rhodopsin, a molecule of significant interest due to its central role in vision, sensing, and energy conversion. First identified in animals in the 19th century and in microbes in 1971, rhodopsins have also served as testing ground for cutting-edge experimental methods. This symposium will revisit fundamental and applied rhodopsin research, examining their functions, novel techniques, and potential applications while fostering discussions to drive future breakthroughs in rhodopsin-based technologies.

はじめに
Opening Remarks

- 2SJA-1** 微生物ロドプシンにおけるプロトン移動の理論解析
Theoretical investigation of proton transfer in microbial rhodopsins
○辻村 真樹^{1,2}, 斉藤 圭亮¹, 石北 央¹ (¹ 東大・院工, ² 理研・開拓研究所)
Masaki Tsujimura^{1,2}, Keisuke Saito¹, Hiroshi Ishikita¹ (¹*Grad. Sch. Eng., Univ. Tokyo*, ²*PRI, RIKEN*)

- [2SJA-2](#) 光駆動プロトンポンプロドプシンの新たな視点：プロトン輸送メカニズムとその方向性
New Insights into Light-Driven Proton Pump Rhodopsins: Proton Transfer Mechanism and Directionality
○潤井 泰斗 (阪大院理)
Taito Urui (*Grad. Sch. Sci., Univ. Osaka*)
- [2SJA-3](#) ウイルスヘリオロドプシン V2HeR3 のプロトン輸送メカニズム
Mechanism of Proton Transport in the Viral Heliorhodopsin V2HeR3
○水島 律¹, Nuemket Nipawan^{2,3}, Fangjia Luo³, 細島 頌子^{1,5}, D'Ascenzi Jacopo⁴, Oliveira Leonardo⁴, 大橋 沙也佳¹, 吉住 玲¹, Palombo Riccardo⁴, 角田 聡^{1,5}, 古谷 祐詞^{1,5}, Bèjà Oded⁶, Olivucci Massimo^{4,7}, 南後 恵理子^{3,8}, 片山 耕大^{1,5}, 神取 秀樹^{1,5} (¹名工大・院工,²高輝度光科学研究センター,³理研・SPRING-8,⁴Univ. Siena,⁵名工大・オプトバイオ,⁶Technion-Israel Inst. Tech.,⁷Bowling Green State Univ.,⁸東北大・多元物質科学研究所)
Ritsu Mizutori¹, Nipawan Nuemket^{2,3}, Luo Fangjia³, Shoko Hososhima^{1,5}, Jacopo D'Ascenzi⁴, Leonardo Oliveira⁴, Sayaka Ohashi¹, Rei Abe-Yoshizumi¹, Riccardo Palombo⁴, Satoshi Tsunoda^{1,5}, Yuji Furutani^{1,5}, Oded Bèjà⁶, Massimo Olivucci^{4,7}, Eriko Nango^{3,8}, Kota Katayama^{1,5}, Hideki Kandori^{1,5} (¹Grad. Sch. Eng., Nagoya Inst. Tech.,²Japan Synchrotron Radiation Research. Inst.,³RIKEN SPRING-8,⁴Univ. Siena,⁵OptoBioTechnology Research Cent.,⁶Technion-Israel Inst. Tech.,⁷Bowling Green State Univ.,⁸Institute of Multidisciplinary Research for Advanced Materials, Tohoku Univ.)
- [2SJA-4](#) 光応答性神経による括約筋の制御と貫通型消化管の進化的起源
Light-modulated neural control of sphincter regulation in the evolution of through-gut
Junko Yaguchi¹, Kazumi Sakai², Atsushi Horiuchi², Takashi Yamamoto³, Takahiro Yamashita², Shunsuke Yaguchi¹ (¹SMRC, Univ. Tsukuba,²Grad. Sch. Sci., Univ. Kyoto,³Genom. Edit. Innov. Cent., Hiroshima Univ.)
- [2SJA-5](#) メダカでは脳下垂体に発現する光受容体が紫外線受容によって色素沈着促進ホルモンの分泌を誘導する
A Photoreceptor Expressed in Pituitary Endocrine Cells Mediates UV-Induced Hormone Release That Enhances Pigmentation in Medaka
○神田 真司¹, 福田 彩華^{1,2}, 佐藤 恵太³ (¹東京大学大気海洋研究所,²基礎生物学研究所神経行動学研究部門,³岡山大学医歯薬学総合研究科)
Sinji Kanda¹, Ayaka Fukuda^{1,2}, Keita Sato³ (¹Atmosphere and Ocean Research Institute, The University of Tokyo,²Division of Behavioral Neurobiology, National Institute for Basic Biology,³Faculty of Medicine, Dentistry, and Pharmaceutical Sciences, Okayama University)
- おわりに
Closing Remarks

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- 2SKA 日韓二国間シンポジウム：拡大する日韓生物物理研究のフロンティア
Korea-Japan Bilateral Symposium: Expanding Frontiers of Biophysics in Two Countries
オーガナイザー：高橋 聡 (東北大学), Young-Ho Lee (Korea Basic Sci. Inst.)
Organizers: Satoshi Takahashi (Tohoku Univ.), Young-Ho Lee (Korea Basic Sci. Inst.)

09:00~11:30

K 会場 (天平ホール) / Room K (Tempyo Hall)

The 2026 annual meeting of the Biophysical Society of Japan will be held in Busan, Korea as the joint meeting with the Federation of Korean Societies for Biomolecular and Biophysical Sciences. This bilateral symposium, which is the pre-event of the 2026 meeting, aims to promote collaboration among scientists in both countries by facilitating the exchange of the latest research in various fields of biophysics. We invite scientists to share their expectations for the future of Korea-Japan collaboration.

はじめに

Opening Remarks

[2SKA-1](#) Assessing druggability based on the structural features of human leucyl-tRNA synthetase 2
Seonha Park¹, Byeongmin Shin¹, Ingyo Park¹, Kyuhyeon Bang¹, Sulhee Kim¹, Ina Yoon²,
Kwang Yeon Hwang¹ (¹*Department of Biotechnology, Korea University*, ²*College of Pharmacy, Yonsei University*)

[2SKA-2](#) クライオ電子顕微鏡を用いた感染症治療薬・ワクチン開発の進展と日韓協力
Advancements in Therapeutic and Vaccine Development for Infectious Diseases Using Cryo-EM: A Potential Japan-Korea Collaboration
Katsumi Maenaka^{1,2} (¹*Facult. Pharm. Sci., Hokkaido Univ.*, ²*Facult. Pharm. Sci., Kyushu University*)

[2SKA-3](#) Accurate Conformational Ensembles of Intrinsically Disordered Proteins using Reweighting based on NMR Chemical Shift
Juhyeong Jeon¹, Wonjin Yang¹, Jin Hae Kim², Young-Ho Lee³, **Wookyoung Yu¹** (¹*Department of Brain Sciences, DGIST, Daegu, Republic of Korea*, ²*Department of New Biology, DGIST, Daegu, Republic of Korea*, ³*Research Center for Bioconvergence Analysis, Korea Basic Science Institute, Republic of Korea*)

[2SKA-4](#) NMR を利用した天然変性タンパク質を標的とした創薬への挑戦
Challenges and perspectives in drug discovery and design against intrinsically disordered proteins by NMR
Hidekazu Hiroaki^{1,2,3} (¹*Grad. Sch. Pharm. Sci., Nagoya Univ.*, ²*BeCellBar, LLC.*, ³*COMIT, Nagoya Univ.*)

[2SKA-5](#) Cellular Mechanobiology in Phagocytosis
Min Chanhuk¹, Cho Hyeokjin², Yu Jeongmin¹, Park Daeho², **Lee Gwangrog¹** (¹*Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST)*, ²*School of Life Sciences, Gwangju Institute of Science and Technology (GIST)*)

[2SKA-6](#) Direct Visualization of Dynamics in Prokaryotic Motility Machinery
Takayuki Nishizaka¹, Masaki Mizutani¹, Daisuke Nakane² (¹*Gakushuin Univ.*, ²*Univ. Electro-Communications*)

おわりに

Closing Remarks

2SAP エピゲノブリッジ: クロマチン構造形成におけるエピゲノムの役割とその複製機構の分子・細胞スケールに渡る理解
EpigenoBridge: Toward Understanding the Epigenome's Role in Chromatin Structure Formation and Replication Mechanisms from the Molecular to the Cellular Scale

共催 学術変革領域研究 (B) 「エピゲノブリッジ」

オーガナイザー: 角南 智子 (QST), 寺川 剛 (京都大学)
Organizers: Tomoko Sunami (QST), Tsuyoshi Terakawa (Kyoto Univ.)

16:15~18:45

A 会場 (会議室 101+102) / Room A (Meeting Room 101+102)

Eukaryotic genomic DNA is intricately packaged into nucleosomes, forming a dynamic beads-on-a-string structure. Various chemical modifications of histones define the “epigenome,” guiding chromatin structure and thus determining gene expression and cell function. Despite their importance, the precise mechanisms by which the epigenome regulates chromatin architecture and influences cell function remain elusive. Moreover, how these epigenetic marks are maintained and transmitted across cell generations through DNA replication is still poorly understood. This symposium brings together leading experts to explore cutting-edge research on epigenome-mediated chromatin formation, its interplay with DNA replication, and potential approaches for its artificial manipulation.

はじめに

Opening Remarks

[2SAP-1](#) クロマチン構造の力学的解析: 分子夾雑とエピゲノム継承の分子機構の理解に向けて
Mechanical Analysis of Chromatin by Optical Tweezers: Molecular Crowding and Inheritance of Epigenome

○角南 智子¹, Kumar Amarjeet¹, 日詰 光治², 河野 秀俊^{1,3} (¹QST・量子生命, ²埼玉医科大・医学部・中央研究施設, ³千葉大院・量子構造創薬センター)

Tomoko Sunami¹, Amarjeet Kumar¹, Kohji Hizume², Hidetoshi Kono^{1,3} (¹*iQLS, QST, ²BRC, Med, Saitama Med U, ³cQUEST, Chiba U*)

[2SAP-2](#) Structure and dynamics of reconstituted chromatin with defined histone modification patterns
Yohsuke T Fukai¹, **Kyogo Kawaguchi**^{1,2} (¹*RIKEN PRI, ²Institute for Physics of Intelligence, Department of Physics, The University of Tokyo*)

[2SAP-3](#) Cryo-EM analysis of basic chromatin architectures isolated from cells
Yoshimasa Takizawa^{1,2}, Haotong Zhuang^{1,2}, Takuro Shioi^{1,3}, Suguru Hatazawa¹, Yuki Kobayashi¹, Mitsuo Ogasawara¹, Yasuyuki Ohkawa⁴, Hitoshi Kurumizaka^{1,3,4} (¹*IQB, Univ.Tokyo, ²Grad. Sch. Fro. Sci., Univ.Tokyo, ³Grad. Sch. Sci., Univ. Tokyo, ⁴MIB, Kyushu Univ.*)

[2SAP-4](#) 化学触媒によるエピゲノム改変技術の開発
Development of epigenome modification technology by chemical catalysis
○川島 茂裕 (東京大学大学院薬学系研究科)
Shigehiro Kawashima (*Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

2SAP-5

複製依存的ヒストン標識 (Repli-Histo 標識) を用いて明らかにする, ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい

Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells

○南 克彦^{1,2}, 仲里 佳子^{1,2}, 井手 聖^{1,2}, 海津 一成^{3,4}, 東 光一^{2,5}, 田村 佐知子¹, 豊田 敦⁶, 高橋 恒一³, 黒川 顕^{2,5}, 前島 一博^{1,2} (¹ 遺伝研・ゲノムダイナミクス研究室, ² 総研大・先端学術院, ³ 理研 BDR・バイオコンピューティング研究チーム, ⁴ 生命創成研究センター・細胞シミュレーション研究グループ, ⁵ 遺伝研・ゲノム進化研究室, ⁶ 遺伝研・先端ゲノミクス支援センター)

Katsuhiko Minami^{1,2}, Kako Nakazato^{1,2}, Satoru Ide^{1,2}, Kazunari Kaizu^{3,4}, Koichi Higashi^{2,5}, Sachiko Tamura¹, Atsushi Toyoda⁶, Koichi Takahashi³, Ken Kurokawa^{2,5}, Kazuhiro Maeshima^{1,2}
(¹Genome Dynamics Laboratory, NIG, ²SOKENDAI, ³Laboratory for Biologically Inspired Computing, RIKEN BDR, ⁴Cell Modeling and Simulation Group, ExCELLS, ⁵Genome Evolution Laboratory, NIG, ⁶Comparative Genomics Laboratory, NIG)

おわりに

Closing Remarks

2SBP 動的溶液環境の観点から紐解く生体分子凝縮体

Understanding Biomolecular Condensation from the Perspective of Dynamic Solution Environments

オーガナイザー: 関山 直孝 (京都大学), 中村 秀樹 (京都大学)

Organizers: Naotaka Sekiyama (Kyoto Univ.), Hideki Nakamura (Kyoto Univ.)

16:15~18:45

B 会場 (会議室 103+104) / Room B (Meeting Room 103+104)

Solution environments in living cells fluctuate spatiotemporally, influencing the formation of biomolecular condensates. This symposium will explore how dynamic changes in solution environments regulate liquid-liquid phase separation and amyloid fibril formation by modulating intermolecular interactions, as well as the subsequent effects on physiological functions and the formation of pathological aggregates. By integrating experimental, computational and theoretical approaches, we aim to uncover the intricate mechanisms underlying biomolecular condensate formation across scales, from microscopic molecular interactions to macroscopic biological outcomes.

2SBP-1

シナプス後肥厚タンパク質のリン酸化による凝縮体および受容体集合への影響: 分子シミュレーションによる検討

Effects of phosphorylation of postsynaptic density proteins on condensates and receptor assembly studied by molecular simulations

○山田 莉彩, 高田 彰二 (京大・理・生物物理)

Risa Yamada, Shoji Takada (Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.)

2SBP-2

Single-Molecule Studies of how Mug20-Rec25-Rec27 (MRR) Complex Mediates DNA Conformational Change and Biomolecular Condensates Formation

Hung-Wen Li¹, Chieh-Yu Tsai¹, Feng-Yu Wang², Ya-Ching Yang², Ya-Chen Gong³, Shyh-Chyang Luo³, Peter Chi² (¹Dept. Chemistry, National Taiwan Univ., ²Inst. Biochem. Sci., National Taiwan Univ., ³Dept. Materials Sci. Eng., National Taiwan Univ.)

2SBP-3

液体の積分方程式理論を用いた 4 残基ペプチドデータベースの構築

A Comprehensive Tetrapeptide Database Using Integral Equation Theory of Liquid

○金丸 恒大^{1,2}, 吉田 紀生² (¹京大・福井セ, ²名大・院情報)

Kodai Kanemaru^{1,2}, Norio Yoshida² (¹FIFC, Kyoto Univ., ²Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.)

- [2SBP-4](#) アミロイド多型とその形成メカニズム
Amyloid polymorphism and formation mechanisms
○宗 正智, 菅瀬 謙治 (京大・院農)
Masatomo So, Kenji Sugase (*Grad. Sch. Agric., Kyoto Univ.*)
- [2SBP-5](#) 動的溶液環境におけるアミロイド β タンパク質の分子集合
Molecular assembly of amyloid- β proteins in dynamic solution environments
○矢木 真穂^{1,2} (¹ 名市大・院薬, ² 自然科学研究機構・生命創成探究セ)
Maho Yagi-Utsumi^{1,2} (¹*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, ²*ExCELLS, Natl. Inst. Nat. Sci.*)
- [2SBP-6](#) 動的細胞内環境における機能性アミロイド線維の可能性の探索
Investigating Neuronal Amyloid Fibrils with Potential Functional Roles in a Dynamic Intracellular Environment
○杉江 淳¹, 小坂 二郎² (¹ 京都工芸繊維大学, ² 東京科学大学)
Atsushi Sugie¹, **Jiro Osaka**² (¹*Kyoto Institute of Technology*, ²*Institute of Science Tokyo*)

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- 2SCP 重力場における生命の適応進化戦略「細胞骨格ダイナミクス」「ホメオスタシス」から超高齢社会のQOLを考える～自己組織化・分子シャペロン・Hippo経路・可視化と意識的活動
Adaptive Evolutionary Strategy of Life in a Gravitational Field "Cytoskeletal Dynamics", "Mechanical Homeostasis" for Quality of Life in a Super-aging Society - Self-organization, Molecular Chaperones, Hippo Pathway, Visualization and Conscious Activity
オーガナイザー：跡見 順子 (帝京大学), 井上 大介 (九州大学)
Organizers: Yoriko Atomi (Teikyo Univ.), **Daisuke Inoue** (Kyushu Univ.)

16:15~18:45

C会場 (会議室 105+106) / Room C (Meeting Room 105+106)

Only intelligent human beings can apply the principles of life to their own existence and life to science themselves and present scientific strategies to revitalize the super-aging society. In this symposium, we aim to gain insight into the essence of "cytoskeletal dynamics" and "mechanical homeostasis" from key factors such as self-organization, molecular chaperones, Hippo pathways, visual understanding, and conscious activity, and to create a new field of biophysics through discussions that link the two horizontally and vertically.

はじめに

Opening Remarks

- [2SCP-1](#) 微小管ダイナミックインスタビリティ 3.1：高精度多次元解析がもたらした意外な高次機能の発見
Microtubule Dynamic Instability 3.1: From Imaging to Insight into Hidden Functions
○清末 優子 (関西医科大学 附属生命医学研究所 分子遺伝学部門)
Yuko Mimori-Kiyosue (*Department of Molecular Genetics, Institute of Biomedical Science, Kansai Medical University*)
- [2SCP-2](#) The Timing of the Acquisition of Eukaryotic Traits during Eukaryogenesis
Robert Charles Robinson (*Vidyasirimedhi Institute of Science and Technology (VISTEC) Thailand*)
- [2SCP-3](#) α B-クリスタリン, チューブリン/微小管のメカノシャペロン：階層的自己組織化とヒト特異性を活用したQOL戦略
 α B-Crystallin, mechanochaperon for tubulin/microtubule: A QOL strategy that utilizes hierarchical self-organization and human specificity
○跡見 順子 (帝京大学先端総合研究機構)
Yoriko Atomi (*Teikyo University, ACRO*)

[2SCP-4](#) 再構成型ヒト翻訳・フォールディング連動システムを利用した変異 β -アクチンの生合成における異常ステップの解析
A Reconstituted Human Translation/Folding Coupled System Defines the Defective Step in the Biogenesis of Mutated β -Actin Proteins
○町田 幸大 (兵庫県立大・院工・応用化学)
Kodai Machida (*Dept. of Appl. Chem., Grad. Sch. of Eng., Univ. of Hyogo*)

[2SCP-5](#) 量子ドットイメージングで観る細胞表面へのアミロイド β 凝集・沈着
Visualization of amyloid β aggregation and deposition on cell surface using quantum dot imaging
○倉賀野 正弘, 徳樂 清孝 (室工大・院工)
Masahiro Kuragano, Kiyotaka Tokuraku (*Grad. Sch. Eng., Muroran Inst. Tech.*)

[2SCP-6](#) 細胞外環境を感知する Hippo シグナル伝達経路の役割
Roles of the Hippo signaling pathway sensing the extracellular environment
○仁科 博史 (東京科学大学)
Hiroshi Nishina (*Institute of Science Tokyo*)

[2SCP-7](#) The expression of the collagen chaperone Hsp47 is regulated by mechanical loading through the YAP/TEAD pathway
Ayano Kasai^{1,2}, Shinya Ito³, Ryo Ushioda^{1,2}, Kazuhiro Nagata^{1,2,4} (¹*Fac. Life Sci., Kyoto Sangyo Univ.*, ²*Inst. Protein Dynamics, Kyoto Sangyo Univ.*, ³*Ctr. Mol. Biol., Heidelberg Univ.*, ⁴*JT Biohistory Research Hall*)

おわりに
Closing Remarks

2SDP 多細胞生物の解明に向けて：組織内で細胞の特徴を捉えるための多彩なアプローチ
Towards the elucidation of multicellular organisms: Diverse approaches to capturing the characteristics of cells within tissues

オーガナイザー：北條 望 (理化学研究所), 神谷 真子 (東京科学大学)
Organizers: Nozomi Hojo (RIKEN), Mako Kamiya (Science Tokyo)

16:15~18:45

D 会場 (会議室 107+108) / Room D (Meeting Room 107+108)

Recent advances in single-cell analysis technologies have revealed that multicellular organisms are composed of diverse cell types, which work in coordination to regulate tissues. Unraveling the detailed mechanisms requires not only the identification of cell types but also the integrated analysis of information such as the spatial location, morphology, and functional activity of cells within three-dimensional biological tissues. This symposium aims to focus on research that captures the characteristics of cells within tissues using various methods, with the goal of achieving a comprehensive understanding of multicellular organisms. We hope to have active discussion on this topic with participants.

はじめに
Opening Remarks

[2SDP-1](#) 一細胞 3 次元空間トランスクリプトーム解析を実現する新規細胞単離法
A novel single-cell isolation method enables single-cell 3D spatial transcriptomics
○北條 望, 城口 克之 (理研・BDR)
Nozomi Hojo, Katsuyuki Shiroguchi (*BDR, Riken*)

- [2SDP-2](#) 線虫の全脳活動計測と遺伝子発現解析
Whole brain activity measurement and gene expression analysis of neurons in *Caenorhabditis elegans*
○豊島 有^{1,2}, 飯野 雄一¹, 楊 曉雄² (¹東大・院理・生物科学, ²東大・新領域・メディカル情報生命)
Yu Toyoshima^{1,2}, Yuichi Iino¹, Xiaoxiong Yang² (¹*Grad. Sch. of Sci., Univ. of Tokyo*, ²*Grad. Sch. of Front. Sci., Univ. of Tokyo*)
- [2SDP-3](#) Unraveling the Mechanisms of Collective Cell Migration in Epithelial Morphogenesis
Erina Kuranaga^{1,2} (¹*Grad Sch Pharmaceu Sci, Kyoto Univ*, ²*Grad Sch Life Sci, Tohoku Univ*)
- [2SDP-4](#) 生きた動物内で標的 GPCR を細胞種選択的に制御する化学遺伝学的アプローチ
Chemogenetic strategy for controlling target GPCRs in a cell-type-specific manner in vivo
○清中 茂樹 (名大・院工)
Shigeki Kiyonaka (*Grad. Sch. Eng., Nagoya Univ.*)
- [2SDP-5](#) Functional Raman probes for multiplexed vibrational imaging
Mako Kamiya (*CLS, Science Tokyo*)
- おわりに
Closing Remarks

2SEP 生物物理からのアクティブマターへのアプローチ

Approaching Active Matter from Biophysics Perspective

オーガナイザー：川又 生吹 (京都大学), 早川 雅之 (京都工芸繊維大学)

Organizers: Ibuki Kawamata (Kyoto Univ.), Masayuki Hayakawa (Kyoto Institute of Technology)

16:15~18:45

E 会場 (会議室 201) / Room E (Meeting Room 201)

This symposium will focus on Active Matter, where the mechanism of active motion of a component is addressed, and further the interaction among them is of interest. Each component can be materialized in a variety of manners from natural organisms to artificially synthesized molecules. In the symposium, Active Matter will be discussed from a wide range of Biophysics, covering experimental research on cells, microorganism, droplets, molecular motors, colloids, and so on. Through the discussion of Active Matter, our symposium will provide insights into the origin and evolution of life, as well as the essence of emergence resulting from autonomy and complexity.

[2SEP-1](#) アクティブに推進する生体分子エージェントとプログラムされた DNA 化学反応ネットワークの統合

Actively Gliding Biomolecular Agents Integrated with Programmed DNA Chemical Reaction Network

○川又 生吹 (京都大学)

Ibuki Kawamata (*Kyoto University*)

[2SEP-2](#) 光照射で駆動される DNA 流体による生命的な動き

Life-like motion of active DNA fluid driven by photo-irradiation

○鵜殿 寛岳¹, 野村 M. 慎一郎², 瀧ノ上 正浩¹ (¹東京科学大学 情報理工学院, ²東北大学大学院工学研究科 ロボティクス専攻)

Hirotake Udono¹, M. Shin-ichiro Nomura², Takinoue Masahiro¹ (¹*Dept. Comp. Sci., Institute of Science Tokyo*, ²*Dept. Robotics, Sch. Eng., Tohoku University*)

- 2SEP-3** 完全な運動一方向性のための DNA 人工分子モーターの構造改変
Geometry engineering of DNA artificial molecular motor for perfect unidirectionality
○原島 崇徳^{1,2}, 飯野 亮太^{1,2} (¹分子科学研究所, ²総合研究大学院大学)
Takanori Harashima^{1,2}, Ryota Iino^{1,2} (¹*Institute for Molecular Science*, ²*Graduate Institute for Advanced Studies, SOKENDAI*)
- 2SEP-4** 非生物由来分子システムの自律的回帰性が駆動する生命性
"Life" Actuated by Autonomous Recursion of Non-Biological Molecular Systems
○松尾 宗征^{1,2} (¹広島大学, ²東京大学)
Muneyuki Matsuo^{1,2} (¹*Hiroshima University*, ²*The University of Tokyo*)
- 2SEP-5** アクティブマター研究としての単細胞の重力生物学
Gravitational biology of unicellular organisms as active matter research
○鹿毛 あずさ (室蘭工業大学)
Azusa Kage (*Muroran Institute of Technology*)
- 2SEP-6** 磁場による遊泳バクテリア集団の秩序形成制御
Magnetically controlled self-organization of swimming bacteria
Kazusa Beppu¹, Joakim Stenhammar², Jaakko V. I. Timonen³ (¹*Dept. of Chem. Eng., Kyoto Univ.*, ²*Div. of Phys. Chem., Lund Univ.*, ³*Dept. of Appl. Phys., Aalto Univ. Sch. of Sci.*)
- 2SEP-7** 走化性を示さない細胞性粘菌にみられる集団運動
Self-organized collective dynamics in *Dictyostelium* cells lacking chemotaxis
○早川 雅之^{1,2}, Bhattacharjee Biplab², 桑山 秀一³, 柴田 達夫² (¹京都工芸繊維大学・機械工学系, ²理研・生命機能科学研究センター, ³筑波大学・生命環境系)
Masayuki Hayakawa^{1,2}, Biplab Bhattacharjee², Hidekazu Kuwayama³, Tatsuo Shibata² (¹*Dept. of Mech. Eng., Kyoto Institute of Technology*, ²*RIKEN BDR*, ³*Life Environ. Sci., Univ. Tsukuba*)

2SFP スーパーコンピュータ「富岳」による創薬と医療の促進
Advancing drug discovery and healthcare through supercomputer Fugaku
共催 「富岳」成果創出加速プログラム 「「富岳」で目指すシミュレーション・AI 駆動型次世代医療・創薬」
オーガナイザー：荒木 望嗣 (京都大学), 寺山 慧 (横浜市立大学)
Organizers: Mitsugu Araki (Kyoto Univ.), Kei Terayama (Yokohama City Univ.)

16:15~18:45

F 会場 (会議室 202) / Room F (Meeting Room 202)

Drug discovery and medical technologies are being innovated by development of high performance computing (HPC). Large-scale molecular simulations performed on supercomputer Fugaku enable atomic-level observation of protein recognition processes of small-molecule ligands, peptides, antigens, and proteins, providing deeper insight into understanding pathogenesis mechanisms of many unexplained diseases and exploring drugs to control them. In this symposium, we will discuss about the forefront of next-generation molecular simulation and artificial intelligence (AI) techniques for drug discovery and medical treatment.

はじめに
Opening Remarks

[2SFP-1](#) 大規模 MD シミュレーションによる DHFR 阻害剤耐性メカニズムの微視的解析
Molecular Dynamics Simulation Unveils Multiple-Site Binding of Inhibitors with Reduced Activity on the Surface of Dihydrofolate Reductase
○荒木 望嗣, 奥野 恭史 (京大・院医)
Mitsugu Araki, Yasushi Okuno (*Grad. Sch. Med., Kyoto Univ.*)

[2SFP-2](#) 富岳を用いた大規模レプリカ交換 MD シミュレーションによる、ペプチド認識に関与するプロテインキナーゼの構造ダイナミクスの解明
Massive Replica-Exchange MD Simulations on Fugaku Reveal Conformational Features of Protein Kinases Relevant to Peptide Recognition
○信夫 愛 (大阪大学)
Ai Shinobu (*Osaka University*)

[2SFP-3](#) In Silico Design of Inhibitors Targeting SARS-CoV-2 Non-Structural Proteins
Duy Tran, Akio Kitao (*School of Life Science and Technology, Institute of Science Tokyo*)

[2SFP-4](#) スパコンによるマルチスケール解析でストレッチアクティベーションが心拍動と昆虫の羽ばたきになぜ必要かを解明する
Supercomputer-based multiscale analysis reveals why stretch activation is necessary for beating the heart and insects' wings
○鷺尾 巧^{1,2}, 久田 俊明¹ (¹UT-Heart 研究所, ² 東京大学)
Takumi Washio^{1,2}, Toshiaki Hisada¹ (¹UT-Heart Inc., ²University of Tokyo)

[2SFP-5](#) 結合自由エネルギー計算に基づくキナーゼ阻害剤の心筋イオンチャネル阻害活性の予測
Prediction of cardiac ion channel inhibitory activities of kinase inhibitors based on binding free energy calculation
○根上 樹, 寺田 透 (東大・院農)
Tatsuki Negami, Tohru Terada (*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*)

[2SFP-6](#) Enhancing Antibody Engineering with Automated Molecular Interaction Descriptors and Structure Modeling
Shuntaro Chiba¹, Tsutomu Yamane¹, Yasushi Okuno^{1,2}, Mitsunori Ikeguchi^{1,3}, Masateru Ohta¹ (¹R-CCS, RIKEN, ²Grad. Sch. Med., Kyoto Univ., ³Grad. Sch. Med. Life Sci., YCU)

[2SFP-7](#) 分子生成 AI とシミュレーションの融合による創薬分子設計
Integrating Molecular Generative AI and Simulation for Drug Discovery
○寺山 慧 (横浜市大・院生命医科学)
Kei Terayama (*Grad.Sch.Med.Life.Sci, Yokohama City Univ.*)

おわりに
Closing Remarks

2SGP あらゆる地球環境で光合成を可能とする超分子構造制御
Supramolecular Complexes and Their Regulations to Enable Photosynthesis All Around the
Globe

共催 学術変革領域研究 (A) 「光合成ユビキティ」

オーガナイザー：斉藤 圭亮（東京大学），白井 剛（長浜バイオ大学）

Organizers: Keisuke Saito (The Univ. of Tokyo), Tsuyoshi Shirai (Nagahama Inst. of Bio-Sci. Tech.)

16:15~18:45

G 会場（会議室 203）／Room G（Meeting Room 203）

Photosynthetic organisms convert water and carbon dioxide into organic compounds using solar energy. They have adapted to diverse environments, sustaining life on Earth. The structure and function of the photosynthetic apparatus dynamically respond to environmental changes. The research project Photosynthetic Ubiquity, supported by a Grant-in-Aid for Transformative Research Areas (A) from JSPS, explores how supramolecular complexes regulate physiological functions based on spatiotemporal structural information. In this symposium, project members from structural biology, plant physiology, biochemistry, and bioinformatics will discuss molecular mechanisms underlying the adaptation of photosynthetic supramolecular complexes to various environments.

はじめに

Opening Remarks

[2SGP-1](#) 暗所従属栄養条件でのシアノバクテリアの微小進化

Microevolution of cyanobacteria in the dark heterotrophic conditions

○藤田 祐一（名古屋大・院生命農）

Yuichi Fujita (*Grad. Sch. Bioagricultural Sci., Nagoya Univ.*)

[2SGP-2](#) 緑色硫黄細菌で見つかった嫌気的な非光化学的消光：その反応機構と生理的意義

Anaerobic non-photochemical quenching of photosynthetic green sulfur bacteria: Its reaction mechanism and physiological significance

○浅井 智広（中央大・理工）

Chihiro Azai (*Fac. Sci. & Eng., Chuo Univ.*)

[2SGP-3](#) 時間分解蛍光分光法による光合成色素-タンパク質複合体の機能解明

Functions of photosynthetic pigment-protein complexes, revealed by time-resolved fluorescence spectroscopy

○秋本 誠志（神戸大・院理）

Seiji Akimoto (*Grad. Sch. Sci., Kobe Univ.*)

[2SGP-4](#) 光合成タンパク質の分子構造と理論構造をつなぐ磁気構造

Linkage of the molecular and theoretical structures of photosynthetic proteins using magnetic spin configurations

○三野 広幸（名古屋大学・院理）

Hiroyuki Mino (*Grad. Sch. Sci., Nagoya Univ.*)

[2SGP-5](#) 光捕集複合体の構造に基づいた海洋性大型緑藻のカルボニルカロテノイドによる緑色光吸収の分子メカニズム

Mechanism of green light absorption by carbonyl carotenoids of marine macroalgae based on the structure of light-harvesting complexes

○藤井 律子^{1,2} (¹大阪公立大学人工光合成研究センター, ²大阪公立大学理学研究科化学専攻)

Ritsuko Fujii^{1,2} (¹Research Center for Artificial Photosynthesis, Osaka Metropolitan University,

²Department of Chemistry, Graduate School of Science, Osaka Metropolitan University)

- [2SGP-6](#) 光合成アンテナのデザインを目指して：in vitro 再構成光合成アンテナの構造解析
Toward the design of photosynthetic antennas: structural determination of in vitro reconstituted light-harvesting complex
○関 莊一郎¹, 川本 晃大^{1,2}, 宮田 知子^{3,4}, 難波 啓一^{3,4}, 藤井 律子⁵, 栗栖 源嗣^{1,2,4} (¹ 阪大・蛋白研, ² 阪大・OTRI, ³ 阪大・生命機能, ⁴ 阪大・日本電子 YOKOGUSHI 協働研, ⁵ 阪公大・人工光合成研究センター)
Soichiro Seki¹, Akihiro Kawamoto^{1,2}, Tomoko Miyata^{3,4}, Keiichi Namba^{3,4}, Ritsuko Fujii⁵, Genji Kurisu^{1,2,4} (¹IPR, Osaka Univ., ²OTRI, Osaka Univ., ³Grad. Sch. Frontier Biosci., Osaka Univ., ⁴JEOL YOKOGUSHI Res. Alliance Labs., Osaka Univ., ⁵ReCAP, Osaka Metropol. Univ.)
- [2SGP-7](#) 光センサータンパク質 RcaE における「水素結合のアクセプター」となるリシン
Deprotonated Lysine Serving as a “H-bond acceptor” in the Photoreceptor Protein RcaE
○三島 正規 (東京薬科大・薬学)
Masaki Misima (*Sch. Pharm., Tokyo Univ. Pharm. and Life Sci.*)
- [2SGP-8](#) AlphaFold と MD シミュレーションを活用したオートファジー駆動機構の解明
Elucidating the mechanism of autophagy utilizing AlphaFold prediction and MD simulations
○野田 展生^{1,2} (¹ 北大・遺制研, ² 微化研)
Nobuo N. Noda^{1,2} (¹IGM, Hokkaido Univ., ²Inst. Microbial Chem.)

おわりに

Closing Remarks

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- 2SHP メゾ複雑体の機能解明に向けた計算科学と実験科学の統合的アプローチ
Towards the Elucidation of Structure of Meso-entangled Bodies through the Integration of Computational and Experimental Approaches

共催 学術変革領域研究 (A) 「クロススケール新生物学」

オーガナイザー：西田 紀貴 (千葉大学), 笠原 健人 (大阪大学)

Organizers: Noritaka Nishida (Chiba Univ.), Kento Kasahara (The Univ. of Osaka)

16:15~18:45

H 会場 (会議室 204) / Room H (Meeting Room 204)

In cells, specific proteins form spatiotemporally regulated complexes, which we refer to as meso-entangled bodies, playing a vital role in maintaining normal cellular functions. To elucidate the structures of these protein complexes, cutting-edge experimental techniques such as cryo-EM, NMR, and X-ray crystallography, along with computational approaches like molecular dynamics simulations and AI-driven structure prediction, have made significant contributions. This symposium will present research that integrates these experimental and computational methods to deepen our understanding of the structural basis and biological functions of meso-entangled bodies.

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- [2SHP-1](#) FUS の液滴形成・成熟過程の in-cell NMR 解析
Structural insights into liquid-liquid phase separation (LLPS) mechanism of FUS using in-cell NMR
○西田 紀貴 (千葉大・院薬)
Noritaka Nishida (*Grad Sch Pharm Sci, Chiba Univ*)

- [2SHP-2](#) 統合的時分割構造解析で捉えるシャペロンのフォールディング制御における速度論的特性
Kinetic Insights into Chaperone-Mediated Protein Folding from Integrative, Dynamic Structural Biology
○熊代 宗弘¹, 久米田 博之², 齋尾 智英¹ (¹徳大・酵素研, ²北大・先端生命)
Munehiro Kumashiro¹, Hiroyuki Kumeta², Tomohide Saio¹ (¹*Inst. Adv. Med. Sci., Tokushima Univ.*,
²*Fac. Adv. Life Sci., Hokkaido Univ.*)
- [2SHP-3](#) Modulation of Structure and Dynamics in Biomolecular Condensates Revealed by Large-Scale Molecular Dynamics Simulations
Cheng Tan, Yuji Sugita (*RIKEN Center for Computational Science*)
- [2SHP-4](#) PROTAC-induced Protein Structural Dynamics in Targeted Protein Degradation
Chia-en Chang, Kingsley Wu, Ta I David Tang (*University of California, Riverside*)
- [2SHP-5](#) Elucidation of the regulation of the Rac1/Cdc42 guanine nucleotide exchange factor DOCK6
Mutsuko Kukimoto-Niino (*RIKEN, Yokohama*)
- [2SHP-6](#) カーゴ受容体 ERGIC-53 によるカーゴ輸送のクライオ電顕構造解析
Cryo-EM analysis of cargo transport and release by a cargo receptor ERGIC-53
○渡部 聡, 本城 恵美, 稲葉 謙次 (九大・生医研)
Satoshi Watanabe, Emi Honjo, Kenji Inaba (*MIB, Kyushu Univ*)
- [2SHP-7](#) 高速 AFM と cryo-EM による, CAMSAP2 によって誘導される微小管およびアスター構造形成過程の直接観察
Direct observation of CAMSAP2-induced microtubule and aster formation processes using high-speed AFM and cryo-EM
Tsuyoshi Imasaki¹, Ayhan Yurtsever², Ryota Kitano¹, Kien Xuan Ngo², Takaaki Kato¹, Hanjin Liu¹, Hideki Shigematsu³, Takeshi Fukuma², Ryo Nitta¹ (¹*Kobe University Graduate School of Medicine*,
²*WPI-NanoLSI*, ³*JASRI*)
- おわりに
Closing Remarks

2SIP 複雑な細胞機能を解き明かす：メカニズム解明と技術革新
Deciphering complex cellular functions: Mechanistic insights and technological innovations
オーガナイザー：出口 真次 (大阪大学), 木戸秋 悟 (九州大学)
Organizers: Shinji Deguchi (The Univ. of Osaka), **Satoru Kidoaki** (Kyushu Univ.)

16:15~18:45

I 会場 (会議室 205) / Room I (Meeting Room 205)

Cells exhibit a variety of complex functions that are vital for life, yet deciphering the mechanisms driving these processes remains a significant scientific challenge. This symposium will focus on recent progress in exploring cellular mechanisms, highlighting the connections between molecular interactions and cellular functions. The discussions will also focus on innovative methods, including advanced imaging and computational tools, that provide new perspectives on cell biology. By presenting these findings, the symposium aims to enhance our understanding of cellular processes and inspire further developments that integrate biological research with technological advancements.

はじめに
Opening Remarks

- [2SIP-1](#) ミスセンス変異モータータンパク質の機能評価に向けた力計測アプローチ
Functional Assessment of Missense Mutations in Motor Proteins via Force Measurements
○林 久美子 (東大・物性研)
Kumiko Hayashi (*ISSP, Univ. Tokyo*)
- [2SIP-2](#) Mechanisms of intracellular force transmission revealed by coiled-coil mechano-sensors
Takumi Saito (*Grad. Sch. of Engineering Science, The University of Osaka*)
- [2SIP-3](#) Alternative Force Transmission Mechanisms at Adherens Junctions with Potential Roles in Cancer Progression
Cristina Bertocchi^{1,2} (¹*Pontificia Universidad Católica de Chile*, ²*The University of Osaka*)
- [2SIP-4](#) A molecular basis for neuronal migration in confined spaces
Naotaka Nakazawa (*Kindai University*)
- [2SIP-5](#) 突起形成による力不均衡がもたらすグリオーマの移動極性
Migratory polarity emerges from protrusion-mediated force imbalance in glioma cells
○作村 諭一^{1,2}, 田川 晴奈², 兼松 大介³, 勝間 亜沙子^{2,3}, 稲垣 直之², 金村 米博³ (¹奈良先端大・DSC, ²奈良先端大・先端科学技術, ³大阪医療センター)
Yuichi Sakumura^{1,2}, Haruna Tagawa², Daisuke Kanematsu³, Asako Katsuma^{2,3}, Naoyuki Inagaki², Yonehiro Kanemura³ (¹*Data Science Center, Nara Inst. of Sci. and Tech.*, ²*Grad. Sch. Sci. and Tech., Nara Inst. of Sci. and Tech.*, ³*NHO Osaka National Hospital*)
- [2SIP-6](#) 運動する細胞の応力ゆらぎ操作と計測
Dynamic Control and Analysis of Intracellular Stress Fluctuations during Cell Migration
○木戸秋 悟 (九大・先導研)
Satoru Kidoaki (*IMCE, Kyushu Univ.*)
- [2SIP-7](#) 細胞内の中間スケールにおけるゆらぎ駆動力の定量解析
Probing mesoscale physical forces in cells
○出口 真次^{1,2}, 上田 唯花¹ (¹阪大・基礎工, ²阪大・国際医工情報センター)
Shinji Deguchi^{1,2}, Yuika Ueda¹ (¹*Grad Sch Eng Sci, Univ Osaka*, ²*MEI-Center, Univ Osaka*)
- おわりに
Closing Remarks

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- 2SJP 日豪台三国間シンポジウム: 量子生命科学による最先端生体計測の新展開(国際量子科学技術年記念シンポジウム)
Japan-Australia-Taiwan Trilateral Symposium: New Frontiers in Biological Measurement Enabled by Quantum Life Science (International Quantum Science and Technology Year Commemorative Symposium)
オーガナイザー: 石綿 整 (QST), David Simpson (The Univ. of Melbourne)
Organizers: Hitoshi Ishiwata (QST), David Simpson (The Univ. of Melbourne)

16:15~18:45

J 会場 (会議室 206) / Room J (Meeting Room 206)

Quantum life science is an emerging interdisciplinary field at the intersection of quantum physics and biology, focused on exploring fundamental life processes at the molecular level. By applying principles of quantum measurement and quantum bioengineering, this field aims to develop advanced techniques for quantifying intracellular nanoscale environments, including temperature, pH, diffusion, and redox activities. This innovative approach has the potential to transform our understanding of biological systems and drive significant advancements in genetics, molecular biology, medicine, and bioengineering.

はじめに

Opening Remarks

[2SJP-1](#) Sub-micron imaging of neuronal action potentials by defect charge-state conversion in diamond
Daniel McCloskey^{1,2}, Kathryn Munro³, Nikolai Dotschuk¹, David Simpson^{1,2} (¹*Sch. of Phys., Univ. Melbourne*, ²*ARC CoE in Quantum Biotechnology*, ³*Dept. Anatomy & Physiology, Univ. Melbourne*)

[2SJP-2](#) Computational 4D imaging for understanding pain-processing neural circuit
Takuma Sugi (*Grad. Sch. Integ. Sci. for Life, Hiroshima Univ.*)

[2SJP-3](#) Quantum Sensing in Healthcare: Spin-Enhanced Immunoassays with Fluorescent Nanodiamonds
Huan-Cheng Chang (*Academia Sinica, Taiwan*)

[2SJP-4](#) *Diamond quantum sensors for iron load quantification of ferritin proteins*
A. Simpson David (*School of Physics, University of Melbourne*)

[2SJP-5](#) Interferometric Scattering Microscopy: Where Light Scatters and Life Reveals
Chia-Lung Hsieh (*Institute of Atomic and Molecular Sciences (IAMS), Academia Sinica*)

[2SJP-6](#) ナノ量子センサが切り拓く細胞機能の新次元定量技術
Next-Generation Quantification of Cellular Functions Enabled by Nanoscale Quantum Sensors
○石綿 整^{1,2} (¹量子科学技術研究開発機構, 量子生命科学研究所, ²千葉大 量子生命構造創薬センター)
Hitoshi Ishiwata^{1,2} (¹*iQLS, QST*, ²*Chiba Univ. cQUEST*)

2SKP 人工細胞そして生命－非生命の境界

Artificial cell and boundary between living and non-living matters

共催 JST CREST 「ゲノム合成」

オーガナイザー：野地 博行（東京大学）、市橋 伯一（東京大学）

Organizers: Hiroyuki Noji (The Univ. of Tokyo), Norikazu Ichihashi (The Univ. of Tokyo)

16:15～18:45

K 会場（天平ホール）／Room K（Tempyo Hall）

In recent years, the field of bottom-up construction of artificial cells as autonomously functioning molecular systems has advanced rapidly, bringing the realization of "living molecular systems" closer to reality. However, the boundary conditions that discriminate "living matters (life)" from "non-living matters (non-life)" remain unclear. This symposium aims to explore the factors that define the boundary between living- and non-living matters by integrating insights from cutting-edge artificial cell research with perspectives from researchers studying this boundary from different viewpoints.

はじめに
Opening Remarks

- [2SKP-1](#) 小さいゲノムを持つ微生物から見る生命と非生命の境界
The Boundary Between Life and Non-Life Seen in Microorganisms with Small Genomes
○鈴木 志野 (理研・開拓研究所)
Shino Suzuki (*PRI, RIKEN*)
- [2SKP-2](#) ヌクレオサイトウイルス門の巨大ウイルスによる感染細胞に対する思いもよらぬ影響について
Giant viruses of the Phylum Nucleocytoviricota induce unexpected behaviors in infected host cells
○武村 政春, ペジワン (東京理科大・院理)
Masaharu Takemura, Jiwan Bae (*Grad. Sch. Sci., Tokyo Univ. Sci.*)
- [2SKP-3](#) Artificial cells with dissipative structures
Sakura Takada, Kei Fujiwara (*Dept. of Biosci. and Info., Keio Univ.*)
- [2SKP-4](#) LLPS ドロプレットを用いた自律成長型人工細胞モデル
Artificial protocell models based on LLPS droplet
○野地 博行, 皆川 慶嘉 (東京大学)
Hiroyuki Noji, Yoshihiro Minagawa (*University of Tokyo*)
- [2SKP-5](#) 生物みたいに自己再生産できる人工システムを作りたい：現状と展望
Toward a self-regenerative in vitro central dogma; progress and future
○市橋 伯一 (東大総合文化)
Norikazu Ichihashi (*Grad. Sch. Arts Sci. Univ. Tokyo*)
- [2SKP-6](#) 動的な人工細胞のための核酸ベースの知的な凝集体
Nucleic Acid-based Smart Condensates for Dynamic Artificial Cells
○瀧ノ上 正浩^{1,2,3} (¹東京科学大・情報理工, ²東京科学大・生命理工, ³東京科学大・自律システム材料科学研究センター)
Masahiro Takinoue^{1,2,3} (¹*Sch. Computing, Science Tokyo*, ²*Sch. Life Sci. Tech., Science Tokyo*, ³*ASMat, IIR, Science Tokyo*)
- [2SKP-7](#) 細胞死の理論と「安定に機能する生化学システム」の珍しさ
A theory of cell death and the rarity of stably functioning biochemical systems
○姫岡 優介 (東京大学大学院理学系研究科生物普遍性研究機構)
Yusuke Himeoka (*Universal Biology Institute, The University of Tokyo*)
- おわりに
Closing Remarks

3 日目 (9 月 26 日 (金)) / Day 3 (Sep. 26 Fri.)

3SAA ノルウェー・日本の二国間シンポジウム
Norway-Japan Bi-lateral Symposium
オーガナイザー：古池 美彦 (分子科学研究所)
Organizers: Yoshihiko Furuike (IMS)

09:00~11:30
A 会場 (会議室 101+102) / Room A (Meeting Room 101+102)

What are the significances of sequence diversity and conformational polymorphism of proteins for biological phenomena? We will introduce cutting-edge research results from Norway and Japan to promote research exchange and future collaboration between the two countries.

3SAA-1 ストレスファイバ直線収縮が引き起こす魚類表皮ケラトサイトの細胞体回転
Cell body rotation by sequential linear contraction of stress fibers in a fish epidermal keratocyte
○沖村 千夏 (山口大・理)
Chika Okimura (*Dept. Biol., Yamaguchi Univ.*)

3SAA-2 Nanoscale motion tracing of spermatozoa
Jean-Claude Tinguely¹, Sunil Bhatt², Ankit Butola¹, Mona Nystadq^{3,4}, Dalip Singh Mehta², Krishna Agarwal¹ (¹*Institute of Physics and Technology, UiT The Arctic University of Norway, Tromsø, Norway*, ²*Department of Physics, Indian Institute of Technology Delhi, New Delhi, India*, ³*Department of Clinical Medicine, UiT The Arctic University of Norway, Tromsø, Norway*, ⁴*Department of Obstetrics and Gynecology, University Hospital of North Norway, Tromsø, Norway*)

3SAA-3 Statistical Physics Meets AlphaFold: Universal Folding–Function Scaling and Evolutionary Trends
Qianyuan Tang¹, Zecheng Zhang¹, Weitong Ren², Jun Wang³ (¹*Hong Kong Baptist University, HKSAR, China*, ²*Wenzhou Institute, Univ. Chin. Acad. Sci., China*, ³*Nanjing Univ, China*)

3SAA-4 Fluorescence and label-free microscopy to study keratocytes from Atlantic salmon
Deanna Lynn Wolfson, Dhivya B. Thiagarajan, Bilal M. Afzal, Marie Mikkelsen, Azeem Ahmad, Balpreet S. Ahluwalia, Roy A. Dalmo (*UiT The Arctic University of Norway*)

3SAA-5 古代地球における時計タンパク質 KaiC の構造的進化
Structural Evolution of Clock Protein KaiC on Ancient Earth
○古池 美彦 (分子科学研究所)
Yoshihiko Furuike (*Institute for Molecular Science*)

3SAA-6 NANOSPACER: Nanofluidics for single molecule metrology of extracellular vesicles, biomacromolecules and amyloids in solution
Oliver Vanderpoorten (*UiT The Arctic University of Norway*)

おわりに
Closing Remarks

3SBA 生物発光における合成・定量計測・理論計算の融合研究
Bioluminescence Interdisciplinary Collaboration between Experimental and Theoretical Approach
オーガナイザー：樋田 みやび (群馬大学), 山本 典史 (千葉工業大学)
Organizers: Miyabi Hiyaama (Gunma Univ.), Norifumi Yamamoto (Chiba Inst. of Tech.)

09:00~11:30

B 会場 (会議室 103+104) / Room B (Meeting Room 103+104)

Bioluminescence, the emission by a substrate and an enzyme, is extensively utilised for investigation of temporal changes in cell proliferation, observation of drug and cancer cell metastasis pathways, detection of microbial pollution in food hygiene testing, and so on. Because of their usefulness, protein mutants and substrate analogues for different bioluminescence colours have been developed as emission probes. However, the emission mechanism, which can explain the colour change and high quantum yield of wild substrates, remains unknown. To understand the bioluminescence mechanisms, the interdisciplinary collaboration of organic synthesis, quantitative measurements, quantum chemistry calculations, molecular dynamics simulations, and molecular biology is indispensable. In this symposium, we exchange information for the newest results for interdisciplinary collaboration between experimental and theoretical studies of bioluminescence.

はじめに

Opening Remarks

[3SBA-1](#)

生体内深部を観察可能な近赤外 in vivo 光イメージング材料

Innovation of NIR luciferin analogues using firefly bioluminescence for in vivo imaging

Nobuo Kitada^{1,2,3}, Genta Kamiya¹, Jumpei Hatakeyama¹, Ryohei Moriya⁴, Masahiro Kiyama⁵, Satoshi Iwano⁵, Takashi Hirano¹, Shojiro Maki^{1,2,3} (¹*Grad. Sch. Info. Eng., UEC*, ²*Env. Saf. San. Mgmt. Ctr., UEC*, ³*CNBE, UEC*, ⁴*Fac. Sci., Kitasato Univ.*, ⁵*Tenure-Track Prom. Off., Univ. Miyazaki*)

[3SBA-2](#)

ホタル生物発光基質類似体の理論的研究

Theoretical study for firefly bioluminescence substrate analogs

○樋山 みやび (群馬大学)

Miyabi Hiyama (*Gunma University*)

[3SBA-3](#)

発光タンパク質イクオリンの時分割シリアルフェムト秒結晶構造解析

Time-resolved serial femtosecond crystallography of the bioluminescent protein Aequorin

○森口 舞子, 中津 亨 (和医大・薬)

Maiko Moriguchi, Toru Nakatsu (*Fac. Pharm. Sci., Wakayama Med. Univ.*)

[3SBA-4](#)

ハイブリッド QM/MM 自由エネルギー法によるイクオリンの生物発光過程についての理論的研究

Theoretical study on the bioluminescent process of Aequorin by hybrid QM/MM free energy method

○安東 智大¹, 船橋 俊也², 中津 亨³, 林 重彦¹ (¹京大院理, ²京大院薬, ³和医大薬)

Tomohiro Ando¹, Toshiya Funahashi², Toru Nakatsu³, Shigehiko Hayashi¹ (¹*Grad. Sch. of Sci. Kyoto Univ.*, ²*Grad. Sch. of Pharm. Sci. Kyoto Univ.*, ³*Sch. of Pharm. Sci. Wakayama Med. Univ.*)

[3SBA-5](#)

古代のルシフェラーゼを復元する

Resurrecting the ancient luciferase

○大場 裕一 (中部大・応用生物)

Yuichi Oba (*Dept. Env. Biol., Chubu Univ.*)

[3SBA-6](#)

分子シミュレーションで探るホタルの太古の光

Molecular Simulations of the Ancient Glow of Fireflies

○山本 典史 (千葉工業大学)

Norifumi Yamamoto (*Chiba Tech*)

3SBA-7

ホシホウネンエソ発光器に局在する紫色素タンパク質の生化学的解析

Biochemical analysis of the purple pigment protein localized in the light organ of the hatchetfish

○水野 雅玖¹, 矢野 大地², 今井 日奈乃¹, バイティオ ジョゼ^{1,3}, 磯貝 泰弘⁴, 白井 剛⁵,
大場 裕一¹ (¹中部大・応用生物, ²和歌山高専・生物応用化学, ³サンパウロ大学, ⁴富山県立大・
工学・医薬品工学, ⁵長浜バイオ大・バイオサイエンス)

Gaku Mizuno¹, Daichi Yano², Hinano Imai¹, Jose Paitio^{1,3}, Yasuhiro Isogai⁴, Tsuyoshi Shirai⁵,
Yuichi Oba¹ (¹*Col. Biosci. Biotech., Chubu Univ.*, ²*Dep. Apl. Chem. Biochem., Nat. Ins. Tech. Wakayama*
Col., ³*Univ. Sao Paulo*, ⁴*Dep. Pharm. Eng., Toyama Pref. Univ.*, ⁵*Fac. Biosci., Nagahama Ins. Biosci.*
Tech.)

3SBA-8

全電子第一原理 GWF 法の開発

Development of all-electron first-principles GWF method

○野口 良史 (静岡大院・工)

Yoshifumi Noguchi (*Grad. Sch. Eng., Shizuoka Univ.*)

3SBA-9

半導体レーザーを用いたポータブルピコ秒パルス光源と生物物理への応用

Semiconductor laser based portable picosecond pulse light source for biophysics applications

○小林 真隆¹, 柴田 桂成^{1,2}, 中前 秀一¹, 金 昌秀^{1,3}, 伊藤 隆³, 樋山 みやび^{4,5}, 秋山 英文^{1,3} (¹東大
物性研, ²筑波大数理物質系, ³㈱LDseed, ⁴群馬大院理工, ⁵群馬大食健康セ)

Masataka Kobayashi¹, Keisei Shibata^{1,2}, Hidekazu Nakamae¹, Changsu Kim^{1,3}, Takashi Ito³,
Miyabi Hiyama^{4,5}, Hidefumi Akiyama^{1,3} (¹*ISSP, Univ. of Tokyo*, ²*Grad. Sch. Pure and Appl. Sci, Univ. of*
Tsukuba, ³*LDseed Co., Ltd.*, ⁴*Grad. Sch. Sci. Tech., Gunma Univ.*, ⁵*Gunma Univ. Center for Food Science*
and Wellness)

おわりに

Closing Remarks

3SEA

NMR の方法論開発と複雑な生体分子系への応用の新展開

Advances in NMR Methodologies and Applications to Complex Biological Systems/Landscapes

オーガナイザー：石井 佳誉 (東京科学大学), 松木 陽 (大阪大学)

Organizers: Yoshitaka Ishii (Science Tokyo), Yoh Matsuki (Univ. Osaka)

09:00~11:30

E 会場 (会議室 201) / Room E (Meeting Room 201)

This symposium highlights cutting-edge development of NMR technology, including ultra-high-field NMR (e.g., with ¹H frequencies exceeding 1 GHz) and hyperpolarization techniques, which enable the study of challenging biological targets, such as amyloid aggregates, glycolipids, high-molecular-weight proteins, and membrane-bound proteins, for structural biology. The program also highlights modern NMR methods/applications to characterize heterogeneous/complex proteins in motion and biological systems under conditions mimicking cells and tissues. Additionally, the symposium explores the integration of NMR with other complementary methods like cryo-electron microscopy (cryoEM) for structural/functional analyses.

はじめに

Opening Remarks

3SEA-1

Innovations in Sensitivity-Enhanced High-Dimensional Protein Solid-state NMR and Applications to Amyloid Proteins

Yoshitaka Ishii (*Institute of Science Tokyo*)

- [3SEA-2](#) 溶解 DNP-NMR 法を用いた蛋白質の相互作用、構造動態解析法の開発
Development of protein interaction and structural dynamics studies using dissolved DNP and isotope-aided NMR
赤木 謙一, 池之上 達哉, ○宮ノ入 洋平 (阪大・蛋白研)
Ken-ichi Akagi, Tatsuya Ikenoue, **Yohei Miyanoiri** (*Inst. Prot. Res., Univ. Osaka*)
- [3SEA-3](#) 固体 NMR を用いた微生物型ロドプシンの残基特異的な知見
Residue-specific insights on microbial rhodopsins using solid-state NMR
○川村 出 (横浜国大・院理工)
Izuru Kawamura (*Grad. Sch. Eng. Sci, Yokohama Natl. Univ.*)
- [3SEA-4](#) 分子シャペロンを対象とした構造・キネティクス解析
Structural and kinetic insights into molecular chaperones
○齋尾 智英 (徳島大・先端酵素)
Tomohide Saio (*LAMS, Tokushima Univ.*)
- [3SEA-5](#) 大腸菌における内在性糖脂質 MPLase の機能的役割
Functional roles of the endogenous glycolipid MPLase in *Escherichia coli*
○野村 薫 (サントリー生科財団)
Kaoru Nomura (*Suntory Foundation for Life Sciences*)
- [3SEA-6](#) Methods and Instruments for High-Field MAS DNP toward Intracellular Structural Biology
Yoh Matsuki (*Inst. Prot. Res., Univ. Osaka*)
- おわりに
Closing Remarks
-

- 3SFA 学際研究で迫る生物物理的視点からの生命の起源研究
Interdisciplinary investigations into the biophysics of the origins of life
オーガナイザー: Tony Z. Jia (広島大学), 車 兪澈 (海洋研究開発機構)
Organizers: Tony Z. Jia (Hiroshima Univ.), Yutetsu Kuruma (JAMSTEC)

09:00~11:30

F 会場 (会議室 202) / Room F (Meeting Room 202)

The origins of life is an interdisciplinary field requiring collaboration and input from many disparate disciplines, including biophysics, chemistry, geology, and more. Each of these fields approaches the question of the origin of life with a different mindset, using different techniques and analyses. Only by combining ideas and research from multiple fields can we begin to approach answer such difficult questions. In this symposium, we highlight new research which combines biophysics with at least one other discipline to answer significant questions related to the origins and evolution of life both on Earth and elsewhere.

はじめに
Opening Remarks

- [3SFA-1](#) Enzymatic Condensates as self-regulating systems for metabolic efficiency
Paola Laurino^{1,2} (¹Okinawa Inst. of Sci. & Tech. Graduate Univ., ²Institute for Protein Research, Osaka Univ.)

- 3SFA-2** 生命における代謝経路選択と熱力学的制約
Thermodynamic constraints and the choice of metabolic pathways in life
○瀬戸 蘭美¹, 佐々木 里瑩¹, 大岡 英史², 中村 龍平^{2,3} (¹ 奈良女子大学, ² 理化学研究所生体機能触媒研究チーム, ³ 東京科学大学地球生命研究所)
Mayumi Seto¹, Risa Sasaki¹, Hideshi Ooka², Ryuhei Nakamura^{2,3} (¹Nara Women's University, ²Biofunctional Catalyst Research Team, RIKEN Center for Sustainable Resource Science, ³Earth-Life Science Institute (ELSI), Institute of Science Tokyo)
- 3SFA-3** 深海における人工細胞の生存可能性について
The Potential of Artificial Cells Functioning under *In Situ* Deep-Sea Conditions
○車 兪澈, 野牧 秀隆, 磯部 紀之, 松岡 大佑, 嶋根 康弘 (海洋研究開発機構)
Yutetsu Kuruma, Hidetaka Nomaki, Noriyuki Isobe, Daisuke Matsuoka, Yasuhiro Shimane (*Japan Agency for Marine-Earth Science and Technology*)
- 3SFA-4** 貨幣分子間のカップリングにおける熱力学的制約
Thermodynamic constraint on the coupling of currency metabolites
○山岸 純平¹, 畠山 哲央² (¹ 理研・神戸 BDR, ² 科学大・ELSI)
Jumpei Yamagishi¹, Tetsuhiro S. Hatakeyama² (¹BDR, Riken, ²ELSI, Science Tokyo)
- 3SFA-5** 電子が導いた生命の起源と生物最古の枝分かれ
Electrons and the origin of three divisions of life
○延 優 (海洋研究開発機構・超先鋭)
Masaru Konishi Nobu (*JAMSTEC*)
- 3SFA-6** 超臨界 CO₂ による脱水反応を介した前生物的な核酸合成
Supercritical CO₂ promotes prebiotic nucleotide synthesis via dehydration condensation
○藤島 皓介¹, 田川 翔大朗², 森野 航平³ (¹ 東京科学大学 地球生命研究所, ² 海洋研究開発機構 超先鋭研究開発プログラム, ³ 東京科学大学 生命理工学院)
Kosuke Fujishima¹, Shotaro Tagawa², Kohei Morino³ (¹Earth-Life Science Institute, Science Tokyo, ²Institute for Extra-cutting-edge Science and Technology Avant-garde Research Japan Agency for Marine-Earth Science and Technology, ³School of Life Science and Technology, Science Tokyo)

3SGA 計測科学 x 情報科学が切り開く生物学の地平線
Integrating Measurement and Information Science: Unlocking New Frontiers in Biology

共催 JST CREST 「革新的計測解析」

オーガナイザー：小松崎 民樹 (北海道大学)
Organizers: Tamiki Komatsuzaki (Hokkaido Univ.)

09:00~11:30

G 会場 (会議室 203) / Room G (Meeting Room 203)

Cutting-edge research, like AlphaFold, highlights the transformative role of information science in life sciences. The integration of measurement and information science is redefining how we approach data acquisition. Traditionally, efforts have focused on optimizing experimental conditions beforehand or analyzing data post-measurement. However, reinforcement learning now enables real-time optimization during measurements, drastically accelerating processes while maintaining mathematical accuracy. This symposium brings together experts from diverse fields, including biophysics and information science, to explore the forefront of measurement informatics in biology. Join us to discover how this interdisciplinary collaboration is reshaping the future of biological research and innovation.

はじめに

Opening Remarks

[3SGA-1](#)

計測インフォマティクスの発展と展開 ―情報計測から革新的計測解析へ―

Development and Evolution of Measurement Informatics - From Intelligent Measurement Analysis to Innovative Measurement and Analysis -

○鷲尾 隆（関西大学ビジネスデータサイエンス学部）

Takashi Washio (*Faculty of Business Data Science, Kansai University*)

[3SGA-2](#)

血小板生物学 x 人工知能

Intelligent platelet biology

○合田 圭介^{1,2,3,4} (¹ 東京大学大学院理学系研究科化学専攻, ² カリフォルニア大学ロサンゼルス校工学部生体工学科, ³ 武漢大学工業科学研究院, ⁴ 東北大学国際放射光イノベーション・スマート研究センター)

Keisuke Goda^{1,2,3,4} (¹*Department of Chemistry, University of Tokyo*, ²*Department of Bioengineering, University of California, Los Angeles*, ³*Institute of Technological Sciences, Wuhan University*, ⁴*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*)

[3SGA-3](#)

Theoretical Perspectives on the Hidden Structures in Biological Systems

Ayaka Sakata^{1,2} (¹*Dept. Infor. Sci. Ochanomizu Univ.*, ²*RIKEN AIP*)

[3SGA-4](#)

2 細胞計測技術を用いた免疫細胞とがん細胞の 1 細胞相互作用解析

Single-cell analysis of interactions between immune cells and cancer cells using dual-cell measurement technology

○山口 哲志（大阪大学産業科学研究所）

Satoshi Yamaguchi (*SANKEN, Univ. of Osaka*)

[3SGA-5](#)

電圧マトリックスを用いたナノボア測定によるタンパク質混合物の識別

Voltage-Matrix Nanopore Profiling for the Discrimination of Protein Mixtures

Sotaro Uemura¹, Ryo Akita¹, Lysenko Artem¹, Keith Boroevich¹, Tatsuya Yokota², Daiki Kawai¹, Ryo Iizuka¹, Tatsuhiko Tsunoda¹ (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Dep. Comp. Sci, Nagoya Inst. Tech*)

[3SGA-6](#)

多階層マルチオミックスデータの統合理解に向けた挑戦：ラマンスペクトルとトランスクリプトームを用いたケーススタディ

Toward a Cross-Layer Understanding through Biological Multimodal Data: A Case Study Using Raman Spectroscopy and Transcriptomes

○渡邊 朋信^{1,2} (¹ 理化学研究所生命機能科学研究センター, ² 広島大学原爆放射線医科学研究所)

Tomonobu M Watanabe^{1,2} (¹*RIKEN BDR*, ²*RIRBM, Hiroshima University*)

[3SGA-7](#)

計測介入型 AI が拓く生物学の展開

Unveiling New Frontiers in Biology with Measurement-Intervening AI

○小松崎 民樹（北大・電子研、化学反応創成拠点）

Tamiki Komatsuzaki (*RIES, WPI-ICReDD, Hokkaido Univ.*)

3SHA 生命の高次元システムを予測と検証により合理的に理解する
Understanding the high-dimensional biological systems rationally through prediction and verification

共催 JST CREST 「予測数学基盤」

オーガナイザー：望月 敦史（京都大学），今吉 格（京都大学）

Organizers: Atsushi Mochizuki (Kyoto Univ.), Itaru Imayoshi (Kyoto Univ.)

09:00~11:30

H 会場（会議室 204）／Room H（Meeting Room 204）

It is thought that biological phenomena such as cell differentiation, homeostasis or intelligence arise from the dynamics of high-dimensional systems consisting of the interactions of numerous biomolecules. In recent years, there has been rapid development in three areas: 1) measurement technology that can capture the dynamics of multiple variables with sufficient time and spatial resolution, 2) information science and theoretical science that can not only interpret dynamics but also provide predictions and experimental guidelines, and 3) technology for dynamically manipulating biomolecules to provide feedback between measurement and prediction. In this symposium, we will invite researchers who have developed these new technologies and have achieved elucidation of the dynamics of high-dimensional biological systems to give presentations and hold discussions. We hope that this symposium will lead to increased interaction between different methods and open up new avenues for systems biology.

はじめに

Opening Remarks

[3SHA-1](#) 光遺伝学的手法を用いた神経幹細胞の新規転写制御メカニズムの同定
Uncovering Novel Transcriptional Regulatory Mechanisms of Neural Stem Cells Using Optogenetic Approaches

○今吉 格^{1,2} (¹京大・院生命科学, ²京大・医研)

Itaru Imayoshi^{1,2} (¹Grad. Sch. Biostudies., Univ. Kyoto, ²LiMe., Univ. Kyoto)

[3SHA-2](#) Nano-electrokinetics が隠れた転写動態と単一細胞の確率的挙動を結びつける
Nano-Electrokinetics Links Hidden Transcriptomic Dynamics to Stochastic Single-Cell Behavior

○新宅 博文^{1,2}, 塩見 晃史^{1,2}, 金子 泰洸^{1,2}, 峯岸 美紗^{1,2}, 鳥井 孝太郎^{1,2}, 土田 新² (¹京大・医研, ²理研・開拓)

Hirofumi Shintaku^{1,2}, Akifumi Shiomi^{1,2}, Taikopaul Kaneko^{1,2}, Misa Minegishi^{1,2}, Kotaro Torii^{1,2}, Arata Tsuchida² (¹LiMe, Kyoto University, ²CPR, RIKEN)

[3SHA-3](#) De co de, predict, and control biological systems through single-cell omics and modelling approaches

Kenji Kamimoto^{1,2,3} (¹Research Institute for Microbial Diseases, The University of Osaka, ²Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka,

³Bioinformatics Center, The University of Osaka)

[3SHA-4](#) 高速・広視野 Ca²⁺イメージングが明らかにする大脳皮質の機能的ネットワーク構造
High-speed, Large-FOV Ca²⁺ Imaging Reveals Functional Cortical Network Architecture

○村山 正宜（理化学研究所 脳神経科学研究センター）

Masanori Murayama (RIKEN Center for Brain Science)

3SHA-5

ネットワークボロロジーに由来する生命機能と機能単位

Biological functions and functional modules originated in the topology of chemical reaction networks

○望月 敦史¹, 山内 悠平¹, 杉山 博紀², 後藤 祐平^{3,4}, 青木 一洋^{3,4,5} (¹京都市大・医研, ²東京大・院工学, ³京都大・院生命科学, ⁴自然科学研究機構・基礎生物学研究所, ⁵自然科学研究機構・生命創成探究センター)

Atsushi Mochizuki¹, Yuhei Yamauchi¹, Hironori Sugiyama², Yuhei Goto^{3,4}, Kazuhiro Aoki^{3,4,5} (¹LiMe, Kyoto Univ., ²Sch. Eng., Univ. Tokyo, ³Grad. Sch. Biostudies, Kyoto Univ., ⁴NIBB, NINS, ⁵ExCELLS, NINS)

おわりに

Closing Remarks

3SIA 人工細胞膜をつくる・つかう分子テクノロジー

Molecular technologies for creating and utilizing artificial cell membranes

オーガナイザー：安原 主馬（奈良先端科学技術大学院大学），森垣 憲一（神戸大学）

Organizers: Kazuma Yasuhara (NAIST), Kenichi Morigaki (Kobe Univ.)

09:00～11:30

I 会場（会議室 205）／Room I（Meeting Room 205）

The cell membrane performs complex functions through the supramolecular assembly of lipids and membrane proteins. Despite significant advances in molecular biology, complete understanding of the intricate design principles remains a challenge. Efforts to construct artificial cell membranes by the hybridization of synthetic and natural molecules provide a reconstructive approach to unravel the functional design principles. This symposium will explore cutting-edge molecular technologies, such as the creation of artificial membranes and membrane protein mimicking molecules, aiming to replicate the complex structures and functions observed in the natural cell membranes.

はじめに

Opening Remarks

3SIA-1

合成両親媒性高分子で膜活性ペプチドを真似る

Mimicking Membrane-Active Peptides with Synthetic Amphiphilic Polymers

○安原 主馬^{1,2,3,4} (¹奈良先端大院物質, ²奈良先端大院デジタルグリーンイノベーションセンター, ³奈良先端大院データ駆動型サイエンス創造センター, ⁴奈良先端大院メディルクス研究センター)

Kazuma Yasuhara^{1,2,3,4} (¹Div. Mat. Sci., Grad. Sch. Sci. Tech., Nara Inst. Sci. Tech., ²Ctr. Digital Green-innovation, Nara Inst. Sci. Tech., ³Data Sci. Ctr., Nara Inst. Sci. Tech., ⁴Medilux Res. Ctr., Nara Inst. Sci. Tech.)

3SIA-2

ペプチドと脂質がもたらす膜相分離型ハイブリッド細胞膜とその応用

Peptide-Lipid Hybrid Vesicle with Phase-Separated Domains

○上田 一樹^{1,2} (¹都立大院 環境応用化学, ²理研 CSRS)

Motoki Ueda^{1,2} (¹Dept. Appl. Chem., Tokyo Metropolitan Univ., ²RIKEN CSRS)

3SIA-3

次世代分子ロボティクスのための脂質膜通型 DNA デバイス

Lipid Membrane-Translocating DNA Devices for Next-Generation Molecular Robotics

○野村 慎一郎（東北大院工・ロボ）

Shin-ichiro M. Nomura (Dept. Robotics, Grad. Sch. Eng., Tohoku Univ.)

- [3SIA-4](#) 触媒システムの構築に向けた赤血球ゴースト-金属化合物ハイブリッドの設計
Design of red blood cell ghost-metal compound hybrids for construction of catalytic systems
○越山 友美 (立命館大 生命科学)
Tomomi Koshiyama (*Coll. Life Sci., Ritsumeikan Univ.*)
- [3SIA-5](#) 人工膜と蛍光 1 分子観察を用いた、膜分子の機能解析
Combining an artificial membrane and a single-molecule imaging technique to investigate the function of membrane protein
○笠井 倫志 (国立がん研究センター研究所)
Rinshi Kasai (*Natl. Cancer Ctr. Res. Inst.*)
- [3SIA-6](#) 人工生体膜分子およびドメインの光操作
Optical Manipulation of Molecules and Domains in Biological Membranes Models
○谷本 泰士, 森山 俊哉, 増井 恭子, 細川 千絵 (阪公大・院理)
Yasushi Tanimoto, Shunya Moriyama, Kyoko Masui, Chie Hosokawa (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)
- [3SIA-7](#) ペプチドナノディスクを用いたパターン化人工膜への膜タンパク質導入技術の開発
Reconstitution of membrane proteins in a micro-patterned model membrane using peptide nanodisc
○森垣 憲一^{1,2}, 小松 愛華², 肥塚 雅人², 杭田 美子², 谷本 泰士^{1,4}, 林 文夫³ (¹神戸大・バイオシグナル, ²神戸大・院農学, ³神戸大・院理学, ⁴大阪公立大・院理学)
Kenichi Morigaki^{1,2}, Aika Komatsu², Masato Koezuka², Fuko Kueda², Yasushi Tanimoto^{1,4}, Fumio Hayashi³ (¹Biosignal, Kobe Univ., ²Grad. Sch. Agri. Sci., Kobe Univ., ³Grad. Sch. Sci., Kobe Univ., ⁴Grad. Sch. Sci., Osaka Metropol. Univ.)

おわりに

Closing Remarks

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- 3SJA 時間タンパク質学: 生命現象の時間をタンパク質から理解する
Chronoproteoinology: protein-driven understanding of biological time

共催 学術変革領域研究 (A) 「時間タンパク質学」

オーガナイザー: 大出 晃士 (東京大学), 原田 慶恵 (大阪大学)

Organizers: Koji Ode (The Univ. of Tokyo), Yoshie Harada (The Univ. of Osaka)

09:00~11:30

J 会場 (会議室 206) / Room J (Meeting Room 206)

Neuronal firing, circadian clocks, and circa-annual rhythms—life's phenomena span a vast range of time scales. “Chronoproteoinology”, launched at 2024 as a KAKENHI Transformative Research Areas, seeks to understand how the biochemical and biophysical properties of specific proteins generate the distinct time information characteristic of each biological process. In this symposium, we will introduce ongoing efforts to elucidate the time scales—from minutes to years—and the protein properties that underlie them.

はじめに
Opening Remarks

- [3SJA-1](#) 開花まで 120 年：タケにおける超長周期タイマーへの挑戦
120 years for flowering: Challenge to the ultra-long timer in bamboo
○村中 智明¹, 高橋 望², 遠藤 求², 久本 洋子³ (¹名古屋大・院生命農学, ²奈良先端大, ³東京大・院農学生命)
Tomoaki Muranaka¹, Nozomu Takahashi², Motomu Endo², Yoko Hisamoto³ (¹*Grad. Sch. Bio. Agri., Naoyga Univ.*, ²*Grad. Sch. Sci. Tech., NAIST*, ³*Grad. Sch. Agri., Univ. of Tokyo*)
- [3SJA-2](#) 緑藻における転写非依存的な概日時計
Transcription-Independent Circadian Rhythms in Green Algae
○松尾 拓哉 (北里大学 理学部 生物科学科 分子生物学講座)
Takuya Matsuo (*Laboratory of Molecular Biology, Department of Biosciences, School of Science, Kitasato University*)
- [3SJA-3](#) Exploring the molecular origin of self-sustained circadian oscillator through clock protein evolution
Atsushi Mukaiyama (*Dept. of Biosci. and Biotech., Fukui Pref. Univ.*)
- [3SJA-4](#) シアノバクテリアの試験管内概日リズムに反応液の pH が与える影響
Effect of pH on the cyanobacterial circadian oscillator in vitro
○三輪 (伊藤) 久美子^{1,2}, 尾上 靖宏³, 近藤 孝男^{1,2}, 寺内 一姫³ (¹名古屋大・院理, ²名古屋大・高等研究院, ³立命館大・生命科学)
Kumiko Ito-Miwa^{1,2}, Yasuhiro Onoue³, Takao Kondo^{1,2}, Kazuki Terauchi³ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*IAR, Nagoya Univ.*, ³*Ritsumeikan Univ.*)
- [3SJA-5](#) 概日リズムの温度補償および同期化に関わる波形歪み
Waveform distortion for temperature compensation and synchronization in circadian rhythms
Shingo Gibo^{1,3}, Teiji Kunihiro², Tetsuo Hatsuda¹, **Gen Kurosawa**¹ (¹*RIKEN iTHEMS*, ²*Yukawa Institute for Theoretical Physics, Kyoto University*, ³*Institute for Basic Science*)
- [3SJA-6](#) 細胞内在性発熱による温度シグナリング機構
A thermal signaling mechanism driven by intracellular endogenous heat generation
中馬 俊祐¹, 原田 慶恵², 岡部 弘基¹ (¹東大・院薬, ²阪大・ヒューマン・メタバース疾患研究拠点)
Shunsuke Chuma¹, Yoshie Harada², **Kohki Okabe**¹ (¹*Graduate School of Pharmaceutical Sciences, The University of Tokyo*, ²*PRiME, The University of Osaka*)
- [3SJA-7](#) 反復刺激による神経オルガノイド回路組織の再編と機能性獲得
Repetitive Input Drives Network Refinement and Stimulus-Specific Output in Connected Neural Organoids
Yoshiho Ikeuchi^{1,2} (¹*Institute of Industrial Science, The University of Tokyo*, ²*Institute for AI and Beyond, The University of Tokyo*)

1日目 (9月24日(水)) / Day 1 (Sep. 24 Wed.)

1MSF ベシクルダイナミクスの最前線：先端イメージング、AI、メディカル応用
Unlocking Vesicle Dynamics: Advanced Imaging, AI, and Biomedical Applications

オーガナイザー：Seohyun Lee (東京大学)、樋口 秀男 (東北大学)

Organizers: Seohyun Lee (The Univ. of Tokyo), Hideo Higuchi (Tohoku Univ.)

18:50~20:30

F会場 (会議室 202) / Room F (Meeting Room 202)

This symposium introduces advanced analytical methods and imaging techniques to explore vesicle dynamics and their broad implications in biology and disease. Topics include cutting-edge approaches to vesicle transport analysis using advanced imaging techniques and artificial intelligence, comprehensive studies on microbial vesicles with potential applications in vaccine development, and pioneering efforts to understand molecular machinery through exosome engineering as well as synthetic vesicle membrane research. Notably, the symposium will highlight MINFLUX, a revolutionary super-resolution imaging technique recently published in *Science*, which enables nanometer-scale insights into molecular mechanisms within live cells. By integrating diverse biophysical perspectives with the latest techniques, this session seeks to enhance our understanding of vesicle dynamics and their implications in the biomedical field.

[1MSF-1](#) AI 技術を活用した生細胞内小胞輸送の理解に向けて
AI-Powered Characterization of Vesicle Transport in Live-Cell Systems

○イ ソヒョン (東京大学)

Seohyun Lee (*The University of Tokyo*)

[1MSF-2](#) High-precision tracking of kinesin-1 stepping inside cells using single- and dual-color MINFLUX nanoscopy

Takahiro Deguchi¹, Tobias Engelhardt², Nikolay Sergeev³, Malina Iwanski⁴, Roman Schmidt²,

Christopher Heidebrecht⁵, Savannah Cattarius⁵, Lukas Kapitein⁴, Timo Zimmermann¹, Jonas Ries³

(¹*European Molecular Biology Laboratory*, ²*Abberior Instruments GmbH*, ³*Max Perutz Labs, University of Vienna*, ⁴*Utrecht University*, ⁵*University of Heidelberg*)

[1MSF-3](#) Structural analysis and advanced live imaging reveal vesicle dynamics of SID1-mediated uptake of large dsRNA molecules

Akira Takai^{1,2}, Kaoru Kumazaki³, Toshikuni Awazu^{2,4}, Taketoshi Kambara², Shunya Murakoshi³,

Takafumi Kato⁵, Masahiro Hiraizumi⁶, Yoshiaki Kise³, Tsukasa Kusakizako³, Tomohiro Nishizawa⁷,

Yasushi Okada^{1,2,4,8,9,10}, Osamu Nureki³ (¹*Grad. Sch. Med., Univ. Tokyo*, ²*BDR, RIKEN*, ³*Dept. Bio. Sci., Grad. Sch. Sci., Univ. Tokyo*, ⁴*Grad. Sch. Front. Biosci., Osaka Univ.*, ⁵*Dept. Biochem., Univ. Oxford*,

⁶*Grad. Sch. Eng., Univ. Tokyo*, ⁷*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, ⁸*Dept. Phys., Grad. Sch. Sci., Univ. Tokyo*, ⁹*UBI, Grad. Sch. Sci., Univ. Tokyo*, ¹⁰*WPI-IRCn, IAS, Univ. Tokyo*)

[1MSF-4](#) Bacterial Membrane Vesicles: Biology, Functions, and Medical Applications

Ryoma Nakao, Takehiro Yamaguchi, Kimihiro Abe, Yukihiro Akeda (*Dept Bacteriol. I, Natl. Inst. Infect. Dis., JIHS*)

[1MSF-5](#) Creation of biological phenomena using asymmetric vesicles

Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

1MSG 若手の会が紡いだ生物物理学のフロンティア
Frontiers in Biophysics Spun by the Society of Young Scientists

オーガナイザー：柴垣 光希（北海道大学），藤井 真子（神戸大学）

Organizers: Mitsuki Shibagaki (Hokkaido Univ.), Masako Fujii (Kobe Univ.)

18:50~20:30

G 会場（会議室 203）／Room G（Meeting Room 203）

The Society of Young Scientists has played an important role in training future generations in scientific research. In biophysics, the Society of Young Scientists in Biophysics started its activities before the foundation of the Biophysical Society of Japan and has produced many prominent researchers. This symposium aims to present the latest development of the Society of Young Scientists in Biophysics and the state-of-the-art science of young researchers who have been involved in the recent advances of this Society.

はじめに

Opening Remarks

[1MSG-1](#) 凝集傾向のある抗菌ペプチドの溶解化戦略およびその多様な多量体化特性の評価
Solubilization strategy of aggregation-prone antimicrobial peptides and evaluation of their diverse multimerization properties

Mitsuki Shibagaki, Jeremia Oktavian Chrisnanto, Kosuke Maeda, Tatsuya Arai, Dessalegn Abeje Tefera, Hiroyuki Kumeta, Fumi Hirai, Tomoyasu Aizawa (*Grad. Sch. Life Sci., Hokkaido Univ.*)

[1MSG-2](#) 分光研究から見てきたウイルスヘリオロドプシンの多様性
Diversity of Viral Heliorhodopsins Uncovered through Spectroscopic Analysis

○水鳥 律（名工大・院工）

Ritsu Mizutori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

[1MSG-3](#) 細菌アクチンの微小管化

Microtubulation of the bacterial actin

○高橋 大地^{1,2}, 沼本 修孝¹, 宮田 真人^{2,3}, 沈 建仁^{1,4}, Robert C. Robinson^{1,5} (¹ 岡山大・異分野基礎, ² 大阪公大・院理, ³ 大阪公大・複合先端, ⁴ 岡山大・環境生命自然科学, ⁵ ウィタヤシリメティ技大・生物工学)

Daichi Takahashi^{1,2}, Nobutaka Numoto¹, Makoto Miyata^{2,3}, Jian-Ren Shen^{1,4}, Robert C. Robinson^{1,5} (¹RIIS, Okayama Univ., ²Grad. Sch. Sci., Osaka Met. Univ., ³OCARINA, Osaka Met. Univ., ⁴Grad. Sch. Environ. Life. Nat. Sci. Tech., Okayama Univ., ⁵Sch. Biol. Sci. Eng., Vidyasirimedhi Inst. Sci. Tech.)

[1MSG-4](#) 葉緑体 ATP 合成酵素に特有の部位によるレドックス制御機構
Mechanism of redox regulation by region specific to chloroplast F₀F₁-ATP synthase

○秋山 健太郎¹, 若林 憲一², 久堀 徹³ (¹ 産業技術総合研究所, ² 京都産業大学, ³ 総合研究大学院大学)

Kentaro Akiyama¹, Ken-ichi Wakabayashi², Toru Hisabori³ (¹The National Institute of Advanced Industrial Science and Technology, ²Kyoto Sangyo University, ³The Graduate University for Advanced Studies)

[1MSG-5](#) 構造解析および反応速度論を用いたアセト酢酸脱炭酸酵素 AAD の触媒機構の解明
Structural and kinetic insights into the catalytic mechanism of acetoacetate decarboxylase AAD

○石坂 優人^{1,2}, Rindfleisch Sören^{1,2}, Auer Florian^{1,2}, Gingeleit Lukas^{1,2}, 鄭 達翔³, Bielecki Michael⁴, Rabe von Pappenheim Fabian^{1,2}, Penka Elke^{1,2}, Kluger Ronald⁴, 坂田 絵理³, Tittmann Kai^{1,2} (¹ ゲッティンゲン大・分子酵素学, ² MPI・複合科学, ³ ゲッティンゲン大・聴覚神経科学, ⁴ トロント大・化学)

Masato Ishizaka^{1,2}, Sören Rindfleisch^{1,2}, Florian Auer^{1,2}, Lukas Gingeleit^{1,2}, Tat Cheung Cheng³, Michael Bielecki⁴, Fabian Rabe von Pappenheim^{1,2}, Elke Penka^{1,2}, Ronald Kluger⁴, Eri Sakata³, Kai Tittmann^{1,2} (¹Dept. Mol. Enzymol., Univ. Göttingen, ²Multidisciplinary Sci., MPI, ³Inst. Auditory Neurosci., Univ. Med. Center Göttingen, ⁴Dept. Chem., Univ. Toronto)

- [1MSG-6](#) 古細菌 SMC 複合体は DNA セグメント捕捉機構によって DNA 上を一方方向にトランスロケーションする
DNA Segment Capture Drives Unidirectional DNA Translocation of a Prokaryotic SMC Complex: A Multiscale Simulation Study
○山内 仁喬, プランダーニ ジョバンニ, 寺川 剛, 高田 彰二 (京都大学・理学)
Masataka Yamauchi, Giovanni Brandani, Tsuyoshi Terakawa, Shoji Takada (*Dept. of Biophys., Kyoto Univ.*)
- [1MSG-7](#) データベース探索とドッキングシミュレーションを活用した, 中鎖アルカン合成酵素の創出と機能解析
Creation of the medium-chain alkane producing enzyme by using the enzyme database search and the docking simulation
○工藤 恒, 近藤 昭彦, 蓮沼 誠久 (神戸大・先端バイオ)
Hisashi Kudo, Akihiko Kondo, Tomohisa Hasunuma (*Engineering Biology Research Center., Kobe Univ.*)
- おわりに
Closing Remarks

1MSH 日本のタンパク質水素可視化最近の動き
Recent developments in protein hydrogen visualization in Japan

オーガナイザー: 田中 伊知朗 (茨城大学), 栗原 和夫 (QST)
Organizers: Ichiro Tanaka (Ibaraki Univ.), Kazuo Kurihara (QST)

18:50~20:30

H 会場 (会議室 204) / Room H (Meeting Room 204)

Determining the positions of hydrogen atoms in biomolecules is an essential theme in life science. A groundbreaking neutron detector developed in Japan about 30 years ago has spread to research reactors around the world and has been of great help in determining hydrogen positions. Nowadays, neutron analysis technology is steadily improving thanks to the next generation of accelerator-based neutron sources in Japan and US. On the other hand, cryo-EM has also been attracting attention for its ability to obtain hydrogen position information, and we are now in an era where AI can predict the structure of biomolecules one after another. In addition to classical neutrons, we will consider future directions, including recent efforts to visualize hydrogen position information.

[1MSH-1](#) 導入と中性子回折装置を中心とした世界的現状
Introduction and current status of neutron diffractometers worldwide
○田中 伊知朗 (茨城大学)

Ichiro Tanaka (*Ibaraki University*)

[1MSH-2](#) TOF 型単結晶中性子回折装置 iBIX の現状と将来計画
Current status and future prospects for TOF type single crystal neutron diffractometer iBIX
Katsuhiko Kusaka, Terutoshi Sakakura, Haruki Sugiyama (*NIAPC, CROSS*)

[1MSH-3](#) Measurement of hydrogen properties using cryo-EM and ED
Koji Yonekura^{1,2} (¹*RIKEN SPring-8*, ²*IMRAM, Tohoku University*)

[1MSH-4](#) 中性子 D/H コントラスト結晶解析による鶏卵白リゾチームの水和構造の研究
Neutron D/H contrast crystallographic study of hydration structure of hen-egg-white lysozyme
○茶竹 俊行¹, 角南 智子², 藤原 悟², 田中 伊知朗³, 日下 勝弘⁴ (¹京大・複合研, ²QST, ³茨大・院理工, ⁴CROSS)
Toshiyuki Chatake¹, Tomoko Sunami², Satoru Fujiwara², Ichiro Tanaka³, Katsuhiko Kusaka⁴ (¹*KURNS*, ²*QST*, ³*Grad. Sch. Sci. Eng., Ibaraki Univ.*, ⁴*CROSS*)

- [1MSH-5](#) タンパク質の主鎖のやわらかさをデザインする。-中性子と ^{15}N NMR が示唆する主鎖ペプチド結合の部位特異的緩和の原理とその利用-
Designing main-chain flexibility of proteins. Principle of site-specific relaxation of peptide bonds and an application in protein design
○千葉 かおり (茨城高専)
Kaori Chiba (*National Institute of Technology, Ibaraki College*)
- [1MSH-6](#) 単色法を用いたタンパク質用中性子回折装置の日本における現状と将来
Monochromatic Neutron Diffractometers for Protein Crystallography at Present and in the Future in Japan
○栗原 和男¹, 河野 史明¹, 清水 瑠美¹, 田村 格良², 大原 高志³, 茶竹 俊行⁴, 井上 倫太郎⁴, 平野 優^{1,5}, 玉田 太郎^{1,5} (¹QST・量生研, ²原子力機構・新試験研究炉, ³原子力機構・J-PARC セ, ⁴京大・複合研, ⁵千葉大・cQUEST)
Kazuo Kurihara¹, Fumiaki Kono¹, Rumi Shimizu¹, Itaru Tamura², Takashi Ohhara³, Toshiyuki Chatake⁴, Rintaro Inoue⁴, Yu Hirano^{1,5}, Taro Tamada^{1,5} (¹*iQLS, QST*, ²*New Res. Reactor Promo. Office, JAEA*, ³*J-PARC Center, JAEA*, ⁴*KURNS, Kyoto Univ.*, ⁵*cQUEST, Chiba Univ.*)

1MSI タンパク質デザインへの誘い
Invitation to Protein Design

オーガナイザー：小杉 貴洋 (分子科学研究所), 新津 藍 (理化学研究所)
Organizers: Takahiro Kosugi (IMS), Ai Niitsu (RIKEN)

18:50~20:30

I 会場 (会議室 205) / Room I (Meeting Room 205)

The field of protein design has been honored with the 2024 Nobel Prize in Chemistry, highlighting its transformative potential and the promising future. Now, the technology is expected to be of interest to many researchers and to be applied across a broad range of research fields. In this symposium, talented early-career researchers introduce their cutting-edge technologies, the latest advancements, and forthcoming challenges in protein design and its applied fields. We aim to provide useful information for researchers in diverse fields, enabling them to incorporate protein design technologies into their own research. Furthermore, we hope this symposium serves as a catalyst for innovations and increased excitement in protein design.

はじめに

Opening Remarks

- [1MSI-1](#) AI が導くバイオ分子デザイン：タンパク質と、その先へ
AI-guided biomolecule design: protein and beyond
○齋藤 裕 (北里大学・未来工)

Yutaka Saito (*Dept. Front. Eng., Kitasato Univ.*)

- [1MSI-2](#) 進化的アルゴリズムとネットワーク理論を融合した酵素リデザイン法の開発
Development of enzyme redesign strategy combining evolutionary algorithm and network theory
○中野 祥吾 (静岡県大・食栄)

Shogo Nakano (*Grad. Div. Nut. Sci., Univ. Shizuoka*)

- [1MSI-3](#) Molecular Programming Using De Novo Designed Proteins

Zibo Chen (*School of Life Sciences, Westlake University*)

- [1MSI-4](#) A Rapid and Universal Pipeline for GPCR Structure Determination through In Silico Construct Optimization and de novo Protein Design

Hideaki Kato (*The University of Tokyo*)

おわりに

Closing Remarks

1MSJ ゲノム構造の原理を紐解く：理論と実験の融合

Elucidating the Principles of Genome Organization: Bringing Together Theory and Experiments

オーガナイザー：Giovanni Brandani (京都大学), 河野 秀俊 (QST)

Organizers: Giovanni Brandani (Kyoto Univ.), Hidetoshi Kono (QST)

18:50~20:30

J 会場 (会議室 206) / Room J (Meeting Room 206)

Functional genome organization emerges from a complex interplay of structural and dynamic factors across multiple scales. This symposium will bring together experimentalists and theoreticians to discuss key aspects of genome organization, including the action of SMC complexes, chromatin structure and dynamics, and 3D genome compartmentalization. By fostering interactions between theory and experiments, we aim to stimulate new insights, where experimental observations inspire theoretical models and computational predictions guide new experiments. This symposium includes contributions from diverse perspectives to advance our understanding of genome organization and create a dynamic exchange of ideas within this rapidly evolving field.

はじめに

Opening Remarks

[1MSJ-1](#) 生きたヒト細胞内の分裂期染色体の化学的・物理的性質

Chemical and physical properties of human mitotic chromosomes in living cells

○日比野 佳代 (阪大・蛋白研)

Kayo Hibino (*Inst. Protein Res., Univ. Osaka*)

[1MSJ-2](#) DNA 複製動態から染色体の振る舞いを明らかにする

Deciphering the behavior of chromosomes through DNA replication dynamics

○平谷 伊智朗 (理化学研究所 生命機能科学研究センター)

Ichiro Hiratani (*RIKEN Center for Biosystems Dynamics Research*)

[1MSJ-3](#) ヒトゲノムのデータ駆動のアノテーションを目指した大規模立体構造比較解析

Large-scale comparative analysis of the 3D genome structure for data-driven annotation of the human genome

○中戸 隆一郎 (東京大学定量生命科学研究所)

Ryuichiro Nakato (*Institute for Quantitative Biosciences, the University of Tokyo*)

[1MSJ-4](#) Enhanced A/B Compartment Assignment: Improved Consistency, Orientation, and Resolution with HiC-SCA

○ジャスティン チャン スオン¹, 河野 秀俊^{1,2} (¹QST, ²千葉大学)

Justin Chan¹, Hidetoshi Kono^{1,2} (¹iQLS, QST, ²Center of Quantum Life Science for Structural Therapeutics (cQUEST), Chiba University)

[1MSJ-5](#) コヒーシンスラブユニット Scc1 ヘリックス領域の構造機能解析

Structural and Functional Analysis of Conserved Helical Regions in the Cohesin Subunit Scc1

○木下 慶美, 西山 朋子 (京都大・院生物)

Yoshimi Kinoshita, Tomoko Nishiyama (*Grad. Sch. Sci., Kyoto University*)

[1MSJ-6](#) Phase diagram approach to elucidate the organization principle of mitotic chromosome

Tetsuya Yamamoto (*ICReDD, Hokkaido Univ.*)

[1MSJ-7](#) クロマチンドメインの生物種間サイズ分布を説明する普遍的な理論

A universal theory describes chromatin domain size distributions across species

○藤城 新 (京大・福井謙一)

Shin Fujishiro (*FIFC, Kyoto Univ.*)

おわりに

Closing Remarks

1日目（9月24日（水））／Day 1 (Sep. 24 Wed.)

1GA タンパク質：構造，機能
Protein: Structure, Function

座長：菅瀬 謙治（京都大学），加藤 英明（東京大学）

Session Chairs: Kenji Sugase (Kyoto Univ.), Hideaki Kato (Univ. Tokyo)

15:10~18:25

A会場（会議室 101+102）／Room A (Meeting Room 101+102)

- [1GA001](#) 赤痢アメーバ由来 adenosine 5'-phosphosulfate kinase の構造解析
Structural analysis of adenosine 5'-phosphosulfate kinase from *Entamoeba histolytica*
○畑中 涼¹, 湯浅 日菜¹, 見市 文香², 岸川 淳一¹, 志波 智生¹ (¹京都工芸繊維大学大学院 工芸科学研究科 応用生物学専攻, ²長崎大学 熱帯医学研究所)
Ryo Hatanaka¹, Hina Yuasa¹, Fumika Mi-ichi², Jyun-ichi Kishikawa¹, Tomoo Shiba¹ (¹Fac. Applied Biol., Kyoto Inst. Tech., ²Inst. Tropical Medicine, Nagasaki University.)
- [1GA002](#) ペプチド結合の平面性の歪みを用いたタンパク質の原子座標データの一次スクリーニング
Primary screening of structural data obtained by electron microscopy using planar distortion of peptide bonds
○國井 真帆¹, 茶竹 俊行², 大原 高志³, 千葉 かおり¹ (¹茨城高専, ²京大 複合研, ³原科研 J-PARC センター)
Mahan Kunii¹, Toshiyuki Chatake², Takashi Ohhara³, Kaori Chiba¹ (¹National Institute of Technology, Ibaraki College, ²KURNS, Kyoto Univ., ³J-PARC, JAEA)
- [1GA003](#) PRMT1 と基質 EWS の複合体構造から考察する基質認識機構
Substrate recognition mechanism considered from the complex structure of PRMT1 with substrate EWS
○遠藤 伸幸¹, 藤間 祥子^{2,3}, 越村 日向子², 川本 晃大¹, 廣瀬 未果¹, 池上 暁子², 葛原 美和², 大徳 浩照^{3,4}, 加香 孝一郎⁵, 加藤 貴之¹, 深水 昭吉^{3,4}, 上久保 裕生², 栗栖 源嗣¹ (¹阪大・蛋白研, ²奈良先端大, ³革新的先端研究開発支援事業, ⁴筑波大・生存ダイナミクス研究センター, ⁵筑波大・生命環境系)
Nobuyuki Endo¹, Sachiko Toma-Fukai^{2,3}, Hinako Koshimura², Akihiro Kawamoto¹, Mika Hirose¹, Akiko Ikegami², Miwa Kuzuhara², Hiroaki Daitoku^{3,4}, Koichiro Kako⁵, Takayuki Kato¹, Akiyoshi Fukamizu^{3,4}, Hironari Kamikubo², Genji Kurisu¹ (¹IPR, Univ. Osaka, ²NAIST, ³AMED-CREST, ⁴TARA, ⁵LES. Univ. Tsukuba)
- [1GA004](#) ダイズ由来メチオニン γ-リアーゼの基質侵入ループ構造による酵素活性への影響
Effects on the enzymatic activity of the loop structures in methionine γ-lyase from *Glycine max*
○森田 宗¹, 牧野 晴菜¹, 井上 幹太¹, 横山 大輝², 大川 敦司², 手嶋 琢³, 岸川 淳一¹, 松井 健二³, 稲垣 賢二², 志波 智生¹ (¹京工繊大・院・応生, ²岡山大・院・環境生命, ³山口大・院・創成科学)
Shu Morita¹, Haruna Makino¹, Kanta Inoue¹, Daiki Yokoyama², Atsushi Okawa², Taku Teshima³, Jun-ichi Kishikawa¹, Kenji Matsui³, Kenji Inagaki², Tomoo Shiba¹ (¹Fac. Appl. Biol., Grad. Sch. Sci. and Tech., Kyoto Inst. Tech., ²Grad. Sch. Env. & Life Sci., Okayama Univ., ³Grad. Sch. Sci. & Tech., Yamaguchi Univ.)

- 1GA005** 天然変性タンパク質 FUS の分子動力学シミュレーションによる構造領域と天然変性領域の協調的な核酸結合機構の普遍性の解明
A Universal Mechanism of Nucleic Acid Binding by Protein Structured and Intrinsically Disordered Regions Revealed by Molecular Simulations
○木島 壮一郎, 北尾 彰朗 (東京科学大学生理工学院)
Soichiro Kijima, Akio Kitao (*Inst. Sci. Tokyo, Sch. Life Sci. Tech.*)
- 1GA006** 放線菌由来 L-メチオニン脱炭酸酵素 MetDC における Tyr421 の役割
Role of Tyr421 in L-Methionine Decarboxylase, MetDC, from *Kitasatospora aureofaciens*
○井上 幹太¹, 牧野 晴菜¹, 森田 宗¹, 茶堂 快渡¹, 大川 敦司², 稲垣 賢二², 岸川 淳一¹, 志波 智生¹
(¹京工繊大・院・応生,²岡山大・院・環境生命)
Kanta Inoue¹, Haruna Makino¹, Shu Morita¹, Kaito Chadou¹, Atsushi Okawa², Kenji Inagaki², Jun-ichi Kishikawa¹, Tomoo Shiba¹ (¹*Dept. Appl. Biol., Grad. Sch. Sci. and Tech., Kyoto Inst. of Tech.*, ²*Grad. Sch. Env. & Life Sci., Okayama Univ.*)
- 1GA007** E. coli-expressed Influenza H1N1 Receptor Binding Domain is immunogenic in mice and produces neutralizing antibodies against live virus
Le Ngoc Thao Tu¹, Md. Din Islam¹, Ching-yu Tseng^{2,3}, Wei-li Hsu^{2,3}, Toshio Yamazaki⁴, Trong Thang Ha^{1,5}, Allen Huynh¹, Yutaka Kuroda^{1,3} (¹*Dept. of Biotech and Life Sci., Grad. Sch. of Engr., TUAT*, ²*Grad. Inst. of Microbiol. & Public Health, Coll. Vet. Med., NCHU*, ³*GIR, TUAT*, ⁴*RIKEN Cent. for Biosyst. Dyn. Res.*, ⁵*Inst. Biotech & Food, CTU*)
- 1GA008** ペプチド結合型 GPCR に対する小分子化合物の異なる作用機構
Small chemical molecules exhibit distinct mechanisms of action towards a peptide-binding GPCR
○顾 羽中¹, 新開 有紗^{3,4}, 小林 和弘^{1,2}, 川上 耕季^{1,2}, 小島 朝翔⁶, 斉藤 毅^{4,5}, 加藤 英明^{1,2} (¹東京大学大学院理学系研究科, ²東京大学先端科学技術センター, ³筑波大学院数理工学物質, ⁴筑波大睡眠研究機構(IIS), ⁵筑波大医学医療系, ⁶東京大学大学院総合文化研究科)
Yuzhong Gu¹, Arisa Shinkai^{3,4}, Kazuhiro Kobayashi^{1,2}, Kouki Kawakami^{1,2}, Asato Kojima⁶, Tsuyoshi Saitoh^{4,5}, Hideaki Kato^{1,2} (¹*Graduate School of Science, The University of Tokyo*, ²*Research Center for Advanced Science and Technology, The University of Tokyo*, ³*Graduate School of Pure and Applied Sciences, University of Tsukuba*, ⁴*International Institute for Integrative Sleep Medicine (WPI-IIS), University of Tsukuba*, ⁵*Institute of Medicine, University of Tsukuba*, ⁶*Graduate School of Arts and Sciences, The University of Tokyo*)
- 1GA009** M₂ および M₄ ムスカリン受容体のサブタイプ選択的活性化に関する赤外分光解析
Infrared Spectroscopic Insights into Subtype-Selective Activation of M₂ and M₄ Muscarinic Receptors
○水野 萌香¹, 杉浦 勇也¹, 井上 明俊², 寿野 千代², 寿野 良二², 神取 秀樹^{1,3}, 片山 耕大^{1,3} (¹名工大・院工, ²関西医大・医, ³名工大・オプトバイオテクノロジー研究センター)
Moeka Mizuno¹, Yuya Sugiura¹, Akitoshi Inoue², Chiyo Suno², Ryoji Suno², Hideki Kandori^{1,3}, Kota Katayama^{1,3} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Kansai Medical University. Medical.*, ³*OptoBioTechnology Research Center, Nagoya Inst. Tech.*)
- 1GA010** オスモライト添加による水のダイナミクス変化が α-アミラーゼ活性に及ぼす影響
Change in water dynamics by osmolytes affect the activity of α-amylase
○古川 幸佳¹, 城田 秀明², 菱田 真史¹ (¹東理大・院理学, ²千葉大・院理学)
Sachika Furukawa¹, Hideaki Shirota², Mafumi Hishida¹ (¹*Grad. Sch. Sci., Univ. TUS*, ²*Grad. Sch. Sci., Univ. Chiba*)
- 1GA011** ラクダムシ由来甲虫型不凍タンパク質の発見と機能解析
Discovery and Functional Characterization of Beetle-type Antifreeze Proteins in Snakeflies
○内澤 風穂¹, 前田 皓丞¹, 津田 栄², 相沢 智康^{1,2}, 新井 達也^{1,2} (¹北大・理, ²北大・先端生命)
Kaho Uchizawa¹, Kosuke Maeda¹, Sakae Tsuda², Tomoyasu Aizawa^{1,2}, Tatsuya Arai^{1,2} (¹*Sch. Sci., Hokkaido Univ.*, ²*Fac. Adv. Life Sci., Hokkaido Univ.*)

- [1GA012](#) 複数のプロトン輸送ユニットを持った天然 F_0F_1 -ATP 合成酵素の探索
Exploring natural F_0F_1 -ATP synthase with multiple proton transport units
○片野 真熙¹, 丸井 里駆², 上野 博史¹, 野地 博行^{1,3} (¹ 東京大学工学系研究科応用化学専攻, ² 東京大学 大学院工学系研究科 バイオエンジニアリング専攻, ³ 東京大学プラネタリーヘルス研究機構)
- Mahiro Katano**¹, Riku Marui², Hiroshi Ueno¹, Hiroyuki Noji^{1,3} (¹*Department of Applied Chemistry, School of Engineering, University of Tokyo.*, ²*Department of Bioengineering School of Engineering, University of Tokyo.*, ³*Research Institute of Planetary Health (RIPH), The University of Tokyo*)
- [1GA013](#) 脂質二重膜中でチャネル活性を有する両親媒性 β ヘルックスペプチドの会合状態の解析
Analysis of the association state of amphiphilic β -helix peptides with channel activity in lipid bilayers
○中嶋 悠人¹, 佐藤 大輔¹, 彭 祖癸², 栢森 史浩³, 白井 健二³, 新津 藍⁴, 川野 竜司², 川村 出¹
(¹ 横浜国立大学 大学院理工学府, ² 東京農工大学 工学研究院, ³ 甲南大学 フロンティアサイエンス学部, ⁴ 理化学研究所 生命医科学研究センター)
- Haruto Nakajima**¹, Daisuke Sato¹, Zugui Peng², Fumihiko Kayamori³, Kenji Usui³, Ai Niitsu⁴, Ryuji Kawano², Izuru Kawamura¹ (¹*Graduate School of Engineering Science, Yokohama National University.*, ²*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology.*, ³*Faculty of Frontiers of Innovative Research in Science and Technology, Konan University.*, ⁴*Laboratory for Dynamic Biomolecule Design, Riken Center for Integrative Medical Science.*)

1GB タンパク質：物性，天然変性
Protein: Property, Intrinsic disorder

座長：櫻井 一正（近畿大学），西田 紀貴（千葉大学）

Session Chairs: Kazumasa Sakurai (KINDAI Univ.), Noritaka Nishida (Chiba Univ.)

15:10～18:10

B 会場（会議室 103+104）／Room B（Meeting Room 103+104）

- [1GB001](#) モルテングロビュール状態を介した同時翻訳のフォールディング経路の可視化
Visualizing co-translational folding pathway mediated by Molten-Globule (MG) state
○小西 雄一朗^{1,2}, 赤松 香奈子³, 丹澤 豪人¹, 加藤 貴之¹ (¹ 大阪大学・蛋白質研究所, ² 大阪大学・大学院生命機能研究科, ³ 大阪大学ワクチン開発拠点・先端モダリティ DDS 研究センター)
- Yuichiro Konishi**^{1,2}, Kanako Akamatsu³, Takehito Tanzawa¹, Takayuki Kato¹ (¹*Institute for Protein Research, The University of Osaka.*, ²*Graduate School Frontier Biosciences, The University of Osaka.*, ³*Center for Advanced Modalities and DDS, The University of Osaka.*)
- [1GB002](#) FUS-ALS 疾患型変異体の相分離や不可逆的凝集に対する ATP の抑制メカニズム
Mechanistic insights into ATP's inhibition of phase separation and aggregation of ALS-linked FUS variants, R495X and P525L
○北村 奎時¹, 津久井 一太¹, 荒山 みゆ², 大島 彩乃¹, 北沢 創一朗¹, 亀田 倫史³, 北原 亮^{1,2} (¹ 立命館大学・院薬学, ² 立命館大学・薬学部, ³ 産総研・人工知能研究センター)
- Keiji Kitamura**¹, Itta Tsukui¹, Miyu Arayama², Ayano Ohshima¹, Soichiro Kitazawa¹, Tomoshi Kameda³, Ryo Kitahara^{1,2} (¹*Grad. Sch. Pharm., Ritsumeikan Univ.*, ²*Col. Pharm., Ritsumeikan Univ.*, ³*Art. Int. Res. Ctr., AIST.*)
- [1GB003](#) *Corynebacterium glutamicum* における反応サイクルと関連したクエン酸合成酵素の集合体形成メカニズム
Catalysis-dependent mechanism of citrate synthase condensation in *Corynebacterium glutamicum*
○長岡 誠¹, 西山 真^{1,2}, 古園 さおり^{1,2,3} (¹ 東大・院農生科, ² 東大・CRIIM, ³ 理研 CSRS)
- Makoto Nagaoka**¹, Makoto Nishiyama^{1,2}, Saori Kosono^{1,2,3} (¹*Grad. Sch. Agric. Life Sci., UTokyo*, ²*CRIIM, UTokyo*, ³*RIKEN CSRS*)

- 1GB004** 圧カジャンプ分光法によるタンパク質液液相分離に関する速度論的解析
Kinetic analysis for Protein liquid-liquid phase separation by pressure-jump spectroscopy
○白砂 雄太郎¹, 森下 愛大², 北村 奎時¹, 北原 亮^{1,2} (¹立命館大・院薬学, ²立命館大・薬学)
Yutaro Shiramasa¹, Manato Morishita², Keiji Kitamura¹, Ryo Kitahara^{1,2} (¹*Grad. Sch. Pharm. Sci., Univ. Ritsumeikan*, ²*Coll. Pharm. Sci., Univ. Ritsumeikan*)
- 1GB005** sm-FRET および蛍光相関分光法による SARS-CoV-2 の N タンパク質リンカー領域の RNA への結合における役割の解明
Roles of the linker region of the N protein of SARS-CoV-2 in the association to RNA by sm-FRET and fluorescence correlation spectroscopies
Shion Ishikawa^{1,2}, Takahiro Kimura^{1,2}, Takuya Katayama^{1,2}, Syamil MA Husna^{2,3}, Yuji Itoh^{1,2,3}, Satoshi Takahashi^{1,2,3} (¹*Graduate School of Life Sciences, Tohoku University*, ²*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*, ³*Department of Chemistry, Graduate School of Science, Tohoku University*)
- 1GB006** αB-クリスタリン及びその断片による α シヌクレイン液滴の老化の阻害
αB-Crystallin and its fragment prevent aging of α-Synuclein droplets
○藤塚 健次¹, 柚 佳祐¹, 道上 佑希¹, Carver John A.², 茶谷 絵理¹ (¹神戸大院・理, ²Res. Sch. Chem., ANU.)
Kenji Fujitsuka¹, Keisuke Yuzu¹, Yuki Michiue¹, John A. Carver², Eri Chatani¹ (¹*Grad. Sch. Sci., Kobe Univ.*, ²*Res. Sch. Chem., ANU.*)
- 1GB007** トランスサイレチン 49-127 断片が形成するプロトフィブリルの解析
Characterization of Protofibril Formed by Transthyretin 49-127 Fragment
○益田 優月¹, 中尾 星哉¹, 柚 佳祐¹, 山本 直樹², 守島 健³, 井上 倫太郎³, 杉山 正明³, 茶谷 絵理¹ (¹神戸大・院理, ²自治医科大・医, ³京都大複合研)
Yuzuki Masuda¹, Seiya Nakao¹, Keisuke Yuzu¹, Naoki Yamamoto², Ken Morishima³, Rintaro Inoue³, Masaaki Sugiyama³, Eri Chatani¹ (¹*Grad. Sch. Sci, Kobe Univ.*, ²*Sch. Med., Jichi Med. Univ.*, ³*KURNS, Kyoto Univ.*)
- 1GB008** アルキル化ペプチドによる液-液相分離液滴の分子取り込みの制御
Controlling the molecular uptake of liquid-liquid phase separated droplets using Alkylated peptides
○山下 息吹 (富山大学 薬学部)
Ibuki Yamashita (Fac. Pharm. Sci., Univ. Toyama)
- 1GB009** アコヤガイの貝殻に含まれる天然変性タンパク質 nacrein の構造ダイナミクス解析
Structural dynamics of nacrein, an intrinsically disordered protein in a shell of *Pinctada fucata*
○浪川 勇人¹, 守島 健², 井上 倫太郎², 杉山 正明², 鈴木 道生¹ (¹東大院農, ²京大複合研)
Yuto Namikawa¹, Ken Morishima², Rintaro Inoue², Masaaki Sugiyama², Michio Suzuki¹ (¹*GSALS, KURNS*)
- 1GB010** IDP 相分離液滴を用いたオリゴ DNA からの効率的なタンパク質発現系
Oligo assembly enhanced by IDP droplet for efficient cell-free expression
○上野 大慈¹, 皆川 慶嘉¹, 野地 博行^{1,2} (¹東京大学・工学系・応用化学, ²東京大学プラネタリーヘルス研究機構)
Taiji Ueno¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Dept. Applied Chemistry, Sch. Eng., Univ. Tokyo.*, ²*Research Institute of Planetary Health (RIPH), Univ. Tokyo*)
- 1GB011** TIA-1 における RRM 間および RRM-LCD 相互作用による相分離制御機構の解明
Mechanistic analysis of TIA-1 phase separation driven by intramolecular RRM-RRM and RRM-LCD interactions
○近藤 千月¹, 楠 真一^{1,2,3,4}, 安田 恭大^{1,2,3}, 多根 奈津美¹, 磯 僚海¹, 荒木 優香¹ (¹広島大・院統合生命, ²広島大・核内クロマチン・ライブダイナミクスの数理研究拠点, ³広島大・持続可能性に寄与するキラルノット超物質拠点, ⁴明治大・先端数理科学インスティテュート)
Kazuki Kondo¹, Shinichi Tate^{1,2,3,4}, Kyota Yasuda^{1,2,3}, Natsumi Tane¹, Tomomi Iso¹, Yuka Araki¹ (¹*Grad. Sch. Sci., Univ. Hiroshima*, ²*ReMcD, Univ. Hiroshima*, ³*WIP-SKCM2, Univ. Hiroshima*, ⁴*MIMS, Univ. Meiji*)

[1GB012](#) 核小体タンパク質 Nopp140 のハイパーリン酸化は有糸分裂期脱凝集を加速させる
Hyperphosphorylation of nucleolar protein Nopp140 accelerates mitotic nucleolar disassembly
○嶋村 悠¹, 乗添 祐樹², 坂上 貴洋², 吉村 成弘¹ (¹ 京都大学生命科学研究科, ² 青山学院大学理工学部)
Hisashi Shimamura¹, Yuki Norizoe², Takahiro Sakae², Shige H. Yoshimura¹ (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*Coll. Sci. Engr. Aoyama Gakuin Univ.*)

1GC タンパク質：計測, タンパク質工学, 膜タンパク質, バイオエンジニアリング
Protein: Measurement, Engineering, Membrane proteins, Bioengineering

座長：古賀 信康（大阪大学），鎌形 清人（岐阜大学）

Session Chairs: Nobuyasu Koga (Osaka Univ.), Kiyoto Kamagata (Gifu Univ.)

15:10~18:25

C 会場（会議室 105+106）／Room C（Meeting Room 105+106）

[1GC001](#) 高速 AFM 観察による真菌機能性アミロイドの線維表面触媒による線維伸長機構の解明
High-speed atomic force microscopy reveals surface-catalyzed elongation mechanism of fungal functional amyloid
○高橋 尚央¹, 木村 竜也², 寺内 裕貴³, 吉見 啓^{4,5}, 中山 隆宏², 阿部 敬悦¹ (¹ 東北大院・農, ² 金沢大・ナノ生命化学研究所, ³ 山口大・中高温研, ⁴ 京大院・農, ⁵ 京大院・地環学)
Nao Takahashi¹, Tatsuya Kimura², Yuki Terauchi³, Akira Yoshimi^{4,5}, Takahiro Watanabe-Nakayama², Keietsu Abe¹ (¹*Grad. Sch. Agri., Tohoku Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*RCTMR, Yamaguchi Univ.*, ⁴*Grad. Sch. Agri., Kyoto Univ.*, ⁵*Grad. Sch. Glob. Env. Stud., Kyoto Univ.*)

[1GC002](#) 一分子蛍光顕微鏡と近接依存性標識による一細胞ミトコンドリアプロテオームの網羅的解析
Single-cell mitochondrial proteome profiling via combining single-molecule fluorescence microscopy and proximity labeling
○土田 美咲^{1,2}, カマルザマン ラティファ^{1,3}, 金 水縁¹, 谷口 雄一^{1,3,4} (¹ 京都大学 物質・細胞統合システム拠点 (iCeMS), ² 京都大学 農学部, ³ 大阪大学 生命機能研究科, ⁴ 京都大学大学院 生命科学研究科)

Misaki Tsuchida^{1,2}, Latiefa Kamarulzaman^{1,3}, Sooyeon Kim¹, Yuichi Taniguchi^{1,3,4} (¹*Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University*, ²*Faculty of Agriculture, Kyoto University*, ³*Graduate School of Frontier Biosciences, Osaka University*, ⁴*Graduate School of Biostudies, Kyoto University*)

[1GC003](#) 構造的制約をタンパク質デザインで取り入れた進化モデルによる祖先ヌクレオソームの再構築
Reconstruction of ancestral nucleosomes using an evolutionary model that incorporates structural constraints through protein design
○林 泰瑤¹, 佐久間 航也², 寺川 剛¹, 高田 彰二¹ (¹ 京大・院理・生物物理, ² 名大・細胞生理学研究所センター)

Taiyo Hayashi¹, Koya Sakuma², Tsuyoshi Terakawa¹, Shoji Takada¹ (¹*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*, ²*CeSPI, Nagoya Univ.*)

[1GC004](#) 複数狭窄部をもつ Epx4 ナノポアのペプチド識別能力の探索
Exploring the peptide discrimination capabilities of multiple constriction Epx4 nanopores
○伊集院 綾子¹, 内藤 航大², 田中 良和², 川野 竜司¹ (¹ 農工大・院生命工学, ² 東北大学・院生命科学研究科)

Ayako Ijuin¹, Kota Naito², Yoshikazu Tanaka², Ryuji Kawano¹ (¹*Grad. Sch. Biotech and Life Sci., TUAT*, ²*Grad. Sch. Life Sci., Tohoku Univ.*)

[1GC005](#) 演題取り下げ Withdrawn

- [1GC006](#) Minimal RNA polymerase reconstruction
Riddhi Prashant Gondhalekar^{1,2}, Shunsuke Tagami³, Sota Yagi⁴, Kosuke Fujishima^{1,2,5} (¹*School of Life Science and Technology, Institute of Science Tokyo*, ²*Earth-Life Science Institute, Institute of Science Tokyo*, ³*RIKEN IMS*, ⁴*Faculty of Human Sciences, Waseda University*, ⁵*Graduate School of Media and Governance, Keio University*)
- [1GC007](#) *De novo* ペプチドナノポアのエミラ化とセンシング精度向上に向けた改変
 Chimeric integration of a *de novo* peptide nanopore and its sequence optimization for improving sensing resolution
 ○中田 彩夏¹, 内藤 航大², 田中 良和², 川野 竜司¹ (¹ 東京農工大・院生命工学, ² 東北大学・院生命科学科学研究科)
Ayaka Nakada¹, Kota Naito², Yoshikazu Tanaka², Ryuji Kawano¹ (¹*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, ²*Graduate School of Life Sciences, Tohoku University*.)
- [1GC008](#) 膜透過性ペプチドを介した汎用的なタンパク質輸送システムの開発
 Development of a wide range of protein delivery systems mediated by cell-penetrating peptides
 ○三輪 明星, 神谷 厚輝 (群大・院理工)
Akari Miwa, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)
- [1GC009](#) 酵素間相互作用の強化による二段階アルカン合成反応の効率化
 Improving efficiency of two-step alkane synthesis reactions by enhancing enzyme interactions
 ○岡田 隼弥¹, 季高 駿士¹, 新井 宗仁^{1,2} (¹ 東大・総合文化・生命環境, ² 東大・理・物理)
Shunya Okada¹, Shunji Suetaka¹, Munechito Arai^{1,2} (¹*Department of Life Sciences, The University of Tokyo*, ²*Department of Physics, The University of Tokyo*)
- [1GC010](#) 酵素を合理的に活性化する普遍的手法の開発
 Development of a universal method to rationally activate enzymes
 ○渡辺 敦也¹, 季高 駿士¹, 新井 宗仁^{1,2} (¹ 東大・総合文化・生命環境, ² 東大・理・物理)
Atsuya Watanabe¹, Shunji Suetaka¹, Munechito Arai^{1,2} (¹*Department of Life Sciences, The University of Tokyo*, ²*Department of Physics, The University of Tokyo*)
- [1GC011](#) アゴニスト誘導コンフォメーションを捉えた TRPM8 の X 線 1 分子動態計測
 Single-molecule X-ray analysis capturing the agonist-induced conformation of TRPM8
 ○町田 温登^{1,2}, 大久保 達成^{2,3}, 佐々木 大輔^{1,2}, 三尾 和弘^{2,3}, 佐々木 裕次^{1,2,4} (¹ 東京大・院新領域, ² 産総研, ³ 横浜市大・院生命医, ⁴ 高輝度光科学研究センター)
Haruto Machida^{1,2}, Tatsunari Ohkubo^{2,3}, Daisuke Sasaki^{1,2}, Kazuhiro Mio^{2,3}, Yuji. C Sasaki^{1,2,4} (¹*Grad. Sch. Frontier Sci., Univ. Tokyo*, ²*Natl. Inst. Adv. Ind. Sci. & Technol.*, ³*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, ⁴*JASRI*)
- [1GC012](#) 電気エネルギー依存性細胞死の電気回路モデルによる解析
 Explaining Electrical Energy Dependent Cell Death Mechanisms Through Electrical Circuit-Based Modeling
 ○廣島 大輝, 田中 蒼大, 本村 英樹, 池田 善久, 神野 雅文 (愛媛大学大学院 理工学研究科)
Taiki Hirohata, Sota Tanaka, Hideki Motomura, Yoshihisa Ikeda, Masafumi Jinno (*Dept. of EEE, Grad. Sch. of Sci. and Eng., Ehime Univ.*)
- [1GC013](#) 新規高輝度蛍光 RNA アプタマーの取得とその特性解析
 Isolation and characterization of novel bright fluorogenic RNA aptamers
 ○山田 智嵩, 伊藤 敬佑, 上村 想太郎, 飯塚 怜 (東大・院理・生科)
Tomotaka Tayama, Keisuke Ito, Sotaro Uemura, Ryo Iizuka (*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

- [1GD001](#) 線維芽細胞の外環境の弾性率に対する受動的応答と心筋細胞への能動的影響
Passive responses of fibroblasts to extracellular stiffness and their active influence on cardiomyocytes
○長井 新^{1,2}, 栗原 宙歩², 守山 裕大², 三井 敏之² (¹京大・院生命科学,²青学大・院理工)
Arata Nagai^{1,2}, Hiromu Kuwabara², Yuuta Moriyama², Toshiyuki Mitsui² (¹Grad. Sch. Bio., Kyoto Univ.,
²Grad. Sch. Sci. and Eng., Aoyamagakuin Univ.)
- [1GD002](#) 三次元位置検出顕微鏡による纖毛虫テトラヒメナの遊泳および纖毛運動解析
Three-dimensional tracking of swimming and ciliary beating in *Tetrahymena*
○石井 裕人, 丸茂 哲聖, 山口 真, 山岸 雅彦, 矢島 潤一郎 (東京大学大学院総合文化研究科)
Hiroto Ishii, Akisato Marumo, Shin Yamaguchi, Masahiko Yamagishi, Junichiro Yajima (Grad. Sch. of Arts and Sci., Univ. Tokyo)
- [1GD003](#) Modified model with myosin accumulation effect for mechanosensitive migration
Yuki Kimura¹, Chika Okimura², Yoshiaki Iwadate², Tatsunari Sakurai¹ (¹Dept. Math. Eng., Musashino Univ.,²Grad. Sch. Sci. & Tech. Innov., Yamaguchi Univ.)
- [1GD004](#) ドリル細菌は鞭毛フックの曲げ剛性を調節する
Bacteria capable of drill-like propulsion adjust bending stiffness of the flagellar hooks
○小倉 尚樹¹, 吉岡 青葉², 中根 大介², 村山 能宏¹ (¹農工大・院生体医用シス工,²電通大・院基盤理工)
Naoki Ogura¹, Aoba Yoshioka², Daisuke Nakane², Yoshihiro Murayama¹ (¹Grad. Sch. Bio-Med. Sys. Eng., TUAT,²Grad. Sch. Fund. Sci. & Eng., UEC)
- [1GD005](#) 改良版 Vicsek モデルによるイエユウレイグモ初期胚の細胞集団運動のシミュレーションと解析
Simulation and Analysis of Collective Cell Migration in Early Embryos of *Pholcus phalangioides* Using a Modified Vicsek Model
○庄司 紘都 (同志社大学生命医科学部)
Hiroto Shoji (Faculty of Life and Medical Sciences, Doshisha University)
- [1GD006](#) ヘリコバクターの多彩な移動戦略はドリル運動によって最適化される
Flagellar wrapping facilitates directional movement in *Helicobacter*
○横濱 さらら¹, 上村 直輝¹, 島田 佳季², 見理 剛³, 林原 絵美子³, 菅 哲朗², 中根 大介¹ (¹電通大院・基盤理工,²電通大院・機械知能,³感染研・細菌二部)
Sarara Yokohama¹, Naoki Uemura¹, Yoshiki Shimada², Tsuyoshi Kenri³, Emiko Rimbara³, Tetsuo Kan², Daisuke Nakane¹ (¹Dep. Eng. Sci., UEC,²Dep. Mech. Intell. Syst., UEC,³Dep. Bact. II, NIID)
- [1GD007](#) 魚類表皮ケラトサイト集団同士の高速な融合は互いのアクトミオシンケーブルを消失させ合うことで実現する
Rapid Integration of Two Keratocyte Sheets by Disassembling Each Other's Actomyosin Cables
○清水 和真, 沖村 千夏, 岩楯 好昭 (山口大・院創成科学・生物)
Kazuma Shimizu, Chika Okimura, Yoshiaki Iwadate (Grad. Sch. Sci. Tech., Univ. Yamaguchi)

- 1GD008** MreB が合成細菌にスピロプラズマ運動能を発生させる方法を *in vivo* で可視化する
In vivo visualization of how MreBs drive *Spiroplasma* motility in minimal synthetic bacterium
 ○田中 芳樹¹, 木山 花², 水谷 雅希¹, 森本 雄祐³, 宮田 真人², 西坂 崇之¹ (¹学習院大・理・物理,
²阪公大・院理,³九工大・情報工学)
- Yoshiki Tanaka**¹, Hana Kiyama², Masaki Mizutani¹, Yusuke V. Morimoto³, Makoto Miyata²,
 Takayuki Nishizaka¹ (¹Dept. Phys., Gakushuin Univ., ²Grad. Sch. Sci., Osaka Metropolitan Univ., ³Fac.
 Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.)
- 1GD009** 脂肪酸代謝酵素 HADH の核内機能において制御される線虫 *C.elegans* の温度順化現象の分子機
 構解析
 Molecular mechanism of temperature acclimation in *C. elegans* regulated by the nuclear
 function of fatty acid metabolizing enzyme HADH
 ○森 雪永¹, 福本 晃久¹, 岡畑 美咲¹, 三浦 徹¹, 水口 洋平², 豊田 敦², 太田 茜¹, 久原 篤^{1,3} (¹甲南
 大学 自然科学研究科生物学専攻 生体調節学 研究室,²国立遺伝学研究所,³PRIME, AMED)
- Yukina Mori**¹, Akihisa Fukumoto¹, Misaki Okahata¹, Toru Miura¹, Yohei Minakuchi², Atsushi Toyoda²,
 Akane Ohta¹, Atushi Kuhara^{1,3} (¹Laboratory of Molecular and Cellular Regulation Graduate school of
 Natural Science Konan University, ²National Institute of Genetics, Japan, ³PRIME, AMED)
- 1GD010** 高速 AFM による分子間相互作用を介した CaMKII クラスターダイナミクスの観察
 High-speed AFM revealed dynamics of CaMKII clusters through intermolecular interactions
 ○鈴木 大晴¹, 炭竈 享司², 村越 秀治³, 柴田 幹大^{2,4} (¹金沢大・院ナノ生命,²金沢大・WPI-
 NanoLSI,³生理研・脳機能計測支援センター,⁴金沢大・新学術創成)
- Taisei Suzuki**¹, Takashi Sumikama², Hideji Murakoshi³, Mikihiro Shibata^{2,4} (¹Grad. Sch. NanoLS.,
 Kanazawa Univ., ²WPI-NanoLSI, Kanazawa Univ., ³Supportive Center for Brain Research, NIPS,
⁴InFiniti, Kanazawa Univ.)
- 1GD011** 高速 AFM による CaMKIIα/β ヘテロオリゴマーの構造と動態の観察
 Architecture and Dynamics of CaMKIIα/β heterooligomers revealed by High-Speed AFM
 ○松島 啓介¹, 炭竈 享司², 村越 秀治³, 柴田 幹大^{2,4} (¹金沢大・院数物,²金沢大・WPI-nanoLSI,
³生理研・脳機能計測支援センター,⁴金沢大・新学術創成)
- Keisuke Matsushima**¹, Takashi Sumikama², Hideji Murakoshi³, Mikihiro Shibata^{2,4} (¹Grad. Sch. Math.
 & Phys., Kanazawa Univ., ²WPI-NanoLSI, Kanazawa Univ., ³Supportive Center for Brain Research,
 National Institute for Physiological Sciences, ⁴InFiniti, Kanazawa Univ.)
- 1GD012** プラス帯電性ナノバブルが及ぼす神経細胞への影響
 Influence of positively charged nanobubbles to neurons
 ○劉 一帆¹, 大平 猛², 北方 恵美², 原田 慈久², 林 久美子² (¹東京大学 大学院新領域創成科学研究
 院科,²東京大学 物性研究所)
- Yifan Liu**¹, Takeshi Ohdaira², Emi Kitakata², Yoshihisa Harada², Kumiko Hayashi² (¹Graduate School of
 Frontier Science, The University of Tokyo, ²The Institute for Solid State Physics, The University of Tokyo)

1GE 分子モーター, 核酸: 結合タンパク質, ナノテクノロジー
 Molecular motor, Nucleic acid: binding protein, nanotechnology

座長: 横田 浩章 (光産業創成大学院大学), 坂上 貴洋 (青山学院大学)

Session Chairs: Hiroaki Yokota (Grad. Sch. New Photon. Indust.), Takahiro Sakaue (Aoyama Gakuin Univ.)

15:10~18:10

E 会場 (会議室 201) / Room E (Meeting Room 201)

- 1GE001** YY1 による DNA スーパークラスターの濃度依存的制御
 Concentration-dependent modulation of DNA superclusters by YY1
 ○晏 晞, 寺川 剛 (京都大学 大学院理学研究科)
Xi Yan, Tsuyoshi Terakawa (Graduate School of science, Kyoto University)

- 1GE002** 一分子 FRET 分光法が示す SARS-CoV-2 のゲノム RNA の構造
Single molecule FRET spectroscopy reveals the structure of genomic RNA of SARS-CoV-2 virus
Takahiro Kimura^{1,2}, Takuya Katayama^{1,2}, Shinnosuke Saitou^{1,2}, Kamila Putridifia Priyambada¹, Yuuhei Yamano¹, Kazumitsu Onizuka^{1,3}, Fumi Nagatsugi^{1,3}, Shilpi Laha⁴, Athi N Naganathan⁴, Yuji Itoh^{1,2,3}, Satoshi Takahashi^{1,2,3} (¹IMRAM, Univ. Tohoku, ²Grad. Sch. Life Sci., Univ. Tohoku, ³Grad. Sch. Sci., Univ. Tohoku, ⁴IITM)
- 1GE003** シリカナノ液滴による DNA 情報処理系の 3D-固体材料化
3D-Solid Materialization of DNA Data Processing Systems by silica nano droplets
○呉松 健吾, 川野 竜司 (東京農工大学 工学部 生命工学科)
Kengo Kurematsu, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology (TUAT)*)
- 1GE004** 異種ポリアミンによる協調/阻害効果: DNA 高次構造転移による遺伝子発現スイッチング制御
Cooperation/inhibition of polyamines on regulation of gene expression switching in relation to higher-order structural changes of DNA
○小川 遥士¹, 西尾 天志^{1,2}, 吉川 祐子¹, 剣持 貴弘¹, 吉川 研一¹ (¹同志社大・院生命医科学, ²産総研・モレキュラーバイオシステム)
Haruto Ogawa¹, Takashi Nishio^{1,2}, Yuko Yoshikawa¹, Takahiro Kenmotsu¹, Kenichi Yoshikawa¹ (¹Grad. Sch. Life and Med Sci., Doshisha Univ., ²MolBiS, AIST)
- 1GE005** *In silico* 解析による GTP 駆動型 F₁-ATPase の設計
Design of GTP-driven F₁-ATPase by *in silico* analysis
○大矢 辰哉¹, 小林 稜平¹, 上野 博史¹, 岡崎 圭一², 野地 博行^{1,3} (¹東大 院工 応化, ²分子科学研究所, ³東大 プラネタリーヘルス研究機構)
Tatsuya Oya¹, Ryohei Kobayashi¹, Hiroshi Ueno¹, Kei-ichi Okazaki², Hiroyuki Noji^{1,3} (¹Grad. Eng. Appl. Chem., Univ. of Tokyo, ²Institute for Molecular Science, ³RIPH., Univ. of Tokyo)
- 1GE006** 複数のプロトン駆動トルク発生ユニットを有する F_oF₁-ATP 合成酵素の設計手法の拡張
Attempt to extend the design strategy for F_oF₁-ATP synthase with multiple proton-driven torque-generating units
○丸井 里駆¹, 上野 博史¹, 野地 博行^{1,2} (¹東京大・院工学, ²東京大・プラネタリーヘルス研究機構)
Riku Marui¹, Hiroshi Ueno¹, Hiroyuki Noji^{1,2} (¹Grad. Sch. Eng., Univ. Tokyo, ²RIPH., Univ. Tokyo)
- 1GE007** axle-less F₁-ATPase の 1 分子回転観察によって発見された新たな回転中間体の解析
A new dwell-time discovery by single-molecule rotation assay of axle-less F₁-ATPase
○内山 友¹, 上野 博史¹, Sobti Meghna^{2,3}, Stewart Alastair G.^{2,3}, 野地 博行^{1,4} (¹東大・院工, ²Mol. Struct. & Comput. Biol. Div., VCCRI, NSW, Australia, ³St Vincent's Clin. Sch., Fac. Med., UNSW Sydney, NSW, Australia, ⁴東大・プラネタリーヘルス研究機構)
Tomo Uchiyama¹, Hiroshi Ueno¹, Meghna Sobti^{2,3}, Alastair G. Stewart^{2,3}, Hiroyuki Noji^{1,4} (¹Grad. Sch. Eng., The Univ. of Tokyo, ²Mol. Struct. & Comput. Biol. Div., VCCRI, NSW, Australia, ³St Vincent's Clin. Sch., Fac. Med., UNSW Sydney, NSW, Australia, ⁴Res. Inst. Planet. Health (RIPH), Univ. Tokyo)
- 1GE008** 1 分子計測及び機械学習を用いた高活性 F₁-ATPase の探索
Exploration of high-speed F₁-ATPase with single-molecule assay and machine-learning
○三宅 皓大¹, 小林 稜平¹, 上野 博史¹, 田口 真衣¹, 齋藤 裕², 野地 博行^{1,3} (¹東大・工・応化, ²北里大・未来工・データサイエンス, ³東大・プラネタリーヘルス研究機構)
Kodai Miyake¹, Ryohei Kobayashi¹, Hiroshi Ueno¹, Mai Taguchi¹, Yutaka Saito², Hiroyuki Noji^{1,3} (¹Dep. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo, ²Dep. Data Sci., Sch. Fro. Eng., Univ. Kitasato, ³RIPH, Univ. Tokyo)

- 1GE009** マイコバクテリア ATP 合成酵素における α サブユニット C 末端伸長による阻害メカニズムの解明
Revealing a Unique Inhibitory Mechanism of C-terminal Extension of α -Subunit in Mycobacterial ATP Synthase
○田村 遼太¹, 渡邊 亮¹, Meghna Sobti^{2,3}, 上野 博史¹, Alastair Stewart^{2,3}, 野地 博行^{1,4} (¹ 東大・理工学応化, ²Mol. Struct. & Comput. Biol. Div., VCCRI, NSW, Australia, ³St Vincent's Clin. Sch., Fac. Med., UNSW Sydney, NSW, Australia, ⁴ 東大プラネタリー研究機構)
Ryota Tamura¹, Ryo Watanabe¹, Sobti Meghna^{2,3}, Hiroshi Ueno¹, Stewart Alastair^{2,3}, Hiroyuki Noji^{1,4} (¹App. Chem., Grad. Sch. Eng., Univ. Tokyo, ²Mol. Struct. & Comput. Biol. Div., VCCRI, NSW, Australia, ³St Vincent's Clin. Sch., Fac. Med., UNSW Sydney, NSW, Australia, ⁴RIPH, Univ. Tokyo)
- 1GE010** 計算機で設計したサプレッサ変異による疾患型 KIF1A キネシンの運動性能の改善と神経機能の修復
Computationally identified suppressors rescue pathogenic mutations in KIF1A kinesin and restore neurological function
○北 智輝¹, 丹羽 伸介^{1,2} (¹ 東北大・生命科学, ² 東北大・学際研)
Tomoki Kita¹, Shinsuke Niwa^{1,2} (¹Grad. Life. Sci., Tohoku Univ., ²FRIS, Tohoku Univ)
- 1GE011** 全原子分子動力学シミュレーションによる F₁-ATPase の 40°サブステップ回転機構の解析
Investigating the 40° substep rotation mechanism of F₁-ATPase using all-atom MD simulations
○本橋 昌大^{1,2}, 宗行 英朗¹, 杉田 有治^{2,3} (¹ 中央大・院理工学, ² 理研・開拓研究所, ³ 理研・計算科学研究センター)
Masahiro Motohashi^{1,2}, Eiro Muneyuki¹, Yuji Sugita^{2,3} (¹Grad. Sch. Sci. Eng., Univ. Chuo, ²RIKEN Pioneering Research Institute, ³RIKEN Center for Computational Science)
- 1GE012** DNA オリガミ製ナノスプリングを用いた Kinesin-3 モータータンパク質 KIF1A の力計測
Force measurement of the kinesin-3 motor KIF1A using a programmable DNA origami nanospring
○高松 宣道^{1,2}, 古元 礼子³, 有賀 隆行⁴, 岩城 光宏^{4,5,6}, 林 久美子² (¹ 東大・院新領域, ² 東大・物性研, ³ 山口大・院医系, ⁴ 阪大・院生命機能, ⁵NICT・未来 ICT, ⁶ 阪大・IFReC)
Nobumichi Takamatsu^{1,2}, Hiroko Furumoto³, Takayuki Ariga⁴, Mitsuhiro Iwaki^{4,5,6}, Kumiko Hayashi² (¹Grad. Sch. Frontier Sci., Univ. Tokyo, ²Inst. Solid State Phys., Univ. Tokyo, ³Grad. Sch. Med., Yamaguchi Univ., ⁴Grad. Sch. Frontier Biosci., Osaka Univ., ⁵Adv. ICT Res. Inst., NICT, ⁶IFReC, Osaka Univ.)

1GF 生体膜・人工膜：構造、物性、ダイナミクス、情報伝達
Biological & Artificial membrane: Structure, Property, Dynamics, Signal transduction
座長：末次 志郎（奈良先端科学技術大学院大学）、渡邊 千穂（広島大学）
Session Chairs: Shiro Suetsugu (NAIST), Chiho Watanabe (Hiroshima Univ.)

15:10~18:10

F 会場（会議室 202）／Room F（Meeting Room 202）

- 1GF001** 嗅覚受容体と温度感受性チャネル TRPV1 の細胞内クロストークの解析
Investigation of Crosstalk between Olfactory Receptors and TRPV1 Channels
○森山 さくら^{1,2}, 日沼 州司², 黒田 俊一^{1,2} (¹ 大阪大学大学院 生命機能研究科, ² 大阪大学 産業科学研究所)
Sakura Moriyama^{1,2}, Shuji Hinuma², Shun'ichi Kuroda^{1,2} (¹Graduate School of Frontier Biosciences, The University of Osaka, ²SANKEN, The University of Osaka)

- 1GF002** 超解像・1分子観察による細胞膜階層構造ドメイン形成機構の解明
Mechanisms of hierarchical domain organization on cell membranes revealed by super-resolution and single-molecule imaging
○川合 登偉¹, 笠井 倫志², 廣澤 幸一郎^{2,3}, 藤原 敬宏⁴, 楠見 明弘⁵, 横田 康成⁶, 鈴木 健一^{1,2,3}
(¹ 岐阜大院・連農, ² 国立がん研究センター研究所, ³ 岐阜大・iGCORE, ⁴ 京都大・iCeMS, ⁵ 沖縄科学技術大学院大学, ⁶ 岐阜大・工)
Touji Kawai¹, Rinshi S. Kasai², Koichiro M. Hirose^{2,3}, Takahiro K. Fujiwara⁴, Akihiro Kusumi⁵, Yasunari Yokota⁶, Kenichi G. N. Suzuki^{1,2,3} (¹UGSAS, Gifu Univ, ²Natl. Cancer. Ctr. Res. Inst., ³iGCORE, Gifu Univ, ⁴iCeMS, Kyoto Univ, ⁵OIST, ⁶Dept. Eng., Gifu Univ)
- 1GF003** Development of nanoforce polydiacetylene-based biosensors and tailoring their properties by integrating additives
Fabiano Altieri^{1,2}, Kaori Sugihara^{2,3} (¹Graduate School of Engineering, University of Tokyo, ²Institute of Industrial Science, University of Tokyo, ³Department of Physical Chemistry, University of Geneva)
- 1GF004** Synergistic Interaction between LL-37 and HNP-1 for Reducing Cytotoxicity on MDCK-I
Jing Zhang¹, Yuge Hou¹, Takashi Yasuda², Siu Yu Angela Chow¹, Soshi Ito¹, Mizuho Otuska¹, Yoshiho Ikeuchi¹, Xiang Li², Kaori Sugihara¹ (¹The University of Tokyo, ²Hokkaido University)
- 1GF005** 蛍光脂質を用いた DHA 含有リン脂質の相分離膜に対する影響評価
Evaluation of the Effects of DHA-Containing Phospholipids on Phase-Separated Membranes Using Fluorescent Derivatives of Phospholipids
○清水 浩太郎¹, 木下 祥尚², 松森 信明¹ (¹九大・院理, ²群大・院理工)
Kotaro Shimizu¹, Masanao Kinoshita², Nobuaki Matsumori¹ (¹Grad. Sch. Sci., Univ. Kyushu, ²Grad. Sch. Sci. & Tech., Univ. Gunma)
- 1GF006** ミニマル合成細菌 JCVI-syn3B の膜電位計測
Measurement of membrane potential in the minimal synthetic bacterium JCVI-syn3B
○金森 智士, 木山 花, 信元 健智, 宮田 真人 (大阪公立大・院理学)
Satoshi Kanamori, Hana Kiyama, Kenji Nobumoto, Makoto Miyata (*Grad. Sch. Sci., Omu*)
- 1GF007** 細胞膜の非対称性と不均一性
Asymmetry and Heterogeneity in the Plasma Membrane
○山田 哲平¹, 篠田 渉² (¹岡山大・院環境生命自然, ²岡山大・異分野基礎研)
Teppei Yamada¹, Wataru Shinoda² (¹Grad. Sch. Env., Life, Sci. and Tech., Okayama Univ., ²Research Institute for Interdisciplinary Science, Okayama Univ.)
- 1GF008** Single Amino Acid Drives LL-37/HNP1 Synergy: Unveiling Antimicrobial Peptide Interactions
Ariane Schwitter¹, Kaori Sugihara² (¹Grad. Sch. Eng., Univ. Tokyo, ²Inst. Ind. Sci., Univ. Tokyo)
- 1GF009** Bilayer lipid packing effects on the structure and electron transfer activity of cytochrome c oxidase
Bon Leif Dominguez Amalla¹, Atsuhiko Shimada², Satoshi Nagao³, Hiroyuki Kumeta⁴, Takeshi Uchida^{1,5}, Koichiro Ishimori^{1,5} (¹Grad. Sch. of Chem. Sci. Eng., Hokkaido Univ., ²Fac. of Appl. Biol. Sci., Gifu Univ., ³JASRI, ⁴Fac. of Adv. Life Sci., Hokkaido Univ., ⁵Fac. of Sci., Hokkaido Univ.)
- 1GF010** マイクロ流体デバイスで作製したリポソームの微小管重合による膜変形制御
Liposomes synthesized by microfluidic devices change shape in response to microtubule polymerization
○西村 拓真, 石井 裕人, 佐藤 優成, 山岸 雅彦, 矢島 潤一郎 (東京大学・総合文化研究科)
Takuma Nishimura, Hiroto Ishii, Yusei Sato, Masahiko Yamagishi, Junichiro Yajima (*Graduate School Art and Science, The University of Tokyo*)
- 1GF011** Machine Learning-Driven Functional Screening of Peptides Using Mechanochromic Lipid Sensors
Jiali Chen, Kaori Sugihara (*IIS., Univ. Tokyo*)

- 1GF012** コレラ菌走化性受容体 Mlp24 による GABA および L-オルニチンのリガンド認識機構
Ligand recognition mechanisms of GABA and L-orithine by the chemoreceptor Mlp24 in *Vibrio cholerae*
○飯田 莉梨香¹, 大森 楓河², 竹川 宜宏³, 西山 宗一郎⁴, 川岸 郁朗^{2,5,6}, 今田 勝巳³ (¹阪大・理,
²法政大・院理工,³阪大・院理,⁴新潟薬大・応用生命,⁵法政大・生命科学,⁶法政大・マイクロ・ナノテクセンター)
Ririka Iida¹, Fuga Omori², Norihiro Takekawa³, So-ichiro Nishiyama⁴, Ikuro Kawagishi^{2,5,6},
Katsumi Imada³ (¹*Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Sci. and Engin., Hosei Univ.*, ³*Grad. Sch. Sci., Osaka Univ.*, ⁴*Dept. Appl Life Sci, Niigata Univ of Pharm and Appl Life Sci.*, ⁵*Dept. Front Biosci., Hosei Univ.*, ⁶*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

1GG 生命の起源・進化, 理論生物学, バイオイメージング
Origin of life & Evolution, Theoretical biology, Bioimaging

座長: 市橋 伯一 (東京大学), 望月 敦史 (京都大学)

Session Chairs: Norikazu Ichihashi (Univ. Tokyo), Atsushi Mochizuki (Kyoto Univ.)

15:10~18:10

G 会場 (会議室 203) / Room G (Meeting Room 203)

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- 1GG001** Molecular Simulation of Prebiotically Plausible Interactions Between Amino Acids and Fatty Acid Membranes
Taren Ginter^{1,2}, Ryoji Abe^{1,2}, Masayuki Imai³, Akiko Baba³, Wataru Shinoda^{4,5}, Yusuke Miyazaki^{4,5}, Kosuke Fujishima^{1,6} (¹*Earth-Life Science Institute*, ²*Institute of Science Tokyo, School of Life Science and Technology*, ³*Tohoku University, Department of Physics*, ⁴*Okayama University, Research Institute for Interdisciplinary Science*, ⁵*Okayama University, Department of Chemistry*, ⁶*Keio University, Graduate School of Media and Governance*)
- 1GG002** 液液相分離系を反応場とした遺伝子の複雑化を伴う進化の実現
Evolution with genomic complexity acquisition under LLPS droplet as a reaction field
○佐々木 弥来¹, 皆川 慶嘉¹, 野地 博行^{1,2} (¹東京大・院工学,²東京大・プラネタリーヘルス研究機構)
Mirai Sasaki¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Grad. Sch. Eng., Univ. Tokyo*, ²*RIPH., Univ. Tokyo*)
- 1GG003** 核酸分子と脂肪酸膜系の相互作用機構および脂肪酸膜系存在下での核酸分子の拡散挙動の全原子分子動力学シミュレーションを用いた解析
Analysis of the interaction and diffusion behavior of nucleic acid molecules with the fatty acid membrane system using AA-MD simulations
○安部 稜士¹, ギンター テーレン¹, 藤島 皓介^{1,2,3} (¹東京科学大学 生命理工学院,²東京科学大学 地球生命研究所,³慶應義塾大学大学院 政策・メディア研究科)
Ryoji Abe¹, Taren Ginter¹, Kosuke Fujishima^{1,2,3} (¹*School of Life Science and Technology, Science Tokyo*, ²*Earth-Life Science Institute, Science Tokyo*, ³*Graduate School of Media And Governance, Keio University*.)
- 1GG004** 遺伝子間の量比保存関係を通した遺伝的摂動効果のグローバルな波及
Global propagation of genetic perturbation effects through stoichiometry conservation architecture
○千葉 元太¹, 亀井 健一郎¹, 小田 有沙^{1,2}, 太田 邦史^{1,2,3}, 若本 祐一^{1,2,3} (¹東大・院総合文化,²東大・複雑系生命システム研究センター,³東大・生物普遍性研究機構)
Genta Chiba¹, Ken-ichiro F Kamei¹, Arisa H Oda^{1,2}, Kunihiro Ohta^{1,2,3}, Yucih Wakamoto^{1,2,3} (¹*Grad. Sch. Arts Sci., Univ. Tokyo*, ²*Res. Cent. Complex Syst. Biol., Univ. Tokyo*, ³*UBI, Univ. Tokyo*)

- [1GG005](#) 生命システムにおける生体要素間相互作用の一般化勾配流モデルに基づく数理表現
Describing Interaction Dynamics in Living Systems via the Generalized Gradient Flow Model of Adaptive Components
○鈴木 龍之介^{1,2}, 安達 泰治^{1,2,3} (¹京大・医生研,²京大・院工,³京大・院生命)
Ryunosuke Suzuki^{1,2}, Taiji Adachi^{1,2,3} (¹LiMe, Kyoto Univ., ²Grad. Sch. Eng., Kyoto Univ., ³Grad. Sch. Life Sci., Kyoto Univ.)
- [1GG006](#) 機械学習を用いた細胞形状情報とストレスファイバー形成機構を考慮した細胞の牽引力推定
Cell Morphology and Stress Fiber Formation Mechanisms-Informed Traction Force Microscopy Using Machine Learning
○藤原 弘貴¹, 藤川 良祐¹, 鈴木 文丈¹, 鈴木 健大^{1,2}, 作村 諭一^{1,2} (¹奈良先端大・院科学技術,²奈良先端大・データ駆動センター)
Koki Fujiwara¹, Ryosuke Fujikawa¹, Yukihiko Suzuki¹, Kenta T. Suzuki^{1,2}, Yuichi Sakumura^{1,2} (¹Grad. Sch. Sci. Tech., NAIST, ²DSC, NAIST)
- [1GG007](#) 麻酔または光遺伝学制御による生きている線虫 *C. elegans* の赤外イメージング手法の開拓
Development of infrared imaging methods for a living nematode, *C. elegans*, using anesthetics or optogenetic control
○脇田 和佳¹, 伊藤 明子¹, 佐藤 龍², 錦野 達郎^{1,3}, 小柳 光正^{2,4}, 古谷 祐詞^{1,3} (¹名古屋工業大学大学院工学研究科,²大阪公立大学大学院理学研究科,³オプトバイオテクノロジー研究センター,⁴大阪公立大学複合先端研究センター)
Nodoka Wakita¹, Akiko Ito¹, Ryu Sato², Tatsuro Nishikino^{1,3}, Mitsumasa Koyanagi^{2,4}, Yuji Furutani^{1,3} (¹Graduate School of Engineering, Nagoya Institute of Technology, ²Graduate School of Science, Osaka Metropolitan University, ³Optobiotechnology Research Center, ⁴The OMU Advanced Research Institute for Natural Science and Technology, Osaka Metropolitan University)
- [1GG008](#) X線回折イメージング・トモグラフィーにおける三次元構造精密化手法の開発とデンプン粒子構造解析への応用
Development of structure refinement protocol for XDIT and its application to structure analysis of rice-starch
○原田 康生^{1,4}, 高山 裕貴^{2,4}, 中迫 雅由^{3,4} (¹慶應義塾大学 大学院理工学研究科,²東北大学 国際放射光イノベーション・スマート研究センター,³慶應義塾大学 理工学部 物理学科,⁴理化学研究所 放射光科学研究センター)
Kosei Harada^{1,4}, Yuki Takayama^{2,4}, Masayoshi Nakasako^{3,4} (¹Graduate School of Science and Technology, Keio University, ²International Center for Synchrotron Radiation Innovation Smart, Tohoku University, ³Department of Physics, Faculty of Science and Technology, Keio University, ⁴RIKEN SPring-8 Center)
- [1GG009](#) 超解像顕微鏡による非凍結性低温環境下における不凍タンパク質の細胞部位特異的局在の解析
Subcellular Localization of Antifreeze Proteins in a Non-Freezing Cold Environment Revealed by Super-Resolution Microscopy
○前田 皓丞¹, 内澤 風穂¹, 津田 栄², 相沢 智康^{1,2}, 新井 達也^{1,2} (¹北海道大学 理学部,²北海道大学 先端生命科学研究院)
Kosuke Maeda¹, Kaho Uchizawa¹, Sakae Tsuda², Tomoyasu Aizawa^{1,2}, Tatsuya Arai^{1,2} (¹School of Science, Hokkaido University, ²Faculty of Advanced Life Science, Hokkaido University)
- [1GG010](#) 蛍光ナノ粒子を用いた細胞質の特性計測
Probing cytoplasmic physics with Genetically Encoded Multimeric nanoparticles
○廣兼 空¹, 岡田 康志^{1,2,3} (¹東大・理,²東大・医,³理研 BDR)
Sora Hirokane¹, Yasushi Okada^{1,2,3} (¹Grad. Sch. Sci., Univ. Tokyo, ²Grad. Sch. Med., Univ. Tokyo, ³BDR, Riken)
- [1GG011](#) 神経突起伸長過程におけるシナプス接着分子の蛍光 1 分子追跡による時空間動態解析
Spatiotemporal dynamics analysis of synaptic adhesion molecules during neurite outgrowth by single molecule fluorescence imaging
○佐々木 洸大, 並木 繁行, 浅沼 大祐, 廣瀬 謙造 (東大・院医)
Kodai Sasaki, Shigeyuki Namiki, Daisuke Asanuma, Kenzo Hirose (Grad. Sch. Med., Univ. Tokyo)

[1GG012](#) トランススケール生細胞イメージングによる希少細胞融合現象から形成されるハイブリッド腫瘍細胞の動態解析
Visualizing rare cell fusion events leading to hybrid tumor cell formation using trans-scale live-cell imaging
○ラフィダー イッサティ^{1,2}, 福島 俊一², 垣塚 太志^{2,3}, 和沢 鉄一², 市村 垂生³, 熊ノ郷 淳⁴, 永井 健治^{2,3} (¹大阪大学薬学研究科, ²大阪大学産業科学研究所, ³大阪大学先導的学際研究機構, ⁴大阪大学大学院医学系研究科)
Izzati Rafidah^{1,2}, Shun-ichi Fukushima², Taishi Kakizuka^{2,3}, Tetsuichi Wazawa², Taro Ichimura³, Atsushi Kumanogoh⁴, Takeharu Nagai^{2,3} (¹The University of Osaka Graduate School of Pharmaceutical Sciences, ²SANKEN, The University of Osaka, ³OTRI, The University of Osaka, ⁴The University of Osaka Graduate School of Medicine)

1GH 計算生物学: 分子シミュレーション, モデリング
Computational biology: Molecular simulation, Modeling

座長: 奥村 久士 (自然科学研究機構), 川口 一朋 (金沢大学)

Session Chairs: Hisashi Okumura (ExCELLS), Kazutomo Kawaguchi (Kanazawa Univ.)

15:10~18:10

H 会場 (会議室 204) / Room H (Meeting Room 204)

[1GH001](#) 分子動力学シミュレーションとアンブレラサンプリングによる神経疾患関連フィラミン A 変異の構造解析
Molecular Dynamics and Umbrella Sampling Reveal Structural Changes in Filamin-A Mutants associated with Neurodegenerative disorders
○伊藤 翔太¹, 辻河 高陽², 佐橋 健太郎¹, 川崎 猛史^{3,4}, 榮 慶文⁵, 勝野 雅央¹ (¹名古屋大学大学院医学系研究科 総合医学専攻 脳神経病態制御学 神経内科学分野, ²名古屋大学 環境医学研究所 発生遺伝分野, ³大阪大学 D3 センター 大規模計算科学研究部門, ⁴大阪大学大学院理学研究科 物理学専攻, ⁵一般財団法人 高度情報科学技術研究機構)
Shota Ito¹, Koyo Tsujikawa², Kentaro Sahashi¹, Takeshi Kawasaki^{3,4}, Yoshitake Sakae⁵, Masahisa Katsuno¹ (¹Department of Neurology, Nagoya University Graduate School of Medicine, ²Department of Genetics, Research Institute of Environmental Medicine, Nagoya University, ³D3 center, Osaka University, ⁴Department of Physics, Osaka University, ⁵Research Organization for Information Science and Technology)

[1GH002](#) 脂質漏洩下におけるナノディスク中の膜タンパク質の構造安定性
Effect of Lipid Leakage on the Structural Stability of Membrane Proteins in Nanodiscs
○井上 紗良, 森 貴治 (東理大院・理)

Sara Inoue, Takaharu Mori (Tokyo University of Science)

[1GH003](#) AlphaFold で予測された多状態の強化サンプリングに基づくタンパク質の自由エネルギー計算手法の開発

Development of Free Energy Calculation Method Based on Enhanced Sampling of Various Protein Conformations Predicted by AlphaFold

○青木 斗真¹, 重田 育照², 原田 隆平² (¹筑波大学 生命環境学群, ²筑波大学 計算科学研究センター)

Toma Aoki¹, Yasuteru Shigeta², Ryuhei Harada² (¹School of Life and Environmental Sciences, University of Tsukuba, ²Center for Computational Sciences, University of Tsukuba)

[1GH004](#) In silico study of transmembrane allosteric effect of CBD on CB1 receptor activation
Vi Toan Lam, Duy Phuoc Tran, Akio Kitao (Institute of Science Tokyo)

- [1GH005](#) Differences in Conformational Dynamics of Glycans on FcγRIIIb Revealed by Molecular Simulation
Yue Zhang¹, Hirokazu Yagi^{2,3}, Koichi Kato^{2,3}, Takumi Yamaguchi^{1,2,3} (¹*Sch. Materials Sci., JAIST*,
²*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, ³*ExCELLS, NINS*)
- [1GH006](#) 構造に基づく機構的理解：SAMを基質とする求核型・求電子型 PLP 酵素の比較
 Structure-Based Mechanistic Insights into Nucleophilic and Electrophilic PLP Enzymes Using SAM
 ○島田 和樹¹, 淡川 孝義², 寺田 透¹ (¹ 東大・院農, ² 理研・環境資源科学研究センター)
Kazuki Shimada¹, Takayoshi Awakawa², Tohru Terada¹ (¹*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*CSRS, Riken*)
- [1GH007](#) Theoretical Study of Drug Resistance Caused by G13D and Q99L Secondary Mutations in KRAS G12C Against Sotorasib and Adagrasib
Riksa Meidy Karim, Kazutomo Kawaguchi, Hidemi Nagao (*Graduate School of Natural Science and Technology, Kanazawa University*)
- [1GH008](#) 細胞スケールの生命現象の解明に向けた新規粗視化分子動力学法の開発
 Innovating Coarse-grained Molecular Dynamics Simulation: beyond Temporal/Spatial Limits
 ○手代木 陽介, 寺田 透 (東大・院農・応生工)
Yosuke Teshirogi, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)
- [1GH009](#) 血流中の酸素の拡散のシミュレーション
 Simulation of oxygen diffusion in blood flow
 ○山本 哲也^{1,2}, 野口 博司², Dmitry Fedosov³ (¹ 慶應大・院理工, ² 東大物性研, ³ FZ Jülich)
Tetsuya Yamamoto^{1,2}, Hiroshi Noguchi², Dmitry Fedosov³ (¹*Grad. Sch. Sci. and Tech., Keio Univ.*, ²*JSSP, Univ. Tokyo*, ³*FZ Jülich*)
- [1GH010](#) De Novo ATPase の触媒活性の合理的改善
 Rational Enhancement of De Novo ATPase Activity
 ○織田 拓也¹, 小杉 貴洋², 林 重彦¹ (¹ 京都大学大学院理学研究科, ² 分子科学研究所 協奏分子システム研究センター)
Takuya Orita¹, Takahiro Kosugi², Shigehiko Hayashi¹ (¹*Graduate School of Science, Kyoto University*, ²*Research Center of Integrative Molecular Systems, Institute for Molecular Science*)
- [1GH011](#) Mesoscale Modeling of Amyloid Formation in Heterogeneous Membraneless Organelles
Kento Fujita, Yusuke Takagi, Eiji Yamamoto (*Grad. Sci., Univ. Keio*)
- [1GH012](#) メロテルペノイドの生合成経路におけるプレニル基転移酵素 Fur7 の触媒機構の計算的研究
 Computational Study on the Catalytic Mechanism of Prenyltransferase Fur7 in the Biosynthetic Pathway of Meroterpenoids
 ○大村 拓登¹, 趙 凡¹, 森脇 由隆², 野口 智弘¹, 白石 太郎¹, 葛山 智久¹, 寺田 透¹ (¹ 東大・院農生工, ² 科学大・難治疾患研)
Takuto Ohmura¹, Fan Zhao¹, Yoshitaka Moriwaki², Tomohiro Noguchi¹, Taro Shiraishi¹, Tomohisa Kuzuyama¹, Tohru Terada¹ (¹*Dept. of Biotechnol., Grad. Sch. of Agri and Life Science., The Univ. of Tokyo*, ²*Med. Res. Lab., Inst. Integr. Res., Science Tokyo*.)

1GI 光生物学：光受容，光合成，生態/環境
 Photobiology: Photoreception, Photosynthesis, Ecology & Environment

座長：栗栖 源嗣（大阪大学），三野 広幸（名古屋大学）

Session Chairs: Genji Kurisu (Osaka Univ.), Hiroyuki Mino (Nagoya Univ.)

15:10~18:10

I 会場（会議室 205）／Room I（Meeting Room 205）

- 1GI001** 紫外光吸収型色覚視物質の構造的洞察
Structural insights into UV sensitivity of mouse SWS1 opsin revealed by low-temperature FTIR spectroscopy
○水野 陽介¹, 新井 想空¹, 神取 秀樹^{1,2}, 片山 耕大^{1,2} (¹名工大 院工, ²名工大 オプトバイオテクノロジー研究センター)
- Yosuke Mizuno**¹, Sora Arai¹, Hideki Kandori^{1,2}, Kota Katayama^{1,2} (¹Grad. Sch. Eng., Nagoya inst. Tech., ²OptoBio Technology Research Center, Nagoya inst. Tech.)
- 1GI002** Chrimson に近縁な新奇チャネルロドプシン HulaChrimson の青色シフト吸収スペクトルとその起源
HulaChrimson—a novel channelrhodopsin homologous to Chrimson with a distinctly blue-shifted absorption spectrum
Hiroto Takahashi¹, Shunki Takaramoto¹, Takashi Nagata¹, Shai Fainsod², Yoshitaka Kato¹, Andrey Rozenberg², Oded Béjà^{2,3}, Keiichi Inoue¹ (¹The Institute for Solid State Physics, The University of Tokyo., ²Faculty of Biology, Technion — Israel Institute of Technology., ³The Nancy and Stephen Grand Technion Energy Program (GTEP), Technion—Israel Institute of Technology.)
- 1GI003** キラル分光を用いた先祖型 Photoactive Yellow Protein 活性部位の構造解析
Structural analysis of the active site of ancestral photoactive yellow protein using chiral spectroscopy
○尾中 良充¹, Dohmen Rosalie², 藤澤 知績¹, Hoff Wouter D.², 海野 雅司¹ (¹佐賀大・院理工学, ²オクラホマ州立大)
- Yoshimitsu Onaka**¹, Rosalie Dohmen², Tomotsumi Fujisawa¹, Wouter D. Hoff², Masashi Unno¹ (¹Fuc. Sci. Eng., Saga Univ., ²Dep. Microbiol. Mol Gen., Oklahoma State Univ.)
- 1GI004** 新規チャネルロドプシン ChR024 の長波長光吸収メカニズムおよびイオン透過機構の構造基盤
Structural basis for the red-shifted absorption and the channel conducting mechanism of the novel channelrhodopsin ChR024
○竹野 有香¹, 渡部 誠也², 岸 孝一郎², 但馬 聖也³, 福田 昌弘³, 辻村 真樹⁴, 寶本 俊輝⁵, 伊藤 佑真⁶, 山下 陽⁶, 杉浦 雅大⁶, 金 穂香³, 片山 耕大⁶, 古谷 祐詞⁶, 神取 秀樹⁶, 石北 央^{3,4}, 井上 圭一⁵, 加藤 英明^{1,2,3} (¹東大・院理, ²東大・院総文, ³東大・先端研, ⁴東大・院工, ⁵東大・物性研, ⁶名工大・院工)
- Yuka E. Takeno**¹, Masaya Watanabe², Koichiro E. Kishi², Seiya Tajima³, Masahiro Fukuda³, Masaki Tsujimura⁴, Shunki Takaramoto⁵, Yuma Ito⁶, Yo Yamashita⁶, Masahiro Sugiura⁶, Suhyang Kim³, Kota Katayama⁶, Yuji Furutani⁶, Hideki Kandori⁶, Hiroshi Ishikita^{3,4}, Keiichi Inoue⁵, Hideaki E. Kato^{1,2,3} (¹Grad. Sch. Sci., Univ. Tokyo, ²Grad. Sch. Arts and Sci., Univ. Tokyo, ³RCAST, Univ. Tokyo, ⁴Grad. Sch. Eng., Univ. Tokyo, ⁵ISSP, Univ. Tokyo, ⁶Grad. Sch. Eng., Nagoya Inst. Tech.)
- 1GI005** L/M 錐体視物質の三次元構造から導く波長制御機構
Unveiling the spectral tuning mechanism through three-dimensional structures of red and green cone pigments
Sayaka Ohashi¹, Kota Katayama^{1,2}, Asato Kojima³, Masahiro Fukuda⁴, Xuchun Yang⁵, Ryoji Suno⁶, Yukihiro Sugita⁷, Nipawan Nuemket^{8,9}, Hiroo Imai¹⁰, So Iwata^{9,11}, Eriko Nango^{9,12}, Takuya Kobayashi⁶, Takeshi Noda⁷, Massimo Olivucci^{5,13}, Hideaki Kato^{3,4}, Hideki Kandori^{1,2} (¹Life Science and Applied Chemistry, Nagoya Institute of Technology, ²OptoBioTechnology Research Center, ³The Graduate School of Arts and Sciences, The University of Tokyo, ⁴Research Center for Advanced Science and Technology, The University of Tokyo, ⁵University of Siena, ⁶Kansai Medical University, ⁷Institute for Life and Medical Sciences, Kyoto University, ⁸Japan Synchrotron Radiation Research Institute, ⁹RIKEN Spring-8 Center, ¹⁰Center for the Evolutionary Origins of Human Behavior, Kyoto University, ¹¹The Graduate School of Medicine, Kyoto University, ¹²Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, ¹³Bowling Green State University)

- [1GI006](#) ヘリオロドプシンの光反応ダイナミクスを決める SNaP bond の赤外分光法による水素結合解析
Direct detection of a crucial Hydrogen Bond in Heliorhodopsin, SNaP bond, using Low-Temperature IR Spectroscopy
○中村 敏規¹, Singh Manish¹, 神取 秀樹^{1,2}, 古谷 祐詞^{1,2} (¹名古屋工業大学大学院工学研究科生命応用化学専攻, ²名古屋工業大学オプトバイオテクノロジー研究センター)
Toshiki Nakamura¹, Manish Singh¹, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology, Nagoya, Japan*, ²*OptoBioTechnology Research Center, Nagoya Institute of Technology, Nagoya, Japan*)
- [1GI007](#) クラゲロドプシンにおける特異な構造変化が示す Gs タンパク質活性化の作用メカニズム
Distinct structural transition in jellyfish rhodopsin reveals the mechanistic basis for Gs protein activation
○大飼 紫乃¹, 小柳 光正², 永田 崇³, 井上 圭一³, 寺北 明久², 神取 秀樹^{1,4}, 片山 耕大^{1,4} (¹名古屋工業大学・院工, ²大阪公立大学・院理, ³東大・物性研, ⁴名古屋工業大学・オプトバイオテクノロジー研究センター)
Shino Inukai¹, Mitsumasa Koyanagi², Takashi Nagata³, Keiichi Inoue³, Akihisa Terakita², Hideki Kandori^{1,4}, Kota Katayama^{1,4} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Grad. Sch. Sci., Osaka Met. Univ.*, ³*ISSP, The Univ. Tokyo*, ⁴*OptoBioTechnology Research Center, Nagoya Inst. Tech.*)
- [1GI008](#) 多周波 EPR による光化学系 II マンガンクラスター S₂ g ~ 5 状態の構造と機能の解析
Role of S₂ g ~ 5 state in photosystem II manganese cluster revealed by multifrequency EPR
○小崎 慎也¹, 中島 芳樹², 沈 建仁², 三野 広幸¹ (¹名古屋大学・院理, ²岡山大学・異分野基礎研)
Shinya Kosaki¹, Yoshiki Nakajima², Jian-Ren Shen², Hiroyuki Mino¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Res. Inst. Interdiscip. Sci., Okayama Univ.*)
- [1GI009](#) 外向きプロトンポンプロドプシンにおける弱有機酸結合の研究
Study of weak organic acid binding on outward proton-pumping rhodopsin
○呂子琨¹, 宝本 俊輝², 井上 圭一^{1,2} (¹東京大学 大学院新領域創成科学研究科 物質系専攻, ²東京大学 物性研究所)
Zikun Lyu¹, Shunki Takaramoto², Keiichi Inoue^{1,2} (¹*The Department of Advanced Materials Science, Graduate School of Frontier Sciences, The University of Tokyo*, ²*The Institute for Solid State Physics, University of Tokyo*)
- [1GI010](#) 内向きプロトンポンプロドプシン NsXeR の新しいプロトン移動メカニズム
A new proton transfer mechanism for inward proton pump rhodopsin NsXeR
○伊藤 侑真¹, 錦野 達郎^{1,2}, 神取 秀樹^{1,2}, 古谷 祐詞^{1,2} (¹名古屋工業大学・院工, ²名古屋工業大学・オプトバイオ)
Yuma Ito¹, Tatsuro Nishikino^{1,2}, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹*Department of Life Science and Applied Chemistry, Nagoya institute of technology*, ²*OptoBioTechnology Research Center, Nagoya institute of technology*)
- [1GI011](#) 摂食による細菌のけいれん運動の制御
Controlling Bacterial Twitching Motility by Feeding
Shufeng Zhao¹, Corrado Salvatore², Nozomu Obana³, Andrew Utada⁴ (¹*Graduate School of Science and technology, University of Tsukuba, Japan*, ²*Department of Computer Engineering, Modelling, Electronics and Systems Engineering, University of Calabria, Italy*, ³*Institute of Medicine, University of Tsukuba, Japan*, ⁴*Institute of Life and Environment Science, Microbial research Center for Sustainability, and Tsukuba Institute for Advanced Research, University of Tsukuba, Japan*)
- [1GI012](#) 油水界面における生物膜の剪断駆動型不安定性
Shear-driven instability in biofilms at oil–water interfaces
Hongtao Zhang¹, Shufeng Zhao¹, Andrew Utada^{2,3,4} (¹*Graduate School of Life and Earth Sciences, Univ. Tsukuba*, ²*Institute of Life and Environment Science, Univ. Tsukuba*, ³*Microbial research Center for Sustainability, Univ. Tsukuba*, ⁴*Tsukuba Institute for Advanced Research, Univ. Tsukuba*)

1GJ 合成生物学・人工細胞, 計測, その他
Synthetic biology & Artificial cells, Measurements, Miscellaneous topics

座長: 日比野 佳代 (大阪大学), 内橋 貴之 (名古屋大学)

Session Chairs: Kayo Hibino (Osaka Univ.), Takayuki Uchihashi (Nagoya Univ.)

15:10~18:10

J 会場 (会議室 206) / Room J (Meeting Room 206)

- 1GJ001** tRNA array 法による 21 種類の tRNA の in vitro 同時発現
Simultaneous in vitro expression of minimal 21 transfer RNAs by tRNA array method
○宮地 亮多¹, 益田 恵子², 清水 義宏², 市橋 伯一^{1,3,4} (¹東京大院 総合文化研究科 広域科学専攻, ²理研 BDR, ³東京大 先進科学研究機構, ⁴東京大 生物普遍性研究機構)
Ryota Miyachi¹, Keiko Masuda², Yoshihiro Shimizu², Norikazu Ichihashi^{1,3,4} (¹Grad. Sch. Arts Sci., Univ. Tokyo, ²Riken BDR, ³Komaba Institute for Sci., Univ. Tokyo, ⁴Research Center for Complex System Biology, Universal Biology Institute Univ. Tokyo)
- 1GJ002** Versatile control of a minimal synthetic bacterium JCVI-syn3B for morphology and fusion
Muhammad Algiffari¹, Hana Kiyama¹, Yoshiki Tanaka², Makoto Miyata^{1,3} (¹Grad. Sch. Sci., Osaka Metropolitan Univ., ²Dept. Phys., Gakushuin Univ., ³OCARINA, Osaka Metropolitan Univ.)
- 1GJ003** 脂質小胞への改変型 β バレルナノポアの再構成手法と分子輸送の検討
Reconstitution method and molecular transport of modified β -barrel nanopore into lipid vesicles
○登坂 俊行, 神谷 厚輝 (群大・院理工)
Toshiyuki Tosaka, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)
- 1GJ004** 人工 DNA 皮質構造による GUV 膜における分子分布制御に向けて
Toward regulation of molecular distribution in giant unilamellar vesicles based on artificial DNA cortex
○吉永 琢朗, 佐藤 佑介 (九州工業大学 大学院 情報工学府)
Takuro Yoshinaga, Yusuke Sato (*Graduate School of Computer Science and Systems Engineering, Kyushu Institute of Technology.*)
- 1GJ005** Design of bioluminescent biosensors via enzymatic kinetic contrast: Demonstration with a Cu²⁺ Sensor
Ti Wu^{1,2}, Hossain Md Nadim¹, Mitsuru Hattori¹, Takeharu Nagai^{1,2} (¹SANKEN, The University of Osaka, ²The Graduate School of Pharmaceutical Sciences, The University of Osaka)
- 1GJ006** 蛍光ナノダイヤモンドを用いた細胞内温度と粒子拡散の同時計測による細胞内環境の解析
Analysis of the intracellular environment by simultaneous measurement of temperature and particle diffusion using fluorescent nanodiamonds
○加藤 祐基¹, 藤田 恵介², 外間 進悟³, 原田 慶恵^{2,4} (¹阪大理・生物, ²阪大 WPI-PRIME, ³京都工繊 分子化学, ⁴阪大 QIQB)
Yuki S. Kato¹, Keisuke Fujita², Shingo Sotoma³, Yoshie Harada^{2,4} (¹Sch. Sci., Univ. Osaka, ²WPI-PRIME, Univ. Osaka, ³Fac. Mol. Chem. Eng., Kyoto Inst. Tech., ⁴QIQB, Univ. Osaka)
- 1GJ007** 液相分離に基づいた新規マイクロリアクタの開発によるデジタル核酸検出の簡便化の実現
New Microreactors from Aqueous Two-Phase Emulsion for the Simplification of Digital Nucleic Acid Detection
○張 畢澄¹, 友原 貫志², 皆川 慶嘉¹, 野地 博行^{1,3} (¹東京大学大学院工学研究科応用化学専攻, ²Laboratoire Guillaiver, UMR7083 CNRS/ESPCI Paris, ³東京大学プラネタリーヘルス研究機構)
Bicheng Zhang¹, Kanji Tomohara², Yoshihiro Minigawa¹, Hiroyuki Noji^{1,3} (¹Graduate School of Engineering, The University of Tokyo, Tokyo, Japan, ²Laboratoire Guillaiver, UMR7083 CNRS/ESPCI Paris, ³Research Institute of Planetary Health (RIPH), The University of Tokyo)

- [1GJ008](#) **ハイスループットイメージングによる適応酵素 CheB 細胞内動態の解析**
 Quantification of CheB's behavior in a single cell by high throughput imaging
 ○黒木 陽一, 内田 裕美子, 石島 秋彦, 福岡 創 (阪大・院生命機能研究)
Yoichi Kuroki, Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)
- [1GJ009](#) **原子間力顕微鏡を用いたアフリカツメガエル初期胚の単一細胞力学マッピング測定**
 Mapping Single-Cell Mechanics in *Xenopus laevis* Embryos during Early Development Using Atomic Force Microscopy
 ○山本 実季¹, 小谷 崇博¹, 山元 孝佳², 道上 達男³, 岡嶋 孝治¹ (¹北海道大学・大学院情報科学
 院 / 研究院, ²東京学芸大学・教育学部, ³東京大学・大学院総合文化研究科)
Miki Yamamoto¹, Takahiro Kotani¹, Takayoshi Yamamoto², Tatsuo Michiue³, Takaharu Okajima¹
 (¹*Graduate School / Faculty of Information Science and Technology, Hokkaido University*, ²*Graduate School / Faculty of Education, Tokyo Gakugei University*, ³*Graduate School / Faculty of Arts and Sciences, The University of Tokyo*)
- [1GJ010](#) **生体内 3D 温度計測技術の開発と応用**
In vivo 3D thermometry by light-field fluorescent nanodiamond microscopy and deep learning
 ○中根 有梨奈¹, 前岡 遥花¹, 高橋 真奈美², 神長 輝一², 田桑 弘之², 白杵 深³, 五十嵐 龍治²,
 杉 拓磨¹ (¹広島大学大学院統合生命科学研究科, ²量子科学技術研究開発機構, ³静岡大学電子工
 学研究科)
Yurina Nakane¹, Haruka Maeoka¹, Manami Takahashi², Kiich Kaminaga², Hiroyuki Takuwa²,
 Shin Usuki³, Ryuji Igarashi², Takuma Sugi¹ (¹*Graduate School of Integrated Sciences for Life, Hiroshima University*, ²*National Institutes for Quantum and Radiological Science and Technology*, ³*Research Institute of Electronics, Shizuoka University*)
- [1GJ011](#) **Developing a label-free and non-destructive method to resolve single cell transition paths**
Tobias Frick^{1,2}, Katsuyuki Shiroguchi¹ (¹*RIKEN Center for Biosystems Dynamics Research (BDR)*,
²*Osaka University*)
- [1GJ012](#) **透過型電子顕微鏡によるヒドラとグリーンヒドラの組織構造比較研究**
 Transmission Electron Microscopy Comparative Study of Histological Structure of Hydra and Green Hydra
 ○梁瀬 智輝 (九工大・情報工)
Tomoki Yanase (*Information Engineering, Univ. Kyusyu kougyou*)

1日目（9月24日（水））／Day 1（Sep. 24 Wed.）

1EA 核酸：結合タンパク質，ナノテクノロジー
Nucleic acid: binding protein, nanotechnology

座長：西尾 天志（産総研・モレキュラーバイオシステム），Archer Richard James（東京科学大）

Session Chairs: Takashi Nishio (MolBis, AIST), Richard James Archer (Inst. Sci. Tokyo)

18:50~20:30

A会場（会議室 101+102）／Room A（Meeting Room 101+102）

- [1EA001](#) 細胞サイズ液滴内における DNA 高次構造変化と局在・液滴物性の相関
Higher-order structure of DNA confined in cell-size droplets modulates its localization and droplet material properties
○西尾 天志（産総研・モレキュラーバイオシステム）
Takashi Nishio (*MolBis, AIST*)
- [1EA002](#) Nuclease-induced stepwise photodrooping (NISP) to investigate single-stranded DNA degradation behaviors of exonucleases and endonucleases
Hsiufang Fan (*National Sun Yat-sen University, Kaohsiung, Taiwan*)
- [1EA003](#) Modulation of RNA transcription through DNA condensates reactions' encapsulation as a model for Chromatin micro rheology studies
Nathan Evangelista¹, Takahiko Chimura², Masahiro Takinoue^{1,2,3} (¹*Dept. of Life Sci. and Tech., Inst. of Science Tokyo*, ²*Dept. of Comp. Sci., Inst. of Science Tokyo*, ³*Research Center for Autonomous Systems Materialogy (ASMat), Inst. of Integrated Research (IIR), Inst. of Science Tokyo*)
- [1EA004](#) Dynamic assembly of complex hierarchical DNA polymer networks by biomolecular active agents
Farhana Afroze¹, **Richard James Archer**^{2,6}, Mahammad Mustakim³, Rakesh Das⁴, Arif Md. Rashedul Kabir¹, Yuuto Miura¹, Rubaya Rashid⁵, Tetsuya Hiraiwa³, Shin-ichiro M. Nomura², Shogo Hamada^{6,7}, Akira Kakugo^{1,5} (¹*Department of Chemistry, Hokkaido University, Sapporo, Japan.*, ²*Department of Robotics, Tohoku University, Sendai, Japan.*, ³*Institute of Physics, Academia Sinica, Taipei, Taiwan.*, ⁴*Max Planck, Institute for the Physics of Complex Systems, Dresden, Germany.*, ⁵*Department of Physics and Astronomy, Kyoto University, Kyoto, Japan.*, ⁶*Department of Computer Science, Institute of Science Tokyo, Yokohama, Japan.*, ⁷*Biomolecular Design Institute, CBI Research Institute, Tokyo, Japan.*)

1EB バイオイメーキング，計測
Bioimaging, Measurement

座長：山崎 健（金沢大・ナノ生命科学研究所），楊 倬皓（東大・先端研）

Session Chairs: Takeru Yamazaki (WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa Univ.), Zhuohao Yang (RCAT, Univ. Tokyo)

18:50~20:30

B会場（会議室 103+104）／Room B（Meeting Room 103+104）

- [1EB001](#) FLIM による温度測定のために粘度応答を抑制した赤色蛍光温度計
Red Fluorescent Thermometer with Suppressed Viscosity Response for FLIM-based Thermometry
○山崎 健¹, 山澤 徳志子², 平田 修造³, 新井 敏¹ (¹金沢大・ナノ生命科学研究所, ²東京慈恵医大・基盤研究施設, ³東京電通大・院情報理工)
- Takeru Yamazaki¹**, Toshiko Yamazawa², Syuzo Hirata³, Satoshi Arai¹ (¹*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa Univ.*, ²*Core Research Facilities, The Jikei Univ. Sch. of Med.*, ³*Dept. of Eng. Sci., Univ. of Electro-Commun.*)
- [1EB002](#) The maturation state of dengue virus particles affects their structural dynamics and nanomechanical properties
Steven John McArthur, Kenichi Umeda, Noriyuki Kodera (*Nano Life Science Inst., Kanazawa Univ.*)
- [1EB003](#) Comprehensive profiling of single-cell proteome based on 3D single-molecule imaging
Latiefia Kamarulzaman^{1,2}, Sooyeon Kim¹, Takuya Hidaka⁴, Yuichi Taniguchi^{1,2,3} (¹*Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University*, ²*Graduate School of Frontier Biosciences, The University of Osaka*, ³*Graduate School of Biostudies, Kyoto University*, ⁴*Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA), Vienna BioCenter (VBC)*)
- [1EB004](#) Single aptamer-modified DNA origami nanopore for specific chemical detection
Hiromu Akai, Kan Shoji (*Nagaoka University of Technology*)
- [1EB005](#) Pixel-Wise Deconvolution of Antibody Binding Kinetics Enables Visualization of Instantaneous Secretion Dynamics
Zhuohao Yang¹, Takashi Kamatani², Mai Yamagishi³, Nobutake Suzuki¹, Yuto Kurisu⁴, Takashi Funatsu^{1,5}, Yasuyuki Ozeki¹, Yoshitaka Shirasaki¹ (¹*RCAST, Univ. Tokyo*, ²*Inst. Integrated Res., Inst. Sci. Tokyo*, ³*Live Cell Diagnosis, Ltd.*, ⁴*Grad. Sch. Pharm. Sci., Univ. Tokyo*, ⁵*Grad. Sch. Integrated Sci. for Life, Hiroshima Univ.*)

1EC 細胞生物学的課題, 分子モーター, 非平衡
Cell biology, Molecular motor, Nonequilibrium

座長: 藤瀬 賢志郎 (金沢大・医薬保健研究域・医), 新谷 正嶺 (中部大学 生命健康科学部 生命医科学科)
Session Chairs: Kenshiro Fujise (Dept. FSIR, Faculty of Medicine, Kanazawa Univ.),
Seine A. Shintani (Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University)

18:50~20:30

C 会場 (会議室 105+106) / Room C (Meeting Room 105+106)

- [1EC001](#) 細胞内再構成アプローチによるドーパミンシナプス小胞の形成機構の解析
Distinct synaptic vesicle populations in dopaminergic neurons: insights into organization and sorting by *in cellulo* reconstitution assay
○藤瀬 賢志郎¹, ニーシャ モハド ラフィク², ピエトロ デカミリ³, 齋藤 敦¹ (¹金沢大・医薬保健研究域・医, ²チュービンゲン大・学際的生化学, ³イエール大・医・神経科学)
- Kenshiro Fujise¹**, Nisha Mohd Rafiq², Pietro De Camilli³, Atsushi Saito¹ (¹*Dept. FSIR, Faculty of Medicine, Kanazawa Univ.*, ²*IFIB, Univ Tübingen, Germany*, ³*Dept Neurosci, YSM, Yale Univ, USA*)
- [1EC002](#) 「遅い」キネシンから「速い」キネシンへのギアチェンジにより実現される高速・高効率な軸索輸送メカニズム
Gear change to go through: Cooperation of two different kinesins enables fast and efficient axonal transport
○岩崎 奏子^{1,2}, 岩城 光宏^{2,3}, 岡田 康志^{1,2} (¹東京大・院医学, ²理研 生命機能科学研究センター, ³情報通信研究機構)
- Kanako Iwasaki^{1,2}**, Mitsuhiro Iwaki^{2,3}, Yasushi Okada^{1,2} (¹*Grad. Sch. Med., Univ. Tokyo*, ²*BDR, Riken*, ³*NICT*)

- 1EC003** がん細胞の増殖と免疫逃避を担う、液状ナノ信号プラットフォームの発見
Nano-liquid signaling platform responsible for both cancer cell growth and immune evasion
Taka-aki Tsunoyama¹, Christian Hoffmann², Daiki Sasaki¹, Bo Tang¹, Koichiro M Hirose³,
Yuri L Nemoto⁴, Rinshi S Kasai⁵, Takahiro K Fujiwara⁶, Kenichi GN Suzuki^{3,5,6}, Reinhard Fässler⁷,
Hiroki Ishikawa¹, Dragomir Milovanovic², Akihiro Kusumi^{1,6} (¹*OIST*, ²*DZNE*, ³*iGCORE, Gifu Univ.*,
⁴*Biosig. Res. Cent., Kobe Univ.*, ⁵*Div. Adv. Bioimag., Natl. Cancer Cent. Res. Inst.*, ⁶*WPI-iCeMS, Kyoto Univ.*, ⁷*Max Planck Inst. Biochem.*)
- 1EC004** 拍動心筋サルコメアに潜む秩序とカオスの動的恒常性
Localized Chaos within Periodic Beating of Cardiomyocyte Sarcomeres: Evidence for Chaordic Homeodynamics
○新谷 正嶺^{1,2,3} (¹中部大学 生命健康科学部 生命医科学科, ²中部大学 AI 数理データサイエンスセンター, ³名古屋大学 高等研究院)
Seine A. Shintani^{1,2,3} (*Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University*, ²*Center for Mathematical Science and Artificial Intelligence, Chubu University*, ³*Institute for Advanced Research, Nagoya University*)
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1ED 生体膜、合成生物学、理論生物学
Biological membrane, Synthetic biology, Theoretical biology

座長：栗栖 実（東北大・院理物理）、木幡 愛（科学大・生命理工）

Session Chairs: Minoru Kurisu (Dept. Physics, Grad. Sch. Sci., Tohoku Univ.),
Ai Kohata (Sch. Life Science and Technology, Science Tokyo)

18:50~20:30

D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

- 1ED001** 浸透圧を利用して出芽型分裂するベシクル系の開発
Osmotic spawning vesicle
○栗栖 実, 今井 正幸（東北大・院理物理）
Minoru Kurisu, Masayuki Imai (*Dept. Physics, Grad. Sch. Sci., Tohoku Univ.*)
- 1ED002** PDA-Based Microfluidic Sensor for pathogenic bacteria Detection
Bratati Das, Kaori Sugihara (*Institute of Industrial Science, The university of Tokyo*)
- 1ED003** グラフによる生態系の定常分布と応答の表現
Diagrammatic expressions for steady-state distribution and static responses in population dynamics
○片山 康矢, 永山 龍那, 伊藤 創祐（東大理）
Koya Katayama, Ryuna Nagayama, Sosuke Ito (*Dept. of Phys., U Tokyo*)
- 1ED004** 界面活性剤の自己集合化による水面に浮かぶ油滴の自律的な振動
Spontaneous oscillation of oil droplets on water surface by self-assembly of surfactants
○木幡 愛¹, 山田 雄平², 前田 真吾^{2,3}, 金原 数^{1,2} (¹科学大・生命理工, ²科学大・総合・自律システム材料科学研究センター, ³科学大・工)
Ai Kohata¹, Yuhei Yamada², Shingo Maeda^{2,3}, Kazushi Kinbara^{1,2} (¹*Sch. Life Science and Technology, Science Tokyo*, ²*ASMat, IIR, Science Tokyo*, ³*Sch. Mechanical Engineering, Science Tokyo*)

1EE 計算生物学: 分子シミュレーション, モデリング
Computational biology: Molecular simulation and modeling

座長: ジェラン ムハマド ディルガンタラ (医薬基盤・健康・栄養研究所 AI 健康・医薬研究センター),
Fan Shujie (Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences)

Session Chairs: **Jelang Muhammad Dirgantara** (Laboratory of In Silico Design, Artificial Intelligence Center for Health and Biomedical Research, National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan),
Shujie Fan (Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences)

18:50~20:30

E 会場 (会議室 201) / Room E (Meeting Room 201)

- [1EE001](#) 親和性を超えて: ペプチドの親和性と生物学的機能との関係性の解明
To Affinity and Beyond: Investigating the Relationship Between Peptide Affinity and Biological Functions
Jelang Muhammad Dirgantara¹, Takuto Nogimori², Kazuma Kiyotani³, Takuya Yamamoto², Suyong Re¹ (¹Laboratory of In Silico Design, Artificial Intelligence Center for Health and Biomedical Research, National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan, ²Laboratory of Precision Immunology, Center for Intractable Diseases and ImmunoGenomics, National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan, ³Laboratory of Immunogenomics, Center for Intractable Diseases and ImmunoGenomics, National Institute of Biomedical Innovation, Health and Nutrition, Osaka, Japan)
- [1EE002](#) Bayesian Inference of the Transport Mechanism of the Zn²⁺/H⁺ Antiporter YiiP from Microscale Thermophoresis and Simulations
Shujie Fan¹, David L. Stokes³, Oliver Beckstein² (¹Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, ²Dept. of Physics, Arizona State University, ³Dept. of Cell Biology, NYU School of Medicine)
- [1EE003](#) An Integrative Computational Framework Using Sequence, Structural, and Functional Analyses to Predict Novel Pathogenic Troponin C Mutants
Pooja Pradipta Bandyopadhyay (School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi- 110067)
- [1EE004](#) 演題取り下げ Withdrawn
- [1EE005](#) Learning Transcription Machinery from Minimal Model, Molecular Dynamics, Genome Profiling, and Directed Evolution
Carmen Masri¹, Biao Wan², Liqiang Dai², Chao E³, **Jin Yu**¹ (¹Department of Physics and Astronomy, University of California-Irvine, USA, ²Wenzhou Institute, UCAS, Wenzhou, Zhejiang, China, ³Beijing Computational Science Research Center, Beijing, China)

3 日目（9 月 26 日（金））／Day 3（Sep. 26 Fri.）

3HL

オーガナイザー：上久保 裕生（奈良先端科学技術大学院大学），安原 主馬（奈良先端科学技術大学院大学），
末次 志郎（奈良先端科学技術大学院大学），作村 諭一（奈良先端科学技術大学院大学）

Organizers: Hironari Kamikubo (NAIST), Kazuma Yasuhara (NAIST), Shiro Suetsugu (NAIST),
Yuichi Sakumura (NAIST)

09:00～11:45

D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

- [3HL0900](#) NARAKITA 放置竹林拡大問題解決プロジェクト～竹コンポスト開発への道のり～
NARAKITA Project to Address the Expansion Abandoned Bamboo Forests: The Road to
Bamboo Compost Development
老本 蓮叶, 谷 明琉乃, 田口 主馬, ○仲村 慶大, 山本 優果, 河野 友乃助, 武内 菜穂子（奈良県立奈良
北高等学校）
Rento Oimoto, Aruno Tani, Kazuma Taguchi, **Keita Nakamura**, Yuka Yamamoto, Yunosuke Kono,
Nahoko Takeuchi (*Nara Prefectural Narakita Senior High School*)
- [3HL0915](#) チャコウラナメクジのカフェインに対する忌避反応を用いた作物への食害防除
Prevention of crop damage using *Ambigolimax valentianus*' repellent reaction to caffeine
○高原 佑真, 飯沼 快友, 塩見 岳（奈良県立奈良北高等学校）
Yuma Takahara, Kaito Iinuma, Gaku Shiomi (*Nara Prefectural Narakita Senior High School*)
- [3HL0930](#) 奈良学園の里山における地下水と植生の関係
Investigation the relationship between the distribution of the groundwater and the ground
vegetation at satoyama in Naragakuen High School
○手塚 陽琉, 安田 悠人, 畚 隆喜, 西田 有希（奈良学園高等学校）
Ataru Tezuka, Haruto Yasuda, Takayoshi Hazama, Yuki Nishida (*Naragakuen High School*)
- [3HL0945](#) 深部静脈血栓症の発生病因子の定量的評価
Quantitative Evaluation of Risk Factors for Deep Vein Thrombosis
○高瀬 祐理菜（西大和学園高等学校）
Yurina Takase (*Nishiyamato Gakuen High School*)
- [3HL1000](#) プラナリアの再生における活性酸素の二面的機能の評価
Evaluation of the Dual Functions of Reactive Oxygen Species in Planarian Regeneration
○高島 柚衣, 山田 壮真, 王 鋭瑾萱（西大和学園高等学校）
Yui Takashima, Soma Yamada, Ruikinshinn Ou (*Nishiyamato Gakuen High School*)
- [3HL1015](#) 学校設備を用いた酵母菌（*Saccharomyces cerevisiae*）のコールドスリープ条件の検討
Investigation of conditions for the freeze tolerance of *Saccharomyces cerevisiae* using school
facilities
○高木 宏輔, 辻 翔成, 錦 一磨, 濱田 勝太, 阮 暁米（西大和学園高等学校）
Kosuke Takagi, Shosei Tsuji, Kazuma Nishiki, Shota Hamada, Xiaomi Ruan (*Nishiyamato Gakuen High School*)
- [3HL1030](#) 葛乳酸菌と植物性ミルクでヨーグルトをつくる ～完全なゲル化を達成する条件の検討～
Make yogurt with kudzu lactobacillus and plant milk～Investigation of conditions to achieve
complete gelation～
○奥田 桃加, 川崎 愛花里, 川本 紗弥（奈良県立青翔高等学校）
Momoka Okuda, Akari Kawasaki, Saya Kawamoto (*Nara Prefectural Seisho Senior High School*)

[3HL1045](#)

ヤマトマナの高亜鉛化

The increasing zinc content of Yamatomana and the number of days of zinc treatment

○島村 冴矢, 阪口 裕哉, 吉川 英里, 田邊 あゆ美 (奈良県立青翔高等学校)

Saya Shimamura, Yuya Sakaguchi, Eri Yoshikawa, Ayumi Tanabe (*Nara Prefectural Seisho Senior High School*)

[3HL1100](#)

アンモニア中のバクテリアの行動の観察

Observation of Bacterial Behavior in Ammonia

○幸田 稜平, 本道 主樹, 濱田 理公, 中田 俊壺 (石川県立小松高等学校)

Ryohei Kouta, Kazuki Hondou, Riku Hamada, Shunichi Nakada (*Komatsu high school*)

[3HL1115](#)

タンパク質の主鎖原子の温度因子が高いとペプチド結合が歪みすぎてしまう？

When the temperature factor of the main chain atoms in a protein molecule is high, does the peptide bond become more twisted?

○島田 明星¹, 國井 真帆¹, 茶竹 俊行², 大原 高志³, 千葉 かおり¹ (¹茨城高専, ²京大 複合研, ³ 原科研 J-PARC センター)

Akari Shimada¹, Mahan Kunii¹, Toshiyuki Chatake², Takashi Ohhara³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*KURNS, Kyoto Univ.*, ³*J-PARC, JAEA*)

[3HL1130](#)

β バレル型タンパク質の生合成におけるループの DGG 配列がもつ折り目効果

ORIME effect of the DGG sequence on the loop in the biosynthesis of β-barrel proteins

○田上 大輝¹, 大島 広夢¹, 星野 大², 鈴木 喜大³, 千葉 かおり¹ (¹茨城高専, ²京大・薬, ³ 農研機構)

Daiki Tagami¹, Hiromu Ohshima¹, Masaru Hoshino², Nobuhiro Suzuki³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll.*, ²*Pharm., Kyoto Univ.*, ³*NARO*)

1 日目 (9 月 24 日 (水)) / Day 1 (Sep. 24 Wed.) 13:00 ~ 15:00

01A. タンパク質：構造 / 01A. Protein: Structure

- [1Pos001](#) Mutation Effect of Terpene Cyclase CotB2 Revealed by Ambient Temperature Crystallography
Atika Nur Rochmah¹, Takaaki Fujiwara¹, Tomohiko Kuzuyama², Eriko Nango¹ (¹*Grad. Sch. Sci., Univ. Tohoku*, ²*Grad. Sch. Agr. Life. Sci., Univ. Tokyo*)
- [1Pos002](#) クライオ電子顕微鏡を用いたヒトパネキシン 3 チャンネルの脂質ナノディスク中での構造解析
Cryo-EM structure of human Pannexin-3 in lipid nanodiscs
Shota Kawaguchi¹, Shota Suzuki², Koki Nishikawa³, Yoshinori Fujiyoshi², Atsunori Oshima^{1,4} (¹*Grad. Sch. PharmSci., Nagoya Univ.*, ²*CeSPL, Inst. Integrated Research, Inst. Science Tokyo*, ³*Tokyo Univ. Agri. and Tech.*, ⁴*CeSPL, Nagoya Univ.*)
- [1Pos003](#) 生細胞内での近接ラベリング法で検出された RAF 複合体の分子構成
Molecular composition of RAF kinase complexes in living cells revealed by proximity labeling
Kenji Okamoto, Yasushi Sako (*RIKEN PRI*)
- [1Pos004](#) Structural rearrangement of DNMT3B driven by histone modifications stimulates its DNA methylation activity
Cho Chao-Cheng¹, Chu Woei-Chyn², **Hanna S. Yuan**¹ (¹*Academia Sinica*, ²*National Yang Ming Chiao Tung University*)
- [1Pos005](#) Structural insight into the mechanism of amyloid fibril formation by hen egg-white lysozyme
Haruka Kawabata¹, Yan Li^{2,3}, Haruka Umezawa¹, Yuxi Lin², Naito Ishimoto¹, Yunseok Heo², Jae-Hyun Park^{1,4}, Jeremy R.H. Tame¹, Young-Ho Lee^{2,5,6,7,8}, Sam-Yong Park¹ (¹*Graduate School of Medical Life Science, Yokohama City University*, ²*Biopharmaceutical Research Center, Korea Basic Science Institute (KBSI)*, ³*Research Institute of Biomedical and Health Science, Konkuk University*, ⁴*Department of Molecular Cell Biology, Sungkyunkwan University*, ⁵*Bio-Analytical Science, University of Science and Technology (UST)*, ⁶*Graduate School of Analytical Science and Technology, Chungnam National University*, ⁷*Department of Systems Biotechnology, Chung-Ang University (CAU)*, ⁸*Frontier Research Institute for Interdisciplinary Sciences (FRIS)*)
- [1Pos006](#) 集光アンテナ複合体であるフィコビリソームの高分解能構造解析に向けた取り組み
Approaches to high-resolution structural analysis of the phycobilisome, a photosynthetic light-harvesting antenna complex
Yuya Fujita^{1,2}, Soichiro Seki², Akihiro Kawamoto^{1,2}, Yuu Hirose³, Genji Kurisu^{1,2} (¹*The University of Osaka, Grad. Sch. Engineering, Japan*, ²*The University of Osaka, Institute for Protein Research (IPR), Japan*, ³*Toyohashi University of Technology, Grad. Sch. Engineering, Applied chemistry and Life science, Japan*)
- [1Pos007](#) Co-crystal structure of a human 8-oxoguanine DNA glycosylase with photocaged substrate toward time-resolved crystallography
Momoko Yumita¹, Tomoki Imura¹, Yuhei Hosokawa², Kai-Chun Yang², Hsuan-Yu Shih², Manuel Maestre-Reyna², Junpei Yamamoto¹ (¹*Graduate School of Engineering Science, Osaka University Department of Chemistry*, ²*National Taiwan University*)
- [1Pos008](#) Structural basis for the mechanisms of complex assembly by the Influenza A virus nucleoprotein and importin
Haruka Umezawa (*Yokohama City Univ., Medical Life Science, Drug Design Lab.*)
- [1Pos009](#) 巨大マルチドメインタンパク質の構造予測
Structure prediction of large multidomain proteins
Ryota Kobayashi¹, Suguru Fujita¹, Yoshitaka Moriwaki², Tohru Terada¹ (¹*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*, ²*Med. Res. Lab., Inst. Integr. Res., Science Tokyo*)

- [1Pos010](#) Improved Resolution of *Enterococcus hirae* V-ATPase by cryo-EM: Structural Insights into the Full Complex
Yuan-E Lee¹, Raymond N. Burton-Smith^{1,2}, Akihiro Otomo^{2,3}, Kano Suzuki⁴, Tsukasa Nakamura⁵, Toshio Moriya⁵, Takeshi Murata⁴, Ryota Iino^{2,3}, Kazuyoshi Murata^{1,2} (¹ExCELLS/NIPS, Okazaki, ²SOKENDAI, Okazaki, ³IMS, Okazaki, ⁴Chiba University, Chiba, ⁵KEK, Tsukuba)
- [1Pos011](#) Crystal structure elucidation of *Rubricoccus marinus* halorhodopsin
Naithok Khachuk Debbarma¹, Takaaki Fujiwara^{1,2}, Eriko Nango^{1,2} (¹Grad. Sch. Life Sci., Univ. Tohoku, ²IMRAM, Univ. Tohoku)

01B. タンパク質：物性（安定性、折れたたみなど）／01B. Protein: Physical property

- [1Pos012](#) Kinetic Analysis of heparin-induced fibrillation of α -synuclein
Takashi Ohgita, Norihiro Namba, Nao Minami, Hiroyuki Saito (Kyoto Pharm. Univ.)
- [1Pos013](#) Rose Bengal を用いたタンパク質凝集プロセスの評価
 Evaluation of Protein Aggregation Process Using Rose Bengal
Gen Takebe¹, Shigetoshi Okazaki¹, Heidi Ottevaere² (¹Hamamatsu Photonics K.K., ²Department of Applied Physics and Photonics, Vrije Universiteit Brussel)
- [1Pos014](#) 残基間距離と局所環境の相関によるアデニル酸キナーゼのアロステリックコミュニケーション経路の同定
 Allosteric communication pathway within adenylate kinase elucidated by correlation between interresidue distances and local environments
Shinichi Kurino, Tomoki P. Terada (Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.)
- [1Pos015](#) VCD を用いたスパイクタンパク質フラグメントのアミロイド多形性および超分子キラリティの解析
 Amyloid Polymorphism and Supramolecular Chirality in Spike Protein Fragment as Studied by Vibrational Circular Dichroism
Shunsaku Nagai¹, Hisako Sato², Izuru Kawamura¹ (¹Grad. Sch. Sci., Yokohama Natl Univ., ²Sch. Sci., Univ. Ehime)
- [1Pos016](#) フッ素化アミノ酸を用いた膜貫通イオンチャネルの設計と特性評価
 Design and characterization of transmembrane ion-channel peptide containing fluorinated amino acids
Keiya Saito¹, Daisuke Sato², Peng Zugui³, Ai Niitsu⁴, Ryuji Kawano³, Izuru Kawamura¹ (¹Grad. Sch. Eng. Sci., Yokohama Natl. Univ., ²Inst. Sci. Eng., Ibaraki Univ., ³Inst. Eng., Tokyo Univ. of Agri. & Tech., ⁴Yokohama Inst., Riken)
- [1Pos017](#) Gum Ghatti の乳化微粒子構造の解析
 Structural Analysis of Emulsified Nanoparticles of Gum Ghatti
Kento Yonezawa^{1,2}, Sawa Fusamae², Yuya Iwao², Ryuki Iida², Shoma Igarashi², Naoya Sagawa³, Keigo Kinoshita³, Yoichi Yamazaki², Sachiko Toma², Hironari Kamikubo^{1,2} (¹NAIST, CDG, ²NAIST, M.S., ³San-Ei Gen F.F.I., inc.)
- [1Pos018](#) エピガロカテキンガラートが LDL の物性に与える影響
 Effect of the binding of epigallocatechin gallate to LDL on physical properties of LDLs
Seiji Takeda, Moeko Kitagawa, Naoya Ishihara, Takahisa Hiruma (Faculty Pharm. Sci. Hokkaido Univ. Sci.)
- [1Pos019](#) シアノバクテリアの概日リズムを司る Kai 時計タンパク質の会合解離挙動
 Association-dissociation behavior of Kai-clock proteins regulating cyanobacterial circadian rhythm
Ken Morishima, Ritsuki Sakamoto, Rintaro Inoue, Masaaki Sugiyama (KURNS, Kyoto Univ.)

- [1Pos020](#) Molecular Dynamics Study on the Taste-Recognition Mechanism of Human Taste Receptor Heterodimers
Yu Yamamori, Rikuri Morita, Yasuteru Shigeta, Ryuhei Harada (*center of computational science, University of Tsukuba*)
- [1Pos021](#) Structural and functional characterization of novel ice-binding protein isoforms discovered via genome and transcriptome analyses
Tatsuya Arai^{1,2}, Kaho Uchizawa², Kosuke Maeda², Sakae Tsuda¹, Tomoyasu Aizawa^{1,2} (¹*Faculty of Advanced Life Science, Hokkaido University*, ²*School of Science, Hokkaido University*)
- [1Pos022](#) Effect of phospholipid composition on binding behavior of α -synuclein to lipid membranes
Norihiko Namba, Shiori Ariyoshi, Honori Shiroshita, Takashi Ohgita, Hiroyuki Saito (*Kyoto Pharm. Univ.*)
- [1Pos023](#) KaiC のリン酸化率に依存した KaiC-KaiA 結合強度の変化
 Phosphorylation-Level-Dependent Changes in KaiC-KaiA Binding Strength
Arisa Nakao¹, Risako Aoyama¹, Yoichi Yamazaki¹, Shuji Akiyama^{2,3}, Kento Yonezawa^{1,4}, Hironari Kamikubo^{1,4} (¹*NAIST, MS*, ²*CIMos, IMS*, ³*NINS*, ⁴*SOKENDAI*, ⁴*NAIST, CDG*)
- [1Pos024](#) Biochemical assay development for kinetic analysis of ATPase cycle of KaiC
Yasuhiro Onoue¹, Yoshihiko Furuie^{1,2}, Shuji Akiyama^{1,2} (¹*Institute for Molecular Science, NINS*, ²*The Graduate University for Advanced Studies (SOKENDAI)*)
- [1Pos025](#) トリプシン様蛋白質分解酵素のプロペプチド領域による酵素活性阻害機構
 Mechanism of Enzyme Activity Inhibition by the Propeptide Region of a Trypsin-Like Protease
Orika Ashida¹, Nana Sakata¹, Kairi Ogawa¹, Miki Matsuzaki¹, Mitsuhiro Miyazawa², Shigeru Shimamoto¹, Yuji Hidaka¹ (¹*Grad. Sch. Sci. Eng., Univ. Kindai*, ²*PrevenTec Inc.*)
- [1Pos026](#) メダカ由来プロスタグランジン結合蛋白質とリボフラビンの相互作用解析
 Interaction analysis of medaka prostaglandin binding protein with riboflavin
Kazuki Mitani¹, Koichi Uegaki², Shigeru Shimamoto¹ (¹*Faculty of Science and Engineering, Kindai University*, ²*Faculty of Agriculture, Kindai University*)
- [1Pos027](#) リポカリン型プロスタグランジン D 合成酵素の系統解析
 Phylogenetic and Functional Analysis of Lipocalin-type Prostaglandin D Synthase
Kodai Nakamoto, Chinatsu Noma, Kei Iida, Shigeru Shimamoto (*Faculty of Science and Engineering, Kindai University*)

- [1Pos028](#) マルチドメインタンパク質のダイナミクスを特徴づける粗視化アプローチ
 A coarse-grained approach to characterizing the dynamics of multi-domain proteins
Chigusa Kobayashi¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS*, ²*RIKEN PRL*)
- [1Pos029](#) リン酸結合タンパクを含む液滴チャンバーアレイにより高感度で検出する F₁-ATPase および PPase からの無機リン酸解離
 Highly sensitive detection of phosphate released from F₁-ATPase and PPase using phosphate-binding protein in droplet chamber arrays
Waren Imaoka¹, Tomohiro Aoyama¹, Yoshihiro Minagawa², Hiroshi Ueno², Nobukiyo Tanaka¹, Hiroyuki Noji², Tomoko Masaie¹ (¹*Dept. Appl. Biol. Sci., Tokyo Univ. Sci.*, ²*Dept. Appl. Chem., Univ. Tokyo*)
- [1Pos030](#) 細胞内タンパク質結晶生成過程とその可視化
 The process of intracellular protein crystal formation and its visualization
Etsuko Tokunaga, Yasufumi Umena (*NUSR, Univ. Nagoya*)

- [1Pos031](#) MD シミュレーションとニューラルネットワークを組み合わせたタンパク質の高速 AFM 画像解析
Analysis of HS-AFM images of proteins combining MD simulation and Neural Network
Katsuki Sato¹, Yui Kanaoka², Tomoya Tsukazaki³, Takayuki Uchihashi², Takaharu Mori¹ (¹Tokyo University of Science, ²Nagoya University, ³Nara Institute of Science and Technology)
- [1Pos032](#) デキストラン結合酵素グルカンスクララーゼはデキストラン-ポリエチレングリコール混合系での液滴形成を誘導する
Dextran-Binding Enzyme Glucanase Induces Droplet Formation in Dextran– Polyethylene Glycol Mixtures
Mikage Iwakiri, Hideyuki Komatsu (Department of Bioscience and Bioinformatics, Faculty of Systems Engineering and Computer Science, Kyushu Institute of Technology)
- [1Pos033](#) ロボット機構学に基づくタンパク質の内部運動特性予測のための計算フレームワークの開発
Development of a Computational Framework for Predicting the Internal Motion Properties of Proteins Based on Robot Kinematics
Keisuke Arikawa (Fcl. Eng., Kanagawa Inst. of Tech.)

01E. タンパク質：タンパク質工学／進化学／01E. Protein: Engineering

- [1Pos034](#) 多様なカーゴ分子を媒介とした非ウイルス性タンパク質カプシドの試験管内形成と形態制御
In vitro assembly of a nonviral protein capsid and its morphological control mediated by versatile cargos
Kenya Tajima¹, Yusuke Sakai^{2,3}, Naohiro Terasaka¹ (¹Earth-Life Science Institution, Institute of Future Science, Institute of Science Tokyo, ²RIKEN Center for Biosystems Dynamics Research, ³Institute for Quantitative Biosciences, The University of Tokyo)
- [1Pos035](#) Model screening of an epitope-tag peptide from a random library consisting of a reduced set of amino acids using PL display
Shingo Ueno, Fumi Toshioka, Takanori Ichiki (iCONM, Kawasaki Inst. Industry. Promo.)
- [1Pos036](#) 分子進化によるウイルス模倣粒子の構造多様化と機能化
Functionalization and structural diversification of artificial nucleocapsids by laboratory evolution
Naohiro Terasaka (Earth-Life Sci. Inst., Inst. Future Sci., Inst. Sci. Tokyo)
- [1Pos037](#) 細胞内タンパク質結晶エンジニアリングによる刺激応答固相転移
Engineering in-cell protein crystals for the stimuli-responsive solid-solid phase transitions
Kosuke Kikuchi¹, Misaki Nagama¹, Junko Tanaka¹, Haonan Kong¹, Satoshi Abe², Takafumi Ueno^{1,3} (¹Sch. of Life Sci. and Tech., Science Tokyo, ²Grad. Sch. of Life and Env. Sci., KPU, ³IIR-ASMat, Science Tokyo)
- [1Pos038](#) アクティブ・ラーニングによる ATP 合成酵素の阻害タンパク質 IF₁ の再設計
Redesign of the inhibitor protein IF₁ for ATP synthase via an active-learning framework
Ryohei Kobayashi^{1,2}, Constantin Guyot^{2,3}, Jun Ohnuki^{2,3}, Hiroyuki Noji^{1,4}, Kei-ichi Okazaki^{2,3} (¹Dep. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo, ²Institute for Molecular Science, ³SOKENDAI, ⁴RIIP, Univ. Tokyo)

01F. タンパク質：天然変性／01F. Protein: Intrinsic disorder

- [1Pos039](#) 高速 AFM・生化学手法による E6AP/E6/p53 複合体の構造動態の統合的解析
Integrated analysis of structural dynamics of E6AP/E6/p53 complex by HS-AFM and biochemical methods
Soma Yamamoto^{1,2}, Holger Flechsig³, Hiroki Konno³ (¹Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ., ²WISE Program for Nano-Precision Medicine, Science, and Technology, Kanazawa Univ., ³WPI Nano Life Sci. Inst. (WPI-Nano LSI), Kanazawa Univ.)

- [1Pos040](#) MAP7 は微小管結合を介して FUS の相分離を制御する：ALS 関連変異体との相互作用比較からの示唆
MAP7 Regulates FUS Condensate Formation via Microtubule Binding: Insights from ALS-Linked Mutant Interactome Analysis
Kyoto Yasuda^{1,5,7}, Hyun-woo Rhee^{4,7}, Tomonobu Watanabe^{1,2,3}, Shin-ichi Tate^{1,5,6,7} (¹*Grad. Sch. Int. Sci. Life., Univ. Hiroshima*, ²*Res. Int. Radiation. Bio. Med., Univ. Hiroshima*, ³*BDR, RIKEN*, ⁴*Chem., SNU*, ⁵*RcMcD, Univ. Hiroshima*, ⁶*MIMS, Univ. Meiji*, ⁷*WPI-SKCM2*)
- [1Pos041](#) 高速原子間力顕微鏡を用いたヒストンテール動態モニタリング
Histone tail dynamics monitoring using high-speed atomic force microscopy
Ryota Imada¹, Quynh Pham², Yusuke Miyanari³, Shoko Sato⁴, Hitoshi Kurumizaka⁴, Mikihiko Shibata^{3,5} (¹*Grad. Sch. Math. & Phys., Kanazawa Univ.*, ²*Grad. Sch. NanoLS., Kanazawa Univ.*, ³*WPI-NanoLSI, Kanazawa Univ.*, ⁴*Institute for Quantitative Biosciences, Tokyo Univ.*, ⁵*InFiniti, Kanazawa Univ.*)
- [1Pos042](#) 酵母プリオン Sup35 の液滴形成過程の高速 AFM 観察
High-speed AFM observation of the droplet formation process of yeast prion Sup35
Aya Ogino¹, Yumiko Ohhashi², Hideki Taguchi², Hiroki Konno³ (¹*Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ.*, ²*Inst. of Integ. Res., Science Tokyo.*, ³*WPI Nano Life Sci. Inst. (WPI-Nano LSI), Kanazawa Univ.*)

02. ヘムタンパク質／02. Heme proteins

- [1Pos043](#) 単結晶およびシリカゲル中機能解析でヘモグロビンのアロステリック平衡を読み解く
Deciphering hemoglobin allosteric equilibria through functional analysis in single crystals and silica gels
Naoya Shibayama (*Div. Biophys., Jichi Med. Univ.*)
- [1Pos044](#) ウシ心筋シトクロム酸化酵素の核 DNA 由来サブユニットにより形成される疎水性チャネルの構造解析
Structural analysis of a hydrophobic channel formed by nuclear DNA-coded subunit of bovine heart cytochrome c oxidase
Kazumasa Muramoto, Kyoko Shinzawa-Itoh (*Grad. Sch. Sci., Univ. Hyogo*)

03. 膜タンパク質／03. Membrane proteins

- [1Pos045](#) 海洋性ビブリオ菌におけるプロトン駆動べん毛モーターのストマチン様タンパク質 Flil と MotAB 固定子複合体の相互作用
Association of stomatin-like protein Flil and MotAB stator complex of proton-driven flagellar motor in marine *Vibrio*
Michio Homma^{1,2}, Kazuki Yokoyama³, Norihiro Takekawa⁴, Tatsuro Nishikino⁵, Hajime Nakatani¹, Seiji Kojima³ (¹*Dep. Biomol. Eng., Grad. Sch. Eng., Nagoya Univ.*, ²*Dep. of Physics, Grad. Sch. Sci., Nagoya Univ.*, ³*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, ⁴*Dep. Macromol. Sci., Grad. Sch. Sci., Osaka Univ.*, ⁵*Dep. Life Sci. Appl. Chem., Nagoya Inst. Tech.*)
- [1Pos046](#) ATR-FTIR による環状ヌクレオチド依存性カリウムチャネル SthK のリガンド選択の分子機構研究
Investigation of molecular mechanisms of ligand selection in a cyclic nucleotide dependent potassium channel SthK by using ATR-FTIR
Taisei Maeda¹, Tatsuro Nishikino^{1,2}, Hiroki Ogasawara³, Hiroto Fukuda³, Yuji Furutani^{1,2} (¹*Graduate School of Engineering, Nagoya Institute of Technology*, ²*Optobiotechnology Research Center*, ³*Nagoya Institute of Technology*)

- [1Pos047](#) Visualization and analysis of P-glycoprotein dynamics by using HS-AFM
Visualization and analysis of P-glycoprotein dynamics by using HS-AFM
Yui Kanaoka¹, Takeshi Murata², Takayuki Uchihashi^{1,3} (¹*Grad. Sch. Sci., Univ. Nagoya*, ²*Grad. Sch. Sci., Univ. Chiba*, ³*ExCELLS*)
- [1Pos048](#) 異種タンパク質結合 OmpG ナノポアの開閉挙動観察
Observation of gating behavior of OmpG nanopore conjugating other protein
Kazuha Endo, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma univ.*)

04. DNA・DNA 結合タンパク質／04. DNA & DNA binding proteins

- [1Pos049](#) 近接した標的 DNA 配列のタンデムリピートに集積する Dof 転写因子の 1 分子観察
Single-molecule observation of Dof transcription factor accumulating to neighboring tandem repeats of target DNA sequences
Hayato Yamashita¹, Akihiro Tsuji¹, Hirotake Furihata², Zhangliang Zhu^{2,3}, Takuya Miyakawa^{2,3}, Masayuki Abe¹ (¹*Grad. Sch. Eng. Sci., Univ. Osaka*, ²*Grad. Sch. Agr. Sci., Univ. Tokyo*, ³*Grad. Sch. Bio., Kyoto Univ.*)
- [1Pos050](#) UvrD ヘリカーゼの野生型と C 末端欠失変異体間の DNA を介した相互作用
DNA-mediated interaction between wild-type and C-terminal deletion mutants of UvrD helicase
Hiroaki Yokota (*Grad. Sch. New Photon. Indust.*)
- [1Pos051](#) 液液相分離により形成するナノスケール凝縮体の蛍光寿命相関解析
Fluorescence lifetime correlation analysis on nanoscale liquid condensates formed through liquid-liquid phase separation
Rene Toyama, Miyuki Sakaguchi, Shoichi Yamaguchi, Takuhiro Otsu (*Grad. Sch. Sci. Eng., Saitama Univ.*)

05. RNA・RNA 結合タンパク質／05. RNA & RNA binding proteins

- [1Pos052](#) Folding of Frameshift-Stimulating RNA Pseudoknots Is Modulated by the Upstream Structures
Jin-Der Wen (*National Taiwan University*)

06. DNA/RNA ナノテクノロジー／06. DNA/RNA nanotechnology

- [1Pos053](#) 自己複製を目指した成長する DNA 液滴の設計
Design of Growing DNA Droplets Toward Self-Replication
Yusei Kudo¹, Tomoya Maruyama³, Masahiro Takinoue^{1,2,3} (¹*Sch. of Computer Science, Institute of Science Tokyo*, ²*Sch. of Life Science and Technology, Institute of Science Tokyo*, ³*Research Center for Autonomous Systems Materialogy (ASMat), Institute of Integrated Research, Institute of Science Tokyo*)
- [1Pos054](#) miRNA の濃度を認識する DNA 液滴コンピュータ構築を目指した化学反応シミュレーション
Chemical reaction simulation for development of DNA droplet computers which recognize concentration of miRNAs
Chisa Kato¹, Yuko Yoshida¹, Masahiro Takinoue^{1,2,3} (¹*Sch. Comp. Sci., Inst. Sci. Tokyo*, ²*Sch. Life Sci. Tech., Inst. Sci. Tokyo*, ³*ASMat, Inst. Sci. Tokyo*)

- [1Pos055](#) 自動分注ロボットと機械学習を用いた DNA 論理回路の自動設計
Automated design of DNA logic circuits using automated pipetting robots and machine learning
Yuko Yoshida¹, Kanta Takagi¹, Masahiro Takinoue^{1,2,3} (¹*School of Computer Science, Institute of Science Tokyo*, ²*School of Life Science and Technology, Institute of Science Tokyo*, ³*Research Center for Autonomous Systems Materialogy (ASMat), Institute of Science Tokyo*)
- [1Pos056](#) DNA ナノミウラ折り：力学的に変形可能なナノ折り紙構造
DNA-Based Miura-ori: A Mechanically transformable Nano-Origami Architecture
Daisuke Ishikawa¹, Ibuki Kawamata², Masahiko Hara³, Masashi Ikeuchi¹ (¹*LBB, Science Tokyo*, ²*Grad. Sch. Sci., Kyoto Univ.*, ³*Sch. Mater. Chem. Technol., Tokyo Tech*)

07. 核酸：その他／07. Nucleic acid: Others

- [1Pos057](#) CRISPR Cas13a システムを用いた *Salmonella* RNA のデジタル検出
Digital Detection of *Salmonella* RNA with CRISPR Cas13a system
Svitlana Kovalchuk¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Graduate School of Engineering, The University of Tokyo*, ²*Research Institute of Planetary Health (RIPH), The University of Tokyo*)
- [1Pos058](#) 静電相互作用により誘起された不均一な DNA 溶液中の力の伝搬
Force propagation in heterogeneous DNA solution induced by electrostatic interactions
Miku Nakao¹, Saki Matsuyama¹, Akinori Miyamoto², Yoshihiro Murayama^{1,2} (¹*Dep. Biomedical Engineering., Grad. Sch. Engineering., Tokyo University of Agriculture and Technology*, ²*Dep. Applied Physics., Grad. Sch. Engineering., Tokyo University of Agriculture and Technology*)

08. クロマチン・染色体／08. Chromatin & Chromosomes

- [1Pos059](#) 分子動力学シミュレーションを用いたインターカレーションした DNA とヌクレオソームの構造ダイナミクス解析
The conformation and dynamics of intercalated DNA and nucleosome analyzed by molecular dynamics simulation
Hisashi Ishida¹, Hidetoshi Kono^{1,2} (¹*Inst. Quantum Life Science, QST*, ²*cQUEST, Chiba Univ.*)
- [1Pos060](#) Unveiling the centromere/kinetochore structure in chicken DT40 cells using expansion microscopy and fluorescence correlation spectroscopy
Yasuhiro Hirano^{1,2}, Akira Kitamura³, Toru Hirota², Tatsuo Fukagawa¹ (¹*Graduate School of Frontier Biosciences, The University of Osaka*, ²*Cancer Institute of JFCR*, ³*Faculty of Advanced Life Science, Hokkaido University*)
- [1Pos061](#) 凝縮体形成と共役した転写動態の粒子ベース反応動力学モデリング
Particle-based modeling of reactive dynamics of transcription coupled with condensate formation
Daiki Sugata, Shoji Takada (*Grad. Sch. Biol., Univ. Kyoto*)

09. 電子状態／09. Electronic

- [1Pos062](#) エネルギー準位統計によるペプチドの分類
Classification of peptides by energy level statistics
Masanori Yamanaka (*CST, Nihon Univ.*)

- [1Pos063](#) 物理学の知識を組み込んだ AI 創薬の開発
Development of drug discovery AI incorporating physics-based knowledge
Yuuka Ogawa¹, Tatsuki Kawauchi², Tomohiko Hayashi² (¹*Faculty of Engineering, Niigata Univ.*, ²*Grad. Sch. Sci. and Tech., Niigata Univ.*)
- [1Pos064](#) トレハロース水溶液を用いた AQP 過剰発現 CHO 細胞の凍結保存
Cryopreservation of AQP4-overexpressing CHO cells using trehalose aqueous solution
Sumire Matsuo¹, Masato Yasui², Youichiro Abe², Tsutomu Uchida³ (¹*Graduate school of engineering, Hokkaido University*, ²*School of Medicine, Keio University*, ³*Faculty of Engineering, Hokkaido University*)

12. 発生・分化／12. Development & Differentiation

- [1Pos065](#) 人工ヒト胚モデルにおける細胞移動とパターン形成
Cell Migration and Pattern Formation in Engineered Human Embryo Models
Kiyoshi Ohnuma¹, Chihiro Takeuchi¹, Hazuki Tsuboi¹, Ryo Kojima¹, Tsuji Shota¹, Emilio Macias Estrada Raul¹, Hayashi Yohei², Miyu Mori¹ (¹*Nagaoka University of Technology*, ²*RIKEN*)
- [1Pos066](#) 画像からの細胞間力の推定と多細胞形態形成
Image-based force inference of pairwise cell-cell interactions for multicellular morphogenesis
Hiroshi Koyama^{1,2}, Toshihiko Fujimori^{1,2} (¹*Div. Embryology, NIBB*, ²*SOKENDAI (Graduate University for Advanced Studies)*)

13. 筋肉（筋蛋白質・収縮）／13. Muscle

- [1Pos067](#) ミオシン頭部の 1 分子実験と筋繊維実験の両方を再現する計算モデルの構築
Construction of a simulation model which reproduces both of the single molecule experiment of myosin head and the muscle fiber experiment
Kenshiro Kaneko, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)
- [1Pos068](#) ファシンにより形成されたアクチン束の崩壊過程ダイナミクスのリアルタイム観察
Real-Time observation of the Disassembly of Fascin-Mediated Actin Bundles
Masayuki Hoshida^{1,2}, Takumi Toji², Tatsuya Iwata³, Noriko Takeuchi¹, Hajime Honda², Ikuko Fujiwara² (¹*School of Health Sciences, Kitasato University*, ²*Materials Sci. & Bioeng., Nagaoka Univ. of Tech.*, ³*Faculty of Pharmaceutical Sciences, Toho University*)

14. 分子モーター／14. Molecular motor

- [1Pos069](#) バクテリア鞭毛モーターにおける MotAB の駆動機構：理論モデルによるアプローチ
Exploring the Driving Mechanism of MotAB in the Bacterial Flagellar Motor via Theoretical Modeling
Shintaro Kubo^{1,2}, Yasushi Okada³, Shoji Takada⁴ (¹*Wako, RIKEN*, ²*Dept. of Applied Chem., the Univ. of Tokyo*, ³*Dept. of Med., the Univ. of Tokyo*, ⁴*Grad. Sch. Sci., Kyoto Univ.*)

- [1Pos070](#) ADP-Pi ミオシン S1 と F-actin 間駆動力の物理原理について
On the physical principle of the driving force between myosin S1 with ADP-Pi and F-actin
Makoto Suzuki (*Tohoku University*)
- [1Pos071](#) キネシン 1 の協調的運動における情報ラチェット機構
Information ratchet mechanism for the coordinated unidirectional movement of kinesin-1
Michio Tomishige¹, Hiroshi Isojima², Kohei Matsuzaki¹ (¹*Dept. Phys. Sci., Aoyama Gakuin Univ.,*
²*Dept. Appl. Phys., Univ. Tokyo*)
- [1Pos072](#) 動的水チャネルを介したべん毛モーターの回転運動の全原子分子動力学解析
All-atom molecular dynamics analysis of rotational motion of flagellar motor mediated by dynamic water channels
Yukinari Kamiyama, Takumi Matsumoto, Tsubasa Nakai, Mitsunori Takano (*Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)
- [1Pos073](#) DNA 人工分子モーターの合理的性能向上
Rational performance improvement of DNA artificial molecular motor
Takanori Harashima^{1,2}, Akihiro Otomo^{1,2}, Ryota Iino^{1,2} (¹*Institute for Molecular Science,* ²*Graduate Institute for Advanced Studies, SOKENDAI*)
- [1Pos074](#) Modulating potential alignment to enhance molecular motor speed
Akihiro Fukuda, Yohei Nakayama, Shoichi Toyabe (*Grad. Sch. Eng., Tohoku Univ.*)
- [1Pos075](#) Rhodamine-Phalloidin によって可視化されたアクチンフィラメントの構造多型性は、リン酸および ATP + ミオシン II によって抑制される
Structural polymorphism of actin filaments revealed by Rhodamine Phalloidin is suppressed by phosphate and ATP + myosin II
Kenta Toshino, Taro Q.P. Uyeda (*Dept. Pure. & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)
- [1Pos076](#) 最高速 AFM によって明らかになった回転子のない F₁-ATPase の化学-力学カップリング
Chemomechanical coupling in rotor-less F₁-ATPase revealed by high-speed atomic force microscopy
Shingo Fukuda¹, Akihiro Otomo^{2,3}, Ryota Iino^{2,3}, Toshio Ando¹ (¹*WPI NanoLSI, Kanazawa Univ.,* ²*Inst. for Mol. Sci., NINS,* ³*SOKENDAI*)
- [1Pos077](#) テザーの改変によるキネシン-1 モータードメインの基本的運動機構の解明
Tether-dependent regulation reveals core motility mechanism of the kinesin-1 motor domain
Rieko Sumiyoshi¹, Masahiko Yamagishi^{1,2}, Junichiro Yajima^{1,2,3} (¹*Grad. Arts & Sci., Univ. Tokyo,*
²*Komaba Inst. Sci., Univ. Tokyo,* ³*RCCSB, UBI, Univ. Tokyo*)
- [1Pos078](#) C.elegans キネシン BMK-1 と有糸分裂キネシン Eg5 阻害剤の生化学的特性と相互作用
Biochemical Characterization and Interaction of *C.elegans* kinesin BMK-1 with Mitotic Kinesin Eg5 Inhibitors
Fofou Yonta Tostani, Shunsuke Kumagai, Nur Fatin Liyana Binti Salwadi, Shinsaku Maruta (*Grad.Sch., Soka Univ.Tokyo*)
- [1Pos079](#) KIF6 による鞭毛運動とエネルギー調節の分子メカニズム
KIF6's Role in Ciliary Motility and Energy Regulation
Tsukasa Makino¹, Chizuru Ito², Takeshi Masuda³, Kazuho Ikeda¹, Daisuke Takao^{1,4}, Yasushi Okada^{1,5}, Kiyotaka Toshimori², Masahide Kikkawa¹ (¹*Univ. Tokyo,* ²*Chiba Univ.,* ³*Keio Univ.,* ⁴*Huazhong Agricultural Univ.,* ⁵*RIKEN BDR*)

15A. 細胞生物学的課題：接着／15A. Cell biology: Adhesion

- [1Pos080](#) 歯周病菌の線毛の先端蛋白質 FimD の X 線結晶構造解析
Structure of FimD, a tip protein of the pill of gum disease bacterium *Porphyromonas gingivalis*
Norihiro Takekawa, Yusuke Ando, Rei Kojima, Katsumi Imada (*Grad. Sch. Sci., Osaka Univ.*)

- [1Pos081](#) 細胞形態切り替え材料による細胞周期の進行速度操作への試み
Modulating Cell Cycle Progression by Dynamic Control of Cell Shape Using Stimuli-Responsive Substrates
Sayaka Masaike, Satoru Kidoaki (IMCE, Univ. Kyushu)

15B. 細胞生物学的課題：運動／15B. Cell biology: Motility

- [1Pos082](#) 巨大纖毛虫 *Spirostomum ambiguum* の細胞伸長に関わる表層微小管束間の滑り運動
Active sliding between microtubule ribbons extending from the ciliary basal bodies elongates the giant ciliate *Spirostomum ambiguum*
Kosuke Nakamura¹, Seiji Sonobe¹, Kazuhiro Oiwa^{1,2} (¹Grad. Sch. Sci., Univ. Hyogo, ²Adv. ICT Res. Inst., NICT, Kobe)
- [1Pos083](#) 時間情報を用いたアメーバ細胞の牽引力場測定
Inference of cellular traction forces using temporal information
Kazuko Hamaoka, Hirokazu Tanimoto (Grad. Sch. Nanobiosci., Yokohama City Univ.)
- [1Pos084](#) CheY Phosphorylation-Mediated Turning Enables Polarity Alignment at the Swarming Front in *Vibrio alginolyticus*
Kakeru Sumitomo, Ikuro Kawagishi, Masatoshi Nishikawa (Grad. Sch. Sci., Univ. Hosei)
- [1Pos085](#) Mechanosensitive adhesion complexes that lead to complex cell crawling behaviors in a one-dimensional track.
Hsuan-Yi Chen (National Central University)
- [1Pos086](#) 制御された局所外力印加により明らかにする細胞境界の変形と分子応答の因果関係
Reveal the causal relationship between tissue deformation and molecular response through optical manipulation
Kenji Nishizawa¹, Shao-Zhen Lin³, Claire Chardès², Jean-François Rupprecht³, Pierre-François Lenne² (¹Graduate School of Engineering, Tohoku University, ²CNRS, Centre de Physique Théorique., ³CNRS, The Institute of Developmental Biology of Marseille.)
- [1Pos087](#) リアルタイムフィードバック機構を用いたサブストレイトの硬さによる機械刺激への拍動応答
Modulation of Beating Response to Mechanical Stimulation by Substrate Stiffness Using Real-Time Feedback Control
Ayaka Namiki, Arisa Mizutani, Yuuta Moriyama, Toshiyuki Mitsui (Dept. Phys. Sch. Sci., Aoyamagakuin Univ.)
- [1Pos088](#) Integrative Spatiotemporal Analysis of Collective Cell Migration and ERK Dynamics in Epithelial MDCK Wound Healing
Lisna Hidayati¹, Kazuhiro Aoki², Yuichi Sakumura¹ (¹Graduate School of Science and Technology, Nara Institute of Science and Technology, ²Graduate School of Biostudies, Kyoto University)

15C. 細胞生物学的課題：細胞骨格・膜骨格／15C. Cell biology: Cytoskeleton & Membrane skeleton

- [1Pos089](#) 破骨細胞融合における membrane-cortex attachment と BAR タンパク質の機械的制御
Mechanical control of cell-cell fusion during osteoclastogenesis by membrane-cortex attachment and BAR proteins
Yuri L. Nemoto^{1,2}, Yumeng Wan², Tsukasa Oikawa³, Kazunori Takano⁴, Takahiro K. Fujiwara⁵, Kazuya Tsujita^{1,2}, Toshiaki Itoh^{1,2} (¹Biosignal Research Center, Kobe University, ²Kobe University Graduate School of Medicine, ³Graduate School of Medicine, Hokkaido University, ⁴Graduate School of Science, Chiba University, ⁵Institute for Integrated Cell-Material Sciences (WPI-iCeMS), Kyoto University)

- [1Pos090](#) 幅広い細胞種に適応した中心体単離手法の開発
Development of centrosome isolation methods adaptable to various cell types
Momoko Miyazawa, Shohei Yamamoto, Daiju Kitagawa (*Grad. Pharm., Univ. Tokyo*)
- [1Pos091](#) TIRF 解析によるアクチン重合ダイナミクスにおける His161 の役割解明
Elucidating the role of His161 in actin polymerization dynamics using TIRF analysis
Kota Onozato¹, Mitsusada Iwasa², Shuichi Takeda², Toshiro Oda³, Hajime Honda¹, Ikuko Fujiwara¹
(¹*Materials Sci. & Bioeng., Nagaoka Univ. of Tech.*, ²*Grad. Sch. Info., Nagoya Univ.*, ³*Faculty of Health and Welfare, Tokai Gakuin University*)
- [1Pos092](#) アクチン重合制御における古細菌ゲルゾリン各ドメインの TIRF および構造解析による機能解明
Dissecting Domain Functions of Archaeal Gelsolin in Actin Assembly by TIRF and Structural Analyses
Houryou Mizuki¹, Shuichi Takeda^{2,3}, Robert Robinson^{3,4}, Ikuko Fujiwara¹ (*¹Materials Sci. & Bioeng., Nagaoka Univ. of Tech.*, *²Grad. Sch. Info., Nagoya Univ.*, *³RIIS, Okayama Univ.*, *⁴VISTEC, Thailand.*)
- [1Pos093](#) TIRF 顕微鏡と構造解析により明らかになった Cytochalasin D のアクチンフィラメント作用機構
Cytochalasin D Inhibits Actin Dynamics through Transient Capping and Severing
Takahiro Mitani¹, Shuichi Takeda², Toshiro Oda³, Akihiro Narita⁴, Yuichiro Maéda², Hajime Honda¹, Ikuko Fujiwara¹ (*¹Materials Sci. & Bioeng., Nagaoka Univ. of Tech.*, *²Grad. Sch. Info., Nagoya Univ.*, *³Fac. Health & Welf., Tokai-gakuin Univ.*, *⁴Grad. Sch. Sci., Nagoya Univ.*)
- [1Pos094](#) 初期胚における一過的な核の物性変化と転写のバーストの促進
Changes in the physical properties of early embryonic nuclei promote a transcriptional burst
Masahito Tanaka¹, Rin Sakanoue², Atsushi Takasu², Yasuki Miyagawa³, Naoko Watanabe¹, Yu-Chia Chen⁴, Aussie Suzuki⁴, Kei Miyamoto^{2,3}, Yuta Shimamoto^{1,5} (*¹Laboratory of Physics and Cell Biology, National Institute of Genetics.*, *²Graduate School of Biology-Oriented Science and Technology, Kindai University.*, *³Faculty of Agriculture, Kyushu University.*, *⁴McArdle Laboratory for Cancer Research, Department of Oncology, University of Wisconsin-Madison.*, *⁵Department of Genetics, Sokenkai University*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

- [1Pos095](#) The mechanical properties of cells grown at the interface of ferroelectric domain walls
Alexis Borowiak, Takeshi Shimi, Yohei Kono, Takeshi Fukuma (*NanoLSI, Kanazawa University*)
- [1Pos096](#) 1 分子 SuperPAINT 法による細胞膜全体にわたる動的ナノスケール不均一性の可視化
SuperPAINT visualization of dynamic nanoscale heterogeneity of the entire plasma membrane
Maoji Wang¹, Bo Tang¹, Takahiro Fujiwara², Taka-Aki Tsunoyama¹, Akihiro Kusumi¹ (*¹Okinawa Institute of Science and Technology.*, *²Institute for Integrated Cell-Material Sciences, Kyoto University*)
- [1Pos097](#) 大腸菌細胞内 Ca²⁺恒常性の再検討
A reconsideration of intracellular Ca²⁺ homeostasis in *Escherichia coli*
Takemasa Nakamura¹, Hiroyuki Noji^{1,2}, Kazuhito Tabata^{1,2} (*¹Department of Applied Chemistry, School of Engineering, University of Tokyo.*, *²Research Institute of Planetary Health (RIPH), The University of Tokyo*)
- [1Pos098](#) 抑制性シナプス形成の開始機構：ゲフリンと Ena/VASP の共凝縮体形成によるアクチン重合
Initiators for inhibitory synapse formation: actin polymerization induced by co-condensation of gephyrin and Ena/VASP family proteins
Amine Aladag¹, Taka-Aki Tsunoyama¹, Irina Meshcheryakova¹, Maoji Wang¹, Jun-Seok Lee¹, Bo Tang¹, Hiroko Hijikata³, Takahiro K Fujiwara³, Sawako Yamashiro², Akihiro Kusumi¹ (*¹Okinawa Institute of Science and Technology.*, *²Kyoto University Graduate School of Biostudies.*, *³Kyoto University Institute for Integrated Cell-Material Sciences, KUIAS*)

- [1Pos099](#) ホスホリパーゼ D によるミリスチル化タンパク質の拡散および Ras/PIP3 ドメインの制御
Phospholipase D regulates on-membrane diffusivity of a myristoylated protein and defines the Ras/PIP3 patch territory
Gen Honda^{1,2}, Satoshi Sawai^{1,3}, Miho Yanagisawa^{1,2,3} (¹Department of Basic Science, Graduate School of Arts and Sciences, University of Tokyo, ²Komaba Institute for Science, Graduate School of Arts and Sciences, University of Tokyo, ³Research Center for Complex Systems Biology, Graduate School of Arts and Sciences, University of Tokyo)
- [1Pos100](#) Two distinct regulatory mechanisms limiting macrophage phagocytosis: membrane backtracking and inhibition of phagocytosis initiation
Dan Horonushi¹, Souta Suzuki¹, Maiha Ando¹, Haruka Yuki¹, Shinya Kato¹, Kenji Yasuda^{1,2} (¹Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ., ²Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.)
- [1Pos101](#) 神経細胞による心筋細胞集団間の興奮伝導接続
Excitatory Connection Between Cardiomyocyte Populations Mediated by Neurons
Ayuri Sakaguchi, Kentaro Kito, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ., Tokyo, Japan*)
- [1Pos102](#) 複数微粒子貪食数に対する細胞膜最大伸長量の応答変化計測からの最大貪食機能の解明
Determining Maximum Macrophage Phagocytosis by Measuring Membrane Extension Response During Sequential Particle Uptake
Shinya Kato¹, Dan Horonushi¹, Haruka Yuki¹, Kei Shibata², Syunya Morikawa², Kenji Yasuda^{1,2} (¹Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ., ²Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.)
- [1Pos103](#) オプソニン化マイクロニードルに対するマクロファージ応答の極性を明らかにする貪食膜伸長と細胞運動の相関解析
Coupled coordination of phagocytic membrane extension and cell migration reveals polarity in macrophage response to opsonized microneedles
Haruka Yuki¹, Dan Horonushi¹, Maiha Ando¹, Sinya Kato¹, Kenji Yasuda^{1,2} (¹Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ., ²Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.)
- [1Pos104](#) 単一細胞レベルにおける直線状心筋細胞ネットワークの伝導速度
Conduction Velocity of Linear Cardiomyocyte Networks at single-cell level
Shinnosuke Mori, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

16A. 生体膜・人工膜：構造・物性 / 16A. Biological & Artificial membrane: Structure & Property

- [1Pos105](#) 環境応答性蛍光色素によるモデル脂質膜とタウタンパク質の相互作用解析
Interactions between Lipid Membranes and Tau Protein Probed by Environment-Sensitive Fluorescent Probes
Chiho Watanabe (*Grad. Sch. Int. Sci. Life, Hiroshima Univ.*)
- [1Pos106](#) Computational studies of the disruption mechanism of pathogenic bacterial membrane by cocoglucoside from coconut oil
Phonphiphat Bamrung (คณะวิทยาศาสตร์ มหาวิทยาลัยเกษตรศาสตร์)
- [1Pos107](#) 人工甘味料スクラロースによる DPPC モデル生体膜における指組ゲル相形成
The artificial sweetener sucralose induces the formation of an interdigitate gel phase in DPPC model biomembranes
Emika Matsumoto¹, Michael Postrado², **Hiroshi Takahashi**² (¹Sch. Sci. Tech. Gunma Univ., ²Grad. Sch. Sci. Tech. Gunma Univ.)

- [1Pos108](#) 2本のうち1本の疎水鎖末端を部分フッ素化したリン脂質が膜タンパク質バクテリオドプシン(bR)の四次構造と光サイクルに及ぼす影響
Quaternary structure and photocycle of bR in bilayers composed of phospholipids with a single partially fluorinated hydrophobic chain
Ai Nakagawara¹, Takafumi Shimoaka¹, Toshiyuki Takagi², Hiroshi Takahashi¹, Takashi Kikukawa³, Hideki Amii^{1,4}, Masashi Sonoyama^{1,4,5} (¹*Grad. Sch. Sci. & Tech., Gunma Univ.*, ²*AIST*, ³*Fac. Adv. Life Sci., Hokkaido Univ.*, ⁴*GLAR, Gunma Univ.*, ⁵*GUCFW, Gunma Univ.*)

16B. 生体膜・人工膜：ダイナミクス／16B. Biological & Artificial membrane: Dynamics

- [1Pos109](#) 表層糖鎖が関与する細菌の細胞外膜小胞形成
Involvement of the surface carbohydrates in bacterial membrane vesicle formation
Jun Kawamoto¹, Taiku Tsudzuki¹, Tomoya Imai², Takuya Ogawa¹, Tatsuo Kurihara¹ (¹*Institute for Chemical Research, Kyoto University*, ²*Research Institution for Sustainable Humansphere*)
- [1Pos110](#) Giant Plasma Membrane Vesicle の膜粘度測定
Viscosity of Giant Plasma Membrane Vesicles
Tatsuya Itoi (*Dept. of Physics, Tohoku University*)
- [1Pos111](#) 自動化技術による膜粘度の顕微鏡画像データ解析の精度向上
Improving accuracy of microscopic image data analysis for membrane viscosity measurement using automation technique
Kenya Haga, Yuka Sakuma, Masayuki Imai (*Grad. Sch. Sci., Tohoku Univ.*)
- [1Pos112](#) パターン化人工膜と光ピンセットによる人工生体膜分子の時空間操作
Spatiotemporal Manipulation of Membrane Molecules in Artificial Membranes Using Membrane Patterning and Optical Tweezers
Yasushi Tanimoto¹, Shunya Moriyama¹, Kyoko Masui¹, Fumio Hayashi², Kenichi Morigaki^{3,4}, Chie Hosokawa¹ (¹*Grad. Sch. Sci., Osaka Metropolitan Univ.*, ²*Grad. Sch. Sci., Kobe Univ.*, ³*Biosignal Res. Center, Kobe Univ.*, ⁴*Grad. Sch. Agri., Kobe Univ.*)

16C. 生体膜・人工膜：興奮・チャネル／16C. Biological & Artificial membrane: Excitation & Channels

- [1Pos113](#) 電位依存性プロトンチャネル活性化のN末端制御
N-terminal control of voltage-gated proton channels
Ryuya Nawata, **Akira Kawanabe**, Yuichiro Fujiwara (*Grad. Sch. Biomed. Health Sci., Hiroshima Univ.*)
- [1Pos114](#) 高速原子間力顕微鏡による非競合阻害剤結合状態のAMPA受容体ナノダイナミクスの解明
High-speed atomic force microscopy reveals nano-dynamics of AMPARs with the non-competitive inhibitors
Keisuke Sato¹, Yimeng Zhao², Motoyuki Hattori², Mikihiro Shibata^{3,4} (¹*Grad. Sch. NanoLS, Kanazawa Univ.*, ²*Sch. Life Sci., Fudan Univ.*, ³*WPI-NanoLSI, Kanazawa Univ.*, ⁴*InFiniti, Kanazawa Univ.*)
- [1Pos115](#) 油中水滴接触膜を用いた膜張力定量下でのアクアポリンの水透過性測定
Measuring aquaporin water permeability using pressure-determined droplet interface bilayers with defined membrane tension
Misuzu Ueki, Takahisa Maki, **Masayuki Iwamoto** (*Dep. Mol. Neurosci., Facul. Med. Sci., Univ. Fukui*)

- [1Pos116](#) Ion translocation mechanism of Na⁺-pumping NADH-quinone oxidoreductase from molecular dynamics simulations
Takehito Seki^{1,2}, Moe Ishikawa-Fukuda^{3,4}, Jun-ichi Kishikawa⁵, Masatoshi Murai³, Takahiro Masuya³, Hideto Miyoshi³, Danielle McFee⁴, Blanca Barquera⁴, Kei-ichi Okazaki^{1,2} (¹*SOKENDAI*, ²*Institute for Molecular Science*, ³*Graduate School of Agriculture, Kyoto University*, ⁴*Department of Biological Science, Rensselaer Polytechnic Institute*, ⁵*Department of Applied Biology, Kyoto Institution of Technology*)
- [1Pos117](#) 糖脂質 MPLase が関与する膜タンパク質輸送機構の物理化学的解析
 Exploring the Role of a Glycolipid MPLase in Membrane Protein Transport through Physicochemical Studies
Shoko Mori¹, Kaoru Nomura¹, Kohki Fujikawa¹, Tsukiho Osawa¹, Ken-ichi Nishiyama², Keiko Shimamoto^{1,3} (¹*Bioorg. Res. Inst., Suntory Fdn. Life Sci.*, ²*Fac. Agric., Iwate Univ.*, ³*Grad. Sch. Sci., Osaka Univ.*)

17. 化学受容／17. Chemoreception

- [1Pos118](#) コレラ菌アミノ酸走性受容体の広範かつ特異的な検知プロフィール
 The versatile and specific sensing profiles of *Vibrio cholerae* amino-acid chemoreceptors
So-ichiro Nishiyama¹, June Minaki¹, Taisei Kumakura¹, Yuta Nogami¹, Fuga Omori^{2,3}, Katsumi Imada⁴, Ikuro Kawagishi^{1,2,3} (¹*Fac. App. Life Sci., Niigata Univ. Pharm. Med. Life Sci.*, ²*Grad. Sch. Sci. and Engin., Hosei Univ.*, ³*Res. Cen. Micro-Nano Tech., Hosei Univ.*, ⁴*Dep. MacroMol. Grad. Sch. Sci., Osaka Univ.*)

18. 神経・感覚（細胞・膜タンパク質・分子）／18. Neuroscience & Sensory systems

- [1Pos119](#) Abnormal differentiation of olfactory sensory neurons in ATF5 upstream open reading frame mutant mice
Haruo Nakano, Sanetoki Koide, Shuya Yoshida, Mariko Umemura, Shigeru Takahashi, Yuji Takahashi, Yasuhiro Shinkai (*Environ. Biol., Life Sci., Tokyo Univ. Pharm. Life Sci.*)
- [1Pos120](#) 飢餓状態における線虫 *C. elegans* の低温耐性獲得機構と人工進化解析による新規因子の探索
 Mechanism of acquisition of cold tolerance in *C. elegans* during starvation and search for novel factors by artificial evolution analysis
Seiya Kamino¹, Miina Fuzisawa¹, Atsushi Doi², Hideki Doi², Akane Ohta¹, Atsushi Kuhara^{1,3} (¹*Institute for Integrative Neurobiology, Konan University*, ²*Kinki University · School of Agriculture Medical Institute of Bioregulation*, ³*PRIME, AMED*)
- [1Pos121](#) *C. elegans* の低温耐性に関わる転写伸長因子 TCEB の機能細胞の絞り込み
 Narrowing down the functional cells of TCEB, a transcription elongation factor involved in cold tolerance in *C. elegans*
Sho Yabuuchi^{1,2}, Hiroaki Teranishi^{1,2}, Toshihiro Iseki^{1,2}, Natsune Takagaki^{1,2}, Yohei Minakuchi³, Atsushi Toyoda³, Akane Ohta^{1,2}, Atsushi Kuhara^{1,2,4} (¹*Dept. Biol. Grad. Sch. Sci. Konan Univ.*, ²*Inst. of Integral NeuroBiol. Konan Univ.*, ³*National Institute of Genetics, Japan*, ⁴*PRIME AMED*)

- [1Pos122](#) カエル神経筋接合部シナプスにおけるカゼインキナーゼ阻害剤の効果: 単発刺激放出の抑制と連続刺激での放出増大短期可塑性の強化
Investigation of effect of a casein kinase 2 inhibitor at the frog NMJ: EPP was reduced and short-term plasticity was intensified
Naoya Suzuki (*Grad.Sch.Sci., Nagoya Univ.*)
- [1Pos123](#) Thermosensory signal processing by multiple thermoreceptors within a single thermosensory neuron in *C. elegans*
Nanako Kanamura^{1,2}, Akane Ohta^{1,2}, Yuki Sato^{1,2}, Akira Kawanabe³, Yuichiro Fujiwara^{3,4}, Atsushi Kuhara^{1,2,5} (¹*Graduate School of Natural Science, Konan University, Kobe, Japan*, ²*Institute for Integrative Neurobiology, Konan University, Kobe, Japan*, ³*Faculty of Medicine, Kagawa University, Kagawa*, ⁴*Graduate School of Biomedical and Health Sciences (Medical), Hiroshima University, Hiroshima, Japan*, ⁵*PRIME, AMED*)

21A. 光生物：視覚・光受容 / 21A. Photobiology: Vision & Photoreception

- [1Pos124](#) クロライドイオンを対イオンとしてもつサングオプシンの分光研究
Spectroscopic studies of a coral opsin with chloride ion as a counterion
Yuri Tominaga¹, Shino Inukai¹, Yusuke Sakai², Mitsumasa Koyanagi², Akihisa Terakita², Hideki Kandori^{1,3}, Kota Katayama^{1,3} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Grad. Sch. Sci., Osaka Met. Univ.*, ³*OptoBio Technology Center, Nagoya Inst. Tech.*)
- [1Pos125](#) アプノモナドが持つ新奇紫外・青色光受容アニオンチャンネルロドプシン ApuRs の分光学的特性
Spectroscopic characterization of ApuRs, novel UV- and blue-absorbing anion channel rhodopsins from Apusomonads
Takashi Nagata¹, Luis Javier Galindo², Shunki Takaramoto¹, Andrey Rozenberg³, Hiroto Takahashi¹, Oded Běja³, Keiichi Inoue¹ (¹*Inst. Solid State Phys., Univ. Tokyo*, ²*Inst. Water Res., Univ. Granada, Spain*, ³*Faculty Biol., Technion – Israel Inst. Tech., Haifa, Israel*)
- [1Pos126](#) 固体 NMR によるヘリオロドプシンのアミノ酸残基特異的なダイナミクスとプロトン化状態の解析
Residue-Specific Characterization of Heliorhodopsin Dynamics and Protonation States by solid-state NMR
Yuki Samatsu¹, Sari Kumagai¹, Kota Katayama², Hideki Kandori², Izuru Kawamura¹ (¹*Grad. Sch. Eng. Sci., Yokohama Natl. Univ.*, ²*Grad. Sch. Eng., Nagoya Inst. Tech.*)
- [1Pos127](#) Time-resolved crystallography reveals structural transitions of a bifunctional cryptochrome bearing a light-harvesting antenna chromophore
Junpei Yamamoto¹, Wei-Ting Lin², Meng-Iao Fong², Kai-Chun Yang², Hikaru Saito¹, Yuhei Hosokawa², Manuel Maestre-Reyna² (¹*Grad. Sch.Eng.Sci., Univ. Osaka*, ²*Dep. Chem., National Taiwan Univ.*)
- [1Pos128](#) 短波長シフトした光駆動内向きプロトンポンプロドプシンの波長制御機構の研究
Study on the color-tuning mechanism of a blue-shifted light-driven inward proton-pumping rhodopsin
Yoshitaka Kato¹, Borja Aldegue-Riquelme², Oded Běja^{3,4}, Josefa Antón², Keiichi Inoue¹ (¹*ISSP, Univ. Tokyo*, ²*Department of Physiology, Genetics and Microbiology, University of Alicante*, ³*Faculty of Biology, Technion—Israel Institute of Technology*, ⁴*The Nancy and Stephen Grand Technion Energy Program, Technion—Israel Institute of Technology*)

- [1Pos129](#) 無脊椎動物由来繊維毛型オプシンの G タンパク質共役特異性の解析
G protein-coupling specificity of ciliary opsins in invertebrates
Kazuki Ohmichi¹, Tomoki Kawaguchi¹, Keita Sato², Hideyo Ohuchi², Hisao Tsukamoto¹ (¹*Grad. Sch. Sci. Kobe Univ.*, ²*Okayama Univ.*)
- [1Pos130](#) 自動化プラットフォームを用いたロドプシン吸収波長変異体の効率的作製
Automated System for High-Throughput Production of Spectral-Tuning Rhodopsin Variants
Masae Konno, Takashi Nagata, Keiichi Inoue (*ISSP, Univ. Tokyo*)
- [1Pos131](#) Expression analysis of heliorhodopsin genes in actinomycetes
Rei Abe-Yoshizumi¹, Hideki Kandori^{1,2} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*OptoBio., Nagoya Inst. Tech.*)
- [1Pos132](#) *Stretomyces alkaliphilus* 由来ヘリオロドプシンは、固相培養で発現する
Heliorhodopsin from *Stretomyces alkaliphilus* is expressed in solid phase culture
Koyo Yamada¹, Rei Abe-Yoshizumi¹, Tatsuro Nishikino^{1,2}, Hideki Kandori^{1,2} (¹*Grad. Sch. of Eng., Nagoya Inst. of Tech.*, ²*OptoBio Tech. Res. Cent., Nagoya Inst. of Tech.*)
- [1Pos133](#) 中温性細菌 *Modestobacter muralis* 由来のロドプシンの発現と光反応
Expression and photoreaction of rhodopsin from the mesothermal bacterium *Modestobacter muralis*
Haruna Matsumura¹, Shota Takahashi¹, Takafumi Shimoaka¹, Fumio Hayashi², Takashi Kikukawa³, Masashi Sonoyama^{1,4,5} (¹*Grad. Sch. Sci. Tech., Gunma Univ.*, ²*Ctr. Inst. Analysis, Gunma Univ.*, ³*Fac. Adv. Life. Sci., Hokkaido Univ.*, ⁴*GIAR, Gunma Univ.*, ⁵*GUCFW, Gunma Univ.*)

21B. 光生物：光合成／21B. Photobiology: Photosynthesis

- [1Pos134](#) 最先端の蛍光顕微分光法による細胞内の多様な光合成超複合体を観る
Capturing *in vivo* dynamic photosynthetic supercomplexes using state-of-the-art fluorescence excitation-emission microscopy
Xianjun Zhang^{1,2}, Ryutaro Tokutsu³, Jun Minagawa⁴, Shen Ye¹, Yutaka Shibata¹ (¹*Tohoku University*, ²*Massachusetts Institute of Technology*, ³*School of Veterinary Science, Kitasato University*, ⁴*National Institute for Basic Biology*)
- [1Pos135](#) 光化学系 II 結晶を用いた Mn₄CaO₅ クラスターの構築機構の時間分解赤外分光解析
Time-resolved infrared study of the photoassembly process of the Mn₄CaO₅ cluster using photosystem II crystals
Yuki Kato¹, Kazuki Ogura¹, Yoshiki Nakajima², Jian-Ren Shen², Takumi Noguchi¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Res. Inst. Interdiscip. Sci., Okayama Univ.*)
- [1Pos136](#) Spectral Shifts in Chromophore Absorption Wavelengths Caused by Three Linkers in the Phycobilisome Rod of *Synechocystis* PCC 6803
Hiroto Kikuchi (*Dept. Phys., Sch. Med., Nippon Med. Sch.*)
- [1Pos137](#) 紅色光合成細菌 *Phaeospirillum molischianum* の LH2 タンパク質の再構築：カロテノイドと界面活性剤の影響
Reconstruction of LH2 protein from a purple photosynthetic bacterium *Phaeospirillum molischianum*: effects of carotenoids and detergents
Taiga Miura, Yoshitaka Saga (*Grad. Sch. Sci. Eng, Kindai Univ.*)
- [1Pos138](#) 光合成酸素発生系における翻訳後アミノ酸修飾によるシステインスルホン酸配位子の形成
Formation of a cysteine sulfonate ligand via post-translational modification in the photosynthetic oxygen-evolving complex
Kazuha Nakamura¹, Takehiro Suzuki², Hatsune Mizue¹, Tomomi Kitajima-Ihara¹, Minako Hirano¹, Yuki Kato¹, Naoshi Dohmae², Takumi Noguchi¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*RIKEN, CSRS*)

- [1Pos139](#) 遠赤色利用可能な光化学系IIの光捕集機能におけるカロテノイドの役割
Light-harvesting functions of carotenoids in the far-red light utilizing photosystemII from *Acaryochloris marina*
Vasco Joris¹, Naoki Suenaga², Miki Bando-Uotani^{1,3}, Kyoko Shinzawa-Ito⁴, Natsuko Inoue-Kashino⁴, Yasuhiro Kashino⁴, Keisuke Kawakami⁵, Koji Yonekura⁵, **Daisuke Kosumi**⁶ (¹Grad. Sch. Sci. and Tech., Kumamoto Univ., ²Facul. Sci., Kumamoto Univ., ³Dev. Tech., Kumamoto Univ., ⁴Grad. Sch. Sci, Hyogo Univ., ⁵RIKEN, SPring-8, ⁶IIna, Kumamoto Univ.)
- [1Pos140](#) 光化学系I超複合体の高分解能AFM観察
High-resolution AFM imaging of photosystem I supercomplex in thylakoid membrane
Azusa Owada¹, **Daisuke Yamamoto**² (¹WDB Co., LTD., ²Fac. Sci., Fukuoka Univ.)
- [1Pos141](#) 光合成酸素発生系における脂肪族アミノ酸の非天然カルボキシレート配位子への翻訳後変換
Post-translational conversion of aliphatic amino acids to non-natural carboxylate ligands in the photosynthetic oxygen-evolving complex
Hatsune Mizue¹, Takehiro Suzuki², Takumi Matsubara¹, Tomomi Kitajima-Ihara¹, Minako Hirano¹, Yuichiro Shimada¹, Yuki Kato¹, Naoshi Dohmae², Takumi Noguchi¹ (¹Department of Physics, Graduate School of Science, Nagoya University, ²Biomolecular Characterization Unit, RIKEN Center for Sustainable Resource Science)

21C. 光生物：光遺伝学・光制御／21C. Photobiology: Optogenetics & Optical control

- [1Pos142](#) カリウムチャネルロドプシン B1ChR2 のK⁺選択性メカニズムの解明と応用に向けて
Towards a mechanistic understanding and application of K⁺ selectivity of potassium channelrhodopsin B1ChR2
Ryotaro Shimamura¹, Shoko Hososhima^{1,2}, Hideki Kandori^{1,2}, Satoshi Tsunoda^{1,2} (¹Grad. School of Engineering, Nagoya Institute of Technology, ²Opto Bio Technology Research Center)
- [1Pos143](#) PYP を用いた光可逆的タンパク質性液液相分離形成の解析
Analysis of photo-reversible proteinaceous liquid-liquid phase separation formation using PYP
Yoichi Yamazaki¹, Ranmaru Shirahama¹, Kento Yonezawa^{1,2}, Hironari Kamikubo^{1,2} (¹NAIST MS, ²NAIST CDG)
- [1Pos144](#) Disordering of cell membrane lipids induced by THz irradiation
Hiromichi Hoshina (RIKEN RAP)
- [1Pos145](#) H⁺輸送活性の低いナトリウムポンプロドプシンにおけるプロトン化レチナール塩基周辺の水素結合ネットワーク
Hydrogen-Bonding Network Around the Protonated Retinal Schiff Base in a Sodium-Pumping Rhodopsin with Low H⁺ Transport Activity
Hiroyuki Takizuka¹, Yuma Ito¹, Akiko Ito¹, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹Graduate School of Engineering, Nagoya Institute of Technology, ²Optobiotechnology Research Center, Nagoya Institute of Technology)
- [1Pos146](#) チャネルロドプシン GtCCR3 の波長制御とチャネル開閉機構
Color tuning and channel gating mechanism of cation-channelrhodopsin GtCCR3
Junichiro Tabe¹, Shoko Hososhima^{1,2}, Hideki Kandori^{1,2}, Satoshi Tsunoda^{1,2} (¹Graduate School of Engineering, Nagoya Institute of Technology, ²Opto Bio Technology Research Center)

- [1Pos147](#) Unveiling Calcium's Role in the Emergence of Molecular Chirality
Chen Chen¹, Ruiqin Yi², Tony Z. Jia³ (¹*Biofunctional Catalyst Research Team, RIKEN Center for Sustainable Resource Science (CSRS)*, ²*Guangzhou Institute of Geochemistry, Chinese Academy of Sciences*, ³*Earth-Life Science Institute, Institute of Future Science, Institute of Science Tokyo*)
- [1Pos148](#) 緑藻類の光応答に及ぼす細胞数と細胞分化の影響
 Effects of cell number and cell differentiation on the photo-response of green algae
Daito Seito, Yoshihiro Murayama (*Tokyo University of Agriculture and Technology, Faculty of engineering, Department of Biomedical Engineering*)
- [1Pos149](#) 最小ゲノム細菌の実験室適応進化
 Adaptive laboratory evolution of minimal genome bacterium
Masaki Mizutani¹, Minoru Moriyama², Ryuichi Koga², Takema Fukatsu^{2,3,4}, Shigeyuki Kakizawa² (¹*Faculty of Science, Gakushuin University*, ²*Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology (AIST)*, ³*Graduate School of Science, University of Tokyo*, ⁴*Graduate School of Life and Environmental Sciences, University of Tsukuba*)
- [1Pos150](#) 短いランダムな RNA 集団に創発する遺伝の解析
 Exploring emergent heritability in short random RNA pools
Jiro Kakizaki¹, Alike Andjani Widada¹, Norikazu Ichihashi², Ryo Mizuuchi¹ (¹*Fac. Sci. Eng., Waseda Univ.*, ²*Grad. Sch. Arts and Sci. Univ. Tokyo*)

24. 合成生物学・人工細胞／24. Synthetic biology & Artificial cells

- [1Pos151](#) 膜結合アクチンネットワークによる人工細胞の形態変化
 Morphological modification of artificial cell encapsulating membrane-bound actomyosin system
Yusei Sato^{1,2}, Rieko Sumiyoshi², Masahiko Yamagishi², Takeshi Haraguchi³, Kyohei Matsuda², Suguru Sato³, Kohji Ito³, Junichiro Yajima² (¹*X-star, JAMSTEC*, ²*Dep. of Life Sci., Grad. Sch. of Arts and Sci., The Univ. of Tokyo*, ³*Dep. of Biology, Grad. Sch. of Sci., Chiba Uni.*)
- [1Pos152](#) DNA で操る合成細胞のアクチン骨格：DNA とタンパク質の橋渡しによる機能拡張
 DNA-Regulatable Actin Cytoskeleton in Synthetic Cells: Bridging DNA and Proteins toward Enhanced Functionality
Daichi Nakajima¹, Keita Abe¹, Satoshi Murata¹, Shinichiro M. Nomura¹, Hideaki Matsubayashi² (¹*Department of Robotics, Graduate School of Engineering, Tohoku University*, ²*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*)
- [1Pos153](#) 人工分子の化学修飾による微小管のプログラム可能な配列制御
 Programmable Microtubule Arrangement via Synthetic Molecular Modification
Kenta Tamaki¹, Hiroto Morita¹, Ryota Iino², Takayuki Uchihashi¹ (¹*Grad. Sch. of Sci., Nagoya Univ.*, ²*IMS, NINS*)
- [1Pos154](#) 翻訳因子の持続的な再生産による *in vitro* 自己増殖系の構築
 Sustainable regeneration of translation factors toward *in vitro* self-regeneration
Kentaro Shoji¹, Katsumi Hagino¹, Norikazu Ichihashi^{1,2,3} (¹*Department of Life Science, Graduate School of Arts and Science, The University of Tokyo*, ²*Komaba Institute for Sciences, University of Tokyo*, ³*Universal Biology Institute, University of Tokyo*)
- [1Pos155](#) A Hybrid *In Silico*/*In-Cell* Controller for Robust Optimization of Microbial Bioprocesses
Katsuyuki Kunida^{1,2}, Tomoki Ohkubo², Yuichi Sakumura² (¹*Department of Computational Biology, School of Medicine, Fujita Health University*, ²*Data-Driven Biology, Division of Biological Science, Nara Institute of Science and Technology*)

- [1Pos156](#) 生体制御モジュールを用いたリボソームの人工制御
Artificial regulation of ribosomes using the trans-acting engineered regulatory module
Maho Fujino, Yoshikazu Tanaka, Takeshi Yokoyama (*Grad. Sch. Life Sci., Tohoku Univ.*)
- [1Pos157](#) マイクロ流路内での水/水相分離が創り出す細胞サイズ液滴の規則配列
Spontaneous generation of linearly-arranged uniform microdroplets through phase separation in microfluidic channel
Mayu Shono¹, Ken Hirano², Akihisa Shioi³, Kenichi Yoshikawa⁴ (¹*Komaba Institute for Science, Graduate School of Arts and Sciences*, ²*Health and Medical Research Institute, National Institute of Industrial Science and Technology (AIST)*, ³*Department of Chemical Engineering and Materials Science, Doshisha University*, ⁴*Faculty of Life and Medical Sciences, Doshisha University*)
- [1Pos158](#) 多細胞様液滴による翻訳と共役した RNA ゲノム複製の空間的分離
Multicell-like communicating droplets enabling spatial control of translation-coupled genomic RNA replication
Hidekazu Sono¹, Keiji Murayama², Kensuke Ueda³, Norikazu Ichihashi^{3,4,5}, Ryo Mizuuchi^{1,6} (¹*Dept. Elect. Eng. & Biosci., Fac. Sci. & Eng., Waseda Univ.*, ²*Dept. Biomol. Eng., Grad. Sch. Eng., Nagoya Univ.*, ³*Komaba Inst. for Sci., Univ. Tokyo*, ⁴*Dept. Life Sci., Grad. Sch. Arts & Sci., Univ. Tokyo*, ⁵*Universal Biol. Inst., Univ. Tokyo*, ⁶*FOREST, JST*)
- [1Pos159](#) Organization of multicellular-like liposome structures with specific shapes
Shun Okada, Kan Shoji (*Nagaoka University of Technology*)

26A. 計算生物学: 生命情報学 / 26A. Computational biology: Bioinformatics

- [1Pos160](#) 構造揺らぎを想定した変異体タンパク質のアンサンブルドッキングによる相互作用解析
Interaction analysis by ensemble docking of mutant proteins assuming structural fluctuations
Nobuyuki Uchikoga¹, Yuri Matsuzaki² (¹*Dept. Network Design, Sch. Interdisip. Math. Sci., Meiji Univ.*, ²*Acad. Leadership, Sci. Tokyo*)
- [1Pos161](#) Towards automation in HS-AFM data analysis and interpretation
Romain Amyot, Holger Flechsig (*NanoLSI, Kanazawa University*)
- [1Pos162](#) 乳がん組織における TP53 ホットスポット変異と発現変動の関連機構
Association between TP53 hotspot mutations and expression alterations in breast cancer tissues
Takaharu Naito, Takanori Sasaki (*Fac. Adv. Math. Sci., Meiji Univ.*)
- [1Pos163](#) RNA-seq を用いた相関分析による転移性乳がんの miRNA 予後予測因子の選出
Selection of miRNA Prognostic Factors for Metastatic Breast Cancer by Correlation Analysis Using RNA-seq
Sota Kageyama, Takanori Sasaki (*I. Fac. Adv. Math. Sci., Meiji Univ.*)
- [1Pos164](#) 内分泌療法による乳がんの予後に関する効果修飾遺伝子と PPI network 領域の予測
Prediction of effect modifiers and PPI network regions involved in endocrine therapy-induced breast cancer prognosis
Shoya Oba, Takanori Sasaki (*I. Fac. Adv. Math. Sci., Meiji Univ.*)
- [1Pos165](#) 大規模なデータセットで学習した事前学習モデルを利用したタンパク質・リガンド結合親和性の予測
Predicting protein-ligand binding affinity using pre-trained models on large-scale dataset
Sei Inoue, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)
- [1Pos166](#) 蛋白質リガンド相互作用の pIC50 の機械学習予測
pIC50 Prediction Using Protein-Ligand Interactions
Shuji Endo, Masanori Yamanaka (*Grad. Sch. Sci. & Tech., Nihon Univ.*)

- [1Pos167](#) 深層学習モデル gr Predictor を用いたタンパク質 2 量体界面の水和分布予測
Predicting the Hydration Structures at the Protein-Protein Interfaces of Dimers using a Deep-Learning Model "gr Predictor
Yuki Ito, **Takashi Yoshidome** (*Dep. of Appl. Phys., Tohoku Univ.*)
- [1Pos168](#) Analysis of water dynamics around antifreeze proteins by molecular dynamics simulations
Nao Abe¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)
- [1Pos169](#) QM/MM Study of the Reaction Mechanism of a SAM-Dependent 3-Amino-3-Carboxypropyl Transferase in Nocardicin Biosynthesis
Masayuki Karasawa¹, Takayoshi Awakawa², Takahiro Mori^{3,4,5}, Ikuro Abe^{3,4}, Tohru Terada^{1,4} (¹*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*RIKEN Cent. Sustain. Res. Sci. (CSRS)*, ³*Grad. Sch. of Pharm. Sci., Univ. of Tokyo*, ⁴*Collab. Res. Inst. Innov. Microbiol. (CRIIM)*, ⁵*JST PRESTO*)
- [1Pos170](#) Elucidating the Binding Pathway of Abltide to Abl Kinase through Enhanced 2D Replica Exchange Molecular Dynamics Simulations
Yichao Wu, Ai Shinobu (*Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka*)
- [1Pos171](#) Free energy analysis of drug inclusion in polymeric micelles using molecular dynamics simulation
Mai Ukawa¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)
- [1Pos172](#) BEMM-GEN: A Toolkit for Generating a Biomolecular Environment-Mimicking Model for Molecular Dynamics Simulation
Takunori Yasuda, Rikuri Morita, Yasuteru Shigeta, **Ryuhei Harada** (*CCS, Univ. of Tsukuba*)
- [1Pos173](#) Effects of Phosphorylation in the Naturally-Denatured Region of TGIF-1 on Functional Regulation
Madoka Nakatani¹, Simon Hikiri², Junichi Higo³, Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*, ³*Grad. Sch. Info. Sci., Univ. Hyogo*)
- [1Pos174](#) Binding Free Energy Analysis of PD-L1 and Macrocyclic Peptide Inhibitors
Hyunji Kim¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)
- [1Pos175](#) Elucidation of the binding mechanism between botulinum toxin and antibodies through binding free energy analysis
Yuka Maeda¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)
- [1Pos176](#) アクチンの分子揺らぎに内在する複数の機能運動
Multiple functional motions of actin are embedded in its intrinsic molecular fluctuation
Ryotaro Koike¹, Kei Moritsugu², Motonori Ota¹ (¹*Grad. Sch. Info., Nagoya Univ.*, ²*Grad. Sch. Sci., Osaka Metro. Univ.*)
- [1Pos177](#) MD シミュレーションを用いた膜の伝熱性解析
Analysis of the Thermal Insulation Properties of Lipid Bilayers Using Molecular Dynamics (MD) Simulations
Ayaka Kiyota¹, Yuichi Togashi^{1,2} (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*RIKEN*)
- [1Pos178](#) Molecular Simulation Study on the Conformational Dynamics and Activation Pathway of Melanopsin
Ruisi Zou¹, Kohe Obayashi², Hisao Tsukamoto², Toshifumi Mori^{1,3} (¹*Grad. Sch. Integr. Sci. & Eng., Univ. Kyushu*, ²*Grad. Sch. Sci., Kobe Univ.*, ³*Inst. Mater. Chem. & Eng., Kyushu Univ.*)

- [1Pos179](#) Investigating Protein Condensation and Ion Contributions with Explicit Solvent Coarse-Grained Models
Yangyang Zhang¹, Cheng Tan¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS, Kobe, Japan*, ²*RIKEN PRI, Wako, Japan*)
- [1Pos180](#) Neuropsin (KLK8)の触媒活性に対する金属添加効果の計算化学的検討
Effect of metal ion addition on the catalytic activity of Neuropsin (KLK8): a computational study
Masami Lintuluoto¹, Mari Fujimoto¹, Humika Nakamura¹, Souma Kai¹, Yoshifumi Fukunishi², Hideki Tamura³, Jua Mikael Lintuluoto⁴ (¹*Graduate School of Life and Environmental Sciences, Kyoto Prefectural University*, ²*Cellular and Molecular Biotechnology Research Institute, National Institute of Advanced Industrial Science and Technology (AIST)*, ³*Laboratory of Biofunctional Science, Hoshi University School of Pharmacy and Pharmaceutical Sciences*, ⁴*Graduate School of engineering, Kyoto University*;))
- [1Pos181](#) 分子動力学シミュレーションを用いた多剤排出輸送体 MdfA の基質特異性と排出機構の解析
Analysis of substrate specificity and efflux mechanism of the multidrug transporter MdfA using MD simulations
Hodaka Tanabe, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ of Tokyo*)
- [1Pos182](#) 阻害剤の柔軟性がレセプタータンパク質への結合に与える影響の拡張アンサンブルによる検証
Verification of the effect of ligand and receptor flexibility on inhibitory activity by generalized-ensemble algorithms
Suzuka Saitou¹, Simon Hikiri², Junichi Higo³, Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*, ³*Grad. Sch. Info Sci., Hyogo Univ.*)
- [1Pos183](#) 計算化学を用いた 2-オキシグルタル酸依存性ジオキシゲナーゼによるオロバンコール環拡大反応の触媒機構の解明
Computational study on the catalytic mechanism of 2-oxoglutarate-dependent dioxygenase in the ring expansion of orobanchol
Hanting Jiang¹, Takatoshi Wakabayashi², Hajime Sato¹, Yoshitaka Moriwaki^{1,4}, Masato Homma³, Yukihiro Sugimoto³, Tohru Terada¹ (¹*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*Dept. of Appl. Biol. Chem., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ³*Dept. of Biochem., Grad. Sch. of Agri. and Life Sci., Kove Univ.*, ⁴*Med. Res. Inst., Inst. of Integr. Res., Science Tokyo.*)
- [1Pos184](#) 薬剤設計のための AQP7 チャネルへの阻害剤侵入に関するインシリコ解析
In silico analysis of inhibitor intrusion into the AQP7 channel for efficient drug design
Koryo Obata¹, Yasuteru Shiget², Ryuhei Harada² (¹*Grad. Sch. degree programs in life and earth sciences, University of Tsukuba*, ²*Center for Computational sciences, University of Tsukuba*)
- [1Pos185](#) 分子動力学を用いた 超音波誘導性の piezo 1 立体構造変化解析
Analysis of ultrasound-induced structure changes in piezo1 using Molecular Dynamics
Yoshio Nakano, Kazuki Arita, Satoka Kasai, Kazumi Yoshizawa, Tsugumi Yamauchi, Daisuke Yamada, Akiyoshi Saitoh, Satoru Miyazaki (*Fac. Pharm. Tokyo Univ. Sci.*)
- [1Pos186](#) 分子動力学計算による脂質スクランブラーゼ Atg9 の開閉運動における脂質及び水分子の挙動解析
Lipid and Water Dynamics during the Functional Cycle of the Lipid Scramblase Atg9: A Molecular Dynamics Study
Ayaka Shimbo, Takaharu Mori (*Grad. Sci., Tokyo Univ. of Sci.*)
- [1Pos187](#) 拡散モデルによる全原子シミュレーションからの粗視化力場の学習
Learning coarse-grained force fields from all-atom simulations via diffusion models
Ryounosuke Kouriki, Tsuyoshi Terakawa (*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)
- [1Pos188](#) AlphaFold と MD シミュレーションによるコラーゲン三重らせん構造の解析
Structural Analysis of Collagen Triple Helices Using AlphaFold and Molecular Dynamics Simulations
Rikuto Noguchi¹, Taiyo Eguchi¹, Aimi Yamashita¹, Kohsuke Adachi², Masato Kinoshita³, Yuuta Moriyama¹, Toshiyuki Mitsui¹ (¹*Grad. Sch. Sci. and Eng., Aoyamagakuin Univ.*, ²*Fac. Agr. and Mar. Sci., Kochi Univ.*, ³*Grad. Sch. Agr., Kyoto Univ.*)

26C. 計算生物学：生体モデリングとシミュレーション／
26C. Computational biology: Biological modeling and simulation

- [1Pos189](#) 細胞の剥離を含む頂点モデルにおける破壊パターンの解析
Analysis of fracture patterns in a vertex model including detachment of cells
Nozomi Fujita¹, Yuichi Togashi^{1,2} (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*BDR, RIKEN*)
- [1Pos190](#) 粗視化格子モデルによるタンパク質の進化とアロステリック制御
Coarse-Grained Lattice Modeling of Protein Evolution and Allostery
Jin Kousaka^{1,2}, Radek Erban³, Yuichi Togashi¹ (¹*Graduate School of Life Sciences, Ritsumeikan University*, ²*Kobe Inst., Riken*, ³*Mathematical Institute University of Oxford*)
- [1Pos191](#) Boosting weak signals with incorrect ligands in the sensory system
Yan-Ru Chen (*Department of Physics, National Central University*)

27. 数理生物学・理論生物学／27. Mathematical & Theoretical biology

- [1Pos192](#) グリオブラストーマ細胞の移動メカニズムを解明するための数理モデリングと解析
Mathematical modeling and analysis to elucidate the migration mechanism of glioblastoma cells
Hauna Tagawa¹, Daisuke Kanematsu², Asako Katsuma², Yonehiro Kanemura², Yuichi Sakumura¹
(¹*Graduate School of Science and Technology, Nara Institute of Science and Technology*, ²*National Hospital Organization Osaka National Hospital*)
- [1Pos193](#) Modeling hysteresis in protrusion mechanics during neuronal polarization
Akane Uchida, Naoyuki Inagaki, Yuichi Sakumura (*Graduate School of Science and Technology, Nara Institute of Science and Technology*)
- [1Pos194](#) シグナル伝達系における時間符号化の進化
Evolution of temporal encoding in signaling network
Thoma Itoh^{1,2}, Yohei Kondo³, Kazuhiro Aoki⁴, Nen Saito² (¹*Dept. Basic Biol., Grad. Sch. Life Sci., SOKENDAI*, ²*Grad. Sch. Integrated Sciences for Life, Univ. Hiroshima*, ³*Grad. Sch. Med., Univ. Nagoya*, ⁴*Grad. Sch. Biostudies, Univ. Kyoto*)
- [1Pos195](#) Mathematical Modeling and Simulation of Epithelial Wound Closure Dominated by Fingering Instability
Hikaru Emoto, Nen Saito (*Graduate School of Integrated Sciences for Life, Hiroshima University*)
- [1Pos196](#) Mechanical balance of adhesions mediates chiral collective rotation induced by cell chirality
Ryohei Nishizawa^{1,2}, Tomoki Ishibashi¹, Goshi Ogita¹, Tatsuo Shibata^{1,2} (¹*BDR, Riken*, ²*Grad Sch. of FBS., Osaka Univ.*)

28. 生態／環境／28. Ecology & Environment

- [1Pos197](#) Multiphase chemistry of bio-related molecules in microdroplets studied aerosol optical tweezers
Yuan-Pin Chang (*Dept. of Chem., National Sun Yat-sen Univ., Taiwan*)

29. 非平衡・生体リズム／29. Nonequilibrium state & Biological rhythm

- [1Pos198](#) 非平衡ナノ逆ミセルのテラヘルツ振動凝縮
Terahertz vibrational condensation in out-of-equilibrium nanoscale reverse micelles
Hiroshi Murakami (*QST*)

- [1Pos199](#) ナノ内視鏡 AFM 法を用いた上皮間葉転換による細胞内核膜硬さ変化測定
Nanodendoscopy-AFM based nanomechanical measurements reveal changes in nuclear elasticity during epithelial-mesenchymal transition
Takehiko Ichikawa, Yohei Kono, Makiko Kudo, Takeshi Shimi, Takeshi Fukuma (*NanoLSI, Kanazawa Univ.*)
- [1Pos200](#) ナノスケール構造・化学変化ダイナミクス分析のための高速 AFM・顕微ラマン複合装置
High-speed AFM/micro-Raman multimodal system for studying nanoscale conformational and chemical dynamics
Keishi Yang¹, Feng-Yueh Zhan², Verma Prabhat¹, Takayuki Uchihashi^{2,3}, Takayuki Umakoshi^{1,4} (*Grad. Sch. Eng., Univ. Osaka, ²Grad. Sch. Sci., Univ. Nagoya, ³ExCELLS, ⁴Inst. Adv. Co-creation Studies, Univ. Osaka*)
- [1Pos201](#) 機械学習画像解析を活用した 3 次元バクテリアバイオフィルムの In vivo マイクロレオロジー計測
In vivo microrheological measurement for 3D bacterial biofilm with machine learning image analysis
Takuya Ohmura¹, Dominic J. Skinner², Konstantin Neuhaus^{3,4}, Gary P.T. Choi⁵, Jörn Dunkel⁶, Knut Drescher³ (*¹RIES, Hokkaido Univ., ²Cent. Comput. Biol., Flatiron Instit., ³Biozentrum, Univ. of Basel, ⁴Dept. Phys., Univ. of Marburg, ⁵Dept. Math., Chinese Univ. of Hong Kong, ⁶Dept. Math., MIT*)
- [1Pos202](#) レーザーマニピュレーション法を用いた超微量ナノポア計測の開発
The development of the ultralow concentration detection using laser manipulation method and nanopore sensing
Masaya Yokono (*Nagaoka Univ. of Tech.*)
- [1Pos203](#) 酸化物/a-Si:H 積層薄膜による光触媒の作製とフラバン分子を用いた水素生成量の検出システム
Fabrication of photocatalysts based on oxide/a-Si:H stacked thin films and detection system of hydrogen production using flavan molecules
Yuki Sato¹, Kohei Saito¹, Akiko Hinoguchi¹, Hiroshi Masumoto², Yutaka Tsujiuchi^{1,2} (*¹Mat. Sci., Akita UNIV., ²FRIS, Tohoku UNIV.*)
- [1Pos204](#) ゲル, 紫外可視光変換物質, FLAVAN 分子, 半導体, を用いた光照射ダイオード特性制御システム
Light irradiation diode characteristic control system using gels, UV-Visible light converting materials, FLAVAN molecules, semiconductors
Yutaka Tsujiuchi^{1,2}, Hiroshi Masumoto², Yuto Takayama¹, Kohei Saito¹, Akiko Hinoguchi¹ (*¹Mat. Sci., Akita UNIV., ²FRIS, Tohoku UNIV.*)
- [1Pos205](#) 分子混雑効果が誘起する HIV-1 グアニン四重鎖 RNA の構造不均一性の単一分子レベルの解析
Analysis of structural heterogeneity in HIV-1 G-quadruplex RNA induced by molecular crowding at the single-molecule level
Miyuki Sakaguchi¹, Atsuki Harada¹, Kunihiro Ishii^{2,3}, Tahei Tahara^{2,3}, Takuhiro Otsu¹, Shoichi Yamaguchi¹ (*¹Grad. Sch. Sci. Eng., Saitama Univ., ²Molecular Spectroscopy Lab., RIKEN, ³RIKEN Center for Advanced Photonics*)
- [1Pos206](#) Single power-law rheology of crowded cytoplasm in living cells
Hiroyuki Ebata, **Daisuke Mizuno** (*Department of Physics, Kyushu University*)

- 1Pos207** 抗血清由来プローブを使った IRIS 多色超解像顕微鏡法による内在性の分子複合体の構成
The composition of endogenous molecular complexes by IRIS, multiplexed super-resolution imaging using antiserum-derived probes
Tai Kiuchi¹, Ryouhei Kobayashi², Shuichiro Ogawa¹, Louis Elverston², Dimitrios Vavylonis³, Naoki Watanabe² (¹Grad. Sch. Med., Kyoto Univ., ²Grad. Sch. Bio., Kyoto Univ., ³Dept. Phys., Lehigh Univ.)
- 1Pos208** Fluorescence lifetime imaging for quantification of subcellular GTP/GDP ratios in mammalian cells
Loan Thi Ngoc Nguyen¹, Cong Quang Vu², Satoshi Arai^{1,2} (¹Div. NanoLSI, Univ. Kanazawa, ²WPI-NanoLSI, Univ. Kanazawa)
- 1Pos209** Development of Organelle Heating Technology to Study the Spatiotemporal Dynamics of HSP Expression
Hettimudalige Dilini Nisansala¹, B.M.K.D. Basnayake¹, Takeru Yamazaki², Kayoko Nomura², Satoshi Arai^{1,2} (¹Grad. Sch. of Frontier Science Initiative, Division of Nano Life Science, Kanazawa University, ²WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University)
- 1Pos210** 酵素のナノスケール運動観察を目指したラベルフリー高精度一分子イメージングシステムの開発
Label-free high-precision single-molecule imaging system for nanoscale enzyme motion
Masato Sawa¹, Yasushi Okada^{1,2,3,4,5} (¹Grad. Sch. Sci., Univ. Tokyo, ²Grad. Sch. Med., Univ. Tokyo, ³Kobe Inst., Riken, ⁴WPI-IRCN, Univ. Tokyo, ⁵UBI, Univ. Tokyo)
- 1Pos211** EMCCD の高精度ノイズモデルを用いた機械学習による細胞の高倍率生物発光イメージングのためのデノイズング
Denosing for high-magnification bioluminescence imaging of cells through machine learning with precise noise modeling of EMCCD
Tetsuichi Wazawa¹, Haiyang Jiang², Ryohei Ozaki-Noma¹, Yinqiang Zheng², Imari Sato³, Takeharu Nagai¹ (¹SANKEN, Univ of Osaka, ²AI Center, Univ of Tokyo, ³Digital Content and Media Sciences Research, NII)
- 1Pos212** 高速 AFM を用いた PfDYN2 の膜構造認識に基づくマラリア原虫分裂機構の探究
Investigation of Plasmodium division mechanisms based on membrane recognition by PfDYN2 using high-speed AFM
Hirona Osaka¹, Hiroshi Yamada², Kohji Takei², Takayuki Uchihashi^{1,3} (¹Grad. Phys. Sci., Univ. Nagoya, ²Grad. Sch. Med., Dent. and Pharm. Sci., Okayama Univ., ³ExCELLS)
- 1Pos213** ミオシン分子に結合したアクチン線維の超解像顕微鏡解析
Super-resolution images of actin filaments bound to myosin molecules using a microscope with a home-built illumination system
Daichi Kobayashi, Taiki Tsujimoto, Kuniyuki Hatori (Graduate School of Science and Engineering, Yamagata University)
- 1Pos214** 一分子蛍光イメージングを用いた分子シャペロンによるアミロイド脱凝集過程のメカニズムの解明
Amyloid conformation-dependent disaggregation of chaperone revealed by single molecule fluorescent imaging
Yoshiko Nakagawa¹, Shingo Tamai¹, Takashi Nomura¹, Takahiro Nakayama², Motomasa Tanaka¹ (¹RIKEN, CBS, ²WPI Nano Life Science Institute, Kanazawa University)
- 1Pos215** 温度ジャンプ高速原子間力顕微鏡の開発と性能評価
Development and characterization of a temperature jump high-speed atomic force microscopy
Mai Tambo, Ayumi Sumino (Grad. Sch. of biostudies, Kyoto univ.)

- [1Pos216](#) Load-induced remodeling of mechanosensing proteins in suspended cell sheets
Madoka Suzuki¹, Keiko Kawauchi², Hiroaki Machiyama³, Hiroaki Hirata⁴, Shin'ichi Ishiwata⁵, Hideaki Fujita⁶ (¹*Inst. Protein Res., Univ. Osaka*, ²*Fac. Front. Innov. Res. Sci. Technol., Konan Univ.*, ³*Dept. Immunol., Tokyo Med. Univ.*, ⁴*Dept. Life Sci. Biotechnol., Kanazawa Inst. Technol.*, ⁵*Fac. Sci. Eng., Waseda Univ.*, ⁶*Res. Inst. Radiation Biol. Med., Hiroshima Univ.*)
- [1Pos217](#) 金ナノ粒子を用いる酸化還元蛋白質の電子移動制御と電気バイオものづくり
 Efficacy of uncapped gold nanoparticles for electron transfer to redox proteins and its application for bioproduction
Yasuhiro Mie¹, Chitose Mikami¹, Kentaro Akiyama², Yoshiaki Yasutake¹ (¹*Biomufacturing Production Res. Ctr., AIST*, ²*Molecular Biosystems Res. Inst., AIST*)
- [1Pos218](#) ARTIFICIAL CONTROL OF A HIGHLY ACTIVATED PLASTIC DEGRADING ENZYME BY PHOTOCROMIC NANODEVICES
Ateke Yanick Besong, Shota Nishida, Shinsaku Maruta (*Grad.Sch.Sci.Eng., Soka Univ.*)

34. Miscellaneous topics その他／34. Miscellaneous topics

- [1Pos219](#) 異常拡散系の初期通過問題における系の総数依存性とその役割
 The role of population for first passage time problem with anomalous diffusion
Yuta Sakamoto, Takahiro Sakaue (*Aoyama Gakuin University*)
- [1Pos220](#) 2点 MSD 解析の基礎と応用
 Two-Point MSD Analysis for Eliminating External Motion
Naoya Katayama, Takahiro Sakaue (*Dept. of Phys. Aoyama Gakuin Univ.*)

2 日目 (9 月 25 日 (木)) / Day 2 (Sep. 25 Thu.) 14:00 ~ 16:00

01A. タンパク質：構造／01A. Protein: Structure

- [2Pos001](#) マウスノロウイルスカプシドと細胞レセプター sCD300lf の結合様式の解明
 Elucidation of the binding mechanism between murine norovirus capsid and sCD300lf receptor
Kentaro Hiraka^{1,2}, Reiko Todaka³, Kei Haga³, Kazuhiko Katayama³, Kazuyoshi Murata^{1,2} (¹*ExCELLS, NINS*, ²*NIPS, NINS*, ³*Grad. Sch. Infection Control Sci., Kitasato Univ.*)
- [2Pos002](#) 細菌の細胞分裂に関与するタンパク質 FtsZ の構造遷移機構の解析
 Structural transition mechanism of Bacterial cell division protein FtsZ
Kodai Yamamoto¹, Taichi Takasawa¹, Takumi Oshiro¹, Yoshio Kodera^{1,2}, Go Watanabe³, Takashi Matsui^{1,2} (¹*Grad. Sch. Sci., Kitasato Univ.*, ²*Center for Disease Proteomics, Sch. Sci., Kitasato Univ.*, ³*Sch. of Front. Eng., Kitasato Univ.*)
- [2Pos003](#) 溶液 NMR による自然免疫シグナルタンパク質 MyD88 の多量化および相互作用解析
 NMR analysis of the interactions of the MyD88 TIR domain in innate immune signaling
Shiho Nukui, Yudai Ito, Kazuki Kasai, Hidehito Tochio (*Dept. of Biol. Sci., Grad. Sch. of Sci., Kyoto Univ.*)

- [2Pos004](#) ATR-FTIR 分光法によるアデノシン A2a 受容体のリガンド誘起構造変化解析
Ligand-induced conformational changes in the adenosine A2a receptor probed by ATR-FTIR spectroscopy
Shuma Tajima¹, Kento Watanabe¹, Shota Nakamura², Mika Hirose², Akitoshi Inoue³, Takayuki Kato², Ryoji Suno³, Hideki Kandori^{1,4}, Kota Katayama^{1,4} (¹*Nagoya Institute of Technology Graduate School of Engineering*, ²*Institute for Protein Research, Osaka University*, ³*Kansai Medical University*, ⁴*Nagoya Institute of Technology OptoBioTechnology Research Center*)
- [2Pos005](#) 性繊維毛 H-Pilus の構造が明らかにした TrhA pilin の環状化
Structural basis of the conjugation H-pilus reveals the cyclic nature of the TrhA pilin
Naito Ishimoto^{1,2,3}, Joshua Wong², Shan Heb², Sally Shirranc⁴, Olivia Paramio², Chloe Seddon^{2,3}, Nanki Singha^{2,3}, Carlos Balsalobre⁵, Ravi Sonanie⁶, Abigail Clements³, Edward Egelman⁶, Gad Frankel², Konstantinos Beis^{2,3} (¹*Grad. Sch. Life Sci., Yokohama City Univ.*, ²*Department of Life Sciences, Imperial College London*, ³*Rutherford Appleton Laboratory, Research Complex at Harwell*, ⁴*Biomedical Sciences Research Complex Mass Spectrometry & Proteomics Facility, University of St Andrews*, ⁵*Department de Genètica, Universitat de Barcelona*, ⁶*Department of Biochemistry and Molecular Genetics, University of Virginia*)
- [2Pos006](#) Structural insights into calcium selectivity of channelrhodopsin CapChR2
Jie Ma¹, Masahiro Fukuda², Seiwa Nakamura³, Seiya Tajima¹, Koichiro Kishi³, Suhyang Kim², Hideaki Kato^{1,2,3} (¹*Graduate School of Science, The University of Tokyo*, ²*Research Center for Advanced Science and Technology, The University of Tokyo*, ³*Graduate School of Arts and Sciences, The University of Tokyo*)
- [2Pos007](#) 非準等価ウイルスカプシドにおけるサブユニット形状の幾何学的制約
Geometric Constraints on Subunit Shapes in Non-Quasi-Equivalence Viral Capsids
Sakura Homma¹, Seri Nishimoto², Tomoya Tendo³, Kanata Warisaya², Hiroki Minami², Issei Tanaka², Ryuya Toyooka³, Takashi Horiyama⁴, Tomohiro Tachi³, Yasuhiro Matsunaga^{1,5} (¹*Grad. Sch. Sci. & Eng., Saitama Univ.*, ²*Grad. Sch. Eng., Univ. Tokyo*, ³*Grad. Sch. Arts & Sci., Univ. Tokyo*, ⁴*Grad. Sch. Fac. Inf. Sci. & Tech., Hokkaido Univ.*, ⁵*RIKEN*)
- [2Pos008](#) Universal scaling laws linking Dynamics and Folding revealed by AlphaFold Database
Zecheng Zhang¹, Qianyuan Tang¹, Weitong Ren², Jun Wang³ (¹*Hong Kong Baptist University, HKSAR, China*, ²*Wenzhou Institute, Univ. Chin. Acad. Sci, China*, ³*Nanjing University, China*)
- [2Pos009](#) クライオ電子顕微鏡を用いた V-ATPase の構造機能解析
Structural and Functional Analysis of V-ATPase Using Cryo-Electron Microscopy
Fuka Ueda¹, Yui Nishida¹, Atsuki Nakano¹, Atsuko Nakanishi², Kaoru Mitsuoka³, Ken Yokoyama¹ (¹*Grad.Sch. Life Sci., Kyoto Sangyo Univ.*, ²*IPR, Osaka Univ.*, ³*Research Center for Ultra-High Voltage Electron Microscopy, Osaka Univ.*)
- [2Pos010](#) 酵母プリオンタンパク質の構造・細胞表現系相関解析
Structural and Phenotypic Correlation Analysis of Yeast Prion Proteins
Takashi Nomura¹, David Boyer², Yusuke Komi¹, Atsushi Yamagata³, Mikako Shirouzu³, Carlos Bustamante⁴, David Eisenberg², Motomasa Tanaka^{1,5} (¹*Wako Inst., Riken*, ²*Dept. Bio. Chem., UCLA*, ³*Yokohama Inst., Riken*, ⁴*QB3, UC Berkeley*, ⁵*Dept. Life Sci. & Tech., TMDU*)
- [2Pos011](#) 放線菌由来新規プレニル基転移酵素の構造-機能相関の解明
Structure-function relationship of novel prenyltransferase from *Streptomyces* sp. KS84
Takumi Oshiro¹, Shuta Uehara¹, Yoshikazu Tanaka², Takuya Ito³, Yoshio Kodera^{1,4}, Takashi Matsui^{1,4} (¹*Grad. Sch. Sci., Kitasato Univ.*, ²*Grad. Sch. Life Sci., Tohoku Univ.*, ³*Fac. of Pharm., Osaka Ohtani Univ.*, ⁴*Center for Disease Proteomics, Sch. Sci., Kitasato Univ.*)
- [2Pos012](#) Protein Language Models Capture Evolutionary Trends via Embedding Variation
Yuxiang Zheng, Zecheng Zhang, Qian-Yuan Tang (*Hong Kong Baptist Univ*)

- [2Pos013](#) 時間分解真空紫外円二色性による SDS ミセル結合過程における β -ラクトグロブリンの構造ダイナミクス観測
Observing structural dynamics of β -Lactoglobulin Binding to SDS Micelle by Time-Resolved Vacuum-Ultraviolet Circular Dichroism
Satoshi Hashimoto¹, Koichi Matsuo^{1,2} (¹*Grad. Sch. Adv. Sci. Eng., Hiroshima Univ.*, ²*HiSOR*)
- [2Pos014](#) ペプチド結合の折り目効果の強化による黄色蛍光タンパク質 Venus の収量増加の試み
Attempts to increase the yield of the yellow fluorescent protein Venus by enhancing the ORIME effect of a peptide bond
Erika Gunji¹, Manami Suwa¹, Masaru Hoshino², Nobuhiro Suzuki³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*Kyoto Univ. Pharm.*, ³*NARO*)
- [2Pos015](#) トリプシン様蛋白質分解酵素のプロ領域による立体構造形成の解明
Propeptide-Mediated Folding of a Trypsin-Like Protease
Kairi Ogawa¹, Nana Sakata¹, Orika Ashida¹, Mitsuhiro Miyazawa², Shigeru Shimamoto¹, Yuji Hidaka¹ (¹*Grad. Sch. Sci. Eng., Univ. Kindai*, ²*PrevenTec Inc.*)
- [2Pos016](#) 変性状態下における BDPA の non-local 相互作用とフォールディング機構の再検討
Revisiting the Folding Mechanism of BDPA through non-local interactions in the Denatured State
Seiichi Hayashi¹, Saeko Yanaka^{1,2,3}, Maho Yagi^{1,2,4}, Yukiko Isono^{1,2}, Koichi Kato^{1,2,4}, Kunihiro Kuwajima⁵ (¹*Institute for Molecular Science, National Institutes of Natural Sciences*, ²*Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences*, ³*Materials and Structures Laboratory at Institute of Integrated Research, Institute of Science Tokyo*, ⁴*Graduate School of Pharmaceutical Sciences, Nagoya City University*, ⁵*Department of Physics, School of Science, University of Tokyo*)
- [2Pos017](#) 構造に基づく単純な統計力学モデルを用いた骨形成タンパク質 2 のフォールディング反応過程の予測
Prediction of the folding process of bone morphogenetic protein 2 using a simple structure-based statistical mechanical model
Yusaku Hirata¹, Koji Ooka², Munechito Arai^{1,2,3} (¹*Department of Physics, The University of Tokyo*, ²*College Arts and Sciences, The University of Tokyo*, ³*Department of Life Sciences, The University of Tokyo*)
- [2Pos018](#) RNA によるタウ凝集の速度論的解析
Kinetics of RNA-induced Tau Aggregation
Hiyori Araki, Hide Miyaguchi, Hideyuki Komatsu (*Department of Bioscience and Bioinformatics, Faculty of Systems Engineering and Computer Science., Kyushu Institute of Technology*)
- [2Pos019](#) がん抑制タンパク質 p53 のアセンブリ形態制御法の確立
Control of the assembly morphology of the tumor suppressor protein p53
Emi Hibino¹, Reiji Hijikata¹, Haruna Yoshida¹, Hidekazu Hiroaki^{1,2,3} (¹*Grad. Sch. Pharm. Sci., Nagoya Univ.*, ²*BeCellBar*, ³*COMIT*)

- [2Pos020](#) Molecular Shape Evolution of the Clock Protein KaiC
Shuji Akiyama^{1,2}, Yoshihiko Furuike^{1,2} (¹*NINS, IMS*, ²*SOKENDAI*)
- [2Pos021](#) オワンクラゲ由来蛍光タンパク質における二量体形成の比較
Comparison of Dimerization Behavior of Fluorescent Proteins from the Jellyfish *Aequorea Victoria*
Yuna Kinoshita, Haruko Hosoi (*Grad. Sch. Sci., Toho Univ.*)

- [2Pos022](#) グライコプロテオミクスのための O-glycoprotease IMPa 活性部位付近の相互作用解析
Analysis around the Active Site of O-glycoprotease IMPa for Glycoproteomics
Hiromitsu Shimoyama, Tomoaki Tamano, Issaku Yamada (*The Noguchi Institute*)
- [2Pos023](#) Functional and Structural Analyses on Clock Protein KaiC to Identify the Essential Step for the Temperature Compensation
Kanta Kondo^{1,2}, Yoshihiko Furuike^{1,2}, Kota Horiuchi^{1,2}, Yasuhiro Onoue², Shuji Akiyama^{1,2}
(¹*SOKENDAI*, ²*IMS*)
- [2Pos024](#) シクロム P450 還元酵素におけるフラビン補因子の還元によるアロステリック応答の分子動力学解析
Molecular dynamics analysis of the allosteric response to reduction of flavin cofactors in cytochrome P450 reductase
Mikuru Iijima, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)
- [2Pos025](#) 一本鎖抗体の活性に対する大腸菌外膜タンパク質 OmpF の効果
Effect of *Escherichia coli* outer membrane protein, OmpF, on the activity of single-chain variable fragments
Keiko Okano, Anna Ogi, Takao Izuka, Toshiyuki Okano (*Department of Electrical Engineering and Bioscience, School of Advanced Science and Engineering, Waseda University*)
- [2Pos026](#) 時計タンパク質 KaiC における第三の周期調節部位
The third period-regulating site in the clock protein of KaiC
Kota Horiuchi^{1,2}, Yoshihiko Furuike^{1,2}, Kumiko Ito-miwa³, Shuji Akiyama^{1,2} (¹*Institute for Molecular Science*, ²*SOKENDAI*, ³*Nagoya University*)
- [2Pos027](#) Time-Resolved Study of Light Intensity-Dependent Clustering Dynamics of TePixD
Chihiro Aramoto¹, Yusuke Masuda¹, Shunro Tokonami², Masahide Terazima¹, Yusuke Nakasone¹
(¹*Grad. Sch. Sci., Kyoto University*, ²*Grad. Sch. Sci., Gakushuin University*)
- [2Pos028](#) 細菌膜内切断プロテアーゼ RseP の基質結合構造と光架橋解析から提案する基質ドッキング機構
Substrate docking mechanism of intramembrane protease RseP revealed by the substrate-bound cryoEM structure and photocrosslinking analysis
Yosuke Shimizu¹, Tatsuya Kobayashi¹, Kikuko Asahi², Terukazu Nogi², Yoshinori Akiyama¹,
Yohei Hizukuri¹ (¹*Inst. Life Med. Sci., Kyoto Univ.*, ²*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

01D. タンパク質：計測・解析の方法論 / 01D. Protein: Measurement & Analysis

- [2Pos029](#) ナノ秒蛍光相関分光法を用いたタンパク質と RNA の高速ダイナミクスの観測
Ultrafast dynamics of protein and RNA investigated by nanosecond fluorescence correlation spectroscopy
Yuji Itoh^{1,2}, Yutaka Sano^{1,2}, Ibuki Soshino^{1,2}, Shrutarshi Mitra^{1,2}, Divya Rajendran³,
Athi N. Naganathan³, Satoshi Takahashi^{1,2} (¹*Grad. Sch. Sci., Tohoku Univ.*, ²*IMRAM*, ³*IIT Madras*)
- [2Pos030](#) 酸化 LDL の高感度検出を目指したバイオセンサーの合成研究
Synthetic study of biosensors for measurement of oxidized LDL
Takahisa Hiruma, Ryota Kumakura, Seiji Takeda (*Pharm. Sci., Hokkaido Univ. of Sci.*)
- [2Pos031](#) 酵素反応を用いたタンパク質の部位特異的蛍光色素ラベル化法の開発
Development of site-specific fluorophore labeling to target protein by using enzymatic reactions
Ai Hanano^{1,2}, Saori Kanbayashi¹, Cassidy Schmitt¹, Hiroyuki Oikawa³, Tateki Suzuki⁴,
Takao Hashiguchi⁴, Yuji Itoh^{1,2}, Satoshi Takahashi^{1,2} (¹*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*, ²*Graduate School of Life Sciences, Tohoku University*, ³*Molcure Inc.*, ⁴*Institute for Life and Medical Sciences, Kyoto University*)
- [2Pos032](#) 分子動力学計算とニューラルネットワークの連携による生体分子小角散乱プロファイルの解析
Interpretation of small-angle scattering profiles of biomolecules by molecular dynamics simulation and neural networks
Masahiro Shimizu (*KURNS, Kyoto Univ.*)

[2Pos033](#) AlphaFold3 を用いた AFM 画像から 3 次元立体構造の高速な再構築手法
Rapid Reconstruction of Atomic 3D Configurations from an AFM image by AlphaFold3
Tsuyoshi Kawai, Yasuhiro Matsunaga (*Grad. School. Sci. Eng., Univ. Saitama*)

01E. タンパク質：タンパク質工学／進化学／01E. Protein: Engineering

[2Pos034](#) The development of AMP-based antibiotics for drug-resistant Gram-negative bacteria
Wei Chun Weng, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo*)

[2Pos035](#) Development of red-color fluorescence lifetime biosensors for quantification of ATP levels in living cells
Tri Minh Phan¹, B.M.K.D Basnayake¹, Quang Vu Cong², Satoshi Arai^{1,2} (¹*Graduate School of Frontier Science Initiative, Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

[2Pos036](#) タンパク質工学を利用した人工セルロソームの構築とセルロース分解の効率化
Construction of an artificial cellulosome using protein engineering toward improvement of cellulose degradation
Momoka Takazawa, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

[2Pos037](#) De novo design of sensor proteins: calcium-binding protein
Rie Tatsumi, Nobuyasu Koga (*IPR, Univ. Osaka*)

[2Pos038](#) 遺伝子にコードされた蛍光バイオセンサーのためのモジュール型設計戦略：VEGF 検出への応用
Modular design strategy for genetically-encoded fluorescent biosensors: Application to VEGF Detection
Momoko Oya^{1,2}, Ryohei Ozaki-Noma¹, Tetsuichi Wazawa¹, Kazunori Sugiura¹, Mitsuru Hattori¹, Masataka Michigami³, Daisuke Fujiwara³, Ikuo Fujii³, Takeharu Nagai¹ (¹*SANKEN, The Univ. of Osaka*, ²*Grad. Sch. Pharm. Sci., The Univ. of Osaka*, ³*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

01F. タンパク質：天然変性／01F. Protein: Intrinsic disorder

[2Pos039](#) FUS タンパク質の天然変性領域と RNA の相互作用機構の解明
Unveiling the Interaction Mechanism between a FUS Intrinsically Disordered Region and RNA by Molecular Dynamics Simulation
Yoshie Iijima, Soichiro Kijima, PhuocDuy Tran, Akio Kitao (*Grad. Sch. Life Sci. and Tech., Science Tokyo*)

[2Pos040](#) TIA1 の自己集合における核酸の寄与の解明
Investigating the contribution of nucleic acids to the self-assembly of TIA1
Anupap Chauyjaroen Suk¹, Naotaka Sekiyama¹, Aya Ogino², Hiroki Konno³, Hidehito Tochio¹ (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ.*, ³*WPI Nano Life Sci. Inst. (WPI-Nano LSI), Kanazawa Univ.*)

[2Pos041](#) 実験とシミュレーションによる Hero 蛋白質のヘリックス形成の研究
The α -Helix Formation of Hero Proteins Studied by Experiments and Simulations
Takao Yoda¹, Ai Niitsu², Cheng Tan³, Naoya Tochio², Haeri Im^{3,4}, Takanori Kigawa², Jaewoon Jung^{3,4}, Yuji Sugita^{3,4} (¹*Nagahama Institute of Bio-Science and Technology*, ²*RIKEN IMS*, ³*RIKEN R-CCS*, ⁴*RIKEN PRJ*)

[2Pos042](#) 超音波照射を用いた夾雑環境下における α -シヌクレインシードの高感度検出
Ultrasonic Cavitation Enhances Selective Detection of α -Synuclein Amyloid Fibrils from a Crowded Environment
Tomoki Ota, Kichitaro Nakajima, Keiichi Yamaguchi, Yuji Goto, Hirotsugu Ogi (*Grad. Sch. Eng., Osaka Univ.*)

02. ヘムタンパク質／02. Heme proteins

- [2Pos043](#) 脱窒タンパク質超分子複合体の可溶化条件の最適化
Optimization of Solubilization Conditions for supramolecular complex of denitrification proteins
Sara Tanibayashi (*Grad. Sch. Sci., Univ. Hyogo*)
- [2Pos044](#) オリゴマー型アロステリック蛋白質の機能に於ける両親媒性溶質の影響 - 疎水性相互作用の役割
Effect of Amphipathic Solutes on the Function of an Oligomeric Allosteric Protein - Role of Hydrophobic Interactions
Antonio Tsuneshige^{1,2}, Takehiko Haga² (¹*Frontier Bioscience, HOSEI UNIVERSITY*, ²*Micro-Nano Tech. Ctr., HOSEI UNIVERSITY*)

03. 膜タンパク質／03. Membrane proteins

- [2Pos045](#) オレキシン受容体 2 の C 末端 IDR と受容体コアドメインとの分子内相互作用に関する溶液 NMR 解析
Solution NMR Analysis of the Intramolecular Interaction between the C-terminal IDR and the Receptor Core Domain of Orexin Receptor 2
Riki Kato¹, Yuki Kanazaki¹, Ken-Ichi Akagi², Yohei Miyanoi², Kayo Imamura¹, Hidehito Tochio¹
(¹*Grad. Sch. Sci., Univ. Kyoto*, ²*Inst. Protein Research, Univ. Osaka*)
- [2Pos046](#) 抗体を用いた膜結合型 CLIC1 を標的としたモノクローナル抗体の作製と機能解析
Development of Monoclonal Antibodies Specifically Targeting Membrane-bound CLIC1 and Their Functional Characterization
Kazuki Imai^{1,2}, Ayana Yamagishi^{1,2}, Masumi Iljima³, Chikashi Nakamura^{1,2} (¹*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, ²*CMB, AIST*, ³*Fac. Appl. BioSci., Tokyo Univ. of Agri.*)
- [2Pos047](#) 多剤排出トランスポーター EmrE の pH 依存的基質結合駆動力変換には Asp84 が関与する
Asp84 Is Involved in the pH-Dependent Driving Force Conversion for Substrate Binding in the Multidrug Efflux Transporter EmrE
Kazumi Shimono¹, Daisuke Takahashi¹, Shuichi Miyamoto¹, Seiji Miyauchi² (¹*Fac. Pharm. Sci., Sojo Univ.*, ²*Fac. Pharm. Sci., Toho Univ.*)
- [2Pos048](#) Allosteric Effects of Sodium Binding on the κ -Opioid Receptor Revealed by FTIR Spectroscopy
Ryo Nishikawa¹, Seiya Iwata¹, Shun Yokoi², Ryoji Suno³, Chiyo Suno-Ikeda³, Ayori Mitsutake², Takuya Kobayashi³, Hideki Kandori^{1,4}, **Kota Katayama**^{1,4} (¹*Grad. Sch. Engi. Univ. Nagoya. Inst.*, ²*Grad. Sch. Phys. Univ. Meiji*, ³*Grad. Sch. Med. Univ. Kansai. Med.*, ⁴*OptBioTech. Res. Cent. Univ. Nagoya. Inst.*)

04. DNA・DNA 結合タンパク質／04. DNA & DNA binding proteins

- [2Pos049](#) 分子動力学シミュレーションを用いた CRISPR Type I-C における DNA 切断前後のダイナミクスの違い
Molecular dynamics simulation study of the differences in dynamics before and after DNA cleavage in CRISPR Type I-C
Ryusei Haruna¹, Yoshihiro Kashiya¹, Ryota Kiyooka¹, Shota Shimogoochi¹, Naoyuki Miyashita^{1,2}
(¹*Grad. Sch. BOST, KINDAI Univ.*, ²*BOST KINDAI Univ.*)

- [2Pos050](#) Advancing Biophysical Protein-DNA Interaction and Dynamics Studies Through Enhanced Sampling
Mohamed Marzouk Sobaih, Ai Shinobu (*Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka*)
- [2Pos051](#) 高速 AFM を用いた ATP 依存的な Smc5/6 の構造ダイナミクスの可視化
 ATP dependent dynamics of Smc5/6 by high-speed atomic force microscopy
Kenichi Umeda^{1,2}, Yumiko Kurokawa³, Yasuto Murayama³, Noriyuki Kodera¹ (¹*Nano Life Science Institute, Kanazawa University*, ²*PRESTO/JST*, ³*Department of Chromosome Science, National Institute of Genetics*)

05. RNA・RNA 結合タンパク質／05. RNA & RNA binding proteins

- [2Pos052](#) NMR による α -シヌクレインと G4RNA の相互作用メカニズム解析
 NMR study of the interaction between α -Synuclein and G4RNA
Yiran Chen¹, Yasushi Yabuki², Norifumi Shioda², Hidehito Tochio¹ (¹*Grad. Sch. Sci., Univ. Kyoto*, ²*IMEG, Univ. Kumamoto*)
- [2Pos053](#) Valosin-containing protein behaved like an ATPase for FUS granules
Hitomi Kimura^{1,2}, Shin-ichi Tate^{1,2,3}, Kyota Yasuda^{1,2,3} (¹*Department of Mathematical and Life Sciences, Graduate School of Integrated Sciences for Life, Hiroshima University*, ²*International Institute for Sustainability with Knotted Chiral Meta Matter*, ³*Research Center for the Mathematics on Chromatin Life Dynamics*)

06. DNA/RNA ナノテクノロジー／06. DNA/RNA nanotechnology

- [2Pos054](#) DNA 液滴の個数制御された分裂を実現する酵素カスケード反応
 Enzymatic cascade reactions for number-controlled division of DNA droplets
Tatsumi Sakuma¹, Tomoya Maruyama², Masahiro Takinoue^{1,2,3} (¹*Department of Life Science and Technology, Institute of Science Tokyo*, ²*Research Center for Autonomous Systems Materialogy, Institute of Integrated Research, Institute of Science Tokyo*, ³*Department of Computer Science, Institute of Science Tokyo*)
- [2Pos055](#) 核酸増幅システムの特性検証
 Characterization of Responsive Nucleic Acid Amplification systems
Ken Komiya¹, Chizuru Noda¹, Takashi Nakakuki² (¹*X-star, JAMSTEC*, ²*Faculty of Comp. Sci. & Sys. Engi., Kyutech*)
- [2Pos056](#) 酵素反応によって活性化された DNA 凝集体
 Active DNA condensates coupled with enzymatic reactions
Tomoya Maruyama¹, Masahiro Takinoue^{1,2} (¹*Research Center for Autonomous Systems Materialogy, Institute of Integrated Research, Institute of Science Tokyo*, ²*Department of Computer Science, Institute of Science Tokyo*)
- [2Pos057](#) PEG-mediated regulation of DNA droplets: Stabilization with bulk PEG and transition to vesicle-like structures via DNA-PEG conjugates
Naoki Yoshida¹, Mayu Shono², Kenichi Yoshikawa³, Masahiro Takinoue^{1,4,5} (¹*Sch. Life Sci. & Tech., Science Tokyo*, ²*Grad. Sch. Art. & Sci., Univ. Tokyo*, ³*Self-organization Sci. Res. Ctr., Doshisha Univ.*, ⁴*Sch. Comp., Science Tokyo*, ⁵*ASMat, IIR, Science Tokyo*)

- [2Pos058](#) サブテラヘルツ波照射が DNA 塩基対の形成に与える影響の溶液 NMR 研究
Investigation of sub-terahertz irradiation effects on DNA base pair formation by solution NMR
Yuji Tokunaga¹, Koh Takeuchi¹, Hiromichi Hoshina², Masahiko Imashimizu³ (¹*Grad. Sch. Pharm. Sci., UTokyo*, ²*RIKEN Center for Advanced Photonics*, ³*CMB, AIST*)
- [2Pos059](#) ポリアミンによる遺伝子発現活性の温度依存性
Temperature dependence of gene expression activity in the presence of polyamines
Shotaro Kato¹, Takashi Nishio^{1,2}, Yuko Yoshikawa¹, Koichiro Sadakane¹, Kenichi Yoshikawa¹ (¹*Grad. Sch. Life and Med Sci., Doshisha Univ.*, ²*MolBis, AIST*)

08. クロマチン・染色体／08. Chromatin & Chromosomes

- [2Pos060](#) Hi-C コンタクトマップのスペクトル分解解析
Spectral decomposition analysis of Hi-C contact maps
Ai Ito, Takahiro Sakaue (*Aoyama Gakuin University*)
- [2Pos061](#) クロマチンドメインの熱力学的サイズ制限について
Thermodynamic size limits in chromatin domains
Fujishiro Shin (*FIFC, Kyoto Univ.*)
- [2Pos062](#) 複製依存的ヒストン標識 (Repli-Histo 標識) を用いて明らかにする, ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい
Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells
Katsuhiko Minami^{1,2}, Kako Nakazato^{1,2}, Satoru Ide^{1,2}, Kazunari Kaizu^{3,4}, Koichi Higashi^{2,5}, Sachiko Tamura¹, Atsushi Toyoda⁶, Koichi Takahashi³, Ken Kurokawa^{2,5}, Kazuhiro Maeshima^{1,2}
(¹*Genome Dynamics Laboratory, NIG*, ²*SOKENDAI*, ³*Laboratory for Biologically Inspired Computing, RIKEN BDR*, ⁴*Cell Modeling and Simulation Group, ExCELLS*, ⁵*Genome Evolution Laboratory, NIG*, ⁶*Comparative Genomics Laboratory, NIG*)

10. 水・水和／電解質／10. Water & Hydration & Electrolyte

- [2Pos063](#) 水中でのタンパク質分子間結合の高速計算に向けた GBSA 陰溶媒モデルの精査
Scrutiny of GBSA implicit solvent model for fast simulation of protein-protein binding in water
Fangqian Wei, Yukinari Kamiyama, Wataru Moriya, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)
- [2Pos064](#) 長距離静電相互作用のカットオフ計算で生じる水の層状構造：格子スピン模型による検証
The electrostatic problem of water revisited: Strange layer structure emerging from the truncated long-range interactions
Yoshiteru Yonetani (*National Institutes for Quantum Science and Technology (QST)*)
- [2Pos065](#) 機械学習による過冷却水のローカル構造と水素結合エネルギーの解析
Machine-Learning Analysis of Local Structural Motifs and Hydrogen-Bond Energetics in Supercooled Water
Taku Mizukami¹, Nguyen Viet Cuong³, Dam Hieu Chi² (¹*Japan Advanced Institute of Science and Technology, Materials Science*, ²*Japan Advanced Institute of Science and Technology, Knowledge Science*, ³*HPC Systems*)

- [2Pos066](#) **Atoh1** 依存的な遺伝子ネットワーク構築に向けたドライ解析
In silico prediction of *Atoh1*-dependent gene networks using target genes of *lin-32*, a homolog of *Atoh1*, in *Caenorhabditis elegans*
Saki Imamura¹, Sayaka Hori² (¹*Graduate School of Humanities and Sciences, Nara Women's University*, ²*Faculty Division of Natural Sciences, Nara Women's University*)

12. 発生・分化／12. Development & Differentiation

- [2Pos067](#) 高速 AFM による Afamin–Wnt3a 相互作用と動態の解明
 Unveiling Afamin–Wnt3a interactions and dynamics using high-speed AFM
Hikaru Ichida¹, Kosuke Mizuno^{1,3}, Amyot Romain², Flechsig Holger², Satoshi Toda³, Noriyuki Kodera² (¹*Grad. Sch. NanoLS, Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*Institute for Protein Research, Osaka Univ.*)
- [2Pos068](#) 神経分化における細胞内の発熱が関与する転写機構の解明
 Elucidation of the Transcriptional Mechanisms Involving Intracellular Heat Generation in Neural Differentiation
Yukiho Shimazaki^{1,2}, Kohki Okabe³, Yoshie Harada^{4,5} (¹*Grad. Sch. Sci., Univ. Osaka*, ²*IPR, Univ. Osaka*, ³*Grad. Sch. Pharm. Sci., Univ. Tokyo*, ⁴*WPI-PRIME, Univ. Osaka*, ⁵*QIQB, Univ. Osaka*)
- [2Pos069](#) 赤血球可視化ゼブラフィッシュを用いた血液循環における物理量評価
 Quantitative Analysis of Hemodynamic Parameters in Blood Circulation Using Red Blood Cell-Visualized Zebrafish
Yusei Inoue, Mana Okada, Toshiyuki Mitsui, Yuuta Moriyama (*Grad. Sch. Sci. and Eng., Aoyamagakuin Univ.*)

13. 筋肉（筋蛋白質・収縮）／13. Muscle

- [2Pos070](#) 重合阻害物質を用いた短いアクチンフィラメントの構造解析
 Structural analysis of short actin filaments using polymerization inhibitors
Yuta Arimura, Takuo Yasunaga (*Grad. Sch. Comp. Sci. & Eng., Kyutech*)

14. 分子モーター／14. Molecular motor

- [2Pos071](#) アミロライド誘導体フェナミルがビブリオ菌べん毛モーター固定子のナトリウムイオン輸送を阻害する分子機構
 Inhibition mechanism of phenamil, an amiloride derivative of sodium channel inhibitor, for the rotation of the *Vibrio* flagellar stator
Tatsuro Nishikino^{1,2}, Norihiro Takekawa³, Jun-ichi Kishikawa⁴, Mika Hirose⁵, Seiji Kojima⁶, Michio Homma⁷, Takayuki Kato⁵, Katsumi Imada³ (¹*Dep. of Life Sci. and Applied Chem., Nagoya Inst. of Tech.*, ²*OptoBioTech. Res. Cent., Nagoya Inst. of Tech.*, ³*Dept. of Macromol. Sci., Grad. Sch. of Sci., Osaka Univ.*, ⁴*Dep. of Applied Bio., Kyoto Inst. of Tech.*, ⁵*Inst. for Protein Res., Univ. of Osaka*, ⁶*Dep. of Bio. Sci., Grad. Sch. of Sci., Nagoya Univ.*, ⁷*Dep. of Biomole. Eng., Grad. Sch. of Eng., Nagoya Univ.*)

- [2Pos072](#) Design and Development of a Novel Photoswitchable Inhibitor Targeting Mitotic Kinesin Eg5
Nur Fatin Liyana Binti Salwadi¹, Islam Md Alradzi², Shinsaku Maruta² (¹*Grad. Sch. Sci. Eng., Soka Univ.*, ²*Sch. Sci. Eng., Soka Univ.*)
- [2Pos073](#) Loop-tethered kinesin-14 reveals factors underlying motility and directionality
Taisei Sano, Rieko Sumiyoshi, Masahiko Yamagishi, Junichiro Yajima (*Grad. Arts & Sci., Univ. Tokyo*)
- [2Pos074](#) 混雑環境下におけるキネシンの動態解析のためのマイクロレオロジー計測
Micro-rheology measurement for dynamic analysis of kinesin in crowded environments
Gai Ohashi¹, Takeshi Yokoyama², Takayuki Ariga¹ (¹*Graduate School of Frontier Biosciences, Osaka University*, ²*Graduate school of life science, Tohoku University*)
- [2Pos075](#) 変異体解析による海洋性ビブリオ菌側ベン毛固定子 MotA/MotB 複合体活性化の探求
Mutational analysis to explore activation of the *Vibrio alginolyticus* lateral flagellar stator, MotA/MotB complex
Kazuki Yokoyama¹, Michio Homma², Norihiro Takekawa³, Seiji Kojima¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Grad. Sch. Eng.*, ³*Grad. Sch. Sci.*)
- [2Pos076](#) 細菌ベン毛モーターにおける固定子 MotB の N 末端へのタンパク質融合はローター-固定子相互作用を阻害する
Inhibition of rotor-stator interaction by protein fusion to the N-terminus of the stator protein MotB in the bacterial flagellar motor
Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)
- [2Pos077](#) バクテリアベン毛モーターの回転データにおける揺らぎ評価手法の開発
Development of a method for evaluating fluctuations in rotational data of bacterial flagellar motors
Kenta Takemori, Yusuke V. Morimoto (*Grad. Sch. Comput. Sci. and Syst. Eng., Kyushu Inst. Tech.*)
- [2Pos078](#) 微小管 C 末端 Tail の伸長と単量体 KIF1A の微小管結合の分子動力学解析
Molecular Dynamics Analysis on the Extension of C-terminal Tail of Tubulin and Monomeric KIF1A Binding to Microtubule
Koki Adachi, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)
- [2Pos079](#) Unveiling the N-type ATPase: A Hidden Player in the Rotary ATPase Family
Hiroshi Ueno, Atsuki Nakano, Tatsuki Matsui, Hiroyuki Noji (*Grad. Sch. Eng., Univ. Tokyo*)
- [2Pos080](#) ミオシンの 2D 投影像の深層学習による構造分類に関する研究
Deep Learning-Based Structural Classification of Myosin from 2D Projection Images
Hikaru Iwasaki, Hitomi Wada, Takuo Yasunaga (*Grad. School. Comp. Sci. Syst., KIT*)

15A. 細胞生物学的課題：接着／15A. Cell biology: Adhesion

- [2Pos081](#) 蛍光顕微鏡と AFM を併用した細胞-基質接着間構造の解析
Analysis of cell-substrate adhesion structures by combined fluorescence microscopy and atomic force microscopy
Shun Sato, Shinji Deguchi (*Grad. Sch. Eng. Sci., The Univ. of Osaka*)
- [2Pos082](#) 高速原子間力顕微鏡を用いた液中における Notch レセプターと Delta リガンドの構造解析
Structural analysis of Notch receptor and Delta ligand in solution using high-speed atomic force microscopy
Shigetaka Nishiguchi (*Kansai Center, National Institute of Advanced Industrial Science and Technology*)

- [2Pos083](#) 微小管結合 RhoGEF である GEF-H1 の *in vitro* 動態解析
In vitro kinetic analysis of microtubule-binding RhoGEF, GEF-H1
Tatsuki Kondo¹, Yukako Nishimura¹, Taketoshi Kambara², Kaori Kuribayashi-Shigetomi³, Yasushi Okada^{2,4,5}, Fumio Motegi¹ (¹*Inst. Gen. Med., Hokkaido Univ.*, ²*RIKEN, BDR*, ³*Inst. Adv. Grad. Edu., Hokkaido Univ.*, ⁴*Grad. Sch. Sci., Tokyo Univ.*, ⁵*Grad. Sch. Med., Tokyo Univ.*)
- [2Pos084](#) 細菌べん毛モーターにおける固定子ユニットへの Flil 結合の定量化
 Characterising the stoichiometry of Flil binding to stator units in bacterial flagellar motors
Momoka Kumagai¹, Tomoya Shoji¹, Tsubasa Ishida², Naoki Hidaka², Yong-Suk Che⁴, Yumiko Uchida⁴, Hajime Fukuoka⁴, Akihiko Ishijima⁴, Yoshiyuki Sowa^{1,2,3} (¹*Grad. Frontier Biosci., Hosei Univ.*, ²*Res. Cent. Micro-nano Tech., Hosei Univ.*, ³*Dept. Frontier Biosci., Hosei Univ.*, ⁴*Grad. Frontier Biosci., Osaka Univ.*)
- [2Pos085](#) 単一微生物の活発な運動を追跡するための広視野顕微鏡法
 Wide-field microscopy for tracking active locomotion of single microorganisms
Kaname Kuroda, Seiichiro Kinoshita, Masayoshi Nishiyama (*Grad. Sch. Sci. Eng., Kindai Univ.*)
- [2Pos086](#) 多孔質培地中における周毛性細菌の運動性
 Motility of peritrichous bacteria in porous media
Naoki Kanda, Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)
- [2Pos087](#) サルモネラにおける cAMP 濃度と運動能の相関の計測
 Measurement of the correlation between cAMP levels and motility in *Salmonella* cells
Keisuke Sakai, Yusuke V. Morimoto (*Grad. Sch. Comp. Sci. and Syst. Eng., Kyushu Inst. Tech.*)
- [2Pos088](#) 高圧力下にある哺乳類精子細胞の鞭毛運動の直接観察
 Direct observation of flagellar motility in mammalian sperm cells at high pressure
 Koji Matsuura¹, Yuka Asano¹, Masatoshi Morimatsu², Yuhkoh Satouh³, Toshiki Yagi⁴, Keiji Naruse², **Masayoshi Nishiyama**⁵ (¹*Okayama Univ. Sci.*, ²*Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ.*, ³*Gunma Univ.*, ⁴*Pref. Univ. Hiroshima*, ⁵*KINDAI Univ.*)
- [2Pos089](#) イオンチャネル領域に変異を持つキメラ固定子複合体 PomA/PotB の機能解析
 Mutational analysis of the ion channel region of PomA/PotB, a chimeric stator of bacterial flagellar motor
Kaito Nagano (*Grad.Sch.Sci.,Osaka Univ.*)

15C. 細胞生物学的課題：細胞骨格・膜骨格／15C. Cell biology: Cytoskeleton & Membrane skeleton

- [2Pos090](#) *Spiroplasma* 由来の MreB を発現した Syn3B 破砕液を内包したリポソームの形態変化
 Deformation of Liposomes by Encapsulation of Syn3B expressing *Spiroplasma* MreB
Ikuko Fujiwara¹, Takahiro Mitani¹, Taiki Nishimura¹, Hana Kiyama², Ali Ahsan², Mone Mimura², Satoshi Kanamori², Hideaki Matsubayashi³, Masahito Hayashi⁴, Kingo Takiguchi⁵, Makoto Miyata² (¹*Materials Sci. & Bioeng., Nagaoka Univ. of Tech.*, ²*Grad. Sch. Sci., OMI, FRIS, Tohoku Univ.*, ⁴*UBI, UTokyo*, ⁵*Grad. Sch., Nagoya Univ.*)
- [2Pos091](#) Regulation of Epithelial Homeostasis by Stretch and Cell Density
Rosario Ibanez¹, Honghan Li², Shinji Deguchi¹ (¹*Osaka University, Graduate School of Engineering Sciences, Deguchi Laboratory*, ²*University of Science and Technology Liaoning, School of Computer Science and Software Engineering*)
- [2Pos092](#) 直接の力学摂動に対する微小管とアクチン骨格の構造応答
 Structural response of microtubule and actin cytoskeletons to direct intracellular load
Ryota Orii, Hirokazu Tanimoto (*Yokohama City Univ.*)

- [2Pos093](#) 機械的ストレス下における微小管束の粘弾性応答
Viscoelastic Behavior of Microtubule Bundles Under Mechanical Stress
Syeda Rubaiya Nasrin¹, Marie Tani¹, Gadiel Saper², Masatoshi Ichikawa¹, Ibuki Kawamata¹, Henry Hess², Akira Kakugo¹ (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*Dept. Biomed. Engg. Columbia Univ.*)
- [2Pos094](#) Actin Network Morphogenesis: From Spots to Rings and Interconnected Bundles
Vivek Semwal, Biplab Bhattacharjee, Tatsuo Shibata (*RIKEN Center for Biosystems Dynamics Research Laboratory for Physical Biology*)
- [2Pos095](#) 電子顕微鏡による細胞性粘菌の多細胞体における細胞間構造の可視化
Intercellular structures in the multicellular body of *Dictyostelium discoideum* visualized by electron microscopy
Yuki Gomibuchi, Yusuke V. Morimoto, Takuo Yasunaga (*Grad. Sch Comp. Sci and Sys. Eng., Kyushu Inst. Tech.*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

- [2Pos096](#) 膜リモデリングを介した TRPV4-GPCR のクロストーク
TRPV4-GPCR crosstalk mediated by membrane remodeling
Masataka Yanagawa^{1,2}, Kota Shimizume¹, Ryoji Kise¹, Asuka Inoue^{1,3} (¹*Grad. Sch. Pharm., Kyoto Univ.*, ²*Riken, CPR*, ³*Grad. Sch. Pharm., Tohoku Univ.*)
- [2Pos097](#) ATP 濃度は CBASS 応答の活性化と抑制を調節する
ATP levels modulate the activation and suppression of CBASS responses
Yoshiaki Kinoshita, Rikiya Watanabe (*RIKEN, PRI*)
- [2Pos098](#) Thermal regulation on EML4-ALK condensates dynamics and signaling activation
Chongxia Zhong¹, Josephina Sampson², Richard Bayliss², Madoka Suzuki¹ (¹*Inst. Protein Res., Univ. Osaka*, ²*Astbury Ctr. Struct. Mol. Biol., Univ. Leeds, UK*)
- [2Pos099](#) 細胞膜脂質による上皮成長因子受容体の活性制御機構の解析
Bilateral regulation of EGFR activity and local PI(4,5)P₂ dynamics in mammalian cells observed with single-molecule microscopy
Mitsuhiro Abe¹, Masataka Yanagawa^{1,2}, Yasushi Sako¹ (¹*RIKEN PRI*, ²*Grad. Sch. Pharm. Sci., Kyoto Uni.*)
- [2Pos100](#) 2 回の忌避刺激に対する大腸菌忌避応答と受容体脱メチル化酵素 CheB 動態
Repellent response of *Escherichia coli* to twice repellent stimuli and kinetics of the receptor demethylase CheB
Yugo Tomoda, Yoichi Kuroki, Yumiko Uchida, Akihiko Ishijima, **Hajime Fukuoka** (*Grad. Sch. Front. Biosci., Univ. Osaka*)
- [2Pos101](#) 心筋細胞集団間の線維芽細胞接続における心筋細胞同期
Synchronization of Cardiomyocytes in Fibroblasts Connections between Cardiomyocyte Clusters
Mayu Yamada, Tomoyuki Kaneko (*LaRC.FB.Hosei Univ.*)
- [2Pos102](#) 溶液中の細胞性粘菌多細胞体への薬物添加
Drug addition to multicellular bodies of *Dictyostelium discoideum* in solution
Sotaro Fukuda¹, Tomohiro Shima², Yusuke V. Morimoto³ (¹*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech.*, ²*Grad. Sch. Sci, Univ. Tokyo*, ³*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech*)
- [2Pos103](#) 海洋性バクテリア *Vibrio alginolyticus* の情報伝達タンパク質 CheY 動態の 1 細胞観察
Observation of CheY-GFP dynamics in a single *Vibrio alginolyticus* cell
Eito Kawamura, Ryoya Takase, Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)

- [2Pos104](#) 心筋細胞クラスターサイズによる薬剤応答の違いの解析
Effect of Cardiomyocyte Cluster Size on Drug Response
Chinatsu Fujita, Kentaro Kito, Tomoyuki Kaneko (*LaRC.FB.Hosei Univ*)
- [2Pos105](#) 細胞性粘菌における新規細胞巨大化法による細胞内高分解能計測
High-resolution intracellular measurements using a novel cell enlargement method in *Dictyostelium discoideum*
Yukihiisa Hayashida¹, Yuki Gomibuti², Chikoo Oosawa², Takuo Yasunaga², Yusuke V Morimoto²
(¹*Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, ²*Dept. Phys. and Info. Eng., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech*)

16A. 生体膜・人工膜：構造・物性／16A. Biological & Artificial membrane: Structure & Property

- [2Pos106](#) スフィンゴミエリンのナノドメイン形成に対するコレステロールの影響
Cholesterol assists gel-like nanodomain formation of biologically relevant sphingomyelins
Masanao Kinoshita¹, Koki Yamane², Nobuaki Matsumori² (¹*Grad. Sch. Sci. Tech., Gunma Univ.*, ²*Grad. Sch. Sci. Tech., Kyushu Univ.*)
- [2Pos107](#) DPPH アッセイとハイパースペクトル顕微鏡を用いた炎症性腸疾患に対する抗酸化ナノザイムの評価
Evaluation of Antioxidant Nanozymes for Inflammatory Bowel Disease Using DPPH Assay and Hyperspectral Microscopy
Ami Saito (*Institute of Industrial Science, The University of Tokyo*)
- [2Pos108](#) アシル鎖長の異なるスフィンゴミエリンは脂質ラフト様秩序膜ドメイン内で異なるナノドメインを形成する
Sphingomyelins with varying acyl chain lengths form segregated nanodomains within lipid raft-like ordered membrane domains
Akane Nakamoto¹, Masanao Kinoshita², Nobuaki Matsumori¹ (¹*Grad. Sch. Sci., Kyushu Univ.*, ²*Grad. Sch. Sci. & Tech., Gunma Univ.*)
- [2Pos109](#) パターン化モデル膜における電気泳動を用いた膜タンパク質の分離
Separation of membrane proteins by electrophoresis in a patterned model membrane
Keigo Kitayama¹, Kenichi Morigaki² (¹*Grad. Sch. Agr., Kobe University*, ²*Biosignal Research Center, Kobe University*)
- [2Pos110](#) 両親媒性モデルペプチド 18A の改変による脂質膜曲率を認識するペプチドの開発
Development of curvature sensitive peptides based on the amphipathic model peptide 18A
Kazuna Ikeuchi, Keisuke Ikeda, Hiroyuki Nako, Minoru Nakano (*Fac. Pharm. Sci. Univ. Toyama*)

16B. 生体膜・人工膜：ダイナミクス／16B. Biological & Artificial membrane: Dynamics

- [2Pos111](#) F₁F_o-ATP 合成酵素の複合体状態によるミトコンドリア形態と機能の制御機構
Regulatory mechanism of mitochondrial dynamics and function via the complex state of F₁F_o-ATP synthase
Aoi Ichikawa¹, Takaya Ishihara^{1,2}, Naotada Ishihara¹ (¹*Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.*, ²*Dept. Life Sci., Faculty of Med., Shimane Univ.*)
- [2Pos112](#) 長さ分布を調整したアクチン封入リポソームの形態変化
Morphological changes in actin-encapsulated liposomes with adjusted length distribution
Yuki Mizutani, Mahito Kikumoto, Ken Bessho, Kingo Takiguchi (*Grad. Sch. Sci., Univ. Nagoya*)
- [2Pos113](#) 脂質二重膜小胞の安定性に対するアクチンの影響
Effect of Actin on the Stability of Lipid Bilayer Vesicles
Ken Bessho, Mahito Kikumoto, Yuki Mizutani, Kingo Takiguchi (*Grad. Sch. Sci., Nagoya Univ.*)

- [2Pos114](#) Reconstitution of actin cytoskeleton into artificial membranes
Yosuke Senju^{1,2}, Feng-Ching Tsai³, Zack Jarin⁴, Ilpo Vattulainen¹, Gregory Voth⁴, Patricia Bassereau³, Pekka Lappalainen¹ (¹*Univ. Helsinki*, ²*Okayama Univ.*, ³*Institut Curie*, ⁴*Univ. Chicago*)

16C. 生体膜・人工膜：興奮・チャネル／16C. Biological & Artificial membrane: Excitation & Channels

- [2Pos115](#) 細胞質側とペリプラズム側の張力センサーの異なる役割により明らかになった MscL の非対称な機械刺激感受性
 Asymmetric Mechanosensitivity of MscL Channel Revealed by Differential Roles of Cytoplasmic and Periplasmic Tension Sensors
Takeshi Nomura¹, Yasuyuki Sawada², Masahiro Sokabe³ (¹*Sch. Human Sci. Environ., Univ. Hyogo*, ²*Institute of Materials Innovation, Nagoya Univ.*, ³*Human Information Systems Labs, Kanazawa Institute of Technology*)
- [2Pos116](#) 点突然変異によるクラミドモナス TRP チャネル TRP11 の機能解析
 Functional analysis of a TRP channel in Chlamydomonas, TRP11, by point mutagenesis
Takanao Miyake, Miyu Kimura, Kenjiro Yoshimura (*Col. Sys. Engineer. Sci., Grad. Sch. Engineer. Sci., Shibaura Inst. Technol.*)
- [2Pos117](#) MscL での二箇所での張力感受：F7 と F78 の間にある機能的関連性
 Dual-Site Tension Sensing in MscL: Functional Link Between F7 and F78
Yasuyuki Sawada¹, Takeshi Nomura², Masahiro Sokabe³ (¹*Inst. Materials, InFuS, Nagoya Univ.*, ²*Sch. Human Sci and Env., Univ. Hyogo*, ³*Human Information Systems Labs, Kanazawa Inst. Tech.*)

16D. 生体膜・人工膜：輸送・情報伝達／16D. Biological & Artificial membrane: Transport & Signal transduction

- [2Pos118](#) DNA チャネル内部の官能基修飾とイオン輸送特性の相関の分子論的解析
 Molecular analysis of the correlation between functional group modifications inside DNA channels and ion transport properties
Taichi Hirano^{1,2}, Hiromu Akai³, Yusuke Sato⁴, Kan Shoji³, Takuya Mabuchi^{1,2} (¹*Graduate School of Engineering, Tohoku University*, ²*Institute of Fluid Science, Tohoku University*, ³*Department of Mechanical Engineering, Nagaoka University of Technology*, ⁴*Department of Intelligent and Control Systems, Kyushu Institute of Technology*)

17. 化学受容／17. Chemoreception

- [2Pos119](#) ストレス応答センサーキナーゼ BaeS のマルチリガンド認識機構
 Multiple ligand recognition mechanisms of the membrane stress sensor kinase BaeS
Hiroataka Tajima^{1,2}, Riku Takei³, Kentaro Yamamoto⁴, Ikuro Kawagishi^{1,2,3} (¹*Dept. Frontier Biosci., Hosei Univ.*, ²*Res. Cen. Micro-Nano Tech., Hosei Univ.*, ³*Grad. Sch. Sci. Eng., Hosei Univ.*, ⁴*Dept. Mycobacteriol., Lepr. Res. Ctr., NIID*)

- [2Pos120](#) 動物と植物間で保存された miRNA 合成分子に関わる遺伝子によって制御される温度耐性機構
Temperature tolerance regulated by a miRNA processing molecule conserved between animals and plants
Sakura Sengoku^{1,2}, Akane Ohta^{1,2}, Teruaki Taji³, Atsushi Kuhara^{1,2,4} (¹Graduate School of Natural Science, Konan University, ²Institute for Integrative Neurobiology, Konan University, ³Department of Bioscience, Tokyo University of Agriculture, ⁴AMED-PRIME, Japan Agency for Medical Research and Development)
- [2Pos121](#) 神経ネットワークを構成する細胞数がバースト発火に与える影響
Effect of Number of Cells in Neural Network on Burst Firing
Takumi Yamaguchi, Kentaro Kito, Tomoyuki Kaneko (*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

19. 神経回路・脳の情報処理／19. Neuronal circuit & Information processing

- [2Pos122](#) 方位選択性を備えた深層ニューラルネットワークモデルによるハーマン格子錯視の定量解析
Quantitative analysis of the Hermann grid illusion using a minimal deep neural network with orientation-specific edge detection
Masayo Inoue¹, Izumi Ohzawa^{2,3}, Kazufumi Hosoda^{2,3,4} (¹Grad. Sch. Eng., Kyutech, ²Grad. Sch. Frontier Biosciences, Osaka Univ., ³CiNet, NICT, ⁴Kobe Univ. Grad. Sch. Health Sciences)
- [2Pos123](#) ミミズ古典的条件づけの神経メカニズムの解明
Molecular mechanism of associative learning in earthworm, *Eisenia fetida*
Yoshihiro Kitamura¹, Sukehiro Kabayama² (¹Dept. Math. Sci. Phys., Col. Sci. Eng., Kanto Gakuin Univ., ²Appl. Mat. Life. Sci., Grad. Sch. Eng., Kanto Gakuin Univ.)

20. 行動／20. Behavior

- [2Pos124](#) 牧羊犬はどのように羊を追いつけるのか？：視覚情報に基づく誘導方法
How Do Shepherd Dogs Herd Sheep? – A Visual Perception-Based Guiding Rule
Kosuke Miyoshi¹, Nen Saito^{1,2} (¹Graduate School of Integrated Science for Life, Hiroshima University, ²Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences)

21A. 光生物：視覚・光受容／21A. Photobiology: Vision & Photoreception

- [2Pos125](#) 発光プローブを用いた哺乳類メラノプシンとアレステインとの相互作用解析
Analyses of the interaction between mammalian melanopsin and arrestin using bystander BRET probes
Kento Takano, Hisao Tsukamoto (*Grad. Sch. Sci., Kobe Univ.*)
- [2Pos126](#) 光依存的シグナル伝達に関する新奇ロドプシンの分子特性
Molecular properties of novel microbial rhodopsins with a photosensory function in light-dependent signal transduction
Qianfan Zhou, Masae Konno, Keiichi Inoue (*ISSP, Univ. Tokyo*)

- [2Pos127](#) PYP と PBP の光依存的多量化反応における PBPC 末端領域の寄与
Contribution of the PBP C-terminal region to the light-dependent multimerization reaction of PYP and PBP
Yusuke Kuwahara¹, Youichi Yamazaki¹, Kento Yonezawa^{1,2}, Sachiko Toma-Fukai¹, Hironari Kamikubo^{1,2} (¹NAIST, MS, ²NAIST, CDG)
- [2Pos128](#) ラマン分光およびアミノ酸置換体を用いたシアノバクテリアオクロム RcaE の光変換機構の研究
Photoconversion mechanism of cyanobacteriochrome RcaE studied by Raman spectroscopy and Mutagenesis
Taisei Koga¹, Masako Hamada², Yuu Hirose², Tomotsumi Fujisawa¹, Masashi Unno¹ (¹Fac. Sci. Eng., Saga Univ., ²Dept. Appl. Chem. Life Sci. Toyohashi Univ. of Tech.)
- [2Pos129](#) 真骨魚類が特異的に持つ緑感受性ピノプシンの解析
Characterization of the unique green-sensitive pinopsin found in teleost fish
Chihiro Fujiyabu¹, Gyoja Fuji², Keita Sato³, Emi Kawano-Yamashita⁴, Hideyo Ohuchi³, Takehiro Kusakabe², **Takahiro Yamashita**¹ (¹Grad. Sch. Sci., Kyoto Univ., ²Grad. Sch. Nat. Sci., Konan Univ., ³Fac. Med., Dent. & Pharm. Sci., Okayama Univ., ⁴Fac. Sci., Nara Women's Univ.)
- [2Pos130](#) ラマン分光法によるセンサリロドプシン II (Natronomonas pharaonis 由来) の O 中間体の発色団構造の特定
Retinal Chromophore Configuration in the O Intermediate of Sensory Rhodopsin II from *Natronomonas pharaonis*
Tomotsumi Fujisawa¹, Nozomi Tanaka¹, Jun Tamogami², Masashi Unno¹ (¹Fac. Sci. Eng., Saga Univ., ²Coll. Pharm. Sci., Matsuyama Univ.)
- [2Pos131](#) 無脊椎動物の非視覚オプシン・アルスロプシンの分子特性の多様性
Molecular diversity of protostome non-visual opsin arthropsin
Kazumi Sakai¹, Kengo Fujii¹, Chihiro Fujiyabu¹, Yasuhiro Shiga², Takahiro Yamashita¹ (¹Grad. Sch. Sci., Kyoto Univ., ²Tokyo Univ. of Pharm. and Life Sci.)
- [2Pos132](#) 可視光感受性を示す甲殻類由来 Opn5 の分子機能解析
Molecular characterization of visible-light sensitive Opn5 from crustaceans
Kuto Takahashi¹, Yuya Nagata¹, Keita Sato², Kohei Obayashi³, Hisao Tsukamoto³, Hideyo Ohuchi², Takahiro Yamashita⁴, Yuki Sudo², Keiichi Kojima² (¹Grad. Sch. Med. Dent. & Pharm. Sci., Okayama Univ., ²Fac. Med, Dent & Pharm Sci., Okayama Univ., ³Grad. Sch. Sci., Kobe Univ., ⁴Grad. Sch. Sci., Kyoto Univ.)
- [2Pos133](#) 幅広い時間スケールでの時分割結晶構造解析により明らかになったクリプトクロムのシグナル伝達機構
Cryptochrome signal transduction mechanism revealed by time-resolved crystallography across broad timescales
Yuhei Hosokawa^{1,2,3,4}, Po-Hsun Wang^{2,5}, Nicolas Caramello⁶, Mai Nakamura³, Sylvain Engilberge⁶, Antoine Royant⁶, Lars-Oliver Essen⁵, Ming-Daw Tsai², Junpei Yamamoto³, Manuel Maestre-Reyna^{1,2} (¹Dept. Chem., National Taiwan Univ., ²Inst. Biol. Chem., Academia Sinica, ³Grad. Sch. Eng. Sci., Osaka Univ., ⁴RIKEN, ⁵Dept. Chem., Philipps Univ. Marburg, ⁶ESRF)

21B. 光生物：光合成／21B. Photobiology: Photosynthesis

- [2Pos134](#) 緑色硫黄細菌の光合成反応中心複合体のカロテノイド配糖体を介する三重項エネルギー移動
Energy transfer pathway forming triplet-excited state of carotenoid in the photosynthetic reaction center of green sulfur bacteria
Tomomi Inagaki¹, Masatoshi Kida², Daisuke Kosumi³, Chihiro Azai⁴ (¹Graduate School of Life Sciences, Ritsumeikan University, ²Graduate School of Science and Technology, Kumamoto University, ³Institute of Industrial Nanomaterials, Kumamoto University, ⁴Faculty of Science and Engineering, Chuo University)

- [2Pos135](#) Evaluating the mobility of LHCII in plant thylakoid membrane using high-speed AFM
Nami Yamano, Yudai Nishitani, Daisuke Yamamoto (*Fukuoka University*)
- [2Pos136](#) モデル植物苔類ゼニゴケ由来の光化学系Ⅰ二量体のクライオ電子顕微鏡単粒子構造解析
 Cyro-EM structures of dimeric PSI-LHCI supercomplex from the model organism *Marchantia polymorpha*
Pi-Cheng Tsai¹, Romain La Rocca¹, Hiroyasu Motose², Jian-Ren Shen¹, Fusamichi Akita¹ (¹*Adv. Res., Univ. Okayama*, ²*Grad. Sch. Envir. Life, Nat. Sci. & Tech., Univ. Okayama*)
- [2Pos137](#) 光化学系ⅡのMn高親和性サイトの配位環境
 Coordination environment of Mn high-affinity site in Photosystem II
Naohiko Nakamura, Shinya Kosaki, Hiroyuki Mino (*Grad. Sch. Sci., Univ. Nagoya*)
- [2Pos138](#) The most stable LH1-RC architecture from a thermophilic purple sulfur bacterium, *Caldichromatium japonicum*
Yukihiro Kimura¹, Mohit. K. Saini², Endang R. Purba³, Malgorzata Hall³, Shinji Takenaka¹, Vera Thiel⁴, Bruno M. Humbel⁵, Michael T. Madigan⁶, Zheng-Yu Wang-Otomo⁷, Kazutoshi Tani⁸ (¹*Grad. Sch. Agric., Kobe Univ.*, ²*Inst. Microbiol., Centre Algatech*, ³*Sci. Imag. Sec., OIST*, ⁴*Leibniz Inst., DSMZ*, ⁵*Provost Office, OIST*, ⁶*Dept. Microbiol., Southern Illinois Univ.*, ⁷*Fac. Sci., Ibaraki Univ.*, ⁸*Cent. Comp. Sci, Univ. Tsukuba*)
- [2Pos139](#) Spectroscopic characterization of the light-harvesting 1 reaction center complexes from psychrophilic photosynthetic purple bacteria
Kazuki Inada¹, Seiji Akimoto², Michael T. Madigan³, Zheng-Yu Wang-Otomo⁴, Yukihiro Kimura¹ (¹*Grad. Sch. Agric., Kobe Univ.*, ²*Grad. Sch. Sci., Kobe Univ.*, ³*Dept. Microbiol., Southern Illinois Univ.*, ⁴*Fac. Sci., Ibaraki Univ.*)
- [2Pos140](#) Spectroscopic and structural characterization of purple bacterial LH1-RC complexes containing bacteriochlorophyll b
Kouta Hirose¹, Kaisei Mori¹, Shinji Takenaka¹, Michael T. Madigan², Zheng-Yu Wang-Otomo³, Kazutoshi Tani⁴, Yukihiro Kimura¹ (¹*Grad. Sch. Agric., Kobe Univ.*, ²*Sch. Biol. Sci., Southern Illinois Univ.*, ³*Fac. Sci., Ibaraki Univ.*, ⁴*Cent. Comp. Sci., Univ. Tsukuba*)

21C. 光生物：光遺伝学・光制御／21C. Photobiology: Optogenetics & Optical control

- [2Pos141](#) 赤色光にตอบสนองするアニオンチャネルロドプシンのイオン輸送機構
 Ion transport mechanism of channel rhodopsin in response to red light
Keito Minamisawa¹, Shoko Hososhima^{1,2}, Satoshi Tsunoda^{1,2}, Hideki Kandori^{1,2} (¹*Graduate School of Engineering, Nagoya Institute of Technology*, ²*Opto Bio Technology Research Center, Nagoya Institute of Technology*)
- [2Pos142](#) 新規内向きプロトンポンプ，PhXeRの分光学的解析
 Spectroscopic Analysis of a Novel Inward Proton Pump, PhXeR
Nanako Hattori¹, Yuma Ito¹, Yuji Furutani^{1,2}, Tatsuro Nishikino^{1,2}, Hideki Kandori^{1,2} (¹*Department of Life Science and Applied Chemistry, Nagoya institute of technology*, ²*OptoBioTechnology Research Center, Nagoya institute of technology*)
- [2Pos143](#) Photoregulation of Ras Function Using Photoresponsive Protein
Nobuyuki Nishibe¹, Zhang Ziyun², Kazunori Kondo¹, Shinsaku Maruta^{1,2} (¹*Department of Science and Engineering for Sustainable Innovation, Faculty of Science and Engineering, Soka University*, ²*Department of Biosciences, Graduate School of Science and Engineering, Soka University*)
- [2Pos144](#) Autonomous Multicolor Bioluminescence Imaging in Bacteria, Mammalian, and Plant Hosts
Subhan Hadi Kusuma (*SANKEN, The University of Osaka*)

- [2Pos145](#) Na⁺ポンプから Cl⁻ポンプに変異させた光駆動イオンポンプロドプシンの時間分解赤外分光に関する研究
Time-resolved FTIR study of light-driven ion pump rhodopsin mutants converted from Na⁺ to Cl⁻ pump
Masahiro Yamamoto¹, Yuma Ito¹, Tatsuya Sakamoto¹, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹*Grad. Sch. Eng., Nagoya Institute of Technology*, ²*OptoBioTechnology Research Center, Nagoya Institute of Technology*)
- [2Pos146](#) 環状ヌクレオチド依存性チャネルを用いた光活性化アデニル酸シクラーゼの活性測定系の開発
Development of a system to measure activity of photoactivated adenylyl cyclase using cyclic nucleotide-gated channels
Shunsuke Kiguchi¹, Kosei Higuchi¹, Koshiro Morita¹, Mami Asakura^{1,2}, Toru Ide¹, Minako Hirano¹ (¹*Graduate School of Interdisciplinary Science and Engineering in Health Systems, Okayama University*, ²*Dept. of Comp. Tech. Soln., Okayama Univ.*)

23. 生命の起源・進化／23. Origin of life & Evolution

- [2Pos147](#) Structural and functional analysis of Heimdallarchaeaota tubulin reveals the origin of eukaryotic microtubules
Linh Tran¹, Makito Miyazaki^{1,2,3}, Samson Ali⁴, Akihiro Narita⁵, Robert Robinson^{4,6} (¹*Center for Integrative Medical Sciences, RIKEN*, ²*Center for Biosystems Dynamics Research, RIKEN*, ³*Graduate School of Medicine, Science and Technology, Shinshu University*, ⁴*Research Institute for Interdisciplinary Science, Okayama University*, ⁵*Division of Biological Science, Graduate School of Science, Nagoya University*, ⁶*School of Bio-molecular Science and Engineering (BSE), Vidyasirimedhi Institute of Science and Technology (VISTEC)*.)
- [2Pos148](#) 古生代ミオグロビンによる高酸素環境への適応
Adaptation of Paleozoic Myoglobins to the Oxygenized Environments
Yasuhiro Isogai¹, Antonio Tsuneshige², Hiroshi Imamura³, Tsuyoshi Shirai³ (¹*Dept. Pharm. Engin., Toyama Pref. Uni.*, ²*Dept. Frontier Biosci., Micro-Nano Tech. Res. Center, Hosei Uni.*, ³*Dept. Frontier Bio-Sci., Nagahama Inst. Bio-Sci. Tech.*)
- [2Pos149](#) 数千種の細菌における走化性遺伝子群の組み合わせ進化ダイナミクス
Combinatorial evolutionary dynamics of chemotaxis genes across thousands of bacterial species
Takao Suzuki (*Juntendo Univ. Grad. Sch. Med.*)

24. 合成生物学・人工細胞／24. Synthetic biology & Artificial cells

- [2Pos150](#) PURE system 内における翻訳阻害効果の解消
Relieving Translation Repression Caused by Inhibitory DNA Sequences in the PURE System
Akari Sakurai (*Graduate School of Arts and Sciences, The University of Tokyo*)
- [2Pos151](#) タンパク質集積による脂質-タンパク質非対称膜小胞内膜での効率的な酵素反応
Protein accumulation enhances enzymatic reactions on inner leaflet of asymmetric lipid-protein vesicles
Masato Suzuki, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)
- [2Pos152](#) 組織再構築を目指したリポソーム内細胞培養系の開発
Development of Cell Culture System in Liposomes for Tissue Reconstruction
Reika Hibi¹, Masahito Hayashi^{1,2}, Tomoyuki Kaneko¹ (¹*Dept. FB., Hosei Univ.*, ²*Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.*)

- [2Pos153](#) ポリリン酸-塩水溶液の液-液相分離における一価イオンの影響
Monovalent Ion Effect on Liquid-Liquid Phase Separation of Aqueous Polyphosphate-Salt Mixtures
Tomohiro Furuki^{1,2}, Azusa Togo³, Hatsuho Usuda⁴, Tomohiro Nobeyama^{2,5}, Atsushi Hirano⁴, Kentaro Shiraki² (¹*Dept. Life Sci. Tech., Sci. Tokyo*, ²*Pure and Appl. Sci., Univ. Tsukuba*, ³*ISC, AIST*, ⁴*NMRI, AIST*, ⁵*WPI-iCeMS, Kyoto Univ.*)
- [2Pos154](#) Retrofitting of antibiotic target sites on ribosomes: A synthetic approach to reveal the molecular basis of antimicrobial resistance
Ryo Muramatsu, Yoshikazu Tanaka, Takeshi Yokoyama (*Grad. Sch. Life Sci., Univ. Tohoku*)
- [2Pos155](#) 細胞サイズ空間への閉じ込めがもたらすタンパク質の遅い拡散と反応拡散波による緩和効果
Enhanced repulsive interactions suppress protein diffusion in membrane-confined systems, alleviated by propagating protein waves
Hiroki Sakuta^{1,2}, Sakura Takada³, Naoya Yanagisawa², Tatsuro Oda⁴, Koichi Mayumi⁴, Koichiro Sadakane⁵, Kei Fujiwara³, Miho Yanagisawa^{1,2,6} (¹*Univ. Biol. Inst., Univ. Tokyo*, ²*Grad. Sch. Arts Sci., Univ. Tokyo*, ³*Dept. Biosci. and Info., Keio Univ.*, ⁴*Inst. Solid State Phys., Univ. Tokyo*, ⁵*Facul. Life Med. Sci., Doshisha Univ.*, ⁶*Dept. Phys., Grad. Sch. Sci., Univ. Tokyo*)
- [2Pos156](#) クラミドモナス封入リポソームの遊泳速度決定要因の解析と光スイッチング
Analysis of Swimming Velocity Determinants and Optical Switching of Chlamydomonas-Encapsulated Liposomes
Koichiro Akiyama¹, Sota Hamaguchi², Hiromasa Shiraiwa¹, Shunsuke Shiomi¹, Daiki Matsunaga², Masahito Hayashi^{1,3}, Tomoyuki Kaneko¹ (¹*Grad. Sch. Eng. Sci., Univ. Hosei*, ²*Grad. Sch. Sci. Eng., Univ. Osaka*, ³*Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.*)
- [2Pos157](#) 細菌ぺん毛とRbodyにより誘導されるリポソームの能動的変形
Active deformation of liposomes induced by bacterial flagella and R-bodies
Yuto Kobashigawa¹, Tsubasa Ishida³, Naoki Hidaka², Masahito Hayashi^{2,4}, Yoshiyuki Sowa^{1,2,3} (¹*Grad. Frontier Biosci., Univ. Hosei*, ²*Dept. Frontier Biosci., Univ. Hosei*, ³*Res. Cent. Micro-nano Tech., Univ. Hosei*, ⁴*Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.*)
- [2Pos158](#) 異なるリポソーム表面で作動するDNA回路をつなぐ「DNAシナプス」
"DNA Synapse" Wiring DNA Circuits Operating on Separate Liposome Surfaces
Masahito Hayashi, Taro Toyota (*Grad. Sch. Arts Sci., Univ. Tokyo*)

26A. 計算生物学: 生命情報学 / 26A. Computational biology: Bioinformatics

- [2Pos159](#) Pfam ドメイン AlphaFold 構造の特徴探索
Features of Pfam domain in Alpha Fold DB
Yamato Nakaya, Ryotaro Koike, Motonori Ota (*Graduate School of Informatics, Nagoya University*)
- [2Pos160](#) タンパク質参照構造との立体構造比較に基づくタンパク質と結合分子の変形構造のモデリング
Deformation Modeling of Proteins and Ligands Based on Structural Comparison with Reference Protein Structures
Takeshi Kawabata, Kengo Kinoshita (*Grad. Sch. Info. Sci., Tohoku Univ.*)
- [2Pos161](#) 水和構造を考慮したタンパク質-基質結合親和性予測機械学習モデル
Machine learning prediction model of protein-ligand binding affinity considering hydration structures
Yukihide Yoshimura, Hazime Satou, Terada Tohru (*Graduate School of Agricultural and Life Science, The University of Tokyo*)

- [2Pos162](#) AlphaFold3 の予測構造に基づく Type-51 R-body 構造変化機構の解明
Mechanism of Type-51 R-body conformational change based on structural predictions using AlphaFold3
Hiroaki Oheda¹, Toru Ekimoto¹, Tsutomu Yamane², Kosuke Kikuchi³, Koki Date³, Takafumi Ueno³, Mitsunori Ikeguchi^{1,2} (¹*Yokohama City University, Graduate School of Medical Life Science*, ²*RIKEN, Center for Computational Science*, ³*Institute of Science Tokyo, School of Life Science and Technology*)
- [2Pos163](#) 深層学習でリガンド結合状態の RNA 構造を生成する
Generate RNA Conformations in Ligand-binding States with Deep Learning
Ikuo Kurisaki¹, Michiaki Hamada^{2,3,4} (¹*Waseda Research Institute for Science and Engineering, Waseda University*, ²*Faculty of Science and Technology, Waseda University*, ³*AIST-Waseda University Computational Bio Big-Data Open Innovation Laboratory*, ⁴*Graduate School of Medicine, Nippon Medical School*)
- [2Pos164](#) インシリコ解析による RseP 阻害剤候補のスクリーニングと構造予測をベースとした基質選択の分子基盤の解明
In Silico Screening of RseP Inhibitor Candidates and Elucidation of the molecular basis of substrate selectivity by Structure Prediction
Remii Takahashi¹, Hiroaki Oheda¹, Masao Inoue¹, Toru Ekimoto¹, Tsutomu Yamane², Yohei Hizukuri³, Terukazu Nogi¹, Yoshinori Akiyama³, Mitsunori Ikeguchi^{1,2} (¹*Yokohama City University, Graduate School of Medical Life Science*, ²*RIKEN Center for Computational Science*, ³*Institute for Life and Medical Sciences, Kyoto University*)
- [2Pos165](#) ESM 埋め込みのアテンションプーリングを用いたタンパク質機能同一性予測
Protein Functional Identity Prediction Using Attention-Pooling of ESM Embeddings
Kotaro Ukai, Tohru Terada, Suguru Fujita (*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)
- [2Pos166](#) AlphaFold3 versus AlphaFold2 in Sampling Alternative Conformational States of Transporter Proteins
Jun Ohnuki, Kei-ichi Okazaki (*Institute for Molecular Science*)

26B. 計算生物学: 分子シミュレーション / 26B. Computational biology: Molecular simulation

- [2Pos167](#) インフルエンザウイルス・ノイラミニダーゼの薬剤耐性機構に関する理論的研究: 酵素反応の自由エネルギープロファイル解析
Computational study of the drug resistance mechanism of influenza virus neuraminidase: Free energy profile analysis of enzyme reaction
Ryotaro Katsumata¹, Manabu Igarashi², Norifumi Yamamoto¹ (¹*Chiba Tech.*, ²*Hokkaido University*)
- [2Pos168](#) ネットワーク解析による 3α-HSD の二量体間における信号伝達機構の解明
Signal transduction mechanism between the subunits of 3α-HSD by network analysis
Naoya Hirooka¹, Niino Yoshiki², Kahoru Amakawa², Daiki Suzuki², Masayuki Oda¹, Juha Lintuluoto³, Masami Lintuluoto¹ (¹*Grad. Sch. Life and Env. Sci., Univ. Kyoto Prefectural*, ²*Fac. Life and Env., Univ. Kyoto Prefectural*, ³*Grad. Sch. Eng., Univ. Kyoto*)
- [2Pos169](#) Prediction of Cross-Species Binding Affinities of GPCR-Targeting Drugs
Ruigeng Ji¹, Masaru Ihara², Han Zhang³, Tohru Terada¹ (¹*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, ²*Fac. Agr. Mar. Sci., Kochi Univ.*, ³*School of Environmental Science and Technology, Dalian University of Technology*)
- [2Pos170](#) FtsZ 重合ダイナミクスの 10 分規模にわたるメソスコピック反応動力学シミュレーション
Mesoscopic Reactive Dynamics Simulation of FtsZ Polymerization Dynamics on the order of 10 minutes
Yoshiki Bessho, Shoji Takada (*Grad. Sch. Sci., Kyoto Univ.*)

- [2Pos171](#) 全ての側鎖の動きを含めた AI を用いたタンパク質の構造変化モーフィング手法の開発: MOVE-DM 3.0
Development of a Protein Structural Change Morphing method with All Side-Chain Consideration using an AI-based approach: MOVE-DM 3.0
Yoshihiro Kashiama¹, Shota Shimogochi¹, Yuma Shiota¹, Kazuya Iwano¹, Ryota Kiyooka¹, Naoyuki Miyashita^{1,2} (¹*Grad. Sch. of BOST, KINDAI Univ.*, ²*BOST, KINDAI Univ.*)
- [2Pos172](#) Aβ 凝集における相互作用ダイナミクスの解明: Aβ40/Aβ42 各種会合状態の比較
Unraveling the Role of Interaction Dynamics in Aβ Aggregation: A Comparative Study of Aβ40/Aβ42 Monomers, Homodimers, and Heterodimers
Ayumu Koike, Norifumi Yamamoto (*ChibaTech*)
- [2Pos173](#) pH 一定の分子動力学シミュレーション由来のトラジェクトデータに基づく結合自由エネルギー計算: FabI 酵素での検証
Binding free energy calculation based on constant-pH molecular dynamics simulation-derived trajectory: application to FabI enzyme
Shin-ichi Fujiwara (*Fac. Med., Tottori Univ.*)
- [2Pos174](#) 分子シミュレーションを用いた PET トレーサー PBB3 と TMEM 繊維の結合と安定性
Binding and Stability of PET Tracer PBB3 with TMEM Fibrils using molecular simulations
Nanami Matsumoto¹, Yoshitaka Tadokoro¹, Naoyuki Miyashita^{1,2} (¹*Grad. Sch. of BOST, KINDAI Univ.*, ²*BOST, KINDAI Univ.*)
- [2Pos175](#) Markov state Model に基づいた環状ペプチド膜透過過程の多次元の反応座標における速度論的な解析
Kinetic analysis of membrane permeation processes of cyclic peptides on multiple reaction coordinates based on the Markov state model
Masatake Sugita^{1,2}, Kei Terakura¹, Takuya Fujie^{1,2}, Keisuke Yanagisawa^{1,2}, Yutaka Akiyama^{1,2} (¹*Sch. Computing, Science Tokyo*, ²*MIDL, Science Tokyo*)
- [2Pos176](#) Molecular dynamics simulations of peptide aggregation properties
Joe Mori^{1,2}, Satoru G Itoh^{1,2,3}, Hisashi Okumura^{1,2,3} (¹*SOKENDAI*, ²*IMS*, ³*ExCELLS*)
- [2Pos177](#) Implementation of Modeling Employing Limited Data in GENESIS
Azuki Mizutani¹, Alberto Perez², Yuji Sugita^{1,3} (¹*Riken, PRI*, ²*Dept. of Chem., Univ. Florida*, ³*Riken, R-CCS*)
- [2Pos178](#) メチル化ヒストン断片と LEDGF の結合安定性に関する分子動力学シミュレーション
Molecular dynamics simulations of the binding stability of methylated histone fragments to LEDGF
Hinako X. Suzuki⁴, Hisashi Okumura^{2,3,4}, **Satoru Itoh**^{1,2,3} (¹*IMS*, ²*ExCELLS*, ³*SOKENDAI*, ⁴*Dept. Sci., Shinshu Univ.*)
- [2Pos179](#) Atomic-Level Analysis of pH-Dependent Switchable Binding in Ipilimumab-CTLA-4 Complex for Designing Therapeutic Antibodies
Wanda Destiarani^{1,2}, Kowit Hengphasatporn², Yasuteru Shigeta², Ryuhei Harada² (¹*Grad. Sch. Sci. Tech., Univ. Tsukuba*, ²*CCS., Univ. Tsukuba*)
- [2Pos180](#) タンパク質の形状を考慮した粗視化モデル分子動力学シミュレーションを用いた ECMO 中空糸膜モデル中の血漿と酸素・二酸化炭素の浸透機構
Permeation Mechanism of Plasma, O₂ and CO₂ in ECMO Hollow Fiber Membrane model Using CG MD Simulation Considering Protein Shape
Ryota Shibasaki¹, Makoto Hukuda^{1,2}, Naoyuki Miyashita^{1,2} (¹*Grad. Sch. BOST, KINDAI Univ.*, ²*BOST KINDAI Univ.*)
- [2Pos181](#) N 結合型糖鎖修飾による Neuropsin (KLK8) の触媒活性の調節機構
Modulation of enzymatic activity in Neuropsin (KLK8) by N-glycosylation
Mai Fujiwara¹, Masami Lintuluoto¹, Yoshifumi Fukunishi², Hideki Tamura³, Juha Lintuluoto⁴ (¹*Grad. Sch. Life and Env. Sci., Univ. Kyoto Pref.*, ²*CMB, AIST*, ³*Lab. Biofunct. Sci., Univ. Hoshi Sch. of Pharm. Sci.*, ⁴*Grad. Sch. Eng., Univ. Kyoto*)
- [2Pos182](#) Theoretical study of competitively ligands binding to AMP-activated protein kinase
Taiga Murakami, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Natu. Sci. Tech., Univ. Kanazawa*)

- [2Pos183](#) 分子シミュレーションを用いた p53N 末端天然変性領域の結合におけるリン酸化と結合相手の影響
Investigating Binding Modes of p53 N-terminal IDR by dPaCS-MD: Impact of Phosphorylation and Partners
Yoshito Hasegawa, Duy Phuoc Tran, Akio Kitao (*Life Science and Technology, Science Tokyo Univ.*)
- [2Pos184](#) KaiC におけるリン酸化状態変化により誘起されるアロステリック応答の全原子分子動力学解析
All-atom molecular dynamics analysis of allosteric response in KaiC induced by phosphorylation state change
Riki Ueno¹, Yudai Terui¹, Koki Adachi¹, Toshifumi Mori², Shuji Akiyama^{3,4}, Mistunori Takano¹ (¹*Grad. Sch. Adv. Sci. Eng., Waseda Univ.*, ²*Inst. Mat. Chem. Eng., Kyushu Univ.*, ³*CIMos, IMS, NINS*, ⁴*SOKENDAI*)
- [2Pos185](#) フラグメント分子動力学を用いたニューロセルピン新規阻害剤の研究開発
Development of Novel Inhibitors for Neuroserpin Using Fragment Molecular Dynamics
Nanase Sakashita¹, Hiroto Terada¹, Daiki Akai¹, Bunzo Mikami^{2,3}, Maki Onda¹, Kei Moritsugu¹ (¹*Grad. Sch. Sci. OMU*, ²*RISH Kyoto Univ.*, ³*IAE Kyoto Univ.*)
- [2Pos186](#) 部位選択的 Gaussian accelerated Molecular Dynamics の開発
Development of site-selective Gaussian accelerated Molecular Dynamics
Hiraku Oshima (*Grad. Sch. Sci., Univ. Hyogo*)
- [2Pos187](#) gREST-ABMD 法によるマルチスケールな自由エネルギー地形探索
New enhanced conformational sampling method for multi-scale molecular dynamics simulations
Shingo Ito¹, Hiraku Oshima², Yuji Sugita^{1,3} (¹*RIKEN Center for Computational Science*, ²*Graduate School of Life Science, University of Hyogo*, ³*Cluster for Pioneering Research, RIKEN*)

26C. 計算生物学：生体モデリングとシミュレーション／
26C. Computational biology: Biological modeling and simulation

- [2Pos188](#) Predicting structural and functional properties of albumins from pets and economic animals by molecular modeling and machine learning
Darunee Traiphophon (*Grad. Sch. Sci., Univ. Kasetsart*)
- [2Pos189](#) シミュレーションによる細菌べん毛周辺の正電荷分布の動態解析
Analysis of the Dynamics of Charged Particle Distributions near a Bacterial Flagellum
Suguru Ushioda, Masashi Tachikawa (*Grad. Sch. Nanobio., Yokohama City Univ.*)
- [2Pos190](#) Cryo-EM and MDSPACE Reveal Continuous Conformational Heterogeneity in Glutamate Dehydrogenase
Tingting Wang¹, Osamu Miyashita¹, Hideki Shigematsu², Masaki Yamamoto³, Florence Tama^{1,4} (¹*IR-CCS, RIKEN*, ²*JASRI, SPring-8*, ³*RIKEN SPring-8 Center*, ⁴*Department of Physics and ITbM, Nagoya Univ.*)
- [2Pos191](#) A tension gradient in a noncoserved cell membrane generates a divergent pattern of cell shape and motility
Valentina Tyukosova¹, Satoru Okuda² (¹*Kanazawa University, Division of Nano Life Science*, ²*Kanazawa University, Nano Life Science Institute*)

27. 数理生物学・理論生物学／27. Mathematical & Theoretical biology

- [2Pos192](#) 「細胞死」の理論
Theoretical Basis for Cell Death
Yusuke Himeoka¹, Shuhei A. Horiguchi^{2,3}, Tetsuya J. Kobayashi^{1,3} (¹*Universal Biology Institute, The University of Tokyo*, ²*Nano Life Science Institute, Kanazawa University*, ³*Institute of Industrial Science, The University of Tokyo*)

- [2Pos193](#) 物理と生物の統一理論；公平な増幅と崩壊による自律的最適化
A Unified Theory of Biology and Physics; Self-Optimization by Martingale Turnover with Amplification
Tomoyuki Yamaguchi (*Research Institute, Nozaki Tokushukai Hospital*)
- [2Pos194](#) 脱分化の力学系モデリング
Dynamical Systems Modeling of Dedifferentiation
Kansuke Sasamori¹, Yusuke Himeoka¹, Chikara Furusawa^{1,2} (¹*Sch. Sci., Univ. Tokyo*, ²*BDR, Riken*)
- [2Pos195](#) 空間変化を伴う反応拡散系
Reaction-diffusion system with spatial deformation
Naoto Yonekura, Shinji Deguchi (*Grad. Sch. Eng. Sci., Univ. Osaka*)

28. 生態／環境／28. Ecology & Environment

- [2Pos196](#) Changes of microbial interactions among core members are one of major driving force to induce community succession
Reika Mimoto¹, Takashi Okada², Yasuhisa Saito³, Hiroyuki Futamata^{1,4,5} (¹*Grad. Sch. Integr. Sci. Tech., Shizuoka Univ.*, ²*Inst. Med. Biol. Kyoto Univ.*, ³*Grad. Sch. Sci. Eng. Shimane Univ.*, ⁴*Grad. Sch. Sci. Tech. Shizuoka Univ.*, ⁵*Res. Inst. Green Sci. Tech., Shizuoka Univ.*)

29. 非平衡・生体リズム／29. Nonequilibrium state & Biological rhythm

- [2Pos197](#) Effects of combined period-modulating mutations on circadian rhythm in a cyanobacterial clock protein system
Eri Hiraiwa, Yuji Nishimura, Kosuke Maki (*Grad. Sch. Sci., Univ. Nagoya*)

30. 計測／30. Measurements

- [2Pos198](#) Polydiacetylene biosensor detecting different binding affinities
Niklas Urs Brenner, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo*)
- [2Pos199](#) Selective IR measurement of only the chromophore part in fluorescent proteins by resonance IR method
Konoka Mifune¹, Hirona Takahashi^{1,2}, Minoru Yamakawa¹, Makoto Sakai^{1,2} (¹*Graduate school of Science and Engineering, Okayama University of Science*, ²*Faculty of Science, Okayama University of Science*)
- [2Pos200](#) Direct observation of single integrin-mediated forces on soft substrates using a DNA-based force sensor
Hiroki Fukunaga¹, Hitomi Matsubara², Yoshihiko Kobayashi³, Fumiko Toyoshima³, Mitsuhiro Iwaki^{1,4,5,6} (¹*Adv ICT Res Inst, NICT*, ²*IMS, RIKEN*, ³*IIR, Science Tokyo*, ⁴*IFReC, Osaka Univ.*, ⁵*FBS, Osaka Univ.*, ⁶*BDR, RIKEN*)
- [2Pos201](#) 低温ラマン光学活性分光装置の開発及び光受容タンパク質への応用
Development of low-temperature Raman optical activity spectrometer and its application to photoreceptor proteins
Naoya Sasaki, Tomotsumi Fujisawa, Masashi Unno (*Fac. Sci. Eng., Saga Univ.*)

- [2Pos202](#) Analysis of *Alcanivorax borkumensis* biofilm on binary oil mixtures
Rei Shimizu¹, Shufeng Zhao¹, Tatsuya Yamamoto³, Andrew S. Utada^{2,3,4} (¹*Grad. Sch. of Sci. and Tech., Univ. of Tsukuba*, ²*Faculty of Life and Environmental Sci., Univ. of Tsukuba*, ³*Microbial Research Center for Sustainability (MiCS), Univ. of Tsukuba*, ⁴*Tsukuba Inst. for Advanced Research, Univ. of Tsukuba*)
- [2Pos203](#) 光ファイバ型蛍光相関分光法によるヒト血清中の細胞外小胞の定量計測
 Measurement of extracellular vesicles in human serum using fiber-optic fluorescent correlation spectroscopy
Johtaro Yamamoto (*Health & Med. Res. Inst., AIST*)
- [2Pos204](#) ソリッドステートナノポアによる tRNA の柔軟性の評価
 Flexibility Evaluation of tRNA by Solid State Nanopore
Gaku Ogino¹, Kazuki Nagashima¹, Hikaru Nozawa¹, Artem Lysenko¹, Tatsuhiko Tsunoda¹, Tsutomu Suzuki², Sotaro Uemura¹ (¹*Graduate School of Science, The University of Tokyo*, ²*Graduate School of Engineering, The University of Tokyo*)
- [2Pos205](#) Contactless Stiffness Measurement of Biomolecular Condensates through Acoustic Trapping
Kichitaro Nakajima, Hirotsugu Ogi (*Graduate School of Engineering, Osaka University*)

31. バイオイメージング / 31. Bioimaging

- [2Pos206](#) 癌の生体ナノイメージングを指向した遠赤色発光性白金ナノクラスターバイオナノプローブの開発
 Far red-emitting Pt nanoclusters based bio-nanoprobes for *in vivo* tumor-targeted imaging
Shin-ichi Tanaka^{1,2}, Hiroki Wadati^{3,4}, Kazuhisa Sato^{5,6} (¹*National Institute of Technology (KOSEN), Kure College*, ²*NHO Kure Medical Center and Chugoku Cancer Center*, ³*Department of Material Science, Graduate School of Science, University of Hyogo*, ⁴*Institute of Laser Engineering, Osaka University*, ⁵*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*, ⁶*Division of Materials and Manufacturing Science, Graduate School of Engineering, Osaka University*)
- [2Pos207](#) ルーピング期心臓形成にエタノールが与える影響の SS-OCT 観測
 Swept-source OCT analysis of ethanol effects on embryonic heart looping
Aimi Yamashita, Taiyo Eguchi, Rikuto Noguchi, Ryuichiro Yamazaki, Yuuta Moriyama, Toshiyuki Mitsui (*Dept. Phys. Sch. Sci., Aoyamagakuin Univ.*)
- [2Pos208](#) Recent Updates to Post-acquisition Super Resolution for Cryo-electron Microscopy
Ray Burton-Smith, Kazuyoshi Murata (*National Institute of Physiological Sciences*)
- [2Pos209](#) 生体分子機能の増強に向けた分子局所加温技術の開発
 Development of Molecular Heating Technology toward the Enhancement of Biomolecular Functions
Yuya Matsuda¹, Kayoko Nomura², Cong Quang Vu², Takeru Yamazaki², Satoshi Arai^{1,2} (¹*Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)
- [2Pos210](#) Ensemble of Deep Neural Network Models for Drug Screening Using 3D Images of *Drosophila* Larvae
Md Al Mehedi Hasan¹, Jean-Emmanuel Clement², Walker Peterson³, Tsubasa Kobayashi³, Soichiro Hata⁴, Takuya Otsuka⁴, Koji Tabata^{1,2}, Masahiro Sonoshita⁴, Keisuke Goda^{3,5}, Tamiki Komatsuzaki^{1,2} (¹*Research Institute for Electronic Science, Hokkaido University, Sapporo, Japan*, ²*Institute for Chemical Reaction Design and Discovery, Hokkaido University, Sapporo, Japan*, ³*Department of Chemistry, Graduate School of Science, The University of Tokyo, Tokyo, Japan*, ⁴*Institute for Genetic Medicine, Hokkaido University, Sapporo, Japan*, ⁵*Department of Bioengineering, University of California, Los Angeles, California 90095, USA*)

- [2Pos211](#) オプティカル光熱赤外分光法 (O-PTIR) の液-液相分離分析への応用可能性についての考察
Consideration of the applicability of optical photothermal infrared spectroscopy (O-PTIR) to liquid-liquid phase separation analysis
Naoki Baden (*Nihon Thermal Consulting Co.*)
- [2Pos212](#) 生物発光による多色同時観察法の開発
A method for simultaneous observation of multiple bioluminescence colors
Mitsuru Hattori¹, Tetsuichi Wazawa¹, Yuki Hiruta², Takeharu Nagai¹ (¹*SANKEN, The University of Osaka*, ²*Faculty of Science and Technology, Keio University*)
- [2Pos213](#) Development of X-ray fluorescence microscope toward non-destructive nanoscale investigation of phase-separated structures in cell nucleus
Yosuke Tomioka¹, Yukako Oma¹, Masahiko Harata^{1,2}, Yuki Takayama^{1,2} (¹*Graduate School of Agricultural Science, Tohoku University*, ²*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*)
- [2Pos214](#) 黄金の蝶々型ナノ粒子を用いた液液相分離液滴の生成消滅制御テクノロジー
Regulatory nanotechnology of liquid-liquid phase separated condensates formation/deformation dynamics by using gold nano-butterflies
Tomohiro Nobeyama¹, Koji Takata³, Tatsuya Murakami³, Yoichi Yamada², Kentaro Shiraki² (¹*Institute for Advanced Study iCEMS, Kyoto University*, ²*Pure and Applied Physics, University of Tsukuba*, ³*Graduate School of Engineering, Toyama Prefectural University*)
- [2Pos215](#) 発蛍光プローブを用いた入れ替わり可能なタンパク質ラベル化システムの開発
Development of Exchangeable Protein Labeling System Using Fluorogenic Probe
Masafumi Minoshima¹, Shahi Imam Reja², Kohei Iijima¹, Kazuya Kikuchi^{1,2} (¹*Grad. Sch. Eng. The University of Osaka*, ²*IFReC, The University of Osaka*)

32. バイオエンジニアリング／32. Bioengineering

- [2Pos216](#) CaM-M13 システムを用いたイオンによる生体分子機械の組み立て制御
Controlling the Assembly of Biomolecular Machines by Ions Using the CaM-M13 System
Ziyun Zhang¹, Nobuyuki Nishibe¹, Shinsaku Maruta^{1,2} (¹*Grad. Sch. Sci., Univ. Soka*, ²*Sch.Sci., Univ. Soka*)
- [2Pos217](#) 大気圧プラズマによるマウス筋芽細胞 C2C12 の成長促進
Growth promotion of murine myoblast cells C2C12 by non-thermal atmospheric pressure plasma exposure
Takeru Kobayashi, **Miho Tsuji**, Kumagai Shinya (*Meijo University*)
- [2Pos218](#) An enzyme discovery approach based on microbial growth in water-in-oil microdroplets
Fumika Hemmi, Kazuma Kouno, Sotaro Uemura, **Ryo Iizuka** (*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

34. Miscellaneous topics その他／34. Miscellaneous topics

- [2Pos219](#) インクジェットパターン植菌法による大腸菌のコロニー成長の評価
Evaluation of microbial colony growth of *Escherichia coli* inoculated via bioprinting
Mikiko Tsudome^{1,2}, Shigeru Deguchi¹, Yutetsu Kuruma^{1,2} (¹*Jamstec*, ²*Yokohama City Univ.*)
- [2Pos220](#) 膜のゆらぎを制御した膜面上の相分離
Phase separation on a membrane surface with controlled membrane fluctuations
Naoki Iso¹, Takahiro Sakaue¹, Shunsuke Yamazaki², Tsutomu Hamada² (¹*Department of Physical Sciences, Aoyama Gakuin University*, ²*School of Materials Science, Japan Advanced Institute of Science and Technology*)

01A. タンパク質：構造 / 01A. Protein: Structure

- [3Pos001](#) ミオシン II の化学反応と力学的反応との共役の分子メカニズムに関する進捗報告
Progress report on the molecular mechanism of the conjugation of chemical and mechanical reactions of myosin II
Riho Sato, Takuo Yasunaga (*Grad. Sch. Comput. Sci. Syst. and Eng. Kyushu Inst. Tech*)
- [3Pos002](#) ファージの宿主認識の構造解析
Structural analysis of phage host recognition
Shuji Kanamaru (*Department of Life Science and Technology, Institute of Science Tokyo*)
- [3Pos003](#) HOIL-1L による HOIP の活性制御機構の構造生物学的解析
Structural biology of the regulation of HOIP activity by HOIL-1L
Marina Koga¹, Kazuki Kasai², Kayo Imamura¹, Kazuhiro Iwai³, Takayuki Kato⁴, Mika Hirose⁴, Keiichi Namba², Tomoko Miyata², Rie Motohashi¹, Hidehito Tochio¹ (¹*Grad. Sch. of Sci., Kyoto Univ.*, ²*Grad. Sch. of Fro., Osaka Univ.*, ³*Grad. Sch. of Med., Kyoto Univ.*, ⁴*inst. for pro., Osaka Univ.*)
- [3Pos004](#) AcrB による薬剤排出の分子基盤の解析
Analysis of the molecular basis of drug efflux by AcrB
Wataru Sakaguchi¹, Yuto Muto¹, Atsuki Nakano¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Department of Molecular Biosciences, Kyoto Sangyo University*, ²*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*)
- [3Pos005](#) Liposome に再構成した LRRC8A の構造解析
Structural analysis of LRRC8A reconstituted into liposome
Ryuga Teramura¹, Atsuki Nakano¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Life, Sci., KSU*, ²*Research Center, Univ. Osaka*)
- [3Pos006](#) ウシ心筋ミトコンドリアの SMP における ATP 合成酵素のオリゴマー構造
Structure of ATP synthase oligomer in SMP membranes of bovine heart mitochondria
Atsuki Nakano¹, **Katsuya Matsuki**¹, Shunsuke Akisada¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Department of Molecular Biosciences, Kyoto Sangyo University*, ²*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*)
- [3Pos007](#) 人工赤色蛋白質 AzamiRed1.0 に復帰変異を導入した変異体シリーズの構造と分光学的性質
Structures and spectroscopic properties of a series of revertant mutant proteins of AzamiRed1.0, an engineered red fluorescent protein
Isamu Nagatomi¹, Hiromi Imamura², Norihiro Takekawa¹, Katsumi Imada¹ (¹*Grad. Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Biost., Kyoto Univ.*)
- [3Pos008](#) HeLa S3 細胞内のヒト UCHL3 の立体構造解析
In-cell NMR study of human UCHL3 in HeLa S3 cells
Hikari Sato¹, Moeka Nagamine¹, Yui Akai¹, Shigeharu Kubota¹, Hiroki Miyata¹, Haruka Sugawara¹, Kohsuke Inomata^{1,2,3}, Teppei Ikeya¹, Yutaka Ito¹ (¹*Department of Chemistry, Tokyo Metropolitan University*, ²*Institute for Molecular Science, National Institutes of Natural Sciences*, ³*Okazaki Collaborative Platform, National Institutes of Natural Sciences*)
- [3Pos009](#) 分子クラウディング環境下での蛋白質の立体構造
Protein 3D structures under macromolecular crowding environment
Shuto Kubo, Seito Kato, Ryouma Tagishi, Akio Horikawa, Sayeesh P.M., Kousuke Inomata, Teppei Ikeya, Yutaka Ito (*Department of Chemistry, Tokyo Metropolitan University*)

- [3Pos010](#) Cryo-EM structure of a putative bicarbonate channel PtBEST1 from diatom *Phaeodactylum tricornutum*
Hiroyasu Koteishi¹, Akihiro Kawamoto¹, Ginga Shimakawa³, Hiroaki Matsui², Yoshinori Tsuji², Yusuke Matsuda², Genji Kurisu¹ (¹IPR, Osaka Univ., ²Dept. Biosci., Sch. Biol & Environ. Sci., Kwansei Gakuin Univ., ³Grad. Sch., Agri. Sci., Kobe Univ.)
- [3Pos011](#) Structural analysis of Ib mutants by cryo-electron microscopy to reveal the membrane pore formation process of Ib
Ren Nakanishi (*kyoto sangyo university*)

01B. タンパク質：物性（安定性、折れたたみなど）／01B. Protein: Physical property

- [3Pos012](#) 分子動力学シミュレーションを用いた IL3Rα N 末端領域の構造揺らぎが IL-3 結合親和性に与える影響評価
Molecular dynamics simulation for IL-3/IL3Rα complexes to verify the effects of fluctuations of IL3Rα N-terminal domain on affinity
Toshiaki Ueda¹, Aiko Hasegawa², Yozo Nakazawa^{1,2}, Koji Umezawa¹ (¹Grad. Sch. of Sci. & Tech., Shinshu Univ., ²Sch. of Med., Shinshu Univ.)
- [3Pos013](#) 分泌発現量に関わる α 接合因子プレプロリーダー配列の動的構造特性
Dynamical structural property of α-mating factor pre-pro-leader sequence and relationship with the expression yield
Kazumasa Sakurai (*Inst. Adv. Tech., Kindai Univ.*)
- [3Pos014](#) The relationship between initial structure and polymorphism of amyloid fibrils from SARS-CoV-2 spike peptide
Manami Yamaguchi¹, Emi Hibino¹, Natsuko Goda¹, Takeshi Tenno^{1,2}, Hidekazu Hiroaki^{1,2,3} (¹Grad. Sch. Pharm. Sci., Nagoya Univ., ²BeCellBar, LLC, ³COMIT)
- [3Pos015](#) GFPuv の発色団形成反応におけるカルボニル基の役割
Role of carbonyl groups in the chromophore formation of GFPuv
Tomoya Adachi¹, Masaru Hoshino², Kaori Chiba¹ (¹Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan, ²Kyoto Univ. Pharm.)
- [3Pos016](#) GFP 様タンパク質 mCherry が分子の内部にもつ酸性アミノ酸の役割
Role of acidic Amino Acids inside the molecule of GFP-like Proteins
Pattarisa Rerganan¹, Masaru Hoshino², Nobuhiro Suzuki³, Kaori Chiba¹ (¹Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan, ²Kyoto Univ. Pharm., ³NARO)
- [3Pos017](#) E222DGFPuv は中性 pH で acidic form の発色団のみを持つ
E222DGFPuv has only chromophores in acidic form at neutral pH
Yutsuki Mimura¹, Masaru Hoshino², Kaori Chiba¹ (¹Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan, ²Kyoto Univ. Pharm.)
- [3Pos018](#) タンパク質をモデルとした生物の超高压力耐性のラマン分光研究
Raman Spectroscopic Study on Ultra-High Pressure Resistance in Small Organisms Using Proteins as a Model
Kantaro Iwasa¹, Toshiki Nakao¹, Minoru Kato^{1,2} (¹Grad. Sch. of Life Sci. Univ. Ritsumei, ²Col. of Life Sci. Univ. Ritsumei)

- [3Pos019](#) 部位特異的変異体を用いた α -イソプロピルリンゴ酸合成酵素(IPMS)のロイシン認識メカニズムの解明
Elucidation of the leucine recognition mechanism of α -isopropylmalate synthase (IPMS) using site-directed mutants
Hanane Nakamura¹, Yuto Miura¹, Hana Kitazume¹, Kanon Sugao², Yoko Akazawa³, Shigeru Shimamoto⁴, Takayuki Ohnuma², Atsushi Kurata², Koichi Uegaki² (¹*Grad.Sch.Agric.Kindai univ.*, ²*Agric.Kindai univ.*, ³*AIST*, ⁴*Fac.Sci. & Eng.Kindai univ*)
- [3Pos020](#) α -イソプロピルリンゴ酸合成酵素のロイシン感受性とリンカードメインの構造変化
Leucine Sensitivity and Structural Changes in the Linker Domain of α -Isopropylmalate Synthase
Yuto Miura¹, Hanane Nakamura¹, Hana Kitadume¹, Kanon Sugao², Yoko Akazawa³, Kazuki Mitani⁴, Shigeru Shimamoto⁴, Kazuki Kawahara^{5,6}, Hiroya Oki⁷ (¹*Grad. Sch. Agric., Kindai Univ.*, ²*Agric., Kindai Univ.*, ³*AIST*, ⁴*Fac. Sci. & Eng., Kindai Univ.*, ⁵*Grad. Sch. Pharm. Sci., Osaka Univ.*, ⁶*CiDER, Osaka Univ.*, ⁷*Res. Inst. Microbial Dis., Osaka Univ.*)
- [3Pos021](#) 均一基質バインダーのダイナミクスと進化
Dynamics and Evolution of Uniform Substrate Binder
Yusran Abdillah Muthahari¹, Yovin Sugijo¹, Paola Laurino^{1,2} (¹*Protein Engineering and Evolution Unit, Okinawa Institute of Science and Technology*, ²*Institute for Protein Research, Osaka University*)
- [3Pos022](#) ヘイムダルアクチンは短いフィラメントを形成し，骨格筋トロポミオシントロポニン複合体と共沈する
Heimdall actin forms short filaments and coprecipitates with the muscle tropomyosin-troponin complexes
Kaoru Takahashi¹, Tomoharu Matsumoto², Akihiro Narita², Taro Q.P. Uyeda¹ (¹*Dept. Pure. & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, ²*Dept. Physics, Grad. Sch. of Science, Nagoya Univ.*)
- [3Pos023](#) EPR 法による南極海および深海細菌由来無機ピロフォスファターゼの低温適応機構の解明
EPR Spectroscopy Reveals the Cold Adaptation Mechanism for Di-Mn²⁺ Inorganic Pyrophosphatase
Ren Sugawara, Yuri Kusu, Kantaro Sakamoto, **Masaki Horitani** (*Fac. Agri., Saga Univ.*)
- [3Pos024](#) ヒト H 鎖フェリチン内部に形成される鉄コアに対するリン酸の影響
Effect of phosphate on the iron core formed in human H-ferritin
Katsuaki Hanabusa¹, Takumi Kuwata², Haruki Sakakibara¹, Kazuo Fujiwara¹, Masamichi Ikeguchi^{1,2} (¹*Department of Biosciences., Graduate School of Science and Engineering, Soka University*, ²*Department of Science and Engineering for Sustainable Innovation, Soka University*)
- [3Pos025](#) NMR による Ubiquitin C-terminal Hydrolase (UCHL3)のユビキチンとの相互作用とダイナミクス解析
NMR analysis of the intermolecular interaction between Ubiquitin C-terminal Hydrolase (UCHL3) and ubiquitin, and their molecular dynamics
Shigeharu Kubota, Hiroki Miyata, Haruka Sugasawa, Yutaka Ito, Teppei Ikeya (*Department of Chemistry, Tokyo Metropolitan University*)
- [3Pos026](#) Purification and functional analysis of Loki archaea actin
Haruka Tatsuta¹, Gaku Sakai¹, Yuta Yanase¹, Tomoharu Matsumoto², Akihiro Narita², Taro Uyeda¹ (¹*Grad. Sch. Adv. Sci. Eng., Univ. Waseda*, ²*Grad. Sch. Sci., Univ. Nagoya*)

- [3Pos027](#) A high-performance software suite for 3D reconstruction from single-particle X-ray scattering
Wenyang Zhao¹, Osamu Miyashita¹, Florence Tama^{1,2,3} (¹*RIKEN Center for Computational Science*,
²*Institute of Transformative Bio-Molecules, Nagoya University*, ³*Graduate School of Science, Nagoya University*)
- [3Pos028](#) CaMKII と GluN2B ペプチドの結合を可視化する高速 AFM 基板の開発
 Development of a HS-AFM substrate to visualize the binding between CaMKII and GluN2B peptides
Kodai Hasegawa¹, Taiki Kobayashi², Hiroki Konno^{3,4}, Yusuke Miyanari^{3,4}, Mikihiro Shibata^{3,4}
 (¹*Grad.Sch.NanoLS, Kanazawa Univ.*, ²*Sch.Math.&Phys., Kanazawa Univ.*, ³*WPI-NanoLSI, Kanazawa Univ.*, ⁴*InFiniti, Kanazawa Univ.*)
- [3Pos029](#) 高速 AFM 用超微小カンチレバーの変位検出レーザーの自動位置アライメント
 Automatic position alignment of the deflection detection laser to ultra-small high-speed AFM cantilever
Taiyo Ogawa¹, Noriyuki Kodera², Kenichi Umeda² (¹*Grad.Sch.Math. & Phys., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*)
- [3Pos030](#) 蛍光明滅を併用した TDP-43-核酸相互作用の定量性向上
 Improving quantitative detection of TDP-43-nucleic acid interactions by combining fluorescence blinking analysis
Haruki Kawai¹, Akira Kitamura² (¹*Grad. Sch. of Life Sci., Hokkaido Univ.*, ²*Fac. of Adv. Life Sci., Hokkaido Univ.*)
- [3Pos031](#) 磁気コンパスの機構解明に向けた共焦点顕微鏡による FAD-Trp 系の蛍光測定
 Fluorescence measurement of the FAD-Trp system by confocal microscopy to elucidate the mechanism of the magnetic compass
Akihiro Tateno¹, Toru Kondo^{1,2} (¹*ExCELLS*, ²*NIBB*)

- [3Pos032](#) Tag/Catcher システムを用いたタンパク質構造体への異種タンパク質の取り込みの検討
 Incorporation of heterologous proteins into protein structures using the Tag/Catcher system
Yume Kosuge, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)
- [3Pos033](#) 耐熱性酵素を用いた無細胞アルカン合成
 Cell-free alkane synthesis using thermostable enzymes
Kaisei Nagao¹, Shunji Suetaka¹, Munchito Arai^{1,2} (¹*Dept. Life Sci., Univ. Tokyo*, ²*Dept. Phys., Univ. Tokyo*)
- [3Pos034](#) 大腸菌における翻訳促進ペプチドの機械学習による予測と実証
 Machine learning-guided identification and validation of translation-enhancing peptides in *Escherichia coli*
Chie Motono¹, Yokoyama Gentaro², Hideo Nakano³, Teruyo Ojima-Kato³, Michiaki Hamada² (¹*Cellular and Molecular Biotechnology Research Institute, AIST*, ²*Graduate School of Advanced Science and Engineering, Waseda University*, ³*Graduate School of Bioagricultural Sciences, Nagoya University*)
- [3Pos035](#) タンパク質ファミリー 2 種の配列を深層学習により混合させた新規タンパク質の特性
 Deep Learning-Guided Generation of "Marble-Type" Hybrid Transcription Factors Bridging Two Subfamilies
 Michio Aiko, Atsushi Minami, Sota Okuda, Kazumasa Ohtake, **Daisuke Kiga** (*Waseda U, Dept. Elect Eng and Biosci*)
- [3Pos036](#) A platform for developing thermogenetic tools to control protein function
Quang Cong Vu, Satoshi Arai (*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

01F. タンパク質：天然変性／01F. Protein: Intrinsic disorder

- [3Pos037](#) SOS1 天然変性領域(IDR)の GRB2 との多価相互作用と液液相分離形成機構の溶液 NMR 解析
NMR analysis of the multivalent interaction between SOS1 intrinsically disordered region and GRB2 and its liquid-liquid phase separation
Rina Kamimura¹, Sangya Yu¹, Maho Watanabe¹, Toshifumi Hayashi¹, Haruka Sugawara¹, Tsutomu Mikawa², Yutaka Ito¹, Teppei Ikeya¹ (¹*Department of Chemistry, Graduate School of Science, Tokyo Metropolitan University*, ²*RIKEN Center for Biosystems Dynamics Research*)
- [3Pos038](#) Kinetic Study on LLPS of Pbp1 by Combining Stopped-Flow and Transient Grating Methods
Ryo Taniguchi, Masahide Terazima, Yusuke Nakasone (*Grad. Sch. Sci., Kyoto Univ.*)
- [3Pos039](#) SAXS-guided prediction of animal-like cryptochrome from green alga *Chlamydomonas reinhardtii* structure via coarse-grained MD simulations
Petlada Rattanasombat¹, Osamu Miyashita², Tsubura Yoshimi³, Sachiko Yanagisawa³, Minoru Kubo³, Florence Tama^{1,2,4} (¹*Graduate School of Science, Nagoya University*, ²*RIKEN Center for Computational Science*, ³*Graduate School of Science, University of Hyogo, Ako-gun, Hyogo, Japan*, ⁴*Institute of Transformative Bio-Molecules, Nagoya University*)
- [3Pos040](#) 高速 A F M による結核菌休眠制御タンパク質 MDP1 のサブ分子観察
Sub-molecular imaging of MDP1, a dormancy-regulating intrinsically disordered protein in *Mycobacterium tuberculosis*, by high-speed AFM
Yuna Goto¹, Kaho Nakamoto¹, Kenichi Umeda², Akihito Nishiyama³, Sohkichi Matsumoto³, Noriyuki Kodera² (¹*Grad. Sch. Math. & Phys., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*Dept. Bacteriol., Niigata Univ. Sch. Med.*)

02. ヘムタンパク質／02. Heme proteins

- [3Pos041](#) Modification of intramolecular electron transfer membrane protein for photo-induced iron reduction
Kanta Kondo¹, Hiroshi Sugimoto^{2,3}, Kimura Tetsunari^{1,4} (¹*Dept. of Chem., Grad Sch. of Sci., Kobe Univ.*, ²*Spring-8Cent., RIKEN*, ³*Dept. of Life Sci., Grad Sch. of Sci., Hyogo Prefectural Uni.*, ⁴*Research Cent. for Molecular Photo Sci., Kobe Uni.*)
- [3Pos042](#) Analysis of the Transport Mechanism in the ABC transporter Based on Spectroscopic Tracking of Heme
Kaito Nakagawa¹, Yoshitsugu Shiro², Hiroshi Sugimoto^{2,3}, Tetsunari Kimura^{1,4} (¹*Dept. of Chem., Grad. Sch. of Sci., Kobe Univ.*, ²*Dept. of Life Sci., Grad. Sch. of Sci., Univ. of Hyogo*, ³*Spring-8 Cent., RIKEN*, ⁴*Mol. Photo. Res. Cent., Kobe Univ.*)

03. 膜タンパク質／03. Membrane proteins

- [3Pos043](#) QM/MM シミュレーションを用いたハロロドプシンの光活性化状態に関する理論的研究
Theoretical studies on halorhodopsin photoactivation using QM/MM simulations
Tomo Ejiri, Shigehiko Hayashi (*Grad. Sci., Univ. Kyoto*)
- [3Pos044](#) 全長構造から読み解く KcsA の構造ダイナミクスと機能
Structural dynamics and function of KcsA revealed by the full-length structures
Kotaku Yano¹, Hiroko Takazaki², Hirofumi Shimizu³, Takuo Yasunaga¹ (¹*Grad. Sch. Comp. Sci. and Sys. Eng. Kyushu Inst. Tech.*, ²*IPR, Osaka University*, ³*University of Fukui*)

- [3Pos045](#) 脂質過酸化能の評価に向けた BRIL 融合型シトクロム b561D2 のナノディスク化
Preparation of BRIL-fused cytochrome b561D2 in nanodisc to evaluate its peroxidation activity for lipid membrane
Haruka Yoshimura¹, Motonari Tsubaki¹, Hisroshi Sugimoto^{2,3}, Tetsunari Kimura^{1,4} (¹*Graduate School of Science, Kobe University*, ²*Spring-8 Center, RIKEN*, ³*Graduate School of Science, University of Hyogo*, ⁴*Molecular PhotoScience Research Center, Kobe University*)
- [3Pos046](#) Affinity between of the ABC transporter BhuUV and the periplasmic binding protein BhuT, investigated by biolayer interferometry
Yusei Toyoda¹, Yoshitsugu Shiro², Hiroshi Sugimoto^{2,3}, Tetsunari Kimura^{1,4} (¹*Dept. of Chem., Grad. Sch. of Sci., Kobe Univ.*, ²*Dept. of Life Sci., Grad. Sch. of Sci., Univ. of Hyogo*, ³*Spring-8 Cent., RIKEN*, ⁴*Mol. Photo. Res. Cent., Kobe Univ.*)

04. DNA・DNA 結合タンパク質／04. DNA & DNA binding proteins

- [3Pos047](#) Molecular Simulations Reveal Phase Separation Mechanisms of Pluripotency Transcription Factor Combinations
Samuel Blazquez Fernandez, Yutaka Murata, Shoji Takada, Tsuyoshi Terakawa (*Department of Biophysics, Graduate School of Science, Kyoto University, Kyoto, Japan*)
- [3Pos048](#) 高速 AFM による形状測定とナノ力学測定を用いた DNA-MDP1 複合体の薬剤応答解析
Structural and nano-mechanical analysis of drug effects on DNA-MDP1 complexes using high-speed AFM
Kaho Nakamoto¹, Yuna Goto¹, Kenichi Umeda², Akihito Nishiyama³, Sohkichi Matsumoto³, Noriyuki Kidera² (¹*Grad. Sch. Math. & Phys., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*Dept. Bacteriol., Niigata Univ. Sch. Med.*)
- [3Pos049](#) Slippage Dynamics of Trinucleotide Hairpins and Their Disruption of the Genome-Maintaining Function of Human Replication Protein A (hRPA)
I-Ren Lee, Yu-Chi Kuang, Cheng-Wei Ni, Szu-Yu Chen (*Department of Chemistry, National Taiwan Normal University*)

05. RNA・RNA 結合タンパク質／05. RNA & RNA binding proteins

- [3Pos050](#) グルタミン tRNA 合成酵素の分子機構に関する理論的研究
Theoretical study on a molecular mechanism of the glutamyl-tRNA synthetase
Ayaka Matsuyama¹, Masahiko Taguchi², Shigehiko Hayashi¹ (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*IMRAM, Tohoku Univ.*)

06. DNA/RNA ナノテクノロジー／06. DNA/RNA nanotechnology

- [3Pos051](#) 紫外線損傷 DNA の低分子化合物による光修復
Photorepair of UV-damaged DNA by small molecules
Tatsuya Iwata, Rina Fuchigami, Risa Inomata, Manato Okabe, Yumika Ochiai, Fumio Takahashi, Mineo Iseki (*Fac. Phar. Sci., Toho Univ.*)
- [3Pos052](#) A Systematic Approach for Integrating DNA Aptamers and DNA-Responsive Nanosystems via Strand Displacement Reactions
Satofumi Kato¹, Masahiro Takinoue², Hiroaki Onoe¹ (¹*Graduate School of Science and Technology, Keio University*, ²*Department of Computer Science, Institute of Science Tokyo*)

- [3Pos053](#) Self-limited assembly of shape-adjustable DNA origami modules into desired polygonal shapes
Ayu Sakamoto, **Yuki Suzuki** (*Grad. Sch. Eng., Mie Univ.*)

07. 核酸：その他／07. Nucleic acid: Others

- [3Pos054](#) DNA 超らせん構造のねじれと伸長による力学的制御
Mechanical control of DNA supercoils by torsion and extension
Shinnosuke Inui, Anzu Kawamura, Yoshihiro Murayama (*Department of Biomedical Engineering, Faculty of Engineering, Tokyo University of Agriculture and Technology*)

08. クロマチン・染色体／08. Chromatin & Chromosomes

- [3Pos055](#) ESR 分光学で捉えた液液相分離中のヘテロクロマチンタンパク質 1(HP1)のダイナミクス
Dynamics of heterochromatin protein 1 (HP1) during phase separation, as studied by ESR spectroscopy
Isao Suetake², Kazunobu Sato¹, Toshiki Takei³, Tomoaki Sugishiata³, Yuichi Mishima³, Yoh Matsuki³, Toshimichi Fujiwara³, Takeji Takui¹, Makoto Miyata¹, Hironobu Hojo³, **Toshiaki Arata**^{1,3} (¹*Grad. Sch. Sci., Osaka Met. Univ.*, ²*Grad. Sch. Home Economics, Kobe Women's Univ.*, ³*Inst. Protein Res., Univ. Osaka*)
- [3Pos056](#) Mechanical Insights into Nucleosome Remodeling by divalent Cations: A Single-molecule study
Amarjeet Kumar¹, Tomoko Sunami¹, Shoko Sato², Hitoshi Kurumizaka², Hidetoshi Kono^{1,3} (¹*Inst. Quant. Life Sci., Nat. Inst. Quant. Sci. Tech., Chiba, Japan*, ²*Inst. Quant. BioSci., Univ. of Tokyo, Tokyo, Japan*, ³*Cent. Quant Life Sci. Str. Therap., Chiba Univ., Chiba, Japan*)
- [3Pos057](#) スクレオソーム DNA 引き剥がしダイナミクスの解読：ナノポアが明らかにするヒストン N 末端テイルの役割
Decoding Nucleosomal DNA Unwrapping Dynamics: The Role of Histone N-Terminal Tails Revealed by Nanopores
Satoshi Ogiwara¹, Hikaru Nozawa¹, Takumi Oishi², Fritz Nagae³, Munetaka Akatsu², Shoji Takada³, Hitoshi Kurumizaka², Sotaro Uemura¹ (¹*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, ²*Institute for Quantitative Biosciences, The University of Tokyo*, ³*Department of Biophysics, Graduate School of Science, Kyoto University*)

10. 水・水和／電解質／10. Water & Hydration & Electrolyte

- [3Pos058](#) 回折 X 線明減法を用いた不凍液中の再結晶過程に伴う水分子動態解析
Molecular dynamics analysis of the recrystallization behavior of water in antifreeze solutions by Diffracted X-ray Blinking
Daisuke Sasaki¹, Umena Yasufumi², Yuji C. Sasaki¹ (¹*Department of Advanced Materials Science, Graduate School of Frontier Sciences, The University of Tokyo*, ²*Synchrotron Radiation Research Center, Nagoya University*)
- [3Pos059](#) サブテラヘルツ波照射による DNA 塩基対形成の非熱的促進
Non-thermal acceleration of DNA base-pair rearrangement using sub-THz irradiation
Masahiko Imashimizu, Johtaro Yamamoto, Tomoya Inose (*AIST*)

- [3Pos060](#) ショウジョウバエ胚の後腸の捻転と伸長は異なる集団細胞移動によって独立して制御される
Distinct collective cell behaviors independently regulate the rotation and elongation of the embryonic gut in *Drosophila*
Mikiko Inaki^{1,2}, Satoru Okuda³, Kenji Matsuno² (¹Grad. Sch. Sci., Univ. Hyogo, ²Grad. Sch. Sci., Univ. Osaka, ³Nano LSI, Kanazawa Univ.)
- [3Pos061](#) 細胞性粘菌における細胞分化・脱分化と細胞内 Ca²⁺動態の相関分析
Correlative analysis of intracellular Ca²⁺ dynamics with cell differentiation and dedifferentiation in *Dictyostelium*
Rintaro Aono, Yusuke V. Morimoto (*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech.*)
- [3Pos062](#) 人工ヒト胚モデルにおけるサイズ依存的なパターン形成：胚葉形成のダイナミクスに関する考察
Size-Dependent Pattern Formation in Engineered Human Embryo Models: Insights into Gastrulation Dynamics
Miyu Mori¹, Hazuki Tuboi¹, Ryo Kojima¹, Chihiro Takeuchi¹, Yohei Hayashi², Kiyoshi Ohnuma¹
(¹Nagaoka University of Technology, ²BioResource Research Center, RIKEN)

13. 筋肉（筋蛋白質・収縮） / 13. Muscle

- [3Pos063](#) 昆虫飛翔筋の回転平均化された 2 次元 X 線回折像からサルコメアの 3 次元構造を復元する
Restoration of the 3D structure of insect flight muscle from a rotationally averaged 2D X-ray diffraction pattern
Hiroyuki Iwamoto (*SPRING-8 · JASRI*)

14. 分子モーター / 14. Molecular motor

- [3Pos064](#) Cilia-like Beating of Clamped Microtubules Driven by Kinesin Motors
Jane Wanja Karanja, Douglas K. Ng'ang'a, Takahiro Nitta (*Applied Physics Course, Faculty of Engineering, Gifu University, Gifu 501-1193, Japan*)
- [3Pos065](#) Buckling and Trajectory Deflections of Microtubules Driven by Kinesin Motors
Douglas Kagoiya Ng'ang'a, Takahiro Nitta (*Applied Physics Course, Faculty of Engineering, Gifu University*)
- [3Pos066](#) Cryo-EM visualization of the conformational states of G_i-ATPase, a rotary motor driving *Mycoplasma mobile* gliding
Takuma Toyonaga¹, Daisuke Unabara¹, Tasuku Hamaguchi¹, Koji Yonekura^{1,2} (¹IMRAM, Tohoku Univ., ²RIKEN SPRING-8 Center)
- [3Pos067](#) Development of gold nanoparticle-based optical switches for reversible artificial muscles driven by kinesin motor proteins
Kensei Hori¹, Taiyo Sato¹, Yuichi Hiratsuka², Keisuke Morishima⁴, Takahiro Nitta³ (¹Grad. Sch. Nat. Sci. & Tech., Univ. Gifu, ²JAIST, ³Univ. Gifu, ⁴Univ. Osaka)
- [3Pos068](#) 二重オブジェクトツールによるキネシン 14 のアンカー位置制御を介した微小管運動方向の光制御
Light-controlled directional reversal of microtubule motility via dual optogenetic switches regulating kinesin-14 anchoring
Masahiko Yamagishi^{1,2}, Junichiro Yajima^{1,2,3} (¹Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo, ²Komaba Institute for Science, The University of Tokyo, ³Research Center for Complex Systems Biology, Universal Biology Institute, The University of Tokyo)

- [3Pos069](#) LOV トロポニンによるアクトミオシンの光制御
Light control of myosin-actin based motility by LOV-Troponin
Koki Yasuda (*JAIST*)
- [3Pos070](#) 脂質二重膜中で機能する ATP 合成酵素のクライオ電子顕微鏡構造解析
Cryo-EM structures of ATP synthases functioning in lipid bilayers
Atsuki Nakano¹, Jun-Ichi Kishikawa², Christoph Gerle⁵, Hideki Shigematsu⁴, Kaoru Mitsuoka³, Ken Yokoyama¹ (¹*Fac. of Life Sci., Kyoto Sangyo Univ.*, ²*Applied Biology, Kyoto Institute of Technology*, ³*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*, ⁴*JASRI*, ⁵*RIKEN Spring-8 Center*)
- [3Pos071](#) 骨格筋の収縮原理を細胞外で模倣したアクトミオシン-フィブリンゲル混合アクチュエータ
Actomyosin-fibrin gel composite actuator mimicking contraction mechanism of skeletal muscle extracellularly
Takuro Kawasumi¹, Koki Yoshida², Yuichi Hiratsuka³, Hiroaki Onoe¹ (¹*Keio University*, ²*Shibaura Institute of Technology*, ³*Japan Advanced Institute of Science and Technology*)
- [3Pos072](#) 情報熱力学による F₁-ATPase 内の相互作用の実験的評価
Experimental evaluation of interactions within F₁-ATPase based on information thermodynamics
Ken Takagi¹, Yohei Nakayama¹, Chun-Biu Li², Stefano Bo³, Takahiro Sagawa⁴, Shoichi Toyabe¹ (¹*Department of Applied Physics, Tohoku University, Japan*, ²*Department of Mathematics, Stockholm University, Sweden*, ³*Department of Physics, King's College London, United Kingdom*, ⁴*Department of Applied Physics, The University of Tokyo, Japan*)
- [3Pos073](#) *Enterococcus hirae* V-ATPase の Na⁺能動輸送を支える a サブユニットの2つのハーフチャネルの非対称な Na⁺結合親和性
Asymmetric Na⁺ binding affinities of two half-channels in a-subunit support active Na⁺ transport of *Enterococcus hirae* V-ATPase
Akihiro Otomo^{1,2}, Yuan-E Lee^{3,4}, Juliette Lahore⁵, Raymond Burton-Smith^{2,3,4}, Kano Suzuki⁶, Takeshi Murata⁶, Kazuhoshi Murata^{2,3,4}, Ryota Iino^{1,2} (¹*Institute for Molecular Science*, ²*SOKENDAI*, ³*ExCELLs*, ⁴*National Institute for Physiological Sciences*, ⁵*Chmie ParisTech*, ⁶*Grad. Sch. Sci., Univ. Chiba*)
- [3Pos074](#) Elucidating Dynein Velocity Enhancement via Binding Affinity Modulation
Haruki Kawase^{1,2}, Kenta Ishibashi², Akane Furuta², Ken'ya Furuta^{1,2} (¹*The university of Osaka*, ²*National institute of information and communications technology*)

15A. 細胞生物学的課題：接着／15A. Cell biology: Adhesion

- [3Pos075](#) アクチン架橋タンパク質による細胞間境界の力安定性維持機構
Actin Crosslinking Proteins Maintain Force Stability at Cell-Cell Boundaries
Hiroki Katsuta¹, Satoru Okuda², Nobutomo Fujimoto³, Duc Doan Manh¹, Hiroaki Hirata⁴, Keiji Naruse¹ (¹*Faculty of Med. Dent. and Pharm Sci., Okayama Univ.*, ²*Nano LSI, Kanazawa Univ.*, ³*Dept. Med., Okayama Univ.*, ⁴*Dept. Life Sci. and Biotech., KIT*)
- [3Pos076](#) Scale-dependent mechanobiological responses of focal adhesions
Gento Takeshima, Takumi Saito, Shinji Deguchi (*Grad. Sch. Eng. Sci. Univ. Osaka*)
- [3Pos077](#) 歯周病菌の Fim 線毛先端タンパク質 FimE の C 末端領域の構造
Structure of the C-terminal region of FimE, a tip protein of the Fim pili from *Porphyromonas gingivalis*
Hikaru Tanizaki¹, Norihiro Takekawa², Katsumi Imada² (¹*Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Sci., Osaka Univ.*)

- [3Pos078](#) Light-Guided Actin Dynamics Drives Protocell Migration
Hideaki Matsubayashi¹, Shiva Razavi², Daichi Nakajima³, Hideki Nakamura⁴, Tomoaki Matsuura⁵, Shin-ichiro Nomura³, Takanari Inoue² (¹*Frontier Research Institute for Interdisciplinary Sciences (FRIS), Tohoku University*, ²*School of Medicine, Johns Hopkins University*, ³*Graduate School of Engineering, Tohoku University*, ⁴*Hakubi Center for Advanced Research, Kyoto University*, ⁵*Earth-Life Science Institute, Science Tokyo*)
- [3Pos079](#) Elucidating the role of *Spiroplasma* fibril protein using synthetic bacterium, JCVI syn3
Ali Ahsan, Hana Kiyama, Makoto Miyata (*Grad. Sch. Sci., Osaka Metropolitan Uni.*)
- [3Pos080](#) Manipulation of rotational direction of the archaeal flagella motor in *Halobacterium salinarum* by light modulation
Jumpei Sega¹, Masaki Mizutani¹, Daisuke Nakane², Takayuki Nishizaka¹ (¹*Gakushuin University*, ²*University of Electro-Communications*)
- [3Pos081](#) クラミドモナス鞭毛におけるマスティゴネマ線維の構造と機能
 Strucutre and function of mastigoneme filaments in *Chlamydomonas* cilium
Toshiki Yagi, Ryuta Yoshizawa, Kakeru Komori (*Dept. Life and Env. Sci, Pref. Univ. Hiroshima*)
- [3Pos082](#) マイクロ構造体を用いた運動性を持つ微生物の運動方向の操作
 Manipulation of the direction of movement of motile microbes using microstructures
Masaru Kojima¹, Mitsuhiro Horade² (¹*Grad. Sch. Eng.Sci., The Univ. of Osaka*, ²*Fac. of Sci. and Eng., Setsunan Univ.*)
- [3Pos083](#) 機械的な力の付加による細胞集団運動の変化から機械走性メカニズムに迫る
 Approaching the Mechanism of Mechanotaxis via Collective Cell Migration Induced by Mechanical Force Loading
Chihori Asano¹, Keitaro Shibata², Shigenobu Yonemura² (¹*Grad. Sch. Med., Tokushima Univ.*, ²*Grad. Sch. Biomed. Sci., Tokushima Univ.*)
- [3Pos084](#) Phototaxis and light-driven accumulation in wild isolates of *Heterosigma akashiwo*
Naoki Uemura¹, Shoko Ueki², Daisuke Nakane¹ (¹*Dept. Eng. Sci., Univ. Electro-Communications*, ²*Inst. Plant Sci. Res., Univ. Okayama*)

15C. 細胞生物学的課題：細胞骨格・膜骨格／15C. Cell biology: Cytoskeleton & Membrane skeleton

- [3Pos085](#) Dynamic response of keratin assemblies to thermal stress in mutant keratinocytes implicated in Epidermolysis bullosa simplex
Doyin Rachael Abiola¹, Tetsuya Kitaguchi², Birgitte E. Lane³, Madoka Suzuki¹ (¹*Inst. Protein Res., Univ. Osaka*, ²*Inst. Integr. Res., Sci. Tokyo*, ³*SRIS, Singapore*)
- [3Pos086](#) 植物左右ねじれ伸長創発メカニズムの解明
 Elucidating the mechanisms of plant chiral growth
Eiki Meguro¹, Masayoshi Nakamura², Toshifumi Mori³ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Grad. Sch. Sci. and Eng., Saitama Univ.*, ³*Institute for Materials Chemistry and Engineering, Kyushu Univ.*)
- [3Pos087](#) 出芽酵母アクチンフィラメントの in situ 構造解析に向けた取り組み
 Towards in situ Structural Analysis of Actin Filaments in Budding Yeast
Hiroko Takazaki¹, Kana Shimamoto^{1,2}, Stephen Mwaniki¹, Misaki Arie¹, Akira Shinohara¹, Takayuki Kato¹ (¹*IPR., Univ. Osaka*, ²*Grad. Sch. Sci., Univ. Osaka*)
- [3Pos088](#) ケモメカニカルモデルによる焦点接着斑とアクトミオシン動態の解析
 Chemomechanical Model of Focal Adhesion-Actomyosin Dynamics
Eiji Matsumoto, Shinji Deguchi (*Graduate School of Engineering Science, The University of Osaka*)

- [3Pos089](#) 分子シャペロン α B-クリスタリンはチューブリン凝集を抑え微小管会合活性を維持する
The molecular chaperone α B-crystallin delays thermal aggregation of tubulin and maintains microtubule polymerization activity
Shinya Horinouchi^{1,2}, Daisuke Inoue³, Shohei Yamamoto⁴, Eri Fujita⁵, Miho Shimizu², Toshiyuki Watanabe¹, Yoriko Atomi² (¹*Grad. Sch. of Eng., Tokyo Univ. Agric. and Technol.*, ²*ACRO, Teikyo Univ.*, ³*Faculty of Design, Kyushu Univ.*, ⁴*Grad. Sch. of Pharmaceutical Sci., The University of Tokyo*, ⁵*Faculty of Medical Tech., Teikyo Univ.*)
- [3Pos090](#) 生細胞内における力伝播
Force propagation inside a living cell
Ayama Tokuyasu, Hirokazu Tanimoto (*Graduate School of Nanobioscience., Univ. Yokohama city*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

- [3Pos091](#) High Hydrostatic Pressure Regulates the TGF- β Signaling Pathway
Xinxuan Li (*Okayama University*)
- [3Pos092](#) 大腸菌のアレイブリンキングにおける活性伝搬の役割
The role of signal transduction in *E. coli* array blinking
Kaho Yoshinari, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka, Yumiko Uchida (*Grad. Sch. Frontier Biosci. Univ. Osaka*)
- [3Pos093](#) 大腸菌の走光性情報伝達の FRET 解析
Investigation of blue light-induced phototaxis in *Escherichia coli* using FRET
Satomi Itoki¹, Naoki Hidaka³, Ikuro Kawagishi^{1,2,3}, Yoshiyuki Sowa^{1,2,3} (¹*Grad. Frontier Biosci., Hosei Univ.*, ²*Res. Cent. Micro-nano Tech., Hosei Univ.*, ³*Dept. Frontier Biosci., Hosei Univ.*)
- [3Pos094](#) 環状心筋細胞ネットワーク中の伝導障害部位による伝導変化
Conduction Changes at Sites of Conduction Defects in Circular Cardiomyocyte Network
Moeno Furuya¹, Momo Akada², Tomoyuki Kaneko^{1,2} (¹*FB, Hosei Univ.*, ²*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)
- [3Pos095](#) 近赤外線レーザー光による周期刺激に対する心筋細胞の応答
Cyclic responses of cardiomyocytes induced by periodic near-infrared laser stimulation
Kanan Tominaga, Takaaki Nishikawa, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)
- [3Pos096](#) 心筋細胞と線維芽細胞を縞状に配置した心筋梗塞線維化モデル心筋細胞ネットワーク
Fibrotic heart model cardiomyocyte network with stripes of cardiomyocytes and fibroblasts
Yuna Honda, Kentaro Kito, **Tomoyuki Kaneko** (*LaRC, FB, Hosei Univ.*)
- [3Pos097](#) 環状心筋細胞ネットワークにおける発火起点からの細胞外電位の振幅の変化
Variation of Extracellular Potential Amplitude in Circular Cardiomyocyte Network from Active Firing Origin
Momo Akada, Kentaro Kito, Tomoyuki Kaneko (*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)
- [3Pos098](#) 高フレーム撮影による2つの心筋細胞の拍動同期解析
Analysis of two Cardiomyocytes beating synchronization with high-frame-rate imaging
Sasa Shimizu, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)
- [3Pos099](#) 近赤外線レーザー照射による心筋細胞のFPD評価
Variation in Field Potential Duration of cardiomyocytes induced by near-infrared laser irradiation
Yuka Motoyama, Tomoyuki Kaneko (*FB, Hosei Univ.*)
- [3Pos100](#) Single-molecule imaging analysis of mutual inhibition and positive feedback for Ras excitability in eukaryotic migrating cells
Satomi Matsuoka, Koji Iwamoto, Masahiro Ueda (*Grad. Sch. Frontier Biosciences, Univ. Osaka*)

- [3Pos101](#) 脂質凝集体の脂質分子パッキングに対するスクラロースとスクロースの効果の比較
Comparison of the effects of sucralose and sucrose on the lipid molecular packing in lipid aggregates
Yuki Homma, Hiroshi Takahashi (*Grad. sch. Sci. Tech. Gunma Univ.*)
- [3Pos102](#) ハイドロゲルで被覆されたモデル生体膜アレイ
Model membrane array sealed with a hydrogel layer
Masako Fujii¹, Kenichi Morigaki^{1,2} (¹*Grad. of Agri. Sci., Kobe Univ.*, ²*Biosignal Res. Ctr., Kobe Univ.*)
- [3Pos103](#) バイオフィルム脱離因子 Dspl が関連する膜リモデリングは緑膿菌バイオフィルムにおける細胞外小胞形成を誘発する
Membrane remodeling by a biofilm dispersion factor Dspl enhances vesicle formation in *Pseudomonas aeruginosa* biofilms
Mizuki Kanno¹, Hiroyuki Futamata^{1,2,3}, Yosuke Tashiro^{1,2} (¹*Grad. Sch. Sci. Tech., Shizuoka Univ.*, ²*Grad. Sch. Integr. Sci. Tech., Shizuoka Univ.*, ³*Res. Inst. Green Sci. Tech., Shizuoka Univ.*)
- [3Pos104](#) 人工膜とナノ空間を用いた生体分子・膜小胞解析技術の開発
Analyzing biomolecules and vesicles using model membranes and nanometric gap junction
Yu Yoshimura¹, Nanami Nagatsuka¹, Taisei Higashihara¹, Rinshi S. Kasai², Kenichi G.N. Suzuki^{2,3}, Kenichi Morigaki⁴ (¹*Grad. Sch. Agri., Kobe Univ.*, ²*National Cancer Center Japan*, ³*iGCORE., Gifu Univ.*, ⁴*Biosignal Research Center., Kobe Univ.*)
- [3Pos105](#) 粗視化分子動カモデルによる SARS-CoV-2 エンベロープ膜の構造と形成の探索
Exploring SARS-CoV-2 envelope structure and formation by coarse-grained molecular dynamics simulation
Ryo Urano, Wataru Shinoda (*Okayama Univ. RIIS*)

- [3Pos106](#) Curcumin and its derivatives modulate membrane domains and induce IL-6 receptor shedding in monocytes
Toshiyuki Murai¹, Yoshikazu Masaki², Kazuma Yasuhara² (¹*Grad. Sch. Med., Osaka Univ.*, ²*Grad. Sch. Sci. Tech., NAIST*)
- [3Pos107](#) 微細穴にマニピレートしたヒト培養細胞と基板支持脂質膜間の脂質移行の促進
Enhanced Lipid Transfer Between Micropore-Manipulated Human Cells and Supported Lipid Bilayers
Asahi Gono¹, Takayuki Nakaya², Reibun Sakane², Naoki Shimura², Takashi Okuno^{3,4} (¹*Grad. Sch. Sci., Univ. Yamagata*, ²*Orbray CO., Ltd.*, ³*Fac. Sci., Univ. Yamagata*, ⁴*CID, Univ. Yamagata*)
- [3Pos108](#) 反応拡散方程式に基づく真核細胞の小胞体におけるタンパク質ドメイン形成に関する数理モデル
Modeling the formation of protein domains on the endoplasmic reticulum in eukaryotic cells with reaction-diffusion equations
Tomoyo Nishigaki, Masashi Tachikawa (*Grad. Sch. of Nanobiosci., Yokohama City Univ.*)
- [3Pos109](#) 無細胞合成されたタンパク質における疎水領域の長さでアミノ酸配列が引き起こすリポソームのエンドサイトーシス様の分裂
Endocytosis-like fission of liposomes induced by the length of hydrophobic domains in cell-free synthesized proteins
Aika Yamamoto, Yuki Nagai, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

- [3Pos110](#) Development of a simple method for the reconstitution of ion channels using agarose gel beads
Mami Asakura^{1,2}, Kohta Takagi³, Miho Ohnishi³, Minako Hirano², Toru Ide² (¹*Dept. of Comp. Tech. Soln., Okayama Univ.*, ²*Grad. Sch. Health Sys., Okayama Univ.*, ³*Fac. Eng., Okayama Univ.*)
- [3Pos111](#) 脂質-オレオシン非対称膜小胞の内膜湾曲による機械刺激依存性チャネルを介した物質輸送
 Molecular transportation via mechanosensitive channel in response to membrane curvature of the asymmetric lipid-oleosin vesicles
Kotaro Baba, Koki Kamiya (*Grad. Sch. Sci & Tech, Gunma Univ.*)

- [3Pos112](#) 脂質膜で隔てられた DNA 振動子の結合に関する研究
 Coupling of DNA oscillators separated by lipid membranes
Kazumo Takahashi¹, Keita Abe¹, Hideaki Matsubayashi², Shinichiro Nomura¹, Ibuki Kawamata³, Satoshi Murata¹ (¹*Department of Robotics, Graduate School of Engineering, Tohoku University*, ²*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*, ³*Division of Physics, Graduate School of Science, Kyoto University*)
- [3Pos113](#) Membrane Translocation of Nucleic Acids via Cholesterol-modified DNA Hybridization
Rinka Aoki, Satoshi Murata, Hideaki Matsubayashi, Keita Abe, Shin-ichiro M. Nomura (*Grad. Sch. Eng., Univ. Tohoku*)

- [3Pos114](#) コレラ菌セロトニン走性受容体の同定および機能解析
 Identification and characterization of the serotonin chemoreceptor in *Vibrio cholerae*
Fuga Omori¹, Sotaro Asaoka¹, Hirotaka Tajima^{2,3}, Ikuro Kawagishi^{1,2,3} (¹*Grad. Sch. Sci. and Engin., Hosei Univ.*, ²*Fac. of Biosci. and Appl. Chem., Hosei Univ.*, ³*Res. Cent. for Micro-Nano Tech., Hosei Univ.*)

- [3Pos115](#) GPCR-mediated signaling in heat tolerance of *C. elegans*
Shiori Mototake^{1,2}, Yuki Sato^{1,2}, Kohei Ohnishi^{1,2,3}, Tohru Miura^{1,2,3}, Akane Ohta^{1,2,3}, Atsushi Kuhara^{1,2,3,4} (¹*Dept. Biol., Facul. Sci & Engineer. Konan Univ.*, ²*Dept. Biol. Grad. Sch. Sci. Konan Univ.*, ³*Inst. of Integral NeuroBiol. Konan Univ.*, ⁴*PRIME AMED*)
- [3Pos116](#) 培地中 Na⁺上昇による神経活動変化
 Neural Activity by Increasing Concentration of Sodium Ion in Culture Medium
Kaito Watanabe¹, Takumi Yamaguchi², Tomoyuki Kaneko^{1,2} (¹*LaRC.FB.Hosei Univ.*, ²*LaRC.FB.Grab.Sch.Sci.&Eng.,Hosei Univ.*)

- [3Pos117](#) The synaptic vesicle cluster restricts the diffusion of cytosolic α -Synuclein via boundary confinement
Kye Kudo¹, Adekunle T. Bademosi¹, S. Sean Millard², Frédéric A. Meunier^{1,2} (¹*Queensland Brain Institute, The University of Queensland*, ²*School of Biomedical Sciences, Faculty of Medicine, The University of Queensland*)

19. 神経回路・脳の情報処理 / 19. Neuronal circuit & Information processing

- [3Pos118](#) ヨーロッパモノアラガイの味覚嫌悪学習に関係する CGC の mGluR を介した抑制作用
 Metabotropic glutamate receptor-mediated inhibition of CGCs associated with conditioned taste aversion memory in *Lymnaea*
Yoshimasa Komatsuzaki¹, Samui Chiba¹, Ayaka Itoh², Ken Lukowiak³, Minoru Saito² (¹*Grad. Sch. Sci. and Tech, Nihon Univ.*, ²*Grad. Sch. Integ. Basic. Sci., Nihon Univ.*, ³*Univ of Calgary, Calgary*)
- [3Pos119](#) mGluR1 と GHS-R1a のクロストークによる小脳シナプス可塑性の制御
 Cross-talk between mGluR1 and GHS-R1a signaling modulates cerebellar synaptic plasticity
Moritoshi Hirono¹, Boyang Zhang¹, Hiroshi Hosoda², Masanori Nakata¹ (¹*Dept. Physiol., Wakayama Med. Univ.*, ²*Dept. Mol. Pathophysiol., Shinshu Univ.*)

20. 行動 / 20. Behavior

- [3Pos120](#) 流れ刺激に対するハルテリアの逃避遊泳行動
 Flow-induced escape behavior of *Halteria* sp.
Koki Kanda¹, Yukinori Nishigami^{1,2}, Takuya Ohmura^{1,2}, Katsuhiko Sato³, Toshiyuki Nakagaki^{1,2} (¹*Graduate School of Life Science, Hokkaido University*, ²*Research Institute for Electronic Science, Hokkaido University*, ³*Faculty of Science, University of Toyama*)

21A. 光生物：視覚・光受容 / 21A. Photobiology: Vision & Photoreception

- [3Pos121](#) Uncovering light-sensitive mechanism of non-visual opsins
Seiwa Nakamura¹, Asato Kojima¹, Kazuhiro Kobayashi², Masahiro Fukuda², Koki Kawakami², Suhyang Kim², Takashi Nagata³, Kota Katayama^{4,5}, Hideki Kandori^{4,5}, Keiichi Inoue³, Hideaki E. Kato^{2,6} (¹*Grad. Sch. Art. Sci., Univ. Tokyo*, ²*RCAS, Univ. Tokyo*, ³*ISSP, Univ. Tokyo*, ⁴*Life Sci. Appl. Chem., Grad. Sch. Eng., Nagoya Inst. Tech.*, ⁵*OptoBio Tech. Res. Cent.*, ⁶*Grad. Sch. of Sci, Univ. Tokyo*)

- 3Pos122** A Structural Approach to the Potassium-Selective Channelrhodopsin HcKCR1 for Its Development as an Optogenetic Tool
Seiya Tajima¹, Seiwa Nakamura², YoungJu Jo^{3,4}, Joseph J. Noh^{3,5}, Peter Y. Wang³, Antonia Drinnenberg³, Chelsea Li³, Masatoshi Inoue³, Masaki Tsujimura⁶, Eamon F. X. Byrne³, Thanh-Nga C. Shenoy³, Sung-Soo Jang⁷, Ki Eun Pyo³, Nadya Andini³, Jenny Shi³, Kishandra A. Patron³, Joseph M. Paggi⁸, Masahiro Fukuda¹, Yuma Ito⁹, Masahiro Sugiura⁹, Kota Katayama^{9,10}, Yuji Furutani^{9,10}, Hisako Ikeda¹, Charu Ramakrishnan¹¹, Linlin Z. Fan³, Sean Quirin³, Hiroshi Ishikita^{1,6}, John R. Huguenard⁷, Hideki Kandori^{9,10}, Ron O. Dror^{5,8,12}, Yoon Seok Kim³, Karl Deisseroth^{3,11,13}, Hideaki E. Kato^{1,2,14} (¹RCAST, Univ. Tokyo, ²Grad. Sch. Arts. Sci., Univ. Tokyo, ³Dept. Bioeng., Stanford Univ., ⁴Dept. Appl. Phys., Stanford Univ., ⁵Biophys. Prog., Stanford Univ., ⁶Grad. Sch. Eng., Univ. Tokyo, ⁷Dept. Neurol. & Neurol. Sci., Stanford Univ., ⁸Dept. Comput. Sci., Stanford Univ., ⁹Dept. Life Sci. & Appl. Chem., Nagoya Inst. Technol., ¹⁰OptoBioTechnology Research Center, Nagoya Inst. Technol., ¹¹CNC Prog., Stanford Univ., ¹²Inst. Comput. Math. Eng., Stanford Univ., ¹³Dept. Psychiatry & Behav. Sci., Stanford Univ., ¹⁴Grad. Sch. Sci., Univ. Tokyo)
- 3Pos123** 低温ラマン分光法による Cl⁻ポンプロドプシン(*Mastigocladopsis repens* 由来)の発色団構造変化の解明
 Cryogenic Raman Study of Chromophore Structural Changes during the Photocycle of a Light-Driven Cl⁻ Pump from *Mastigocladopsis repens*
Kana Miyazaki¹, Takashi Kikukawa², Masashi Unno¹, Tomotsumi Fujisawa¹ (¹Fac. Sci. Eng., Saga Univ., ²Fac. Adv. Life Sci., Hokkaido Univ.)
- 3Pos124** 細胞性粘菌の発生と細胞骨格に対するレチナールの影響
 Effect of retinal on development and cytoskeleton in *D. discoideum*
Shuhei Tsuchihashi¹, Kazuki Akiyama¹, Yusuke V. Morimoto² (¹Grad. Sch. Comput. Sci. Syst. and Eng., Kyushu Inst. Tech., ²Grad. Sch. Comput. Sci. Syst. and Eng., Kyushu Inst. Tech.)
- 3Pos125** 有機溶媒中における微生物ロドプシンの物理化学的特性の解析
 Comparative analysis of the physicochemical properties of microbial rhodopsins in organic solvents
Miyu Inokuchi¹, Keiichi Kojima², Yuki Sudo² (¹Grad. Sch. Med. Dent. & Pharm. Sci., Okayama Univ., ²Fac. Med, Dent & Pharm Sci., Okayama Univ.)
- 3Pos126** 微生物ロドプシンによる光駆動型有機アニオン輸送の発見
 Discovery of light-powered organic anion transport by microbial rhodopsins
 Simiao Shen¹, Kaisei Ohno², Takashi Tsukamoto^{1,2,3}, Kwang-Hwan Jung⁴, Yuki Sudo⁵, **Takashi Kikukawa**^{1,2,3} (¹Grad. Sch. Life Sci., Hokkaido Univ., ²Sch. Sci., Hokkaido Univ., ³Fac. Adv. Life Sci., Hokkaido Univ., ⁴Dept. Life Sci. & Bionano Cent., Sogang Univ., ⁵Fac. Med., Dent. & Pharm. Sci., Okayama Univ.)
- 3Pos127** 一分子蛍光 in situ hybridization 法によるメダカ組織におけるオプシン発現細胞の解析
 Single-Molecule FISH Analysis of Opsin-Expressing Cells in Medaka
Keita Sato, Hideyo Ohuchi (Fac. Med, Dent & Pharm Sci., Okayama Univ.)
- 3Pos128** Light Intensity-Dependent Reaction Dynamics of the Photoresponsive Enzyme MsLadC
Dai Takeuchi, Masahide Terazima, Yusuke Nakasone (Grad. Sch. Sci., Kyoto Univ.)
- 3Pos129** センサリーロドプシン II (SRII) からトランスデューサー (HtrII) への情報伝達におけるシグナリング中間体の同定
 Identification of signaling states of sensory rhodopsin II (SRII) in the signal transduction to its cognate transducer protein (HtrII)
Jun Tamogami¹, Miki Takeguchi¹, Risa Matsunami-Nakamura¹, Takashi Kikukawa², Naoki Kamo², Toshifumi Nara¹ (¹College Pharm. Sci., Matsuyama Univ., ²Fac. Adv. Life Sci., Hokkaido Univ.)

- [3Pos130](#) 高速原子間力顕微鏡を用いた植物光合成膜におけるタンパク質複合体のダイナミクス解析
Analysis of protein complex dynamics in plant photosynthetic membranes by high-speed atomic force microscopy
Yudai Nishitani, Daisuke Yamamoto (*Fac. Sci., Fukuoka Univ.*)
- [3Pos131](#) 機械学習を用いた光合成タンパク質複合体における環境適応アミノ酸残基の推定
Estimating environmentally adaptive residues in photosynthetic complexes using machine learning
Atsushi Hijikata¹, Ryuhei Minei², Satoshi Omori², Yuko Tsuchiya³, Tsuyoshi Shirai² (¹*Tokyo Univ. of Pharm. Life Sci.*, ²*Nagahama Inst. Bio-Sci. Tech.*, ³*AIST*)
- [3Pos132](#) 暗発酵および光発酵による最適化
Optimization by dark and photo fermentation
Masahiro Hibino, Kousei Miyamoto (*Div. Sust. Enviro. Eng., Muroran Inst. Tech.*)
- [3Pos133](#) 光合成タンパク質超複合体の空間分解分光にむけた超解像吸収顕微鏡の開発
Super-resolution absorption microscopy toward spatially-resolved spectroscopy of photosynthetic protein supercomplexes
Yoshihiro Tojo^{1,2}, Tomomi Inagaki³, Chihiro Azai⁴, Toru Kondo^{2,5} (¹*Dept. of Life Sci. Tech., Science Tokyo*, ²*NIBB*, ³*Grad. Sch. of Life Sciences, Ritsumeikan Univ.*, ⁴*Grad. Sch. of Sci. Eng., Chuo Univ.*, ⁵*ExCELLS*)
- [3Pos134](#) 網羅的単一分子分光を用いた光阻害修復途上光化学Ⅱの観測
Observation of photosystem II under repair from photoinhibition by exhaustive single-molecule spectroscopy
Kyosuke Watanabe, Shen Ye, Yutaka Shibata (*Graduate school of science, Tohoku Univ.*)
- [3Pos135](#) Localization of auxiliary proteins of LHC assembly during its insertion into thylakoid membrane
Yuiki Shimamura¹, Hiroshi Kuroda², Yuichiro Takahashi², Shen Ye³, Yutaka Shibata³ (¹*Grad. Sch. Sci., Tohoku Univ.*, ²*Research Institute for Interdisciplinary Science, Okayama University*, ³*Grad. Sch. Sci., Tohoku Univ.*)
- [3Pos136](#) 重合脂質膜鑄型法による再構成チラコイド膜のタンパク質込み合いの評価
Evaluation of protein crowding in reconstituted thylakoid membrane supported by polymerized lipid membranes
Hayata Sakai¹, Koki Takagi², Kenichi Morigaki³, Shen Ye¹, Yutaka Shibata¹ (¹*Graduate School of Science Tohoku Univ.*, ²*Agricultural Science, Graduate School of Kobe Univ.*, ³*Graduate School of Biosignal Reserch Center Kobe Univ.*)
- [3Pos137](#) 一分子時間分解蛍光分光測定による光合成光捕集アンテナ複合体のエネルギー移動解析
Single-molecule time-resolved fluorescence spectroscopy of energy transfer in photosynthetic antenna complex
Shinnosuke Masuda^{1,2,3}, Mai Watanabe⁴, Toru Kondo^{1,2,3} (¹*SOKENDAI*, ²*NIBB*, ³*ExCELLS*, ⁴*Dept. of Science, Tokyo Metropolitan Univ.*)

3Pos138 *Oscillatoria acuminata* 由来の光活性化アデニル酸シクラーゼの C 末端領域による活性制御機構の解明

The role of the C-terminal region in regulating the activity of the photoactivated adenylyl cyclase from *Oscillatoria acuminata*

Reito Yasui¹, Masahiko Taguchi^{2,3}, Syun Sakuraba^{4,5}, Masumi Takebe⁶, Saiko Akizuki¹, Mami Asakura^{1,7}, Akiya Hukuda², Eriko Nango^{2,3,8}, Hidetoshi Kono^{4,5}, Toru Ide¹, Minako Hirano¹
(¹Graduate School of Interdisciplinary Science and Engineering in Health Systems, Okayama University, ²Graduate School of Science, Tohoku University, ³Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, ⁴Institute for Quantum Life Science, National Institutes for Quantum Science and Technology, ⁵Center of Quantum Life Science for Structural Therapeutics, Chiba University, ⁶Hamamatsu Photonics K.K., ⁷Dept. of Comp. Tech. Soln., Okayama Univ., ⁸International Center for Synchrotron Radiation Innovation Smart, Tohoku University)

3Pos139 光活性化アデニル酸シクラーゼの活性調節機構の解明

Regulatory mechanism of photoactivated adenylyl cyclase activity

Hinase Kondo¹, Masahiko Taguchi^{2,3}, Syun Sakuraba^{4,5}, Masumi Takebe⁶, Koki Shimomae¹, Mei Kawamoto¹, Mami Asakura^{1,7}, Akiya Hukuda², Eriko Nango^{2,3,8}, Hidetoshi Kono^{4,5}, Toru Ide¹, Minako Hirano¹ (¹Grad. Sch. Health Sys., Okayama Univ., ²Graduate School of Science, Tohoku Univ., ³IMRAM, Tohoku Univ., ⁴iQLS, QST, ⁵cQUEST, Chiba Univ., ⁶Hamamatsu Photonics K.K., ⁷Dept. of Comp. Tech. Soln., Okayama Univ., ⁸SRIS, Tohoku Univ.)

3Pos140 リジン主鎖同位体標識ロドプシンの赤外分光解析

FTIR Analysis of microbial rhodopsins with ¹⁵N-labeled lysine backbone

Mako Ooka¹, Tatsuro Nishikino^{1,2}, Teppei Sugimoto¹, Yuma Ito¹, Yuji Furutani^{1,2}, Hideki Kandori^{1,2}
(¹Graduation school of Engineering, Nagoya institute of technology, ²OptoBio Technology Research Center, Nagoya institute of technology)

3Pos141 低温赤外分光法によるウイルス由来カチオンチャネルロドプシンの構造解析

Structural analysis of viral cation channelrhodopsin using low-temperature FTIR spectroscopy

Mako Aoyama¹, Kota Katayama^{1,2}, Hideki Kandori^{1,2} (¹Grad. Sch. Eng., Nagoya Inst. Tech., ²Nagoya Inst. Tech., OptoBioTechnology Research Center)

3Pos142 短波長応答チャネルロドプシン KnChR の分子機能

Unraveling the Functional Mechanism of KnChR: A Short-Wavelength Absorbing Cation Channelrhodopsin

Satoshi Tsunoda^{1,2}, Koki Natsume¹, Yuzhu Wang³, Tatsuki Tanaka³, Shoko Hososhima^{1,2}, Wataru Shihoya⁴, Osamu Nureki³, Hideki Kandori^{1,2} (¹Grad. Sch. Eng., Nagoya Institute of Technology, ²OptoBio Technology Research Center, Nagoya Institute of Technology, ³Grad. Sch. Sci., The University of Tokyo, ⁴Keio University School of Medicine)

3Pos143 Photocontrol of GTPase Cycle of the small G-protein H-Ras using its regulator RASGRF1 with photochromic molecular devices

Isra Lilatul, Nobuyuki Nishibe, Shinsaku Maruta (Grad.Sch.Sci.Eng., Univ.Soka)

23. 生命の起源・進化／23. Origin of life & Evolution

3Pos144 ペプチド液滴による原始的な自己区画の確立

Establishment of Primitive Self-Compartments with Peptide-Droplets

Yota Tabata, Tomoyuki Kaneko (FB, Grad. Sch. Sci. & Eng., Hosei Univ.)

- [3Pos145](#) ベイズ学習と統計力学による進化の理論：タンパク質を例に
An Evolutionary Theory Based on Bayesian Learning and Statistical Mechanics: The Case of Proteins
Tomoei Takahashi¹, George Chikenji², Kei Tokita³, Yoshiyuki Kabashima¹ (¹*Inst. for Physics of Intelligence, Grad. Sch. of Sci., The Univ. of Tokyo*, ²*Grad. Sch. of Eng., Nagoya Univ.*, ³*Grad. Sch. of Inf., Nagoya Univ.*)
- [3Pos146](#) 微生物進化実験を用いた進化可能性ランドスケープと増殖-死滅トレードオフの定量
Quantifying Evolutionary Landscapes and the Growth-Death Trade-off in Microbial Experimental Evolution
Atsushi Shibai¹, Riku Kamiura¹, Shumpei Sato¹, Shigeyuki Kakizawa³, **Chikara Furusawa**^{1,2} (¹*BDR, RIKEN*, ²*UBI, Univ. Tokyo*, ³*AIST*)

24. 合成生物学・人工細胞 / 24. Synthetic biology & Artificial cells

- [3Pos147](#) ミニマル合成細菌 syn3B のゲノムサイレンシング
Silencing a genome of minimal synthetic bacterium syn3B
Hana Kiyama¹, Sohkiichi Matsumoto², Makoto Miyata^{1,3} (¹*Grad. Sch. Sci., Osaka Metropolitan Univ.*, ²*Grad. Sch. Med., Niigata Univ.*, ³*OCARINA, Osaka Metropolitan Univ.*)
- [3Pos148](#) ミニマル合成細菌 syn3B のゾンビと生き返り
Zombie cells and revival of minimal synthetic bacterium syn3B
Nanase Oda¹, Hana Kiyama¹, Yuhei O Tahara^{1,2}, Masaki Mizutani³, Shigeyuki Kakizawa⁴, Makoto Miyata^{1,5} (¹*Grad. Sch. Sci., Osaka Metropolitan Univ.*, ²*Grad. Sch. Eng., Osaka Metropolitan Univ.*, ³*Dept. Phys., Gakushuin Univ.*, ⁴*MolBiS, AIST*, ⁵*OCARINA, Osaka Metropolitan Univ.*)
- [3Pos149](#) Myosin distribution and the deformation and behavior of the droplets formed by phase separation
Tatsuyuki Waizumi¹, Hiroki Sakuta², Mahito Kikumoto¹, Kanta Tsumoto³, Kingo Takiguchi¹, Kenichi Yoshikawa⁴ (¹*Grad. sch. Sci., Univ. Nagoya*, ²*Grad. Sch. Arts and Sci., Univ. Tokyo*, ³*Grad. Sch. Eng., Univ. Mie*, ⁴*Sci Ctr. Self-Organization., Univ. Doshisha*)
- [3Pos150](#) Scalable preparation of GUVs using freeze-dried gelatin gel
Takumi Furusawa¹, Keita Abe¹, Hideaki Matsubayashi², Satoshi Murata¹, Shin-Ichiro Nomura¹, Richard James Archer³ (¹*Department of Robotics, Graduate School of Engineering, Tohoku University*, ²*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*, ³*Department of Computer Science, School of Computing, Institute of Science Tokyo*)
- [3Pos151](#) 巨大リボソーム内でのクラミドモナスの片腕変異株の運動解析
Motion Analysis of Uniflagellate *Chlamydomonas* Mutants inside Giant Liposomes
Yuka Matsukawa¹, Koichiro Akiyama², Masahito Hayashi³, Tomoyuki Kaneko^{1,2} (¹*LaRC, FB, Hosei Univ.*, ²*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ.*, ³*Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.*)
- [3Pos152](#) クラミドモナス封入リボソームの運動能力の解明に向けた微小物質の共封入
Co-encapsulation of Micro-objects in *Chlamydomonas*-Encapsulated Liposomes for Motility Characterization
Hiromasa Shiraiwa¹, Koichiro Akiyama¹, Shunsuke Shiomi¹, Masahito Hayashi^{1,2}, Tomoyuki Kaneko¹ (¹*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ.*, ²*Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.*)
- [3Pos153](#) リン脂質添加による細胞モデル液滴の界面張力変化
Interfacial Tension Changes of Cell-Mimicking Droplets Induced by Phospholipid Addition
Sota Miura, Koichiro Sadakane (*Grad. Sch. Life and Med Sci., Doshisha Univ.*)
- [3Pos154](#) Insights into Gel-in-Giant Unilamellar Vesicle System as Artificial Cell Model
Wancheng Zhang¹, Aileen Cooney², Lorenzo Di Michele³, Yuval Elani², Tomoaki Matsuura¹ (¹*Earth-Life Science Institute, Institute of Science Tokyo*, ²*Department of Chemical Engineering, Imperial College London*, ³*Department of Chemical Engineering and Biotechnology, University of Cambridge*)

- [3Pos155](#) PEG/DEX 系における相分離に対するリン脂質・界面活性剤等の影響：光散乱測定を用いた解明
Effects of Phospholipids, Surfactants, etc. on Phase Separation in PEG/DEX Systems:
Elucidation Using Light Scattering
Ryuya Bamba, Koichiro Sadakane (*Grad. Sch. Life and Med Sci., Doshisha Univ.*)

25. ゲノム生物学／25. Genome biology

- [3Pos156](#) 膜タンパク質の膜—内外領域における同義コドン使用頻度解析：原核—真核生物の比較
Synonymous Codon Usage Comparison in Membrane Protein Inner/Extra transmembrane
Regions Between Prokaryotes and Eukaryotes
Riki Haida¹, Makiko Suwa^{1,2}, Kenji Etchuya² (¹*Biological Science Course, Graduate School of Science
and Engineering, Aoyama Gakuin University, Kanagawa, Japan*, ²*Chem. Biological Science Course,
Department. Science and Engineering, Aoyama Gakuin University, Kanagawa, Japan*)

26A. 計算生物学: 生命情報学／26A. Computational biology: Bioinformatics

- [3Pos157](#) Evaluating Protein Generative AI for Exploring Uncharted Sequence Space
Hafumi Nishi^{1,2,3} (¹*Grad. Sch. Info. Sci., Tohoku Univ.*, ²*Fac. Core. Res. Ochanomizu Univ.*, ³*ToMMo,
Tohoku Univ.*)
- [3Pos158](#) Structure prediction of protein complexes using cross-linking mass-spectrometry data with the
estimated error rate
Hiroto Matsubara, Takaharu Mori (*Tokyo University of Science*)
- [3Pos159](#) EpiLoop：説明可能なグラフ・トランスフォーマーによる細胞特異的クロマチンループのストラ
イプ型／ドット型識別と分類
EpiLoop: explainable graph transformer for identifying and classifying cell-specific chromatin
loops into stripe or dot structures
Bingxin Xie^{1,2}, Yuichi Taniguchi^{1,2,3} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*CeMS, Kyoto Univ.*, ³*Inst.
for Advanced Study, Kyoto Univ.*)
- [3Pos160](#) 金属イオン結合部位を予測する機械学習モデルの開発
Development of Machine Learning Models for Predicting Metal Ion-binding Sites
Yamato Maehara, **Masafumi Shionyu** (*Grad. Sch. Biosci. Nagahama Inst. Bio-Sci. and Tech.*)
- [3Pos161](#) アルツハイマー病特異的タウ線維構造の Inverse folding
Inverse folding of Alzheimer disease-specific tau filaments
Motoharu Tajitsu¹, Maria Kano², Taeko Kimura², Sakura Homma¹, Taisuke Tomita²,
Yasuhiro Matsunaga^{1,3} (¹*Grad. Sch. Sci. Eng., Saitama Univ.*, ²*Grad. Sch. Pharm. Sci., Tokyo Univ.*,
³*RIKEN*)
- [3Pos162](#) 環境変化と損傷に対するロバストネスの進化
Evolution of Robustness to Environmental Change and Damage
Mao Sakae (*Ritsumeikan LifeScience*)
- [3Pos163](#) The Impact of Environmental Factors on the Predatory Behavior of Marine Organisms
Haruki Kawakami (*Ritsumeikan university*)
- [3Pos164](#) 深層学習を用いた筋小胞体形態と Ca²⁺濃度の関係の解析
Analysis of the relationship between sarcoplasmic reticulum morphology and Ca²⁺ concentration
using deep learning
Katsuya Saito¹, Kenji Etchuya², Jun Nakamura³, Chikara Sato^{1,3,4,5}, Makiko Suwa^{1,2} (¹*Biol. Sci., Grad.
Sch. Sci. Eng., Aoyama Gakuin Univ.*, ²*Chem. Biol. Sci., Dept. Sci. Eng., Aoyama Gakuin Univ.*, ³*Natl.
Inst. Adv. Ind. Sci. Techno. (AIST)*, ⁴*Div. Immune Homeostasis, Dept. Pathol. Microbiol., Nihon Univ.*
Sch. Med., ⁵*Div. Microbiol., Dept. Pathol. Microbiol., Nihon Univ. Sch. Med.*)

- [3Pos165](#) スクレオチドリン酸の長時間結合は細胞質中の蛋白質間相互作用を抑制する
Prolonged Bindings of Nucleoside Triphosphates Reduces Protein-Protein Interaction in Cytoplasm
Isseki Yu¹, Michael Feig², Yuji Sugita³ (¹*Maebashi Institute of Technology*, ²*Michigan State Univ.*, ³*Riken*)
- [3Pos166](#) 光応答性膜モジュレータ分子の分子動力学シミュレーション
Molecular Dynamics of Light-Responsive Twistable Membrane Modulators
Reo Kadowaki¹, Huo Wenting², Koji Miki², Kouichi Ohe², Wataru Shinoda³ (¹*Grad. Sch. Env. Life and Nat. Sci., Univ. Okayama*, ²*Grad. Sch. Eng. Sci., Univ. Kyoto*, ³*Res. Inst. Interdiscip. Sci., Univ. Okayama*)
- [3Pos167](#) Binding free energy shift of Barnase-Barstar complex due to single and double mutations
Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)
- [3Pos168](#) Molecular Dynamics Study of Potential Inhibitors Targeting VP28 from White Spot Syndrome Virus in Tiger Shrimp
Fachruddin Hari Anggara Putera, Kazutomo Kawaguchi, Hidemi Nagao (*Graduate School of Natural Science and Technology, Kanazawa University*)
- [3Pos169](#) MD シミュレーションによる脂質フリッパーゼ MurJ の構造変化とイオン相互作用の解析
Analysis of Structural Changes and Ion Interactions of the Lipid Flippase MurJ by Molecular Dynamics Simulations
Keina Murata, Takaharu Mori (*Tokyo Univ. of Science*)
- [3Pos170](#) Investigation of the Reason Why Ornithine Was Excluded from the Proteinogenic Amino Acids by Quantum Chemical Calculations
Ayato Mizuno¹, Tomoki Nakayoshi^{1,2}, Koichi Kato^{1,3}, Akifumi Oda^{1,4} (¹*Grad. Sch. Pharm., Meijo Univ.*, ²*Inst. Adv. Res., Nagoya Univ.*, ³*Fac. Pharm. Sci., Shonan Univ. Med. Sci.*, ⁴*Inst. Protein Res., Osaka Univ.*)
- [3Pos171](#) MD 計算によるタンパク質透過チャネル SecY と分泌モニタータンパク質 VemP との相互作用解析
Elucidating the interactions between the protein-conducting channel SecY and translocating VemP via steered MD simulations
Shunsuke Muraoka¹, Hiroyuki Mori², Takaharu Mori¹ (¹*Tokyo University of Science*, ²*Kyoto University*)
- [3Pos172](#) 分子動力学シミュレーションによる HaloKbp1a₆₃₅ 蛍光タンパク質の理論研究
Theoretical Study of HaloKbp1a₆₃₅ Fluorescence Protein Sensor by Molecular Dynamics Simulations
Natthanan Kongchu, Shigehiko Hayashi (*Grad. Sch. Sci., Kyoto Univ.*)
- [3Pos173](#) Analysis of water dynamics around antifreeze proteins by molecular dynamics simulations
Shinnosuke Nakamura¹, Nao Abe¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)
- [3Pos174](#) カーボンドットとがん細胞膜脂質との相互作用に関する Steered 分子動力学シミュレーション
Steered Molecular Dynamics Study of Carbon Dot Interactions with Cancer Cell Membrane Lipids
Atsunori Yuki (*Grad. Sch. Bioinformatics, Ritsumeikan University, Shiga*)
- [3Pos175](#) 水中およびクロロホルム中における鎖状と環状のグリシンペプチドに関する立体構造集団解析
Conformational ensembles of linear and cyclic glycine peptides in water and chloroform
Koji Umezawa^{1,2}, Yoshiyuki Yamaoka¹, Yuzuki Takase¹, Rei Kitajima¹, Jumpei Morimoto³, Shinsuke Sando³ (¹*Agri., Shinshu Univ.*, ²*Grad. Sch. of Sci. & Tech., Shinshu Univ.*, ³*Grad. Sch. of Eng., Univ. of Tokyo*)

- [3Pos176](#) Thermal Modulation of NOMPC Gating Springs in *Aedes aegypti*: Insights from Comparative Modeling and MD Simulations
Roberto Carlos Pestana Nobles¹, Martin Pavlovich¹, YuMin M. Loh^{1,2}, Matthew P. Su^{1,2,3}, Azusa Kamikouchi^{1,2}, Osamu Miyashita⁴, Florence Tama^{1,2,4} (¹*Institute of Transformative Bio-Molecules (ITbM), Nagoya University, Nagoya, Japan*, ²*Graduate School of Science, Nagoya University, Nagoya, Japan*, ³*Institute for Advanced Research, Nagoya University, Nagoya, Japan*, ⁴*RIKEN Center for Computational Science, Kobe, Hyogo, Japan*)
- [3Pos177](#) Analysis of the Interconversion Mechanisms of “CO-in” and “CO-out” Conformations of Ferredoxin Using Molecular Dynamics Simulations
Tomoki Nakayoshi^{1,2,3}, Yusuke Ohnishi^{4,5}, Hideaki Tanaka⁵, Genji Kurisu⁵, Akifumi Oda¹, Yu Takano² (¹*Fac. Pharm., Meijo Univ.*, ²*Inst. Adv. Res., Nagoya Univ.*, ³*Grad. Sch. Inf. Sci., Hiroshima City Univ.*, ⁴*Core Facility Center, Univ. Osaka*, ⁵*Inst. Protein Res., Univ. Osaka*)
- [3Pos178](#) Distinct Structural Responses of CRY1 and CRY2 to Small Molecule Binding: A Coarse-Grained Molecular Dynamics Simulation Study
Ajeet Kumar Yadav¹, Florence Tama^{1,2,3} (¹*Department of Physics, Nagoya University*, ²*ITbM, Nagoya University*, ³*Riken Center for Computational Science*)
- [3Pos179](#) Multiscale modeling of spatiotemporal heterogeneity in biomolecular condensates
Eiji Yamamoto¹, Kento Fujita², Yusuke Takagi², Youtaro Takeda² (¹*Dept. Sys. Des. Eng., Keio Univ.*, ²*Grad. Sch. Sci. Tech., Keio Univ.*)
- [3Pos180](#) High-throughput virtual screening and *de novo* design of functionalised nanographenes targeting the FAD binding site of CRY clock proteins
Ben Cree¹, Manami Hayashi², Masaya Hagai², Kazuhiro J. Fujimoto², Hideya Kono⁴, Kazuma Amaike⁴, Takeshi Yanai^{2,3}, Kenichiro Itami⁴, Florence Tama^{1,2,3} (¹*Computational Structural Biology Research Team, RIKEN R-CCS*, ²*Graduate School of Science, Nagoya University*, ³*Institute of Transformative BioMolecules, Nagoya University*, ⁴*Molecule Creation Laboratory, RIKEN*)
- [3Pos181](#) Temperature-Dependent Conformational Changes of Dengue Virus Envelop protein
Dokainish Hisham, Yoshimasa Takahashi (*Research Center for Vaccine Development, NIID, Japan Institute for Health Security*)
- [3Pos182](#) シスチン/グルタミン酸アンチポーター xCT 輸送体の基質輸送過程の分子シミュレーション
Molecular Simulation of Substrate Transport Mechanisms in the Cystine/Glutamate Antiporter xCT
Ikumi Mizuno, Kei Moritsugu (*Grad. Sch. Sci., OMU*)
- [3Pos183](#) ALS における SOD1 の構造動態・金属結合部位の反応性・毒性機構に関する理論的解析
Computational Insights into SOD1 Conformational Dynamics, Metal Site Reactivity, and Toxic Mechanisms in ALS
Shun Fujimaki¹, Shinya Tahara², Takakazu Nakabayashi², Norifumi Yamamoto¹ (¹*Chiba Tech.*, ²*Tohoku Univ.*)
- [3Pos184](#) D30N/L90M 変異を持つ HIV-1 プロテアーゼにおける薬剤耐性メカニズムの解明：残基間相互作用ネットワーク解析
Unveiling Drug Resistance Mechanisms in HIV-1 Protease with D30N and L90M Mutations: Residue Interaction Network Analysis
Keidai Yamase (*Chiba Tech*)
- [3Pos185](#) D2-L29/卵白リゾチーム複合体の変異による親和性向上メカニズム
Molecular Dynamics Elucidation of Mutation-Induced Affinity Enhancement in the D2-L29 VHH/ Hen Egg Lysozyme Complex
Rika Munakata, Motoki Inoue, Takefumi Yamashita (*Univ. Hoshi*)

26C. 計算生物学：生体モデリングとシミュレーション／
26C. Computational biology: Biological modeling and simulation

- [3Pos186](#) ニューラルネットワークを用いた溶液系の adaptive QM/MM 法の改善
Enhancement of Adaptive QM/MM Approaches for Solution-Phase Systems via Neural Networks
Hiroshi Watanabe, Takuma Ikeda, Haruyuki Nakano (*Dep. Chem., Fac. Sci., Kyushu Univ.*)
- [3Pos187](#) Engineering Epithelial Layer Structures via Cell Surface Tension Using a 3D Vertex Model
Chayanit Thitichareontam¹, Satoru Okuda² (¹*Division of Nano Life Science, Kanazawa University*,
²*WPI Nano Life Science Institute, Kanazawa University*)
- [3Pos188](#) Discovery of novel inhibitor candidate compounds using accurate *in silico* screening protocol
Hiroto Terada, Kei Moritsugu (*Grad. Sch. Sci., OMU*)
- [3Pos189](#) Structural dynamics analysis of actin filament formation using molecular dynamics simulation
Kenta Omoto (*Grad. Sch. Sci., OMU*)

27. 数理生物学・理論生物学／27. Mathematical & Theoretical biology

- [3Pos190](#) 変動環境下での代謝恒常性を支える Bowtie 型代謝ネットワーク
Bowtie-Structured Metabolic Networks Maintain Homeostasis under Fluctuating Environments
Yudai Iyoda¹, Chikara Furusawa^{1,2}, Yusuke Himeoka¹ (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*BDR, Riken*)
- [3Pos191](#) 一細胞と組織における力学応答の矛盾を統合する張力ホメオスタシスモデルの構築
Tension homeostasis model integrating contradictory mechanical responses in a single cell and tissues
Yoshihito Sawazaki¹, Yohei Kondo², Naoki Honda^{1,2} (¹*Grad. Sch. Integr. Life Sci., Univ. Hiroshima*,
²*Grad. Sch. med., Univ. Nagoya*)
- [3Pos192](#) 代謝動力学モデルを用いた細胞の低温ストレス応答解析
Analysis of Cellular Responses to Cold Stress Using a Metabolic Kinetics Model
Atsuki Hishida¹, Yusuke Himeoka², Chikara Furusawa^{2,3} (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*Univ. Biol. Inst., Grad. Sch. Sci., Univ. Tokyo*, ³*BDR., Riken*)
- [3Pos193](#) 液滴勾配による遺伝子誘導の数理モデル
Gene Guidance by Droplet Gradients: A Theory
Takeshi Sugawara (*Center for Data Science, Kochi Univ.*)

29. 非平衡・生体リズム／29. Nonequilibrium state & Biological rhythm

- [3Pos194](#) 回帰的な無機膜ダイナミクスで歩行するソフトロボット
A Walking Soft Robot Actuated by Recursive Inorganic Membrane Dynamics
Ryusei Kubota, Muneyuki Matsuo (*Graduate School of Integrated Sciences for Life, Hiroshima University*)
- [3Pos195](#) 擬二次元環境下における繊毛虫テトラヒメナの疎密波形成と伝播
Formation and propagation of the density wave by Ciliate *Tetrahymena* under a Quasi-2D Environment
Ryuhei Itoh¹, Kohei Okuyama¹, Ibuki Kawamata¹, Marie Tani¹, Akira Kakugo¹, Masatoshi Ichikawa^{1,2}
(¹*Grad. Sch. of Sci., Kyoto Univ.*, ²*Grad. Sch. Integr. Sci. Life, Hiroshima Univ.*)

- [3Pos196](#) Development of a Micro-Acoustic Resonator for Micro-Rheological Measurement of Biomolecular Condensates
Taichi Yoshikawa, Hirotsugu Ogi, Kichitaro Nakajima (*Graduate School of Engineering, Osaka University*)
- [3Pos197](#) 光学的手法を用いた選択的 DNA 増幅技術の開発
 Development of selective DNA amplification technology by optical method
Ren Saito¹, Hironori Sugiyama³, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Dep. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, ²*RIPH., Univ. Tokyo*, ³*ELSI., Science Tokyo*)
- [3Pos198](#) 硫酸アンモニウム混合液で加工したナノポアを用いた高解像度一分子構造解析
 High-resolution single-molecule structural analysis of nanopore sensing using ammonium sulfate assisted fabrication
Wataru Tsuchiya¹, Lin Liu², Kyosuke Matsuda¹, Fan-Yan Wei³, Hirohito Yamazaki⁴ (¹*Grad. Mech., Nagaoka Univ. of Tech.*, ²*Grad. Sch. Med., Tohoku Univ.*, ³*IDAC, Tohoku Univ.*, ⁴*Mech., Nagaoka Univ. of Tech.*)
- [3Pos199](#) Vibrational relaxation process of flavin compounds measured by resonance IR method
Minori Yamakawa¹, Hirona Takahashi^{1,2}, Konoka Mifune¹, Makoto Sakai^{1,2} (¹*Graduate School of Science and Engineering, Okayama University of Science*, ²*Faculty of Science, Okayama University of Science*)
- [3Pos200](#) Design of nanodiamonds for subcellular thermal manipulation
Daisuke Watanabe¹, Yoshie Harada^{1,2} (¹*WPI-PRIME, Univ. Osaka*, ²*QIQB, Univ. Osaka*)
- [3Pos201](#) 液性相分離を用いたオイルフリーデジタルバイオアッセイ
 Oil-free Digital Bioassay with Aqueous Two-Phase Separation
Yoshihiro Minagawa¹, Kai Matsumoto¹, Hiroyuki Noji^{1,2} (¹*Dept. App. Chem., Univ. Tokyo*, ²*RIPH., Univ. Tokyo*)
- [3Pos202](#) プログラム可能な DNA 応答型発光センサープラットフォーム：スプリット Cas12a とルシフェラーゼ再構成に基づくシステム
 Programmable DNA-responsive bioluminescent sensor platform based on split Cas12a and luciferase reconstitution
Figureiredo Diogo^{1,2}, Mitsuru Hattori², Takeharu Nagai^{1,3} (¹*Graduate School of Frontier Biosciences, Osaka University, Suita, Osaka*, ²*Department of Biomolecular Science and Engineering, SANKEN, Osaka University, Ibaraki, Osaka*, ³*Trans dimensional Life Imaging Division, Institute for Open and Transdisciplinary Research Initiatives, Osaka University, Suita, Osaka*)
- [3Pos203](#) 細胞内温度変動を支配する非伝導性熱散逸
 Non-conductive heat dissipation governs intracellular temperature variations
Masaharu Takarada¹, Takashi Funatsu², Kohki Okabe¹ (¹*Graduate School of Pharmaceutical Sciences, The University of Tokyo*, ²*Graduate School of Integrated Sciences for Life, Hiroshima University*)

31. バイオイメージング / 31. Bioimaging

- [3Pos204](#) Development of a Homo-FRET-Based Approach to Monitor Protein Conformational Changes
Tomoya Mukai^{1,3}, Yasushi Okada^{1,2,3} (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Grad. Sch. Med., Univ. Tokyo*, ³*Kobe Inst., Riken*)
- [3Pos205](#) 蛍光多重イメージングのための、青色と緑色光で光スイッチングする緑色蛍光タンパク質の開発
 A green fluorescent protein reversibly photoswitched by blue and teal light for multiplexed imaging
Ryohei Ozaki-Noma, Tetsuichi Wazawa, Kazunori Sugiura, Takeharu Nagai (*SANKEN, The Univ. of Osaka*)

- [3Pos206](#) 鶏卵の孵卵中のレーザースペckル法による血管の可視化に適した露光時間の探索
Searching for Optimal Exposure Time for Visualization of Blood Vessel of Chicken Egg During Incubation Using Laser Speckle Imaging Method
Hiroki Tamura^{1,2,3}, Tetsuhito Suzuki⁴, Keiichiro Shiraga^{1,5}, Naoshi Kondo¹, Yuichi Ogawa⁶ (¹Graduate School of Agriculture, Kyoto University, ²Distinguished Doctoral Program of Platforms (WISE), Kyoto University, ³JSPS Research Fellowship for Young Scientists DC1, ⁴Graduate School of Bioresources, Mie University, ⁵PRESTO, JST, ⁶Department of Medicine, Hyogo Medical University)
- [3Pos207](#) XYクロストークを低減した高速AFMスキャナーの開発
Development of a high-speed AFM scanner with reduced XY crosstalk
Sora Nishida¹, Kenichi Umeda², Noriyuki Kodera² (¹Grad. Sch. Math & Phys., Kanazawa Univ., ²WPI-NanoLSI, Kanazawa Univ.)
- [3Pos208](#) Correlation Analysis of Intracellular Temperature Heterogeneity and Subcellular Structures
Keisuke Fujita¹, Yoshie Harada^{1,2} (¹WPI-PRIME, Univ. Osaka, ²QIQB, Univ. Osaka)
- [3Pos209](#) 急速凍結ディープエッチングレプリカ電子顕微鏡を用いた滑走細菌のペプチドグリカン層の可視化
Visualization of peptidoglycan layer of gliding bacteria by using quick-freeze deep-etch replica electron microscope
Yuhei Tahara^{1,2}, Makoto Miyata² (¹Grad. Sch. Eng., Osaka Metropolitan Univ., ²Grad. Sch. Sci., Osaka Metropolitan Univ.)
- [3Pos210](#) 電子顕微鏡における複素観測：シェルツァー限界を超える
Complex Observation in Electron Microscopy : Surpassing the Scherzer Limit
Kuniaki Nagayama (Science Communication Laboratory LLC)
- [3Pos211](#) Non-invasive Evaluation of iPSC-derived Cardiomyocytes Using Deep Learning
Taishi Kakizuka^{1,2}, Taro Ichimura², Takeharu Nagai^{1,2} (¹SANKEN, Univ. Osaka, ²OTRI, Univ. Osaka)
- [3Pos212](#) 赤外STEDと共焦点顕微鏡の組み合わせによる、細胞周期と細胞内の構造の同時計測
Observation of cell cycle and fine structures by using the combination of confocal and Infrared STED microscopy
Kaoru Katoh^{1,2,3}, Totai Mitsuyama^{1,2} (¹ExCELLS, National Institutes of Natural Sciences, ²AIRC, AIST, ³SIGMA, Univ. Tsukuba)
- [3Pos213](#) High-speed in-line force mapping - imaging of mechanical properties from microtubules to bacteria
Christian Ganser¹, Shigetaka Nishiguchi², Feng-Yueh Chan³, Takayuki Uchihashi^{1,3} (¹National Institutes of Natural Sciences, Exploratory Research Center on Life and Living Systems, ²National Institute of Advanced Industrial Science and Technology, Department of Life Science and Biotechnology, ³Nagoya University, Department of Physics)

32. バイオエンジニアリング／32. Bioengineering

- [3Pos214](#) Fabrication of Periodic Inorganic Nanoparticles Using a Fusion Protein of Dps and Nanofiber-Forming Peptide
Mitsuhiro Okuda^{1,2,3}, Gabriela Pretre^{2,3} (¹Meiji Univ., ²CIC nanoGUNE, ³Komie Corp.)
- [3Pos215](#) 淘汰圧制御に向けた溶液交換技術の開発
Development of Solution Exchange Technology for Controlling Selection Pressure
Nanato Takaso¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹Graduate School of Engineering, The University of Tokyo, ²Research Institute of Planetary Health (RIPH), The University of Tokyo)
- [3Pos216](#) キネシン-微小管系を内包したゲル人工筋肉の収縮特性評価
Characterization of contractile behavior of artificial muscle gel incorporating Kinesin-Microtubule networks
Shuichi Ishino (JAIST)

- [3Pos217](#) 油気界面における生体分子からなる膜状構造の形成とその応用
Film-like biomolecular structures at the oil-air interface and their potential application
Daichi Tominaga¹, Shogo Hamada², Yusuke Sato¹ (¹*Grad. Sch. Com., Kyushu. Inst. Tech.*, ²*Grad. Sch. Com., Inst. Sci. Tokyo*)

34. Miscellaneous topics その他 / 34. Miscellaneous topics

- [3Pos218](#) The Role of Fluid Dynamics in Active Phase-Separating Systems
Charu Datt^{1,3}, Jonathan Bauermann^{2,3}, Nazmi Burak Budanur³, Frank Julicher³ (¹*Department of Mechanical Engineering, Keio University*, ²*Department of Physics, Harvard University*, ³*Max Planck Institute for the Physics of Complex Systems, Dresden*)
- [3Pos219](#) OptoChaperone – A biohybrid tool for regulating protein condensates in cells and *in vitro*
Thanh Tuan Do, Motonori Matsusaki, Soichiro Kawagoe, Hiroyuki Kumeta, Tomohide Saio (*Division of Molecular Science (Saio's Lab), Institute of Advanced Medical Sciences, Tokushima University, Tokushima, Japan*)
- [3Pos220](#) Attenuation of TDP-43 proteinopathy by graphene quantum dots in amyotrophic lateral sclerosis
Yunseok Heo, Yuxi Lin, Young-Ho Lee (*Korea Basic Science Institute*)

- [1SA-A-1](#) Visualization of domain motion in multi-domain protein as studied by neutron scattering and molecular dynamics simulation

Rintaro Inoue (*Institute for Integrated Radiation and Nuclear Science, Kyoto University*)

Multi-domain protein (MDP), which is ubiquitously found in eukaryotic, exhibits various biologically significant function. Recently, it is recognized that its function is regulated by domain motion. Hence, direct observation and identification of domain motion in MDP is crucial for understanding the mechanism of biological function of MDP. Quasielastic neutron scattering (QENS) can cover both the temporal and spatial scales of domain motion, however the resolution is quite limited. To overcome the shortcoming of QENS, the complementary uses of QENS and all-atom molecular dynamics simulation is adopted for the observation and identification of domain motion. In the presentation, we also take about selective deuteration of concerned domain in MDP.

- [1SA-A-2](#) 情報幾何学による実験データと MD の統合: 蛋白質構造アンサンブル可視化への適用
Visualization of protein conformational ensembles by integrating experiments and MD via information geometry

Tomotaka Oroguchi (*Dept. Phys., Keio Univ.*)

Since protein conformational ensembles are essential for biological functions, techniques to visualize them are in high demand. A promising approach is to reconstruct the true ensemble from an MD-derived ensemble with reference to experimental data. A key challenge is the divergent behavior of the reconstruction. Recent methods, such as Bayesian statistics, suppress this divergence by constraining the MD-derived ensemble, often at the cost of accuracy. Here, we show that the divergence originates from the manifold structure of the probability distribution space representing the ensemble. Our manifold-based optimization enables accurate reconstruction, and successfully visualizes a functionally important ensemble of an enzyme from small-angle X-ray scattering data.

- [1SA-A-3](#) 高速原子間力顕微鏡データと分子シミュレーションの融合による生体分子の構造ダイナミクスのデータ同化解析
Data assimilation analysis of structural dynamics of biomolecules by combining HS-AFM data and molecular simulations

Sotaro Fuchigami¹, Toru Niina², Suguru Kato², Yasuhiro Matsunaga³, Shoji Takada⁴ (¹Sch. Pharm. Sci., Univ. Shizuoka, ²RIKEN BDR, ³Grad. Sch. Sci. & Eng., Saitama Univ., ⁴Grad. Sch. Sci., Kyoto Univ.)

High-speed atomic force microscopy (HS-AFM) is a powerful technique for observing structural dynamics of biomolecules in real time with nanometer resolution. However, its spatiotemporal resolution is not sufficient to reveal atomic-level details. In this study, we have performed data assimilation analyses of structural dynamics of biomolecules using several protocols developed for data assimilation between HS-AFM data and coarse-grained molecular dynamics simulations. Flexibly fitting revealed the structural details of observed biomolecules, and particle filter and particle smoother were confirmed to be effective in examining biomolecular dynamics. Markov state model and hidden Markov model uncovered the details of long-term behavior of myosin-V walking.

- [1SA-A-4](#) クライオ電子顕微鏡単粒子画像からの 3D モデル直接推定によるタンパク質マルチコンフォメーション状態の解明
Uncovering Multiple Conformational States of Protein via Direct 3D Models Estimation from CryoEM single-particle images

Atsushi Tokuhisa (*RIKEN Center for Computational Science*)

Understanding protein function requires capturing their diverse conformational states. However, directly visualizing these states remains challenging, even with advanced cryoEM, due to low S/N ratios in single-particle images and loss of structural detail, especially in flexible regions, during 3D reconstruction. To address these issues, we introduce cryoMDM, a molecular dynamics-based structural matching method. This approach enables direct estimation of atomic-resolution 3D structures from individual cryoEM images by comparing them with conformers generated from MD simulations. Applying cryoMDM to the SARS-CoV-2 spike protein, we identified multiple conformational states, demonstrating the method's potential in resolving structural heterogeneity at atomic resolution.

1SAA-5 SAXS/SANS と MD シミュレーションを用いた分子複合体の統合的構造モデリング
Integrative structural modeling of macromolecular complexes using SAXS/SANS and MD simulations

Atsushi Matsumoto (*iQLS, QST*)

We perform integrative structural modeling of biomolecular complexes using low-resolution data such as small-angle X-ray scattering (SAXS) and small-angle neutron scattering (SANS). Unlike 3D information from cryo-EM, SAXS and SANS provide one-dimensional profiles, making it difficult to directly evaluate how well a model fits the data. To address this, we generate diverse 3D models and calculate theoretical scattering profiles. These are compared with experimental data to select appropriate models. However, this approach does not always give a unique solution, and multiple candidate structures may remain. We therefore perform molecular dynamics (MD) simulations to assess their structural stability in aqueous environments and identify the most plausible model.

1SBA-1 タンパク質構造変化の AI ベースモーフィングと構造ダイナミクスの Transformer 解析
AI-based Morphing of Protein Structural Changes and Transformer-based Analysis of Conformational Dynamics

Naoyuki Miyashita^{1,2}, Yoshihiro Kashiwaya², Rin Hirasawa¹, Shota Shimogochi², Yuma Shiota², Ryota Kiyooka²
(¹BOST, KINDAI Univ., ²Grad. Sch. BOST, KINDAI Univ.)

Structural changes in biomolecules such as enzymes occur on timescales ranging from microseconds to seconds, making it difficult to capture them using conventional molecular dynamics (MD) simulations. Conventional morphing methods are simple and widely used to examine structural changes between two states, but usually cannot represent detailed motions. To overcome this, we developed an AI-based non-linear morphing method (MOVE-DM) that uses MD data to reproduce complex structural changes, including side-chain movements. Furthermore, to analyze key events such as triggers of conformational changes, we developed a Transformer-based method (DeKE-MD) for analyzing MD and morphing data. In this presentation, we introduce these two novel approaches.

1SBA-2 CGBack : 拡散モデルを用いたバックマッピングによる粗視化タンパク質シミュレーションからの原子レベル構造の大規模再構築
CGBack: Large Scale Reconstruction of Atomistic Detail from Coarse-Grained Protein Structures with a Diffusion Model

Diego Renato Ugarte La Torre¹, Yuji Sugita^{1,2} (¹RIKEN R-CCS, ²RIKEN PRI)

Bridging coarse-grained (CG) sampling and atomistic insight demands fast, accurate back-mapping of millions of protein configurations. We present a diffusion model that generates full atomic coordinates directly from CG beads while preserving bond, angle, and rotamer statistics. Trained on the SidechainNet dataset, the model restores 99.7 % of covalent bonds and cuts steric clashes to <0.6 %. Included in CGBack's pipeline, a lightweight post-processing routine also eliminates residual ring penetrations and incorrect chiralities. We find CGBack enables seamless CG exploration followed by all-atom analysis of biomolecular function of multi-million-atom assemblies such as viral capsids and phase-separated condensates.

1SBA-3 Deciphering allosteric regulation in disease-associated proteins with MD simulation and deep learning

Yuko Tsuchiya (*AIRC, AIST*)

Allosteric signal transduction, the process by which events such as ligand binding or amino-acid substitutions at a site distinct from a protein's active site (the allosteric site) modulate the structure and function of that active site, plays a central role in the regulation of physiological processes. In this study, we aim to elucidate disease-relevant signaling pathways by characterizing the activation mechanisms triggered by ligand binding to signaling proteins and the pathogenic mechanisms induced by disease-associated mutations. To obtain an atomistic understanding of the allosteric processes underlying disease onset, we propose an integrated analytical framework combining molecular dynamics simulations with deep learning.

1SBA-4 機械学習を用いたタンパク質ダイナミクスや細胞ダイナミクスの次元縮約とデータ生成
Machine Learning-Based Dimensionality Reduction and Data Generation for Protein and Cellular Dynamics

Hiroshi Fujisaki (*Nippon Med. Sch.*)

Understanding high-dimensional protein and cellular dynamics is crucial for uncovering fundamental biological mechanisms. In this research, we aim to develop machine learning-based methods for dimensionality reduction and data generation tailored to these systems. Building on our experience with diffusion maps, time-lagged autoencoders, and variational autoencoders for protein dynamics, and with CNN-based architectures such as AlexNet for cellular image data, we explore unified frameworks that extract low-dimensional representations capturing essential temporal and spatial features. Additionally, we will employ generative models to simulate realistic dynamical trajectories and cellular images, enabling predictive modeling and hypothesis testing in biological systems.

1SBA-5 蛋白質 MD シミュレーションデータの動的特徴量とその時間依存性を精密に同時抽出する新規機械学習法
A novel machine learning method for the simultaneous and accurate extraction of dynamic features and time dependence from MD simulations

Yasushige Yonezawa (*Kindai University Institute of Advanced Technology*)

Understanding allosteric effects caused by the dynamic properties of proteins is expected to be the most important issue in the future. Molecular dynamics (MD) simulations are expected to be an important tool for studying protein allosteric effects, but conventional methods for analyzing time-dependent dynamic fluctuations of molecules have various problems and room for improvement. In this presentation, we report an enhanced machine learning (AI) method that overcomes the problems of conventional MD simulation data analysis methods, which can simultaneously and precisely separate and determine low-dimensional dynamic features and the time-dependence from the spatio-temporal data information of protein molecular simulations.

1SBA-6 機械学習手法を用いたヘムタンパク質における配列構造機能相関の解析
Analysis of sequence-structure-function relationships in heme proteins by using machine learning methods

Hiroko X. Kondo (*Kitami Inst. Tech.*)

Cytochrome P450 is a superfamily of enzymes that catalyze monooxygenase reactions. They are essential for metabolism and biosynthesis, and catalyze a variety of reactions for various substrates. In this study, to clarify the relationship between amino acid sequence, active site structure, and catalytic reaction in cytochrome P450, we analyzed the correlation between the structure of the active site and catalytic reactions or substrates using statistical analysis and machine learning methods on a small dataset (samples in P450Rdb). In addition, we are working on extending the machine learning dataset with AlphaFold3 to enable the prediction of catalytic reactions for a greater variety of proteins.

1SBA-7 大規模分子動力学計算・動的モンテカルロ法・機械学習を統合した不均一系における物質輸送の研究手法
Integration of large-scale MD calculation, dynamic MC method, and machine learning to study mass transport in heterogeneous systems

Tetsuro Nagai¹, Nobuaki Kikkawa², Ryosuke Jinnouchi², Masayuki Kimura³, Susumu Okazaki⁴ (¹*Department of Chemistry, Faculty of Science, Fukuoka University*, ²*Toyota Central R&D Labs., Inc.*, ³*Toyota Motor Corporation*, ⁴*Graduate School of Nanobioscience, Yokohama City University*)

Molecular diffusion in heterogeneous media is a ubiquitous phenomenon observed in a wide variety of physical, chemical, and biological systems. As the timescale of mass transport in the heterogeneous systems is typically longer than that of all-atom molecular dynamics (MD) calculations, we propose a method to overcome this timescale challenge. Here, we use large-scale MD simulations to obtain the free energy landscape and position-dependent diffusion constant, which are used as input for the successive Monte Carlo (MC) method to evaluate the diffusive dynamics on the long timescale. We further advocate the use of machine learning to efficiently evaluate the free energy landscape and position-dependent diffusion constant to address even larger systems.

1SBA-8 疾患の複雑性を解読する：難病創薬のためのデータ駆動的アプローチ
Decoding Disease Complexity: Integrative Data-Driven Approaches for Rare Disease Drug Discovery

Yayoi Natsume-Kitatani^{1,2} (¹*National Institutes of Biomedical Innovation, Health and Nutrition*, ²*Institute of Advanced Medical Sciences, Tokushima University*)

The growing volume of clinical data holds great promise for advancing drug discovery, while omics analyses have become more accessible, providing deeper insights into disease mechanisms. However, the complexity and heterogeneity of these data remain major challenges for effective utilization. To address this, we developed novel patient stratification techniques that integrate clinical and omics data to identify subgroup-specific therapeutic targets. We also established an analytical method for extracting clinically relevant features from limited medical imaging data to support stratification. This presentation outlines our data-driven strategies to transform conventional paradigms in drug target discovery, with a focus on rare diseases.

1SCA-1 生物物理学のための Structured Light
Structured light for biophysics

Takashige Omatsu (*Chiba University*)

Structured light possesses unique features, such as an annular spatial form, an orbital angular momentum, and non-diffractive propagation, and it has been widely investigated in a variety of fields. In recent years, it has been discovered that the orbital angular momentum of structured light twists a liquid-phase resin to shape a helical fiber via photopolymerization. Such helical fibers will have potentially the capacity to be applied to the tissue engineering scaffolds. We herein review the fundamentals and applications of structured light for biophysics.

1SCA-2 らせんの組織工学の創製
Development of Helical Tissue Engineering

Michiya Matsusaki (*The University of Osaka*)

No perfect linear structure exists in biological tissues and living tissues have helical structures such as the double helix of DNA at the molecular level, the collagen triple helix at micrometer level, and the helical structures of blood vessels at the millimeter level, respectively. Why do living organisms prefer helical structures? There have been no reports to reproduce the helical structures mimicking living organisms. In this study, we focused on optical vortex to construct cell-scaffold tissues with helical structures at micrometer pitch and to analyze cellular functions. We expect to understand the meaning and functions of helical structures and develop them into creative “helical tissue engineering” technology.

1SCA-3 細胞内温度計測：蛍光性ナノ材料を用いた細胞機能の探索
Intracellular thermometry: Probing cell function with fluorescent nanomaterials

Yoshie Harada (*PRiME, The University of Osaka*)

Intracellular temperature is deeply involved in vital biological processes. Using fluorescent polymer thermometers and fluorescent nanodiamonds, we have found that spontaneous intracellular temperature increases—associated with transcription and translation—play a critical role in the differentiation of neuronal model cells, and that the thermal conductivity inside cells is lower than that in water. Recently, we synthesized more than ten types of carbon quantum dots, and found that several of them function effectively as intracellular thermometers. In this talk, I will provide an overview of intracellular temperature measurement using fluorescent polymer thermometers, fluorescent nanodiamonds, and our newly developed carbon quantum dots.

1SCA-4 光渦/高速 AFM 複合機で光の螺旋性を可視化する
High-speed AFM combined with optical vortex visualizes optical helicity

Takayuki Umakoshi (*Dept. Appl. Phys., Univ. Osaka*)

Chirality is essential in life science, and plays a vital role in biological functions. Optical vortex has attracted significant attention as light sources that measure or even manipulate chirality. Here, we developed a system of high-speed AFM (HS-AFM) combined with an optical vortex. HS-AFM is an indispensable measurement tool for visualizing nanoscale dynamics in the field of biophysics. Our HS-AFM can observe the area where the optical vortex was irradiated. As the first demonstration, we show the spiral motions of a photo-active polymer film under an optical vortex. We also include our recent developments in the integration of HS-AFM with other optical techniques. This novel technique would be a great tool to analyze chirality at high spatio-temporal resolutions.

1SCA-5 液滴およびアミロイド線維形成に至るタンパク質の光捕捉ダイナミクス
Optical trapping dynamics of protein assembly into condensates and amyloid fibrils

Eri Chatani¹, Keisuke Yuzu^{1,2}, Yi-Sian Chien², Hiroshi Masuhara² (¹*Grad. Sch. Sci., Kobe Univ.*, ²*Dept. Appl. Chem., National Yang Ming Chiao Tung Univ.*)

Optical trapping is one of the most attractive techniques for manipulating biomolecules. We recently found it effective for fabricating protein assemblies. With α -synuclein, a single liquid-like condensate was formed when a near-infrared laser beam was focused on the air-liquid interface of a protein solution. The condensate grew beyond the focus, and subsequently underwent a liquid-to-solid transition to form amyloid fibrils. Condensate formation was also observed with lysozyme, where the properties of the condensate were sensitively modulated by the charge state of the protein molecules, offering a perspective on the spatiotemporal and structural control of protein assemblies enabled by this method.

1SCA-6 紫外域における放射光キラル分光と生体分子の構造観測
Synchrotron radiation chiral spectroscopy in ultraviolet region and structural characterization of biomolecules

Koichi Matsuo (*Res. Inst. Synchrotron Rad. Sci., Hiroshima Univ.*)

Chirality is an important structural element in biomolecules and circular dichroism (CD), which observes the interaction with ultraviolet circularly-polarized light (UV-CPL), is widely used as a chiral spectroscopy to characterize the structures and functions of biomolecules. UV synchrotron radiation as a light source has brought great advantages to the CD measurement and analysis, and to the developments of linear dichroism and spatial- and time-resolved apparatus. The applied research is also explored the use of optical vortex or helical dichroism with UV-CPL. Here, we introduce recent developments in synchrotron radiation chiral spectroscopy and its further potential in the research of biomolecule structures.

1SCA-7 集光フェムト秒光渦レーザーによる単一神経細胞の刺激
Single-neuron stimulation with a focused femtosecond optical vortex laser

Chie Hosokawa (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

Neurons form a highly complex network that communicates among cells through synaptic connections. Measurement of neuronal stimulation and evoked responses at the single-cell level is necessary to elucidate the communication mechanisms of neural networks. We recently found that focused femtosecond Gaussian beam irradiation of neurons generated transient micro-perforations in the cell membrane due to laser ablation and induced high-frequency action potentials in a target single neuron. In this study, we demonstrate neuronal stimulation using a femtosecond optical vortex laser to achieve less invasive neuronal stimulation. We evaluated changes in neuronal activity and cell membrane morphology induced by focused femtosecond optical vortex laser irradiation.

1SCA-8 マウスノード不動繊毛は変形の向きを感知して左右軸を決定する
Immotile cilia mechanically sense the direction of fluid flow for left-right determination

Takanobu Kato (*Grad. Sch. Med., The Univ. of Tokyo*)

Immotile cilia at the node of mouse embryos are required for sensing of a leftward fluid flow that breaks L-R symmetry of the body. The flow-sensing mechanism has long remained elusive, however. Here we show that immotile cilia at the node undergo asymmetric deformation along the D-V axis in response to the flow. Application of mechanical stimuli to immotile cilia by optical tweezers induced Ca^{2+} transient and degradation of *Dand5* mRNA in the targeted cells. The *Pkd2* channel protein was preferentially localized to the dorsal side of immotile cilia, and Ca^{2+} transients were preferentially induced by mechanical stimuli directed toward the ventral side. Our results explain the biophysical mechanism as to how immotile cilia at the node sense the direction of fluid flow.

1SDA-1 微細加工温度センサが導く単一細胞の独特な熱挙動
Unique thermal behaviors of single cells revealed by microfabricated thermometer

Naoki Inomata (*Tohoku University*)

Temperature is a crucial parameter influencing the physical states of animals. Understanding cellular behaviors in response to temperature is a topic of significant interest. This presentation introduces the use of microfabricated thermometers that offer high sensitivity, small-scale measurements, and fast response times. Dynamic temperature measurements at the single-cell level have revealed distinctive thermal phenomena, including periodic sharp heat bursts, frequency spectra of self-heating signals, and unique thermal properties. These findings—enabled by the simultaneous temporal and thermal resolution of microfabricated thermometers—demonstrate the potential of such devices to uncover novel thermal behaviors in cellular environments.

1SDA-2 天然変性タンパク質の凝集を決定する配列ルールの解読
Decoding Sequence Rules for Condensation of Disordered Proteins

Kyosuke Adachi^{1,2}, Kyogo Kawaguchi^{2,3} (¹*RIKEN iTHEMS*, ²*RIKEN PRI*, ³*IPI, Grad. Sch. Sci., Univ. Tokyo*)

Protein condensates—such as nucleoli and nuclear speckles—coexist within cells and are central to numerous cellular processes. Although condensation is known to be driven primarily by interactions among intrinsically disordered regions, the precise amino acid sequence rules that allow distinct condensates to coexist remain unclear. In this presentation, I will introduce a theoretical framework we have developed to predict heteropolymer interactions among disordered protein sequences [1]. Using this framework, we can determine key condensate properties, such as critical temperatures, and elucidate the conditions required for the coexistence of multiple types of condensates.

[1] K. Adachi and K. Kawaguchi, *Phys. Rev. X* 14, 031011 (2024).

1SDA-3 The cellular basis of long-term memory: L-LTP-dependent extension of endoplasmic reticulum into spines via septin 3

Natsumi Ageta-Ishihara (*Fac. Sci., Toho Univ.*)

Transient memories are converted to persistent memories at the synapse and systems levels. The synapse-level consolidation parallels electrophysiological transition from early- to late-phase long-term potentiation of synaptic transmission (E-/L-LTP). However, cellular basis conferring persistence on L-LTP remain unclear. Here we show that L-LTP causes fast spine enlargement, followed by SEPT3-dependent smooth endoplasmic reticulum (sER) extension into enlarged spines. Spines containing sER show greater Ca^{2+} responses and local synaptic activity. Consistently, *Sept3*^{-/-} mice impairs long-term memory and causes a scarcity of sER-containing spines. These findings indicate a concept that sER extension into active spines serves as a synaptic basis of long-term memory.

1SDA-4 How does the nucleus move within 'super crowded' plant cells?**Hirotomo Takatsuka**^{1,2}, Toshiki Amari³ (¹Dept. Biol. Sci., NWU, ²JST · Presto, ³Div. Biol. Sci. Tech., Kanazawa Univ.)

The vacuole, an organelle that characterizes plant cells, absorbs water and expands the cell from within, thereby acting as a driving force for active plant cell growth. On the other hand, as the vacuole develops to occupy more than 90% of the cell volume, it can also be a physical obstacle. However, the mechanism that places the organelles to the appropriate location in such a 'super crowded' environment remains largely unknown. To tackle this issue, we have focused on the dynamic yet precise nuclear movement that occurs within fully vacuolated root hair cells by employing the 4D imaging technique. In this symposium, we shall discuss how plant cells cope with large vacuoles to ensure the spatiotemporal dynamics of intracellular structures.

1SDA-5 **TIGR-Tas(タイガー-タス): Nop ドメインタンパク質群によるモジュラーな RNA 誘導性システム**
TIGR-Tas: Modular RNA-guided systems with Nop domain-containing proteins**Makoto Saito** (RIKEN PRI Biophenomena Engineering RIKEN ECL Research Team)

RNA-guided systems provide remarkable versatility, enabling diverse biological functions. Through iterative structural and sequence homology-based mining starting with a guide RNA-binding domain of Cas9, we identified a family of RNA-guided DNA-targeting proteins in phage and parasitic bacteria. Each system consists of a Tandem Interspaced Guide RNA (TIGR) array and a TIGR-associated (Tas) protein containing a Nop domain, sometimes fused to HNH or RuvC nuclease domains. Here, I will introduce the molecular mechanisms of TIGR-Tas systems and their potential application in human genome editing.

(This work was conducted during my postdoctoral time in Feng Zhang's lab at the Broad Institute, in collaboration with Guilhem Faure, Max E. Wilkinson, and others.)

1SDA-6 **リボソーム液滴を標的とする新規抗菌ペプチド**
A Novel Antimicrobial Peptide that Targets Liquid Ribosomal Condensates**Hirofumi Toda** (IUIS, University of Tsukuba)

Antimicrobial peptides (AMPs) are key components of innate immunity, typically disrupting bacterial membranes or inhibiting intracellular processes. Previously, we identified Nemuri (Nur), a sleep-inducing factor from *Drosophila melanogaster*, as a novel AMP. Nur is processed into short peptides enriched with arginine-glycine repeats, exhibiting potent bactericidal activity. Unlike conventional AMPs, Nur peptides penetrate bacterial membranes without causing disruption and interact intracellularly with ribosomal RNAs. Nur specifically targets bacterial ribosomal liquid-like condensates, reducing their fluidity and inhibiting protein translation. Importantly, Nur peptides show broad-spectrum antimicrobial activity, including efficacy against drug-resistant pathogens.

1SEA-1 **コヒーシオン HEAT サブユニット IDR のクロマチン高次構造形成における重要性**
Impact of IDR in the HEAT repeat protein STAG in building higher-order chromatin structure**Tomoko Nishiyama** (Grad. Sch. Sci., Kyoto Univ.)

Cohesin, which mediates sister chromatid cohesion (SCC), is essential for higher-order chromatin structure formation via DNA loop extrusion (LE) activity. The mechanism of LE and the mechanistic difference between LE and SCC are still elusive. Using a single-molecule assay, we show that the IDR in a HEAT repeat subunit, STAG1, is required for LE and AT-hook in IDR is essential for the function. STAG1^{ΔAT} is more dynamic on DNA than wild type. However, in human HCT116 cells, AT-hook is not essential for SCC, suggesting that stable DNA binding is only essential for LE but not for SCC, presumably because of the Sororin-dependent cohesion establishment mechanism. We will discuss the mechanistic differences between loop extrusion and sister chromatid cohesion.

1SEA-2 Repli-Histo 標識によって明らかにする生細胞におけるユークロマチンとヘテロクロマチンの物性
Replication-dependent histone labeling dissects the physical properties of euchromatin and heterochromatin in living human cells

Kazuhiro Maeshima^{1,2} (¹*National Institute of Genetics*, ²*SOKENDAI*)

A string of nucleosomes is organized in the cell as chromatin, ranging from euchromatin to heterochromatin, with distinct genome functions. Here, we developed replication-dependent histone (Repli-Histo) labeling to mark nucleosomes in euchromatin and heterochromatin. Using this approach, we investigated local nucleosome motion in the four known chromatin classes, from euchromatin to heterochromatin, of living human and mouse cells. The more euchromatic (earlier-replicated) and more heterochromatic (later-replicated) regions exhibit greater and lesser nucleosome motions, respectively. Genome chromatin is essentially replicated from regions with greater nucleosome motions. Our study reveals physical properties of euchromatin and heterochromatin in living cells.

1SEA-3 Physical modeling of chromatin dynamics

Soya Shinkai (*RIKEN BDR*)

Genomic DNA is folded and compacted in the micrometer-sized nucleus, and its 3D organization plays a key role in gene regulation. To analyze its dynamic nature, we developed a framework called PHI-C, integrating Hi-C and live-cell imaging data via a polymer model. This model, with optimized pairwise interactions, predicts time-resolved chromatin behavior at single-locus resolution. It bridges population-averaged contact data with real-time dynamics. We also showed that monomer motion in this model follows a generalized Langevin equation, consistent with chromatin tracking experiments. I will present this integrated approach and its implications for understanding chromatin organization.

1SEA-4 精子クロマチン凝縮過程の追跡
Tracking the Process of Sperm Chromatin Condensation

Yuki Okada¹, Masashi Hada¹, Yoshinori Makino^{1,2}, Satoru Kaneko^{1,3} (¹*Institute for Quantitative Biosciences, The University of Tokyo*, ²*Sapporo Kosei Hospital*, ³*SSET clinic*)

In mammals, sperm chromatin is highly compacted, largely replacing histones with protamines. Despite its biological importance, the spatiotemporal regulation of the histone-to-protamine transition remains poorly understood. In this study, we applied next-generation sequencing techniques, including ATAC-seq and CUT&Tag, to systematically track chromatin dynamics throughout the transition. Our analyses revealed marked chromatin reorganization coinciding with the timing of protamine incorporation, a strong correlation between large-scale chromatin architecture and protamine insertion sites, and a potential association between chromatin organization and sperm quality. These findings offer new insights into the epigenetic regulation of sperm development and male fertility.

1SEA-5 Target-DNA searching process of a light-regulated transcription factor, Photozipper, observed by high-speed atomic force microscopy

Akihiro Tsuji¹, Hayato Yamashita¹, Osamu Hisatomi², Masayuki Abe¹ (¹*Grad. Sch. Eng. Sci., UOsaka*, ²*Grad. Sch. Sci., UOsaka*)

Transcription factors (TFs) are DNA-binding proteins that regulate gene expression and diverse cellular processes. To achieve gene regulation, TFs often recognize short target sequences (6–10 bp) by forming oligomers, most commonly dimers. Although oligomerization is thought to enhance DNA-binding affinity, it remains unclear whether it also facilitates the search process for efficiently locating these small targets. Using high-speed atomic force microscopy (HS-AFM), we visualized the target-binding dynamics of Photozipper (PZ), a TF that undergoes light-induced dimerization. Single-molecule observations under dark and light conditions enabled direct comparison between monomeric and dimeric PZ. We will discuss how dimerization alters PZ's target recognition mechanism.

[1SEA-6](#) 核小体における DNA 二重らせん構造の力学的制御メカニズム Mechano-regulation of DNA duplex structure in a nucleolus

Koichiro Maki^{1,2,3,4}, Jumpei Fukute^{1,3}, Taiji Adachi^{1,2,3,4} (¹*Institute for Life and Medical Sciences, Kyoto University*,
²*Grad. Sch. Eng., Kyoto University*, ³*Grad. Sch. Biostudies, Kyoto University*, ⁴*Grad. Sch. Med., Kyoto University*)

Inside a eukaryotic nucleus, dynamic genomic processes result in DNA untwisting and melting. In this study, to gain mechanical insights into DNA conformational change, we performed *in situ* super-resolution microscopy for underwound (untwisted) and single-stranded DNA. As a result, underwound DNA was found abundantly inside a nucleolus. The abundance of underwound DNA was reduced by blocking G-quadruplex (G4), implying the importance of RNA polymerase I-generating torque coupled with G4-based constraints of axial rotation. Interestingly, single-stranded DNA accumulated outside the nucleolar shell. This suggested a positive feedback in which underwound DNA in the nucleolar core transits to single-stranded DNA toward the shell, to supply G4 structures for DNA untwisting.

[1SFA-1](#) 細胞膜由来の細胞外小胞を介した効率的タンパク質伝達 Efficient protein transfer through the protrusion-derived extracellular vesicles

Tamako Nishimura, Shiro Suetsugu (*NAIST*)

Extracellular vesicles (EVs) transfer intracellular proteins from producer to recipient cells. EVs are produced either from plasma membrane protrusions or endosomes. Comparing with the endosome-derived EVs, the mechanisms and the efficiency of the protein transfer by the plasma membrane-derived EVs are poorly understood. We show that the protrusion-derived EVs deliver the natural and functional small GTPase Rac1 protein efficiently to the recipient cells. Applying this superior system, we packaged the genome-editing protein Cas12f into the protrusion-derived EVs, which delivered Cas12f with higher efficiency than endosome-derived EVs. Thus, the protrusion-derived EVs as a powerful tool for the efficient and bioactive delivery of both native and engineered proteins.

[1SFA-2](#) 1 粒子追跡と超解像顕微鏡観察による細胞外小胞の結合・取り込み機構の解明 Mechanisms of extracellular vesicle binding and internalization uncovered by single-particle tracking and super-resolution microscopy

Kenichi G. N. Suzuki^{1,2} (¹*Gifu Univ.* · *iGCORE*, ²*NCCRI*)

Small extracellular vesicles (sEVs) mediate intercellular communication, yet the mechanisms governing their selective binding and uptake remain elusive. Using dual-color single-molecule and super-resolution imaging, we found that tumor-derived sEV subtypes predominantly bind to laminin on the target cell plasma membranes via $\alpha 6 \beta 4$ or $\alpha 6 \beta 1$ integrins, with minimal affinity for fibronectin. All sEV subtypes are internalized through galectin-3- and LAMP-2C-mediated clathrin-independent endocytosis, while some also utilize the caveolae pathway. Paracrine sEV binding triggers intracellular signaling, calcium response, and calcineurin-dynamin-dependent uptake of sEVs. These findings demonstrate that laminin engagement facilitates both sEV-cell binding and internalization.

[1SFA-3](#) 大腸菌生細胞からのメンブレンベシクル創発：バイオポリマー合成が"引き金" Controllable secretion of membrane vesicles (MVs) from viable *Escherichia coli* triggered by intracellular polymer accumulation

Sangho Koh, Seiichi Taguchi (*Inst. ARG, Shinshu Univ.*)

In this study, we discovered a novel mechanism of bacterial membrane vesicle (MV) biogenesis that is triggered by the intracellular accumulation of poly(3-hydroxybutyrate) (PHB) in *Escherichia coli*. This mechanism, termed the Polymer Interacellular Accumulation-triggered system for MV production (PIA-MVP), demonstrated a strong correlation between PHB accumulation and MV biogenesis, which can be finely modulated by the glucose concentration in the culture medium. To gain further mechanistic insights, we are currently conducting live-cell imaging at the single-cell level. These efforts aim to elucidate the causal relationship between intracellular polymer accumulation and MV biogenesis, offering a controllable platform for vesicle production in viable bacterial cells.

1SFA-4 細胞外小胞の物質送達機構の解明と薬物送達への応用
Analysis of intracellular trafficking of extracellular vesicles for drug delivery applications

Masaharu Somiya (*SANKEN, The University of Osaka*)

Extracellular vesicles (EVs) have been considered as messengers to deliver various types of cargo molecules, including RNA and proteins. However, the detailed mechanism and efficiency of the cytoplasmic cargo delivery by EVs have been elusive. We've recently revealed that the cargo delivery of EVs is unexpectedly inefficient in a line of studies by developing new functional EV cargo delivery assays. The potential solutions to overcome the inefficiency in cargo delivery for drug delivery applications will be discussed.

[1] M. Somiya and S. Kuroda, *Anal. Chem.*, 93, 2021

[2] M. Somiya and S. Kuroda, *Journal of Extracellular Vesicles*, 2021

[3] M. Somiya and S. Kuroda, *bioRxiv*, 2022

[4] M. Somiya and S. Kuroda, *Mol. Pharmaceutics*, 2022

1SFA-5 生物材料ナノマシーンによるゲノム編集送達
Genome Editing Delivery by Biomaterial Nanomachines

Akitsu Hotta (*CiRA, Kyoto University*)

With genome editing technologies like CRISPR-Cas9, therapeutic applications for gene mutation diseases are expanding. However, safe and efficient in vivo delivery to skeletal muscle remains a challenge. We have developed a virus-like particle (VLP) system that packages CRISPR-Cas9 protein and guide RNA using self-assembling viral particles. Additionally, we are working on RNA delivery using lipid nanoparticles (LNPs) and analyzing their in vivo dynamics. Both VLPs and LNPs are biocompatible nanomachines capable of transiently delivering CRISPR-Cas9 to skeletal muscle. I will discuss the technical needs, current challenges, and future clinical prospects, focusing on Duchenne muscular dystrophy and related conditions.

1SFA-6 バーコード化細胞外小胞を活用した細胞外小胞研究の新展開
Barcoded Extracellular Vesicles for Next-generation Extracellular-vesicle Research

Ryosuke Kojima (*Graduate School of Medicine, The University of Tokyo*)

Small extracellular vesicles (sEVs) are attracting attention as intercellular messengers and therapeutic delivery tools. Thus, understanding and controlling sEV release and fate is important in both basic biology and biotechnology. However, the mechanisms regulating sEVs remain poorly understood. To address this, we use “barcoded” sEVs that encode information from donor cells. Combined with CRISPR screening, this enables a high-throughput platform to identify regulators of sEV release. In this talk, we introduce this assay system and also present our perspective on extending this approach to discover factors that govern sEV fate and quality.

1SGA-1 人工設計したタンパク質構造に機能を埋め込む試み
Embedding Functional Sites in De Novo Designed Protein Structures

Nobuyasu Koga^{1,2} (¹*ASPiRE, IPR, Univ. Osaka*, ²*ExCELLS, NINS*)

We have developed principles and methods to design protein structures from scratch. Our successes include a diverse range of alpha-beta and all-alpha proteins, including novel topologies not found in nature, all designed with atomic-level accuracy. This presentation will highlight these achievements and our attempts to embed functional sites in de novo designed protein structures as a means to generate functional proteins.

1SGA-2 Toward generative design of circadian clock modulators: Chemical and structural analyses of mammalian CRY

Tsuyoshi Hirota (*ITbM, Nagoya Univ.*)

Dysfunction of the circadian clock due to shift work or genetic mutations has been associated with many diseases in modern society. For a deeper understanding and to enable control of the circadian clock system, we have been applying chemical biology. By conducting cell-based phenotypic screening of circadian clock modulators followed by functional characterization, we discovered first-in-class compounds targeting the core clock protein CRY. By using these compounds, we revealed unique structural features of CRY. In this presentation, I will discuss our newly identified CRY-targeting compounds and the characteristics of CRY revealed by functional and structural analyses. These findings will form the basis of the generative design of circadian clock modulators.

1SGA-3 DNAの光修復：分子進化とメカニズム進化
Light-Driven DNA Repair: Mechanistic Insights and Molecular Evolution

Minoru Kubo (*Grad. Sch. Sci., Univ. Hyogo*)

UV light damages DNA by inducing photoproducts such as (6-4) photoproducts, which can lead to harmful effects such as skin cancer. These lesions are repaired by (6-4) photolyase, which uses a flavin cofactor to initiate electron transfer upon blue-light absorption, triggering the repair reaction. While this light-dependent repair is often considered to follow a common mechanism, our time-resolved UV spectroscopy analysis of the photolyases from various species revealed that the number of photons required for repair differs across organisms. This unexpected species-dependent photon requirement uncovers mechanistic diversity and provides new evolutionary insights into light-driven DNA repair.

1SGA-4 新奇イオン輸送型微生物ロドプシンを用いた光遺伝学ツールの探索と開発
Exploration and development of optogenetic tools based on novel ion-transporting microbial rhodopsins

Keiichi Inoue (*ISSP, Univ. Tokyo*)

Ion-transporting microbial rhodopsins, found in diverse microorganisms, actively (light-driven ion pumps) or passively (light-gated ion channels) transport ions in a light-dependent manner. They also serve as essential tools in optogenetics to regulate neural firing and other biological events by light. To expand their optogenetic versatility, we have explored and developed ion-transporting microbial rhodopsins with novel molecular properties distinct from conventional ones. In this study, we discovered new anion-conducting channelrhodopsins responding to near-UV light. The results of spectroscopic and electrophysiological studies on the color-tuning mechanism will also be discussed. Furthermore, other novel ion-transporting microbial rhodopsins will be introduced.

1SGA-5 高精度量子化学が解き明かす光生物学の分子メカニズム
Exploring Photobiology via High-Precision Quantum Chemistry

Kazuhiro Fujimoto (*ITbM, Nagoya Univ.*)

Photobiological systems fine-tune light capture via pigment-protein interactions, and high-accuracy exciton calculations reveal key mechanisms. (1) In diatom FCP II tetramers, fucoxanthin-S introduces absorption at 500–560 nm and channels energy to chlorophyll *a*. (2) In purple-bacterial LH1, tight bacteriochlorophyll *a* packing enhances charge-transfer mixing, red-shifting the Q_y band beyond that of LH2 and maximizing energy flow to the reaction center. (3) In microbial rhodopsins, opposite signs of retinal-retinal excitonic coupling—negative in channelrhodopsin and positive in heliorhodopsin—yield biphasic vs. single CD bands, distinguishing the two. These results show how advanced quantum chemistry uncovers diverse light-harvesting strategies in photobiology.

1SGA-6 チャンネルロドプシンの光感度に対する電気生理学的アプローチ
A new model of light sensitivity in Channelrhodopsins

Shoko Hososhima^{1,2} (¹*Graduate School of Engineering, Nagoya Institute of Technology*, ²*Opto Bio Technology Research Center, Nagoya Institute of Technology*)

Microbial rhodopsins are mostly reactive to visible light which does not effectively penetrate through biological tissue. Furthermore, optogenetic tools are required high reactivity to weak light. The cryptophyte has 46 rhodopsins, including with 5 cation channelrhodopsins, named GtCCR1-5. We previously reported that GtCCR4 is 30 times more sensitive to light than either ChR2 or GtCCR2. However, the mechanism of high light sensitivity in GtCCR4 was still unknown. Here we compare the light dependency of various microbial rhodopsins by using whole-cell patch clamp with continuous light (LED) or a flash laser. When using a flash laser, GtCCR2 and GtCCR4 exhibited similar light sensitivity. We propose that the mechanism of light sensitivity in microbial rhodopsins.

1SGA-7 タンパク質の古典的機能動態を高速 AFM でとらえる
Visualizing Classical Functional Dynamics of Proteins by High-Speed AFM

Takayuki Uchihashi (*Nagoya University*)

Understanding the transition from quantum mechanical initial reactions to classical macroscopic conformational changes is a central challenge in elucidating protein function. High-speed atomic force microscopy (HS-AFM) enables real-time visualization of large-scale protein dynamics in aqueous environments and has been widely applied to study classical functional processes of proteins. In this talk, we present recent HS-AFM studies of membrane-embedded ATPase in a nanodisc system, focusing on its conformational dynamics during ATP hydrolysis and the effects of substrate binding on its structural transitions. We will discuss how such dynamic structural insights can contribute to the rational design of next-generation functional molecular tools.

1SHA-1 Force Transmission and Mechanical Memory at Integrin-Based Adhesions Revealed by Live-Cell Single-Molecule Imaging

Sawako Yamashiro^{1,2}, Ying Liu¹, David Rutkowski³, Dimitrios Vavylonis³, Naoki Watanabe^{1,2} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*Grad. Sch. Medicine, Kyoto Univ.*, ³*Dept. Physics, Lehigh Univ.*)

Force transmission at integrin-based adhesions is important for cell migration and mechanosensing. The prevailing model describes talin and vinculin as static linkers between F-actin and integrins. Using Single-Molecule Speckle (SiMS) Microscopy, we reveal the dynamic behavior of talin and vinculin. We show evidence that transient stretch of talin and its stochastic linkage are sufficient for force transmission between F-actin and ECM. We further show that the vinculin-talin complex is present in the cytoplasm and shuttles between the cytoplasm and F-actin. Our findings overturn the static view of integrin-based adhesions and provide new insights into mechanotransduction mechanisms.

1SHA-2 Kindlin converts the talin•integrin slip bond under mechanical load to an ideal bond

Reinhard Faessler (*Max Planck Institute, Martinsried, Germany*)

Integrins mediate cell adhesion. A hallmark of integrins is that ligand binding requires an activation step that depends on talin and kindlin binding to the β -integrin cytoplasmic tail and the transmission of forces (up to 40pN) from the actomyosin via talin to the integrin•ligand bonds. An unsolved mystery is how the low talin affinity to integrin tails (100-300 μ M) can resist the high actomyosin forces. We identified kindlin as allosteric activator for talin that converts the talin•integrin slip bond into a force-independent, ideal bond. NMR, biochemistry and cell biology revealed that kindlin also increases talin•integrin affinity. Our findings define the cooperativity of kindlin and talin, which is required to enable strong integrin binding and cell adhesion.

1SHA-3 Deciphering the mechano-sensitive properties of the membrane periodic skeleton in neurons

Gregory Giannone¹, Zhou Xuesi¹, Théo Dudon¹, Jean-Baptiste Trebbia², Anna Brachet¹, Brahim Lounis² (¹*University Bordeaux, CNRS, Interdisciplinary Institute for Neuroscience, UMR 5297, Bordeaux, France*, ²*Laboratoire Photonique Numerique et Nanosciences (LP2N), Institut d'Optique Graduate School and CNRS, UMR 5298, Talence, France*)

In neurons, spectrin-actin forms the periodic membrane skeleton (MPS) revealed by super-resolution. MPS molecular composition and architecture provide essential properties for mechanosensing, yet direct evidence is lacking. Combining axon stretching and super-resolution, we show reversible spectrin unfolding in response to rapid (1s) extracellular mechanical stimuli. Strain rate controlled MPS mechanical response, faster (0.1s) stretching induced irreversible spectrin-actin reorganization, slower (100s) deformations led to molecular adaptation. Mechanical stimuli triggered reversible dissociation of the actin-capping adducin from the actin-spectrin scaffolds. Thus, the MPS is a mechanosensitive scaffold that actively and reversibly reorganizes in response to force.

1SHA-4 SuperPAINT ライブラリー：1 分子超解像観察のために系統的にデザインしたタグタンパク質と蛍光リガンドのペア

SuperPAINT Library: Systematically designed pairs of tag proteins and fluorescent ligands for single-molecule super-resolution imaging

Bo Tang¹, Taka A. Tsunoyama¹, Maoji Wang¹, Ryuto Shinozaki¹, Amine Aladag¹, Takahiro K. Fujiwara², Akihiro Kusumi¹ (¹*Okinawa Institute of Science and Technology*, ²*Institute for Advanced Study, Institute for Integrated Cell-Material Sciences, Kyoto University*)

Points accumulation for imaging in nanoscale topography (PAINT) is a powerful tool to generate super-resolved images and observe single-molecule dynamics under physiological conditions, by utilizing transient binding of fluorescent probes to molecules of interest. In this study, we established a library of truly monomeric avidin-like proteins (tIMAs), which bind to fluorescent biotin with systematically varied k_{off} and high k_{on} . The binding lifetime ($1/k_{\text{off}}$) ranging from 1 ms to >2,000 s allows us to detect and characterize nanoscale hotspots with various lifetimes and molecular exchange rates. PAINT using this library, termed superPAINT, identified hotspots of lymphocyte antigen 6 complex (Ly6E) at later formation stages of large-sized clathrin-coated structures.

1SHA-5 細胞膜上で形成分解を繰り返す準安定ナノ液状シグナル統合プラットフォーム：iTRVZ によるガン増殖の促進

Metastable nano-liquid signal integration hub on the plasma membrane, iTRVZ, which enhances cancer development

Akihiro Kusumi (*Okinawa Institute of Science and Technology Graduate University (OIST)*)

First, I will talk about the world's fastest single-molecule imaging and PALM/dSTORM we developed (0.1-ms time resolution; 29-nm localization precision; simultaneous two-color PALM/dSTORM imaging from 10,000 images obtained for only 10 s). Second, I will present our finding of a platform on the plasma membrane, responsible for integrating the signals downstream from very different receptors: PDGF receptor, which induces cell proliferation and CD59, a GPI-anchored receptor, responsible for cellular immune evasion. This platform, termed iTRVZ, is a 34-nm-diameter liquid-like condensate formed via zyxin's liquid-liquid phase separation enhanced on the surfaces of raft domains and actin membrane skeleton. In mice, iTRVZ promotes tumor growth by enhancing the CD59 signal.

1SIA-1 Lamins regulating nuclear stiffness, genome dynamics and early embryonic development

Yuta Shimamoto (*Nat'l Inst Genetics*)

In our pursuit to understand how subcellular mechanics influence genome dynamics and cell physiology, we recently uncovered a striking transformation in the shape and mechanics of the nucleus during early mouse embryogenesis. This nuclear change was pronounced specifically at the 2-cell stage, when embryos transcribe thousands of zygotic genes and launch a new developmental program. Our data also highlighted key roles of lamin B1 in regulating nuclear deformability and transcription, acting through an autophagy-dependent mechanism. Embryos with soft nuclei successfully initiated zygotic gene activation, but those with stiffened nuclei did not. Our findings reveal that the transient, physical nuclear remodeling is a vital force for successful embryogenesis.

1SIA-2 脳皮質発生におけるニューロン隘路遊走の細胞機構

The cellular mechanism and lifelong impact of neuronal migration in confined brain tissue

Mineko Kengaku^{1,2}, Naotaka Nakazawa¹, Zhejing Zhang², Gianluca Greci³, Andres Canela⁴ (¹WPI-iCeMS, Kyoto Univ., ²Grad. Sch. Biostudies, Kyoto Univ., ³Mechanobiol. Inst., Natl. Univ. Singapore, ⁴Rad. Biol. Cent., Kyoto Univ.)

Newborn neurons migrate long distances in developing mammalian brains. The large and stiff nucleus presents physical challenge for neurons to pass through the narrow interstitial space. Actomyosin contraction is a major driving force, yet the mechanism by which the actomyosin force is generated is not yet understood.

We have demonstrated that migrating cerebellar neurons switch between multiple actomyosin engines depending on the local tissue environment. In 2D conditions, actomyosin is enriched in the leading process, exerting traction force to the cell soma. In 3D confined space, a mechanosensor PIEZO1 is activated and triggered actomyosin translocation to the posterior membrane.

The lifelong effect of mechanostress during neuronal migration will be discussed.

1SIA-3 微小管によるメカノケミカルクロストークが細胞移動の方向性を制御する

Mechano-chemical crosstalk induced by microtubules in directed cell migration

Yukako Nishimura¹, Tatsuki Kondo¹, Ryota Orii², Taketoshi Kambara³, Kaori Kuribayashi-Shigetomi⁴, Yasushi Okada^{3,5,6}, Hirokazu Tanimoto², Fumio Motegi¹ (¹Inst. Gen. Med., Hokkaido Univ., ²Dept. Sci., Yokohama City Univ., ³BDR, Riken, ⁴Inst. Adv. Grad. Edu., Hokkaido Univ., ⁵Grad. Sch. Sci., Tokyo Univ., ⁶Grad. Sch. Med., Tokyo Univ.)

Directed cell migration is a fundamental process in many biological events. To migrate in a given direction, cells must dynamically protrude/retract their leading edges, but their spatio-temporal regulation remains poorly understood. Here, we show that the activation-inactivation cycle of RhoGEF GEF-H1 by microtubules facilitates the periodic cycles of leading edge movement. Both *in vitro* and *in vivo* assays demonstrate that the GEF activity of GEF-H1 is required for its microtubule-binding affinity. Furthermore, GEF-H1 specifically targets microtubules trapped in protruding edges. These findings provide a mechano-chemical framework for the regulation of GEF-H1 activity by microtubules, which controls the cycle of leading edge movement during cell migration.

1SIA-4 加齢にともなう卵子の染色体数異常の細胞生物学的な原因

Cell biological mechanisms of age-associated egg aneuploidy

Tomoya Kitajima (RIKEN Biosystems Dynamics Research)

Chromosomal numerical abnormality (aneuploidy) in eggs is a leading cause of miscarriage and congenital disorders such as Down syndrome. Egg aneuploidy is caused by errors in chromosome segregation during meiosis in oocytes. Using mouse oocytes as a research model, we are tackling this problem through cell biological approaches including live imaging. In this talk, I would like to discuss our recent findings on the cell biological mechanisms of chromosome segregation errors in oocytes, including the results of our new live imaging technology that identifies and tracks individual chromosomes, as well as the potential of error prevention strategies using artificial kinetochores that are currently under development.

1SIA-5 マウス Metaphase II 卵の紡錘体局在を細胞質流動から守るアクチン構造

Cytoplasmic Flow-Resistant Spindle Positioning by Actin Structures in Mouse Metaphase II Oocytes

Miho Ohsugi, Kotoku Terai (Dept. Biol. Sci., Grad. Sch. Sci., Univ. of Tokyo)

Oocytes undergo highly asymmetric division, requiring prolonged cortical spindle positioning before fertilization. Outward cytoplasmic streaming has been considered essential for maintaining this localization.

However, we found that most non-labeled oocytes showed no streaming or inward flow. Despite this, cortical spindle localization was preserved even with inward flow. We show that streaming direction is controlled by the balance between Arp2/3 complex and myosin II activities. Furthermore, an Arp2/3-dependent actin structure fills the gap between the spindle and plasma membrane and blocks cytoplasmic influx. Our findings indicate that outward streaming is not required for spindle positioning and that chromosome-directed actin assembly ensures its stability.

[1SIA-6](#)細胞骨格のエネルギー動態：アクチン線維構造から細胞分裂へ
Energetics of the Cytoskeleton: From F-actin Architecture to Cell DivisionRyota Sakamoto^{1,2}, Michael Murrell^{2,3} (¹*Inst. Phys., Academia Sinica*, ²*Dept. Biomed. Engr., Yale Univ.*, ³*Dept. Phys., Yale Univ.*)

The spatio-temporal dynamics of intracellular forces drive key behaviors such as cell division and migration, powered by the conversion of chemical energy into mechanical work. The force generation is primarily driven by actin filaments and myosin motors, orchestrating cytoskeletal reorganization and membrane deformation, yet how these forces coordinate division and their energetic costs remain unclear. Using biomimetic model cells composed of purified actin, myosin, and lipid membranes, we show that stress relaxation is key to enable faster and deeper cell division. The efficiency of energy conversion peaks just before division and is also modulated by F-actin architecture. Our findings provide quantitative insights into the mechanics and energetics of cell division.

[1SIA-7](#)アクチン重合の光操作で探る密度依存的な細胞骨格の機能制御
Optogenetic control of actin network assembly reveals density-dependent functions of actin binding proteinsMakito Miyazaki^{1,2,3} (¹*RIKEN IMS*, ²*RIKEN BDR*, ³*Grad. Sch. Med., Sci., & Tech., Shinshu Univ.*)

The actin cytoskeleton forms a dynamic meshwork essential for cell morphogenesis. While the biological functions of actin networks depend on actin-binding proteins (ABPs), how network density influences their activities remains elusive. Here, we developed an optogenetic tool to spatiotemporally control Arp2/3-mediated actin assembly on membranes. Using this tool in a reconstituted system, we examined how density affects two ABPs. We found that myosin penetration into the network was hindered at high densities due to steric hindrance. In contrast, cofilin entered regardless of density, but its network disassembly activity was suppressed in dense networks. These findings demonstrate how actin network density modulates ABP functions and cytoskeletal dynamics.

[1SJA-1](#)小胞体関連分解におけるタンパク質の逆行輸送を促進する膜上ナノクラスター構造
A nanocluster mesh on ER membranes facilitates protein retrotranslocation in ERADKeisuke Mochida^{1,2}, Kenichi Umeda³, Hitoshi Nakatogawa¹, Noriyuki Kodera³, Motomasa Tanaka² (¹*IIR, Science Tokyo*, ²*CBS, Riken*, ³*NanoLSI, Kanazawa Univ.*)

ER-associated degradation (ERAD) maintains ER proteostasis by targeting misfolded proteins for proteasomal degradation. However, the mechanisms enabling diverse ER protein substrates to efficiently traverse the ER membrane remain poorly understood. Here, we show that an ERAD retrotranslocon assembles into nanometer-scale clusters on the ER membrane through its unique intrinsically disordered region. These nanoclusters consist of a dense meshwork that facilitates the retrotranslocation of proteins, including those with aggregation-prone domains. Our findings suggest intriguing structural and functional similarities between the ERAD retrotranslocon and the nuclear pore complex for macromolecular transport across membranes.

[1SJA-2](#)高速 AFM によるアミロイドタンパク質の構造動態と凝集機構の解明
High-speed AFM visualization of structural dynamics and aggregation mechanisms in amyloidogenic proteinsTakahiro Watanabe-Nakayama (*WPI-Nano Life Science Institute, Kanazawa University*)

Amyloidogenic proteins form diverse aggregates linked to neurodegenerative diseases. Structural differences affect pathology, but coexisting aggregate species hinder understanding of aggregation dynamics. High-speed atomic force microscopy (HS-AFM) enables real-time, single-aggregate visualization, including intrinsically disordered regions (IDRs). HS-AFM revealed dynamic fibril features and IDR involvement. Fibrils had stable cores with fluctuating IDRs affecting aggregation and interactions. Notably, all fibrils showed clear elongation polarity, suggesting structural asymmetry is fundamental to aggregation. These findings enhance understanding of amyloid pathogenesis and may inform therapeutic strategies.

1SJA-3 α シヌクレイノパチーの病理とバイオマーカー (seed amplification assay)
Pathology and Biomarkers of Alpha-Synucleinopathies: Focus on Seed Amplification Assays

Ayami Okuzumi (*Juntendo University, Department of Neurology*)

Parkinson's disease (PD) is a neurodegenerative disorder marked by dopaminergic neuron loss and Lewy bodies containing aggregated α -synuclein (α S). Current therapies are symptomatic, and disease-modifying treatments are lacking. Misfolded α S acts as a seed, inducing pathogenic aggregation and spreading in a prion-like manner, leading to neurodegeneration through mitochondrial dysfunction, oxidative stress, and impaired proteostasis. We identified α S seeds in blood, suggesting systemic propagation between brain and periphery. These findings support targeting α S seeds for therapy. This presentation focuses on α S-based pathology and biomarkers using seed amplification assays.

1SJA-4 アミロイド繊維形成とアミノ酸残基レベルの自由エネルギーとの相関
Amyloid Fibril Formation Correlates with Residue-Level Free Energy Profiles

Daisuke Fujinami¹, Seichiro Hayashi², An Ito¹, Sohei Ito¹, Daisuke Kohda³ (¹*Grad. Sch. Integr. Pharm. Nutr. Sci., Univ. of Shizuoka*, ²*NINS, Institute for Molecular Science*, ³*MIB, Kyushu Univ.*)

The log-log plot of kinetic and thermostability perturbations, known as a free energy relationship, reveals features of the folding transition state. The slope reflects its position along the reaction coordinate and the degree of structure formation. Using NMR, we measured residue-specific parameters during folding of the α -spectrin SH3 domain. Observed residues and five point mutations were treated as local perturbations. Three mutations deviated from linearity, suggesting alterations in the folding pathway. Amyloid formation correlated with the dispersion of kinetic and thermostability parameters and with thermodynamic stability. We propose that energetic cooperativity and folded-state stability are key determinants of amyloid formation.

1SJA-5 Unveiling Protein Dynamics through Data Integration Simulations

Osamu Miyashita (*RIKEN Center for Computational Science*)

Understanding the functional mechanisms of biological macromolecules requires structural and dynamic information. However, there are no experimental methods for observing these macromolecules in motion with structural detail. Simulations can help fill this gap, but are limited by computational constraints when capturing large-time-scale dynamics. Integrating simulations with experimental data, particularly from time-resolved or single-particle techniques, can help to overcome these limitations. We have developed hybrid modeling approaches that combine data from X-ray free-electron lasers, atomic force microscopy, and other sources to capture dynamic structural information. In this talk, I will highlight recent integrative modeling projects using these techniques.

1SJA-6 ブリオン株多様性の構造および分子基盤の解明
Structural and mechanistic basis for prion strain diversity

Motomasa Tanaka (*RKEN Center for Brain Science*)

The yeast prion protein Sup35 can form structurally distinct amyloid fibrils that lead to distinct transmissible prion states, or strains. However, our understanding of how different Sup35 fibril structures arise, how fibrils differ at the atomic level, and how structural differences dictate phenotypic variation is limited. Here we study four wild-type and S17R mutant fibrils of the Sup35NM fragment that underlie markedly different [*PST*⁺] strains. We show that the four fibrils have strikingly distinct core structures, which exhibit varying stability and chaperone-accessibility. Our results provide a structure-based mechanism for the yeast prion strain phenomenon with implications for understanding amyloid propagation in other biological systems.

[2SAA-1](#) Integrative Structure Modeling of Protein Complexes Using Experimental Data with Errors and Noise

Takaharu Mori (*Tokyo University of Science*)

In recent years, cryo-electron microscopy (cryo-EM) has been widely used to determine three-dimensional structures of protein complexes, while AlphaFold has achieved remarkable success in structure prediction. However, accurate modeling remains challenging for entirely novel folds or when experimental data are noisy or low in resolution. In this study, we introduce a novel integrative structure modeling approach based on Bayesian inference to effectively incorporate cryo-EM and cross-linking mass spectrometry (XL-MS) data with high levels of noise and uncertainty. In this method, estimated error rates are used as input to perform restrained molecular dynamics (MD) simulations. We evaluate and discuss the predictive performance of the method.

[2SAA-2](#) ゲノム分子モデリングにおける統合的多階層手法 An Integrative Multi-Scale Approach to Genome Molecular Modeling

Giovanni Bruno Brandani (*Department of Biophysics, Graduate School of Science, Kyoto University*)

Eukaryotic genomes are hierarchically organized from the basic unit of the nucleosome to loops linking together distant genomic regions. This 3D organization supports the regulation of gene expression, but we still lack a clear understanding of this process at the molecular level. I will illustrate how to integrate genomic experimental data into molecular dynamics simulations, applying our approach to model the entire Nanog locus of mouse embryonic stem cells down to near-atomic resolution. This allows us to explore the multi-scale functional dynamics of genes: from nucleosome plasticity and transcription factor binding, up to the long-distance communication between promoters and enhancers.

[2SAA-3](#) Investigation of conformational landscape from single-particle cryoEM data via reference based approach

Mao Oide¹, Yuji Sugita^{2,3} (¹*IPR, Osaka Univ*, ²*CPR, RIKEN*, ³*R-CCS, RIKEN*)

Recent advances In single-particle cryo-electron microscopy (cryoEM) enables us to analyze structural heterogeneity encoded in the vast number of particle images. However, low signal-to-noise ratio (SNR) of cryoEM image makes difficult to infer correct conformation of each particle image and consequently structural heterogeneity analysis is still non-trivial task. To address this problem, we have been developing a method to analyze structural heterogeneity by utilizing reference structures. Especially, well-sampled ensemble with molecular dynamics (MD) simulation gives us not only references, but also good collective variables. In this presentation, we will introduce our previous and ongoing works for reference-based structural heterogeneity analysis with cryoEM data.

[2SAA-4](#) 生体分子の機能推定のための高速原子間力顕微鏡動画に基づく理論的考察 Theoretical considerations based on high-speed atomic force microscopy movies to estimate biomolecular functions

Takashi Sumikama^{1,2} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*Nano Life Sci. Inst., Kanazawa Univ.*)

A common and modern approach to infer the biomolecular structure beyond the observed experimental data is the development of mathematical and computational methods. I will talk another but traditional approach: simple theoretical considerations are still useful to estimate complex structures of biomolecules and the relation with functions. Such two examples are the interactions of Na⁺ channels and CaMKII based on high-speed atomic force microscopy (HS-AFM) measurements. Another topic I would like to discuss, time permitting, is the comparison of the configurations obtained by AFMfit for HS-AFM movies, recently developed flexible fitting technique, with molecular dynamics simulations.

2SAA-5 **AFM 画像セグメンテーション誘導フレキシブルフィッティングによるオートファジー関連天然変性蛋白質構造の推論**
Inferring autophagy-related intrinsically disordered protein structures using AFM image segmentation guided flexible fitting

Naoyuki Karasawa¹, Tsuyoshi Ishizone², Sakura Homma¹, Ryota Maejima³, Noriyuki Kodera⁴, Kazuyuki Nakamura⁵, Yasuhiro Matsunaga^{1,6} (¹*Grad. Sch. Sci. Eng., Saitama Univ.*, ²*Organ. Strateg. Coord. Res. Intellect. Prop., Meiji Univ.*, ³*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, ⁴*WPI-NanoLSI, Kanazawa Univ.*, ⁵*Sch. Interdiscip. Math. Sci., Meiji Univ.*, ⁶*R-CCS, RIKEN*)

Intrinsically disordered proteins (IDPs) are involved in key biological processes such as autophagy, while their structural flexibility makes characterization challenging. High-speed atomic force microscopy (HS-AFM) enables real-time imaging of IDPs; however, its limited spatial resolution restricts detailed structural analysis. To address this, we developed a computational method combining semantic segmentation and flexible fitting. A neural network is first trained on pseudo-AFM images created from molecular dynamics simulations. Using the trained model, we generate an initial conformation from a target AFM image, which is then refined through flexible fitting. We report the results of applying this method to AFM images of an autophagy-related IDP.

2SAA-6 **Development of high performance coarse-grained molecular dynamics for large-scale biomolecular simulations**

Jaewoon Jung^{1,2}, Cheng Tan¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS*, ²*RIKEN PRI*)

In multiscale computational simulations of biomolecules, residue-level coarse-grained (CG) models has proven valuable for investigating large-scale biological phenomena. However, efficient parallelization algorithms for these models remain limited, hindering their application on modern supercomputers. In this study, we present a new parallelization scheme using residue-level CG models. This method has been implemented in the GENESIS MD engine as a new module, termed CGDYN. We apply this framework to simulate the dynamics of intrinsically disordered protein (IDP) droplets, capturing fusion events and, notably the direct observation of Ostwald ripening, the dissolution of smaller droplets and the redeposition of their molecules into larger ones.

2SAA-7 **Integrative modeling approaches to characterize the dynamics of biomolecules**

Florence Tama^{1,2} (¹*Grad. Sch. Sci., Nagoya University*, ²*RIKEN Center for Computational Science*)

The function of biomolecules is closely tied to their dynamic behavior, which involves transitions among multiple conformational states. A thorough comprehension of such dynamics involves a description at the atomic level of these conformational states. Experimental techniques such as cryo-electron microscopy and atomic force microscopy provide 2D images that capture different views—and potentially different conformations—of these molecules. To connect these 2D observations with detailed atomic models, simulation approaches can be used to generate conformations consistent with the experimental data. In this talk, we will present our efforts to develop such methods and highlight several of their applications.

2SBA-1 **Understanding Activation Mechanisms in GPCRs - 1) Biophysical studies 2) Computational Validation, and 3) Drug discovery strategies**

Robert Scott Prosser¹, Akio Kitao², Duy Phuoc Tran Tran², Adnan Sljoka³, David Young⁴ (¹*Chemistry & Biochemistry Departments, University of Toronto, Toronto, Ontario, Canada*, ²*School of Life Science and Technology, Tokyo Institute of Technology, Tokyo, Japan*, ³*RIKEN Center for Advanced Intelligence Project, Tokyo, Japan*, ⁴*KisoJi Biotechnology, Canada*)

The human adenosine A_{2A} receptor (A_{2A}R 1-317) was reconstituted in detergent micelles and lipid nanodiscs and studied by ¹⁹F NMR, focusing on specific labeling sites and all tryptophan residues. The resulting activation ensemble is validated by computational studies (MD, Monte Carlo, and rigidity theory) with the goal of better understanding underlying activation mechanisms. Building on this ensemble description of this human GPCR, we present new results toward biased therapeutics consisting of heavy domain antibodies that interact with the receptor, single domain antibodies that are tethered to receptor drugs, and new fragments derived by NMR and Mass Spec which allosterically influence receptor activation pathways.

2SBA-2 プロテアーゼ活性化受容体の活性化機構と G タンパク質結合の構造的基盤
Structural Basis of Activation Mechanism and G Protein Coupling in Protease-Activated Receptors

Hidetugu Asada, Dohyun Im, Makoto Adachi (*Kyoto University Graduate school of Medicine*)

Proteinase-activated receptor (PAR)-4 is a GPCR activated by thrombin-mediated N-terminal cleavage, playing a key role in platelet activation and thrombosis alongside PAR-1. Unlike PAR-1, PAR-4 elicits more sustained and moderate signaling, suggesting its potential as a safer therapeutic target. Here, we report cryo-EM structures of active PAR-4 bound to heterotrimeric G proteins and the ligand-free apo state. A peptide mimicking the tethered ligand bound shallowly at the extracellular surface, in contrast to deep binding pockets in other GPCRs. The apo form revealed a closed ligand-binding site, indicating high flexibility. Structural and functional analyses suggest a unique activation mechanism, offering a foundation for rational PAR-4-targeted anticoagulant design.

2SBA-3 活性化時の構造変化に基づく GPCR の化学遺伝学的制御
Chemogenetic regulation of GPCRs based on structural changes upon activation

Tomohiro Doura (*Grad. Sch. Eng., Nagoya Uni.*)

G protein-coupled receptors (GPCRs) are membrane proteins that induce a variety of cellular functions. Therefore, elucidating the physiological functions of GPCRs will lead to the development of drugs targeting GPCRs. Many structural analyses of GPCRs have provided detailed knowledge of the conformational changes of GPCRs upon activation. We focused on the fact that the structural changes in GPCRs are common to many GPCRs, and developed “coordination chemogenetics” as a method for chemogenetic regulation of GPCRs that is independent on endogenous ligands to elucidate the physiological functions of GPCRs. In this presentation, we will discuss the principles of coordination chemogenetics and the applications to various GPCRs, including an orphan GPCR.

2SBA-4 G タンパク質バイアスリガンドによるヒト GPR84 のシグナル伝達機構
Mechanism of human GPR84 signaling by G-protein biased ligands

Shota Suzuki¹, Duy Phuoc Tran², Koki Nishikawa³, Akio Kitao², Yoshinori Fujiyoshi¹ (¹*Adv. Res. Init., Science Tokyo*, ²*Sch. of Life Sci. and Tech., Science Tokyo*, ³*Joint Res. Crs. Adv. Biomol. Character., TUAC*)

GPR84, a medium-chain fatty acid receptor, is linked to inflammatory/metabolic disorders. The GPR84 antagonist GLPG1205 is in Phase II trials for ulcerative colitis. While fatty acid recognition by GPR84 was known, limited structural data for its inactive or biased agonist-bound active states have hindered drug development. We used cryo-EM to determine antagonist-bound inactive GPR84 and biased agonist-bound active GPR84-Gi complex structures at ~3 Å resolution. We found that biased agonists distinctively alter TM6 conformation. Integrating these structures with mutagenesis and molecular dynamics simulations, we elucidated GPR84's biased activation mechanism. These findings should facilitate the development of selective GPR84 modulators with fewer side effects.

2SBA-5 G タンパク質共役型受容体活性化・不活性化メカニズムのインシリコ研究
In silico investigation of the activation and inactivation mechanisms of G protein-coupled receptors

Akio Kitao (*Sch. Life Sci. Tech, Science Tokyo*)

G protein-coupled receptors (GPCRs) are activated and inactivated by extracellular stimuli, such as ligand binding. This further affects the function of G proteins and other downstream molecules inside the cell. Molecular dynamics (MD) and parallel cascade selection MD (PaCS-MD) are powerful simulation tools for studying complex formation, dissociation, and conformational dynamics, which were employed to investigate GPCR activation and inactivation mechanisms. This talk will cover the effects of ligand binding and mutations on GPCR activation and inactivation, as well as G protein binding, as revealed by the simulations.

[2SBA-6](#) Probing Allosteric and biased signaling with rigidity theory, NMR, and geometric Monte-Carlo simulations in GPCRs

Adnan Slijoša (*RIKEN*)

We apply Rigidity Transmission Allostery (RTA), a method grounded in mathematical rigidity theory, to uncover allosteric signaling and G protein selectivity mechanisms in GPCRs. Combining RTA with ¹⁹F-NMR, we demonstrate how ligands and G protein subunits, especially the βγ dimer, induce long-range conformational changes in the A2A adenosine receptor (A2AR). We identify a precoupled intermediate and two active states stabilized by G protein binding. RTA reveals distinct allosteric pathways responsible for differential selectivity and efficacy with different G protein subtypes. We also demonstrate the complexity of allosteric coupling between all residues across the receptor G-protein complex.

[2SCA-1](#) 3次元立体構造を用いた酵素機能の予測：FUJISANの開発と応用
Predicting enzyme functions using 3D Structures: Development and application of FUJISAN

Suguru Fujita, Tohru Terada (*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

The 3D structure of a protein determines its function. Despite the UniProt Knowledgebase surpassing 200 million entries, only 0.2% have experimentally determined 3D structures. The rise of deep learning models like AlphaFold2 has provided access to predicted 3D structures. We have advanced research to predict protein functions using structural information. We developed FUJISAN, a machine learning tool that predicts if a pair of enzymes catalyze the same reaction on the same substrate based on sequence and structural similarities. We also introduce the development of a flexible discrimination method using deep learning and the results of function prediction using FUJISAN for proteins registered in the secondary metabolite biosynthesis gene cluster database MIBiG.

[2SCA-2](#) 非生物学的化学反応を指向した酵素データベースの探索
Database Mining-driven Enzyme Discovery for Abiotic Chemical Transformations

Shunsuke Kato (*Grad. Sch. Eng., UOsaka*)

Along with the recent significant progress of biotechnology, biocatalysis has been recently attracting an increasing attention as a sustainable way for manufacturing valuable chemical feedstocks. One of the main challenges associated with biocatalysis is to expand the catalytic repertoire of natural enzymes to meet the requirements of synthetic chemistry. In this presentation, we will report our recent research on database mining-driven discovery of novel enzymes capable of catalyzing new-to-nature chemical transformations, such as carbene transfer reactions and NHC-mediated radical acylation reactions.

[2SCA-3](#) 機械学習モデルによる新規酸素反応性 PLP 依存性酵素の発見
Machine learning-guided discovery of novel oxygen and PLP-dependent enzymes

Tomohiro Noguchi^{1,2}, Takayoshi Awakawa¹, Yutaka Saito² (¹*Graduate School of Frontier Engineering, Kitasato Univ.*, ²*CSRS, RIKEN*)

PLP-dependent enzymes represent a large group, catalyzing various reactions like transamination, epimerization, and decarboxylation. A small number of oxygen-reactive PLP-dependent enzymes have recently been discovered, which are scattered in phylogenetically distinct subfamilies. This study aims to create a predictive model for oxygen-reactive amino acid sequences using experimental data and machine learning, enabling comprehensive searches for novel oxygen-reactive PLP-dependent enzymes from genome information. Successful identification and validation of a novel enzyme, 4-guanidinobutanal synthase (GBS) from the genus *Nocardia*, were achieved using this model. Furthermore, GBS forms a biosynthetic gene cluster, which produces cluster-dependent natural products.

2SCA-4 Transformer 言語モデルを用いた天然化合物合成遺伝子クラスターの予測と設計に向けて
A transformer-based platform for the prediction and design of biosynthetic gene clusters

Maiko Umemura (*Appl. Biol., Kyoto Inst. Tech.*)

Biosynthetic gene clusters (BGCs) encode diverse natural products, including antibiotics and anticancer agents. Identifying and designing BGCs in microbial genomes is crucial for creating new bioactive compounds. We developed a transformer-based deep learning model that treats protein domains as language-like tokens and learns their genomic arrangement. Trained on both known BGCs and whole genomes, the model accurately predicted functional domains and proposed novel, biologically plausible combinations. Experimental validation of one prediction implied the model's utility, demonstrating the potential of transformer-based language models for designing natural product biosynthetic pathways.

2SCA-5 人工設計タンパク質を利用した新規酵素機能改変戦略
Engineering by Proxy: A Novel Strategy for Enzyme Function Redesign Using Synthetic Designer Proteins

Shun-ichi Tanaka (*Grad. Sch. Life and Environ. Sci., Kyoto Pref. Univ.*)

Synthetic binding proteins, built on non-antibody scaffolds, mimic the high affinity and specificity of antibodies while overcoming key drawbacks such as long development times, high production costs, and instability under reducing conditions. Though initially developed for medical use, their applications are expanding into industrial fields. This presentation introduces "Enzyme Engineering by Proxy," a novel strategy that redefines enzyme engineering. Instead of mutating the enzyme gene, this method alters substrate specificity by positioning a synthetic binding protein near the active site. I will present the concept, methodology, and several case studies demonstrating its feasibility and potential for industrial use.

2SCA-6 酵素反応の理論的予測と改良
Computational prediction and improvement of enzymatic reactions

Munchito Arai^{1,2} (¹*Dept. Life Sci., Univ. Tokyo*, ²*Dept. Phys., Univ. Tokyo*)

Enzymes fold into specific structures and carry out their functions in multiple steps. However, predicting these reactions has been challenging. Recently, we developed a physical theory called the WSME-L model that can predict the folding reactions of proteins of various sizes and shapes. A modified version of the WSME model predicted the turnover rate of an enzyme in agreement with experimental results. In addition, based on molecular dynamics simulations of an enzyme/product complex, we successfully developed mutants that improve the efficiency of two-step alkane biosynthesis. Furthermore, we are developing a theoretical method to enhance enzyme activity. These computational studies will be useful for elucidating and improving enzymatic reactions.

2SDA-1 液体足場：細胞の未知との遭遇
Fluid Scaffolds: An Encounter with the Unknown for Cells

Jun Nakanishi (*NIMS*)

Mammalian cells are typically cultured on stiff plastic or glass dishes. This is because cells have intrinsic contractility and exert mechanical force on their substrates. It is critical for cells to receive sufficient mechanical feedback, so stiff materials are chosen for cell culturing scaffolds. Our group is developing cell scaffolds based on the interface of water and hydrophobic liquids, such as perfluorocarbons and ionic liquids. By engineering the interfacial and bulk properties of these fluids, we can make the cells attach and grow thereon, where we can witness unique cellular behaviors.

[2SDA-2](#) Design of non-sticking microdroplets toward single cell analysis

Mizuki Tenjimbayashi (*National Institute for Materials Science*)

We study non-wetting microdroplets, where micrometre-sized droplets are coated with liquid-repellent nanoparticles and made non-wetting. These non-wetting droplets can be handled like solid materials, but retain the unique shape reconfigurability of liquids, which enhances droplet handling. Various applications are possible by changing the type of liquid inside. For example, cells can be enclosed in droplets in single units, opening a new class of cell-handling technology.

In this presentation, the dynamics and manipulability of non-wetting microdroplets will be introduced and examples of their use in cell culture will be reported.

[2SDA-3](#) 生体分子集合体の階層構造が導く非球形凝縮体の創生 Supramolecular Hierarchical Assembly Involving Peptides and Oligonucleotides Forming Non-Spherical Biomolecular Condensates

Hiroka Sugai (*IIR, Science Tokyo*)

Biomolecular self-assembly offers a fundamental framework for understanding molecular mechanisms in biology and for guiding the rational design of functional systems in materials science. These assemblies encompass a wide variety of structural organizations, ranging from fluidic architectures such as phase-separated droplets to highly ordered structures like fibrils. We focus on non-spherical, cell-sized biomolecular condensates that integrate both fluidity and structural order, formed through hierarchical supramolecular assemblies of chemically defined peptides and oligonucleotides. In this presentation, we report on the design strategies, assembly dynamics, and structural characteristics of these systems.

[2SDA-4](#) 低分子コアセルベートの形成と内部環境や機能化に対する化学構造の影響 Impact of Molecular Structure on Low-Molecular-Weight Coacervates: Formation, Internal Environments, and Functionalization

Sayuri Higashi^{1,2,3}, Ryutaro Fujimoto⁴, Koichiro Hirose^{5,6}, Kodai Kanemaru^{7,8}, Norio Yoshida⁷, Kenichi Suzuki^{5,6}, Masato Ikeda^{2,3,4,5} (¹*Inst. Adv. Study, Gifu Univ.*, ²*Grad. Sch. Drug Disc. & Med. Info. Sci., Gifu Univ.*, ³*COMIT, Gifu Univ.*, ⁴*Dept. Life Sci. & Chem., Grad. Sch. Nat. Sci. & Technol., Gifu Univ.*, ⁵*iGCORE, Gifu Univ.*, ⁶*Div. Adv. Bioimaging, NCCRI*, ⁷*Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.*, ⁸*FIFC, Kyoto Univ.*)

In living systems, compartmentalization allows biomolecules to perform complex functions. Coacervates—cell-like soft materials formed by liquid-liquid phase separation (LLPS) of polyelectrolytes—have drawn attention as mimics of membraneless organelles. Recently, peptide-based coacervates made of sticker-spacer molecules showed functions similar to membraneless organelles. We synthesized various sticker-spacer molecules and studied their effects on coacervate formation. Their physical properties, including stimuli responsiveness and guest uptake, were examined using methods such as molecular dynamics simulations and single-molecule fluorescence microscopy. These results provide insights into designing hierarchical coacervate systems like living cells.

[2SDA-5](#) コアセルベートによる革新的生体高分子送達 Innovative Delivery of Biomacromolecules via Coacervates

Yoshimasa Kawaguchi (*Inst. Chem. Res*)

Antibodies are widely used in life science research and therapeutics due to their high specificity and affinity for target molecules. However, their lack of membrane permeability limits their use in live-cell studies to extracellular targets. Developing a method for intracellular antibody delivery would significantly advance our understanding of cellular functions. Here, we demonstrate that coacervates formed by trimeric attenuated cationic membrane-lytic peptide L17E and engineered negatively charged antibodies enable cytosolic delivery upon addition to cells. This presentation outlines the design of the negatively charged antibodies, the physicochemical characteristics of the coacervates, and the mechanism underlying their intracellular delivery.

2SEA-1**生命の起源：ペプチド集合体・区画による RNA 合成の活性化****The origin of life: Enhancement of RNA synthesis by peptide aggregates and compartments****Shunsuke Tagami** (*RIKEN IMS*)

To recreate the emergence of life on ancient Earth, we aim to reconstruct RNA-peptide macromolecular compartments that mimic primordial cell-like systems. Our focus is particularly on simple peptides that enhance the RNA polymerase ribozyme (RPR), an artificial model for ancient self-replicating RNA. For example, a cationic-hydrophobic peptide (KKVVVVVV) forms insoluble aggregates that concentrate RNA on their surface and enhance the RPR activity (Li et al., Nat Commun, 2022). Recently, we also found that RPR can be activated on surfaces of peptide-based LLPs (unpublished). These findings suggest that such self-assembling peptides could have facilitated the emergence of longer, functional RNAs on prebiotic Earth.

2SEA-2**RNA が導く膜のない細胞内区画の形成：その機構と分子論的理解****RNA-Guided Formation of Membraneless Intracellular Compartments: Mechanisms and Molecular Insights****Tomohiro Yamazaki** (*Front. Biosci., The University of Osaka*)

Cells contain diverse membraneless compartments, known as biomolecular condensates, formed without lipid membranes. RNA serves as a key structural component in their formation. This presentation outlines how RNA collaborates with proteins to drive phase separation and organize these compartments. A novel mechanism called “micellization,” where RNA-protein complexes behave as block copolymers to form micelle-like condensates, will be introduced. Mechanistic insights gained from synthetic RNA-based reconstitution systems will also be discussed, highlighting the cellular functions and molecular basis of RNA-driven compartmentalization.

2SEA-3**人工細胞回路による多細胞パターンのデザイン****Programming multicellular patterns with synthetic cell-cell communication****Satoshi Toda** (*IPR, Univ. Osaka*)

During tissue development, cells communicate with each other to generate multicellular behavior and complex tissue morphologies. To understand and control morphogenetic processes, we have been developing bottom-up approaches to design cell-cell communication rules in the cultured cell systems and analyze emergent multicellular behavior. Recently, we found that we can reconstruct robust pattern formation of tissue compartments by the interplay of cell signaling and responsive cell behavior such as cell adhesion and apoptosis. In this talk, I will introduce our synthetic biology technologies to engineer cell-cell communication and discuss the functions of basic cell-cell communication rules for tissue patterning.

2SEA-4**植物に寄生するシストセンチュウは破壊者か？建築家か？****Cyst nematodes: Destroyers or Architects? ~Insights from the 3D structure of host plant tissues~****Mina Ohtsu** (*NAIST, Bio.*)

Cyst nematodes, which are plant-parasitic nematodes, induce unique infected cells called syncytia in host plant roots. Syncytia are large multinucleate cells formed by cell fusions following cell wall degradation. However, the 3D structure of syncytia and the process of their induction remain largely unknown, as they form deep within root tissues. To address this, we established an in planta 3D imaging system using a tissue-clearing solution and two-photon excitation microscopy (2PEM). Interestingly, 3D imaging revealed unique “pillar-like structures” specifically located at syncytial cell walls. These results suggest that cyst nematodes are not destroyers that randomly degrade cell walls, but rather architects that systematically remodel them.

2SEA-5 ライブイメージングのための透明化試薬の開発
Minimally invasive optical clearing media for live cell imaging ex vivo and in vivo

Shigenori Inagaki (*Grad. Sch. Med. Sci., Kyushu Univ*)

We develop minimally invasive optical clearing media (SeeDB-Live) for fluorescence imaging of live mammalian tissue. SeeDB-Live allows for structural and functional imaging in the deeper regions of spheroids, organoids, acute brain slices, and the mouse brain in vivo. SeeDB-Live minimally affects cell proliferation, electrophysiological properties, and sensory responses. We demonstrate its utility for widefield imaging of subcellular voltage dynamics, such as backpropagating action potentials, in acute brain slices. We also utilize SeeDB-Live for widefield voltage imaging of dozens of dendrites in vivo, demonstrating population dynamics. Thus, SeeDB-Live expands the scale and modalities of fluorescence imaging of live mammalian tissues.

2SEA-6 区画・領域依存的生命現象を可視化する 3D 蛍光顕微鏡法の開発
Novel 3D Fluorescence Microscopy to Visualize Compartment- and Region-Dependent Biological Phenomena

Kohei Otomo^{1,2,3} (¹*Sch. Med., Juntendo Univ.*, ²*NIPS, NINS*, ³*ExCELLS, NINS*)

Fluorescence microscopy is one of the essential analytical techniques in biological and medical research from the subcellular to the tissue level. However, fluorescence microscopy is an optical microscopy, resulting in difficulties to visualize internal structures in untransparent, heterogeneous, and 3D volumetric biological specimens. To overcome these limitations, multiphoton excitation processes using near-infrared light pulses and tissue-clearing techniques have been developed and implemented. In this talk, the direction of technological developments required by end-users will be discussed with several compartment and region-dependent biological examples visualized by our developed microscopy systems.

2SFA-1 In vitro における微小管の機械的適応
Mechanical adaptation of in vitro microtubules

Daisuke Inoue (*Fac. Des., Kyushu Univ.*)

The cytoskeleton is a fundamental cellular component that governs cell morphogenesis and motility. It is recognized as a mechanosensor that responds to external mechanical stress. However, elucidating the mechanisms by which the cytoskeleton senses the stress and dynamically reorganizes itself in response to stimuli in living cells remains challenging due to its complexity. In this talk, I report on the mechanisms underlying the mechanical stress response of a reconstituted cytoskeleton. A dynamic microtubule network, reconstituted with kinesin motor proteins, undergoes remodeling to mitigate external mechanical stress, thereby adapting to the applied stress. Furthermore, I discuss studies that motor proteins facilitate the turnover of the microtubule lattice structure.

2SFA-2 CD44 を介した細胞集団内の力学ネットワーク感知と集団運動
CD44-Mediated Mechanical Network Sensing within Cell Populations and Collective Cell Migration

Keitaro Shibata¹, Chihori Asano¹, Koki Ishida², Takuto Hori², Shigenobu Yonemura¹ (¹*Grad. Sch. Biomed. Sci., Tokushima Univ.*, ²*Med. Faculty, Tokushima Univ.*)

CD44 is a membrane protein that binds to hyaluronic acid, a component of the extracellular matrix, and promotes cell proliferation and cell migration. Individual cells engaged in collective migration exchange mechanical stimuli generated by their mutual movements, and CD44 is one of the molecules that mediates this process, but the details remain unclear. We performed wound healing assays using epithelial cell sheets and a detailed analysis of individual cell migration, and found that CD44 may detect surrounding hyaluronic acid and determine the direction of collective cell migration. This suggests that CD44 transmits changes in the mechanical state of the extracellular environment into the cell and precisely controls cell migration in a context-dependent manner.

[2SFA-3](#)

カルマンフィルタで上皮組織の力の時間変化を推定する

Kalman force inference for epithelial deformation: a force inference method for time-lapse movies

Goshi Ogita¹, Takemasa Miyoshi², Tatsuo Shibata¹ (¹BDR, RIKEN, ²R-CCS, RIKEN)

Mechanical forces are essential for driving morphogenesis. However, direct measurement of forces is still technically difficult. Therefore, inferring cellular forces from the image of epithelial tissue is important. However, methods to accurately infer these dynamics have not been well developed. Here, we propose a new method, Kalman Force Inference (KFI), to infer these dynamics from time-lapse movies using the Kalman filter, a common tool for time-series analysis. KFI will help us to elucidate the role of force dynamics in epithelial mechanics.

[2SFA-4](#)

Mechanical Instability Induces Transition in Epithelial Layer Structure via Nucleation and Growth

Shuya Fukamachi¹, Datta Razib¹, Makiko Arai¹, Rei Yagasaki², Shuhei Horiguchi², Satoru Okuda² (¹Grad. Sch. NanoLS, Kanazawa Univ, ²WPI-NanoLSI, Kanazawa Univ.)

The epithelium transitions from a monolayer to a multilayer structure during organogenesis, influenced by factors like junctional tension, cell density, and geometry. However, how these factors drive stratification remains unclear. Here, we identify a mechanism resembling a phase transition in physics. Through cell culture and three-dimensional mechanical modeling, we demonstrate that stratification occurs via a nucleation-growth process: multilayer seeds spontaneously emerge, and stratified domains expand. This mirrors a phase transition driven by mechanical instability in the foam-like epithelial geometry. This concept also applies to embryonic skin development and cancerous transformation, framing epithelial stratification as a nucleation-driven phase transition.

[2SFA-5](#)

変形可能細胞の数理モデルから迫る、高密度細胞集団動態

Modeling Collective Dynamics in Densely Packed Deformable Cells

Nen Saito (Grad. Sch. Integr. Sci. Life, Hiroshima Univ.)

Cell deformability within dense tissues can play a crucial role in determining tissue-scale mechanical properties. Simulation-based theoretical studies are essential for characterizing such collective behaviors. However, large-scale simulations of deformable cells have typically been limited to simple convex polygonal shapes due to computational constraints.

In this talk, I will present a novel simulation framework that enables efficient modeling of large populations of freely deformable cells, offering significantly improved computational performance over existing methods. Using this framework, we analyze various biological phenomena, including collective dynamics in densely packed cell populations and cell assembly processes guided by chemotactic cues.

[2SFA-6](#)メカノ勾配による Wnt モルフォゲンノイズ除去システムは組織パターン形成の頑強性を支える
"Mechano-gradients" drive morphogen-noise correction to ensure robust patterning

Kana Aoki, Tohru Ishitani (Dept. of Homeostatic regulation, RIMD, Univ. Osaka)

Activity gradients of morphogen signaling instructs cell identities to achieve tissue patterning. However, developing tissues often produce cells with unfit morphogen signaling and consequent noisy morphogen gradients. Here we show that intercellular tension generated by cadherin-actomyosin interaction corrects noisy morphogen gradients to ensure robust morphogen gradient formation. Imaging analyses reveal that Wnt morphogen gradients generate intercellular tension gradients via cadherin-actomyosin interaction in early zebrafish embryos. Unfit cells producing noisy gradients changes cadherin-actomyosin levels and local tension, and neighboring fit cells sense this change and initiate cell competition-mediated apoptotic elimination of unfit cells to correct the gradient.

2SFA-7 軟骨細胞のカラム形成を介して骨形態形成を制御する力学場
Mechanical stress field regulating bone morphogenesis through chondrocyte column formation

Yuka Yokoyama¹, Yoshitaka Kameo², Junko Sunaga³, Koichiro Maki^{3,4}, Taiji Adachi^{3,4} (¹*Med. Res. Lab., Science Tokyo*, ²*Col. Eng., Shibaura Inst. Tech.*, ³*Inst. Life Med. Sci., Kyoto Univ.*, ⁴*Grad. Sch. Eng., Kyoto Univ.*)

Bone shape is determined by the multicellular dynamics of chondrocytes during tissue morphogenesis. Especially, column formation by proliferative chondrocytes and subsequent hypertrophy are critical for bone length and width and are known to be influenced by mechanical forces. We investigated the regulatory mechanism of bone shape by assuming an energy function composed of membrane elasticity and adhesion and performing bone morphogenesis simulations based on continuum-based particle models. As a result, it was found that an anisotropic stress field in the proliferative zone of the growth plate is promoted by chondrocyte hypertrophy and can induce column formation of proliferative chondrocytes to regulate bone elongation.

2SGA-1 走査型蛍光相関分光法により明らかとなったタンパク質凝集体内における低移動性 TDP-25
Scanning fluorescence correlation spectroscopy reveals slowly mobile TDP-25 within protein aggregates

Yuta Hamada¹, Akira Kitamura² (¹*Grad. Sch. Sci. of Life Sci., Hokkaido Univ.*, ²*Fac. of Adv. Life Sci., Hokkaido Univ.*)

TDP-43 and its 25 kDa C-terminal fragment (TDP-25) form cytoplasmic aggregates implicated in neurodegeneration. Although FRAP analyses have shown that TDP-43 and TDP-25 are largely immobile within the aggregates, it remains unclear whether they are completely immobilized or exhibit extremely slow dynamics, and the physicochemical properties of the aggregates remain poorly understood. Here, we applied scanning fluorescence correlation spectroscopy (Scanning FCS) to detect fluorescence fluctuations of GFP-tagged TDP-25. This approach revealed that TDP-25 is not statically immobilized but exhibits slow mobility within the aggregates. This technique may broadly help elucidate the physicochemical properties of tightly packed aggregation-prone biomolecules in the aggregates.

2SGA-2 平衡および非平衡条件におけるアミロイド β 凝集の分子動力学シミュレーション
Molecular dynamics simulation of amyloid- β aggregation under equilibrium and nonequilibrium conditions

Hisashi Okumura^{1,2,3} (¹*Exploratory Research Center on Life and Living Systems*, ²*Institute for Molecular Science*, ³*SOKENDAI*)

Alzheimer's disease is known to be caused by aggregated amyloid beta (A β) peptides. We performed molecular dynamics (MD) simulations to understand the aggregation of A β peptides under equilibrium and nonequilibrium conditions. For the equilibrium MD simulation, we found that the β -hairpin structure in an A β peptide enhances the intermolecular β sheet between multiple A β peptides. We also found that the electrostatic attraction between Arg5 and the C-terminus plays the key role in aggregation. For the MD simulation under non-equilibrium condition, we found that shear in the A β solution enhances the aggregation and revealed its mechanism.

2SGA-3 興奮性シナプス形成の開始誘導：ナノモラー濃度での SynGAP 液状凝縮体形成とそれが誘導する PSD95 と受容体のアセンブリー
Initiation of excitatory synapse formation: SynGAP LLPS at nanomolar concentrations induces PSD95 and receptor oligomer recruitment

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Synapse formation is at the core of neuronal circuit regulation. We found that an excitatory synaptic protein SynGAP forms micron-scale LLPS condensates at submicromolar concentrations, which begins at <10 nM, forming nanoclusters. Our results suggest that trimers of SynGAP's intrinsically disordered region induced by the adjacent coiled-coil domain may act as units for LLPS, while CaMKII-mediated phosphorylation moderately suppressed it. PSD95 does not form clusters at these concentrations, but is recruited to SynGAP condensates via PDZ-mediated interactions. This enables recruitment of Neuroligin1 and TARP2, enhanced by their homo-oligomerization. These results suggest that SynGAP LLPS acts as an initiator for the synapse assembly, challenging PSD95-centered models

[2SGA-4](#) トランスクリプトームおよび画像解析による枯草菌の遊走コロニーの時空間プロファイリング Multimodal Spatiotemporal Profiling of *Bacillus subtilis* Swarm Development via Integrated Transcriptomics and Microscopy

Kazuki Noshio^{1,2,3}, Hannah Jeckel³, Konstantin Neuhaus³, Alasdair Hastewell⁴, Dominic Skinner⁴, Dibya Saha³, Niklas Netter³, Nicole Paczia⁵, Jörn Dunkel⁴, Knut Drescher³ (¹*Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo*, ²*Collaborative Research Institute for Innovative Microbiology, The University of Tokyo*, ³*Biozentrum, University of Basel*, ⁴*Department of Mathematics, Massachusetts Institute of Technology*, ⁵*Max Planck Institute for Terrestrial Microbiology*)

In microbial communities like biofilms and colonies, environmental variations create subpopulations with distinct traits, even among genetically identical cells. *B. subtilis* exhibits a specialized surface motility called swarming, forming colonies with dynamic spatial and temporal motility patterns. We examined spatiotemporal heterogeneity in *B. subtilis* colonies using transcriptomics and microscopy. With a custom robot, we sampled cells from different colony regions at various growth stages and performed RNA-Seq, while simultaneously tracking motility by microscopy. Our results reveal a strong link between carbon metabolism and motility, as well as metabolite exchange between subpopulations, highlighting division of labor and cooperation within *B. subtilis* communities.

[2SGA-5](#) 上皮の細胞間接着形成過程におけるダイナミクス Dynamic processes of cell-cell adhesion in epithelial cells

Yukako Oda (*Kyoto University*)

Epithelial cells adhere to each other and form barriers against various external stresses. This barrier function is contributed by tight junctions (TJs). We previously identified a novel physiologically active peptide, JIP (tight junction-inducing peptide), which induces TJ formation. JIP is derived from C-terminus of the anti-inflammatory protein alpha1-antitrypsin. Recently, we found that JIP regulates the reorganization of F-actin at the apical junctional complex, and that factors involved in cell-cell adhesion exhibit spatiotemporally dynamic behavior during the adhesion process. In this presentation, we will focus on the epithelial response to stress and discuss the role of adhesion-related factor dynamics in promoting epithelialization.

[2SGA-6](#) クライオ光電子相関顕微鏡の開発と現在の状況 Development and Current Status of Cryogenic Correlative Light and Electron Microscopy

Satoru Fujiyoshi (*Dept. Phys., Science Tokyo*)

To visualize individual molecules and their networks in cells, we have been developing a cryogenic correlative light and electron microscopy (cryo-CLEM) system. In this approach, cells are rapidly frozen to below 100 K. While maintaining this cryogenic temperature, the cells are thinned using a cryo-focused ion beam, and imaged with a cryo-fluorescence microscope (cryo-FM) and a cryo-electron microscope (cryo-EM). We have developed cryo-FM with a lateral resolution of 5 nm. By incorporating this system into the cryo-CLEM workflow, we aim to achieve nanometer-scale resolution in cryo-FM and cryo-EM imaging. In this presentation, I will show the current status of cryo-CLEM development, share our latest findings, and discuss future directions and potential applications.

[2SHA-1](#) 試験管内自律的セントラルドグマへの挑戦と鏡像生命に向けた展望 Challenges to realizing in vitro autonomous central dogma and prospects for mirror life

Wataru Aoki (*The University of Osaka*)

The development of self-replicating artificial cells, or a self-replicating central dogma, has been a long-standing goal in synthetic biology, with the potential to drive profound scientific advances. Achieving ribosome biogenesis outside living cells is an essential step toward creating artificial cells, as synthesizing ribosomes from DNA is vital for building artificial cells. In this presentation, I will discuss the latest results from our laboratory on ribosome biogenesis in vitro. I will also discuss the potential advantages and disadvantages of artificial cell research for the realization of mirror life.

2SHA-2

翻訳システムから考える鏡像生命創成への展望

Toward Mirror-Image Life: Insights from Translation Systems

Yoshihiro Shimizu (*RIKEN, BDR*)

Richard Feynman's dictum "What I cannot create, I do not understand" often motivates the quest to build synthetic cells. This principle should extend beyond recreating known systems: fabricating entities absent from nature can likewise deepen insight and spur applications. Mirror-image life, cells built from enantiomeric biomolecules, is one of the important targets. Its absence on Earth leaves open why terrestrial life chose a single chirality; engineered synthesis could test this. Although full reconstruction of natural cells remains unfinished, achieving it may bring mirror-life within reach. In this talk, I will outline how a self-replicating protein-synthesis network underlies both goals, highlighting expected technological hurdles and their solutions.

2SHA-3

タンパク質化学合成と In vitro セレクションによる鏡像抗体ミメティックの創成

Mirror-image Antibody Mimetic Generated via Chemical Protein Synthesis and mRNA Display

Gosuke Hayashi (*Grad. Sch. Eng., Nagoya Univ.*)

Antibody mimetic functions as binders against various target molecules with high affinity and specificity comparable to conventional IgG antibodies. However, biologically produced protein drugs are generally degraded by proteases and often exhibit immunogenicity. To increase protease resistance and decrease immunogenicity of peptides and proteins, mirror-image peptide/protein binders consisting of *D*-amino acids have been developed so far mainly through the mirror-image phage display technique. Here, we present a mirror-image protein binder derived from a monobody, one of the most promising protein scaffolds, using two notable technologies: chemical protein synthesis and TRAP display, which is an improved version of mRNA display.

2SHA-4

Perspective on the Evolution of Mirror-Life Based on Microbial Experimental Evolution

Chikara Furusawa^{1,2} (¹*BDR, RIKEN*, ²*Univ. Biol. Inst., Univ. Tokyo*)

Evolvability, defined as a system's capacity to adapt to changing environmental conditions, is a fundamental property of life. Artificially constructed mirror-image organisms are also expected to possess this capacity. To scientifically evaluate the potential utility and risks of such organisms, it is essential to understand how their evolvability may manifest in environments inhabited by non-mirror-image life. Our research group conducts experimental evolution using non-mirror-image prokaryotes to analyze the properties of evolvability and to explore the predictability and controllability of evolutionary processes. In this talk, I will present our recent findings and discuss the potential evolvability of mirror-image life in light of these insights.

2SHA-5

新興技術における「責任ある研究イノベーション (RRI)」のあり方を考える

Navigating the Future of Emerging Technologies: Responsible Research and Innovation (RRI)

Makiko Matsuo (*Grad. Sch. Public Policy, Univ. Tokyo*)

Research and development of emerging technologies, including Mirror Life, are advancing rapidly. This rapid advancement may lead to the "pacing problem," where the negative impacts of technological development outpace societal responses and oversight. To keep pace with technological development, those engaged in research and development must address gaps in current regulatory science and incorporate "safety by design" in their development to promote responsible research innovation (RRI). They must also be more proactive in engaging in rule-making with policymakers and regulators to ensure that the rules are proportionate to the risks posed. This presentation will explore what is needed to build "anticipatory governance" in ensuring RRI.

[2SIA-1](#)

人工液-液相分離ペプチドのデザインと物性制御

Design and control of physicochemical properties of artificial liquid-liquid phase-separating peptides

Keisuke Ikeda (*Fac. Pharm. Sci., Univ. Toyama*)

We have developed the phase-separating peptide, RD9, for mimicking characteristics of biological condensates and investigated the physicochemical properties of liquid-like droplets formed by the peptide in detail. We revealed that the peptide formed droplets through electrostatic interactions in aqueous phase under physiological conditions. In addition, the surface modification of the droplets with PEGylated peptide inhibited the droplet fusion and led to the long-term stability of the droplet suspension. Our observations under manipulation of the droplets with optical tweezers revealed different behavior of the surface modified droplets in terms of adhesion, fusion, and separation of the droplets in contact depending on the molecular weight of PEG.

[2SIA-2](#)ペプチドによる α -シヌクレインの液-液相分離誘導と物性制御Peptide-Mediated Modulation of α -Synuclein Liquid-Liquid Phase Separation and Its Biophysical Properties**Tatsuya Ikenoue** (*IPR, Univ. Osaka*)

Liquid-liquid phase separation (LLPS) of proteins has been extensively investigated, yet precise control over LLPS remains challenging, with no de novo molecules reported to directly regulate protein-specific LLPS. Here, we present the identification of de novo peptides that effectively induce LLPS of α -synuclein (α Syn), a Parkinson's disease-associated protein, using a peptide screening platform. Moreover, we show that these peptides and their variants modulate the biophysical properties of α Syn condensates and influence subsequent liquid-to-solid phase transitions. These findings offer valuable tools for elucidating the mechanisms of α Syn LLPS and provide a foundation for broader applications in phase separation research.

[2SIA-3](#)

酵母プリオン Sup35 配列由来のデザインタンパク質を用いた液-液相分離に影響を及ぼすアミノ酸の解析

Analysis of amino acids affecting liquid-liquid phase separation using a design protein based on the yeast prion Sup35 sequence

Yumiko Ohhashi¹, Haru Takabatake², Hideki Taguchi^{1,2} (¹*CBC, IIR, Science Tokyo*, ²*Sch. of Life Sci. Tech, Science Tokyo*)

Many proteins involved in intracellular liquid-liquid phase separation (LLPS) contain low-complexity domains (LCDs) composed of a limited set of amino acids. These regions form droplets via multivalent intermolecular interactions. Prion domains, a type of LCD, include residues like Y and F that are involved in interactions. However, the roles of abundant residues such as Q, N, and P in LLPS remain unclear.

To explore these roles, we designed a simplified amino acid sequence based on the N-terminal LCD of the yeast prion protein Sup35, which exhibits phase-separation properties. By adding one or two specific residues and analyzing changes in droplet behavior, we identified amino acids that increase droplet reversibility and others that enhance droplet formation.

[2SIA-4](#)

ALS 関連 FUS 変異体の相挙動に対する圧力・温度および低分子の影響

Effects of pressure, temperature, and small molecules on phase behavior of amyotrophic lateral sclerosis-linked FUS variants

Ryo Kitahara^{1,2} (¹*Coll. Pharm. Sci., Ritsumeikan Univ.*, ²*Grad. Sch. Pharm., Ritsumeikan Univ.*)

In familial amyotrophic lateral sclerosis (ALS), aggregation of the RNA-binding protein fused in sarcoma (FUS) in motor neurons contributes to disease onset. FUS undergoes liquid-liquid phase separation (LLPS), which can lead to irreversible aggregation. To clarify its mechanism, we constructed pressure-temperature phase diagrams for wild-type FUS and ALS variants R495X and P525L using turbidity and microscopy. Two LLPS types were identified: LP-LLPS (<2 kbar) and HP-LLPS (>2 kbar). Pressure-jump assays showed that HP-LLPS has higher aggregation propensity. ATP, a biological hydrotrope, also affected FUS-LLPS. These findings suggest that targeting HP-LLPS offers a new therapeutic approach for ALS.

Kiyoto Kamagata (*Fac. Eng. & Grad. Sch. Eng., Gifu Univ.*)

Phase-separating proteins utilize the liquid-liquid phase separation phenomenon and work as an ensemble. Although high concentration in protein droplets enables highly efficient chemical reactions and other processes, there is a risk of forming abnormal aggregates. Based on the above, we are working on understanding the liquid-liquid phase separation phenomena of naturally denatured proteins p53 and FUS using single molecule fluorescence microscopy, controlling the phase separation phenomena using peptide binder technology, and designing phase-separating mini-proteins. In the presentation, I would like to introduce selected topics from these studies.

Masaki Tsujimura^{1,2}, Keisuke Saito¹, Hiroshi Ishikita¹ (¹*Grad. Sch. Eng., Univ. Tokyo*, ²*RIKEN*)

Proton transfer plays a central role in the light-induced functions of microbial rhodopsins. Here, we present our recent studies on proton transfer in microbial rhodopsins, including (i) investigation of protonation states in the anion channelrhodopsin GtACR1 using an electrostatic continuum model, and (ii) analysis of proton transfer in the sodium-pumping rhodopsin KR2 using a quantum mechanical/molecular mechanical (QM/MM) approach. We also demonstrate relationships (iii) between stretching vibrational frequencies of hydrogen bond donor groups and pK_a differences between hydrogen bond donor and acceptor groups (ΔpK_a), and (iv) between hydrogen bond distances and ΔpK_a , enabling the estimation of pK_a values of residues that are involved in proton transfer.

Taito Urui (*Grad. Sch. Sci., Univ. Osaka*)

Light-driven proton pump rhodopsins unidirectionally transport a proton across membranes by utilizing light energy. The first outward proton pump was discovered in 1971. Then, the first inward proton pump was discovered in 2016. The discovery of proton pumps with opposite transport directions raised a fundamental question: what determines the direction of the proton transport. To address this question, we employed time-resolved resonance Raman spectroscopy to examine the retinal chromophore structures of photointermediates in both outward and inward proton pumps. In the presentation, we will discuss the mechanism of unidirectional proton transfer by comparing the structural changes between outward and inward proton pumps.

Ritsu Mizutori¹, Nipawan Nuemket^{2,3}, Luo Fangjia³, Shoko Hososhima^{1,5}, Jacopo D'Ascenzi⁴, Leonardo Oliveira⁴, Sayaka Ohashi¹, Rei Abe-Yoshizumi¹, Riccardo Palombo⁴, Satoshi Tsunoda^{1,5}, Yuji Furutani^{1,5}, Oded Béja⁶, Massimo Olivucci^{4,7}, Eriko Nango^{3,8}, Kota Katayama^{1,5}, Hideki Kandori^{1,5} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Japan Synchrotron Radiation Research. Inst.*, ³*RIKEN SPring-8*, ⁴*Univ. Siena*, ⁵*OptoBioTechnology Research Cent.*, ⁶*Technion-Israel Inst. Tech.*, ⁷*Bowling Green State Univ.*, ⁸*Institute of Multidisciplinary Research for Advanced Materials, Tohoku Univ.*)

V2HeR3 is a proton transporting heliorhodopsin. Although positions E191, E205, and E215 were identified as important residues, the detailed mechanism remains unclear. Here, we investigated the proton transport mechanism of V2HeR3 using X-ray crystallography, spectroscopy, electrophysiology, and theoretical calculations. We determined two structures of V2HeR3 containing all-*trans* and 13-*cis*, and 15-*syn* retinal with 2.1 Å resolution. Spectroscopic analyses of mutants E191Q/D, E205Q, and E215Q, provided insights into intra-protein proton transfer. Patch-clamp measurements identified additional residues crucial for proton conduction. Together with theoretical calculation results, molecular mechanism of this unique heliorhodopsin will be discussed.

[2SJA-4](#)

光応答性神経による括約筋の制御と貫通型消化管の進化的起源

Light-modulated neural control of sphincter regulation in the evolution of through-gut

Junko Yaguchi¹, Kazumi Sakai², Atsushi Horiuchi², Takashi Yamamoto³, Takahiro Yamashita², **Shunsuke Yaguchi¹** (¹SMRC, Univ. Tsukuba, ²Grad. Sch. Sci., Univ. Kyoto, ³Genom. Edit. Innov. Cent., Hiroshima Univ.)

Light plays a crucial role in sustaining life on Earth. For instance, visual systems heavily rely on light reflection, and the circadian rhythms of most organisms are regulated by the cycles of sunlight. However, the acquisition and diversification of light-dependent systems during deuterostome evolution remain poorly understood, mainly due to the limited knowledge of the light response signaling pathway in Ambulacraria, a major group of deuterostomes and a sister group of chordates. In this study, we demonstrate that sea urchin larvae utilize light to regulate digestive tract activity. Remarkably, our experiments reveal that exposure to light induces pyloric and anal opening even in the absence of food stimuli. Through our investigations, we have identified a light>Opsin3.2>serotonin>nitric oxide pathway responsible for regulating pyloric opening, while different opsins and neurotransmitters are involved in anal opening. Our findings shed light on the evolution of light-dependent systems related to digestive tract activities and neurotransmitter function, providing valuable insights into their establishment during the animal evolution. Drawing from previous research on brain-gut interactions in vertebrates, we speculate that one primitive function of anterior neuroectodermal neurons (brain neurons) might have been to regulate digestive tract function in the common ancestor of deuterostomes. Considering the fundamental importance of food consumption and nutrient absorption for animals, the acquisition and development of a sophisticated gut regulatory system driven by the brain could have played a significant role in deuterostome evolution.

[2SJA-5](#)

メダカでは脳下垂体に発現する光受容体が紫外線受容によって色素沈着促進ホルモンの分泌を誘導する

A Photoreceptor Expressed in Pituitary Endocrine Cells Mediates UV-Induced Hormone Release That Enhances Pigmentation in Medaka

Sinji Kanda¹, Ayaka Fukuda^{1,2}, Keita Sato³ (¹Atmosphere and Ocean Research Institute, The University of Tokyo, ²Division of Behavioral Neurobiology, National Institute for Basic Biology, ³Faculty of Medicine, Dentistry, and Pharmaceutical Sciences, Okayama University)

It is well recognized that non-visual photoreceptors are expressed in non-ocular organs. However, their biological significance remains largely unknown. While performing Ca²⁺ imaging of pituitary hormone-producing cells in a model fish medaka, we unexpectedly observed a robust increase in intracellular Ca²⁺ concentration in response to blue excitation light. This observation led us to identify a novel pathway in which short-wavelength light activates a photoreceptor Opn5m and promotes the release of melanocyte-stimulating hormone (MSH). At the organismal level, this light-responsive pathway enhances melanogenesis through MSH action on the pigments, thereby contributing to protection against harmful short-wavelength radiation, including ultraviolet light.

[2SKA-1](#)

Assessing druggability based on the structural features of human leucyl-tRNA synthetase 2

Seonha Park¹, Byeongmin Shin¹, Ingyo Park¹, Kyuhyeon Bang¹, Sulhee Kim¹, Ina Yoon², **Kwang Yeon Hwang¹** (¹Department of Biotechnology, Korea University, ²College of Pharmacy, Yonsei University)

Leucyl-tRNA synthetase 2 (LARS2) is synthesized in the cytosol and imported into mitochondria, where it charges leucine onto cognate tRNAs to form Leu-tRNA^{Leu} for mitochondrial translation. Unlike cytosolic LARS1, LARS2 lacks post-transfer editing. Biallelic LARS2 variants cause Perrault Syndrome, marked by ovarian failure and hearing loss. We present the crystal structure of LARS2 bound to a leucyl-sulfamoyl-adenylate analog (Leu-AMS). Structural comparison reveals divergence in editing motifs (GTG and threonine-rich regions), explaining the absence of editing. R228H mutation impairs tRNA^{Leu} binding and aminoacylation.

[2SKA-2](#)

クライオ電子顕微鏡を用いた感染症治療薬・ワクチン開発の進展と日韓協力

Advancements in Therapeutic and Vaccine Development for Infectious Diseases Using Cryo-EM: A Potential Japan-Korea Collaboration

Katsumi Maenaka^{1,2} (¹Facult. Pharm. Sci., Hokkaido Univ., ²Facult. Pharm. Sci., Kyushu University)

This talk will focus on the use of cryo-electron microscopy (cryo-EM) in developing therapeutics and vaccines for infectious diseases, including SARS-CoV-2. Cryo-EM provides structural insights into viral proteins and their interactions with antibodies, making it a crucial tool in designing effective treatments and vaccines. Recent studies on SARS-CoV-2 variants highlight its potential in identifying drug targets and optimizing antibody therapies. The talk will also discuss opportunities for further collaboration between Japanese and Korean biophysics researchers to advance these efforts and contribute to the global fight against infectious diseases.

2SKA-3 **Accurate Conformational Ensembles of Intrinsically Disordered Proteins using Reweighting based on NMR Chemical Shift**

Juhyeong Jeon¹, Wonjin Yang¹, Jin Hae Kim², Young-Ho Lee³, **Woogyung Yu¹** (¹*Department of Brain Sciences, DGIST, Daegu, Republic of Korea*, ²*Department of New Biology, DGIST, Daegu, Republic of Korea*, ³*Research Center for Bioconvergence Analysis, Korea Basic Science Institute, Republic of Korea*)

IDR/PSs underpin a wide range of vital biological processes but exhibit dynamic and heterogeneous conformations. But previous researches still struggle to fully capture their conformational diversity. Here, we integrate structural libraries of various IDR/PSs—derived from CGMD and machine learning models—with NMR chemical shifts. Through a maximum entropy approach, we obtain reliable ensembles that more accurately reflect observed chemical shifts and reveal transient states. Our results highlight the importance of comprehensive sampling strategies for capturing diverse conformational states. Furthermore, we demonstrate that these weighted ensembles faithfully track conformational rearrangements under various conditions, which are not fully captured by experiments alone.

2SKA-4 **NMR を利用した天然変性タンパク質を標的とした創薬への挑戦**
Challenges and perspectives in drug discovery and design against intrinsically disordered proteins by NMR

Hidekazu Hiroaki^{1,2,3} (¹*Grad. Sch. Pharm. Sci., Nagoya Univ.*, ²*BeCellBar, LLC.*, ³*COMIT, Nagoya Univ.*)

IDPs are polypeptides that lack a stable, compact folding under physiological conditions. Recently, there has been growing interest in whether IDPs are suitable drug targets. This stems from their propensity to appear as hubs in protein interaction networks and the observation that many proteins involved in liquid-liquid phase separation are IDPs. However, IDPs pose challenges for structural determination by X-ray crystallography or cryo-EM, thereby not fully benefited from drug discovery acceleration methods, such as recent AI technologies. Meanwhile, NMR is an excellent technique for monitoring interactions between IDPs and drug candidates. This presentation will focus on the potential and limitations of NMR in drug discovery efforts targeting IDPs.

2SKA-5 **Cellular Mechanobiology in Phagocytosis**

Min Chanhhyuk¹, Cho Hyeokjin², Yu Jeongmin¹, Park Daeho², **Lee Gwangrog¹** (¹*Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST)*, ²*School of Life Sciences, Gwangju Institute of Science and Technology (GIST)*)

Phagocytes undergo cytoskeletal remodeling and membrane deformation to engulf apoptotic cells, but whether mechanical cues influence signaling during efferocytosis remains unclear. Here, we show that tension between phosphatidylserine (PS) and its receptors (PSRs) at the phagocytic synapse acts as a mechanical signal that determines engulfment. Rac1-driven actin polymerization and apoptotic cell rigidity generate PS-PSR tension, which recruits PI3K to PSRs, leading to Rac1 inactivation and myosin II phosphorylation. These events are required for phagocytic cup closure. Thus, PS-PSR tension serves as a mechanical checkpoint to ensure selective clearance of apoptotic cells.

2SKA-6 **Direct Visualization of Dynamics in Prokaryotic Motility Machinery**

Takayuki Nishizaka¹, Masaki Mizutani¹, Daisuke Nakane² (¹*Gakushuin Univ.*, ²*Univ. Electro-Communications*)

In addition to bacterial flagellar motor that has been extensively studied in biophysics research field, other rotary motors were found in organisms: archaeal flagellar motor, and F₁-ATPase, the soluble subcomplex of ATP synthase. Both motors generate torque using chemical energy of ATP hydrolysis, and a common and general mechanism based on torque measurements will be discussed in the presentation. Finally, by applying microscopic techniques, (1) our research group successfully manipulated rotational direction of archaeal motor by light modulation, which could address the regulation of rotation switching, and (2) detailed behavior of type IV pili (TFP) machinery was visualized in 3D, which gives a new insight into how bacterial TFP machinery evolved to archaeal motor.

2SAP-1 クロマチン構造の力学的解析：分子夾雑とエピゲノム継承の分子機構の理解に向けて
Mechanical Analysis of Chromatin by Optical Tweezers: Molecular Crowding and Inheritance of Epigenome

Tomoko Sunami¹, Amarjeet Kumar¹, Kohji Hizume², Hidetoshi Kono^{1,3} (¹*iQLS, QST, ²BRC, Med, Saitama Med U,*
³*cQUEST, Chiba U*)

Regulation of the chromatin structure and the unwrapping of nucleosomal DNA is essential for the proper utilization of genomic information. However, these processes are inherently transient and dynamic, posing significant challenges for experimental observation. To overcome these limitations, we employ optical tweezers to mechanically stretch polynucleosomes, thereby perturbing their structures and allowing us to investigate how cellular factors modulate chromatin structure and DNA accessibility. In this symposium, we will present two topics. First, we investigate how molecular crowding conditions affect chromatin condensation. Second, we explore the molecular mechanisms by which histone chaperones, such as MCM2 and Asf1, ensure the inheritance of the epigenome.

2SAP-2 Structure and dynamics of reconstituted chromatin with defined histone modification patterns

Yohsuke T Fukai¹, **Kyogo Kawaguchi**^{1,2} (¹*RIKEN PRI, ²Institute for Physics of Intelligence, Department of Physics, The University of Tokyo*)

The physical contribution of epigenetic marks to chromatin architecture and dynamics still remains unclear. We have recently isolated histone acetylation's effect on gene-scale structure using reconstituted 20kb, 96-nucleosome arrays [bioRxiv: 10.1101/2024.11.08.622658]. Single-molecule tracking showed higher acetylation density increases conformational fluctuations and relaxation times, consistent with a model taking into account the hydrodynamic interactions. The in vitro Hi-C (contact map) experiment confirmed how acetylation lowers nucleosome contact frequency and shifts ensembles to more open configurations. A refined physical model to explain the situation is in development; updated results will be presented in the talk.

2SAP-3 Cryo-EM analysis of basic chromatin architectures isolated from cells

Yoshimasa Takizawa^{1,2}, Haotong Zhuang^{1,2}, Takuro Shioi^{1,3}, Suguru Hatazawa¹, Yuki Kobayashi¹, Mitsuo Ogasawara¹, Yasuyuki Ohkawa⁴, Hitoshi Kurumizaka^{1,3,4} (¹*IQB, Univ.Tokyo, ²Grad. Sch. Fro. Sci., Univ.Tokyo, ³Grad. Sch. Sci., Univ. Tokyo, ⁴MIB, Kyushu Univ.*)

Chromatin organizes genomic DNA in the nucleus, with nucleosomes as its basic units, and its higher-order architecture is modulated by histone modifications, variants, and regulatory factors. While numerous in vitro chromatin structures have been determined by cryo-EM, the mechanisms underlying chromatin organization and regulation in cells remain poorly understood. In this study, we aim to elucidate chromatin function in cells by targeting specific nucleosomes, particularly those containing histone variants that influence chromatin architecture, using ChIP-CryoEM, a method combining chromatin immunoprecipitation with cryo-EM. This work will enable us to conduct structural studies of chromatin with diverse histone variants, histone modifications and associated proteins.

2SAP-4 化学触媒によるエピゲノム改変技術の開発
Development of epigenome modification technology by chemical catalysis

Shigehiro Kawashima (*Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

The epigenome plays a pivotal role in chromatin structure and gene expression. Tools for the regioselective introduction of histone PTMs in living cells are critical for dissecting the functions of these epigenetic marks. Here, we report the design and development of three regioselective catalysts that acetylate distinct lysine residues (K43, K108, and K120) on histone H2B. Biochemical and cellular analyses of the catalytic histone acetylation revealed that each lysine acetylation elicited unique effects on transcriptional programs and cellular phenotypes. These findings establish a framework for designing regioselective histone acetylation catalysts and advance our understanding of the regulatory mechanisms underlying epigenome.

2SAP-5 複製依存的ヒストン標識 (Repli-Histo 標識) を用いて明らかにする, ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい
Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells

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Chromatin in living cells serves not only as a repository of genome sequence but also significantly influences cellular functions through its physical properties. We have recently identified unique physical properties of euchromatin (more liquid-like) and heterochromatin (more gel-like), using live-cell single-nucleosome imaging with a novel euchromatin/heterochromatin-specific labeling method (replication-dependent histone labeling, or Repli-Histo labeling). Chromatin is replicated from regions with greater nucleosome motion, suggesting that local chromatin motion can influence replication timing by regulating chromatin accessibility to replication initiation factors. We will further discuss how various factors influence the motion of euchromatin and heterochromatin.

2SBP-1 シナプス後肥厚タンパク質のリン酸化による凝縮体および受容体集合への影響: 分子シミュレーションによる検討
Effects of phosphorylation of postsynaptic density proteins on condensates and receptor assembly studied by molecular simulations

Risa Yamada, Shoji Takada (*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)

Postsynaptic density (PSD), a protein condensate situated beneath the postsynaptic membrane, regulates receptor localization through multivalent interactions, thereby playing an indispensable role in synaptic plasticity. Recent *in vitro* studies have demonstrated that phosphorylation of CaMKII, SynGAP, GKAP alter their interactions with NMDARc and PSD-95, all of which enhances PSD condensation. However, as these changes occur concurrently *in vivo*, the relative contribution of each interaction to receptor assembly remains unclear. Using experimentally derived binding affinities, we perform mesoscale molecular simulations with a membrane-mimetic system and elucidate the critical determinants requisite for stable receptor nanodomain assembly.

2SBP-2 Single-Molecule Studies of how Mug20-Rec25-Rec27 (MRR) Complex Mediates DNA Conformational Change and Biomolecular Condensates Formation

Hung-Wen Li¹, Chieh-Yu Tsai¹, Feng-Yu Wang², Ya-Ching Yang², Ya-Chen Gong³, Shyh-Chyang Luo³, Peter Chi² (¹*Dept. Chemistry, National Taiwan Univ.*, ²*Inst. Biochem. Sci., National Taiwan Univ.*, ³*Dept. Materials Sci. Eng., National Taiwan Univ.*)

During meiosis, double-strand breaks occur at genomic hotspots. In *S. pombe*, the Mug20-Rec25-Rec27 (MRR) complex defines hotspot identity, but how it shapes chromatin architecture is unclear. We developed single-molecule tethered particle motion and fluorescence microscopy across DNA length scales, we show MRR binds DNA cooperatively and induces ~170-bp shortening steps. AFM reveals DNA looping consistent with condensate proximity. MRR forms liquid-liquid phase separation (LLPS) co-condensates that fuse along DNA, driven by MRR-induced shortening. Our work highlights how a meiotic chromatin regulator can sculpt genome architecture through LLPS-mediated condensate behavior, linking local DNA mechanics with long-range genomic organization during meiotic recombination.

2SBP-3 液体の積分方程式理論を用いた 4 残基ペプチドデータベースの構築
A Comprehensive Tetrapeptide Database Using Integral Equation Theory of Liquid

Kodai Kanemaru^{1,2}, Norio Yoshida² (¹*IFIC, Kyoto Univ.*, ²*Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.*)

The development of peptide-based materials increasingly relies on data-driven approaches, highlighting the need for comprehensive and well-curated datasets. In this study, we constructed a tetrapeptide database covering all possible combinations of the 20 natural amino acids. Our approach integrates integral equation theory with molecular dynamics simulations, allowing us to evaluate thermodynamic properties while accounting for peptide structural fluctuations. This hybrid method enables the prediction of key solvation-related properties and intermolecular interactions essential for understanding peptide behavior in condensed phases.

[2SBP-4](#) アミロイド多型とその形成メカニズム Amyloid polymorphism and formation mechanisms

Masatomo So, Kenji Sugase (*Grad. Sch. Agric., Kyoto Univ.*)

Amyloid fibrils are associated with more than 30 amyloidoses, including neurodegenerative diseases. Recent advances in cryo-electron microscopy (cryo-EM) have resolved numerous amyloid structures, revealing that a single sequence can form various amyloid conformations associated with different diseases. Conversely, we have demonstrated that distinct sequences can form the same structure, even when they are linked to separate diseases. Understanding the formation process of amyloid polymorphism—which has remained a significant challenge—is also a crucial topic in amyloid research. In the presentation, we will present the current status of research on the mechanisms of amyloid formation.

[2SBP-5](#) 動的溶液環境におけるアミロイドβタンパク質の分子集合 Molecular assembly of amyloid-β proteins in dynamic solution environments

Maho Yagi-Utsumi^{1,2} (¹*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, ²*ExCELLS, Natl. Inst. Nat. Sci.*)

Aberrant aggregation of amyloid-β (Aβ) proteins is a major pathological hallmark of Alzheimer's disease. Understanding the fibril formation process at the molecular level is crucial for developing effective preventive and therapeutic strategies. In this presentation, I will report our recent findings obtained using high-speed atomic force microscopy, which enabled real-time visualization of Aβ fibril growth and the dynamic interactions of antibodies with fibril ends. I will also present structural analyses of Aβ fibrils formed under microgravity aboard the International Space Station, and discuss the impact of dynamic solution environments on protein assembly and consequent structures.

[2SBP-6](#) 動的細胞内環境における機能性アミロイド線維の可能性の探索 Investigating Neuronal Amyloid Fibrils with Potential Functional Roles in a Dynamic Intracellular Environment

Atsushi Sugie¹, Jiro Osaka² (¹*Kyoto Institute of Technology*, ²*Institute of Science Tokyo*)

Recent studies show that some intrinsically disordered proteins can undergo liquid–liquid phase separation and form amyloid fibrils. While many pathological amyloids are linked to neurodegeneration, we hypothesize that some neuronal proteins may form functional amyloids essential for neuronal survival. Using PLAAC, we identified 85 candidates from 1282 neuronally expressed genes in *Drosophila*. High-throughput RNAi screening revealed 17 factors affecting neurodegeneration, and Thioflavin T assay confirmed amyloid formation in one protein. These findings suggest amyloids may serve not only pathological but also physiological roles in neuronal dynamic solution environments, prompting a paradigm shift in how biomolecular condensation is understood.

[2SCP-1](#) 微小管ダイナミックインスタビリティ 3.1：高精度多次元解析がもたらした意外な高次機能の発見 Microtubule Dynamic Instability 3.1: From Imaging to Insight into Hidden Functions

Yuko Mimori-Kiyosue (*Department of Molecular Genetics, Institute of Biomedical Science, Kansai Medical University*)

Microtubule dynamic instability was first described as 1D behavior at microtubule ends (ver.1.0). High-resolution 2D imaging resolved microtubules in cells (ver.2.0), and the integration of time, multicolor imaging, and analytical techniques (ver.2.1 and further) has elucidated how microtubules coordinate with cell structure and function. Yet, these approaches remained limited in revealing how cells function in their native 3D context. High spatiotemporal volumetric imaging (ver.3.0) and subsequent analytical integration now allow us to uncover spatially regulated modes of cell function. In this talk, I will introduce new links between cellular organization and biological function, revealed through multidimensional analyses of spindle microtubules and chromosomes.

[2SCP-2](#) The Timing of the Acquisition of Eukaryotic Traits during Eukaryogenesis

Robert Charles Robinson (*Vidyasirimedhi Institute of Science and Technology (VISTEC) Thailand*)

Life on our planet can be divided into two classes of organisms, prokaryotes and eukaryotes. The origin of the eukaryotic cell is one of the greatest mysteries in modern biology. Recently, Asgard archaea were discovered that possess genes that appear to have similarity to distinctive eukaryotic genes. Our laboratory has been exploring the properties of some of the protein machines. We have focused on the putative cytoskeletal proteins from Asgard archaea. We have shown that Asgard archaea possess an ancient, regulated actin system, which is likely to integrate force into membrane remodeling processes through directed actin polymerization. Furthermore, we have characterized an Asgard tubulin that forms tubules with a different morphology to microtubules.

[2SCP-3](#) α B-クリスタリン, チューブリン/微小管のメカノシャペロン: 階層的自己組織化とヒト特異性を活用した QOL 戦略 α B-Crystallin, mechanochaperon for tubulin/microtubule: A QOL strategy that utilizes hierarchical self-organization and human specificity

Yoriko Atomi (*Teikyo University, ACRO*)

“Know thyself science and education” has not been realized today. Humans are descendants of prokaryotes, eukaryotes, multicellular animals, vertebrates, mammals, and primates, and have evolved by increasing the number of hierarchical levels while retaining the constraints of each level. Therefore, the layers are nested. Each layer has its own environment, and accurate material systems and activities connecting the layers constitute the conditions for the survival of individuals, thereby improving their quality of life. We attempt to construct a hierarchical logical framework linking mechanochaperon α B-crystallin (relating to tubulin/microtubules), which is highly expressed in axial skeletal muscles that automatically or consciously support and move the bipedal body.

[2SCP-4](#) 再構成型ヒト翻訳・フォールディング運動システムを利用した変異 β -アクチンの生合成における異常ステップの解析 A Reconstituted Human Translation/Folding Coupled System Defines the Defective Step in the Biogenesis of Mutated β -Actin Proteins

Kodai Machida (*Dept. of Appl. Chem., Grad. Sch. of Eng., Univ. of Hyogo*)

In recent years, advances in analytical techniques have led to the discovery of various disorders associated with amino acid mutations in cytoplasmic β -actin and γ -actin protein. However, due to the high sequence homology, it has been difficult to study the effects of individual mutations on actin biogenesis in living cell systems. In addition, since the folding of nascent actin polypeptide requires the assistance of eukaryote-specific chaperones, prokaryotic protein expression systems cannot be used for the study of actin biogenesis. To address this, we established a cell-free protein synthesis system reconstituted with human translation factors and chaperones. Using this system, we found that mutant β -actins show defects in folding and/or polymerization.

[2SCP-5](#) 量子ドットイメージングで観る細胞表面へのアミロイド β 凝集・沈着 Visualization of amyloid β aggregation and deposition on cell surface using quantum dot imaging

Masahiro Kuragano, Kiyotaka Tokuraku (*Grad. Sch. Eng., Muroran Inst. Tech.*)

The aggregation and deposition of amyloid β ($A\beta$) in the brain are believed to be the main cause of Alzheimer's disease and cerebral amyloid angiopathy. However, the mechanism of interaction between $A\beta$ aggregates and the cell surface remains unclear. Previously, we developed real-time imaging methods for $A\beta$ using a quantum dot nanoprobe (Tokuraku et al., PLoS ONE, 2009). Utilizing this method, we succeeded in the simultaneous observation of $A\beta$ aggregation on the cell surface and F-actin organization in the cell. It was revealed that the accumulation of aggregated $A\beta$ disrupted the actin cytoskeleton and caused abnormal actin aggregation, resulting in the attenuation of cell motility. In this presentation, we will provide an overview of our studies and new findings.

[2SCP-6](#)

細胞外環境を感知する Hippo シグナル伝達経路の役割

Roles of the Hippo signaling pathway sensing the extracellular environment

Hiroshi Nishina (*Institute of Science Tokyo*)

The cytoskeleton, which supports the cell lining, is a structure that generates physical forces and induces changes in cell morphology and movement. Therefore, cytoskeletal changes and gene expression are closely related. The Hippo pathway is known as one of the intracellular signaling pathways that senses extracellular stress and regulates gene expression via the cytoskeleton. However, the cellular responses involved in this signaling pathway are still unknown. We isolated and analyzed morphologically abnormal mutants of medaka fish and found that the Hippo pathway and its target molecule, the transcriptional coactivator YAP, are important for gravity tolerance. We have also found that this signaling pathway is also involved in cell competition, which is involved in mammalian quality control. In this symposium, these research results will be presented.

[2SCP-7](#)

The expression of the collagen chaperone Hsp47 is regulated by mechanical loading through the YAP/TEAD pathway

Ayano Kasai^{1,2}, Shinya Ito³, Ryo Ushioda^{1,2}, Kazuhiro Nagata^{1,2,4} (¹*Fac. Life Sci., Kyoto Sangyo Univ.*, ²*Inst. Protein Dynamics, Kyoto Sangyo Univ.*, ³*Ctr. Mol. Biol., Heidelberg Univ.*, ⁴*JT Biohistory Research Hall*)

Heat shock protein 47 (Hsp47) is essential for collagen maturation and maintenance of extracellular matrix (ECM) integrity. Although its transcriptional regulation by heat shock and tissue-specific factors is known, the effect of mechanical stress on its expression remains unclear. Using a mouse tail suspension model, we showed that mechanical unloading suppresses Hsp47 expression via the Hippo pathway through YAP/TEAD-mediated transcriptional regulation. These findings reveal a mechanosensitive regulatory mechanism for collagen homeostasis and suggest an adaptive strategy to physical stress, with implications for tissue maintenance and quality of life (QOL) during aging.

[2SDP-1](#)

一細胞 3 次元空間トランスクリプトーム解析を実現する新規細胞単離法

A novel single-cell isolation method enables single-cell 3D spatial transcriptomics

Nozomi Hojo, Katsuyuki Shiroguchi (*BDR, Riken*)

Multicellular organisms are maintained by the interactions of diverse cells that are appropriately arranged in three-dimensional (3D) tissues. To elucidate this cellular arrangement and interaction, integrated analysis of the 3D positions and comprehensive gene expression profiles of each cell is essential. Here, we developed a novel cell isolation method by which all individual cells are collected from a 3D sample while recording their original positions. We applied this method to lung organoids and small intestinal crypts successfully. By performing single-cell RNA-seq on the isolated cells, we achieved single-cell 3D spatial transcriptomics. In this talk, we will show the scheme of this method and some analyses on cellular interaction based on the 3D cell positions.

[2SDP-2](#)

線虫の全脳活動計測と遺伝子発現解析

Whole brain activity measurement and gene expression analysis of neurons in *Caenorhabditis elegans*

Yu Toyoshima^{1,2}, Yuichi Iino¹, Xiaoxiong Yang² (¹*Grad. Sch. of Sci., Univ. of Tokyo*, ²*Grad. Sch. of Front. Sci., Univ. of Tokyo*)

The Nervous system of *C. elegans* is one of multi-cellular systems and provides unique opportunities to understand their dynamics because all the neurons and their connections had been identified. We have measured the whole-brain activity with single cell resolution and developed a time series prediction model that can be useful for estimating the strength of neural connections and simulating whole-brain activity. We are developing a tracking-4D imaging system to measure whole-brain activity while automatically tracking free-moving animals, and investigating the relationship between neural activity and behavior in detail. Furthermore, we would like to report on a gene expression measurement method modified for nematodes.

[2SDP-3](#) Unraveling the Mechanisms of Collective Cell Migration in Epithelial Morphogenesis

Erina Kuranaga^{1,2} (¹*Grad Sch Pharmaceu Sci, Kyoto Univ*, ²*Grad Sch Life Sci, Tohoku Univ*)

Coordinated cell migration is fundamental to tissue morphogenesis. Using *Drosophila* epithelia, we previously showed that directional movement in male genitalia development is driven by planar polarity-mediated junction remodeling and actomyosin contractility. Our recent work highlights additional roles of dynamic cytoskeletal changes and membrane processes. High-resolution imaging reveals transient cytoskeletal structures linked to polarized vesicle activity. Disruption of membrane trafficking impairs migration, suggesting that spatially regulated membrane-cytoskeleton interactions are essential for collective behavior in epithelial tissues. We aim to discuss how local membrane and cytoskeletal dynamics contribute to coordinated cell behavior and tissue organization.

[2SDP-4](#) 生きた動物内で標的 GPCR を細胞種選択的に制御する化学遺伝学的アプローチ Chemogenetic strategy for controlling target GPCRs in a cell-type-specific manner in vivo

Shigeki Kiyonaka (*Grad. Sch. Eng., Nagoya Univ.*)

Manipulating target cells in a cell-type-specific manner in living animals has become an essential strategy for elucidating complex brain functions. Chemogenetics offers a non-invasive approach to control the function of target cells. We have developed unique chemogenetic approaches to selectively control target receptors in a cell-type-specific manner. Recently, we reported “coordinated chemogenetics” for artificial activation of glutamate receptors using coordination chemistry and genetic engineering. While this method is useful for controlling receptor functions, its applicability in vivo remains limited. To address this, we are developing a new chemogenetic system for GPCR-type glutamate receptors using clinically relevant drug candidates, aiming for in vivo use.

[2SDP-5](#) Functional Raman probes for multiplexed vibrational imaging

Mako Kamiya (*CLS, Science Tokyo*)

Raman probes based on alkyne or nitrile tags hold promise for highly multiplexed imaging. In order to functionalize the Raman probes to be responsive to biological phenomena in live cells and tissues, we have established a general strategy to control Raman signals intensity based on the resonant Raman effect that show enhanced stimulated Raman scattering (SRS) signals upon reaction with enzymes or by photo-irradiation. We also expanded our molecular design strategy to develop a new series of functional Raman probes based on the control of aggregate formation. In this symposium, I would like to introduce our molecular design strategy and their application to live cells and tissues.

[2SEP-1](#) アクティブに推進する生体分子エージェントとプログラムされた DNA 化学反応ネットワークの統合 Actively Gliding Biomolecular Agents Integrated with Programmed DNA Chemical Reaction Network

Ibuki Kawamata (*Kyoto University*)

Programming and analyzing the behavior of molecular-scale active matter is of interest and importance towards the realization and understanding of molecular-scale robots. For this purpose, we have been engineering DNA chemical reaction networks that can interact with biomolecular active matter systems.

As an agent of active matter systems, we utilize microtubules propelled by kinesin molecular motor placed on glass surface, whose behavior can be controlled by DNA. The versatility of DNA is one of the reasons to employ DNA because DNA interactions can be rationally designed using DNA computing technology. In the presentation, autonomous temporal evolution of active matter controlled by programmed DNA chemical reaction network and related recent results will be introduced.

2SEP-2 光照射で駆動される DNA 流体による生命的な動き Life-like motion of active DNA fluid driven by photo-irradiation

Hirotake Udono¹, M. Shin-ichiro Nomura², Takinoue Masahiro¹ (¹*Dept. Comp. Sci., Institute of Science Tokyo*, ²*Dept. Robotics, Sch. Eng., Tohoku University*)

Life-like motion of synthetic cells using various biomolecules has been an eagerly pursued topic in the molecular robotics research. Here, we show life-like motion of DNA droplets, liquid-state condensates self-assembled from DNA nanostructures (motifs), under constant visible light irradiation. Their photo-responsiveness is realized by inserting azobenzene (azo) in the sticky end (SE) of the motifs. They show life-like motion (elongation and migration) in the form of non-diffusive flow, enabled by constant visible light irradiation. This is in marked contrast to our recent report showing diffusive directional motion driven by UV-Vis switching. Under polarized Vis irradiation, they even showed extreme elongation, reminiscent of cell division.

2SEP-3 完全な運動一方向性のための DNA 人工分子モーターの構造改変 Geometry engineering of DNA artificial molecular motor for perfect unidirectionality

Takanori Harashima^{1,2}, Ryota Iino^{1,2} (¹*Institute for Molecular Science*, ²*Graduate Institute for Advanced Studies, SOKENDAI*)

DNA nanoparticle (DNA-NP) motor is the fastest artificial nano-motor, and exhibits two-dimensional super-diffusion on an RNA-modified surface as a burnt-bridge Brownian ratchet (BBR) driven by enzymatic RNA hydrolysis. However, its motion cannot be perfectly unidirectional because BBR on 2D surface only prohibits backward steps but allows forward and side steps. Here, we introduced anisotropy in the motor or rail geometry to achieve perfectly unidirectional motion. First, nanoparticle motor was replaced with a nanorod to restrict the direction of rolling motion, and unidirectionality increased with the aspect ratio of the nanorod. Second, we engineered one-dimensional RNA/DNA nanotube rail, and visualized unidirectional motion of DNA-NP motors along the nanotube rail.

2SEP-4 非生物由来分子システムの自律的回帰性が駆動する生命性 "Life" Actuated by Autonomous Recursion of Non-Biological Molecular Systems

Muneyuki Matsuo^{1,2} (¹*Hiroshima University*, ²*The University of Tokyo*)

Autonomous recursion in life exemplifies an ideal feature of molecular systems. Here, we introduce non-biological molecular systems designed by incorporating such recursion. These systems "sense" via chemical reactions, "move," and "function" through self-oscillations. The key lies in a feedback loop linking a simple chemical reaction with the system's physical properties. The chemical reaction alters these properties, which then influence the reaction rate, completing the loop. The system returns to its initial state, promoting continuous, life-like dynamics. We highlight the emergent, life-like dynamics of non-biological auto-recursion.

2SEP-5 アクティブマター研究としての単細胞の重力生物学 Gravitational biology of unicellular organisms as active matter research

Azusa Kage (*Muroran Institute of Technology*)

Gravitational biology aims to elucidate how biological processes are influenced by gravity. Not only large animals and plants but also unicellular organisms, such as the ciliates *Paramecium* and *Tetrahymena*, as well as the green alga *Chlamydomonas*, exhibit behavioral responses to gravity, known as gravitaxis. Understanding gravitaxis in such systems could provide insights relevant to space biology and the design of bioinspired microswimmers. In this presentation, I will focus on the collective motion and gravity-dependent behavior of these microorganisms, and discuss how such systems can be positioned within the broader context of active matter research. I will also briefly outline future directions for gravitational biology involving microorganisms.

2SEP-6 磁場による遊泳バクテリア集団の秩序形成制御
Magnetically controlled self-organization of swimming bacteria

Kazusa Beppu¹, Joakim Stenhammar², Jaakko V. I. Timonen³ (¹*Dept. of Chem. Eng., Kyoto Univ.*, ²*Div. of Phys. Chem., Lund Univ.*, ³*Dept. of Appl. Phys., Aalto Univ. Sch. of Sci.*)

We demonstrate magnetic control of collective behavior in bacterial suspensions using ferrofluids and external magnetic fields. The magnetic torque on non-magnetic swimmers in a magnetizable medium enables real-time alignment, revealing latent orientational and density instabilities. Horizontal fields control active turbulence into a long-range nematic state with slight undulations. Our continuum model predicts the intrinsic undulation instability and magnetic criteria for switching collective states. Vertical fields generate chiral flows and condensates through hydrodynamic interactions between chiral dipole pushers, corroborated by Lattice-Boltzmann simulations. Our approach offers a powerful tool to probe and control instability-driven phases in active matter.

2SEP-7 走化性を示さない細胞性粘菌にみられる集団運動
Self-organized collective dynamics in *Dictyostelium* cells lacking chemotaxis

Masayuki Hayakawa^{1,2}, Biplab Bhattacharjee², Hidekazu Kuwayama³, Tatsuo Shibata² (¹*Dept. of Mech. Eng., Kyoto Institute of Technology*, ²*RIKEN BDR*, ³*Life Environ. Sci., Univ. Tsukuba*)

Research on active matter covers a wide range of scales and systems, including biomolecules, cells, and droplets. Among them, the self-organization of eukaryotic cells is important not only for understanding physical principles but also for gaining insights into biological phenomena such as morphogenesis. *Dictyostelium discoideum* serves as a useful model for studying collective cell behavior due to its simple genetic background and well-characterized motility. In this presentation, we introduce the collective motion and pattern formation observed in a mutant strain of *Dictyostelium* cells lacking chemotactic ability. These findings contribute to the understanding of the behavior of cell collectives in both biology and physics.

2SFP-1 大規模 MD シミュレーションによる DHFR 阻害剤耐性メカニズムの微視的解析
Molecular Dynamics Simulation Unveils Multiple-Site Binding of Inhibitors with Reduced Activity on the Surface of Dihydrofolate Reductase

Mitsugu Araki, Yasushi Okuno (*Grad. Sch. Med., Kyoto Univ.*)

In this study, we analyzed the thermodynamics and kinetics of inhibitor binding to the surface of wild-type and mutant dihydrofolate reductase (DHFR) using molecular dynamics simulations combined with Markov state modeling. While a strong inhibitor of methotrexate (MTX) showed a preference for the active site of wild-type DHFR, deletion of a side-chain fragment in MTX or the F31V mutation in DHFR largely destabilized the active site-bound state, with clear evidence of binding to unrelated (secondary) sites. These results reveal the presence of multiple-bound states whose stabilities are comparable to or higher than those of the unbound state, suggesting that a reduction in the binding affinity for the active site significantly elevates the fractions of these states.

2SFP-2 富岳を用いた大規模レプリカ交換 MD シミュレーションによる、ペプチド認識に関与するプロテインキナーゼの構造ダイナミクスの解明
Massive Replica-Exchange MD Simulations on Fugaku Reveal Conformational Features of Protein Kinases Relevant to Peptide Recognition

Ai Shinobu (*Osaka University*)

Protein kinases regulate key signaling pathways through dynamic interactions with regulatory motifs and substrates. To gain mechanistic insight, we performed large-scale replica-exchange molecular dynamics (MD) simulations on the supercomputer Fugaku. Focusing on EGFR kinase and Abl kinase, we examined how conformational transitions shape peptide binding and influence activity. In EGFR, distinct structural states help explain mutation-dependent changes in phosphorylation. In Abl, simulations reveal metastable encounter and intermediate states. Fugaku enabled massive sampling of the conformational landscape of protein-protein binding, opening the door to integration with signaling network models and new modality drug design.

2SFP-3 In Silico Design of Inhibitors Targeting SARS-CoV-2 Non-Structural Proteins**Duy Tran**, Akio Kitao (*School of Life Science and Technology, Institute of Science Tokyo*)

The non-structural proteins (Nsps) of SARS-CoV-2 play critical roles in viral replication, transcription, and immune evasion, making them attractive targets for antiviral drug development. We systematically sampled the conformational landscape of the Nsps to identify non-functional states by comparing with the available structures. We then conducted virtual screening to discover ligands capable of stabilizing these inactive conformations, leveraging generative AI models and molecular docking techniques. Our findings provide new insights into the rational design of therapeutics targeting SARS-CoV-2 and highlight the potential of conformational modulation as an antiviral strategy.

2SFP-4 スパコンによるマルチスケール解析でストレッチアクティベーションが心拍動と昆虫の羽ばたきになぜ必要かを解明する
Supercomputer-based multiscale analysis reveals why stretch activation is necessary for beating the heart and insects' wings**Takumi Washio**^{1,2}, Toshiaki Hisada¹ (¹*UT-Heart Inc.*, ²*University of Tokyo*)

Stretch activation (SA) is a delayed increase in force following a rapid increase in muscle length. As its name suggests, the function of SA in insect asynchronous flight muscle has been thought to be the activation of contraction by pre-stretching the muscle rather than by electrical stimulation. However, our supercomputer-based multiscale analysis using the trapping mechanism of motor proteins suggests that the function of SA is more likely to help synchronize relaxation at the end of contraction in spontaneous oscillatory contraction. Furthermore, the trapping mechanism provides a rational interpretation for the role of SA in the beating heart, which requires fast blood filling in diastole against the calcium ions' slowly decreasing concentration.

2SFP-5 結合自由エネルギー計算に基づくキナーゼ阻害剤の心筋イオンチャネル阻害活性の予測
Prediction of cardiac ion channel inhibitory activities of kinase inhibitors based on binding free energy calculation**Tatsuki Negami**, Tohru Terada (*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*)

All drug candidates are tested for cardiotoxicity in clinical trials. Predicting drug interactions with cardiac ion channels, in particular hERG, Na_v1.5, and Ca_v1.2, is important for assessing proarrhythmic risk. Previously, we have calculated binding free energies of various drugs to these three ion channels by combining molecular docking and the MP-CAFE method, demonstrating that the calculated values correlate with experimental values of half maximal inhibitory concentration (IC₅₀). In this study, to estimate the proarrhythmic risk in the treatment of cancers, we calculated binding free energies of four kinase inhibitors and predicted their IC₅₀ values based on the regression models obtained in the previous study. We will discuss the accuracy of the prediction.

2SFP-6 Enhancing Antibody Engineering with Automated Molecular Interaction Descriptors and Structure Modeling**Shuntaro Chiba**¹, Tsutomu Yamane¹, Yasushi Okuno^{1,2}, Mitsunori Ikeguchi^{1,3}, Masateru Ohta¹ (¹*R-CCS, RIKEN*, ²*Grad. Sch. Med., Kyoto Univ.*, ³*Grad. Sch. Med. Life Sci., YCU*)

Antibody drugs require optimization to improve properties like affinity and stability. While single-point mutation (SPM) is commonly used for the optimization, a double-point mutation (DPM) strategy—simultaneously mutating two neighboring residues—has shown greater potential. We developed a software tool to support this strategy. It automates the detection and labeling of various molecular interactions around mutated sites in 3D structures, enabling efficient analysis of complex mutational effects. It supports both SPM and DPM and generates descriptors that quantify interaction changes. Furthermore, a machine learning model by this tool predicts structural validity of modeled mutants, aiding in the rational design and evaluation of antibodies.

2SFP-7 分子生成 AI とシミュレーションの融合による創薬分子設計
Integrating Molecular Generative AI and Simulation for Drug Discovery

Kei Terayama (*Grad.Sch.Med.Life.Sci, Yokohama City Univ.*)

Recent advances in molecular generative models, particularly those based on deep learning, have opened up new possibilities for data-driven molecular design in drug discovery. However, molecular design using prediction models trained on known activity and ADMET data often lacks physical feasibility or biological relevance. To address this, we have developed ChemTSv2, a practical molecular design method that improves the reliability by integrating physical-chemical simulations with reinforcement learning based optimization. In this presentation, we will introduce the design principles behind ChemTSv2 and showcase its applications in drug discovery and other fields.

2SGP-1 暗所従属栄養条件でのシアノバクテリアの微小進化
Microevolution of cyanobacteria in the dark heterotrophic conditions

Yuichi Fujita (*Grad. Sch. Bioagricultural Sci., Nagoya Univ.*)

The prevalence of parasitic plants suggests that photosynthetic organisms frequently evolved to lose the photosynthetic ability in the adaptation process to environments where organic compounds are continuously supplied and photosynthesis is not required. However, there are no reports of actual observations of specific evolution leading to the loss of photosynthesis. In this presentation, I will present the results of the microevolution to the loss of photosynthetic growth ability through genome analysis of dark-adapted variants obtained by long-term cultivation under dark-heterotrophic conditions in the filamentous cyanobacterium *Leptolyngbya boryana*.

2SGP-2 緑色硫黄細菌で見つかった嫌氣的な非光化学的消光：その反応機構と生理的意義
Anaerobic non-photochemical quenching of photosynthetic green sulfur bacteria: Its reaction mechanism and physiological significance

Chihiro Azai (*Fac. Sci. & Eng., Chuo Univ.*)

Non-photochemical quenching (NPQ) of the electronically excited chlorophyll is a well-known and essential process in the oxygenic photosynthesis to protect against the photosensitized formation of reactive oxygen species (ROS). Meanwhile NPQ had been considered physiologically nonsense under anaerobic conditions, where ROS cannot be generated. Recently, however, an empirical refutation of this understanding was found in the anoxygenic photosynthesis of the green sulfur bacterium *Chlorobaculum tepidum*, which is an obligate anaerobe. The carotenoid specifically bound to the reaction center complex constitutively drives NPQ under anaerobic and high-light conditions. This will change our knowledge of the universal function of carotenoids and their evolutionary origin.

2SGP-3 時間分解蛍光分光法による光合成色素-タンパク質複合体の機能解明
Functions of photosynthetic pigment-protein complexes, revealed by time-resolved fluorescence spectroscopy

Seiji Akimoto (*Grad. Sch. Sci., Kobe Univ.*)

The combination of time-resolved fluorescence spectroscopy and global analysis is a useful technique for elucidating excitation relaxation dynamics in photosynthetic systems. This is because the former detects signals only from excited states, whereas the latter gives fluorescence decay-associated spectra (FDAS) to highlight the energy-transfer and energy-dissipation processes with both spectral and temporal information. The energy distribution between photosystem I and photosystem II can also be estimated by FDAS. In the present talk, the functions of several photosynthetic super/megacomplexes, such as light-harvesting, energy transfer, and energy quenching, will be discussed by showing FDAS with high time- and wavelength-resolution.

2SGP-4**光合成タンパク質の分子構造と理論構造をつなぐ磁気構造**

Linkage of the molecular and theoretical structures of photosynthetic proteins using magnetic spin configurations

Hiroyuki Mino (*Grad. Sch. Sci., Nagoya Univ.*)

Recent advances in X-ray crystallography and electron microscopy techniques have led to developments in structural biology. Detailed structural data are utilized for functional analyses using quantum chemical calculations. However, experimental techniques for verifying functional models are limited. Photosynthetic oxygen evolution involves a series of reactions in which the arrangement of a single proton significantly influences the overall reaction. Therefore, accurate proton configurations are required at the quantum-mechanical level. In this presentation, we introduce the assignment of magnetic structures to spatial coordinates and theoretical orbitals, which were derived using pulsed EPR.

2SGP-5**光捕集複合体の構造に基づいた海洋性大型緑藻のカルボニルカロテノイドによる緑色光吸収の分子メカニズム**

Mechanism of green light absorption by carbonyl carotenoids of marine macroalgae based on the structure of light-harvesting complexes

Ritsuko Fujii^{1,2} (¹*Research Center for Artificial Photosynthesis, Osaka Metropolitan University*, ²*Department of Chemistry, Graduate School of Science, Osaka Metropolitan University*)

Underwater, photosynthetic organisms efficiently use the available blue-green light for photosynthesis. We focus on the role of carbonyl carotenoids in green lineages. An intertidal green alga *Codium fragile* accumulates siphonaxanthin, a carbonyl carotenoid found in its major light-harvesting complex (LHCII), to use green light for photosynthesis. However, siphonaxanthin does not absorb green light in organic solvents, and the mechanism by which LHCII absorbs green light remains unknown. Therefore, we investigated the structure of LHCII in *C. fragile* using cryo-EM single-particle analysis. We discovered a hydrogen bond between a cysteine residue and the carbonyl group of siphonaxanthin. We will discuss how this or other structural features enable green light absorption.

2SGP-6**光合成アンテナのデザインを目指して：in vitro 再構成光合成アンテナの構造解析**

Toward the design of photosynthetic antennas: structural determination of in vitro reconstituted light-harvesting complex

Soichiro Seki¹, Akihiro Kawamoto^{1,2}, Tomoko Miyata^{3,4}, Keiichi Namba^{3,4}, Ritsuko Fujii⁵, Genji Kurisu^{1,2,4} (¹*IPR, Osaka Univ.*, ²*OTRI, Osaka Univ.*, ³*Grad. Sch. Frontier Biosci., Osaka Univ.*, ⁴*JEOL YOKOGUSHI Res. Alliance Labs., Osaka Univ.*, ⁵*ReCAP, Osaka Metropol. Univ.*)

Light-harvesting complex (LHC) is a membrane-bound pigment-protein complex essential for capturing sunlight in photosynthesis. In vitro reconstitution method enables the artificial formation of LHCs from recombinant proteins and natural pigments, allowing control of the pigment composition and site-directed mutagenesis. However, the structural reproducibility in this method remained unclear. Here, we determined the structure of in vitro reconstituted LHCII by cryo-EM and compared it to native LHCII. The overall structure was nearly identical, confirming its structural reproducibility. Furthermore, analysis of a mutant lacking the axial ligand showed selective loss of the corresponding chlorophyll, demonstrating that pigment binding can be controlled by mutation.

2SGP-7**光センサータンパク質 RcaE における「水素結合のアクセプター」となるリシン**

Deprotonated Lysine Serving as a “H-bond acceptor” in the Photoreceptor Protein RcaE

Masaki Misima (*Sch. Pharm., Tokyo Univ. Pharm. and Life Sci.*)

Deprotonated lysine and its interactions have been elusive. Here, a deprotonated lysine serving as a “H-bond acceptor” in the photosensor protein RcaE is reported. X-ray crystallography indicates that Lys261 sidechain switches its H-bonding partner from a propionic group to an NH group of the chromophore upon light absorption. Signal splitting and trans-H-bond *J* coupling observed by nuclear magnetic resonance (NMR) spectroscopy provide direct evidence that Lys261 is deprotonated and serves as a H-bond acceptor for the chromophore NH group. Quantum mechanical/molecular mechanical calculations also indicate this H-bond exists stably. These results provide novel insights into the dual role of this lysine which swatches from a H-bond donor to acceptor.

2SGP-8 AlphaFold と MD シミュレーションを活用したオートファジー駆動機構の解明
Elucidating the mechanism of autophagy utilizing AlphaFold prediction and MD simulations

Nobuo N. Noda^{1,2} (¹*IGM, Hokkaido Univ.*, ²*Inst. Microbial Chem.*)

Autophagosome formation, an essential step in autophagy, requires supplying millions of lipid molecules from the ER within 10 min, which is performed by the Atg2-Atg18 complex in yeast. The molecular mechanism of its bulk lipid transport has long been a mystery. We predicted the full-length Atg2-Atg18 structure by AlphaFold and examined its interactions with lipids/membranes via all-atom MD simulations. By designing and testing structure-based mutants in silico, in vitro, and in vivo, we proposed a model for the bulk lipid transport by the Atg2-Atg18 complex. In this presentation, I will introduce our lipid transport model and discuss the utility of AI-driven analysis in life science research.

2SHP-1 FUS の液滴形成・成熟過程の in-cell NMR 解析
Structural insights into liquid-liquid phase separation (LLPS) mechanism of FUS using in-cell NMR

Noritaka Nishida (*Grad Sch Pharm Sci, Chiba Univ*)

Fused in sarcoma (FUS) is an RNA-binding protein that forms biomolecular condensates through liquid-liquid phase separation (LLPS). While LLPS is essential for physiological functions such as RNA processing, the maturation of FUS droplets into amyloid-like fibrils is thought to contribute to the pathogenesis of neurodegenerative diseases. To elucidate the LLPS mechanism of FUS under intracellular conditions, we performed in-cell NMR analysis. By introducing ¹⁵N-labeled FUS into HeLa cells, we monitored chemical shift changes and time-dependent reductions in signal intensity as indicators of droplet formation and maturation. In this presentation, we report the molecular mechanism of intracellular FUS droplet formation, maturation, and transition to fibrillation.

2SHP-2 統合的時分割構造解析で捉えるシャペロンのフォールディング制御における速度論的特性
Kinetic Insights into Chaperone-Mediated Protein Folding from Integrative, Dynamic Structural Biology

Munchiro Kumashiro¹, Hiroyuki Kumeta², Tomohide Saio¹ (¹*Inst. Adv. Med. Sci., Tokushima Univ.*, ²*Fac. Adv. Life Sci., Hokkaido Univ.*)

Protein folding is a crucial process by which nascent chains acquire functional structures. Chaperones assist folding by preventing aggregation and promoting proper folding. While recent NMR studies revealed structures of ~200-kDa chaperone-extended client complexes, how chaperones act on folding intermediates remains unclear. Here, we studied transient complexes between Trigger factor (TF) chaperone and folding intermediates of maltose-binding protein (MBP) using NMR, time-resolved spectroscopy, and computational analysis. Our data showed that local binding kinetics of TF regulate segmental folding of MBP. This provides insight into how chaperones promote folding and highlights the value of integrating experimental and theoretical methods to study transient complexes.

2SHP-3 Modulation of Structure and Dynamics in Biomolecular Condensates Revealed by Large-Scale Molecular Dynamics Simulations

Cheng Tan, Yuji Sugita (*RIKEN Center for Computational Science*)

Biomolecules such as intrinsically disordered proteins form dynamic condensates through highly entangled networks of weak interactions. Although extensive research has elucidated their formation mechanisms, how these condensates are regulated to prevent aggregation remains unclear. Using large-scale all-atom molecular dynamics simulations (~2.5 million atoms, Fugaku supercomputer), we studied TDP-43 condensates and their regulation by the highly charged protein Hero11. Hero11 reduces condensate density, increases fluidity and ion influx, and alters water dynamics. It modulates protein diffusion and promotes coupling between reduced intermolecular contacts and decreased α -helical propensity in TDP-43's C-terminal domain, revealing mechanisms of condensate regulation.

2SHP-4 **PROTAC-induced Protein Structural Dynamics in Targeted Protein Degradation****Chia-en Chang**, Kingsley Wu, Ta I David Tang (*University of California, Riverside*)

PROteolysis Targeting Chimeras (PROTACs) are small molecules that induce target protein degradation via the ubiquitin-proteasome system. In this study, we constructed degradation machinery complexes with Culling-Ring Ligase 4A (CRL4A) E3 ligase scaffolds to model protein dynamics associated with a series of PROTACs, featuring different linkers but different degradation ability. The series of PROTACs all formed ternary complexes with Cereblon (CRBN) E3 ligase and the target protein bromodomain-containing protein 4 (BRD4^{BD1}). Atomistic MD simulations illustrated how PROTAC-dependent protein dynamics facilitate ubiquitination. These findings offer a structural dynamic perspective on ligand-induced protein degradation, providing insights to guide future PROTAC design.

2SHP-5 **Elucidation of the regulation of the Rac1/Cdc42 guanine nucleotide exchange factor DOCK6****Mutsuko Kukimoto-Niino** (*RIKEN, Yokohama*)

DOCK proteins are evolutionarily conserved atypical guanine nucleotide exchange factors (GEFs) for the Rho GTPases that regulate the actin cytoskeleton. DOCK proteins are large multi-domain proteins consisting of approximately 2,000 amino acid residues and have been shown to function in a homodimer. However, by using cryo-electron microscopy and high-speed atomic force microscopy, we have shown that DOCK6, a GEF of Rac1 and Cdc42, regulates its GEF activity through tetramer and even larger multimer formation. On the other hand, there are flexible regions in the DOCK6 sequence that are not captured experimentally, and we have used AlphaFold3 predictions to gain structural insight into the regulation of DOCK6 by phosphorylation at Ser1194.

2SHP-6 **カーゴ受容体 ERGIC-53 によるカーゴ輸送のクライオ電顕構造解析**
Cryo-EM analysis of cargo transport and release by a cargo receptor ERGIC-53**Satoshi Watanabe**, Emi Honjo, Kenji Inaba (*MIB, Kyushu Univ*)

ERGIC-53 is a cargo receptor that transports various glycoproteins such as coagulation factors V/VIII from the ER to the Golgi apparatus by unknown mechanisms. Here we present cryo-EM structures of full-length ERGIC-53 in complex with its functional partner MCFD2. ERGIC-53 comprises a four-leaf clover-like head, a long stalk composed of three sets of four-helix coiled-coils, and a transmembrane helix. 3D variability analysis visualizes the unique motions of its stalk and head, suggesting that ERGIC-53 captures target cargo via dynamic movements of these regions. Furthermore, we found a Zn²⁺ binding site in MCFD2 that regulates cargo release from the receptor. We leveraged these findings to develop a strategy for trapping the transient cargo-ERGIC-53-MCFD2 complex.

2SHP-7 **高速 AFM と cryo-EM による, CAMSAP2 によって誘導される微小管およびアスター構造形成過程の直接観察****Direct observation of CAMSAP2-induced microtubule and aster formation processes using high-speed AFM and cryo-EM****Tsuyoshi Imasaki¹**, Ayhan Yurtsever², Ryota Kitano¹, Kien Xuan Ngo², Takaaki Kato¹, Hanjin Liu¹, Hideki Shigematsu³, Takeshi Fukuma², Ryo Nitta¹ (¹*Kobe University Graduate School of Medicine*, ²*WPI-NanoLSI*, ³*JASRI*)

Microtubules are multi-protein complex that play diverse roles in the cell, including spindle assembly, intracellular transport, and cytoskeletal organization. They are formed through the self-assembly of tubulin, but their dynamics are regulated by microtubule-associated proteins. In this study, we investigated the molecular mechanism of microtubule nucleation and network formation by CAMSAP2 using cryo-EM and hsAFM. Our structural analyses revealed that CAMSAP2 promotes nucleation by binding to tubulin and straightening its conformation to facilitate the formation of nucleation intermediates. Furthermore, hsAFM imaging successfully captured the dynamic process by which tubulin progresses through various intermediates to assemble into mature microtubules.

Kumiko Hayashi (*ISSP, Univ. Tokyo*)

Mutations in KIF1A, a member of the kinesin superfamily, cause KIF1A Associated Neurological Disorder (KAND). Recent studies have examined correlations between clinical phenotypes, as measured by the VABS ABC score, and protein structure-based ESM (Evolutionary Scale Modeling) scores. However, the correlation remains weak, suggesting that phenotypic impact may also stem from biophysical changes in motor proteins caused by mutations. To address this, we aim to advance in-cell force measurement techniques and provide a novel energetic perspective to complement sequence-based phenotype prediction for missense mutations.

Takumi Saito (*Grad. Sch. of Engineering Science, The University of Osaka*)

Mechanical forces regulate cellular behaviors, known as mechanotransduction. To measure forces at the molecular level in living cells, FRET-based techniques are often used. However, these sensors typically exhibit around 20% S/N ratio and require two fluorophores, making their size comparable to that of a protein of interest. To overcome these limitations, we developed a novel mechano-sensor composed of two α -helices forming a coiled-coil structure, hence called coiled-coil mechano-sensors. The coiled-coil mechano-sensors inserted into a protein of interest open in all-or-none fashion, depending on the amino-acid sequence of the helices. The sensor module requires only a single fluorophore or luminescent tag and extends to several tens of nanometers in its open state.

Cristina Bertocchi^{1,2} (¹*Pontificia Universidad Católica de Chile*, ²*The University of Osaka*)

Force transmission through adherens junctions (AJs) plays a key role in maintaining multicellularity. While recent research has advanced our understanding of the molecular basis of mechanotransduction at AJs, the classical model fails to explain how mechanical forces are propagated when key mechanotransducers are absent or mutated. Here I show that β -catenin can directly interact with open vinculin, even in the absence of α -catenin, and that this interaction can bear physiological force. These findings support a model in which force transmission at AJs is a multi-step process, mediated by cooperative and compensatory interactions between β -catenin and α -catenin with vinculin. This mechanism may explain collective invasion of metastatic cells lacking α -catenin.

Naotaka Nakazawa (*Kindai University*)

During brain development, migrating neurons move through confined spaces in brain tissue. However, the molecular mechanisms that control their movement in response to the size of the confined spaces are not well understood. To address this issue, we designed a microfluidic device that mimics the confined spaces in brain tissue. The combination of live cell imaging both in the microfluidic device and in cultured brain tissue revealed that a mechanosensing mechanism is critical for generating the driving force of neuronal migration in confined spaces. In this talk, we will introduce our experimental system using microfluidic devices for neuronal migration, as well as the molecular basis of the mechano-sensing and -response mechanism for confined migration in the neuron.

2SIP-5 突起形成による力不均衡がもたらすグリオーマの移動極性
Migratory polarity emerges from protrusion-mediated force imbalance in glioma cells

Yuichi Sakumura^{1,2}, Haruna Tagawa², Daisuke Kanematsu³, Asako Katsuma^{2,3}, Naoyuki Inagaki², Yonehiro Kanemura³ (¹*Data Science Center, Nara Inst. of Sci. and Tech.*, ²*Grad. Sch. Sci. and Tech., Nara Inst. of Sci. and Tech.*, ³*NHO Osaka National Hospital*)

Glioma is a highly invasive brain tumor with poor prognosis due to its high cell motility. Time-lapse imaging of GDC40 cells on fibronectin- and laminin-coated substrates revealed persistent migration without clear morphological polarity. We define this directional persistence as "migratory polarity" and investigated its controllability. Using a simplified physical model incorporating protrusion dynamics and adhesion kinetics, we manipulated the protrusion formation rate. Increased protrusion generation led to antagonistic forces among protrusions, reduced migratory polarity, and ultimately suppressed motility. This suggests a potential strategy to control tumor invasion through mechanical intervention.

2SIP-6 運動する細胞の応力ゆらぎ操作と計測
Dynamic Control and Analysis of Intracellular Stress Fluctuations during Cell Migration

Satoru Kidoaki (*IMCE, Kyushu Univ.*)

We developed a platform to manipulate and analyze intracellular stress fluctuations in migrating cells using patterned gels with defined stiffness gradients. Non-stationary migration was induced via dual-directional durotaxis, enhancing long-period stress fluctuation components. Wavelet analysis of cell area change acceleration revealed increased low-frequency energy density, particularly in mechanically activated mesenchymal stem cells. These fluctuations may reflect periodic stress-energy buffering linked to ATP cycling. UMAP-based clustering of wavelet features allowed identification of fluctuation-intensified populations. This provides a metric for mechanostate assessment and potential control of cell function.

2SIP-7 細胞内の中間スケールにおけるゆらぎ駆動力の定量解析
Probing mesoscale physical forces in cells

Shinji Deguchi^{1,2}, Yuika Ueda¹ (¹*Grad Sch Eng Sci, Univ Osaka*, ²*MEI-Center, Univ Osaka*)

We investigate how cells generate and regulate physical forces at functionally relevant mesoscale levels, beyond individual molecular interactions yet involving coordinated dynamics of multiple structural components. Using a fluorescence correlation spectroscopy-based framework, we probe intracellular non-thermal fluctuations and quantify active forces. Pharmacological perturbations to specific molecular pathways revealed that both the magnitude of these forces and a responsiveness parameter vary systematically across conditions. These findings suggest that cells adaptively redistribute physical load within cytoplasmic structures, providing new insights into how mesoscale mechanics contribute to cellular function.

2SJP-1 Sub-micron imaging of neuronal action potentials by defect charge-state conversion in diamond

Daniel McCloskey^{1,2}, Kathryn Munro³, Nikolai Dontschuk¹, David Simpson^{1,2} (¹*Sch. of Phys., Univ. Melbourne*, ²*ARC CoE in Quantum Biotechnology*, ³*Dept. Anatomy & Physiology, Univ. Melbourne*)

Voltage imaging techniques are used in electrophysiology to study neural signalling and connectivity, but thus far cannot achieve sub-micron resolutions with sufficient signal-to-noise to reliably resolve dynamics of synaptic plasticity, ion channel expression, and seldom-explored phenomena such as dendritic backpropagation. Here, we demonstrate sub-micron voltage imaging of action-potential propagation in mammalian neurons using conversion between charge-states of diamond nitrogen-vacancy (NV) centres. Ensembles of NV centres formed near a two-dimensional conductive layer at the diamond surface provide a means to optically probe local image charge accumulation at the surface, enabling rapid, label-free, and quantitative voltage imaging at the diffraction limit.

[2SJP-2](#) Computational 4D imaging for understanding pain-processing neural circuit

Takuma Sugi (*Grad. Sch. Integ. Sci. for Life, Hiroshima Univ.*)

Computational imaging is a technology based on optics and information science. One of the key techniques in computational imaging, light-field (LF) imaging, optically encodes a 3D space into a 2D image and computationally decodes the 3D spatial information from the 2D image. Here, we have developed high-resolution LF imaging technology. This high-resolution LF imaging demonstrated its capacity to unveil the logics of information flow and network organization. By combining this imaging technology with other advancements, we have developed single-cell 4D optogenetics, 4D super-resolution imaging, and 4D quantum sensing using fluorescent nanodiamond particles, which allow for the measurement of physical and chemical changes, such as temperature and reactive oxygen species.

[2SJP-3](#) Quantum Sensing in Healthcare: Spin-Enhanced Immunoassays with Fluorescent Nanodiamonds

Huan-Cheng Chang (*Academia Sinica, Taiwan*)

Quantum sensing leverages materials with unique quantum properties to achieve exceptional precision and sensitivity in measurement. Despite its transformative potential, the application of quantum sensing in applied chemistry and healthcare diagnostics remains largely underexplored. In this study, we present two innovative immunoassay platforms that exploit the quantum properties of nitrogen-vacancy (NV) centers in fluorescent nanodiamonds (FNDs). By integrating quantum sensing with both lateral and vertical flow technologies, these assays deliver unprecedented speed, sensitivity, and analytical throughput. Our results demonstrate their broad clinical utility, particularly in the detection of disease biomarkers and circulating tumor cells.

[2SJP-4](#) Diamond quantum sensors for iron load quantification of ferritin proteins

A. Simpson David (*School of Physics, University of Melbourne*)

Ferritin is a key iron-storage metalloprotein essential for iron homeostasis, making its study highly relevant to biochemistry and clinical analysis of iron status. Beyond this, ferritin's magnetic core properties are of growing interest for understanding nanoscale magnetism and developing biomedical nanotechnologies. We investigate ferritin core development using diamond-based quantum spin relaxometry, sensitive to magnetic fluctuations from low protein concentrations. Our data reveal anomalous magnetism linked to morphological changes at low iron loads, supported by electron microscopy. These findings position quantum sensors as powerful tools for noninvasive studies of metalloprotein magnetism.

[2SJP-5](#) Interferometric Scattering Microscopy: Where Light Scatters and Life Reveals

Chia-Lung Hsieh (*Institute of Atomic and Molecular Sciences (IAMS), Academia Sinica*)

Scattering-based optical microscopy enables label-free imaging of biological systems by detecting light interactions such as absorption and scattering. Among these techniques, interferometric scattering (iSCAT) microscopy stands out for its ability to detect nanoscopic objects with exceptional sensitivity, speed, and resolution. In this talk, I will introduce the principles and capabilities of iSCAT microscopy and highlight its advantages for live-cell imaging. Through examples including virus-membrane interactions, intracellular transport, and chromatin condensation, I will illustrate how iSCAT provides new insights into dynamic cellular processes. I will conclude by discussing future directions and the growing potential of label-free iSCAT microscopy in bioimaging.

[2SJ-P-6](#)

ナノ量子センサが切り拓く細胞機能の新次元定量技術

Next-Generation Quantification of Cellular Functions Enabled by Nanoscale Quantum Sensors

Hitoshi Ishiwata^{1,2} (¹iQLS, QST, ²Chiba Univ. cQUEST)

Recent advances in nanoscale quantum sensors, capable of optical detection under ambient conditions, are transforming biochemical detection in biological systems. Core advantage of quantum sensing lies in high-precision quantification, such as temperature sensing below 0.1 °C and nanoscale NMR with <1 nm resolution.

This talk presents two emerging approaches: (1) 2D quantum imaging for analyzing membrane radical generation, and (2) Molecular Quantum Nanosensors (MQNs). Using MQNs, we perform organelle-specific intracellular thermometry, revealing heat shock responses in cancer cell nuclei that correlate with DNA concentration, enabling molecularly precise monitoring of cellular function.

[2SKP-1](#)

小さいゲノムを持つ微生物から見る生命と非生命の境界

The Boundary Between Life and Non-Life Seen in Microorganisms with Small Genomes

Shino Suzuki (*PRI, RIKEN*)

Life, including humans, depends on other organisms, except for primary producers. Over evolutionary time, this dependency deepened, leading to the transformation of aerobic bacteria into mitochondria and photosynthetic bacteria into chloroplasts, which lost their ability to live independently. In strongly alkaline and reducing subsurface environments, we revealed that Candidate Phyla Radiation (CPR) bacteria, with genomes around 500 kbp, dominate, comprising up to 80% of the community. These organisms lack essential genes for biosynthesis, respiration, ATP synthesis, and membrane formation but survive as probable episymbionts. Here, we explore the boundary between life and non-life through the microbe with highly reduced genomes that inhabit extreme environments.

[2SKP-2](#)ヌクレオサイトウイルス門の巨大ウイルスによる感染細胞に対する思いもよらぬ影響について
Giant viruses of the Phylum Nucleocytoviricota induce unexpected behaviors in infected host cellsMasaharu Takemura, Jiwan Bae (*Grad. Sch. Sci., Tokyo Univ. Sci.*)

Giant viruses belonging to the phylum Nucleocytoviricota exhibit highly unique strategies for “living” in ecosystems of living things. Medusaviruses of the family *Mamonoviridae*, discovered in 2019, encode a full set of histones similar to those in eukaryotes and replicate their genome within the host cell nucleus. Genomic studies of medusaviruses have revealed that several lateral gene transfers have occurred that have affected the evolution of eukaryotes and the medusavirus itself. New momovirus strains of the family *Mimiviridae* and new faustovirus strains of the putative family *Asfarviridae* have been found to provide host cells with resistance against these viruses, suggesting linked evolutionary strategies between giant viruses and eukaryotic hosts.

[2SKP-3](#)

Artificial cells with dissipative structures

Sakura Takada, Kei Fujiwara (*Dept. of Biosci. and Info., Keio Univ.*)

Life is a dissipative structure that sustains its activities by consuming energy and utilizes dissipative structures to maintain its functions. Reaction-diffusion (RD) waves, including Turing patterns, are representative dissipative structures, and recent studies have shown that those formed within cells orchestrate various cell functions such as division, motility, and polarity. However, due to their nonlinear dynamics under far-from-equilibrium conditions, it remains challenging to understand how RD waves are regulated and formed in cell-size spaces. In this presentation, we introduce recent findings obtained by using artificial cell systems reconstituting the Min wave and modifying its reaction network.

2SKP-4 LLPS ドロプレットを用いた自律成長型人工細胞モデル
Artificial protocell models based on LLPS droplet

Hiroyuki Noji, Yoshihiro Minagawa (*University of Tokyo*)

I present self-growing artificial cell models based on dextran-rich droplets in an aqueous two-phase system of poly(ethylene glycol) (PEG) and dextran (DEX) (Nat. Commun. 2025a). After finding that DNA induces the generation of DEX-rich droplets, we implement the protocells with cell-free transcription-translation systems coupled with DNA amplification/replication, which show active self-growth. I will also introduce DEX-based protocell with an artificial nucleus like a droplet (Nat. Commun. 2025b). Considering the chemical and mechanistic simplicity of DEX and PEG, Dex droplet systems furnish a promising platform for higher autonomy—including self-division and proliferation. I will discuss these prospects together with potential engineering applications.

2SKP-5 生物みたいに自己再生産できる人工システムを作りたい：現状と展望
Toward a self-regenerative in vitro central dogma; progress and future

Norikazu Ichihashi (*Grad. Sch. Arts Sci. Univ. Tokyo*)

Self-regeneration is a unique characteristic of living organisms that allows the synthesis of its own components (DNA, RNA, and proteins) from low molecular weight compounds. A self-regenerative system requires DNA replication, transcription, and translation (i.e., the central dogma). In this meeting, I will share three of our recent progress: simpler DNA replication, sustained regeneration of 20 aminoacyl-tRNA synthetases, one of the main components in the translation system, and expression of the minimal but sufficient tRNA set from a single polycistronic DNA using a novel tRNA array method. Although these results bring us a step closer to establishing an in vitro central dogma, much remains to be done. I would like to discuss future research directions.

2SKP-6 動的な人工細胞のための核酸ベースの知的な凝集体
Nucleic Acid-based Smart Condensates for Dynamic Artificial Cells

Masahiro Takinoue^{1,2,3} (¹*Sch. Computing, Science Tokyo*, ²*Sch. Life Sci. Tech., Science Tokyo*, ³*ASMat, IIR, Science Tokyo*)

Synthetic liquid-like condensates have gained attention in biophysics and nanobiotechnology. While thermodynamic properties are well-studied, dynamic control remains challenging. Our research focuses on nucleic-acid-based liquid-like condensates, which are programmable and allow tuning of physicochemical properties. We have discovered spatiotemporal dynamics such as division and fusion in these condensates by coupling the condensates with enzymatic and nucleic acid reactions. This enables us to construct condensate-based molecular computers and autonomously moving droplets via sensing biomolecules such as microRNAs. Our findings suggest that spatiotemporal control of nucleic-acid-based condensates can advance the design of smart, dynamic artificial cells.

2SKP-7 細胞死の理論と「安定に機能する生化学システム」の珍しさ
A theory of cell death and the rarity of stably functioning biochemical systems

Yusuke Himeoka (*Universal Biology Institute, The University of Tokyo*)

Understanding deaths and life-death boundaries of cells is a fundamental challenge in biological sciences. Recently, we have developed a theoretical framework for cell death. We conceptualize cell death as a controllability problem within dynamical systems. By computing the controllability of the kinetic model of *E. coli* central carbon metabolism, we revealed its life-death boundary.

Another approach to dissecting life-death boundaries is quantifying the rarity of biochemical systems performing certain functions, such as cell growth and ATP production. We have developed a method to calculate the number of parameter combinations that lead to such functional states in a given in silico cellular model. We will share our preliminary findings on the quantification of rarity.

3SAA-1 ストレスファイバ直線収縮が引き起こす魚類表皮ケラトサイトの細胞体回転
Cell body rotation by sequential linear contraction of stress fibers in a fish epidermal keratocyte

Chika Okimura (*Dept. Biol., Yamaguchi Univ.*)

Crawling migration plays an essential role in a variety of biological phenomena. Fish epidermal keratocytes are wound-healing motile cells. Each cell consists of a frontal crescent-shaped lamellipodium and a rear spindle-shaped cell body. The cell body is rotating during crawling migration of keratocytes. Recently, we showed that multiple stress fibers (SFs) are arranged around the nucleus like a spindle and rotating with the cell body. SFs are molecular machines that contract linearly like myofibrils and are a candidate power source for cell body rotation. We construct a toy robot using a gel and coils. The robot's motion predicts that the cell body, deformed by the stress fiber contraction, would push the substrate and rotate, which is confirmed by live-cell imaging.

3SAA-2 Nanoscale motion tracing of spermatozoa

Jean-Claude Tinguely¹, Sunil Bhatt², Ankit Butola¹, Mona Nystadq^{3,4}, Dalip Singh Mehta², Krishna Agarwal¹
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We present a method for studying cell dynamics combining a label-free microscopy method (quantitative phase imaging - QPI) with a computational nanoscopy tool (multiple signal classification algorithm - MUSICAL). This technique is demonstrated for the study of sperm cells, where nanoscale motion trajectories are correlated with the linear velocity. The alternative strategy for the classification of sperm cell quality potentially enhances the accuracy of sperm selection to improve the success rates of assisted reproductive technologies. Beyond the presented application, we anticipate that this method will be of interest for studying cell dynamics in various biological models.

3SAA-3 Statistical Physics Meets AlphaFold: Universal Folding–Function Scaling and Evolutionary Trends

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The integration of statistical physics with AI-predicted structural data opens new avenues for uncovering universal principles in biology. Using AlphaFold (AF)'s predictions, we examine protein structures across diverse proteomes to identify global trends. Analyzing AF structures, we uncover a universal scaling law linking contact order with fluctuation entropy, revealing the relationship between folding and functional dynamics. This relation holds consistently across chain lengths and species. We observe that proteins from complex organisms show lower contact order and higher entropy, indicating evolution toward enhanced flexibility. These findings reveal physical principles implicitly captured by AI, offering insights into proteome evolution and biomolecule design.

3SAA-4 Fluorescence and label-free microscopy to study keratocytes from Atlantic salmon

Deanna Lynn Wolfson, Dhivya B. Thiyagarajan, Bilal M. Afzal, Marie Mikkelsen, Azeem Ahmad, Balpreet S. Ahluwalia, Roy A. Dalmo (*UiT The Arctic University of Norway*)

Salmon is a vital resource which is facing increasing environmental challenges. Keratocyte cells are their first line of defense against disease, so the mechanisms which they use to communicate and handle exogenous threats are critical to understand. In response to the growing threat of plastic pollution, we have studied how individual and collective cells respond to microplastics. We have shown that single cells can internalize plastic particles from 0.5 – 15 µm, with cells working collectively to surround and move even larger particles. We have further observed that keratocytes form tunneling nanotubes between cells, particularly when stressed, and have used quantitative phase microscopy to map differences in structural integrity of these nanotubes.

3SAA-5 古代地球における時計タンパク質 KaiC の構造的進化
Structural Evolution of Clock Protein KaiC on Ancient Earth

Yoshihiko Furuie (*Institute for Molecular Science*)

The circadian rhythm of modern cyanobacteria arises from the allosteric regulation of ATP-dependent reactions in KaiC. In this study, we traced the evolutionary origin of this sophisticated clock mechanism. We found that the ancestral KaiC from 2.2 billion years ago, reconstructed using phylogenetic analyses, functioned *in vitro* and *in vivo* and synchronized with ancient Earth's rotation. In contrast, a more ancient KaiC dated to 3 billion years ago lacked a clock function. A series of structural analyses revealed that the emergence of key residues mediating ADP-ATP exchange was a crucial evolutionary step. This atomic-scale evolution in KaiC contributed to the development of global ecosystems by enabling temporally regulated photosynthesis in cyanobacteria.

3SAA-6 NANOSPACER: Nanofluidics for single molecule metrology of extracellular vesicles,
biomacromolecules and amyloids in solution

Oliver Vanderpoorten (*UiT The Arctic University of Norway*)

Nanofluidics has proven itself for applications in life sciences and biophysical single molecule metrology. To make this technology more available to a broader community, I present NANOSPACER: a versatile method to size and detect single molecules in solution without permanent surface immobilization using conventional available microscopy equipment. This allows to study label-free protein dynamics and interactions using the Stokes-Einstein relation and open-source NTA software (Fiji) at single particle level. In particular, I demonstrate detection and diffusional sizing of various specimen ranging from highly motile bacteria (1µm), nanoparticles (500-44nm), EVs (200-40nm), viruses (45-40nm), proteins (3-1nm), DNA (1kbp-100bp) to amyloid protein aggregates (tau, a-syn).

3SBA-1 生体内深部を観察可能な近赤外 in vivo 光イメージング材料
Innovation of NIR luciferin analogues using firefly bioluminescence for in vivo imaging

Nobuo Kitada^{1,2,3}, Genta Kamiya¹, Jumpei Hatakeyama¹, Ryohei Moriya⁴, Masahiro Kiyama⁵, Satoshi Iwano⁵, Takashi Hirano¹, Shojiro Maki^{1,2,3} (¹Grad. Sch. Info. Eng., UEC, ²Env. Saf. San. Mgmt. Ctr., UEC, ³CNBE, UEC, ⁴Fac. Sci., Kitasato Univ., ⁵Tenure-Track Prom. Off., Univ. Miyazaki)

Firefly bioluminescence, a key life science tool, typically emits yellow-green light, limiting deep-tissue imaging. As NIR light highly permeates tissues, we've systematically developed NIR luciferin analogues.

NIR luciferin "AkaLumine" proved effective in mouse in vivo imaging. Further optimization yielded commercially available TokeOni and seMpai. The recent development of Akaluc, an artificial enzyme specific to TokeOni, now enables in vivo imaging in larger animals like minipigs and marmosets.

Our current work focuses on synthesizing novel NIR luciferin analogues emitting beyond 700 nm for even deeper, clearer imaging. This presentation will detail the characteristics of these recently developed NIR probes and their potential as advanced imaging tools.

3SBA-2 ホタル生物発光基質類似体の理論的研究
Theoretical study for firefly bioluminescence substrate analogs

Miyabi Hiyama (*Gunma University*)

Firefly bioluminescence is the emission produced by the oxidation reaction of firefly luciferin (LH2) and ATP in firefly luciferase enzyme (fLuc). This bioluminescence is widely used in life science area. Especially, the LH2 analogs producing red emission, such as AkaLumine, are developed because this emission can penetrate through biological tissues. The elucidation of the detail of emission mechanism in firefly bioluminescence is important for the development of LH2 analogs. Thus, the fundamental scientific data including not only bioluminescence but also absorption/fluorescence spectra are needed. In this talk, the theoretical studies for these spectra of LH2 analogs will be presented.

3SBA-3 発光タンパク質イクオリンの時分割シリアルフェムト秒結晶構造解析
Time-resolved serial femtosecond crystallography of the bioluminescent protein Aequorin

Maiko Moriguchi, Toru Nakatsu (*Fac. Pharm. Sci., Wakayama Med. Univ.*)

Aequorin, a bioluminescent protein from *Aequorea victoria*, emits blue light upon specific Ca^{2+} binding. Coelenterazine is oxidized and retained as a peroxide form within the protein. Ca^{2+} binds to three EF-hand motifs (I, III, IV), inducing conformational changes essential for light emission. Previous studies showed preferential Ca^{2+} binding to EF-hands III and IV over I, but the precise binding order and associated structural transitions remained unclear. In this study, we used time-resolved serial femtosecond crystallography with two-solution mixing at the SACLA XFEL. Aequorin microcrystals were mixed with 1, 2, or 3 mM Ca^{2+} and reacted for 5 s. Structures with one, two, and three Ca^{2+} ions bound were successfully determined at resolutions better than 2.0 Å.

3SBA-4 ハイブリッド QM/MM 自由エネルギー法によるイクオリンの生物発光過程についての理論的研究
Theoretical study on the bioluminescent process of Aequorin by hybrid QM/MM free energy method

Tomohiro Ando¹, Toshiya Funahashi², Toru Nakatsu³, Shigehiko Hayashi¹ (¹*Grad. Sch. of Sci. Kyoto Univ.*, ²*Grad. Sch. of Pharm. Sci. Kyoto Univ.*, ³*Sch. of Pharm. Sci. Wakayama Med. Univ.*)

Aequorin is a blue light emitting protein extracted from jellyfish. It is experimentally known that the binding of calcium ions to aequorin initiates its structural changes of protein that triggers the chemical reaction of the luminescent substrate molecule, coelenterazine (CTZ). In this study, we analyzed the correlation between the luminescent reaction of CTZ, and structural changes of the protein through QM/MM RWFE-SCF method and BAR method. The calculations accurately determined molecular interaction between the CTZ and the surrounding amino acid side chains, and revealed the dynamics of the hydrogen bonding network near the active site due to water influx, and explored the proton transfer reaction pathway leading to the luminescent state in terms of free energy.

3SBA-5 古代のルシフェラーゼを復元する
Resurrecting the ancient luciferase

Yuichi Oba (*Dept. Env. Biol., Chubu Univ.*)

The luminescence color of firefly (Hotaru, in Japanese) is determined by the structure of luciferase protein. Firefly's glow ranges in color from green to orange-yellow. Here, we reconstructed ancestral firefly luciferase gene using the ancestral sequence reconstruction methods, characterized the enzymatic properties of the recombinant proteins, and determined the crystal structures with binding of luciferin analogue. Results showed that the last common firefly ancestor, appeared about 100 million year ago, exhibited green light caused by a spatial constraint on the luciferin molecule in enzyme. These results suggest that the first firefly at Cretaceous Period glowed in green, and this green color was accomplished by the tight binding of luciferin in luciferase.

3SBA-6 分子シミュレーションで探るホタルの太古の光
Molecular Simulations of the Ancient Glow of Fireflies

Norifumi Yamamoto (*Chiba Tech*)

Bioluminescence is a widespread natural phenomenon. Professor Oba's group (Chubu University) reconstructed ancestral firefly luciferase, discovering that Cretaceous-era fireflies emitted shorter-wavelength light than modern species.

Building upon these findings, our research group investigates the molecular mechanisms responsible for these distinct bioluminescence colors. We employ advanced computational approaches, including QM/MM TD-DFT simulations to reproduce emission spectra and a "charge scanning" method we developed to identify critical residues. These techniques show how the microenvironment surrounding the light-emitting chromophore varies between modern and ancestral luciferases and how such variations drove the evolutionary shift in emission color.

3SBA-7 ホシホウネンエソ発光器に局在する紫色素タンパク質の生化学的解析
Biochemical analysis of the purple pigment protein localized in the light organ of the hatchetfish

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Approximately 1,500 species of bioluminescent fishes are known, most of them live in deep-sea. It is known that each group possesses specially evolved luminescent organs, and that luminescence is modified to the optimum wavelength by reflectors or pigment filters located in the light organ. Here, we focused on the purple pigment protein localized in the light organ of the hatchetfish *Polyipnus matsubarae*. Peptide mass spectrometry and transcriptome analysis in the light organ revealed that the purple pigment is an unknown protein with homology to myoglobin. Amino acid sequence information and oxidation/reduction processing experiments suggest that purple pigment has lost its oxygen-binding ability, an original function of myoglobin, and has evolved as a pigment protein.

3SBA-8 全電子第一原理 GW Γ 法の開発
Development of all-electron first-principles GW Γ method

Yoshifumi Noguchi (*Grad. Sch. Eng., Shizuoka Univ.*)

The conventional GW approximation, known as the lowest-order approximation to a three-point vertex function, is a well-established method to simulate single excitation energy spectra. However, it generates non-negligible errors for core-electron excitations and even for valence-electron excitations of some molecular systems. We developed a first-principles GWT method that considers the first-order three-point vertex function, and applied it to simulate the core-electron binding energies (BEs) of 19 small-sized molecules. We discuss the computational accuracy of our method in comparison to the experimental BEs.

3SBA-9 半導体レーザーを用いたポータブルピコ秒パルス光源と生物物理への応用
Semiconductor laser based portable picosecond pulse light source for biophysics applications

Masataka Kobayashi¹, Keisei Shibata^{1,2}, Hidekazu Nakamae¹, Changsu Kim^{1,3}, Takashi Ito³, Miyabi Hiyama^{4,5}, Hidefumi Akiyama^{1,3} (¹ISSP, Univ. of Tokyo, ²Grad. Sch. Pure and Appl. Sci, Univ. of Tsukuba, ³LDseed Co., Ltd., ⁴Grad. Sch. Sci. Tech., Gunma Univ., ⁵Gunma Univ. Center for Food Science and Wellness)

Advances in light sources are essential in the development of spectroscopy for biophysics. While traditional spectroscopy has relied on gas or solid-state lasers, semiconductor-laser-based approaches are rapidly emerging. We developed a system of semiconductor lasers and acousto-optic modulators (AOMs) for time-resolved Raman spectroscopy, offering good temporal control with electronic pulse generators. Moreover, we developed nanosecond to sub-picosecond short optical pulses from directly modulated or gain-switched semiconductor lasers. We hope that this light source enables high-speed, time-domain spectroscopy with compact and cost-effective setups toward next-generation biophysics applications.

3SEA-1 Innovations in Sensitivity-Enhanced High-Dimensional Protein Solid-state NMR and Applications to Amyloid Proteins

Yoshitaka Ishii (*Institute of Science Tokyo*)

We discuss recent progress and relevant innovations in biological solid-state NMR (SSNMR) using fast magic angle spinning (MAS) and its applications to amyloid and other proteins. First, we present our progress in the structural examination of misfolded amyloid- β (Ab) by SSNMR. Increasing evidence suggests that the propagation of misfolded A β 42 provokes the Alzheimer's. Here, we discuss our ongoing efforts to characterize the structure of trace amounts of brain-derived A β 42 fibrils and other proteins by sensitivity-enhanced ¹H-detected 3D-5D SSNMR. CryoEM and SSNMR analysis of Ab fibril associated with familial Alzheimer's will be also presented. Some NMR data from a home-built 1.01 GHz NMR system will be presented with future development prospects of 1.3 GHz NMR.

3SEA-2 溶解 DNP-NMR 法を用いた蛋白質の相互作用, 構造動態解析法の開発
Development of protein interaction and structural dynamics studies using dissolved DNP and isotope-aided NMR

Ken-ichi Akagi, Tatsuya Ikenoue, **Yohei Miyanoiri** (*Inst. Prot. Res., Univ. Osaka*)

Solution NMR spectroscopy is an excellent method for analyzing the structures, dynamics, and interactions of biomolecules with atomic resolution. As a result, it is widely used across various life science fields. However, as the molecular weight of the target increases, signal sensitivity decreases significantly, limiting its broader application. To address this issue, we have developed a specific isotope labeling technique that enables high-sensitivity NMR studies of larger proteins. In recent years, we have also incorporated Dynamic Nuclear Polarization (DNP) methods to capture high-sensitivity NMR signals in shorter experimental times. In this session, we will introduce our latest techniques for analyzing protein-drug interactions using these advanced methods.

3SEA-3 固体 NMR を用いた微生物型ロドプシンの残基特異的な知見
Residue-specific insights on microbial rhodopsins using solid-state NMR

Izuru Kawamura (*Grad. Sch. Eng. Sci, Yokohama Natl. Univ.*)

Microbial rhodopsins are seven trans-membrane proteins that function as proton pumps, ion channels, or sensors. Their mechanisms are closely linked to photoinduced structural changes triggered by retinal photoisomerization and residue-level alterations in interactions. To fully understand these mechanisms, it is essential to investigate the structures and dynamics under membrane-mimicking conditions. Here, we employed solid-state NMR to investigate the structural features of microbial rhodopsins, focusing on inward-proton pumping rhodopsin and so on. In particular, analysis of changes in signal intensity, chemical shifts, and line widths revealed structural alterations at specific residues. These findings provide the utility of NMR in probing structure and dynamics.

3SEA-4 分子シャペロンを対象とした構造・キネティクス解析
Structural and kinetic insights into molecular chaperones

Tomohide Saio (*IAMS, Tokushima Univ.*)

Molecular chaperones alter the folding properties of proteins through unknown mechanism. Dynamic and transient character of chaperone-client complexes has prevented the high-resolution structural analysis by X-ray crystallography and cryo-electron microscopy. Here we utilized solution NMR integrated with other spectroscopic techniques to investigate molecular chaperones, especially regarding structure and binding kinetics. Our data show how the chaperones recognize the unfolded proteins as well as folding intermediates, highlighting how the chaperones prevent misfolding and facilitate proper folding.

3SEA-5 大腸菌における内在性糖脂質 MPlase の機能的役割
Functional roles of the endogenous glycolipid MPlase in *Escherichia coli*

Kaoru Nomura (*Suntory Foundation for Life Sciences*)

Membrane protein integrase (MPlase) is an endogenous glycolipid found in the cell membranes of *Escherichia coli* (*E. coli*). Although MPlase is a minor component of the *E. coli* membrane, it plays a crucial role in facilitating the integration of nascent membrane proteins released from ribosomes on the cytoplasmic side of the *E. coli* membrane. We have recently discovered that MPlase has the ability to induce membrane tubule formation from giant unilamellar vesicles. Using a combination of solid-state and solution NMR spectroscopy and microscopic techniques, we have been elucidating the molecular basis of these functions. In this symposium, we will present our findings on MPlase, with particular emphasis on its interactions with cytosolic molecules.

[3SEA-6](#) Methods and Instruments for High-Field MAS DNP toward Intracellular Structural Biology

Yoh Matsuki (*Inst. Prot. Res., Univ. Osaka*)

We have been implementing dynamic nuclear polarization (DNP) at ultra-low temperatures (~30 K) using helium gas that greatly improved the NMR sensitivity at high field (16.4 T). **Beyond the sensitivity gain**, we have been also exploring new methods such as nano-selective DNP and background signal suppression DNP, looking toward high sensitivity, target-selective NMR within unpurified mixture samples. We also demonstrate nanodiamond is a promising polarizing agent for DNP within biological cells. These basic technical advances combined should open up a new avenue toward high-sensitivity intra-cellular structural biology. In the presentation, we will discuss the latest results on such methods, instrument and applications.

[3SFA-1](#) Enzymatic Condensates as self-regulating systems for metabolic efficiency

Paola Laurino^{1,2} (¹*Okinawa Inst. of Sci. & Tech. Graduate Univ.*, ²*Institute for Protein Research, Osaka Univ*)

We show that enzyme reactions actively remodel condensate properties, defying classical crowding effects: catalytic activity stabilizes low-energy enzyme states that *enhance* reaction rates while increasing molecular mobility. Enzyme-generated pH gradients can drive directed droplet migration, enabling synthetic chemotaxis. Reconstituting metabolic clusters (e.g., MDH/ICD) reveals how non-consecutive enzyme interactions regulate kinetic sequestration and carbon-nitrogen flux. These findings position enzymatic condensates as self-regulating systems where phase separation and catalysis co-evolve to optimize metabolism, spatial organization, and even motility—offering insights into concentrated enzymatic microenvironments and life's origins.

[3SFA-2](#) 生命における代謝経路選択と熱力学的制約 Thermodynamic constraints and the choice of metabolic pathways in life

Mayumi Seto¹, Risa Sasaki¹, Hideshi Ooka², Ryuhei Nakamura^{2,3} (¹*Nara Women's University*, ²*Biofunctional Catalyst Research Team, RIKEN Center for Sustainable Resource Scienc*, ³*Earth- Life Science Institute (ELSI), Institute of Science Tokyo*)

Energy is essential for life, and organisms acquire it mainly via direct interactions with electromagnetic forces. Photosynthetic organisms use light to drive electron transfer and synthesize ATP, while chemosynthetic organisms rely on redox reactions. While animals use aerobic respiration with organic matter and oxygen, prokaryotes exploit a wider range of redox reactions. The direction and energy yield of these reactions can be calculated thermodynamically. In energy-limited settings like early Earth, life may have evolved to favor reactions with more negative Gibbs free energy. This study explores how thermodynamic constraints may have shaped nitrogen-based metabolism and microbial community functions.

[3SFA-3](#) 深海における人工細胞の生存可能性について The Potential of Artificial Cells Functioning under *In Situ* Deep-Sea Conditions

Yutetsu Kuruma, Hidetaka Nomaki, Noriyuki Isobe, Daisuke Matsuoka, Yasuhiro Shimane (*Japan Agency for Marine-Earth Science and Technology*)

Understanding protocell viability in extreme environments where life may have arisen is key to origin-of-life research. We explored the survivability of lipid vesicles and artificial cells in deep-sea conditions by deploying samples to the ocean floor using the human-occupied vehicle *Shinkai 6500*. Most artificial cells were disrupted, but some remained intact after submersion to 1,390 m and successfully synthesized protein in nutrient-rich buffer. Complementary onshore experiments confirmed protein synthesis under high pressure. These findings suggest that artificial cells can maintain gene expression in deep-sea environments, potentially utilizing thermal energy from hydrothermal vents.

[3SFA-4](#)

貨幣分子間のカップリングにおける熱力学的制約

Thermodynamic constraint on the coupling of currency metabolites

Jumpei Yamagishi¹, Tetsuhiro S. Hatakeyama² (¹*BDR, Riken*, ²*ELSI, Science Tokyo*)

Cellular metabolism is regulated by various "currency metabolites," such as ATP. Although these metabolites are believed to regulate distinct metabolic functions, they are generally interconvertible through metabolic reactions. Consequently, the ratios of their high- and low-energy states influence each other. However, the biological implications of this coupling are rarely discussed. In this study, we present a basic model of currency metabolite coupling and demonstrate a trade-off between controllability and thermodynamic cost in metabolism. Additionally, given that ATP and GTP serve as both currency metabolites and as building blocks of RNA, we discuss their connection to the evolutionary trend of genomic GC content as well as the origin of metabolism.

[3SFA-5](#)

電子が導いた生命の起源と生物最古の枝分かれ

Electrons and the origin of three divisions of life

Masaru Konishi Nobu (*JAMSTEC*)

Life has always relied on pushing electrons to harness energy. At seafloor hydrothermal vents, where life likely began, serpentinization generated H₂-rich fluids that enabled abiotic carbon reduction and early metabolism. As life spread beyond these reducing environments, it faced new energy challenges. Thermodynamic models, phylogenetics, and microbial physiology suggest that one lineage adopted light energy, giving rise to photosynthetic Bacteria, while another refined H₂ use, leading to methanogenic Archaea. These innovations, and later electron scarcity, set the stage for the Bacteria-Archaea merger that birthed Eukarya.

[3SFA-6](#)超臨界 CO₂ による脱水反応を介した前生物的な核酸合成Supercritical CO₂ promotes prebiotic nucleotide synthesis via dehydration condensation**Kosuke Fujishima**¹, Shotaro Tagawa², Kohei Morino³ (¹*Earth-Life Science Institute, Science Tokyo*, ²*Institute for Extra-cutting-edge Science and Technology Avant-garde Research Japan Agency for Marine-Earth Science and Technology*, ³*School of Life Science and Technology, Science Tokyo*)

Prebiotic nucleotide synthesis in aqueous environments is thermodynamically unfavourable due to hydrolytic instability. Inspired by the presence of deep-sea liquid CO₂ pools, we investigated nucleoside phosphorylation in a simulated supercritical CO₂ (ScCO₂)-water two-phase system. This setup produced a variety of phosphorylated nucleotide products, including 5'- and 3'-NMPs and diphosphates, via dehydration condensation driven by water migration into the ScCO₂ phase. No reaction occurred in pure water, underscoring the essential role of ScCO₂. Furthermore, carbonate-rich acidic water enabled orthophosphate release from hydroxyapatite. These findings suggest that ScCO₂-water interfaces could support prebiotic condensation reactions in deep-sea environments.

[3SGA-1](#)

計測インフォマティクスの発展と展開 ―情報計測から革新的計測解析へ―

Development and Evolution of Measurement Informatics - From Intelligent Measurement Analysis to Innovative Measurement and Analysis -

Takashi Washio (*Faculty of Business Data Science, Kansai University*)

Measurement technologies are key in our IoT society. In most cutting-edge measurement, large volumes of noisy output data must be processed using advanced information science to extract essential information. However, systematic research on synthesis of measurement and information sciences remains insufficient worldwide. Against this backdrop, the importance of "Measurement Informatics" has been recognized in Japan. From FY2016, the JST CREST and PRESTO programs titled "Intelligent Measurement Analysis", "Innovative Measurement and Analysis" and "Measurement and Analysis Foundation" were launched. In this lecture, we will provide an overview of these projects and introduce some of the advanced research outcomes emerging from them.

[3SGA-2](#) 血小板生物学 x 人工知能 Intelligent platelet biology

Keisuke Goda^{1,2,3,4} (¹*Department of Chemistry, University of Tokyo*, ²*Department of Bioengineering, University of California, Los Angeles*, ³*Institute of Technological Sciences, Wuhan University*, ⁴*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*)

Advances in high-throughput optical imaging and deep learning have transformed platelet analysis, enhancing our understanding of their complex and dynamic nature. This emerging field of "intelligent" platelet biology enables classification of platelet aggregates by agonist and real-time assessment of thrombotic conditions and antiplatelet therapy efficacy in coronary artery disease. These technologies open new frontiers in platelet biology and offer significant potential for next-generation diagnostics, quantitative pharmacology, and targeted therapeutics, which I will discuss in my presentation.

[3SGA-3](#) Theoretical Perspectives on the Hidden Structures in Biological Systems

Ayaka Sakata^{1,2} (¹*Dept. Infor. Sci. Ochanomizu Univ.*, ²*RIKEN AIP*)

Biological systems have complex, hidden structures that shape their behavior but are often hard to observe directly. This talk explores how theoretical tools from statistical physics, information theory, and machine learning can help us understand these underlying patterns. We show that low-dimensional structures, often observed in biological systems, can naturally emerge in theoretical models shaped by evolutionary or functional constraints. These insights deepen our understanding of biological complexity and may inform new approaches to measurement and analysis. We also discuss how such structures may guide the design of more effective measurement strategies.

[3SGA-4](#) 2細胞計測技術を用いた免疫細胞とがん細胞の1細胞相互作用解析 Single-cell analysis of interactions between immune cells and cancer cells using dual-cell measurement technology

Satoshi Yamaguchi (*SANKEN, Univ. of Osaka*)

Conventional evaluations of immune cell cytotoxicity against cancer cells have relied on population averages, limiting insights into single-cell behaviors. To address this, we developed a dual-cell measurement technology using a photoactivatable cell-anchoring surface to position single immune and cancer cells adjacent on a substrate for single-cell interaction analysis [1,2]. Using NK cells from human blood and K562 leukemia cells, we observed NK cell-induced killing. Machine learning analysis of time-lapse imaging further revealed NK cells that trigger either apoptosis or necrosis cell death. This technology offers a powerful platform for immune diagnostics, therapeutic cell discovery, and CAR-T cell quality control.

[1] JACS 2022, 144, 13154, [2] JACS 2022, 144, 17980

[3SGA-5](#) 電圧マトリックスを用いたナノポア測定によるタンパク質混合物の識別 Voltage-Matrix Nanopore Profiling for the Discrimination of Protein Mixtures

Sotaro Uemura¹, **Ryo Akita**¹, **Lysenko Artem**¹, **Keith Boroevich**¹, **Tatsuya Yokota**², **Daiki Kawai**¹, **Ryo Iizuka**¹, **Tatsuhiko Tsunoda**¹ (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Dep. Comp. Sci., Nagoya Inst. Tech*)

Solid-state nanopores provide powerful label-free single-molecule detection, but accurate target identification in complex mixtures remains challenging. We present a voltage-matrix nanopore profiling strategy that captures subtle differences in molecular identity and binding states by systematically varying the applied voltage. Using cancer biomarkers and their aptamer complexes as models, we show that voltage-dependent behavior enhances classification, reveals structural changes upon binding, and exposes hidden biases in capture dynamics. This multiparametric approach enables high-dimensional molecular analysis and supports future development of parallelized nanopore systems for advanced biological diagnostics.

- [3SGA-6](#) 多階層マルチオミックスデータの統合理解に向けた挑戦：ラマンスペクトルとトランスクリプトームを用いたケーススタディ
Toward a Cross-Layer Understanding through Biological Multimodal Data: A Case Study Using Raman Spectroscopy and Transcriptomes

Tomonobu M Watanabe^{1,2} (¹RIKEN BDR, ²RIRBM, Hiroshima University)

Biological phenomena are complex systems of interacting elements. These systems exhibit recursive structures, where fluctuating components form ensembles that also fluctuate. This principle applies across hierarchical levels. Biological states carry multiple meanings, as different measurement modalities reflect distinct aspects of the same condition. Such shared links to a biological state may allow mutual prediction across multivariate datasets, regardless of modality. Clustering these relationships could help reconstruct cross-layer interaction networks, supporting a data-driven, integrative multi-omics approach beyond reductionist methods. In this symposium, we present the conceptual basis, the proof of it using Raman spectroscopy and future directions.

- [3SGA-7](#) 計測介入型 AI が拓く生物学の展開
Unveiling New Frontiers in Biology with Measurement-Intervening AI

Tamiki Komatsuzaki (*RIES, WPI-ICReDD, Hokkaido Univ.*)

Measurements are mother of science and have often triggered scientific advancement. When the aim of a measurement such as classifying phenotypes is defined a priori, the conventional paradigm that separates data acquisition from analysis becomes inefficient. Our key lies in embedding AI-driven analysis directly into the measurement loop, dynamically guiding the process toward optimal acquisition conditions. For example, traditional pipelines in drug screening fail to account for inter-individual variability in drug efficacy, largely due to logistical constraints and cost. We address how AI can design to optimize drug selection by balancing efficacy and risk as well as accelerating Raman measurements in discriminating cell phenotypes.

- [3SHA-1](#) 光遺伝学的手法を用いた神経幹細胞の新規転写制御メカニズムの同定
Uncovering Novel Transcriptional Regulatory Mechanisms of Neural Stem Cells Using Optogenetic Approaches

Itaru Imayoshi^{1,2} (¹Grad. Sch. Biostudies., Univ. Kyoto, ²LiMe., Univ. Kyoto)

NSCs are regulated by the unique sets of functional gene network. However, the mechanism of these gene network formations remains poorly understood. With the optogenetic approach, we have unveiled that oscillatory expression of a bHLH-type transcription factor Ascl1 promoted NSC proliferation, and sustained Ascl1 expression facilitated neuronal differentiation with activating many downstream target genes. Strikingly, both common and unique sets of downstream genes were identified between the oscillatory and sustained Ascl1 expressions. We also showed that the expression mode-specific Ascl1 chromatin remodeling activities and its contribution to establishment of functional gene networks which critically regulate coordinated proliferation and differentiation of NSCs.

- [3SHA-2](#) Nano-electrokinetics が隠れた転写動態と単一細胞の確率的挙動を結びつける
Nano-Electrokinetics Links Hidden Transcriptomic Dynamics to Stochastic Single-Cell Behavior

Hirofumi Shintaku^{1,2}, Akifumi Shiomi^{1,2}, Taikopaul Kaneko^{1,2}, Misa Minegishi^{1,2}, Kotaro Torii^{1,2}, Arata Tsuchida²
(¹LiMe, Kyoto University, ²CPR, RIKEN)

Nano-electroporation is a minimally invasive technique that enables molecular transport while preserving cell viability. Using this along with nano-electrokinetics, we present two single-cell methods integrating cellular traits and gene expression. Live-organismal transcriptomics tracks gene expression over time in living cells via picogram-scale mRNA sampling, revealing stochastic bifurcations in *C. elegans* development. ELASTomics quantifies both cell surface tension and gene expression by importing DNA-labeled macromolecules and sequencing them. Together, these approaches reveal hidden links between transcriptomic dynamics and stochastic single-cell behavior.

[3SHA-3](#) De co de, predict, and control biological systems through single-cell omics and modelling approaches

Kenji Kamimoto^{1,2,3} (¹*Research Institute for Microbial Diseases, The University of Osaka*, ²*Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka*, ³*Bioinformatics Center, The University of Osaka*)

The human body is composed of diverse cell types and molecules. We aim to elucidate the systematic coordination mechanisms of genes and cells during development and disease processes by constructing computational regulatory models using multimodal experimental datasets. We made a new computational method, CellOracle, for gene regulatory network inference and analysis. We use the gene regulatory network models constructed from scRNA-seq and scATAC-seq data to perform in silico transcription factor perturbations. Our GRN models are designed to simulate changes in cell identity in response to gene perturbations in each cell. This simulation enables network configurations to be interrogated in relation to cell-fate regulation, facilitating their interpretation.

[3SHA-4](#) 高速・広視野 Ca²⁺イメージングが明らかにする大脳皮質の機能的ネットワーク構造
High-speed, Large-FOV Ca²⁺ Imaging Reveals Functional Cortical Network Architecture

Masanori Murayama (*RIKEN Center for Brain Science*)

Functional brain-wide Ca²⁺ imaging at single-cell resolution is limited by trade-offs between FOV, speed, resolution, and SNR. We overcame these by combining a resonant-galvo scanner with large optics, enabling fast, wide, and contiguous FOV imaging with minimal aberration. This system captured ~17,000 cortical neurons over a 3×3 mm² area at 15 Hz during behavior—exceeding prior microscope performance in neuron count and speed. Functional network analysis revealed weak scale-free but prominent small-world topology, supporting economical and robust signal propagation via long-distance neuronal correlations. Our method opens new avenues for network-level neuroscience.

[3SHA-5](#) ネットワークトポロジーに由来する生命機能と機能単位
Biological functions and functional modules originated in the topology of chemical reaction networks

Atsushi Mochizuki¹, Yuhei Yamauchi¹, Hironori Sugiyama², Yuhei Goto^{3,4}, Kazuhiro Aoki^{3,4,5} (¹*LiMe, Kyoto Univ.*, ²*Sch. Eng., Univ. Tokyo*, ³*Grad. Sch. Biostudies, Kyoto Univ.*, ⁴*NIBB, NINS*, ⁵*ExCELLS, NINS*)

Biological functions emerge from dynamics of reaction networks, and are regulated by change in enzymes. However, it is not understood why different functions can be regulated independently in a connected network. We developed structural sensitivity analysis (SSA) by which responses of reaction systems by parameter changes are determined from network structure alone. Nonzero responses are localized in finite extents in a network, and each of the extents is determined by a "buffering structure" defined from local topology of network. We analyzed cell cycle network using SSA and predicted that two buffering structures in the network achieve independent control of two checkpoints, G₁-S and G₂-M. Experimental validation confirmed the existence of one buffering structure.

[3SIA-1](#) 合成両親媒性高分子で膜活性ペプチドを真似る
Mimicking Membrane-Active Peptides with Synthetic Amphiphilic Polymers

Kazuma Yasuhara^{1,2,3,4} (¹*Div. Mat. Sci., Grad. Sch. Sci. Tech., Nara Inst. Sci. Tech.*, ²*Ctr. Digital Green-innovation, Nara Inst. Sci. Tech.*, ³*Data Sci. Ctr., Nara Inst. Sci. Tech.*, ⁴*Medilux Res. Ctr., Nara Inst. Sci. Tech.*)

In nature, various biologically active peptides—such as pore-forming toxins, antimicrobial peptides, and cell-penetrating peptides—function by modulating the structure and properties of lipid membranes. A common characteristic among these membrane-active peptides is their globally amphiphilic architecture, which arises from the spatial arrangement of hydrophobic and hydrophilic amino acid residues. Inspired by this structural motif, we have developed synthetic amphiphilic polymers that mimic the membrane-interacting behavior of these peptides. In this presentation, we will describe the molecular design and synthesis of these polymers, as well as their mechanisms of action in modulating lipid membrane structure and dynamics.

3SIA-2 ペプチドと脂質がもたらす膜相分離型ハイブリッド細胞膜とその応用 Peptide-Lipid Hybrid Vesicle with Phase-Separated Domains

Motoki Ueda^{1,2} (¹*Dept. Appl. Chem., Tokyo Metropolitan Univ.*, ²*RIKEN CSRS*)

Liposomes formed by lipid self-assembly serve as models for biological membranes and drug delivery carriers, but their native functions—such as fusion and fluidity—can be disrupted by artificial modification.

We developed an amphiphilic polypeptide that co-assembles with lipids yet forms nanoscale phase-separated vesicles. The peptide and lipid domains remain distinct within a single structure. This allows simultaneous membrane fusion ability and high stability, while enabling independent functionalization of each domain. This approach offers a new strategy for engineering advanced, functionally modular liposomes.

3SIA-3 次世代分子ロボティクスのための脂質膜通型 DNA デバイス Lipid Membrane-Translocating DNA Devices for Next-Generation Molecular Robotics

Shin-ichiro M. Nomura (*Dept. Robotics, Grad. Sch. Eng., Tohoku Univ.*)

Molecular robotics aims to enable molecular-level information processing and control. We developed a novel membrane-penetrating signal transmission system, "Chabashira," using cholesterol-modified DNA. It allows DNA-based signals to cross lipid membranes and activate internal reactions in artificial cells (GUVs). This system facilitates compartmentalized molecular communication, contributing to DNA computing and artificial molecular systems. Recent advances also include self-propelling molecular devices and centimeter-scale artificial multicellular bodies, offering new possibilities in automatic molecular robots.

3SIA-4 触媒システムの構築に向けた赤血球ゴースト-金属化合物ハイブリッドの設計 Design of red blood cell ghost-metal compound hybrids for construction of catalytic systems

Tomomi Koshiyama (*Coll. Life Sci., Ritsumeikan Univ.*)

Cell membranes hierarchically integrate various functional components and play an important role in controlling complicated chemical reactions inside cells. Inspired by cell membranes, artificial and natural lipid vesicles have been used as environments for controlling chemical reactions. We focused on red blood cell ghosts (RBCGs), which are red blood cells from which cytoplasmic components are removed. The structural features of RBCGs include an asymmetric membrane with a cytoskeleton network on the inner membrane surface, and a micro-sized membrane with a high surface area. Taking advantage of these structural features, we worked on the construction of catalytic systems by hybridizing RBCGs with metal compounds such as metal complexes and nanoparticles.

3SIA-5 人工膜と蛍光 1 分子観察を用いた、膜分子の機能解析 Combining an artificial membrane and a single-molecule imaging technique to investigate the function of membrane protein

Rinshi Kasai (*Natl. Cancer Ctr. Res. Inst.*)

Investigating the function of membrane protein using an intact plasma membrane is often excessively complicated due to the complex mixture of various proteins and lipids, which makes research difficult. Conversely, removing indispensable factors from a plasma membrane leads to rapid cell death or damage, rendering observation impossible. Therefore, we have been exploring the use of an artificial membrane as an observation platform. Samples are placed on an artificial membrane supported on the glass surface, and we then observed this system using fluorescence microscopy, enabling the visualization of biophysical events at the single molecule level. In this presentation, we will share recent results obtained using this system.

3SIA-6**人工生体膜分子およびドメインの光操作****Optical Manipulation of Molecules and Domains in Biological Membranes Models**

Yasushi Tanimoto, Shunya Moriyama, Kyoko Masui, Chie Hosokawa (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

Optical trapping is widely used to study biomolecular dynamics by labeling with single- μm particles, enabling their manipulation at the laser focus. Although direct optical trapping of biomolecules is difficult owing to their small size and low refractive index, weak optical forces have the potential to bias their diffusion in solutions. To explore the dynamics of membrane molecules at the laser focus, we demonstrated the direct manipulation of membrane components and observed their dynamics using model membranes. Our results indicate that optical forces can act even on small membrane molecules, suggesting that optical trapping can control the dynamics of the membrane molecules. These methods offer a novel approach for the study of biological membranes.

3SIA-7**ペプチドナノディスクを用いたパターン化人工膜への膜タンパク質導入技術の開発****Reconstitution of membrane proteins in a micro-patterned model membrane using peptide nanodisc**

Kenichi Morigaki^{1,2}, Aika Komatsu², Masato Koezuka², Fuko Kueda², Yasushi Tanimoto^{1,4}, Fumio Hayashi³ (¹*Biosignal, Kobe Univ.*, ²*Grad. Sch. Agri. Sci., Kobe Univ.*, ³*Grad. Sch. Sci., Kobe Univ.*, ⁴*Grad. Sch. Sci., Osaka Metropol. Univ.*)

Supported lipid bilayers (SLBs) are a powerful platform for evaluating the physicochemical properties and functions of membrane proteins. However, reconstituting membrane proteins into an SLB constitutes technological challenges. Here, we present a novel approach for reconstituting membrane proteins using nanodisc formed from a short amphiphilic peptide (18A). We reconstituted rhodopsin (Rh), a G-protein-coupled receptor, into a patterned SLB with lateral diffusivity. We controlled the orientation of Rh by attaching G protein transducin to Rh in the nanodisc, and examined the functionality by its activation-dependent dissociation. The model system has the potential to serve as a platform for quantitative analysis of protein-protein and protein-lipid interactions.

3SJA-1**開花まで 120 年：タケにおける超長周期タイマーへの挑戦****120 years for flowering: Challenge to the ultra-long timer in bamboo**

Tomoaki Muranaka¹, Nozomu Takahashi², Motomu Endo², Yoko Hisamoto³ (¹*Grad. Sch. Bio. Agri., Naoyga Univ.*, ²*Grad. Sch. Sci. Tech., NAIST*, ³*Grad. Sch. Agri., Univ. of Tokyo*)

Bamboos are perennial plants belonging to the grass family, Poaceae. Their aboveground shoots are interconnected through an extensive underground rhizome system. Depending on the species, bamboo exhibits synchronized mass flowering followed by death at fixed intervals ranging from 5 to 120 years. Remarkably, this synchronization occurs even among geographically distant individuals, implying the existence of a highly accurate, long-term biological timer. Despite its biological significance, the molecular basis of this phenomenon remains largely unknown due to its extraordinary time scale. To challenge this mystery, we performed comparative RNA-seq and DNA methylation analysis using Japanese collection of Moso bamboo with three ages, 24, 44 and 67 (flowering).

3SJA-2**緑藻における転写非依存的な概日時計****Transcription-Independent Circadian Rhythms in Green Algae**

Takuya Matsuo (*Laboratory of Molecular Biology, Department of Biosciences, School of Science, Kitasato University*)

The eukaryotic circadian clock is typically based on a transcription-translation feedback loop (TTFL) involving clock genes. However, rhythms can persist without transcription, suggesting a transcription-independent clock, though its mechanism is unclear. Algal clock research began in the 1960s with *Acetabularia* and continued in the 1970s with *Chlamydomonas*. Recent work in *Chlamydomonas* and *Ostreococcus* showed that their TTFLs partly resemble those of land plants, but algae also have unique genes and mechanisms, indicating evolutionary divergence. Over 50 years ago, *Acetabularia* was shown to maintain rhythms without a nucleus. This talk will present recent findings and consider the basis of transcription-independent clocks in algae.

3SJA-3 Exploring the molecular origin of self-sustained circadian oscillator through clock protein evolution

Atsushi Mukaiyama (*Dept. of Biosci. and Biotech., Fukui Pref. Univ.*)

Cyanobacteria utilize a circadian clock to predict the light-dark cycle in order to achieve efficient photosynthetic reactions. Primitive cyanobacteria are thought to be the first organisms to acquire a circadian clock, but the evolutionary history remains a mystery.

The circadian clock form *Synechococcus elongatus* PCC 7942 is composed of the three kinds of proteins, KaiA, KaiB, and KaiC (Kai-proteins), and can be reconstructed in a test tube. We examined oscillation ability of Kai-proteins from extant species as well as their ancestral form. Our results show that the oldest Kai-protein oscillator emerged at approximately 2.2 billion years ago and that the trait was inherited by the extant Kai-proteins from most freshwater cyanobacteria and some marine cyanobacteria.

3SJA-4 シアノバクテリアの試験管内概日リズムに反応液の pH が与える影響 Effect of pH on the cyanobacterial circadian oscillator in vitro

Kumiko Ito-Miwa^{1,2}, Yasuhiro Onoue³, Takao Kondo^{1,2}, Kazuki Terauchi³ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*IAR, Nagoya Univ.*, ³*Ritsumeikan Univ.*)

The cyanobacterial clock protein KaiC exhibits robust 24-h oscillation of phosphorylation when incubated with KaiA, KaiB, and ATP in vitro. We shows that the period of the in vitro phosphorylation rhythm of KaiC is correlated with solution pH. The solution pH altered the autophosphorylation and autodephosphorylation of KaiC and the effect of KaiB on KaiC but had little effect on its ATPase activity. It also modified the surface charge of the interface between two ATPase domains in KaiC, thereby affecting the autophosphorylation and autodephosphorylation activity of this protein via interdomain communication. We discuss the essential biochemical properties of the Kai oscillator and how this circadian clock has adapted to environmental changes in cyanobacterial cells.

3SJA-5 概日リズムの温度補償および同期化に関わる波形歪み Waveform distortion for temperature compensation and synchronization in circadian rhythms

Shingo Gibo^{1,3}, Teiji Kunihiro², Tetsuo Hatsuda¹, **Gen Kurosawa**¹ (¹*RIKEN iTHEMS*, ²*Yukawa Institute for Theoretical Physics, Kyoto University*, ³*Institute for Basic Science*)

Many biological processes speed up as temperature rises, but the circadian rhythm period remains stable - a phenomenon called temperature compensation- while synchronizing with the 24-hour light-dark cycle. We theoretically explore how waveform in circadian gene-protein oscillations relate to temperature compensation and synchronization. Analyzing the simple model for circadian rhythms, we provide an explanation for most existing hypotheses about temperature compensation. Also, we theoretically show that more distorted waveform at higher temperature is necessary for temperature compensation. Reanalysis of existing experimental data supports our findings on waveform distortion. We conclude that waveforms are fundamental to circadian rhythms.

3SJA-6 細胞内在性発熱による温度シグナリング機構 A thermal signaling mechanism driven by intracellular endogenous heat generation

Shunsuke Chuma¹, Yoshie Harada², **Kohki Okabe**¹ (¹*Graduate School of Pharmaceutical Sciences, The University of Tokyo*, ²*PRiME, The University of Osaka*)

Recent advances in single-cell thermometry revealed temporal and spatial changes related to organelles and cellular processes. Therefore, we propose that spontaneous intracellular temperature changes drive cellular functions, a phenomenon we call intracellular thermal signaling. To determine whether these changes are a product of or a driving force for intracellular reactions, we manipulated intracellular temperature using infrared laser irradiation. Manipulating the local temperature of living cells caused unique cellular responses, including the induction of neuronal differentiation via transcription activation, which proves the existence of intracellular thermal signaling. These results suggest a new principle of intracellular signal transduction.

3SJA-7 反復刺激による神経オルガノイド回路組織の再編と機能性獲得
Repetitive Input Drives Network Refinement and Stimulus-Specific Output in Connected Neural Organoids

Yoshiho Ikeuchi^{1,2} (¹*Institute of Industrial Science, The University of Tokyo*, ²*Institute for AI and Beyond, The University of Tokyo*)

In the developing brain, sensory input during early life shapes neural circuits. To mimic this *in vitro*, we cultured networks composed of one, two, or three human-derived brain organoids on high-density microelectrode arrays and applied spatially distinct stimuli at two input sites daily for two weeks. After repeated stimulation, three-organoid networks exhibited improved discrimination of input locations. This enhancement was accompanied by circuit-level reorganization. These findings demonstrate that stimulation drives network refinement in hierarchically connected organoid circuits.

1MSF-1 AI 技術を活用した生細胞内小胞輸送の理解に向けて
AI-Powered Characterization of Vesicle Transport in Live-Cell Systems

Seohyun Lee (*The University of Tokyo*)

Vesicles are small organelles that bud from the cell membrane and travel within cells, serving as crucial messengers in processes such as infection and drug delivery. Understanding how these tiny carriers function is key to both biological insight and medical applications. In our research, we have developed a range of computational approaches—from numerical modeling to AI-based analysis—spanning single-vesicle tracking to whole-cell-level interpretations. In this talk, I will introduce these methods, share key findings from their application, and discuss the broader potential of AI-powered analysis in uncovering vesicle dynamics.

1MSF-2 High-precision tracking of kinesin-1 stepping inside cells using single- and dual-color MINFLUX nanoscopy

Takahiro Deguchi¹, Tobias Engelhardt², Nikolay Sergeev³, Malina Iwanski⁴, Roman Schmidt², Christopher Heidebrecht⁵, Savannah Cattarius⁵, Lukas Kapitein⁴, Timo Zimmermann¹, Jonas Ries³ (¹*European Molecular Biology Laboratory*, ²*Abberior Instruments GmbH*, ³*Max Perutz Labs, University of Vienna*, ⁴*Utrecht University*, ⁵*University of Heidelberg*)

Molecular machines perform cellular functions through structural changes, but studying these dynamics is challenging due to their small size and speed. MINFLUX (minimal photon flux) super-resolution fluorescence microscopy is highly photon-efficient and enables direct observation of protein conformational dynamics under physiological conditions.

In this study, we focus on kinesin-1, a processive motor protein responsible for intracellular cargo transport along microtubules. By tracking fluorescently labeled kinesin-1 on cellular microtubules, we resolve alternating walking steps using single- and dual-color MINFLUX. Our results will facilitate further *in vivo* studies of motor protein kinetics and other biomolecules.

1MSF-3 Structural analysis and advanced live imaging reveal vesicle dynamics of SID1-mediated uptake of large dsRNA molecules

Akira Takai^{1,2}, Kaoru Kumazaki³, Toshikuni Awazu^{2,4}, Taketoshi Kambara², Shunya Murakoshi³, Takafumi Kato⁵, Masahiro Hiraizumi⁶, Yoshiaki Kise³, Tsukasa Kusakizako³, Tomohiro Nishizawa⁷, Yasushi Okada^{1,2,4,8,9,10}, Osamu Nureki³ (¹*Grad. Sch. Med., Univ. Tokyo*, ²*BDR, RIKEN*, ³*Dept. Bio. Sci., Grad. Sch. Sci., Univ. Tokyo*, ⁴*Grad. Sch. Front. Biosci., Osaka Univ.*, ⁵*Dept. Biochem., Univ. Oxford*, ⁶*Grad. Sch. Eng., Univ. Tokyo*, ⁷*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, ⁸*Dept. Phys., Grad. Sch. Sci., Univ. Tokyo*, ⁹*UBI, Grad. Sch. Sci., Univ. Tokyo*, ¹⁰*WPI-IRCn, IAS, Univ. Tokyo*)

SID1 protein has been reported as a dsRNA-gated dsRNA channel facilitating systemic RNAi in *C. elegans*, while its precise dsRNA transport mechanism remained unclear. Here, we determined the cryo-EM structures of SID1, which reveal that SID1 lacks a channel-like pore, instead forming self-organized multimeric complexes with bound dsRNA. Live-cell imaging demonstrates an endocytic dsRNA internalization by SID1 against concentration gradients. Imaging at single-molecule levels revealed that SID1 multimerizes upon dsRNA binding, suggesting that SID1 multimer folds a large dsRNA molecule into a compact size to be packaged in a size-limited endosome. Collectively, these findings provide a novel perspective on SID1-mediated dsRNA uptake, a self-organizing endocytic mechanism.

[1MSF-4](#) Bacterial Membrane Vesicles: Biology, Functions, and Medical Applications

Ryoma Nakao, Takehiro Yamaguchi, Kimihiro Abe, Yukihiro Akeda (*Dept Bacteriol. I, Natl. Inst. Infect. Dis., JIHS*)

Bacteria commonly release small proteoliposomes, known as bacterial membrane vesicles (BMVs), which range in diameter from 20 to 200 nm. BMVs have versatile functions in bacteria-host interactions by serving as structurally stable vehicles carrying virulence factors, antigens, immunomodulatory molecules, and signals for communication. This talk will present recent advances in immunologically active and safe BMVs produced from a probiotic *Escherichia coli* derivative and discuss their potential as vaccines and adjuvants against a wide range of infectious diseases and the related diseases including non-communicable diseases. We will also introduce our efforts to develop BMV-based vaccine for periodontal disease in murine and canine model studies.

[1MSF-5](#) Creation of biological phenomena using asymmetric vesicles

Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Asymmetric lipid vesicles mimicking eukaryotic cells have been generated to clarify biological functions associated with the asymmetric lipid membranes. The cell-sized asymmetric lipid vesicles containing phosphatidylserine in the inner leaflet showed efficient DNase I translocation into the vesicles via cell-penetrating peptides (CPP). Recently, we generated asymmetric lipid-protein vesicles containing the lipid membrane in the outer leaflet and the protein membrane in the inner leaflet. The asymmetric lipid-protein vesicles enabled the reconstitution of the membrane proteins and the membrane fission. The enzyme reactions were caused by the accumulation of the enzymes on the protein membranes using this asymmetric vesicle.

[1MSG-1](#) 凝集傾向のある抗菌ペプチドの溶解化戦略およびその多様な多量体化特性の評価 Solubilization strategy of aggregation-prone antimicrobial peptides and evaluation of their diverse multimerization properties

Mitsuki Shibagaki, Jeremia Oktavian Chrisnanto, Kosuke Maeda, Tatsuya Arai, Dessalegn Abeje Tefera, Hiroyuki Kumeta, Fumi Hirai, Tomoyasu Aizawa (*Grad. Sch. Life Sci., Hokkaido Univ.*)

LL-37, a human antimicrobial peptide, exhibits immunomodulatory activity via membrane receptors. Previous recombinant expression systems suffered from aggregation, and structural insight for understanding the mode of action was limited. We designed a calmodulin (CaM) fusion tag based on AlphaFold2 predictions and MD simulations, achieving nearly 100% solubility and successful recovery of active LL-37. Cross-linking showed that LL-37 selectively multimerizes in SDS, but not DPC micelles. Other structural analyses were integrated and revealed that only human LL-37 forms a "segregated" α -helix at neutral membrane, while mouse and rat orthologs were associated. These findings suggest that LL-37 has evolved unique structural properties for receptor signaling.

[1MSG-2](#) 分光研究から見てきたウイルスヘリオロドプシンの多様性 Diversity of Viral Heliorhodopsins Uncovered through Spectroscopic Analysis

Ritsu Mizutori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

More than 3,000 heliorhodopsins have been identified across archaea, bacteria, unicellular eukaryotes, and viruses. Among them, 32 heliorhodopsins have been discovered in coccolithoviruses, giant viruses that infect the marine phytoplankton *Emiliana huxleyi* (VHeRs), which are classified into four groups, VHeR1–VHeR4. VHeR3 and VHeR4 transport protons, whereas the functions of VHeR1 and VHeR2 remain unknown. The *Emiliana huxleyi* virus 202 (EhV-202) encodes VHeR1, VHeR2, and VHeR3, whose functional roles may be distinct within a single viral genome. In fact, our spectroscopic data provides highly different molecular properties among them. Diversity of viral heliorhodopsins will be discussed based on our spectroscopic analysis.

1MSG-3 細菌アクチンの微小管化
Microtubulation of the bacterial actin

Daichi Takahashi^{1,2}, Nobutaka Numoto¹, Makoto Miyata^{2,3}, Jian-Ren Shen^{1,4}, Robert C. Robinson^{1,5} (¹*RIIS, Okayama Univ.*, ²*Grad. Sch. Sci., Osaka Met. Univ.*, ³*OCARINA, Osaka Met. Univ.*, ⁴*Grad. Sch. Environ. Life. Nat. Sci. Tech., Okayama Univ.*, ⁵*Sch. Biol. Sci. Eng., Vidyasirimedhi Inst. Sci. Tech.*)

Life relies on a polymerized protein network, cytoskeleton, which includes distinct major classes, actin filaments and microtubules. Here, we report the formation of a microtubule-like structure by the fifth isoform of the bacterial actin MreB in a wall-less helical bacterium *Spiroplasma* (MreB5). While MreB5 forms sheets under neutral pH conditions, it forms a unique filament under acidic conditions. CryoEM revealed that under acidic conditions, MreB5 filaments adopt a loose, left-handed, hollow, cylindrical structure composed of eight parallel protofilaments linked by interactions common to the sheet formation, one of which is longitudinally displaced similar to the microtubule seam. We refer to this unique filament formation of MreB5 as "microtubulation".

1MSG-4 葉緑体 ATP 合成酵素に特有の部位によるレドックス制御機構
Mechanism of redox regulation by region specific to chloroplast F_0F_1 -ATP synthase

Kentaro Akiyama¹, Ken-ichi Wakabayashi², Toru Hisabori³ (¹*The National Institute of Advanced Industrial Science and Technology*, ²*Kyoto Sangyo University*, ³*The Graduate University for Advanced Studies*)

F_0F_1 -ATP synthase generates ATP by using the electrochemical proton gradient formed across the membrane. In chloroplast ATP synthase (CF_0CF_1), its activity is regulated by the redox states of a pair of Cys residues located on the central axis subunit γ of this motor-shaped enzyme. How this Cys pair affects enzymatic activity has remained unclear. We prepared CF_0CF_1 complexes with a mutation at this Cys pair-containing region from *Chlamydomonas reinhardtii*. Our results suggest that the conformational change of CF_0CF_1 -specific region, including the Cys pair, occurs in a redox-dependent manner, thereby regulating the activity. In this symposium, we will discuss the mechanism of this redox regulation from structural and biochemical perspectives.

1MSG-5 構造解析および反応速度論を用いたアセト酢酸脱炭酸酵素 AAD の触媒機構の解明
Structural and kinetic insights into the catalytic mechanism of acetoacetate decarboxylase AAD

Masato Ishizaka^{1,2}, Sören Rindfleisch^{1,2}, Florian Auer^{1,2}, Lukas Gingeleit^{1,2}, Tat Cheung Cheng³, Michael Bielecki⁴, Fabian Rabe von Papenheim^{1,2}, Elke Penka^{1,2}, Ronald Kluger⁴, Eri Sakata³, Kai Tittmann^{1,2} (¹*Dept. Mol. Enzymol., Univ. Göttingen*, ²*Multidisciplinary Sci., MPI*, ³*Inst. Auditory Neurosci., Univ. Med. Center Göttingen*, ⁴*Dept. Chem., Univ. Toronto*)

A crystallographic study of AAD proposed that the hydrophobic nature of the catalytic pocket and electrostatic repulsion are driving forces. However, some computational studies support that polar attraction around the catalytic residue is critical. Furthermore, a novel Schiff-base-independent reaction mechanism was proposed in 2023.

Here, we obtained crystal and cryo-EM structures of AAD, including substrate-binding state, pre- and post-decarboxylation Schiff-base intermediates, and CO_2 -binding state. Moreover, steady-state kinetics of AAD mutants showed cooperativity within the dimer. Our results emphasize that the essence of enzymatic reactions is the interaction between polar residues and the substrate rather than desolvation effects and electrostatic repulsion.

1MSG-6 古細菌 SMC 複合体は DNA セグメント捕捉機構によって DNA 上を一方方向にトランスロケーションする
DNA Segment Capture Drives Unidirectional DNA Translocation of a Prokaryotic SMC Complex: A Multiscale Simulation Study

Masataka Yamauchi, Giovanni Brandani, Tsuyoshi Terakawa, Shoji Takada (*Dept. of Biophys., Kyoto Univ.*)

Structural maintenance of chromosomes (SMC) complexes are essential for chromosome organization through DNA loop extrusion. This study elucidates the DNA translocation mechanism of a prokaryotic SMC complex using multiscale molecular dynamics simulations. Extensive coarse-grained simulations of the prokaryotic SMC complex with dsDNA over the ATP cycle revealed unidirectional DNA translocation via the DNA segment capture mechanism. The process exhibited a step size of ~200 bp, wherein the complex captured a DNA segment of about the same size within the SMC ring in the engaged state, followed by its pumping into the kleisin ring as ATP was hydrolyzed. We identified the asymmetric path of the kleisin as a critical factor for this unidirectionality.

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- 1MSG-7** データベース探索とドッキングシミュレーションを活用した、中鎖アルカン合成酵素の創出と機能解析
Creation of the medium-chain alkane producing enzyme by using the enzyme database search and the docking simulation

Hisashi Kudo, Akihiko Kondo, Tomohisa Hasunuma (*Engineering Biology Research Center., Kobe Univ.*)

We efficiently develop an aldehyde deformylating oxygenase (ADO) with a high productivity for synthesizing medium-chain alkane by computational design. Firstly, we selected the template ADO candidates from the natural enzyme database by using the original clustering method, and selected the best one. Secondly, we used docking simulation to design mutants with increasing substrate affinity. We obtained the mutants with a higher productivity for medium-chain alkane (C11 alkane) or with that for only C11 alkane. We also succeeded in identifying the residues that are important for ADO activity by mutational analysis into the sub-family specific residues. This enzyme design method may be useful not only for ADO but also for useful enzymes for biomaterial production.

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- 1MSH-1** 導入と中性子回折装置を中心とした世界的現状
Introduction and current status of neutron diffractometers worldwide

Ichiro Tanaka (*Ibaraki University*)

Focusing on the current status of single crystal structural analysis of biopolymers using neutrons, we will outline the possibility of visualizing hydrogen using cryo-electron microscopy (cryoEM) and the movement to install neutron diffractometers at new domestic research reactors. Neutron diffraction is the classic method, but recently, the development of highly sensitive hydrogen detection methods and large single crystal growth technology have attempted to make up for the small number of analyses. On the other hand, there have been many reports of hydrogen being visible using synchrotron radiation and cryoEM. We will consider future technological developments, the characteristics of each method, and their significance.

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- 1MSH-2** TOF 型単結晶中性子回折装置 iBIX の現状と将来計画
Current status and future prospects for TOF type single crystal neutron diffractometer iBIX

Katsuhiko Kusaka, Terutoshi Sakakura, Haruki Sugiyama (*NIAPC, CROSS*)

IBARAKI biological crystal diffractometer so-called iBIX is a TOF neutron single crystal diffractometer to elucidate the hydrogen, protonation and hydration structure of biological macro-molecules. The iBIX can collect a full data set of biological macromolecules and organic compounds for neutron structure analysis in less than one week at the accelerator power of 900 kW. Currently, we are working on accelerating and automating the data measurement, reduction and analysis, in order to shorten the time it takes to obtain the experimental results. For example, development of a new 3-axis goniometer, new measurement method, automatic sample change and so on. In this presentation, we will introduce current status of development, and future plans.

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- 1MSH-3** Measurement of hydrogen properties using cryo-EM and ED

Koji Yonekura^{1,2} (¹RIKEN SPring-8/, ²IMRAM, Tohoku University)

While neutrons and X-rays are scattered by atomic nuclei and the surrounding electrons, respectively, electron beams interact with the Coulomb potential along their transmission path, offering significantly higher sensitivity to valence electrons. Given this property, we have demonstrated the visualization of charges and hydrogen atoms at positions consistent with neutron diffraction, using high-resolution single-particle cryo-electron microscopy (cryo-EM) and three-dimensional electron diffraction (3D ED) from small and thin crystals of organic compounds. In this mini-symposium, I will present our approach and recent results, and discuss the limitations and prospects of cryo-EM and 3D ED, particularly in comparison with X-ray free-electron laser crystallography.

1MSH-4 中性子 D/H コントラスト結晶解析による鶏卵白リゾチームの水和構造の研究
Neutron D/H contrast crystallographic study of hydration structure of hen-egg-white lysozyme

Toshiyuki Chatake¹, Tomoko Sunami², Satoru Fujiwara², Ichiro Tanaka³, Katsuhiro Kusaka⁴ (¹KURNS, ²QST, ³Grad. Sch. Sci. Eng., Ibaraki Univ., ⁴CROSS)

Proper hydration is essential for protein structure and function. The hydration layer consists of various water molecules with different mobilities. Such water molecules are more difficult to observe than protein molecules. All the atoms of the water molecules in the hydration layer cannot yet be determined, even by ultra-high resolution X-ray crystallography. The neutron scattering length of hydrogen atoms is comparable to that of other atoms and differs significantly from that of its isotope, hence the difference in neutron scattering between light and heavy water (D/H contrast) provides the high contrast of water molecules in Fourier maps. In this study, the detailed hydration structure of hen-egg-white lysozyme was determined by neutron D/H contrast crystallography.

1MSH-5 タンパク質の主鎖のやわらかさをデザインする。-中性子と ¹⁵N NMR が示唆する主鎖ペプチド結合の部位特異的緩和の原理とその利用-
Designing main-chain flexibility of proteins. Principle of site-specific relaxation of peptide bonds and an application in protein design

Kaori Chiba (National Institute of Technology, Ibaraki College)

The uniform planarity of peptide bonds is one of the most fundamental factors in molecular dynamics and molecular simulation studies of protein, using its atomic coordinates deposited in the Protein Data Bank, and even in the structure analysis itself of protein. We have recently proposed a site-specific relaxation model for peptide bonds in protein molecules, using the newly observed deuterium by neutron crystallography in the vicinity of the main-chain carbonyl oxygen, and the high-field shift of the amide nitrogen in the peptide bond observed by NMR, and the local intramolecular electrostatic potential around the peptide bond (Chiba et al., *Protein Science*. 2023). We present the principle of individual relaxation of peptide bonds and an application using GFP.

1MSH-6 単色法を用いたタンパク質用中性子回折装置の日本における現状と将来
Monochromatic Neutron Diffractometers for Protein Crystallography at Present and in the Future in Japan

Kazuo Kurihara¹, Fumiaki Kono¹, Rumi Shimizu¹, Itaru Tamura², Takashi Ohhara³, Toshiyuki Chatake⁴, Rintaro Inoue⁴, Yu Hirano^{1,5}, Taro Tamada^{1,5} (¹QLS, QST, ²New Res. Reactor Promo. Office, JAEA, ³J-PARC Center, JAEA, ⁴KURNS, Kyoto Univ., ⁵cQUEST, Chiba Univ.)

In Japan, two protein diffractometers using monochromatic neutron beams, BIX-3 and BIX-4, are operated in the research reactor, JRR-3. The BIX-3 uses thermal neutrons and is equipped with a double-bunk monochromator system where Si (111) and Si (311) monochromators are arrayed at the bottom and top bunk, respectively. This system contributed to the successful determination of a protein structure with sub-angstrom resolution. The BIX-4 uses cold neutrons and is equipped with a variable wavelength selection system suitable for use with an optimal wavelength depending on crystal quality and/or lattice length. This talk will also present a brief introduction to a plan to install new diffractometers in a new research reactor to be constructed at the “Monju” site.

1MSI-1 AI が導くバイオ分子デザイン：タンパク質と、その先へ
AI-guided biomolecule design: protein and beyond

Yutaka Saito (Dept. Front. Eng., Kitasato Univ.)

Proteins and nucleic acids are widely used in medicine and bio-manufacturing. While conventional biomolecule design relied on extensive trial-and-error, AI-driven smart design is now gaining attention. Treating sequences as “language” enables the use of language models, while structures as “images” allow diffusion models. Since 2016, we have advanced AI-based biomolecule design in collaboration with experimentalists, including applications to fluorescent proteins, enzymes, antibodies, and mRNA. We also develop original methods such as evolution-aware protein language model pre-training. Now we are building a “digital lab” integrating AI with robotic automation. I will introduce these efforts.

1MSI-2 進化的アルゴリズムとネットワーク理論を融合した酵素リデザイン法の開発
Development of enzyme redesign strategy combining evolutionary algorithm and network theory

Shogo Nakano (*Grad. Div. Nut. Sci., Univ. Shizuoka*)

Enzymes are expected to be candidates for next-generation biocatalysts in the manufacture of biopolymers and fine chemicals. In this study, we introduce two protein-redesign strategies to design highly functional enzymes. GAOptimizer employs a genetic algorithm to optimize combinatorial mutation sets in a target enzyme with referring to the homolog sequences of the template (H. Ozawa *et al.*, *Cell Rep. Phys. Sci.*, **5**(1), 101758, 2024). GArNet extends on this framework, using a bagging-like approach in GAOptimizer and employing network theory to unify mutations and their co-occurrence. (H. Ozawa *et al.*, *J. Chem. Inf. Model.*, just accepted.). Both GAOptimizer and GArNet are available from the following url: <https://github.com/shognakano/>.

1MSI-3 Molecular Programming Using De Novo Designed Proteins

Zibo Chen (*School of Life Sciences, Westlake University*)

In cells, circuits of proteins interacting, genes, and other biomolecules implement complex molecular algorithms. Compared to nucleic acids, protein circuits could directly interface with endogenous pathways and provide new interactions for the cell, but have been difficult to engineer in a generalizable way. A scalable design for creating specific protein-protein, analogous to base pairing in nucleic acids, would enable this vision. Here, I will describe DNA-like powerful modular specificity in proteins based on de novo designed hydrogen bond networks, and show how it allows the creation of mutually orthogonal protein heterodimers, protein-based logic operations, self-assembling protein materials, and protein-based neural network computation inside cells.

1MSI-4 A Rapid and Universal Pipeline for GPCR Structure Determination through In Silico Construct Optimization and de novo Protein Design

Hideaki Kato (*The University of Tokyo*)

G protein-coupled receptors (GPCRs) orchestrate many physiological signals and dominate drug-target space, yet inactive-state structures remain hard to obtain. Cryo-EM can now resolve small GPCRs by attaching fusion partners or binders that raise molecular weight, but current workflows demand extensive construct screening and BRIL-Fab scaffolds often blur maps owing to flexibility. We present a universal pipeline that couples NOAH, an AI-driven in silico fusion-construct screening tool, with ARK1, a rigid de novo-designed fiducial marker, to streamline GPCR structure determination. This approach removes labor-intensive optimization, delivering rapid, high-resolution structures and accelerating structure-based drug discovery in the GPCR field.

1MSJ-1 生きたヒト細胞内の分裂期染色体の化学的・物理的性質
Chemical and physical properties of human mitotic chromosomes in living cells

Kayo Hibino (*Inst. Protein Res., Univ. Osaka*)

Mitotic chromosome assembly during cell division is an extraordinary example of the self-organization of biological supramolecules. To understand the fundamental principles of chromosome organization and its functional regulation, it is essential to investigate chemical composition and physical properties of the mitotic chromosomes. In this study, we employed Raman and Brillouin imaging to characterize the spatial heterogeneity in the chemical composition and viscoelastic properties of human mitotic chromosomes in living cells. Based on the nanoscopic dynamics of genomic chromatin that underlie these chemical and physical characteristics, we discuss the principles that govern genome organization within mitotic chromosomes.

1MSJ-2 DNA複製動態から染色体の振る舞いを明らかにする
Deciphering the behavior of chromosomes through DNA replication dynamics

Ichiro Hiratani (*RIKEN Center for Biosystems Dynamics Research*)

Hi-C has revealed that mammalian chromosomes are organized into topologically associating domains, which can exhibit either early (A-compartment) or late (B-compartment) DNA replication timing (RT). In 2019, we developed scRepli-seq, a single-cell DNA replication sequencing method. Using scRepli-seq and Hi-C, we have uncovered key features of 3D genome dynamics during mouse ES cell differentiation, embryogenesis, and X-inactivation. Furthermore, we recently discovered several novel modes of DNA replication regulation during early mouse embryogenesis linked to its unique 3D genome dynamics. I will present our latest findings on DNA replication control in early development and efforts to uncover the principles of 3D genome organization through the lens of DNA replication.

1MSJ-3 ヒトゲノムのデータ駆動的アノテーションを目指した大規模立体構造比較解析
Large-scale comparative analysis of the 3D genome structure for data-driven annotation of the human genome

Ryuichiro Nakato (*Institute for Quantitative Biosciences, the University of Tokyo*)

Recent advances in 3D genome analysis have revealed that the genome folds hierarchically within the nucleus. One such structure is the topologically associating domain (TAD), which is a chromatin folding unit on the megabase scale. While many TAD boundaries are conserved across human cell types, recent studies have identified cell-type-specific boundaries and subgroups regulated by different architectural factors. However, their full classification and biological roles remain unclear. In this study, we performed a data-driven analysis of large-scale comparative analysis of 3D genome data to classify TAD boundaries and stripes, regions where they interact with multiple loci within the TAD. Here I will share several findings from it.

1MSJ-4 Enhanced A/B Compartment Assignment: Improved Consistency, Orientation, and Resolution with HiC-SCA

Justin Chan¹, Hidetoshi Kono^{1,2} (¹*iQELS, QST*, ²*Center of Quantum Life Science for Structural Therapeutics (cQUEST), Chiba University*)

HiC experiments reveal chromatin's A/B-compartments—preferential loci interactions forming characteristic checkerboard patterns, typically denoting active/inactive euchromatin/heterochromatin. Current methods like POSSUM (used in ENCODE's pipeline), lack robust quality/resolution metrics and require prior knowledge for orientation assignment. We introduce HiC-SCA (HiC Spectral Compartment Assignment), which outperforms POSSUM by: (1) demonstrating superior consistency across replicates, (2) inferring orientation directly from HiC data, (3) determining optimal resolution, and (4) providing per-chromosome confidence scores. HiC-SCA advances A/B-compartment analysis with improved accuracy and objective assessment capabilities.

1MSJ-5 コヒーシサブユニット Scc1 ヘリックス領域の構造機能解析
Structural and Functional Analysis of Conserved Helical Regions in the Cohesin Subunit Scc1

Yoshimi Kinoshita, Tomoko Nishiyama (*Grad. Sch. Sci., Kyoto University*)

The cohesin complex, composed of SMC1, SMC3, and non-SMC subunits including Scc1 and STAG1/2, mediates sister chromatid cohesion and chromatin organization. While recent studies have revealed aspects of DNA loading and loop extrusion, the mechanistic roles of non-SMC components remain unclear. Conserved helical regions in Scc1 contribute to the STAG1/2 interface and may impact how cohesin interacts with DNA and associated factors. Using Scc1 deletion variants lacking conserved helical regions, we examine their effects on DNA affinity, ATPase activity, topological loading, and loop extrusion in vitro, as well as chromosomal behavior and dynamics in vivo. These analyses provide insights into how Scc1 structure regulates cohesin function.

1MSJ-6 Phase diagram approach to elucidate the organization principle of mitotic chromosome**Tetsuya Yamamoto** (*ICReDD, Hokkaido Univ.*)

Condensin-mediated loop extrusion has been thought to be one of the primary mechanisms of mitotic chromosome assembly. However, how condensins assemble mitotic chromosomes through their interactions with other essential factors in a crowded environment is not well understood. In *Xenopus* egg extracts co-depleted of topoisomerase II α and nucleosomes, nucleosome-free, entangled DNA strands assemble a compact chromatin structure, “sparkler”, is assembled. To understand the mechanisms underlying sparkler assembly, we construct a model predicting that DNA loops extruded from the entangled DNA undergo phase separation into two domains: loops enriched in condensin I remain as protrusions, whereas those enriched in H1.8 are reeled into the central region.

1MSJ-7 クロマチンドメインの生物種間サイズ分布を説明する普遍的な理論
A universal theory describes chromatin domain size distributions across species**Shin Fujishiro** (*FIFC, Kyoto Univ.*)

Eukaryotic chromatin forms domains. In vitro, nucleosome arrays form condensates, suggesting this drives domain formation in cells. A crucial question is why domains do not merge and exhibit species-dependent size distributions. We propose that active, acetylated chromatin regions act as surfactants and limit domain growth. Our simple free energy model, parameterized by acetylated nucleosome fraction, predicts a critical domain size where active chromatin covers the surface. This theoretical size describes the distributions of domain sizes in yeast, arabidopsis, fruit fly, mouse, and human, all with a single common parameter. Our result reinforces the notion that chromatin domains are nucleosomal condensates stabilized by architectural proteins such as cohesin.

1GA001 赤痢アメーバ由来 adenosine 5'-phosphosulfate kinase の構造解析
Structural analysis of adenosine 5'-phosphosulfate kinase from *Entamoeba histolytica*

Ryo Hatanaka¹, Hina Yuasa¹, Fumika Mi-ichi², Jyun-ichi Kishikawa¹, Tomoo Shiba¹ (¹*Fac. Applied Biol., Kyoto Inst. Tech.*, ²*Inst. Tropical Medicine, Nagasaki University*.)

Entamoeba histolytica is a globally endemic parasite, particularly prevalent in developing countries. However, there are only a limited number of clinical treatments. Therefore, the development of new medicines is an urgent issue. Adenosine 5'-phosphosulfate kinase from *E. histolytica* (EhAPSK) is essential for maintaining its life cycle within the host. Hence, APSK is an effective drug target for this disease. In this study, we determined the substrate-free structure of EhAPSK at 2.6 Å by X-ray crystallography. Furthermore, cryo-EM analysis captured several distinct structures of EhAPSK. These structures indicate the dynamic conformational change between catalytic domain and another domain of EhAPSK, suggesting the insight into the reaction mechanism of the enzyme.

1GA002 ペプチド結合の平面性の歪みを用いたタンパク質の原子座標データの一次スクリーニング
Primary screening of structural data obtained by electron microscopy using planar distortion of peptide bonds

Mahan Kunii¹, Toshiyuki Chatake², Takashi Ohhara³, Kaori Chiba¹ (¹*National Institute of Technology, Ibaraki College*, ²*KURNS, Kyoto Univ.*, ³*J-PARC, JAEA*)

Although the planarity of the main-chain peptide bond is one of the most fundamental restraint in protein structure analysis, it has been found that protein models in the Protein Data Bank (PDB) contain many distorted peptide bonds. Recently, we have proposed a model for site-specific relaxation of peptide bonds caused by intramolecular electrostatic potential (Chiba et al., *Protein Science*, 2023). To investigate the versatility of this model, the proportion of distorted peptide bonds was examined using all protein data registered in the PDB. The results showed that the structural models obtained by crystallography and electron microscopy contained significantly different proportions of distorted peptide bonds, even though they were treated equally as structural data.

1GA003 PRMT1 と基質 EWS の複合体構造から考察する基質認識機構
Substrate recognition mechanism considered from the complex structure of PRMT1 with substrate EWS

Nobuyuki Endo¹, Sachiko Toma-Fukai^{2,3}, Hinako Koshimura², Akihiro Kawamoto¹, Mika Hirose¹, Akiko Ikegami², Miwa Kuzuhara², Hiroaki Daitoku^{3,4}, Koichiro Kako⁵, Takayuki Kato¹, Akiyoshi Fukamizu^{3,4}, Hironari Kamikubo², Genji Kurisu¹ (¹*IPR, Univ. Osaka*, ²*NAIST*, ³*AMED-CREST*, ⁴*TARA*, ⁵*LES. Univ. Tsukuba*)

Protein arginine methyltransferase 1 (PRMT1) is the predominant enzyme responsible for catalyzing protein arginine methylation. To elucidate its catalytic mechanism, a few structures of PRMT1 in complex with substrate peptides, cofactors, or inhibitors have been reported. In addition, no structure of PRMT1 bound to a full-length substrate protein has been determined to date. To investigate the substrate recognition mechanism, we determined the cryo-EM structure of PRMT1 in complex with its substrate protein, Ewing sarcoma (EWS). The structure revealed the interaction sites of PRMT1 when forming a complex with EWS. In this presentation, we will discuss the substrate recognition mechanism of PRMT1 based on the structural analysis of this complex.

1GA004 ダイズ由来メチオニン γ-リアーゼの基質侵入ループ構造による酵素活性への影響
Effects on the enzymatic activity of the loop structures in methionine γ-lyase from *Glycine max*

Shu Morita¹, Haruna Makino¹, Kanta Inoue¹, Daiki Yokoyama², Atsushi Okawa², Taku Teshima³, Jun-ichi Kishikawa¹, Kenji Matsui³, Kenji Inagaki², Tomoo Shiba¹ (¹*Fac. Appl. Biol., Grad. Sch. Sci. and Tech., Kyoto Inst. Tech.*, ²*Grad. Sch. Env. & Life Sci., Okayama Univ.*, ³*Grad. Sch. Sci. & Tech., Yamaguchi Univ.*)

Methionine γ-lyase from soybean, *Glycine Max* (GmMGL) 1 and 2 function as methionine degrading enzymes. The K_m values of GmMGL1 and 2 for methionine are 24.1 and 55.4 mM, which are much higher than that of MGL (~0.5 mM) from *Pseudomonas putida* (PpMGL), indicating that GmMGL1/2 have lower affinity for methionine than PpMGL. From comparing the structures of GmMGL1/2 and PpMGL, we found GmMGL1/2 had the loops that didn't exist in PpMGL near the entrance of substrate pocket. To investigate the roles of the loops in the enzymatic activity of GmMGL1/2, we mutated the loop structures and confirmed the enzymatic parameters of the mutated GmMGL1/2. The results suggest the loops are related to regulating the affinity for its substrate through gating the substrate entrance.

1GA005 天然変性タンパク質 FUS の分子動力学シミュレーションによる構造領域と天然変性領域の協調的な核酸結合機構の普遍性の解明
A Universal Mechanism of Nucleic Acid Binding by Protein Structured and Intrinsically Disordered Regions Revealed by Molecular Simulations

Soichiro Kijima, Akio Kitao (*Inst. Sci. Tokyo, Sch. Life Sci. Tech.*)

Many proteins comprise both structured regions and intrinsically disordered regions (IDRs), and these regions often function cooperatively. However, the molecular mechanisms of substrate binding in concert with structured regions and IDRs remain largely unexplored.

In this study, we performed molecular dynamics simulations of the model protein FUS, which contains both structured regions and IDRs, in complex with RNA. Our simulations revealed that the structured regions of FUS determine the RNA sequence specificity, while the IDR enhances the binding affinity between FUS and RNA.

Furthermore, by analyzing IDRs sequence database, we demonstrated that cooperative nucleic acid binding by structured regions and IDRs is a widespread feature among many proteins.

1GA006 放線菌由来 L-メチオニン脱炭酸酵素 MetDC における Tyr421 の役割
Role of Tyr421 in L-Methionine Decarboxylase, MetDC, from *Kitasatospora aureofaciens*

Kanta Inoue¹, Haruna Makino¹, Shu Morita¹, Kaito Chadou¹, Atsushi Okawa², Kenji Inagaki², Jun-ichi Kishikawa¹, Tomoko Shiba¹ (¹*Dept. Appl. Biol., Grad. Sch. Sci. and Tech., Kyoto Inst. of Tech.*, ²*Grad. Sch. Env. & Life Sci., Okayama Univ.*)

L-methionine decarboxylase, MetDC, is a pyridoxal 5'-phosphate (PLP)-dependent enzyme and catalyzes the decarboxylation of L-methionine (L-Met). The crystal structure of MetDC from *Kitasatospora aureofaciens*, previously we determined, indicated Y421 residue at active site plays an important role for its catalysis. In this study, we performed structural and functional analysis of the mutant Y421F to evaluate its role.

The crystal structure of MetDC_Y421F with substrates, L-Met or L-Methionine methyl ester, were determined at 1.79-1.94 Å. These intermediate structures revealed conformational changes around the active site associated with substrate binding. These structural features suggest the mutant reacts through the uncommon pathway among PLP-dependent enzymes.

1GA007 *E. coli*-expressed Influenza H1N1 Receptor Binding Domain is immunogenic in mice and produces neutralizing antibodies against live virus

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Recombinant proteins produced in *E. coli* are not the first vaccine choice due to their low immunogenicity and questionable ability to generate neutralizing antibodies. Here, we describe the *E. coli* expression of the Influenza H1N1 receptor-binding domain (RBD), and experiments to confirm the immunogenicity of this protein. The H1N1-RBD was purified using RP-HPLC, yielding 40 mg/L of pure protein, which was later confirmed to be natively folded using various techniques. However, this protein is poorly immunogenic, so we studied its soluble aggregates to alter its immunogenicity. Results showed that the soluble aggregates of H1N1-RBD protein are strongly immunogenic in mice and induced antisera with vigorous neutralizing activity against the live H1N1 virus.

1GA008 ペプチド結合型 GPCR に対する小分子化合物の異なる作用機構
Small chemical molecules exhibit distinct mechanisms of action towards a peptide-binding GPCR

Yuzhong Gu¹, Arisa Shinkai^{3,4}, Kazuhiro Kobayashi^{1,2}, Kouki Kawakami^{1,2}, Asato Kojima⁶, Tsuyoshi Saitoh^{4,5}, Hideaki Kato^{1,2} (¹*Graduate School of Science, The University of Tokyo.*, ²*Research Center for Advanced Science and Technology, The University of Tokyo*, ³*Graduate School of Pure and Applied Sciences, University of Tsukuba*, ⁴*International Institute for Integrative Sleep Medicine (WPI-IIIS), University of Tsukuba*, ⁵*Institute of Medicine, University of Tsukuba*, ⁶*Graduate School of Arts and Sciences, The University of Tokyo*)

GPCRs are membrane proteins that sense various signals. Their intracellular parts are highly conserved, while their extracellular ligand-binding sites vary to recognize diverse molecules. For flexible peptides, they activate peptide-binding GPCRs through broad contacts. On the other hand, small chemical ligands are rigid and bind in limited but specific ways. In this research, we determined cryo-EM structures of Bradykinin Type 2 receptor (B2R) in apo, inverse agonist-bound and partial agonist-bound states. The partial agonist was derived from the inverse agonist scaffold. It activates B2R by clashing with a key tryptophan, unlike bradykinin's indirect activation, revealing distinct mechanisms of action.

1GA009 **M₂ および M₄ ムスカリン受容体のサブタイプ選択的活性化に関する赤外分光解析**
Infrared Spectroscopic Insights into Subtype-Selective Activation of M₂ and M₄ Muscarinic Receptors

Moeka Mizuno¹, Yuya Sugiura¹, Akitoshi Inoue², Chiyo Suno², Ryoji Suno², Hideki Kandori^{1,3}, Kota Katayama^{1,3} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Kansai Medical University. Medical.*, ³*OptoBioTechnology Research Center., Nagoya Inst. Tech.*)

Muscarinic acetylcholine receptors (M₁R–M₅R) are class A GPCRs that bind the neurotransmitter acetylcholine (ACh). Among them, M₄R is involved in learning, memory, and cognition, and is a potential target for neuropsychiatric drug development. Although static ligand-bound structures have been solved, activation-related dynamics remain unclear. Here, we used ATR-FTIR spectroscopy to monitor conformational changes in M₄R upon ligand binding. ACh-bound M₄R showed unique signals at 1641 and 1546 cm⁻¹, differing from M₂R despite conserved binding residues. We analyzed side-chain orientations of key residues, constructed mutants, and compared their spectra with wild-types. Based on these results, we discuss the differences in ligand-binding mechanisms between M₂R and M₄R.

1GA010 **オスモライト添加による水のダイナミクス変化が α-アミラーゼ活性に及ぼす影響**
Change in water dynamics by osmolytes affect the activity of α-amylase

Sachika Furukawa¹, Hideaki Shirota², Mafumi Hishida¹ (¹*Grad. Sch. Sci., Univ. TUS*, ²*Grad. Sch. Sci., Univ. Chiba*)

The effect of added osmolyte molecules on α-amylase reaction rate was investigated. The results of UV-visible and terahertz time-domain spectroscopy showed a good correlation between the enzyme activity in each osmolyte solution and the number of water molecules whose dynamics was changed by the osmolyte molecules. α-Amylase dynamics in the osmolyte solutions were also measured by Raman-Induced Kerr Effect Spectroscopy.

1GA011 **ラクダムシ由来甲虫型不凍タンパク質の発見と機能解析**
Discovery and Functional Characterization of Beetle-type Antifreeze Proteins in Snakeflies

Kaho Uchizawa¹, Kosuke Maeda¹, Sakae Tsuda², Tomoyasu Aizawa^{1,2}, Tatsuya Arai^{1,2} (¹*Sch. Sci., Hokkaido Univ.*, ²*Fac. Adv. Life Sci., Hokkaido Univ.*)

Antifreeze proteins (AFPs) help organisms survive freezing temperatures by binding to ice crystals and inhibiting their growth. While AFPs are well characterized in beetles (Coleoptera), their presence in other insect groups remains unclear. Here, we identified 19 beetle-type AFP-like sequences in the genome of the snakefly (Raphidioptera), a lineage that diverged from beetles over 300 million years ago. One isoform expressed in *E. coli* exhibited strong antifreeze activity, whereas another with multiple mutations exclusively at the ice-binding site showed no detectable activity. The coexistence of active and inactive AFP-like sequences in the snakefly suggests the occurrence of functional divergence and offers new insight into AFP evolution in insects.

1GA012 **複数のプロトン輸送ユニットを持った天然 F₀F₁-ATP 合成酵素の探索**
Exploring natural F₀F₁-ATP synthase with multiple proton transport units

Mahiro Katano¹, Riku Marui², Hiroshi Ueno¹, Hiroyuki Noji^{1,3} (¹*Department of Applied Chemistry, School of Engineering, University of Tokyo.*, ²*Department of Bioengineering School of Engineering, University of Tokyo.*, ³*Research Institute of Planetary Health (RIPH), The University of Tokyo*)

F₀F₁-ATP synthase catalyzes ATP synthesis coupled with proton translocation across a membrane, and interconverts the free energy of ATP and proton-motive force (*pmf*). The H⁺/ATP ratio is a key parameter in ATP synthesis, and a higher ratio allows ATP synthesis even under low *pmf* conditions. Recently, we engineered F₀F₁ with the highest H⁺/ATP ratio by increasing *a*-subunits. Based on that new strategy, we searched gene databases and identified several ATP synthase operons with similar features, suggesting that natural F₀F₁ variants may also possess three *a*-subunits. Here, we present functional and structural analyses of these natural F₀F₁ complexes to determine whether F₀F₁ with three proton transport units indeed exists in nature.

1GA013 脂質二重膜中でチャネル活性を有する両親媒性βヘリックスペプチドの会合状態の解析
Analysis of the association state of amphiphilic β-helix peptides with channel activity in lipid bilayers

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Nanopore measurement is a rapid, label-free technique for detecting electrical changes as molecules pass through nanoscale pores in biological membranes at the single-molecule level and in real time. De novo design of peptides that incorporate unnatural amino acids (UAAs), including D-amino acids, into their sequences and self-assemble to form nanopores in lipid bilayers provides structural and functional diversity, but is limited by current computer structure prediction.

We designed several amphiphilic β-helical peptides formed by alternating L- D-amino acids, including uuaa, and analyzed its structure and function by channel current measurements, solid-state NMR, and molecular dynamics simulations.

1GB001 モルテングロブール状態を介した同時翻訳的フォールディング経路の可視化
Visualizing co-translational folding pathway mediated by Molten-Globule (MG) state

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Many proteins in the cell can begin folding as they are being synthesized by the ribosome. However, **how nascent chains fold on the ribosome** and **when folding intermediates form remain largely unknown**. In particularly, knotted proteins, whose backbones form topological knots in three-dimensional space, follow exceptionally complex folding pathways, and the principles by which they acquire their native conformations are still poorly understood. In this study, we aim to visualize the intermediate states of knotted proteins during translation to uncover how they fold into their knotted structures on the ribosome.

1GB002 FUS-ALS 疾患型変異体の相分離や不可逆的凝集に対する ATP の抑制メカニズム
Mechanistic insights into ATP's inhibition of phase separation and aggregation of ALS-linked FUS variants, R495X and P525L

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Fused in sarcoma (FUS) is one of the causative proteins of amyotrophic lateral sclerosis (ALS). Both wild-type (WT) FUS and its pathological variants, R495X and P525L, undergo cytotoxic aggregation in motor neurons through liquid-liquid phase separation (LLPS). ATP is an intriguing biomolecule that acts as a solubility modulator due to its hydrotrope-like properties. However, how cytoplasmic concentrations of ATP inhibit LLPS and aggregation remains unclear. We conducted ultraviolet-visible (UV-Vis) spectroscopy and molecular dynamics simulation for WT and the pathogenic variants under multiple temperature and pressure conditions. We demonstrated that ATP, at physiologically relevant concentrations, suppresses both LLPS and aggregation of the proteins.

1GB003 *Corynebacterium glutamicum* における反応サイクルと関連したクエン酸合成酵素の集合体形成メカニズム
Catalysis-dependent mechanism of citrate synthase condensation in *Corynebacterium glutamicum*

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We found that citrate synthase (CS) formed droplet-like condensates in *Corynebacterium glutamicum*, which is a bacterium known as L-glutamate producer. Inactive CS variants with a substitution of catalytic residues lost the ability to form condensates. In vivo and in vitro studies indicated that oxaloacetate (OAA, a substrate of CS) was a factor affecting CS condensation. Turbidity assay and intrinsic fluorescence measurement using recombinant CS indicated that OAA had an effect to reduce CS aggregation through binding to catalytic residues, and OAA-dependent conformational changes occurred less in the inactive CS than in CS^{WT}. We consider that catalysis-dependent conformational changes contribute to multivalent interactions necessary for CS condensation.

1GB004 圧カジャンプ分光法によるタンパク質液液相分離に関する速度論的解析
Kinetic analysis for Protein liquid-liquid phase separation by pressure-jump spectroscopy

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The RNA-binding protein fused in sarcoma (FUS) is localized in the nucleus and plays a key role in RNA processing. FUS has been shown to undergo liquid-liquid phase separation (LLPS), leading to the formation of irreversible aggregates. Two types of LLPS are observed for FUS: low-pressure LLPS (LP-LLPS), which is stable below 2 kbar, and high-pressure LLPS (HP-LLPS), which is stable above 2 kbar. The latter is closely associated with the formation of irreversible aggregates. In this study, we conducted pressure-jump ultraviolet-visible spectroscopy experiments on both LLPS states of wild-type FUS and two pathological FUS variants, R495X and P525L. We also report the inhibitory effects of small molecules on irreversible aggregation.

1GB005 sm-FRET および蛍光相関分光法による SARS-CoV-2 の N タンパク質リンカー領域の RNA への結合における役割の解明
Roles of the linker region of the N protein of SARS-CoV-2 in the association to RNA by sm-FRET and fluorescence correlation spectroscopies

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³*Department of Chemistry, Graduate School of Science, Tohoku University*)

The N protein of SARS-CoV-2 is a dimeric protein and has two different functions. 1) In the early stage of infection, the intrinsically disordered region (LKR) is phosphorylated to form droplets and to promote transcription and translation of genome RNA (gRNA). 2) In the later stage of infection, the intact N protein binds to gRNA, forming ribonucleoprotein complex that promotes the viral assembly. In this study, I prepared several mutants of the N protein in LKR and performed single-molecule FRET spectroscopy and fluorescence correlation spectroscopy measurements with the labeled RNAs complexed with the mutants. It was suggested that the N protein regulates its functions by altering the self-association properties of the LKR region and the its RNA-binding properties.

1GB006 αB-クリスタリン及びその断片による α シヌクレイン液滴の老化の阻害
αB-Crystallin and its fragment prevent aging of α-Synuclein droplets

Kenji Fujitsuka¹, Keisuke Yuzu¹, Yuki Michiue¹, John A. Carver², Eri Chatani¹ (¹*Grad. Sch. Sci., Kobe Univ.*, ²*Res. Sch. Chem., ANU*)

Liquid-liquid phase separation forms droplets of high protein concentration. While droplets are involved in cellular functions, they sometimes undergo “aging”: liquid to solid transition and form amyloid fibrils. In this study, we examined the inhibitory effect of αB-crystallin (αB-C), a small heat shock protein, and its middle domain (ACD) on the aging of α-synuclein (α-Syn) droplets. When α-Syn droplets were formed in the presence of αB-C, αB-C colocalized with α-Syn in the droplets. Moreover, FRAP and ThT fluorescence monitoring showed that αB-C maintained droplet fluidity and inhibited internal aggregation. The inhibitory effect was exhibited even in ACD, suggesting ACD is a key domain to prevent the aging of the α-Syn droplets.

1GB007 トランスサイレチン 49-127 断片が形成するプロトフィブリルの解析
Characterization of Protofibril Formed by Transthyretin 49-127 Fragment

Yuzuki Masuda¹, Seiya Nakao¹, Keisuke Yuzu¹, Naoki Yamamoto², Ken Morishima³, Rintaro Inoue³,
Masaaki Sugiyama³, Eri Chatani¹ (¹*Grad. Sch. Sci. Kobe Univ.*, ²*Sch. Med., Jichi Med. Univ.*, ³*KURNS, Kyoto Univ.*)

Transthyretin (TTR) is a 127-residue plasma protein that forms amyloid fibrils in vivo, leading to ATTR. TTR49-127 fragment is known as one of important components of ATTR amyloid fibrils and we recently identified that it forms protofibrils in vitro. In this study, we aimed to elucidate the structural characteristics of these protofibrils and their role in fibril formation. CD spectroscopy and TEM revealed distinct structural differences between protofibrils and fibrils. Thioflavin T assays indicated that protofibrils formed under quiescent conditions can convert into fibrils upon agitation. These findings suggest that TTR49-127 protofibrils are metastable aggregates that may act as precursors of TTR amyloid fibrils.

- 1GB008** アルキル化ペプチドによる液-液相分離液滴の分子取り込みの制御
Controlling the molecular uptake of liquid-liquid phase separated droplets using Alkylated peptides

Ibuki Yamashita (*Fac. Pharm. Sci., Univ. Toyama*)

We have developed a model peptide RD9 for liquid-liquid phase separation in water and controlled the molecular uptake into the droplets. To increase the retention of hydrophobic molecules in the droplets, stearyl-RD9 (stearyl-CONH-WR₉G₄D₉-COOH) was synthesized. Observation using Confocal laser scan microscopy showed that the incorporation of hydrophobic molecules into the droplets were increased depending on the concentration of stearyl-RD9. Diffusion rates of molecules in the droplets were evaluated using FRAP measurements. The diffusion rates of stearyl-RD9 and hydrophobic molecules were almost identical and slower than that of RD9. This result suggests that hydrophobic molecules form a complex with stearyl-RD9 in the droplets.

- 1GB009** アコヤガイの貝殻に含まれる天然変性タンパク質 nacrein の構造ダイナミクス解析
Structural dynamics of nacrein, an intrinsically disordered protein in a shell of *Pinctada fucata*

Yuto Namikawa¹, Ken Morishima², Rintaro Inoue², Masaaki Sugiyama², Michio Suzuki¹ (¹GSALS, ²KURNS)

Pinctada fucata, a marine invertebrate used in pearl aquaculture, has a shell comprising 95% CaCO₃ and 5% organic matrices regulating shell growth. Nacrein has a carbonic anhydrase domain and an intrinsically disordered GXN (poly Gly-Xaa-Asn) domain that inhibits CaCO₃ precipitation. However, whole structure of nacrein is still unclear due to the highly repeated GXN domain. Small-angle neutron scattering (SANS) revealed distinct scattering profiles in 100% D₂O and H₂O, with large differences in radius of gyration, which was a novel phenomenon. The theoretical scattering profile from AlphaFold-predicted structure reproduced the experimental data, showing the combination of SANS and structural modeling refines possible conformations of intrinsically disordered region.

- 1GB010** IDP 相分離液滴を用いたオリゴ DNA からの効率的なタンパク質発現系
Oligo assembly enhanced by IDP droplet for efficient cell-free expression

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Recent advances in deep learning have enabled rapid design of hundreds of candidate protein sequences with desired functions. However, the experimental validation remains a bottleneck due to the cost and time required for DNA synthesis, assembly, and protein expression. In this study, we developed a novel approach that enhances oligo assembly by using phase-separated droplets formed by intrinsically disordered proteins (IDPs), specifically Ddx4N1. These droplets concentrate oligos, eliminating the need for prior amplification and improving parallel assembly efficiency. Furthermore, we combined this method with microreactor-based cell-free protein expression, allowing direct protein synthesis from assembled DNA within hours.

- 1GB011** TIA-1 における RRM 間および RRM-LCD 相互作用による相分離制御機構の解明
Mechanistic analysis of TIA-1 phase separation driven by intramolecular RRM-RRM and RRM-LCD interactions

Kazuki Kondo¹, Shinichi Tate^{1,2,3,4}, Kyota Yasuda^{1,2,3}, Natsumi Tane¹, Tomomi Iso¹, Yuka Araki¹ (¹Grad. Sch. Sci., Univ. Hiroshima, ²RcMcD, Univ. Hiroshima, ³WIP-SKCM2, Univ. Hiroshima, ⁴MIMS, Univ. Meiji)

T-cell intracellular antigen-1 (TIA-1) is a component of biomolecular condensates such as stress granules. TIA-1 contains three RNA recognition motifs (RRMs) and a low-complexity domain (LCD), and drives liquid-liquid phase separation (LLPS). Although RRM-LCD interactions have been implicated in LLPS, the full range of intramolecular interactions involved remains unclear.

In this study, we investigated the molecular basis of TIA-1-mediated LLPS by analyzing both RRM-LCD and RRM-RRM interactions. Spectroscopic analysis revealed not only transient RRM-LCD interactions, but also contacts between RRM's themselves, suggesting a cooperative network that enhances LLPS. These findings provide novel insights into the regulation of phase separation.

1GB012 核小体タンパク質 Nopp140 のハイパーリン酸化は有糸分裂期脱凝集を加速させる
Hyperphosphorylation of nucleolar protein Nopp140 accelerates mitotic nucleolar disassembly

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Mitotic disassembly of nucleolus, a multi-layered membrane-less organelle for ribosome biogenesis in nucleus, begins at an early prophase even before nuclear envelope breakdown. Here, we explored how protein hyperphosphorylation and inhibition of ribosomal RNA (rRNA) transcription affect this process. Nopp140, a nucleolar protein with 17 mitotic phosphosites, disassembles earlier than both its alanine-substituted mutant and fibrillarin, which colocalizes with Nopp140 and has one mitotic phosphosite. Additionally, the delayed disassembly of the alanine mutant was independent of rRNA transcription. These results indicate that hyperphosphorylation accelerates nucleolar disassembly.

1GC001 高速 AFM 観察による真菌機能性アミロイドの線維表面触媒による線維伸長機構の解明
High-speed atomic force microscopy reveals surface-catalyzed elongation mechanism of fungal functional amyloid

Nao Takahashi¹, Tatsuya Kimura², Yuki Terauchi³, Akira Yoshimi^{4,5}, Takahiro Watanabe-Nakayama², Keietsu Abe¹ (¹*Grad. Sch. Agri., Tohoku Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*RCTMR, Yamaguchi Univ.*, ⁴*Grad. Sch. Agri., Kyoto Univ.*, ⁵*Grad. Sch. Glob. Env. Stud., Kyoto Univ.*)

Amphipathic protein hydrophobin RoIA self-assembles into an amyloid-like fibrous form called rodlet. Rodlets are densely aligned and cover the cell wall surface of mycelia, however, their formation mechanisms remain unclear. Here, we used high-speed AFM to observe rodlet formation and elucidate its mechanism. Interestingly, we found that when one rodlet elongates along with the other rodlet, the energy barrier of the elongation was decreased and the elongation was promoted: we call this reaction surface-catalyzed elongation. In addition, Monte Carlo simulations showed that surface-catalyzed elongation facilitates the alignment of rodlets. Surface-catalyzed elongation may be a universal mechanism that contributes to amyloid aggregation in general.

1GC002 一分子蛍光顕微鏡と近接依存性標識による一細胞ミトコンドリアプロテオームの網羅的解析
Single-cell mitochondrial proteome profiling via combining single-molecule fluorescence microscopy and proximity labeling

Misaki Tsuchida^{1,2}, Latiefia Kamarulzaman^{1,3}, Sooyeon Kim¹, Yuichi Taniguchi^{1,3,4} (¹*Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University*, ²*Faculty of Agriculture, Kyoto University*, ³*Graduate School of Frontier Biosciences, Osaka University*, ⁴*Graduate School of Biostudies, Kyoto University*)

Mitochondrial proteins are essential for energy production, metabolism, and apoptosis, but their expression varies across cells. While understanding cell-to-cell heterogeneity and its dynamics is crucial, their low abundance hampers analysis at the single-cell level by conventional proteomics methods. Here, we developed a molecularly sensitive single-cell proteome profiling platform, composed of gel electrophoresis, single-molecule fluorescence imaging, and innovative proximity labeling method. This approach enables mitochondria-specific proteome analysis at the single-cell level, allowing us to investigate the diverse dynamics of the mitochondrial proteome and thereby gain critical insights into disease mechanisms.

1GC003 構造的制約をタンパク質デザインで取り入れた進化モデルによる祖先ヌクレオソームの再構築
Reconstruction of ancestral nucleosomes using an evolutionary model that incorporates structural constraints through protein design

Taiyo Hayashi¹, Koya Sakuma², Tsuyoshi Terakawa¹, Shoji Takada¹ (¹*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*,
²*CeSPI, Nagoya Univ.*)

Despite high conservation of histone proteins, their origins and early roles of primitive eukaryotes remain unclear. Here we developed a pipeline that jointly infers ancestral sequences of all four histones by integrating evolutionary probability profiles with LigandMPNN-based side-chain design algorithm. **Structurally and evolutionarily consistent histone reconstruction at LECA and a virus-eukaryote ancestor** were achieved, overcoming limitation of conventional methods. Recombinant ancient nucleosomes were assembled and tested for oligomerization in vitro, **revealing primitive nucleosome stacking property and key residues. This study is the first to resurrect a complete ancestral nucleosome** and provides a **novel framework for reconstructing multi-subunit protein complexes.**

[1GC004](#)

複数狭窄部をもつ Epx4 ナノポアのパепチド識別能力の探索

Exploring the peptide discrimination capabilities of multiple constriction Epx4 nanopores

Ayako Ijuin¹, Kota Naito², Yoshikazu Tanaka², Ryuji Kawano¹ (¹*Grad. Sch. Biotech and Life Sci., TUAT*, ²*Grad. Sch. Life Sci., Tohoku Univ*)

DNA nanopore sequencer has inspired the application of nanopore technology to peptide sequencing. Distinguishing 20 amino acids requires high sensing resolution. Complexes with multiple constrictions have been reported to improve resolution. We focused on Epx4, which has multiple constrictions without complex formation. Electrophysiological measurements and molecular dynamics simulations revealed that Epx4 could distinguish between two polypeptides. Our findings indicate that Epx4 is suitable for peptide detection due to its high event frequency and interaction with peptides. To obtain higher resolution, our design of a constriction to enhance peptide interactions represents a key step toward this goal.

[1GC005](#)

演題取り下げ Withdrawn

[1GC006](#)

Minimal RNA polymerase reconstruction

Riddhi Prashant Gondhalekar^{1,2}, Shunsuke Tagami³, Sota Yagi⁴, Kosuke Fujishima^{1,2,5} (¹*School of Life Science and Technology, Institute of Science Tokyo*, ²*Earth-Life Science Institute, Institute of Science Tokyo*, ³*RIKEN IMS*, ⁴*Faculty of Human Sciences, Waseda University*, ⁵*Graduate School of Media and Governance, Keio University*)

Today's cellular RNA polymerases are huge (~4,000 aa), and no evolutionary intermediates exist to trace their origin. It is recaptured that the core domains of the present-day polymerases may have once acted as cofactors for ancient ribozymes, and through evolution, proteins took over the functions of ribozymes. However, the details of this takeover and the following evolution of proteinaceous RNA polymerase are largely unknown. We use structure-based engineering and mRNA display to intermediate identify RNA-protein complexes that reveal coevolutionary stages in the early evolution of proteinaceous RNA polymerases.

[1GC007](#)

De novo ペプチドナノポアのキメラ化とセンシング精度向上に向けた改変

Chimeric integration of a *de novo* peptide nanopore and its sequence optimization for improving sensing resolution

Ayaka Nakada¹, Kota Naito², Yoshikazu Tanaka², Ryuji Kawano¹ (¹*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, ²*Graduate School of Life Sciences, Tohoku University*.)

Nanopore technology, which uses nanometer-sized pores, enables rapid, simple, and label-free detection of single molecules by electrically monitoring their translocation. We previously reported a *de novo* designed peptide nanopore, SVG28, capable of detecting polypeptides. However, SVG28 mainly assembles into three different oligomeric states, resulting in nanopores of varying sizes. To address this issue, we designed a chimeric nanopore by integrating SVG28 with α -hemolysin. This approach improved the pore's stability and uniformity, providing a more stable platform for further functionalization. To progress this technology toward peptide sequencing, we designed sensing regions within the pore lumen and are evaluating their specific interactions with target peptides.

1GC008 膜透過性ペプチドを介した汎用的なタンパク質輸送システムの開発
Development of a wide range of protein delivery systems mediated by cell-penetrating peptides

Akari Miwa, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

The regulation of biomolecular transportations plays an important role in the biochemical and biomedical fields. However, the biomolecular transportation across the cell membrane is not easy. Cell-penetrating peptides (CPPs) have attracted attention for their ability to transport biomolecules into living cells. In this study, we discovered that both the combination of CPPs and the conformation of fused proteins affect the efficiency of protein transport into living cells. Furthermore, we established a strategy for transporting a wide range of proteins using DogTag/DogCatcher system that spontaneously ligates two different proteins. This protein transport system enables the flexible and trackable delivery of water-soluble proteins for modulations of cell functions.

1GC009 酵素間相互作用の強化による二段階アルカン合成反応の効率化
Improving efficiency of two-step alkane synthesis reactions by enhancing enzyme interactions

Shunya Okada¹, Shunji Suetaka¹, Munchito Arai^{1,2} (¹*Department of Life Sciences, The University of Tokyo*,
²*Department of Physics, The University of Tokyo*)

Biofuels produced by cyanobacteria using acyl-ACP reductase (AAR) and aldehyde deformylating oxygenase (ADO) are attracting attention as a new sustainable energy source. AAR converts acyl-ACP, an intermediate in fatty acid synthesis, into aldehydes. Then, ADO converts the aldehydes into alkanes that are equivalent to diesel oil. Our recent simulation studies suggest that AAR and ADO can function as a dimer without dissociation and can efficiently transfer aldehydes from AAR to ADO. However, their affinity is low. To improve the efficiency of alkane production by AAR/ADO, here we have rationally designed AAR/ADO mutants with enhanced mutual affinity using ProteinMPNN, Rosetta, and AlphaFold 2. We will present our experimental results at the meeting.

1GC010 酵素を合理的に活性化する普遍的手法の開発
Development of a universal method to rationally activate enzymes

Atsuya Watanabe¹, Shunji Suetaka¹, Munchito Arai^{1,2} (¹*Department of Life Sciences, The University of Tokyo*,
²*Department of Physics, The University of Tokyo*)

Advancing industrial biotechnology requires a rational method of enhancing enzymatic activity. We previously proposed a universal strategy for achieving this: stabilizing the substrate-bound form while destabilizing the product-bound form. However, this strategy has only been successfully applied to the model enzyme dihydrofolate reductase. To establish a universal method to rationally activate enzymes, we applied this strategy to catechol 1,2-dioxygenase, which converts catechol to *cis,cis*-muconic acid, a compound used in plastics production. Using combination of structure modeling and machine learning, we predicted six amino acid substitutions that align with our strategy. We are currently characterizing the activity of the mutants experimentally.

1GC011 アゴニスト誘導コンフォメーションを捉えた TRPM8 の X 線 1 分子動態計測
Single-molecule X-ray analysis capturing the agonist-induced conformation of TRPM8

Haruto Machida^{1,2}, Tatsunari Ohkubo^{2,3}, Daisuke Sasaki^{1,2}, Kazuhiro Mio^{2,3}, Yuji. C Sasaki^{1,2,4} (¹*Grad. Sch. Frontier Sci., Univ. Tokyo*, ²*Natl. Inst. Adv. Ind. Sci. & Technol.*, ³*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, ⁴*JASRI*)

TRPM8 is a cation channel activated by icilin and menthol and implicated in diseases such as neuralgia and cancer. While cryo-EM has revealed static structures, ligand-induced intramolecular dynamics remain unclear.

Using single-molecule X-ray techniques, we combined DXT and DXB to visualize TRPM8 dynamics from micro- to millisecond timescales. DXT showed increased angular displacement upon menthol or icilin addition, indicating enhanced sub-millisecond C-terminal motion. DXB in living cells showed shortened autocorrelation decay and faster fluctuations.

These findings demonstrate chemical-induced TRPM8 dynamics in both purified protein and cells, providing insights into its molecular mechanism.

[1GC012](#)

電気エネルギー依存性細胞死の電気回路モデルによる解析

Explaining Electrical Energy Dependent Cell Death Mechanisms Through Electrical Circuit-Based Modeling

Taiki Hirohata, Sota Tanaka, Hideki Motomura, Yoshihisa Ikeda, Masafumi Jinno (*Dept. of EEE, Grad. Sch. of Sci. and Eng., Ehime Univ.*)

We studied the mechanism of cell death associated with plasma molecular/gene introduction using electrical equivalent circuit network (EECN) analysis. L-929 cells were treated with sinusoidal plasma discharge, and the relationship between treatment time and the radius of the cell death area was measured. Modeling the system with EECN and assuming two thresholds—instantaneous power (P_{th}) and electrical energy (W_{th})—explained the results. The analysis suggests cell death is not due to physical damage like Joule heating, but a biological response involving programmed cell death, such as apoptosis. EECN-based modeling helps understand the introduction mechanism. We will also discuss these findings and results using various cell death inhibitors at the conference as well.

[1GC013](#)

新規高輝度蛍光 RNA アプタマーの取得とその特性解析

Isolation and characterization of novel bright fluorogenic RNA aptamers

Tomotaka Tayama, Keisuke Ito, Sotaro Uemura, Ryo Iizuka (*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

Fluorogenic RNA aptamers enhance fluorescence upon binding to specific fluorogens and are valuable tools for live-cell RNA imaging and metabolite detection. However, conventional in vitro selection methods like SELEX focus on binding affinity and are less effective for isolating aptamers with strong fluorogenic properties. To overcome this, we developed a combined selection strategy using water-in-oil microdroplets and affinity-based screening. This method led to the discovery of novel RNA aptamers for a thiazole orange derivative, some of which showed greater fluorescence enhancement than Mango I. Conserved structural and sequence features among these aptamers provide new insights into the mechanisms of fluorescence activation.

[1GD001](#)

線維芽細胞の外環境の弾性率に対する受動的応答と心筋細胞への能動的影響

Passive responses of fibroblasts to extracellular stiffness and their active influence on cardiomyocytes

Arata Nagai^{1,2}, Hiromu Kuwabara², Yuuta Moriyama², Toshiyuki Mitsui² (¹*Grad. Sch. Bio., Kyoto Univ.*, ²*Grad. Sch. Sci. and Eng., Aoyamagakuin Univ.*)

The heart functions as a pump composed of cells, including cardiomyocytes and fibroblasts. Fibroblasts respond to mechanical stimulation by changing their shape and dynamics and are involved in cardiomyocyte remodeling. We examined both the passive responses of fibroblasts and their active influence on cardiomyocytes. On soft substrates, fibroblasts showed back-and-forth movement, delaying retraction, while stiffer ones induced high-frequency morphological changes and diffusive movement. In co-culture, the contracting directions of cardiomyocytes aligned, suggesting they followed the orientation of fibroblasts. These findings indicate that fibroblast morphological changes regulate the motility and contribute to the pattern of cardiac tissue.

[1GD002](#)

三次元位置検出顕微鏡による纖毛虫テトラヒメナの遊泳および纖毛運動解析

Three-dimensional tracking of swimming and ciliary beating in *Tetrahymena*

Hiroyo Ishii, Akisato Marumo, Shin Yamaguchi, Masahiko Yamagishi, Junichiro Yajima (*Grad. Sch. of Arts and Sci., Univ. Tokyo*)

Ciliates swim using motile cilia with a 9+2 arrangement. Because both swimming and ciliary motion are three-dimensional (3D), we used 3D tracking optical microscopy to analyze *Tetrahymena* by tracking microbeads within cells or bound to ciliary tips at millisecond resolution. The cells swam along right-handed helical paths, and ciliary tips showed counterclockwise semicircular motion within a single plane. Effective stroke was directed from right-anterior to left-posterior, consistent with the swimming pattern. Knockdown of kinesin-9A or Hydin reduced swimming speed and ciliary beat frequency, but helical swimming was maintained, suggesting that these central pair associated proteins are not essential for helical swimming but are required for efficient ciliary beating.

[1GD003](#) Modified model with myosin accumulation effect for mechanosensitive migration

Yuki Kimura¹, Chika Okimura², Yoshiaki Iwadata², Tatsunari Sakurai¹ (¹*Dept. Math. Eng., Musashino Univ.*, ²*Grad. Sch. Sci. & Tech. Innov., Yamaguchi Univ.*)

Increased attention has been focused on mechanosensitive migration such as directional cell migration by extracellular stiffness, durotaxis, and by stretching substrate, and so on. To reveal the mechanisms underlying the crossover between intracellular processes and cell-substrate adhesions, we propose a modified mathematical model integrating a reaction-diffusion system of the signaling molecules, PIP2, PIP3, and a mechanosensing via the motor clutch model. In addition, myosin II accumulation in the cell cortex is introduced to represent contraction of pseudopod. Our proposed model numerically demonstrates that the pseudopodia elongated by actin polymerization may contract via myosin II accumulation, leading to the directional cell migration in Dictyostelium.

[1GD004](#) ドリル細菌は鞭毛フックの曲げ剛性を調節する Bacteria capable of drill-like propulsion adjust bending stiffness of the flagellar hooks

Naoki Ogura¹, Aoba Yoshioka², Daisuke Nakane², Yoshihiro Murayama¹ (¹*Grad. Sch. Bio-Med. Sys. Eng., TUAT*, ²*Grad. Sch. Fund. Sci. & Eng., UEC*)

Flagellar wrapping plays an important role in the process for host-microbe interaction. However, the mechanism of this transition remains an open question. Here, we analyzed bacterial motility in motion with physical modelling and investigated changing of bending stiffness of the flagellar hook in *Caballeronia insecticola* (capable of wrapping) and *Burkholderia anthina* (incapable of wrapping). In the result, when flagella rotate CCW, bending stiffness in two species increased linearly. This stiffening allows the buckled flagella to unwind and resume the normal pushing configuration. These findings provide a valuable implication for understanding the behavior of animal symbionts and pathogens to establish successful infection inside their hosts.

[1GD005](#) 改良版 Vicsek モデルによるイエユウレイグモ初期胚の細胞集団運動のシミュレーションと解析 Simulation and Analysis of Collective Cell Migration in Early Embryos of *Pholcus phalangioides* Using a Modified Vicsek Model

Hiroto Shoji (*Faculty of Life and Medical Sciences, Doshisha University*)

To model the random collective migration of cells in early embryos of *Pholcus phalangioides*, we proposed a modified Vicsek model emphasizing biological realism. The key improvement was introducing a minimum intercellular distance to reflect finite cell size. This constraint prevented unrealistic aggregation and enabled reproduction of the observed random migration. Additional modifications included Gaussian distributions for speed and angular noise, based on analysis of actual cell tracking data. The simulations successfully reproduced the experimentally observed order parameter (~0.414) and demonstrated how effective cell size and density influence collective migration, highlighting cell size as a critical factor in embryonic cell dynamics.

[1GD006](#) ヘリコバクターの多彩な移動戦略はドリル運動によって最適化される Flagellar wrapping facilitates directional movement in *Helicobacter*

Sarara Yokohama¹, Naoki Uemura¹, Yoshiki Shimada², Tsuyoshi Kenri³, Emiko Rimbara³, Tetsuo Kan², Daisuke Nakane¹ (¹*Dep. Eng. Sci., UEC*, ²*Dep. Mech. Intell. Syst., UEC*, ³*Dep. Bact. II, NIHD*)

Bacterial motility is essential for infection, but how bacteria move at confined and viscous environments remains unclear. We visualized the motility of *Helicobacter pylori* and three non-*H. pylori* *Helicobacter* (NHPH) species using microfluidic devices mimicking host cell surface. *H. pylori* moved directionally in narrow passages with low viscosity, while NHPH exhibited better motility with higher viscosity, and the motility was fine-tuned with the width of narrow passages in each NHPH species. Direct visualization of flagellar filaments revealed that *Helicobacter* utilizes flagellar wrapping to enhance motility at optimal environments for their survivals. These findings suggest a conserved yet flexible motility strategy among *Helicobacter* species in natural habitats.

1GD007 魚類表皮ケラトサイト集団同士の高速な融合は互いのアクトミオシンケーブルを消失させ合うことで実現する
Rapid Integration of Two Keratocyte Sheets by Disassembling Each Other's Actomyosin Cables

Kazuma Shimizu, Chika Okimura, Yoshiaki Iwadate (*Grad. Sch. Sci. Tech., Univ. Yamaguchi*)

Fish keratocytes migrate collectively as sheets and repair skin wounds. The rate of re-epithelialization in fish wound repair is 50 times faster than in humans. In the keratocyte sheet, all cells at the leading edge are connected with each other via actomyosin cables and migrate as leader cells to pull the followers. We previously showed that when two keratocyte sheets collided head-on, the actomyosin cables of the sheets disassembled rapidly and the two sheets integrated. This reaction should be one of the factors contributing to the fast wound repair. Here, we show the unique mechanism for the rapid integration of two keratocyte sheets, i.e., a leader cell pushes the other leader cell on the opposite sheet, causing the actomyosin cable disassembly in the pushed cell.

1GD008 MreB が合成細菌にスピロプラズマ運動能を発生させる方法を *in vivo* で可視化する
In vivo visualization of how MreBs drive *Spiroplasma* motility in minimal synthetic bacterium

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Spiroplasma swims by switching the handedness of its helical body, driven by bacterial actins MreB4 and MreB5. To elucidate the mechanism, we analyzed their intracellular behavior. Small-sized tags allowed limited MreB4 labeling, with rare motile cells. MreB4 expression to constitutive MreB5 caused motility more efficiently than the reverse, suggesting distinct roles in initiating movement. MreB polymerization inhibitor A22 caused MreB5 dissociation, helix deformation, and motility stall. However, MreB5 diffusion did not alter after A22 treatment, suggesting that MreB5 still interacted with cellular components. Using single-molecule polarization, we are now evaluating MreB5 polymerization based on molecular orientation and anisotropy.

1GD009 脂肪酸代謝酵素 HADH の核内機能において制御される線虫 *C. elegans* の温度順化現象の分子機構解析
Molecular mechanism of temperature acclimation in *C. elegans* regulated by the nuclear function of fatty acid metabolizing enzyme HADH

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We show here that fatty acid metabolic enzyme HADH acts in "nucleus" not mitochondria to regulate temperature acclimation of *C. elegans*. HADH was expressed in neurons and intestine, and is unexpectedly localized in nucleus. Abnormal temperature acclimation was observed in *hadh* mutant, which was rescued by expressing *hadh* cDNA in 13 pairs of neurons. Also, knockdown of *hadh* in four neurons caused the similar abnormalities, suggesting that HADH acts in only four neurons. Forced nuclear export of HADH failed to rescue the *hadh* mutant abnormality. Moreover, knockdown of epigenetic factors suppressed *hadh* overexpression-induced phenotype. In summary, HADH regulates temperature acclimation in the nucleus, in which *hadh* may be involved in epigenetic modification.

1GD010 高速 AFM による分子間相互作用を介した CaMKII クラスターダイナミクスの観察
High-speed AFM revealed dynamics of CaMKII clusters through intermolecular interactions

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Ca²⁺/calmodulin-dependent protein kinase II (CaMKII) plays a pivotal role in synaptic plasticity. CaMKII is highly abundant in the post-synaptic density (PSD) and is concentrated upon synaptic stimulation. However, the shape and dynamics of high-density CaMKII assemblies remain unclear. Here, we used high-speed AFM to visualize CaMKIIα clusters in solution at its concentration in the PSD. In the basal state, CaMKIIα formed worm-like chain clusters through kinase domains, and larger clusters were formed by Ca²⁺/CaM binding. Conversely, the autism spectrum disorder-associated E183V mutant did not form the clusters, unlike the wild type. These findings provide insights into how CaMKII cluster contributes to synaptic plasticity.

1GD011 高速 AFM による CaMKII α / β ヘテロオリゴマーの構造と動態の観察
Architecture and Dynamics of CaMKII α / β heterooligomers revealed by High-Speed AFM

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Ca²⁺/calmodulin-dependent protein kinase II (CaMKII) assembles predominantly into 12-meric rings composed of the α and β variants. Their ratios were reported to differ among brain regions at the cellular level; however, direct evidence for the formation of CaMKII α / β heterooligomers at the single-molecule level has been lacking. Here, we employed high-speed atomic force microscopy [Tsuijoka, Sci. Adv. 2023] to visualize the conformational dynamics of CaMKII α / β at a 3:1 ratio, which is the ratio in the forebrain. Our findings demonstrated that the α and β subunits are intermixed within the 12-meric ring assembly, with more than 83% probability that β subunits are adjacent. We will discuss the structural role of CaMKII α / β heterooligomers in synaptic plasticity.

1GD012 プラス帯電性ナノバブルが及ぼす神経細胞への影響
Influence of positively charged nanobubbles to neurons

Yifan Liu¹, Takeshi Ohdaira², Emi Kitakata², Yoshihisa Harada², Kumiko Hayashi² (¹*Graduate School of Frontier Science, The University of Tokyo*, ²*The Institute for Solid State Physics, The University of Tokyo*)

The nucleation of micro and nanoscale liquid drops and gaseous bubbles on surfaces has drawn attention, particularly nanobubbles (NBs). NBs are gas filled spherical bubbles that 100 nm in diameter with charged interfaces and high stability. Recently, NBs have widely been applied in the biology, such as killing cancer cells. In this study, we apply NBs to neurons, essential for brain function. We prepared positively and negatively charged NBs and, for the first time, successfully incorporated positively charged NBs into neurons worldwide. As a result, we observed that neurons exposed to positively charged NBs exhibited a lower survival rate compared to those exposed to negatively charged NBs. We consider positively charged nanobubbles incorporation is more active.

1GE001 YY1 による DNA スーパークラスターの濃度依存的制御
Concentration-dependent modulation of DNA superclusters by YY1

Xi Yan, Tsuyoshi Terakawa (*Graduate School of science, Kyoto University*)

Transcriptional regulation in eukaryotes is essential for cell fate determination. It involves not only transcription factors but also the organization of chromatin. We investigated the transcription factor YY1 using single-molecule DNA curtain fluorescence imaging. YY1 induced distinct DNA structures depending on its concentration: no structural change at ~1–5 nM, dynamic superclusters at ~100 nM, and stable superclusters at ~500 nM. Mutational analysis showed that its histidine-rich and glycine/lysine-rich intrinsically disordered regions regulate weak YY1-mediated interactions essential for the formation of dynamic superclusters. These findings suggest that YY1 modulates chromatin organization, and thus gene expression, in a concentration-dependent manner.

1GE002 一分子 FRET 分光法が示す SARS-CoV-2 のゲノム RNA の構造
Single molecule FRET spectroscopy reveals the structure of genomic RNA of SARS-CoV-2 virus

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SARS-CoV-2 has ~30-kb genomic RNA (gRNA). Some studies have reported that gRNA is bound to nucleocapsid (N) proteins and forms a ribonucleoprotein (RNP) complex with compact granular structures. However, the structure of gRNA in RNP has not been resolved. Here, we established a method to label long RNAs with two fluorophores and performed single-molecule fluorescence resonance energy transfer (sm-FRET) measurements of a long fragment of gRNA, gRNA₁₂₂₃₀₋₁₂₆₈₆. We found that the sample formed a compact domain with interaction between the two termini even in the absence of N protein. Furthermore, N protein abolished the interaction, which is contrary to previous studies. These data suggest a new model of gRNA structure and viral life cycle.

1GE003 シリカナノ液滴による DNA 情報処理系の 3D-固体材料化
3D-Solid Materialization of DNA Data Processing Systems by silica nano droplets

Kengo Kurematsu, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology (TUAT)*)

DNA is expected to be used as a DNA data processing system(DDPS) due to its characteristics, such as parallel computing capacity and ease of replication. However, its liquid-phase reaction limits integration with solid substrates, restricting its application range. Here, we propose solid-phase materialization of DDPS using liquid marble surrounded by silica nanoparticles(SNPs) and UV-curable resin. Aqueous droplets with DNA were coated with SNPs, then treated with the resin and UV irradiation. We confirmed the successful coating of droplets with SNPs and the operation of a DNA amplification system inside them. Moreover, the droplet-resin mixture was successfully solidified, preserving droplet structures. The next step is 3D printing of the mixture into arbitrary shapes.

1GE004 異種ポリアミンによる協調/阻害効果：DNA 高次構造転移による遺伝子発現スイッチング制御
Cooperation/inhibition of polyamines on regulation of gene expression switching in relation to higher-order structural changes of DNA

Haruto Ogawa¹, Takashi Nishio^{1,2}, Yuko Yoshikawa¹, Takahiro Kenmotsu¹, Kenichi Yoshikawa¹ (¹*Grad. Sch. Life and Med Sci., Doshisha Univ.*, ²*MolBiS, AIST*)

Biological polyamines interacting electrostatically with DNA in cell environments are organic compounds that promote cell division and proliferation. Polyamines cause higher-order structure transition of giant DNA from coil to globule states. In this study, we investigated how the higher-order structural changes of giant DNA contribute to the gene expression activity in coexisting of bivalent putrescine(PUT) and trivalent spermidine(SPD). We revealed that PUT promotes gene expression ca. five times larger than that for SPD, by forming “Network-like” structure on giant DNA. The parallel ordering known to “Flower-like” structure formed by SPD were disrupted by the addition of PUT, suggesting the mechanism of competitive effect between SPD and PUT on gene expression.

1GE005 *In silico* 解析による GTP 駆動型 F₁-ATPase の設計
Design of GTP-driven F₁-ATPase by *in silico* analysis

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F₁-ATPase (F₁), a rotary enzyme driven by ATP hydrolysis, can also hydrolyze other NTPs, but with lower affinity than ATP. However, the molecular basis for the broad substrate specificity remains unclear. To address this, we aim to redesign F₁ into a GTP-specific enzyme. From the MD simulation starting from F₁-ATP/GTP structures, we found that the GTP-bound state is less stable than the ATP-bound state. Considering steric hindrance from α R383, we introduced α R383A/K/E mutations to relieve this effect. Although these mutants did not improve GTP affinity, the α R383K mutant exhibited a significant increase in rotation rates for ATP, revealing an unexpected regulatory role. We will design further mutations using machine learning tools to modulate substrate specificity.

1GE006 複数のプロトン駆動トルク発生ユニットを有する F_oF₁-ATP 合成酵素の設計手法の拡張
Attempt to extend the design strategy for F_oF₁-ATP synthase with multiple proton-driven torque-generating units

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F_oF₁-ATP synthase (F_oF₁) is the rotary molecular motor that converts proton motive force (*pmf*) into ATP by coupling ATP synthesis/hydrolysis in F₁ and proton transport in F_o via mechanical rotation. In this study, we attempted to create a F_oF₁ with multiple proton-driven torque-generating units by redesigning the interaction site of δ -subunit and α -subunit. As a result, the mutant F_oF₁ was able to synthesize ATP even under low *pmf* conditions where the wild type could not. Furthermore, cryogenic single-particle analysis suggested that this F_oF₁ possesses multiple peripheral stalks, although further analysis is required for verification. These results indicate that the new design strategy successfully created F_oF₁ with multiple proton-driven torque-generating units.

1GE007 axle-less F_1 -ATPase の 1 分子回転観察によって発見された新たな回転中間体の解析
A new dwell-time discovery by single-molecule rotation assay of axle-less F_1 -ATPase

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F_1 -ATPase is a rotary molecule motor composed of $\alpha_3\beta_3$ stator ring and central rotor γ . The γ is known to contribute to efficient catalysis although it is dispensable for the allosteric communication among β s. Recently, cryo-EM analysis of axle-less F_1 , lacking the axle part of γ , have suggested that the missing part of γ is important for rapid ATP binding. However, it is not obvious whether the structure corresponds to an actual intermediate state during rotation, since this structure was obtained in the presence of an inhibitor. In the present study, we performed a single molecule analysis of axle-less F_1 . Axle-less F_1 showed 9 pauses, whereas wild type showed 6 pauses. This suggested that axle-less F_1 has novel rotational states not been found in the wild type.

1GE008 1 分子計測及び機械学習を用いた高活性 F_1 -ATPase の探索
Exploration of high-speed F_1 -ATPase with single-molecule assay and machine-learning

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F_1 -ATPase (F_1) hydrolyzes ATP to rotate the central stalk via large conformational changes. Despite extensive research so far, few mutations have been found to enhance the activity. Here, we performed machine-learning guided directed evolution. To construct an initial library composed of candidate mutations, we first compared three genuine F_1 s with different activities. Point mutations were introduced by replacing residues in the low-active F_1 with those from the higher-active F_1 s: notably, several mutants exhibited 1.3-fold higher activity than the wild-type. We then trained a machine-learning model to design the 2nd round library, which also yielded mutants with 1.2-fold higher activity. This iterative cycle continues to explore the structure–function relationship.

1GE009 マイコバクテリア ATP 合成酵素における α サブユニット C 末端伸長による阻害メカニズムの解明
Revealing a Unique Inhibitory Mechanism of C-terminal Extension of α -Subunit in Mycobacterial ATP Synthase

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The α -subunit of mycobacterial ATP synthase has a unique C-terminal extension domain (α CTD) that selectively inhibits ATP hydrolysis, suppressing wasteful ATP consumption under hypoxic conditions. To study this inhibitory mechanism, we created a “hybrid F_1 ” by integrating the mycobacterial α CTD and $\gamma\epsilon$ -subunits into TF_1 . This hybrid showed a 13-fold reduction in ATP hydrolysis activity in bulk assays, while single-molecule rotation assays revealed no significant change in rotation rate. Additionally, single-molecule analysis using a femtoliter reactor array device demonstrated fewer active molecules when α CTD was present, indicating that the inhibitory effect is persistent and that the hybrid F_1 remains in a stably inhibitory state without spontaneous activation.

1GE010 計算機で設計したサプレッサー変異による疾患型 KIF1A キネシンの運動性能の改善と神経機能の修復
Computationally identified suppressors rescue pathogenic mutations in KIF1A kinesin and restore neurological function

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KIF1A kinesin moves along microtubules (MTs) to transport synaptic vesicle precursors in axons. Pathogenic mutations in KIF1A impair both its velocity and MT affinity; however, it remains unclear which parameter is most critical for successful axonal transport and neurological function. Focusing on MT affinity, we computationally engineered pathogenic KIF1A mutants to enhance their binding to MTs. TIRF assays revealed a corresponding increase in run length, but not velocity. This modification suppressed the effects of the pathogenic mutations on axonal transport and behavioral activity in *C. elegans* disease models, fully restoring both. These findings suggest that MT affinity—rather than motor velocity—is the key determinant of effective axonal transport by KIF1A.

1GE011 全原子分子動力学シミュレーションによる F₁-ATPase の 40°サブステップ回転機構の解析
Investigating the 40° substep rotation mechanism of F₁-ATPase using all-atom MD simulations

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Thermophilic bacterial F₁-ATPase is a molecular motor driven by ATP hydrolysis, rotating in 120° steps composed of 80° and 40° substeps. This study focused on the 40° substep and conducted several tens of microseconds of all-atom molecular dynamics simulations using 18 structures based on recent cryo-EM structures. The analysis revealed that ATP hydrolysis induces minimal rotation, but the related conformational changes of subunits strongly correlate with rotary motion. In contrast, Pi release tended to increase the rotation angle, but the direct contribution of the subunit involved in Pi release to the rotary motion was limited. These findings suggest a coordinated, stepwise mechanism in which ATP hydrolysis and Pi release cooperatively drive rotation.

1GE012 DNA オリガミ製ナノスプリングを用いた Kinesin-3 モータータンパク質 KIF1A の力計測
Force measurement of the kinesin-3 motor KIF1A using a programmable DNA origami nanospring

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DNA origami technology enables the design of nanoscale structures using DNA and is applied across various fields. Iwaki et al. developed a DNA origami-based "nanospring," the world's smallest spring, which measures molecular-level forces based on its extension and demonstrated its utility by measuring forces generated by myosin. In this study, we applied the nanospring to quantify forces produced by the kinesin-3 motor protein KIF1A, which transports synaptic vesicles in axons and is essential for neurotransmission. We measured forces of both wild-type and disease-associated mutant KIF1A. The mutants showed reduced forces, implicating mechanical dysfunction in the pathogenesis of KIF1A-associated neurological disorders (KAND).

1GF001 嗅覚受容体と温度感受性チャネル TRPV1 の細胞内クロストークの解析
Investigation of Crosstalk between Olfactory Receptors and TRPV1 Channels

Sakura Moriyama^{1,2}, Shuji Hinuma², Shun'ichi Kuroda^{1,2} (¹Graduate School of Frontier Biosciences, The University of Osaka, ²SANKEN, The University of Osaka)

Olfactory receptors (ORs) in nasal sensory neurons detect odorants and initiate brain signals. TRPV1, a temperature-sensitive ion channel co-expressed with ORs, also responds to certain odorants, but their functional crosstalk remains unclear. We co-expressed ORs and TRPV1 in HEK293T cells to investigate this crosstalk. OR activation modulated TRPV1-mediated Ca²⁺ influx depending on ligand: capsaicin-like enhanced, eugenol-like suppressed, and 10-shogaol-like unchanged, likely via PKA-mediated phosphorylation. Conversely, TRPV1 activation attenuated OR51E1-driven cAMP production, possibly through Ca²⁺-dependent OR desensitization. These findings reveal bidirectional modulation between ORs and TRPV1, suggesting complex interplay in odorant signaling.

1GF002 超解像・1分子観察による細胞膜階層構造ドメイン形成機構の解明
Mechanisms of hierarchical domain organization on cell membranes revealed by super-resolution and single-molecule imaging

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Raft domains serve as key signaling platforms. Our group previously showed that GPI-anchored proteins (GPI-APs), representative raft markers, form transient homodimer rafts (~5 nm) via specific protein-protein interactions. Another group reported that GPI-APs assemble microdomains by non-specific transbilayer coupling between saturated fatty acyl chains and actin-bound phosphatidylserine (PS). Using real-time dual-color super-resolution movie observation, we found GPI-APs transiently form mesoscale domains (~100 nm), induced by specific protein interactions and stabilized by both lateral and transbilayer lipid interactions with actin-anchored PI(4,5)P₂ or PS. Furthermore, these mesoscale domains form by accumulating GPI-AP homodimers by transbilayer lipid coupling.

1GF003 Development of nanoforce polydiacetylene-based biosensors and tailoring their properties by integrating additives

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Despite their role in virus control, COVID-19 highlighted the limitations of current rapid tests, which provide only binary results. More informative and probability-based tests, like a rain forecast, are preferable. This work introduces a potential rapid test based on polydiacetylene (PDA), derived from 10,12-tricosadiynoic acid. PDA's mechanochromic properties—blue-to-red transition at the macroscale and fluorescence at the nanoscale—enable quantification of target concentration by correlating nanoscale shear forces (via Nano-Friction Force Microscopy) with fluorescence. Moreover, incorporating phosphatidylcholines during PDA preparation further tunes PDA mechanochromic sensitivity, and modifying the PDA's sidechain chemistry enables the functional reversibility.

1GF004 Synergistic Interaction between LL-37 and HNP-1 for Reducing Cytotoxicity on MDCK-I

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The synergistic antibacterial mechanisms of antimicrobial peptides (AMPs) have been extensively studied, but much less is known about their cooperative roles in protecting mammalian cells. Here, inspired by the crosstalk observed in α -synuclein and β -amyloid aggregation, we report how the synergistic interaction between LL-37 and HNP-1 reduces cytotoxicity toward MDCK-I cells. The results show that, compared to LL-37 or HNP-1 alone, the HNP-1/LL-37 mixture at appropriate ratios exhibits enhanced aggregation kinetics and mutually cytotoxic antagonism, leading to reduced cytotoxicity in MDCK-I cells.

1GF005 蛍光脂質を用いた DHA 含有リン脂質の相分離膜に対する影響評価
Evaluation of the Effects of DHA-Containing Phospholipids on Phase-Separated Membranes Using Fluorescent Derivatives of Phospholipids

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Docosahexaenoic acid-containing phospholipids (DHA-PL), composed of one saturated chain and DHA, have been hypothesized to localize at the boundary between the ordered (Lo) and disordered (Ld) phases and influenced lipid rafts formation. To test this, we synthesized a fluorescent derivative of PDPC, and POPC as a control, using an established labeling method (Kinoshita *et al.*, *J. Cell Biol.* **2017**). These probes were introduced into phase-separated membranes, but neither probes of PDPC nor POPC localized at the Lo/Ld phase boundary. Next, increasing PDPC content led to a higher affinity of PDPC to the Lo phase and a lower affinity of SM, while POPC showed no changing of the Lo phase. This is attributed to Lo phase fluidization, supported by monitoring SM diffusion.

1GF006 ミニマル合成細菌 JCVI-syn3B の膜電位計測
Measurement of membrane potential in the minimal synthetic bacterium JCVI-syn3B

Satoshi Kanamori, Hana Kiyama, Kenji Nobumoto, Makoto Miyata (*Grad. Sch. Sci., OMU*)

Membrane potential is critical for responsible and respiratory membranes such as neural and mitochondrial ones. However, some bacteria are known to keep membrane potential even they lack these activities. This study aims to discuss the role using JCVI-syn3B (syn3), a minimal synthetic bacterium featured by its only essential gene sets. We measured membrane potentials of syn3 and related species with using a fluorescent dye DiSC3(5), and valinomycin. The potentials were -14.9, -80.0, -17.3, -25.8 mV for syn3, *Bacillus subtilis*, *Mycoplasma mycoides*, and *Spiroplasma ericheimae*, respectively. The membrane potential of *Spiroplasma*, decreased by adding itaconic acid, a glycolysis inhibitor, suggesting a role of membrane potential as a cellular energy storage.

[1GF007](#) 細胞膜の非対称性と不均一性 Asymmetry and Heterogeneity in the Plasma Membrane

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Plasma membranes (PMs) exhibit lipid asymmetry between their two leaflets. Lateral heterogeneity, including the formation of lipid domains, is another crucial aspect of PMs with significant biological implications. However, the nature and even the existence of lipid domains in the two leaflets of PMs remain elusive, hindering a understanding of the significance of lipid asymmetry. Using coarse-grained molecular dynamics simulation of the PM, we find that the outer leaflet is predominantly ordered, whereas the inner leaflet separates into dynamic nanoscale ordered and disordered domains. This membrane organization suggests distinct functional roles for the two leaflets in PMs: the outer leaflet acts as a barrier while the inner leaflet modulates protein localizations.

[1GF008](#) Single Amino Acid Drives LL-37/HNP1 Synergy: Unveiling Antimicrobial Peptide Interactions

Ariane Schwitter¹, Kaori Sugihara² (¹*Grad. Sch. Eng., Univ. Tokyo*, ²*Inst. Ind. Sci., Univ. Tokyo*)

Synergistic antimicrobial peptides (AMPs) offer promise against antibiotic-resistant infections. Two human AMPs, LL-37 and α -defensin HNP1, display "double cooperativity"—synergistic bacterial killing with reduced host damage—yet the structural basis remains unclear. We combined LL-37 with HNP1-4 and β -defensin hBD1 to identify key secondary structures using POPC model membranes. FRAP and calcein leakage assays showed LL-37's membrane disruption was suppressed by HNP1, HNP3, HNP4, and hBD1. DLS revealed faster, looser aggregate formation in mixtures, but CD showed no structural changes. Our results suggest HNP2's unique N-terminal residue is critical for synergy with LL-37.

[1GF009](#) Bilayer lipid packing effects on the structure and electron transfer activity of cytochrome *c* oxidase

Bon Leif Dominguez Amalla¹, Atsuhiko Shimada², Satoshi Nagao³, Hiroyuki Kumeta⁴, Takeshi Uchida^{1,5}, Koichiro Ishimori^{1,5} (¹*Grad. Sch. of Chem. Sci. Eng., Hokkaido Univ.*, ²*Fac. of Appl. Biol. Sci., Gifu Univ.*, ³*JASRI*, ⁴*Fac. of Adv. Life Sci., Hokkaido Univ.*, ⁵*Fac. of Sci., Hokkaido Univ.*)

The electron transfer (ET) reaction between cytochrome *c* (Cyt *c*) and its transmembrane oxidase (CcO) contributes to the membrane potential across the inner mitochondrial membrane (IMM) used in ATP synthesis. Recent studies on the ET reaction with micelle-solubilized CcO have provided detailed insights into its regulation. However, the lipid environment in micelles significantly differs from the lipid bilayer structure of the IMM and is presumed to influence the structure and dynamics of CcO substantially. Consequently, we used bicelles, disklike membrane models composed of long and short-chain lipids, to provide a near-native bilayer environment around CcO. This study details how compression in lipid bilayers alters CcO structure and enhances its ET activity with Cyt *c*.

[1GF010](#) マイクロ流体デバイスで作製したリボソームの微小管重合による膜変形制御 Liposomes synthesized by microfluidic devices change shape in response to microtubule polymerization

Takuma Nishimura, Hiroto Ishii, Yusei Sato, Masahiko Yamagishi, Junichiro Yajima (*Graduate School Art and Science, The University of Tokyo*)

Liposomes, artificial vesicles composed of lipid bilayers, have attracted attention as platform materials for functional biomolecular devices due to their high biocompatibility. Particularly, liposomes prepared using microfluidic devices can be produced with high efficiency and uniform size, which is advantageous for the reproducible control of molecular robot behavior. In this study, we synthesized uniformly sized liposomes encapsulating tubulin using microfluidic devices and investigated their deformation induced by tubulin polymerization in response to external stimuli and the activity of motor proteins such as kinesin. This study demonstrates that liposomes fabricated using microfluidic devices can undergo shape deformation in response to microtubule polymerization.

1GF011 Machine Learning-Driven Functional Screening of Peptides Using Mechanochromic Lipid Sensors

Jiali Chen, Kaori Sugihara (*IIS., Univ. Tokyo*)

Membrane-targeting antimicrobial peptides offer a promising strategy against bacterial resistance, as their killing mechanisms are difficult for bacteria to evade through mutation. However, the multifaceted and complex nature of peptide-bacterial interactions means that some peptides exhibit not only antimicrobial activity but also harmful effects on human tissues. Furthermore, characterizing peptide function requires substantial specialized expertise and financial investment. To address these challenges, we have developed a streamlined approach that combines cost-effective, easily synthesized mechanochromic lipid sensors with machine learning to enable rapid and accessible classification of peptide functionality.

1GF012 コレラ菌走化性受容体 Mlp24 による GABA および L-オルニチンのリガンド認識機構
Ligand recognition mechanisms of GABA and L-ornithine by the chemoreceptor Mlp24 in *Vibrio cholerae*

Ririka Iida¹, Fuga Omori², Norihiro Takekawa³, So-ichiro Nishiyama⁴, Ikuro Kawagishi^{2,5,6}, Katsumi Imada³ (¹*Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Sci. and Engin., Hosei Univ.*, ³*Grad. Sch. Sci., Osaka Univ.*, ⁴*Dept. Appl Life Sci, Niigata Univ of Pharm and Appl Life Sci.*, ⁵*Dept. Front Biosci., Hosei Univ.*, ⁶*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

Toxigenic *Vibrio cholerae* has at least 44 genes for putative chemoreceptor proteins. Among them, Mlp24 mediates chemoattractant response to various α -amino acids, and its ligand-binding affinity is enhanced by calcium ions. Recent study showed that γ -aminobutyric acid (GABA) and L-ornithine elicit attractant responses via Mlp24. However, GABA has no α -amino group, and calcium ions do not increase the attractant response to L-ornithine. Here we determined the X-ray crystal structures of the ligand-binding domain of Mlp24 in complex with GABA and L-ornithine and conducted the ligand-binding assays using isothermal titration calorimetry (ITC). The results revealed how Mlp24 binds GABA, and how calcium ions contribute to ligand-binding.

1GG001 Molecular Simulation of Prebiotically Plausible Interactions Between Amino Acids and Fatty Acid Membranes

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Interactions between fatty acids, vesicles, acids amino, and peptides may have supported the selection and emergence of the first protocells on Earth. The precise binding mechanisms and systemic trends have not been identified. All-atom molecular dynamics simulations of the 20 canonical amino acids and lauric acid membranes were thus conducted to investigate the specific interactions and systemic trends. Hydrophobicity, charge, and size of amino acid side chain were all important physicochemical properties that differentiated between distinct binding trends and mechanisms. This research provides valuable insight into prebiotically plausible mechanisms which may have stabilized vesicles and supported aggregation of small organic molecules.

1GG002 液液相分離系を反応場とした遺伝子の複雑化を伴う進化の実現
Evolution with genomic complexity acquisition under LLPS droplet as a reaction field

Mirai Sasaki¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Grad. Sch. Eng., Univ. Tokyo*, ²*RIPH., Univ. Tokyo*)

In the evolutionary process toward the origin of life, increasing genetic/functional complexity is considered essential. Yet, in primitive in vitro evolution experiments of ligase ribozymes or self-replicating systems, short species often emerges, and no experimental conditions have yet realized spontaneous evolution toward longer ones. This study aims to demonstrate such evolution based on LLPS droplets, specifically the DEX-PEG phase separation. In this system, longer RNAs are enriched in the DEX phase, while shorter ones remain dispersed. By removing shorter RNAs through solution exchange, selection pressure favors elongation. This setup is used to evolve longer ribozymes, offering insights into mechanisms driving genetic complexity evolution.

1GG003 核酸分子と脂肪酸膜系の相互作用機構および脂肪酸膜系存在下での核酸分子の拡散挙動の全原子分子動力学シミュレーションを用いた解析
Analysis of the interaction and diffusion behavior of nucleic acid molecules with the fatty acid membrane system using AA-MD simulations

Ryoji Abe¹, Taren Ginter¹, Kosuke Fujishima^{1,2,3} (¹*School of Life Science and Technology, Science Tokyo.*, ²*Earth-Life Science Institute, Science Tokyo.*, ³*Graduate School of Media And Governance, Keio University*.)

Understanding how membrane compartments accumulate nucleic acid molecules is crucial for elucidating the origin of life and the emergence of cells containing genetic material. Recent experimental studies have revealed two different diffusion behaviors of nucleic acid molecules in the presence of primitive membrane systems made of fatty acids, which are simple amphipathic molecules, suggesting an interaction between the fatty acid membrane system and nucleic acid molecules. In this study, we used all-atom molecular dynamics simulations to investigate the detailed mechanisms of these interactions and to analyze the diffusion behavior of nucleic acid molecules in the context of primitive fatty acid membranes.

1GG004 遺伝子間の量比保存関係を通じた遺伝的摂動効果のグローバルな波及
Global propagation of genetic perturbation effects through stoichiometry conservation architecture

Genta Chiba¹, Ken-ichiro F Kamei¹, Arisa H Oda^{1,2}, Kunihiro Ohta^{1,2,3}, Yuchi Wakamoto^{1,2,3} (¹*Grad. Sch. Arts Sci., Univ. Tokyo*, ²*Res. Cent. Complex Syst. Biol., Univ. Tokyo*, ³*UBI, Univ. Tokyo*)

Understanding the design principles behind global gene expression state changes to genetic perturbations is important, but systems-level studies are lacking in any organism. In this study, we approached this problem by analyzing the gene expression profiles of single-gene deletion strains of *Escherichia coli*. We found that, regardless of the type of genetic perturbation, the expression stoichiometry between genes is tightly coordinated within various functionally related gene groups beyond operons. In addition, genes that conserve higher expression stoichiometry with the perturbed gene tended to show differential expression. This relationship also holds true in human and worm cells, suggesting that it is a universal property shared by a wide range of cellular systems.

1GG005 生命システムにおける生体要素間相互作用の一般化勾配流モデルに基づく数理表現
Describing Interaction Dynamics in Living Systems via the Generalized Gradient Flow Model of Adaptive Components

Ryunosuke Suzuki^{1,2}, Taiji Adachi^{1,2,3} (¹*LiMe, Kyoto Univ.*, ²*Grad. Sch. Eng., Kyoto Univ.*, ³*Grad. Sch. Life Sci., Kyoto Univ.*.)

Living systems are composed of interacting components whose adaptive responses to the interaction shape system-level functions. As interactions temporally change with adaptation, understanding function emergence requires capturing these dynamic interactions. This study develops a theory for describing adaptation of living components in response to changing interactions. By formulating internal and environmental state changes and modeling adaptation as gradient flow on energy landscapes, we represent interaction dynamics as temporal changes in energy and energy rate landscapes. Case studies show how this framework describes system-level function emergence. Applying this approach to real living systems could offer a unified perspective on diverse adaptive phenomena.

1GG006 機械学習を用いた細胞形状情報とストレスファイバー形成機構を考慮した細胞の牽引力推定
Cell Morphology and Stress Fiber Formation Mechanisms-Informed Traction Force Microscopy Using Machine Learning

Koki Fujiwara¹, Ryosuke Fujikawa¹, Yukihiro Suzuki¹, Kenta T. Suzuki^{1,2}, Yuichi Sakumura^{1,2} (¹*Grad. Sch. Sci. Tech., NAIST*, ²*DSC, NAIST*)

Traction force microscopy quantifies cellular traction forces, but its accuracy degrades under sparse observations. To date, no standardized dataset has been established, as validation settings—including random force distributions on the substrate, cell size, and bead density—vary across studies. Based on the biophysical mechanism in which cellular traction forces are transmitted through stress fibers to the substrate via clutch proteins and focal adhesions, we constructed a dataset. We proposed a novel machine learning model that incorporates cell shape information obtained through observation, and designed a loss function that accounts for force magnitude and direction. As a result, our method achieves highly accurate force estimation with sparse observations.

1GG007 麻酔または光遺伝学制御による生きている線虫 *C. elegans* の赤外イメージング手法の開拓
Development of infrared imaging methods for a living nematode, *C. elegans*, using anesthetics or optogenetic control

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C. elegans is widely used as a model organism in life science. IR imaging of a living nematode is a challenging task due to its motility and water absorption. We have been trying to develop a method to immobilize *C. elegans* with Na₂Na₃ or optogenetic control under D₂O hydration conditions. IR imaging was performed on a CaF₂ plate fabricated with a trough of 50μm depth or slide. IR images showed that protein amide I was uniformly distributed, while lipid C=O str. and C-H str. were distributed locally in the tail and abdomen. The protein Amide I bands were split into α-helical and β-sheet structures in the second derivative spectra, and this split differed depending on the body region of the worm. After the measurements, the recovery of the *C. elegans* was confirmed.

1GG008 X線回折イメージング・トモグラフィーにおける三次元構造精密化手法の開発とデンプン粒子構造解析への応用
Development of structure refinement protocol for XDIT and its application to structure analysis of rice-starch

Kosei Harada^{1,4}, Yuki Takayama^{2,4}, Masayoshi Nakasako^{3,4} (¹*Graduate School of Science and Technology, Keio University*, ²*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*, ³*Department of Physics, Faculty of Science and Technology, Keio University*, ⁴*RIKEN Spring-8 Center*)

Cryogenic X-ray diffraction imaging tomography (cXDIT) has the potential to visualize the internal structures of micrometer-sized non-crystalline particles at a resolution of several ten nanometers without fatal radiation damage. Although the 3D structure of a particle is reconstructed immediately after the diffraction data collection using our custom-made cXDIT apparatus, the structure amplitude from the reconstructed map is inconsistent with the observation at high resolution. Therefore, any structure refinement protocol dedicated to cXDIT is necessary. In the presentation, we will show a structure-refinement protocol and demonstrate its effectiveness through the application to the structure analysis of rice-starch at a resolution of 37.5 nm.

1GG009 超解像顕微鏡による非凍結性低温環境下における不凍タンパク質の細胞部位特異的局在の解析
Subcellular Localization of Antifreeze Proteins in a Non-Freezing Cold Environment Revealed by Super-Resolution Microscopy

Kosuke Maeda¹, Kaho Uchizawa¹, Sakae Tsuda², Tomoyasu Aizawa^{1,2}, Tatsuya Arai^{1,2} (¹*School of Science, Hokkaido University*, ²*Faculty of Advanced Life Science, Hokkaido University*)

Non-freezing preservation of cells at low temperatures is crucial for biomedical applications. However, current methods typically allow preservation only for a few days. While antifreeze proteins (AFPs) are known for their ice-binding properties, there is increasing evidence that they can extend the preservation periods through binding to cellular membranes. To better understand site-specific interactions of AFPs, we employed 3-dimensional structured illumination microscopy (3D-SIM). Our observations showed that AFPs were not uniformly distributed on the cell membrane but were localized to specific membrane regions and other subcellular domains. This suggests that AFPs probably exert cytoprotective effects at both the cell surface and within intracellular compartments.

1GG010 蛍光ナノ粒子を用いた細胞質の特性計測
Probing cytoplasmic physics with Genetically Encoded Multimeric nanoparticles

Sora Hirokane¹, Yasushi Okada^{1,2,3} (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Grad. Sch. Med., Univ. Tokyo*, ³*BDR, Riken*)

The crowded and active environment within living cells affects the kinetics of intracellular processes. Understanding this biophysical environment is essential for cell biology, yet its quantitative assessment is challenging. To address this, we optimized Genetically Encoded Multimeric nanoparticles (GEMs) as robust, non-invasive intracellular probes. GEMs are self-assembling fluorescent nanoparticles. Their defined size (25-50 nm), structural uniformity, and brightness allow precise tracking in cytoplasm to infer its physical properties. Our optimization of GEMs reduced tracking errors, enabling stable, long-term particle tracking in living cells. Optimized GEMs are a powerful tool to quantify cytoplasmic physical states and probe their effects on cellular function.

1GG011 神経突起伸長過程におけるシナプス接着分子の蛍光 1 分子追跡による時空間動態解析
Spatiotemporal dynamics analysis of synaptic adhesion molecules during neurite outgrowth by single molecule fluorescence imaging

Kodai Sasaki, Shigeyuki Namiki, Daisuke Asanuma, Kenzo Hirose (*Grad. Sch. Med., Univ. Tokyo*)

Synaptic adhesion molecules (SAMs), such as neurexin and neuroligin, are essential for synapse formation, yet their dynamics during early development (1–7 days in vitro) remain poorly understood due to technical limitations in expressing tagged proteins at these stages.

To address this, we established an analysis system combining rapid expression of tagged neurexin via Sindbis viral vectors with single-particle tracking in cultured rat hippocampal neurons. Neurexin mobility was assessed by calculating mean square displacement and diffusion coefficients, typically centered around $0.1 \mu\text{m}^2/\text{s}$.

This platform enables high-resolution analysis of SAM dynamics in the earliest phase of synaptogenesis and provides insights into the molecular basis of synaptic assembly.

1GG012 トランススケール生細胞イメージングによる希少細胞融合現象から形成されるハイブリッド腫瘍細胞の動態解析
Visualizing rare cell fusion events leading to hybrid tumor cell formation using trans-scale live-cell imaging

Izzati Rafidah^{1,2}, Shun-ichi Fukushima², Taishi Kakizuka^{2,3}, Tetsuichi Wazawa², Taro Ichimura³, Atsushi Kumanogoh⁴, Takeharu Nagai^{2,3} (¹The University of Osaka Graduate School of Pharmaceutical Sciences, ²SANKEN, The University of Osaka, ³OTRI, The University of Osaka, ⁴The University of Osaka Graduate School of Medicine)

Rare cellular events, though infrequent, can play critical roles in biological systems, yet their low occurrence makes them difficult to study using conventional methods. Cell fusion, for example, occurs at extremely low frequencies (<0.1%), highlighting the need for advanced imaging technologies. We utilized AMATERAS, a trans-scale imaging system that enables long-term, time-lapse imaging over a wide field of view (~1.5 cm²) with single-cell resolution. Focusing on circulating hybrid cells (CHCs) formed by fusion between cancer cells and immune cells such as macrophages, we co-cultured fluorescently labeled cell lines and successfully captured rare fusion events (1/10,000 cells) initiated at filopodia-like membrane protrusions, suggesting potential fusion mechanisms.

1GH001 分子動力学シミュレーションとアンブレラサンプリングによる神経疾患関連フィラミン A 変異の構造解析
Molecular Dynamics and Umbrella Sampling Reveal Structural Changes in Filamin-A Mutants associated with Neurodegenerative disorders

Shota Ito¹, Koyo Tsujikawa², Kentaro Sahashi¹, Takeshi Kawasaki^{3,4}, Yoshitake Sakae⁵, Masahisa Katsuno¹ (¹Department of Neurology, Nagoya University Graduate School of Medicine, ²Department of Genetics, Research Institute of Environmental Medicine, Nagoya University, ³D3 center, Osaka University, ⁴Department of Physics, Osaka University, ⁵Research Organization for Information Science and Technology)

Filamin-A (FLNA) is an actin cross-linker. Mutant FLNA proteins associated with progressive supranuclear palsy, a neurodegenerative disease, show excessive F-actin stability. To elucidate the mechanisms, we performed 500 ns all-atom molecular dynamics (MD) simulations of FLNA domains 18–19 in wild-type and mutants, applying umbrella sampling to calculate potential of mean force (PMF) profiles as a function of the N–C terminal distance. MD simulations revealed altered domain interactions, with PMF values at the maximum separation (9.2 nm) 12.4–35.6 kJ/mol higher in mutants than in the wild-type. These structural changes may contribute to excessive stabilization of the actin network in the disease.

1GH002 脂質漏洩下におけるナノディスク中の膜タンパク質の構造安定性
Effect of Lipid Leakage on the Structural Stability of Membrane Proteins in Nanodiscs

Sara Inoue, Takaharu Mori (*Tokyo University of Science*)

Nanodiscs (NDs) are widely used to mimic lipid bilayers in the structural analysis of membrane proteins. Recently, high-speed atomic force microscopy (HS-AFM) has been employed to investigate the dynamics of membrane proteins in NDs. HS-AFM scans samples using a cantilever and provides height information. However, such experiments may induce lipid leakage due to the cantilever's mechanical effects. To assess the impact of this artifact on membrane protein structure within NDs, we conducted MD simulations by adjusting the lipid filling rate to mimic lipid leakage. We found that in the case of SecY-ND complex even under low lipid filling conditions, the structure of SecY is largely unaffected.

[1GH003](#) AlphaFold で予測された多状態の強化サンプリングに基づくタンパク質の自由エネルギー計算手法の開発
Development of Free Energy Calculation Method Based on Enhanced Sampling of Various Protein Conformations Predicted by AlphaFold

Toma Aoki¹, Yasuteru Shigeta², Ryuhei Harada² (¹*School of Life and Environmental Sciences, University of Tsukuba*, ²*Center for Computational Sciences, University of Tsukuba*)

AlphaFold (AF) predicts protein conformations with high precision using coevolutionary information from multiple sequence alignments (MSA). Recent studies have revealed that reducing the depth of input MSA increases uncertainty in coevolutionary signals, allowing AF to generate structurally diverse protein conformations. However, these predictions are static conformations without information on protein dynamics, making their structural stability uncertain. In this study, to evaluate AF-predicted conformations, we combined our efficient conformational sampling method called outlier flooding method (OFLOOD) with the multi-state AF prediction using reduced MSA depth, evaluating AF-predicted structures with their free-energy values.

[1GH004](#) In silico study of transmembrane allosteric effect of CBD on CB1 receptor activation

Vi Toan Lam, Duy Phuoc Tran, Akio Kitao (*Institute of Science Tokyo*)

The CB1 receptor plays a central role in the endocannabinoid system, maintaining brain function. THC acts as a phyto-agonist directly activating CB1, while CBD functions as its allosteric phyto-antagonist. However, the transmembrane allosteric binding sites of CBD on CB1 remain unclear, prompting us to investigate them via MD simulations. Multiple structures were used: active (6KPG), apo (6KQI) and inactive (9B9Y). The ligand was removed from 6KQI, THC was modeled to replace the ligand in 6KPG, and CBD binding poses were extensively scanned across the CB1 surface. We identified three distinct transmembrane CBD binding sites. The allosteric effects were evaluated through binding free energy analysis, CBD stability, and CB1 dynamics with and without bound CBD.

[1GH005](#) Differences in Conformational Dynamics of Glycans on FcγRIIIb Revealed by Molecular Simulation

Yue Zhang¹, Hirokazu Yagi^{2,3}, Koichi Kato^{2,3}, Takumi Yamaguchi^{1,2,3} (¹*Sch. Materials Sci., JAIST*, ²*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, ³*ExCELLS, NINS*)

Glycan structures on glycoproteins generally exhibit heterogeneity, but factors that specify glycan structure remain unclear. We explored the determinants of glycan structures on FcγRIIIb by molecular simulations. It has been reported that FcγRIIIb has multiple glycosylation sites while only one site carries predominantly specific glycans. Analysis of the static structure of the protein did not reveal any features corresponding to differences in the glycan structure. Meanwhile, replica-exchange MD simulations of the glycoprotein indicated that differences in the conformational dynamics of glycans between the glycosylation sites are an important factor. It was found that interactions between neighboring glycans significantly restrict their conformational space.

[1GH006](#) 構造に基づく機構的理解：SAM を基質とする求核型・求電子型 PLP 酵素の比較
Structure-Based Mechanistic Insights into Nucleophilic and Electrophilic PLP Enzymes Using SAM

Kazuki Shimada¹, Takayoshi Awakawa², Tohru Terada¹ (¹*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*CSRS, Riken*)

Insights into the dynamic and electronic nature of enzymes are necessary to understand their catalytic mechanisms. Combining complex structure prediction with **AlphaFold3** with **molecular dynamics (MD)** and **QM/MM** techniques, we examined catalytic mechanisms of two **PLP-dependent enzymes using SAM, PseP and Mur24**. Though their active sites resemble each other, PseP yields a β,γ -unsaturated quinonoid (a **nucleophilic intermediate**) whereas Mur24 yields a **vinylglycine ketimine (an electrophilic intermediate)**. Comparison of the model structures indicates that a **histidine** in PseP is replaced by a **phenylalanine** in Mur24. Results from MD simulations and QM/MM calculations suggested that the difference in this residue should cause the difference in the reaction of the enzymes.

1GH007 Theoretical Study of Drug Resistance Caused by G13D and Q99L Secondary Mutations in KRAS G12C Against Sotorasib and Adagrasib

Riksa Meidy Karim, Kazutomo Kawaguchi, Hidemi Nagao (*Graduate School of Natural Science and Technology, Kanazawa University*)

KRAS is a GTPase that plays a critical role in cell signaling, with the G12C mutation driving several cancers. Although KRAS G12C inhibitors such as sotorasib and adagrasib have shown clinical benefit, drug resistance remains a major challenge. Secondary mutations like G13D and Q99L have been observed to confer varying levels of resistance, yet the molecular mechanisms underlying these effects are not well understood. This study aims to uncover how such mutations influence inhibitor binding and efficacy. We use molecular dynamics simulations, binding free energy calculations, and dynamic interaction analyses to identify key changes in protein–ligand behavior. Our results provide insights into resistance mechanisms and inform future KRAS inhibitor design

1GH008 細胞スケールの生命現象の解明に向けた新規粗視化分子動力学法の開発
Innovating Coarse-grained Molecular Dynamics Simulation: beyond Temporal/Spatial Limits

Yosuke Teshirogi, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

Molecular dynamics (MD) simulation is a useful method to investigate the dynamics of biomolecules underlying their functions. However, the time- and spatial-scales of conventional all-atom simulations are restricted because of their high computational cost. In this study, we developed a novel coarse-grained MD simulation method that enables long-time, large-scale simulations. In this method, each protein molecule in a system is coarse-grained at the residue level and is treated as a rigid body. The dynamics of the system is described by the overdamped Langevin equation, which is integrated with a larger timestep using an implicit algorithm. The validity of this method was evaluated in barnase-barstar binding simulations and microtubule nucleation simulations.

1GH009 血流中の酸素の拡散のシミュレーション
Simulation of oxygen diffusion in blood flow

Tetsuya Yamamoto^{1,2}, Hiroshi Noguchi², Dmitry Fedosov³ (¹*Grad. Sch. Sci. and Tech., Keio Univ.*, ²*ISSP, Univ. Tokyo*, ³*FZ Jülich*)

In this study, we modeled blood flow to numerically investigate oxygen transport by red blood cells (RBCs). We adopted a mesoscopic model of blood flow based on the smoothed dissipative particle dynamics (SDPD) method. The setup consists of RBCs, blood plasma, and vessel walls, which were all created using SDPD particles. Oxygen diffusion was additionally modeled by solving the diffusion equation between SDPD particles.

In addition to RBC deformation into a parachute-like shape typically seen in capillaries, we observed that the concentration profiles of oxygen within blood flow depend strongly on its boundary conditions. Specifically, oxygen concentration decays either linearly or exponentially along the flow depending on the flux at the vessel walls.

1GH010 De Novo ATPase の触媒活性の合理的改善
Rational Enhancement of De Novo ATPase Activity

Takuya Orita¹, Takahiro Kosugi², Shigehiko Hayashi¹ (¹*Graduate School of Science, Kyoto University*, ²*Research Center of Integrative Molecular Systems, Institute for Molecular Science*)

Rational enzyme design remains a challenging task, as poor catalytic efficiency and low success rates continue to limit practical applicability. Kosugi et al. developed a de novo ATPase by incorporating a phosphate-binding motif (P-loop) into a scaffold protein. However, its catalytic efficiency was still markedly lower than that of natural enzymes. In this study, we conducted a statistical analysis of natural ATP-binding protein structures to identify structural features critical for catalytic activity. Based on these insights, we employed molecular dynamics simulations to design mutant models of Kosugi's enzyme. One such mutant model reproduced key properties of natural ATP-binding proteins, and thus is expected to exhibit enhanced catalytic activity.

[1GH011](#) Mesoscale Modeling of Amyloid Formation in Heterogeneous Membraneless Organelles

Kento Fujita, Yusuke Takagi, Eiji Yamamoto (*Grad. Sci., Univ. Keio*)

Membraneless organelles are biomolecular condensates formed through phase separation of proteins and RNAs. Spatial heterogeneity in molecular concentration may play biological roles and influence pathological processes such as amyloid nucleation and growth. In this study, we modeled amyloid nucleation and growth using particle-based representations and performed mesoscale simulations to examine the dynamics of inhomogeneous fields. By coupling particles with a continuous concentration field, the framework captured key processes such as nucleation, diffusion, and fibril elongation. This approach enables investigation of droplet heterogeneity and dynamics, offering insights into how spatial variation affects aggregation in phase-separated systems.

[1GH012](#) メロテルペノイドの生合成経路におけるプレニル基転移酵素 Fur7 の触媒機構の計算的研究 Computational Study on the Catalytic Mechanism of Prenyltransferase Fur7 in the Biosynthetic Pathway of Meroterpenoids

Takuto Ohmura¹, Fan Zhao¹, Yoshitaka Moriawaki², Tomohiro Noguchi¹, Taro Shiraishi¹, Tomohisa Kuzuyama¹, Tohru Terada¹
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Meroterpenoids are compounds with terpenoid skeletons fused to other structures, widely found in nature, and known for various biological activities. Furaquinocin D, an antitumor meroterpenoid produced by *Streptomyces*, is synthesized via a pathway involving the prenyltransferase Fur7, which catalyzes a “reverse” prenylation reaction, adding the 3' carbon of geranyl diphosphate to a polyketide backbone. In this study, structure prediction, molecular dynamics, and quantum chemical calculations were employed to analyze Fur7's catalytic mechanism. Computational results demonstrated that Fur7 catalyzes stereoselective “reverse” prenylation via an S_N2 reaction followed by a Claisen rearrangement and identified amino acid residues that stabilize the transition states.

[1GI001](#) 紫外光吸収型色覚視物質の構造的洞察 Structural insights into UV sensitivity of mouse SWS1 opsin revealed by low-temperature FTIR spectroscopy

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The short-wavelength sensitive cone opsin (SWS1) detects blue light in human but UV light in many animals, including mice. This spectral tuning is attributed to the protonation state of the Schiff base of 11-*cis*-retinal: protonated in blue/violet-sensitive and deprotonated in UV-sensitive. Although several residues involved in this tuning have been identified, the detailed molecular mechanism remains unclear. Here, we analyzed the mouse SWS1 (MUV) using FTIR spectroscopy at 77 K. Spectral comparison with a blue-sensitive pigment revealed shared internal water clusters, but distinct structural changes. Moreover, specific water-associated signatures were observed only in MUV. Together with mutational analysis, these results provide new insights into the UV-sensitivity.

[1GI002](#) Chrimson に近縁な新奇チャネルロドプシン HulaChrimson の青色シフト吸収スペクトルとその起源 HulaChrimson—a novel channelrhodopsin homologous to Chrimson with a distinctly blue-shifted absorption spectrum

Hiroyo Takahashi¹, Shunki Takamoto¹, Takashi Nagata¹, Shai Fainsod², Yoshitaka Kato¹, Andrey Rozenberg², Oded Bèjà^{2,3}, Keiichi Inoue¹
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Channelrhodopsins (ChRs) are light-gated ion channels composed of seven transmembrane helices and an all-*trans* retinal chromophore bound to a conserved lysine residue. Ion transport of ChRs is triggered by the photoisomerization of the retinal. Chrimson, a member of cation-conducting ChRs (CCR), responds to around 590-nm light and is one of the most promising optogenetic tools. In this study, we identified a novel CCR, HulaChrimson, from the metatranscriptome of Lake Hula, Israel. While HulaChrimson shares >50% amino-acid sequence identity with Chrimson, its absorption maximum wavelength is 501 nm. In this presentation, we will present the results of amino-acid mutants and the mechanisms underlying the distinct absorption spectrum of HulaChrimson compared to Chrimson.

[1GI003](#)

キラル分光を用いた先祖型 Photoactive Yellow Protein 活性部位の構造解析 Structural analysis of the active site of ancestral photoactive yellow protein using chiral spectroscopy

Yoshimitsu Onaka¹, Rosalie Dohmen², Tomotsumi Fujisawa¹, Wouter D. Hoff², Masashi Unno¹ (¹*Fuc. Sci. Eng., Saga Univ.*, ²*Dep. Microbiol. Mol Gen., Oklahoma State Univ.*)

A cofactor molecule in a protein is usually non-planar, and such structural distortions have been shown to be functionally important. The non-planar structure can be elucidated by chiroptical spectroscopy such as Raman optical activity. In this study, we applied the techniques to a blue light receptor photoactive yellow protein (PYP). PYP has *p*-coumaric acid (*p*CA) as a chromophore, and its chromophore structure is out of plane distorted. Here, we reconstructed ancestral PYP genes and characterized the active site structure of the gene from ancestral PYP. Results showed that the synthetic PYP for the last common PYP ancestor exhibited a planar *p*CA structure. This result implies that the distorted chromophore structure in PYP was obtained during the course of evolution.

[1GI004](#)

新規チャネルロドプシン ChR024 の長波長光吸収メカニズムおよびイオン透過機構の構造基盤 Structural basis for the red-shifted absorption and the channel conducting mechanism of the novel channelrhodopsin ChR024

Yuka E. Takeno¹, Masaya Watanabe², Koichiro E. Kishi², Seiya Tajima³, Masahiro Fukuda³, Masaki Tsujimura⁴, Shunki Takaramoto⁵, Yuma Ito⁶, Yo Yamashita⁶, Masahiro Sugiura⁶, Suhyang Kim³, Kota Katayama⁶, Yuji Furutani⁶, Hideki Kandori⁶, Hiroshi Ishikita^{3,4}, Keiichi Inoue⁵, Hideaki E. Kato^{1,2,3} (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Grad. Sch. Arts and Sci., Univ. Tokyo*, ³*RCAST, Univ. Tokyo*, ⁴*Grad. Sch. Eng., Univ. Tokyo*, ⁵*ISSP, Univ. Tokyo*, ⁶*Grad. Sch. Eng., Nagoya Inst. Tech.*)

Channelrhodopsins underpin optogenetics, yet phototoxicity limits their use, prompting a search for red-shifted variants. A recent machine-learning screen identified ChR024 ($\lambda_{\text{max}} = 578 \text{ nm}$), but the mechanism of its red-shifted absorption and channel conductance has remained unclear. Through cryo-EM, spectroscopy, computational calculations, and electrophysiology, we revealed that residues outside the immediate chromophore pocket critically influence spectral tuning, while subtle residue rearrangements forge an ion-conducting pathway. Furthermore, a key mutation converted an ion-pumping rhodopsin into a light-gated ion channel. Our work elucidates ChR024's color-tuning and ion conducting mechanisms and offers a blueprint for safer, deep-penetrating optogenetic tools.

[1GI005](#)

L/M 錐体視物質の三次元構造から導く波長制御機構 Unveiling the spectral tuning mechanism through three-dimensional structures of red and green cone pigments

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Primate eyes have three types of cone pigments (red, green, and blue), which enable color perception. Although these pigments bind 11-*cis*-retinal as a common chromophore, they exhibit distinct spectral tuning.

In this study, we successfully determined the three-dimensional structures of the red and green cone pigments using cryo-EM and clarified the molecular mechanisms underlying spectral tuning. Furthermore, by combining vibrational spectroscopy and multiconfigurational quantum chemical calculations, we identified the key factors for spectral properties. In addition, our structural analysis revealed the presence of an opening in both red and green cone pigmental feature not observed in rhodopsin. We also discuss the potential structural role of this opening.

[1GI006](#)

ヘリオロドプシンの光反応ダイナミクスを決める SNaP bond の赤外分光法による水素結合解析 Direct detection of a crucial Hydrogen Bond in Heliorhodopsin, SNaP bond, using Low-Temperature IR Spectroscopy

Toshiki Nakamura¹, Manish Singh¹, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology, Nagoya, Japan*, ²*OptoBioTechnology Research Center, Nagoya Institute of Technology, Nagoya, Japan*)

Heliorhodopsins (HeRs) are light-responsive proteins discovered in 2018 and classified as a novel rhodopsin superfamily. We proposed that a hydrogen bond between Ser in helix 3 and Asn in helix 4 regulates the conformational dynamics of active intermediates of HeRs (named SNaP bond). In this study, we used low-temperature infrared (IR) spectroscopy. IR difference spectra of the K intermediate allowed assignment of both C=O and N-H stretching vibrations of Asn from the SNaP bond, which was the first direct detection of the SNaP bond. It is hard to prove the SNaP bond even by modern structural biology methods. We will discuss differences between the SNaP bond and the DC gate in channelrhodopsins, which are far distant from HeRs in the molecular phylogenetic tree.

1GI007 クラゲロドプシンにおける特異な構造変化が示す Gs タンパク質活性化の作用メカニズム
Distinct structural transition in jellyfish rhodopsin reveals the mechanistic basis for Gs protein activation

Shino Inukai¹, Mitsumasa Koyanagi², Takashi Nagata³, Keiichi Inoue³, Akihisa Terakita², Hideki Kandori^{1,4}, Kota Katayama^{1,4} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Grad. Sch. Sci., Osaka Met. Univ.*, ³*ISSP, The Univ. Tokyo.*, ⁴*OptoBioTechnology Research Center, Nagoya Inst. Tech.*)

Jellyfish rhodopsin (JelRh) is unique among animal rhodopsins for its Gs protein activation and the presence of a counterion at a noncanonical position in transmembrane helix 2 (TM2). We previously showed by FTIR spectroscopy that its initial photo-intermediate shares structural features with vertebrate rhodopsins. In this study, we further investigated the transition to the Lumi intermediate. Comparative analysis with vertebrate and invertebrate rhodopsins revealed that, while retinal isomerization in JelRh resembles that of vertebrate rhodopsins, structural changes in the peptide backbone and amino acid side-chains are distinct. These findings suggested that the unique counterion position in JelRh may facilitate Gs-specific activation.

1GI008 多周波 EPR による光化学系 II マンガンクラスター S₂ g ~ 5 状態の構造と機能の解析
Role of S₂ g ~ 5 state in photosystem II manganese cluster revealed by multifrequency EPR

Shinya Kosaki¹, Yoshiki Nakajima², Jian-Ren Shen², Hiroyuki Mino¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Res. Inst. Interdiscip. Sci., Okayama Univ.*)

Photosynthetic oxygen evolution occurs in the Mn cluster of photosystem II. The Mn cluster has five intermediate states S_i (i = 0-4) during water oxidation. X-band EPR showed that the S₂ state had some isomers (g = 2, g = 4.1, g ~ 5). However, the role of these isomers in the S₂-to-S₃ transition remains unclear. We investigated the g ~ 5 state using X- and Q-band EPR. The activation energy in the transition from the S₃ to the S₂ g ~ 5 states was very small (0.54 kcal/mol), indicating that the structure of the g ~ 5 state is very similar to the S₃ state. T₁ measurements show that the g ~ 5 state originates from the S = 7/2 state. By comparison with the QM calculation, the g ~ 5 state was concluded to work as an intermediate state during the S₂-to-S₃ transition.

1GI009 外向きプロトンポンプロドプシンにおける弱有機酸結合の研究
Study of weak organic acid binding on outward proton-pumping rhodopsin

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Outward proton-pumping rhodopsins utilize light energy captured by the retinal chromophore to transport H⁺ from the inside to the outside of the cells. In this study, we found that the pump activity of an outward proton-pumping rhodopsin (*PspR*) from *Pseudomonas putida* is enhanced by extracellular weak organic acids (WOAs). Through mutation analysis, we investigated the WOA binding sites in *PspR*. Interestingly, D73W/F mutants exhibited large blue-shifts in the presence of acetate, suggesting its interaction near the retinal Schiff base. By contrast, R70Q mutant exhibited reduced WOA-binding ability—a smaller enhancement of pump-activity by WOAs and a faster photocycle compared to the wild type, indicating R70 is essential for H⁺ transport and WOA binding.

1GI010 内向きプロトンポンプロドプシン NsXeR の新しいプロトン移動メカニズム
A new proton transfer mechanism for inward proton pump rhodopsin NsXeR

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NsXeR exhibits strong inward proton transport activity. The underlying molecular mechanism would be hidden in the first proton transfer process from the protonated retinal Schiff base (PRSB) to a proton acceptor. By using infrared spectroscopy, we revealed that the hydrogen bond of the PRSB is weakened in the K intermediate and then strengthened in the L intermediate. An aspartic acid residue in the cytoplasmic side was identified as the proton acceptor in a homolog of NsXeR. NsXeR conserves the aspartic residue (D220), however D220 does not directly accept the proton from the PRSB. Our results suggest that the hydrogen bonding network between the PRSB and D220 may be divided by other amino acid residues (H48 and Y212) and water molecules in the L intermediate.

1GI011 摂食による細菌のけいれん運動の制御 Controlling Bacterial Twitching Motility by Feeding

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Alcanivorax borkumensis SK2 (*Alca*) is a model hydrocarbon-degrading marine bacterium known for its role in oil spill bioremediation. *Alca* is typically found at very low concentrations, bloom at the site of oil spills, becoming the dominant bacteria.

Despite lacking flagella and previously being classified as non-motile, we report that *Alca* exhibits pili-mediated surface motility. Moreover, both its motility is strongly regulated by its carbon source preference, as demonstrated through direct observation and gene expression analysis. This preference enables external control of *Alca*'s motility via carbon source switching.

Our findings shed light on how non-swimming bacteria adapt to and thrive in dynamic marine environments.

1GI012 油水界面における生物膜の剪断駆動型不安定性 Shear-driven instability in biofilms at oil–water interfaces

Hongtao Zhang¹, Shufeng Zhao¹, Andrew Utada^{2,3,4} (¹Graduate School of Life and Earth Sciences, Univ. Tsukuba, ²Institute of Life and Environment Science, Univ. Tsukuba, ³Microbial research Center for Sustainability, Univ. Tsukuba, ⁴Tsukuba Institute for Advanced Research, Univ. Tsukuba)

Hydrocarbonoclastic bacteria are marine bacteria that form biofilms at oil-water interfaces, which they use as a sole carbon and energy source. Using microfluidics, we trap and observe dynamic boundary fluctuations of their biofilms under varying flow conditions. The biofilm exhibits wave-like undulations, asymmetric deformation, as well as biofilm-fragmentation and coalescence-like dynamics, which are indicative of a fluid-like responsiveness. Time-lapse imaging and image analysis suggest that interfacial shear may promote boundary instability, supporting the view that the biofilm behaves as an active viscoelastic material. These insights may inform future strategies for biointerface control and synthetic membrane design.

1GJ001 tRNA array 法による 21 種類の tRNA の in vitro 同時発現 Simultaneous in vitro expression of minimal 21 transfer RNAs by tRNA array method

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Transfer RNA (tRNA) plays a central role in translation. The simultaneous in vitro synthesis of minimal yet sufficient tRNA species (at least 21) remains a challenge for building self-reproducible artificial cells. We developed a novel tRNA synthesis method that avoids run-off transcription, which impairs DNA replication. By combining direct tRNA linkage and HDVR attachment (termed the tRNA array method), **we achieved simultaneous expression of 21 tRNAs from a single polycistronic DNA template in the PURE system** (Miyachi et al., 2025). This also enabled replication of the template DNA, laying the foundation for minimal self-replicating gene expression. Moreover, the method's modularity makes it a promising platform for genetic code reprogramming.

1GJ002 Versatile control of a minimal synthetic bacterium JCVI-syn3B for morphology and fusion

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The minimal synthetic bacterium JCVI-syn3B (syn3B) serves as a powerful model to study the essential features of cellular life due to its reduced genome and lack of a cell wall. Our study explores three aspects of syn3B: (1) cell elongation through cytoskeletal protein expression and high-pH conditions, revealing multinucleate cells, (2) detergent-induced division showing asymmetric cytoplasmic partitioning, and (3) PEG-mediated cell fusion, enabling mixing of cytosolic components and altered cell morphology. These findings offer new experimental tools for understanding morphology, organization, and dynamics in minimal cells.

1GJ003 脂質小胞への改変型 β バレルナノポアの再構成手法と分子輸送の検討
Reconstitution method and molecular transport of modified β -barrel nanopore into lipid vesicles

Toshiyuki Tosaka, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Protein nanopore has been used as a biological molecule that transports ions, substrates, and products across a membrane of a cell-sized liposome. To transport various sizes of biological molecules using protein nanopore, it is necessary to construct the protein nanopore with a constant pore diameter. In this study, we modified BtuB to build a stable nanopore that can transport the molecules into the liposome. The BtuB nanopore was designed by deleting the plug domain within the β -barrel. BtuB nanopores were reconstituted in giant unilamellar vesicles (GUV) by membrane fusion between nanodiscs containing BtuB nanopores and GUVs. Transportation of fluorescent molecules was observed from the outer aqueous phase to the inner aqueous phase of the GUV via the BtuB nanopore.

1GJ004 人工 DNA 皮質構造による GUV 膜における分子分布制御に向けて
Toward regulation of molecular distribution in giant unilamellar vesicles based on artificial DNA cortex

Takuro Yoshinaga, Yusuke Sato (*Graduate School of Computer Science and Systems Engineering, Kyushu Institute of Technology*.)

In GUVs containing multiple lipid species, phase separation forms domains, similar to raft models where functions like molecular uptake are thought to be enhanced by accumulating molecules. The actin cortex is suggested to regulate these functions. This study aims to regulate membrane domain distribution by constructing an artificial cortex-like DNA structure inside GUVs, inspired by the cellular actin cortex. We designed two types of six-branched DNA nanostructures, S-motif and orthogonal S-motif (orthS-motif). These motifs were encapsulated in GUVs (DOPC/DPPC/Cholesterol) to form the DNA cortex on the inner leaflet. As a result the membrane domain distribution on the GUV surface corresponded with the patterned distribution of S- and orthS-motifs in the DNA cortex.

1GJ005 Design of bioluminescent biosensors via enzymatic kinetic contrast: Demonstration with a Cu^{2+} Sensor

Ti Wu^{1,2}, Hossain Md Nadim¹, Mitsuru Hattori¹, Takeharu Nagai^{1,2} (¹*SANKEN, The University of Osaka*, ²*The Graduate School of Pharmaceutical Sciences, The University of Osaka*)

Bioluminescence, an enzyme-catalyzed light-emitting reaction, provides a unique basis for designing versatile biosensors. We propose a novel design strategy that exploits difference in enzymatic kinetics between luciferase variants to achieve ratiometric signal outputs. By combining two luciferases with distinct catalytic efficiencies and emission colors, we made their luminescence ratio serve as a quantitative sensor for molecular interactions or environmental changes. As a proof of concept, we developed a ratiometric bioluminescent sensor for Cu^{2+} , named DERK-Cu(II), which enables accurate detection of micromolar Cu^{2+} in real water samples. The kinetic-based design framework offers a promising platform for developing a broad range of enzyme-driven biosensors.

1GJ006 蛍光ナノダイヤモンドを用いた細胞内温度と粒子拡散の同時計測による細胞内環境の解析
Analysis of the intracellular environment by simultaneous measurement of temperature and particle diffusion using fluorescent nanodiamonds

Yuki S. Kato¹, Keisuke Fujita², Shingo Sotoma³, Yoshie Harada^{2,4} (¹*Sch. Sci., Univ. Osaka*, ²*WPI-PRIME, Univ. Osaka*, ³*Fac. Mol. Chem. Eng., Kyoto Inst. Tech.*, ⁴*QIQB, Univ. Osaka*)

To elucidate the mechanism behind local temperature inhomogeneity within cells, we focused on the relationship between local intracellular temperature and viscosity. To measure these two physical quantities, we used fluorescent nanodiamonds (FNDs) and introduced them into cells.

Temperature was estimated from the fluorescence intensity of the FNDs, while information on the surrounding viscosity was obtained by analyzing their positional trajectories.

As a result, we found that viscosity in the cytoplasm is spatially heterogeneous. Moreover, the temperature of FNDs located in regions with low viscosity was lower than that of FNDs in regions with higher viscosity.

Based on these findings, we discuss the physical properties of cells using non-equilibrium physics.

1GJ007 液液相分離に基づいた新規マイクロリアクタの開発によるデジタル核酸検出の簡便化の実現
New Microreactors from Aqueous Two-Phase Emulsion for the Simplification of Digital Nucleic Acid Detection

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Digital bioassay is a single-molecular analytical method that enables highly sensitive detection and absolute quantification of biomolecules. Microreactors prepared from microdevices are essential, since they keep the generated signals inside, allowing single-molecule resolution. However, the fabrication and manipulation of microdevices are often costly and technically complicated, limiting their application and popularization. In this research, we developed a simplified and low-cost digital detection method using microparticles as microreactors. These microparticles are generated from Dextran/Polyethylene Glycol (Dex/PEG) phase separation and can introduce different functions with specific modification, giving a novel prospect of broader application of digital assay.

1GJ008 ハイスループットイメージングによる適応酵素 CheB 細胞内動態の解析
Quantification of CheB's behavior in a single cell by high throughput imaging

Yoichi Kuroki, Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)

E. coli responds to chemical stimuli and this behavior is termed chemotaxis. Recently, we showed the dynamics of the adaptation enzyme CheB represents the active level of chemotaxis system. However, the previous study could measure only one cell at a time, making it difficult to analyze true cellular responses without experimental errors. Therefore, we developed high-throughput imaging system, enabled simultaneously analysis hundreds of cells in a homogeneous condition. This system improved experimental efficiency over 300-fold compared to previous one, and we succeeded in a substantial reduction of the variation in measurement values derived from experimental errors. We confirmed residual variation was due to differences in CheB concentration among individual cells.

1GJ009 原子間力顕微鏡を用いたアフリカツメガエル初期胚の単一細胞力学マッピング測定
Mapping Single-Cell Mechanics in *Xenopus laevis* Embryos during Early Development Using Atomic Force Microscopy

Miki Yamamoto¹, Takahiro Kotani¹, Takayoshi Yamamoto², Tatsuo Michiue³, Takaharu Okajima¹ (¹*Graduate School / Faculty of Information Science and Technology, Hokkaido University*, ²*Graduate School / Faculty of Education, Tokyo Gakugei University*, ³*Graduate School / Faculty of Arts and Sciences, The University of Tokyo*)

During embryogenesis, cells are regulated not only by gene expression and biochemical factors but also by mechanical forces. Direct measurement of mechanical properties at the single-cell level is thus essential for understanding morphogenetic mechanisms. In this study, we used atomic force microscopy (AFM) to investigate the stiffness and rheological properties of *Xenopus laevis* embryos during rapid cleavage stages. To ensure reliable contact with the AFM probe, we chemically removed the jelly coat and vitelline membrane, and immobilized embryos in custom agarose molds. Fluorescent labeling enabled regional identification. This approach revealed spatiotemporal heterogeneity in embryonic mechanics.

1GJ010 生体内 3D 温度計測技術の開発と応用
In vivo 3D thermometry by light-field fluorescent nanodiamond microscopy and deep learning

Yurina Nakane¹, Haruka Maeoka¹, Manami Takahashi², Kiichi Kaminaga², Hiroyuki Takuwa², Shin Usuki³, Ryuji Igarashi², Takuma Sugi¹ (¹*Graduate School of Integrated Sciences for Life, Hiroshima University*, ²*National Institutes for Quantum and Radiological Science and Technology*, ³*Research Institute of Electronics, Shizuoka University*)

To what extent is body temperature regulated at the single-cell resolution? In fluorescent nanodiamond-based spectroscopic thermometry, its blurred fluorescence due to Brownian motion in 3D space and time-consuming 3D scanning hamper accurate thermometry *in vivo*. We here establish *in vivo* 3D thermometry that achieves 10⁴ times faster than previous methods using scanless, high spatiotemporal resolution light-field microscopy and deep learning. Using this method, we discovered that heat diffusion is heterogeneous in *C. elegans*, particularly in dauer larvae. Furthermore, 3D thermometry of the cerebral cortex in a head-fixed mouse suggested that temperature fluctuates by up to 3.0 K in a feedback manner. Thus, we propose existence of *in vivo* cellular homeostasis regulation.

[1GJ011](#) Developing a label-free and non-destructive method to resolve single cell transition paths

Tobias Frick^{1,2}, Katsuyuki Shiroguchi¹ (*RIKEN Center for Biosystems Dynamics Research (BDR)*, ²*Osaka University*)

Understanding of cell state transition in a hypothesis free way over time is essential in many biological phenomena, such as cancer metastasis and differentiation. Imaging can follow cells over time but is limited to reducing cell state to a few molecules. Omics methods measure thousands of molecules but generally cannot follow cells over time. We use deep learning to combine imaging and omics to perform a non-destructive data driven approach which enables untargeted cell state measurements over entire single cell transitions. Using our developed cell picker, ALPS, we produced paired cell-image scRNA-seq data and trained models to infer cell states from bright-field cell images. We apply our method to a cancer metastasis model epithelial-to-mesenchymal transition (EMT).

[1GJ012](#) 透過型電子顕微鏡によるヒドラとグリーンヒドラの組織構造比較研究
Transmission Electron Microscopy Comparative Study of Histological Structure of Hydra and Green Hydra

Tomoki Yanase (*Information Engineering, Univ. Kyusyu kougyou*)

Hydra is the generic name for freshwater invertebrates belonging to the Hydraridae family of cnidarians, the hydrozoans. Here, we concentrated on the difference between the non-photosynthetic species, such as Hydra, and the photosynthetic species, such as Green Hydra. Ultra-thin sections was prepared from Hydra and green hydra samples. Cells and tissues of hydra and green hydra were observed using transmission electron microscopy (TEM) to compare tissue structures. TEM revealed more vacuoles and lysosomes in the hydra than in the green hydra. These vacuoles and lysosomes may have developed because, compared to green hydra, which can synthesize organic matter mainly through photosynthesis by its symbiont Chlorella, the more animal-like hydra needs to digest biomolecules.

[1EA001](#) 細胞サイズ液滴内における DNA 高次構造変化と局在・液滴物性の相関
Higher-order structure of DNA confined in cell-size droplets modulates its localization and droplet material properties

Takashi Nishio (*MolBis, AIST*)

Liquid-liquid phase separation has emerged as a fundamental organizing principle in cell biology, forming membraneless organelles with dynamic physical properties. Inspired by this, we investigated how the higher-order structure of DNA confined within cell-size droplets modulates both its intradroplet localization and the viscoelastic properties of the droplets by using an aqueous two-phase system. We found that tightly compacted DNA molecules were localized at the surface of microdroplets. In addition, the shape of microdroplets was changed depending on the spermidine concentration, which changes the higher-order structure of large DNA molecules. We will discuss our findings with quantitative analysis of the material properties of microdroplets.

[1EA002](#) Nuclease-induced stepwise photodropping (NISP) to investigate single-stranded DNA degradation behaviors of exonucleases and endonucleases

Hsiufang Fan (*National Sun Yat-sen University, Kaohsiung, Taiwan*)

We employed a fluorescence-based single molecule method called nuclease-induced stepwise photodropping (NISP) to measure the DNA degradation process in real-time. Using NISP, we successfully determined the DNA degradation rates of 6.3 ± 0.4 nucleotides (nt) s^{-1} and 2.0 ± 0.1 nt s^{-1} for MGME1 in the 5'-to-3' and 3'-to-5' directions, respectively. Moreover, the degradation behaviors of Mung bean nuclease (MBN), an ss-specific endonuclease, and λ -exonuclease, a double-stranded (ds) specific exonuclease, can be differentiated. Here, we demonstrate NISP as a powerful tool for investigating the ssDNA degradation behavior of nucleases at the single-molecule level.

1EA003 Modulation of RNA transcription through DNA condensates reactions' encapsulation as a model for Chromatin micro rheology studies

Nathan Evangelista¹, Takahiko Chimura², Masahiro Takinoue^{1,2,3} (¹*Dept. of Life Sci. and Tech., Inst. of Science Tokyo*, ²*Dept. of Comp. Sci., Inst. of Science Tokyo*, ³*Research Center for Autonomous Systems Materialogy (ASMat), Inst. of Integrated Research (IIR), Inst. of Science Tokyo*)

In structural biology, cell organization and compartmentalization has emerged as an interesting topic, with chromatin condensation and its impacts on DNA transcription being unclear questions. Here, we proposed the use of artificial and programmable DNA condensates as a potential model to study chromatin condensates properties. Our model is composed of a DNA triplex-based linker, which inserts the gene inside of different DNA condensates and a transcription is performed. We have successfully showed the enzymatic inhibition correlation to condensates micro rheology, underlying enzymatic activity effects upon lower diffusive systems, in a very promising tool towards the molecular mechanism of transcription inhibition in crowded environments.

1EA004 Dynamic assembly of complex hierarchical DNA polymer networks by biomolecular active agents

Farhana Afroze¹, **Richard James Archer**^{2,6}, Mahammad Mustakim³, Rakesh Das⁴, Arif Md. Rashedul Kabir¹, Yuuto Miura¹, Rubaya Rashid⁵, Tetsuya Hiraiwa³, Shin-ichiro M. Nomura², Shogo Hamada^{6,7}, Akira Kakugo^{1,5} (¹*Department of Chemistry, Hokkaido University, Sapporo, Japan.*, ²*Department of Robotics, Tohoku University, Sendai, Japan.*, ³*Institute of Physics, Academia Sinica, Taipei, Taiwan.*, ⁴*Max Planck, Institute for the Physics of Complex Systems, Dresden, Germany.*, ⁵*Department of Physics and Astronomy, Kyoto University, Kyoto, Japan.*, ⁶*Department of Computer Science, Institute of Science Tokyo, Yokohama, Japan.*, ⁷*Biomolecular Design Institute, CBI Research Institute, Tokyo, Japan.*)

Biological systems use active agents to chemically and mechanically assemble complex structures through multi-step energy dissipative processes. Inspired by this we demonstrate the in-vitro use of modified bioactive agents to dynamically assemble DNA into hierarchical networks by consuming chemical energy for synthesis and mechanical manipulation. Specifically, $\Phi 29$ DNA polymerase performs rolling circle amplification (RCA) on DNA-primed microtubules, generating long ssDNA. These are transferred to kinesin-coated surfaces, where ATP-driven microtubule motion stretches the DNA into fibrous morphologies. 2D networks arise from filament interconnection. This work showcases the utility of bioactive agents to form structurally complex microscale materials from the bottom up.

1EB001 FLIM による温度測定のために粘度応答を抑制した赤色蛍光温度計 Red Fluorescent Thermometer with Suppressed Viscosity Response for FLIM-based Thermometry

Takeru Yamazaki¹, Toshiko Yamazawa², Syuzo Hirata³, Satoshi Arai¹ (¹*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa Univ.*, ²*Core Research Facilities, The Jikei Univ. Sch. of Med.*, ³*Dept. of Eng. Sci., Univ. of Electro-Commun.*)

Fluorescence thermometry is a live-cell imaging method that visualizes temperature gradients in cells via fluorescence signals from temperature-sensitive nanomaterials. For this purpose, fluorescence lifetime imaging (FLIM) provides condition-independent microscopy, enabling quantitative temperature mapping with a single fluorophore. Previously, we developed green fluorescent thermometers for FLIM-based thermometry to visualize temperature increases in heat-producing cells. However, these thermometers also responded to intracellular viscosity, compromising measurement reliability. Herein, we designed and synthesized a red fluorescent thermometer with reduced viscosity sensitivity. Here, we demonstrate the applicability of this red thermometer in FLIM-based thermometry.

1EB002 The maturation state of dengue virus particles affects their structural dynamics and nanomechanical properties

Steven John McArthur, Kenichi Umeda, Noriyuki Kodera (*Nano Life Science Inst., Kanazawa Univ.*)

Dengue virus (DENV) maturation, though required for infectivity, is inefficient. Fully mature (smooth) and immature (spiky) virions are well-studied; however, despite their abundance, little is known about partially mature particles. Moreover, DENV sub-particle structural dynamics are enigmatic and nanomechanical properties are unknown. Here, we observe individual mature, partially mature, and immature DENV particles using high-speed AFM and 3D force mapping. We show that partially mature virions are highly dynamic, while immature virions show correlations in spike movement. We also find a maturation-dependent increase in stiffness as well as locally impaired recovery post-deformation. These findings provide insight into the biophysical nature of DENV maturation states.

1EB003 Comprehensive profiling of single-cell proteome based on 3D single-molecule imaging

Latiefa Kamarulzaman^{1,2}, Sooyeon Kim¹, Takuya Hidaka⁴, Yuichi Taniguchi^{1,2,3} (¹*Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University*, ²*Graduate School of Frontier Biosciences, The University of Osaka*, ³*Graduate School of Biostudies, Kyoto University*, ⁴*Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA), Vienna BioCenter (VBC)*)

Rapid advancement of single-cell technologies has transformed our understanding of cellular heterogeneity. Here, we introduced single-cell PAGE-PISA, a molecular-sensitive proteome analysis coupled with single-molecule fluorescence imaging. By labelling all proteins in single cells with fluorescent dyes, separating them by molecular sizes, and counting each protein with 3D single-molecule imaging, our method quantified 10⁷ protein copies per mammalian cell with the sensitivity to detect as few as 100 copies per species. Importantly, our single-cell proteome data strongly correlated with the expected developmental stages during cardiomyocyte differentiation. Altogether, single-cell PAGE-PISA offers comprehensive and unprecedented sensitivity for proteome profiling.

1EB004 Single aptamer-modified DNA origami nanopore for specific chemical detection

Hiromu Akai, Kan Shoji (*Nagaoka University of Technology*)

Nanopore sensors, which can electrically detect analytes, attract attention as a single-cell secretion measurement technique due to their high spatiotemporal resolution and label-free measurement. Although the single-cell secretion was measured using aptamer-modified glass nanopipettes, the temporal resolution was not enough to observe cell secretion in real-time due to the long time to equilibrate the interaction between numerous aptamers and analytes. Here, we propose a hybrid nanopore sensor, which is a glass nanopipette trapping a DNA origami nanopore modified with a single ATP-binding aptamer. In this paper, we designed an aptamer-modified DNA origami nanopore that can open/close the pore entrance in response to ATP, and evaluated the ATP responsivity.

1EB005 Pixel-Wise Deconvolution of Antibody Binding Kinetics Enables Visualization of Instantaneous Secretion Dynamics

Zhuohao Yang¹, Takashi Kamatani², Mai Yamagishi³, Nobutake Suzuki¹, Yuto Kurisu⁴, Takashi Funatsu^{1,5}, Yasuyuki Ozeki¹, Yoshitaka Shirasaki¹ (¹*RCAST, Univ. Tokyo*, ²*Inst. Integrated Res., Inst. Sci. Tokyo*, ³*Live Cell Diagnosis, Ltd.*, ⁴*Grad. Sch. Pharm. Sci., Univ. Tokyo*, ⁵*Grad. Sch. Integrated Sci. for Life, Hiroshima Univ.*)

Cells communicate through the secretion of humoral factors. While several methods visualize secretion in real time, most rely on fluorescent immunoassays, where signals are temporally accumulated and delayed due to antibody binding kinetics. In this study, we modeled this binding behavior and developed a pixel-wise image processing method using temporal differentiation and deconvolution. This enabled high-resolution reconstruction of momentary secretion events. We visualized dynamic secretion events such as IL-1 β release during cell death and CTL-mediated secretion toward cancer cells at single-cell resolution. This method provides a new strategy to understand cell-cell communication.

1EC001 細胞内再構成アプローチによるドーパミンシナプス小胞の形成機構の解析

Distinct synaptic vesicle populations in dopaminergic neurons: insights into organization and sorting by *in cellulo* reconstitution assay

Kenshiro Fujise¹, Nisha Mohd Rafiq², Pietro De Camilli³, Atsushi Saito¹ (¹*Dept. FSIR, Faculty of Medicine, Kanazawa Univ.*, ²*IFIB, Univ Tübingen, Germany*, ³*Dept Neurosci, YSM, Yale Univ, USA*)

Impairment of dopaminergic (DA) neurons is linked to several neuronal diseases, highlighting the need to clarify their molecular and morphological features. Accumulated evidence suggests DA neurons contain distinct synaptic vesicle (SV) types that differ in neurotransmitter content and exocytotic regulation. However, their ultrastructural features remain poorly understood. Here, we show axonal varicosities in iPSC-derived DA neurons possess classical 40nm SVs and VMAT2-positive larger pleomorphic vesicles. Additionally, we reconstitute large vesicle clusters by co-expression of synapsin and VMAT2, which segregate from typical 40nm SV clusters and require adaptor protein AP3, indicating DA SVs exhibit distinct size, localization, and sorting mechanisms.

- 1EC002** 「遅い」キネシンから「速い」キネシンへのギアチェンジにより実現される高速・高効率な軸索輸送メカニズム
Gear change to go through: Cooperation of two different kinesins enables fast and efficient axonal transport

Kanako Iwasaki^{1,2}, Mitsuhiro Iwaki^{2,3}, Yasushi Okada^{1,2} (¹*Grad. Sch. Med., Univ. Tokyo*, ²*BDR, Riken*, ³*NICT*)

Kinesin-1 and kinesin-3 are key players in anterograde axonal transport. Amyloid precursor protein (APP), one of the cargos of kinesin-1, is delivered at faster velocities than single-molecule velocity of kinesin-1 *in vitro*. The mechanism of this acceleration is unknown. This study revealed that kinesin-1 and kinesin-3 cooperatively transport APP. Knockdown and reconstitution assays showed kinesin-1 is required for APP to go through axon initial segment and kinesin-3 is important to achieve fast transport velocity. Further *in vitro* evaluations suggest that switching between two kinesins is mechanically regulated by cytoplasmic environments. This study demonstrates a general mechanism of fast and efficient axonal transports and updates the view of multimotor cooperation.

- 1EC003** がん細胞の増殖と免疫逃避を担う、液状ナノ信号プラットフォームの発見
Nano-liquid signaling platform responsible for both cancer cell growth and immune evasion

Taka-aki Tsunoyama¹, Christian Hoffmann², Daiki Sasaki¹, Bo Tang¹, Koichiro M Hirotsawa³, Yuri L Nemoto⁴, Rinshi S Kasai⁵, Takahiro K Fujiwara⁶, Kenichi GN Suzuki^{3,5,6}, Reinhard Fässler⁷, Hiroki Ishikawa¹, Dragomir Milovanovic², Akihiro Kusumi^{1,6} (¹*OIST*, ²*DZNE*, ³*IGCORE, Gifu Univ.*, ⁴*Biosig. Res. Cent., Kobe Univ.*, ⁵*Div. Adv. Bioimag., Natl. Cancer Cent. Res. Inst.*, ⁶*WPI-iCeMS, Kyoto Univ.*, ⁷*Max Planck Inst. Biochem.*)

Advanced single-molecule imaging identified a nanoscale (≈ 34 nm), liquid-like signaling platform, iTRVZ, which integrates the signals of RTKs and GPI-anchored receptors: Upon simultaneous PDGFR and CD59 stimulation, the PLC γ -IP₃-Ca²⁺ signal was cooperatively amplified. iTRVZ mainly consists of Integrins, Talin, RIAM, VASP, and Zyxin, and is a nanoscale condensates formed via zyxin's LLPS, with further interactions with the inner plasma membrane surface prewet with lipid rafts, PI(4,5)P₂, and actin filaments. iTRVZ is required for CD59-mediated protection from complement attack. In mice, iTRVZ was essential for enhancing CD59 functions, leading to tumor growth. These results identify iTRVZ as a crucial site responsible for both cell growth and immune evasion.

- 1EC004** 拍動心筋サルコメアに潜む秩序とカオスの動的恒常性
Localized Chaos within Periodic Beating of Cardiomyocyte Sarcomeres: Evidence for Chaordic Homeodynamics

Seine A. Shintani^{1,2,3} (¹*Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University*, ²*Center for Mathematical Science and Artificial Intelligence, Chubu University*, ³*Institute for Advanced Research, Nagoya University*)

Cardiomyocyte sarcomeres generate hyperthermal sarcomeric oscillations (HSOs) that keep a constant period while amplitude and phase wander chaotically. High-speed SL-nanometry (3 nm, 500 fps) captured these waves; recurrence quantification and Lyapunov analyses gave a positive maximal exponent (0.17 step⁻¹), DET > 0.99, and surrogate $p < 0.01$, proving deterministic chaos. Yet the period's coefficient of variation was ~ 1 %. Simultaneous imaging showed spontaneous phase flips between adjacent sarcomeres, flattening global tension and stabilizing beating. I will present these quantitative markers of "Chaordic Homeodynamics", discuss how local chaos enhances robustness, and outline plans to couple cryo-EM snapshots with oscillation states.

- 1ED001** 浸透圧を利用して出芽型分裂するベシクル系の開発
Osmotic spawning vesicle

Minoru Kurisu, Masayuki Imai (*Dept. Physics, Grad. Sch. Sci., Tohoku Univ.*)

We discovered a cascade vesicle division system driven by osmotic inflation. Giant unilamellar vesicles (GUVs) composed of AOT and cholesterol were subjected to an osmotic pressure difference by encapsulating sucrose solution in an external glucose solution containing additional AOT molecules. This simple setup enabled the mother GUVs to repeatedly form small membrane buds and undergo fissions, resulting in the production of 30–300 daughter GUVs from one mother GUV. This "osmotic spawning" behavior of GUVs does not rely on chemical reactions or functional macromolecules. Therefore, this cascade division system is compatible with various chemical systems and has the potential to implement reproduction ability in artificial cells, drug delivery systems, and protocells.

1ED002 PDA-Based Microfluidic Sensor for pathogenic bacteria Detection

Bratati Das, Kaori Sugihara (*Institute of Industrial Science, The university of Tokyo*)

We present a polydiacetylene (PDA)-based microfluidic sensor for rapid, label-free, colorimetric detection of pathogenic bacteria. PDA exhibits a blue-to-red color shift in response to surface interactions or mechanical stress. In the device, PDA films are integrated within a microfluidic channel, where fluid flow generates shear forces. Bacterial interactions with the PDA surface trigger a visible color change, amplified by mechanical stress. This response is easily quantified with digital imaging or spectral analysis, without complex instruments. The system is portable, cost-effective, and adaptable to different bacterial targets, offering a simple, real-time diagnostic solution.

1ED003 グラフによる生態系の定常分布と応答の表現

Diagrammatic expressions for steady-state distribution and static responses in population dynamics

Koya Katayama, Ryuna Nagayama, Sosuke Ito (*Dept. of Phys., U Tokyo*)

Understanding the mean fitness and steady-state distribution of a biological population is essential because they reflect how well the whole population or each trait adapts to the environment, respectively. In this presentation, we study a simple model of evolvable populations and present diagrammatic expressions for the steady-state distribution and static responses of mean fitness [1]. As applications, we propose practical methods to approximate static properties when either mutation or natural selection has a dominant effect. Our results allow us to predict static responses of mean fitness using only measurable quantities. Moreover, they offer a graph-theoretic framework for analyzing static properties in population dynamics.

[1] arXiv:2505.11296

1ED004 界面活性剤の自己集合化による水面に浮かぶ油滴の自律的な振動

Spontaneous oscillation of oil droplets on water surface by self-assembly of surfactants

Ai Kohata¹, Yuhei Yamada², Shingo Maeda^{2,3}, Kazushi Kinbara^{1,2} (¹*Sch. Life Science and Technology, Science Tokyo*, ²*ASmat, IIR, Science Tokyo*, ³*Sch. Mechanical Engineering, Science Tokyo*)

Cells convert chemical energy to mechanical energy by restructuring their cytoskeletons, enabling them to move, deform, and divide. For studying these mechanisms, droplets that autonomously drive themselves while consuming energy have garnered attention as simple yet useful models. There is room for discussion regarding models that can comprehensively explain spontaneous non-linear oscillations taking into account the properties of actual substances.

In this study, we introduce the non-linear oscillations of oil droplets floating on a water surface, coupled with the self-assembly of positively- and negatively charged surfactants. We report on the mechanism and theoretical model of the oscillating phenomena.

1EE001 親和性を越えて：ペプチドの親和性と生物学的機能との関係性の解明

To Affinity and Beyond: Investigating the Relationship Between Peptide Affinity and Biological Functions

Jelang Muhammad Dirgantara¹, Takuto Nogimori², Kazuma Kiyotani³, Takuya Yamamoto², Suyong Re¹ (¹*Laboratory of In Silico Design, Artificial Intelligence Center for Health and Biomedical Research, National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan*, ²*Laboratory of Precision Immunology, Center for Intractable Diseases and ImmunoGenomics, National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan*, ³*Laboratory of Immunogenomics, Center for Intractable Diseases and ImmunoGenomics, National Institute of Biomedical Innovation, Health and Nutrition, Osaka, Japan*)

In the early twentieth century, German scientist Paul Ehrlich introduced a paradigm that has guided pharmaceutical development: *corpora non agunt nisi fixata*—a substance will not act unless bound to its target. However, clinical observations increasingly reveal that peptide–target binding affinity alone often fails to predict biological efficacy, largely due to the flexible and dynamic nature of peptides. In this study, we present a high-resolution, integrative pipeline combining **machine learning**, **molecular simulations**, and **experimental data** to predict peptide efficacy. We showcase its application in the design of peptide-based protein–protein interaction inhibitors and in predicting **T cell receptor activation** for epitopes.

[1EE002](#) Bayesian Inference of the Transport Mechanism of the $\text{Zn}^{2+}/\text{H}^{+}$ Antiporter YjiP from Microscale Thermophoresis and Simulations

Shujie Fan¹, David L. Stokes³, Oliver Beckstein² (¹*Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences*, ²*Dept. of Physics, Arizona State University*, ³*Dept. of Cell Biology, NYU School of Medicine*)

We studied the $\text{Zn}^{2+}/\text{H}^{+}$ antiporter YjiP using Bayesian inference of a thermodynamic model informed by microscale thermophoresis (MST) and constant pH molecular dynamics (CpHMD) data. MST measured pH-dependent Zn^{2+} binding at the transport site, while CpHMD provided initial pKa estimates for Zn^{2+} -binding residues. Microscopic parameters were inferred using Differential Evolution Markov Chain Monte Carlo. The model suggests possible transport stoichiometries and predicts ion binding behavior under membrane potential. We also discuss the limitations of MST in resolving detailed microscopic mechanisms of the $\text{Zn}^{2+}/\text{H}^{+}$ antiporter.

[1EE003](#) An Integrative Computational Framework Using Sequence, Structural, and Functional Analyses to Predict Novel Pathogenic Troponin C Mutants

Pooja Pradipta Bandyopadhyay (*School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi- 110067*)

Muscle contraction is regulated by Ca^{2+} binding to troponin C (TnC) and single mutation can lead to cardiomyopathy. To bridge the gap between disease causing mutants and their mechanism, we developed an integrative pipeline that combines experimental binding affinity (BA), structural modeling, and sequence analysis. We curated 24 experiment mutants BA and developed an optimized protocol that shows correlation of 0.87. From the statistical probability model, 61 novel mutants were identified as potentially causing disease. Analysis of all mutants (76) revealed that BA, functionally critical region, substitution type are key determinants of pathogenicity. We develop a predictive model using these features and it achieve 75% concordance with the benchmark model.

[1EE004](#) 演題取り下げ Withdrawn

[1EE005](#) Learning Transcription Machinery from Minimal Model, Molecular Dynamics, Genome Profiling, and Directed Evolution

Carmen Masri¹, Biao Wan², Liqiang Dai², Chao E³, **Jin Yu**¹ (¹*Department of Physics and Astronomy, University of California-Irvine, USA*, ²*Wenzhou Institute, UCAS, Wenzhou, Zhejiang, China*, ³*Beijing Computational Science Research Center, Beijing, China*)

Combining minimal model construction with molecular dynamics simulations from atomic to coarse-grained level, along with stochastic dynamics/kinetic approach and machine learning methods, we have derived transcription factor (TF) target search diffusion/association free energy landscape around DNA binding sites with flanking sequences, and zoomed into structural dynamics detail of eukaryotic TF domain and dimeric TFs for stepwise 1D search along DNA with sequence recognition. We also studied mechanochemical and fidelity control of RNA polymerases (RNAPs). We particularly investigated a phage RNAP on its DNA promoter recognition and switching recognition from one promoter to the other following the path of lab directed evolution.

3HL0900 NARAKITA 放置竹林拡大問題解決プロジェクト～竹コンポスト開発への道のり～
NARAKITA Project to Address the Expansion Abandoned Bamboo Forests: The Road to
Bamboo Compost Development

Rento Oimoto, Aruno Tani, Kazuma Taguchi, **Keita Nakamura**, Yuka Yamamoto, Yunosuke Kono, Nahoko Takeuchi
(*Nara Prefectural Narakita Senior High School*)

To address the issue of the expansion of abandoned bamboo forests, we conducted a study on the development of bamboo compost. Bamboo-degrading fungi were screened from bamboo stumps, and their CMC-degrading activity was investigated. A large number of colonies formed on agar medium inoculated by stamping bamboo stumps (with bamboo powder as the sole carbon source), and six strains with a high frequency of colony formation were isolated. Among them, two strains exhibited CMC-degrading activity. We are currently planning to measure the CMC-degrading activity of culture supernatants using liquid media and to conduct preliminary experiments on bamboo composting using these candidate fungal strains. We also intend to report the results of these ongoing studies.

3HL0915 チャコウラナメクジのカフェインに対する忌避反応を用いた作物への食害防除
Prevention of crop damage using *Ambigolimax valentianus*' repellent reaction to caffeine

Yuma Takahara, Kaito Iinuma, Gaku Shiomi (*Nara Prefectural Narakita Senior High School*)

Ambigolimax valentianus is known to dislike bitterness and to perform associative learning, which links its dislike to other behaviors. We used caffeine as a bitter agent to protect crops from slugs, and studied the effects of caffeine on crops and whether associative learning occurs with caffeine. The results showed that a 0.5% caffeine solution did not affect the growth of leaf lettuce. In the associative learning experiment using caffeine, it was found that the learning memory remained even after 24 hours exposure to a 1% caffeine solution. Currently, we are conducting experiments on the effects of a 1% caffeine solution on leaf lettuce and whether slugs prefer leaf lettuce that has been sprayed with caffeine or leaf lettuce that has not been sprayed with caffeine.

3HL0930 奈良学園の里山における地下水と植生の関係
Investigation the relationship between the distribution of the groundwater and the ground
vegetation at satoyama in Naragakuen High School

Ataru Tezuka, Haruto Yasuda, Takayoshi Hazama, Yuki Nishida (*Naragakuen High School*)

At satoyama in Naragakuen High School, the direction of the groundwater was changed because of having dug the well for the research. For this reason, the population of the rare plants may decrease. Therefore, we have decided to make the map of the groundwater in Naragakuen High School, and to investigate the relationship between the distribution of the groundwater and the ground vegetation. We investigated the distribution of the groundwater with the Wenner's Four Electrodes Arrangement and checked the depth and the direction of the groundwater. We installed quadrat (the frame of 50cm square) in the investigated place and made the investigation into vegetation by checking the sort and the quantity of the plants in the frame.

3HL0945 深部静脈血栓症の発生病因子の定量的評価
Quantitative Evaluation of Risk Factors for Deep Vein Thrombosis

Yurina Takase (*Nishiyamato Gakuen High School*)

[Introduction]

Deep vein thrombosis is caused by clot formation in deep veins, often in the legs, and can lead to fatal pulmonary embolism. Although Virchow's triad explains the risk factors, the role of each, especially stasis, remains unclear.

[Method]

To examine stasis-induced thrombosis, *Xenopus laevis* was used. Leg vein was compressed to induce pooling.

[Result]

Dissection confirmed leg veins are suitable for inducing stasis. One leg was compressed with surrounding tissue and fixed after one hour. Thrombus was not clearly identified, but stasis was achieved.

[Discussion]

These findings suggest *Xenopus* is a useful model for studying venous stasis. Further histological analysis is needed to verify thrombus formation and investigate the underlying mechanisms.

3HL1000 プラナリアの再生における活性酸素の二面的機能の評価 Evaluation of the Dual Functions of Reactive Oxygen Species in Planarian Regeneration

Yui Takashima, Soma Yamada, Ruikinshinn Ou (*Nishiyamato Gakuen High School*)

[Introduction]

Planaria are known for their high regenerative capacity. Reactive oxygen species (ROS) are involved in regeneration signaling, but their temporal roles remain unclear.

[Method]

We applied ascorbic acid (Asc), a ROS scavenger, to regenerating planaria during early, mid, or late phases. Regeneration rates were assessed on day 14.

[Result]

Asc treatment in the early or late phase had no significant effect. However, mid-phase treatment enhanced regeneration.

[Discussion]

These findings suggest a stepwise model: ROS are required in early regeneration, become unnecessary but persistently present—and possibly harmful—in the middle, and are cleared in the late phase. ROS thus play dual roles depending on timing, promoting and later impairing regeneration.

3HL1015 学校設備を用いた酵母菌 (*Saccharomyces cerevisiae*) のコールドスリープ条件の検討 Investigation of conditions for the freeze tolerance of *Saccharomyces cerevisiae* using school facilities

Kosuke Takagi, Shosei Tsuji, Kazuma Nishiki, Shota Hamada, Xiaomi Ruan (*Nishiyamato Gakuen High School*)

[Introduction]

Freeze tolerance occurs in various organisms. A recent study revived nematodes from 46,000-year-old permafrost. While molecular mechanisms are being revealed, effects of abiotic factors remain unclear.

[Method]

We assessed the effect of glycerol, out of cell, on freeze tolerance in *Saccharomyces cerevisiae*. Cells were frozen in solutions with varying glycerol levels and plated on agar for viability.

[Result]

Moderate concentrations of glycerol improved post-freeze cell survival. However, both low and high concentrations of glycerol reduced cell viability.

[Discussion]

These results indicate an optimal glycerol concentration enhances freeze tolerance in *S. cerevisiae*, while excess is harmful. Abiotic factors like solute concentration are key in freeze survival.

3HL1030 葛乳酸菌と植物性ミルクでヨーグルトをつくる ~完全なゲル化を達成する条件の検討~ Make yogurt with kudzu lactobacillus and plant milk~Investigation of conditions to achieve complete gelation~

Momoka Okuda, Akari Kawasaki, Saya Kawamoto (*Nara Prefectural Seisho Senior High School*)

Previous studies was concluded that it is impossible to make yogurt from plant-based milk other than soy milk using kuzu lactic acid bacteria. Therefore, the purpose of this experiment is to produce yogurt using almond milk by changing the amount of sugar, the amount of lactic acid bacteria, and the temperature. To check if yogurt was made, we measured the viscosity of the yogurt and pH.

The experiment showed that the pH decreased, regardless of whether sugar was added or not, and regardless of the amount of sugar or lactic acid bacteria added. However, no gel was formed. This suggests that lactic acid was produced, but the protein did not solidify. We believe the reason is related to the type or the amount of protein.

3HL1045 ヤマトマナの高亜鉛化 The increasing zinc content of Yamatomana and the number of days of zinc treatment

Saya Shimamura, Yuya Sakaguchi, Eri Yoshikawa, Ayumi Tanabe (*Nara Prefectural Seisho Senior High School*)

To address zinc deficiency and preserve the traditional vegetable "Yamatomana", we increased its zinc content. We determined the optimal duration of zinc treatment to increase zinc content without affecting the growth of Yamatomana.

The plants were grown hydroponically for 6 weeks. The zinc concentration was adjusted to 5 ppm, after which the plants were grown for 3, 7 or 14 days before harvest. The zinc content of Yamatomana increased in all plots. Longer treatment durations led to higher zinc content. Chlorophyll content was lower in the 14-day treatment than in the other treatment durations. These results suggest that plant growth was inhibited.

Based on these results, we determined that the optimal duration of zinc treatment for Yamatomana is 7 days.

[3HL1100](#) アンモニア中のバクテリアの行動の観察
Observation of Bacterial Behavior in Ammonia

Ryohei Kouta, Kazuki Hondou, Riku Hamada, Shunichi Nakada (*Komatsu high school*)

Our school's men's restroom often has an unpleasant odor due to heavy use. We found that ammonia, produced from urea in urine, is a major cause. To reduce this odor, we focused on bacteria that decompose ammonia and observed their activity and movement under a microscope during the process. We also examined how bacterial motion changes with ammonia concentration by using solutions of different pH. This allowed us to investigate collective behaviors and responses to environmental conditions. This study aims to understand how ammonia levels affect bacterial motility and to identify optimal conditions for efficient ammonia breakdown.

[3HL1115](#) タンパク質の主鎖原子の温度因子が高いとペプチド結合が歪みすぎてしまう？
When the temperature factor of the main chain atoms in a protein molecule is high, does the peptide bond become more twisted?

Akari Shimada¹, Mahan Kunit¹, Toshiyuki Chatake², Takashi Ohhara³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*KURNS, Kyoto Univ.*, ³*J-PARC, JAEA*)

Peptide bonds in small molecules in water exhibit a planar structure due to electronic resonance. In contrast, we proposed a site-specific relaxation model for peptide bonds caused by the intramolecular electrostatic potential in proteins (Chiba et al., *Protein Science*, 2023). To investigate the extent to which this phenomenon occurs in protein molecules, we examined all protein data in the Protein Data Bank (PDB). We investigated the proportion of distorted peptide bonds within a single molecule and examined the resolution dependence. We found that the frequency of distortion tended to increase in molecular models obtained from data with low resolution. We report on the relationship between this phenomenon and temperature factors.

[3HL1130](#) β バレル型タンパク質の生合成におけるループの DGG 配列がもつ折り目効果
ORIME effect of the DGG sequence on the loop in the biosynthesis of β -barrel proteins

Daiki Tagami¹, Hiromu Ohshima¹, Masaru Hoshino², Nobuhiro Suzuki³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll.*, ²*Pharm., Kyoto Univ.*, ³*NARO*)

In a protein molecule, the peptide bond planarity is relaxed specifically (Chiba et al., *Protein Science*, 2023). Based on the hypothesis that such a soft peptide bond is placed at the loop to fold the β -strand in an ideal position during β -protein biosynthesis, we have performed substitution experiments between two acidic amino acids, Asp and Glu (Chiba, 1MSB05). Results showed that replacing an Asp on a loop between two beta structures with Glu, which has a shorter side chain, reduces the softness of the main chain (ORIME effect) and drastically reduces the biosynthetic yield in *E. coli*. In this study, amino acid substitution experiments were performed to investigate the ORIME-effect of DGG sequences between two loops of the red fluorescent protein, mCherry.

1Pos001 Mutation Effect of Terpene Cyclase CotB2 Revealed by Ambient Temperature Crystallography

Atika Nur Rochmah¹, Takaaki Fujiwara¹, Tomohiko Kuzuyama², Eriko Nango¹ (¹*Grad. Sch. Sci., Univ Tohoku*, ²*Grad. Sch. Agr. Life. Sci., Univ. Tokyo*)

Terpenes are one of the most structurally diverse organic compounds with various functions, such as vitamins, drugs, and flavorings. In nature, the synthesis of terpenes is catalyzed by terpene cyclase from their linear precursors. Due to its high potential, terpene cyclase attracts considerable interest in protein design to search for a novel terpene. To date, such protein design is based on cryogenic structures of proteins, even though cryogenic conditions can hide some conformations essential for catalysis. Here, we compare the crystal structure of CotB2 mutants obtained at cryogenic and ambient temperatures to gain some insights into its catalysis.

1Pos002 クライオ電子顕微鏡を用いたヒトパネキシン 3 チャンネルの脂質ナノディスク中での構造解析
Cryo-EM structure of human Pannexin-3 in lipid nanodiscs

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Human Pannexin-3 (Panx3) forms a nonselective, single membrane channel in vertebrates. In osteoblasts, it is reported that Panx3 channels are involved in osteogenic differentiation by allowing the passage of ATP and Ca²⁺ at the plasma membranes and endoplasmic reticulum membranes. In this study, human Panx3 channels are reconstituted in lipid nanodiscs, followed by single particle analysis using cryo-electron microscopy. A structure of the heptameric human Panx3 channel was determined at 2.95Å resolution. Densities corresponding to lipid acyl chains are found at the interfaces between adjacent subunits, and double-layer densities along the membrane plane are observed inside the channel pore, suggesting that Panx3 channels adopt a gating mechanism using lipid molecules.

1Pos003 生細胞内での近接ラベリング法で検出された RAF 複合体の分子構成
Molecular composition of RAF kinase complexes in living cells revealed by proximity labeling

Kenji Okamoto, Yasushi Sako (*RIKEN PRI*)

RAF kinases are critical components of the RAS-MAPK signaling pathway, which transduces signals from membrane receptors such as the epidermal growth factor receptor (EGFR) to downstream effectors. RAF proteins are thought to undergo conformational changes and dimerization for activation, while forming complexes with other proteins. However, their molecular dynamics remain poorly understood. To elucidate the molecular composition of RAF-containing complexes in living cells, we applied TurboID-based proximity labeling (PL) to RAFs. As a result, MEK1/2 were identified as the most enriched interactor of both CRAF and BRAF, while 14-3-3s, HSP90 and CDC37, which are thought to be structural partners of RAF complexes, showed weaker signals.

1Pos004 Structural rearrangement of DNMT3B driven by histone modifications stimulates its DNA methylation activity

Cho Chao-Cheng¹, Chu Woei-Chyn², **Hanna S. Yuan¹** (¹*Academia Sinica*, ²*National Yang Ming Chiao Tung University*)

DNA methyltransferase 3B (DNMT3B) plays a vital role in shaping DNA methylation patterns during mammalian development. DNMT3B is intricately regulated by histone modifications, however, the precise interplay mechanism between DNA methylation and histone modifications remained elusive. Here, employing small-angle X-ray scattering (SAXS), we reveal that the regulatory PWWP and ADD domains within the DNMT3B-3L complex exhibit remarkable flexibility. In the presence of the H3 peptide, both PWWP and ADD domains undergo a transition from auto-inhibitory to active conformations. This study thus unveils the underlying mechanism by which histone H3 modifications induce conformational rearrangement in DNMT3B, ultimately unleashing its enzymatic activity in DNA methylation.

1Pos005 Structural insight into the mechanism of amyloid fibril formation by hen egg-white lysozyme

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Several human diseases, including Parkinson's disease and Alzheimer's disease, are characterized by the abnormal formation of insoluble protein fibrils known as amyloid. The mechanism of amyloid fibril formation by precursor proteins in many hereditary types of amyloidosis remains unresolved due to a lack of detailed experimental structural information. Here we show a model of amyloid fibrils of hen egg-white lysozyme (HEWL), solved by cryo-EM at 2.3 Å resolution. The structure forms intramolecular π -stacking between amino acids, and all four disulfide bonds present in the globular HEWL structure are conserved in the amyloid. This amyloid model provides new insights that help to explain the mechanism of fibril formation.

1Pos006 集光アンテナ複合体であるフィコビリソームの高分解能構造解析に向けた取り組み Approaches to high-resolution structural analysis of the phycobilisome, a photosynthetic light-harvesting antenna complex

Yuya Fujita^{1,2}, Soichiro Seki², Akihiro Kawamoto^{1,2}, Yuu Hirose³, Genji Kurisu^{1,2} (¹*The University of Osaka, Grad. Sch. Engineering, Japan*, ²*The University of Osaka, Institute for Protein Research (IPR), Japan*, ³*Toyohashi University of Technology, Grad. Sch. Engineering, Applied chemistry and Life science, Japan*)

Red algae utilize phycobilisomes (PBSs) as antenna to capture light energy and transfer it to photosynthetic reaction centers. PBS consist of bilin-binding proteins and linker proteins. To optimize the light-harvesting efficiency under diverse light conditions, red algae adjust the composition of bilins and linkers. High-resolution structural analysis of PBS is essential to understand their diverse light-harvesting strategies. Although structural analysis has been performed by Cryo-EM, local resolution remains limited due to preferred particle orientation. We isolated PBS from a thermophilic red alga *Cyanidioschyzon merolae* and considered grid preparation and data collection conditions for obtaining high-resolution structure.

1Pos007 Co-crystal structure of a human 8-oxoguanine DNA glycosylase with photocaged substrate toward time-resolved crystallography

Momoko Yumita¹, Tomoki Imura¹, Yuhei Hosokawa², Kai-Chun Yang², Hsuan-Yu Shih², Manuel Maestre-Reyna², Junpei Yamamoto¹ (¹*Graduate School of Engineering Science, Osaka University Department of Chemistry*, ²*National Taiwan University*)

DNA in all living beings is damaged by various agents. Such DNA damage can lead to mutagenesis and carcinogenesis and thus needs to be repaired by various enzymes.

The aim of this study is to visualize DNA repair reactions at atomic resolution by time-resolved serial femtosecond X-ray crystallography (TR-SFX). However, due to the characteristics of TR-SFX, where the reaction is triggered by light, its application has been limited to light-dependent reactions. Human 8-oxoguanine DNA glycosylase (hOGG1) is an enzyme responsible for initiating light-independent DNA repair. We crystallized hOGG1 in complex with photocaged DNA and solved the dark-adapted and light-activated structures of the complex, where the uncaged DNA damage was accommodated into the active site.

1Pos008 Structural basis for the mechanisms of complex assembly by the Influenza A virus nucleoprotein and importin

Haruka Umezawa (*Yokohama City Univ., Medical Life Science, Drug Design Lab.*)

The viral genome RNA of the influenza A virus is encapsulated within a ribonucleoprotein (RNP) complex. Within this complex, NP encapsulates viral RNA and promotes transcription and replication. NP contains a nuclear localization signal (NLS) that interacts with importin- α 5 and facilitates its transport into the nucleus. To elucidate the nuclear transport mechanism of NP, we determined the 3.7 Å resolution structure of the human importin- α 5/NP complex by electron microscopy. In the model, NP forms a 1:1 complex with importin- α 5. In addition, the loop of NP undergoes significant structural changes upon binding to importin- α 5, leading to steric hindrance in NP trimer formation. This structural information may contribute to the development of antiviral drugs.

1Pos009 巨大マルチドメインタンパク質の構造予測
Structure prediction of large multidomain proteins

Ryota Kobayashi¹, Suguru Fujita¹, Yoshitaka Moriawaki², Tohru Terada¹ (¹*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*,
²*Med. Res. Lab., Inst. Integr. Res., Science Tokyo*)

Although AlphaFold2 (AF2) can accurately predict the structures of proteins from their amino acid sequences, it has a limitation on the sequence length of around 3,000 residues. The structures of the long-sequence proteins should be composed of multiple structural domains of several hundred residues. Some structural domains interact with the other domains only weakly and are therefore considered to evolve independently. Under this consideration, we developed a method to predict the structures of large multidomain proteins by decomposing them into structurally independent fragments of shorter than 2,000 residues. The fragment boundaries were determined based on graph clustering of predicted aligned errors and the structure of each fragment was predicted by AF2.

1Pos010 Improved Resolution of *Enterococcus hirae* V-ATPase by cryo-EM: Structural Insights into the Full Complex

Yuan-E Lee¹, Raymond N. Burton-Smith^{1,2}, Akihiro Otomo^{2,3}, Kano Suzuki⁴, Tsukasa Nakamura⁵, Toshio Moriya⁵, Takeshi Murata⁴, Ryota Iino^{2,3}, Kazuyoshi Murata^{1,2} (¹*ExCELLS/NIPS, Okazaki*, ²*SOKENDAI, Okazaki*, ³*IMS, Okazaki*, ⁴*Chiba University, Chiba*, ⁵*KEK, Tsukuba*)

Enterococcus hirae vacuolar-type ATPase (EhV-ATPase) is an ATP-driven Na⁺ pump that enables bacterial survival under alkaline conditions. Although previous cryo-EM studies provided insights into the overall structure of the EhV-ATPase, the resolution is insufficient to address the detailed mechanism of Na⁺ transport, especially the coupling between ATP hydrolysis in the cytoplasmic V₁ domain and ion movement in the transmembrane V_o domain. Here, we present high-resolution cryo-EM structures of LMNG-solubilized EhV-ATPase in conformationally distinct nucleotide-bound states. The improved resolution reveals structural details of the full protein complex, providing insights into the conformational transitions between the catalytic V₁ domain and the ion-transport V_o domain.

1Pos011 Crystal structure elucidation of *Rubricoccus marinus* halorhodopsin

Naithok Khachuk Debbarma¹, Takaaki Fujiwara^{1,2}, Eriko Nango^{1,2} (¹*Grad. Sch. Life Sci., Univ. Tohoku*,
²*IMRAM, Univ. Tohoku*)

Microbial rhodopsin is a photoreceptive membrane protein where the photoisomerisation of retinal drives various processes in the organism, including light-driven ion pumping. Recently, it was found that a marine bacterium, *Rubricoccus marinus*, has an inward chloride ion pumping rhodopsin (RmHR) containing a TSA motif. Here we present the crystal structure of RmHR in resting state and shows its structural characteristics, including the key residues involved in the chloride ion pumping mechanism.

1Pos012 Kinetic Analysis of heparin-induced fibrillation of α -synuclein

Takashi Ohgita, Norihiro Namba, Nao Minami, Hiroyuki Saito (*Kyoto Pharm. Univ.*)

In Parkinson's disease, α -synuclein (α S), an intraneural intrinsically disordered protein, deposits as amyloid fibrils. Heparin, a homolog of heparan sulphate found on cellular surfaces, induces α S fibrillation. This study aimed to investigate the mechanism behind heparin-induced α S fibrillation. The results showed that heparin increased the mass of fibrillar α S, leading to the formation of longer fibrils in a concentration-dependent manner, and suggested that the α S fibrillation is a reversible process. Kinetic analysis of the time-traces for heparin-induced α S fibrillation using a model considering reversibility indicated that heparin promotes the growth of α S fibrils by favoring fibril elongation over dissociation.

1Pos013 Rose Bengal を用いたタンパク質凝集プロセスの評価
Evaluation of Protein Aggregation Process Using Rose Bengal

Gen Takebe¹, Shigetoshi Okazaki¹, Heidi Ottevaere² (¹*Hamamatsu Photonics K.K.*, ²*Department of Applied Physics and Photonics, Vrije Universiteit Brussel*)

Protein aggregates are linked to various diseases, including neurodegenerative disorders. This study explored the capability of Rose Bengal, a xanthene dye derivative, to track the protein aggregation process. Lysozyme was used as a model protein, and its aggregated forms were prepared by heating under acidic conditions. The absorption spectra, steady-state fluorescence spectra, and fluorescence lifetime of Rose Bengal changed significantly during the formation of protein aggregates and showed fluorescence quenching in the aggregation intermediates. Raman spectra also changed quantitatively depending on the degree of aggregation, confirmed by partial least square analysis. Rose Bengal is considered a sensitive indicator for detecting aggregated proteins.

1Pos014 残基間距離と局所環境の相関によるアデニル酸キナーゼのアロステリックコミュニケーション経路の同定
Allosteric communication pathway within adenylate kinase elucidated by correlation between interresidue distances and local environments

Shinichi Kurino, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

We propose a method to analyze the all-atom molecular dynamics trajectories to elucidate the allosteric communication within proteins by evaluating correlations between C_{α} distances and changes in local environments. Here, we define the local environment as the set of residues interacting with a given residue pair and introduce a local reaction coordinate to quantify the changes in the local environments. We have applied this method to the molecular dynamics trajectory of adenylate kinase from the closed state to the open state. The residue pairs showing strong correlations with the local environment constitute the allosteric pathway from the LID domain to the CORE domain to the NMP domain, which is consistent with the single-molecule FRET experiments.

1Pos015 VCDを用いたスパイクタンパク質フラグメントのアミロイド多形性および超分子キラリティの解析
Amyloid Polymorphism and Supramolecular Chirality in Spike Protein Fragment as Studied by Vibrational Circular Dichroism

Shunsaku Nagai¹, Hisako Sato², Izuru Kawamura¹ (¹*Grad. Sch. Sci., Yokohama Natl Univ.*, ²*Sch. Sci., Univ. Ehime*)

A spike protein fragment (SPF-12: RSAIEDLLFDKV), derived from the coronavirus spike protein, forms amyloid fibrils at pH 4.4 despite low β -sheet propensity. Fibrils formed under stirring and static conditions were analyzed by vibrational circular dichroism (VCD) and atomic force microscopy (AFM). AFM revealed distinct morphologies: flat tape-like fibrils under stirring and twisted fibrils under static conditions. IR spectra showed β -sheet absorption at 1615 cm^{-1} , while VCD spectra displayed couplet peaks that inverted with repeated measurements. The VCD signals eventually vanished after 5 days under stirring. To further elucidate the β -sheet packing mode, isotope dilution experiments using ^{13}C -labeled phenylalanine indicated an antiparallel β -sheet arrangement.

1Pos016 フッ素化アミノ酸を用いた膜貫通イオンチャネルの設計と特性評価
Design and characterization of transmembrane ion-channel peptide containing fluorinated amino acids

Keiya Saito¹, Daisuke Sato², Peng Zugui³, Ai Niitsu⁴, Ryuji Kawano³, Izuru Kawamura¹ (¹*Grad. Sch. Eng. Sci., Yokohama Natl. Univ.*, ²*Inst. Sci. Eng., Ibaraki Univ.*, ³*Inst. Eng., Tokyo Univ. of Agri. & Tech.*, ⁴*Yokohama Inst., Riken*)

The formation of ion channel activity through the self-assembly of synthetic peptides represents a technique relevant to the activation of molecular systems in cellular membranes, and depending on the size of the resulting pore, it can also be applied to nanopore sensing. In this study, we focused on an α -helical peptide composed of repeating hydrophilic serine and hydrophobic leucine residues, conferring amphiphilic character suitable for membrane integration. To enhance its performance, we incorporated 4-fluorophenylalanines (4-F-Phe) and assessed their effects through molecular dynamics simulations, solid-state NMR, and electrophysiological measurements. 4-F-Phe not only increases hydrophobicity but also serves as a highly sensitive NMR probe.

Kento Yonezawa^{1,2}, Sawa Fusamae², Yuya Iwao², Ryuki Iida², Shoma Igarashi², Naoya Sagawa³, Keigo Kinoshita³, Yoichi Yamazaki², Sachiko Toma², Hironari Kamikubo^{1,2} (¹NAIST, CDG, ²NAIST, M.S., ³San-Ei Gen F.F.I., inc.)

Gum Ghatti (GG), composed of hydrophobic proteins and hydrophilic polysaccharides, exhibits excellent emulsifying ability. While its amphiphilic nature has suggested micelle formation at the water–oil interface, this model does not fully explain its high emulsion stability. To investigate the underlying mechanism, we analyzed the structures of GG and MCT-emulsified GG (MCT/GG). SAXS measurements revealed a ~20 nm protein core in GG, and the scattering profiles showed no significant changes with MCT addition, suggesting the absence of core aggregation or structural changes. We propose a core–shell structural model: in MCT/GG particles, oil droplets are organized around the protein core, and their outer surfaces are effectively shielded by polysaccharide chains.

Seiji Takeda, Moeke Kitagawa, Naoya Ishihara, Takahisa Hiruma (*Faculty Pharm. Sci. Hokkaido Univ. Sci.*)

Low density lipoproteins are consisted of lipids, cholesterol, cholesteryl-ester, triacyl glycerol and apoB-100. LDL contributes to deliver lipids and cholesterol to tissues and it also transport various type of molecules that binds to LDL. However, it is not well investigated the effects of binding of these molecules to LDL on physical properties of LDL. In this study, we measured the binding of epigallocatechin gallate to LDL by ultrafiltration and investigated the effects of the binding of epigallocatechin gallate to LDL on physical properties, size and Young's modulus, of LDL by AFM.

Ken Morishima, Ritsuki Sakamoto, Rintaro Inoue, Masaaki Sugiyama (*KURNS, Kyoto Univ.*)

Cyanobacterial circadian clock is composed of three clock proteins, KaiA, KaiB, and KaiC, and its rhythm is observed as a 24-hour oscillation in the phosphorylation degree of KaiC. The oscillation of phosphorylation degree is coupled with the complex formation of Kai-proteins: KaiA-KaiC (AC) complex promotes phosphorylation, whereas KaiB-KaiC (BC) and KaiA-KaiB-KaiC (ABC) complexes promote dephosphorylation. Therefore, the complex switching between AC and BC/ABC complexes is a driving force behind the circadian oscillation. In this study, to reveal the mechanism of the circadian oscillation, we investigated the static and kinetic behavior of the complexes in solution with analytical ultracentrifugation and small-angle X-ray/neutron scatterings.

Yu Yamamori, Rikuri Morita, Yasuteru Shigeta, Ryuhei Harada (*center of computational science, University of Tsukuba*)

Type I human taste receptors (hTAS1R) are responsible for umami and sweet tastes sensation, recognizing substrates as heterodimers: the hTAS1R1-hTAS1R3 for umami and hTAS1R2-hTAS1R3 for sweet taste. However, the detailed mechanism of the specific recognition remains unclear. We performed molecular dynamics (MD) simulations to investigate how hTAS1R acts as a taste receptor. Apo-state atomic models of monomers and all possible dimer combinations were built using AlphaFold2, and subjected to MD simulations. Finally, we found greater openness of the binding site in the dimers compared with monomers. In addition, we discuss the relationship between these findings and the recognition mechanism, along with the computational results of holo-state hTAS1R monomers and dimers.

1Pos021 Structural and functional characterization of novel ice-binding protein isoforms discovered via genome and transcriptome analyses

Tatsuya Arai^{1,2}, Kaho Uchizawa², Kosuke Maeda², Sakae Tsuda¹, Tomoyasu Aizawa^{1,2} (¹*Faculty of Advanced Life Science, Hokkaido University*, ²*School of Science, Hokkaido University*)

Ice-binding proteins (IBPs) are structurally and genetically diverse molecules that inhibit the growth of ice crystals, allowing host organisms to survive in subzero environments. In nature, IBPs are often produced as mixtures of many isoforms in various organisms such as fish, insects, and microorganisms. However, most of these isoforms remain uncharacterized. Here, we investigated IBP isoforms using transcriptome analysis and publicly available genome data, and characterized their protein structures and functions. Our results revealed significant diversity in the size, ice-binding sites, and activities of IBPs. The observed diversity suggests functional specialization among isoforms, which we will discuss in more detail during the presentation.

1Pos022 Effect of phospholipid composition on binding behavior of α -synuclein to lipid membranes

Norihiro Namba, Shiori Ariyoshi, Honori Shiroshita, Takashi Ohgita, Hiroyuki Saito (*Kyoto Pharm. Univ.*)

Aggregation of α -synuclein (α S) in the brains is strongly associated with Parkinson's disease. α S is folded as α -helical structure upon binding to the phospholipid surface, which is known to regulate the aggregation behavior of α S on lipid membranes. In this study, we examined the effect of phospholipid composition on the binding behavior of α S to lipid membranes. We found that phosphatidylserine (PS), an acidic phospholipid, is essential for binding of α S to lipid membranes, while phosphatidylethanolamine (PE) enhances binding propensity of the C-terminus region in α S to lipid membranes. These results indicate a potential role of PS and PE in modulating the α S aggregation induced by membrane interaction.

1Pos023 KaiC のリン酸化率に依存した KaiC-KaiA 結合強度の変化
Phosphorylation-Level-Dependent Changes in KaiC-KaiA Binding Strength

Arisa Nakao¹, Risako Aoyama¹, Yoichi Yamazaki¹, Shuji Akiyama^{2,3}, Kento Yonezawa^{1,4}, Hironari Kamikubo^{1,4} (¹*NAIST, MS*, ²*CIMos*, *IMS*, *NINS*, ³*SOKENDAI*, ⁴*NAIST, CDG*)

The cyanobacterial circadian clock rhythmically changes the phosphorylation state of KaiC by mixing Kai proteins and ATP. KaiC forms a hexamer with two phosphorylation sites per protomer, resulting in diverse phosphorylation states; however, how KaiA binds to these states remains unclear. We evaluated the binding between KaiA and KaiC, phosphorylated or dephosphorylated in stages, using SAXS. The binding affinity exhibited cooperative changes with hysteresis depending on the phosphorylation level and was categorized into strong and weak modes. Cross-term analysis suggested a structural transition in the KaiC₆-KaiA complex. We propose a model in which the complex undergoes a structural transition along the phosphorylation level, accompanied by a switch in binding mode.

1Pos024 Biochemical assay development for kinetic analysis of ATPase cycle of KaiC

Yasuhiro Onoue¹, Yoshihiko Furuike^{1,2}, Shuji Akiyama^{1,2} (¹*Institute for Molecular Science, NINS*, ²*The Graduate University for Advanced Studies (SOKENDAI)*)

KaiC is a clock protein consisting of tandemly duplicated CI and CII domains and functions as the central oscillator of the circadian rhythm in cyanobacteria. The overall ATPase activity of KaiC is considered as the basis for the clock function, because it is closely correlated with the frequency of the circadian rhythm and robustly temperature-compensated. To determine the reaction rate and its temperature dependence for each elementary step of the ATPase cycle, we have developed biochemical assay based on the nucleotide exchange reaction. At the annual meeting, we will present an example using a truncated CI fragment of KaiC, and discuss the clock function on the basis of the ATPase cycle.

1Pos025

トリプシン様蛋白質分解酵素のプロペプチド領域による酵素活性阻害機構

Mechanism of Enzyme Activity Inhibition by the Propeptide Region of a Trypsin-Like Protease

Orika Ashida¹, Nana Sakata¹, Kairi Ogawa¹, Miki Matsuzaki¹, Mitsuhiro Miyazawa², Shigeru Shimamoto¹, Yuji Hidaka¹ (¹*Grad. Sch. Sci. Eng., Univ. Kindai*, ²*PrevenTec Inc.*)

Cocoonase (CCN), produced by *Bombyx mori*, is a trypsin-like enzyme. CCN folds into its native conformation as a precursor form (proCCN) and is activated upon removal of the pro-region. Recently, we reported that the propeptide region plays important roles not only in the inhibition of protease activity but also in assisting the folding of the mature region. In this study, we identify the amino acid residues in the propeptide region responsible for its functional roles. For this purpose, the mutant proteins in which each residue in the pro-region (KDEE) was sequentially replaced by Ala were expressed in *E. coli* cells. The results revealed the significance of each residue in folding and in protease inhibition activity.

1Pos026

メダカ由来プロスタグランジン結合蛋白質とリボフラビンの相互作用解析

Interaction analysis of medaka prostaglandin binding protein with riboflavin

Kazuki Mitani¹, Koichi Uegaki², Shigeru Shimamoto¹ (¹*Faculty of Science and Engineering, Kindai University*, ²*Faculty of Agriculture, Kindai University*)

Lipocalin-type prostaglandin D synthase (L-PGDS) is a protein that synthesizes prostaglandin D₂ (PGD₂), which acts as a somnogen in the brain. Homologs of L-PGDS with similar amino acid sequences are found in non-mammalian species. Among them, fish homologs are predicted to lack enzymatic activity and may instead function as transporters. However, their ligands and physiological roles remain unclear. In this study, we identified riboflavin as a ligand of the L-PGDS homolog from medaka, referred to as PGBP. Using isothermal titration calorimetry (ITC), we determined the stoichiometry and dissociation constant of the PGBP-riboflavin interaction. Furthermore, riboflavin binding was found to confer protection against light-induced degradation.

1Pos027

リポカリン型プロスタグランジン D 合成酵素の系統解析

Phylogenetic and Functional Analysis of Lipocalin-type Prostaglandin D Synthase

Kodai Nakamoto, Chinatsu Noma, Kei Iida, Shigeru Shimamoto (*Faculty of Science and Engineering, Kindai University*)

L-PGDS, a member of the lipocalin family, catalyzes the isomerization of prostaglandin H₂ (PGH₂) to prostaglandin D₂ (PGD₂) and is found only in vertebrates. Although homologous proteins with similar sequences exist in fish, they lack enzymatic activity, while amphibian homologs exhibit lower activity than those of mammals. This study aims to identify amino acid residues contributing to L-PGDS activity through phylogenetic and functional analyses. Sequence comparisons revealed clade-specific features in L-PGDS proteins. Functional analyses further suggest that substrate and product recognition differs between mammalian/reptilian L-PGDS and amphibian homologs. Currently, we are constructing human-toad L-PGDS chimeras to investigate these differences.

1Pos028

マルチドメインタンパク質のダイナミクスを特徴づける粗視化アプローチ

A coarse-grained approach to characterizing the dynamics of multi-domain proteins

Chigusa Kobayashi¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS*, ²*RIKEN PRI*)

Structural biology advances have revealed multi-domain protein structures under various conditions. Molecular dynamics simulations give atomic-scale insight into their dynamics. However, extracting key insights from such data remains challenging. Protein dynamics can often be decomposed into domain motions as rigid-body movements and local fluctuations of flexible regions. We propose a coarse-grained method that represents proteins using a small number of pseudo-particles, modeling domains and hinge regions. An additional point is placed on each domain to capture rotational and twisting motions. We apply this method to ribose-binding protein, adenylate kinase, and the spike protein, and show that it effectively describes their large-scale dynamics.

1Pos029 リン酸結合タンパクを含む液滴チャンバーアレイにより高感度で検出する F_1 -ATPase および PPase からの無機リン酸解離
Highly sensitive detection of phosphate released from F_1 -ATPase and PPase using phosphate-binding protein in droplet chamber arrays

Waren Imaoka¹, Tomohiro Aoyama¹, Yoshihiro Minagawa², Hiroshi Ueno², Nobukiyo Tanaka¹, Hiroyuki Noji², Tomoko Msaikae¹
(¹Dept. Appl. Biol. Sci., Tokyo Univ. Sci., ²Dept. Appl. Chem., Univ. Tokyo)

We have developed a digital assay for detection of inorganic phosphate (P_i) with high sensitivity using a chamber-array device. The PEG-coated femtoliter droplet chambers contained a biosensor MDCC-labeled phosphate-binding protein. The model enzymes that produce P_i were encapsulated in the chambers, and their activity of P_i production was estimated. In the case of bovine heart mitochondrial F_1 -ATPase, the time-course measurement of single-molecule ATPase activity was achieved. In the case of yeast inorganic pyrophosphatase (Y-PPase), we found a positive correlation between the number of droplets showing increased fluorescence intensity and the calculated number of chambers containing one or more Y-PPase molecules. Thus, digital P_i assay has been largely established.

1Pos030 細胞内タンパク質結晶生成過程とその可視化
The process of intracellular protein crystal formation and its visualization

Etsuko Tokunaga, Yasufumi Umena (*NUSR, Univ. Nagoya*)

In recent years, in vivo crystallography (ivMX) has been studied, in which overexpressed proteins are accumulated in organelles to artificially form intracellular crystals (in vivo crystals). In order to perform protein crystal structure analysis using intracellular crystals, it is important to capture crystal growth within the cellular environment, but it remains difficult to capture and observe protein crystals that are expressed sporadically with a low probability. To establish a standard protocol for capturing this intracellular protein crystallization, we decided to use the protein Xpa, which shows fluorescence when expressed intracellularly. We transfected the Xpa gene into HEK293 cells, expressed the fluorescent protein in the cells.

1Pos031 MD シミュレーションとニューラルネットワークを組み合わせたタンパク質の高速 AFM 画像解析
Analysis of HS-AFM images of proteins combining MD simulation and Neural Network

Katsuki Sato¹, Yui Kanaoka², Tomoya Tsukazaki³, Takayuki Uchihashi², Takaharu Mori¹ (¹Tokyo University of Science, ²Nagoya University, ³Nara Institute of Science and Technology)

High-speed atomic force microscopy (HS-AFM) has been widely used for real-time, direct observation of protein conformational changes. Typical resolution of the HS-AFM images is ~0.15 nm in the vertical direction, while 2–3 nm in the lateral direction, making the identification of the protein conformation difficult. To solve this problem, we developed a new algorithm combining molecular dynamics (MD) simulation and neural network (NN). In the method, MD simulation is first carried out to sample conformational changes of the target protein, and then pseudo-AFM images are generated from each MD snapshot as training data set of NN. The results demonstrated that the well-trained NN could identify a conformational state of the target protein even in experimental AFM images.

1Pos032 デキストラン結合酵素グルカンスクラーゼはデキストラン–ポリエチレングリコール混合系での液滴形成を誘導する
Dextran-Binding Enzyme Glucanase Induces Droplet Formation in Dextran–Polyethylene Glycol Mixtures

Mikage Iwakiri, Hideyuki Komatsu (*Department of Bioscience and Bioinformatics, Faculty of Systems Engineering and Computer Science., Kyushu Institute of Technology*)

Liquid-liquid phase separation (LLPS) is a phenomenon in which biomacromolecules form dynamic and liquid-like aggregates in solution. LLPS plays important roles in intracellular compartmentalization and extracellular matrix formation. A dextran-polyethylene glycol (PEG) mixture system is useful for analysis of LLPS. Glucanase (GS), a glucosyltransferase from oral bacteria, specifically binds to dextran. Here, we have investigated the effect of GS on LLPS in a dextran-PEG mixture system. Although LLPS was not observed in a 4% dextran / 5% PEG solution, the supplement of 16 μ M GS to this solution induced micron-sized droplet formation. The result suggests that GS interacts with dextran to promote the formation of phase-separated condensates.

1Pos033 ロボット機構学に基づくタンパク質の内部運動特性予測のための計算フレームワークの開発
Development of a Computational Framework for Predicting the Internal Motion Properties of
Proteins Based on Robot Kinematics

Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

A computational framework has been developed for predicting the internal motion characteristics of proteins based on robot kinematics. In this framework, proteins are modeled as robotic mechanisms composed of serial kinematic chains constrained by linear springs, where the joint angles correspond to the dihedral angles of the main chains in proteins. Flexible mode motions are extracted by applying singular value decomposition to the structural compliance matrix of the model. The prediction is based on the concept that flexible mode motions occur more easily. The proposed framework provides commands for interactively performing the prediction sequence (e.g., setting analysis conditions, creating a model from PDB data, and visually expressing the results).

1Pos034 多様なカーゴ分子を媒介とした非ウイルス性タンパク質カプシドの試験管内形成と形態制御
In vitro assembly of a nonviral protein capsid and its morphological control mediated by
versatile cargos

Kenya Tajima¹, Yusuke Sakai^{2,3}, Naohiro Terasaka¹ (*¹Earth-Life Science Institution, Institute of Future Science, Institute of Science Tokyo, ²RIKEN Center for Biosystems Dynamics Research, ³Institute for Quantitative Biosciences, The University of Tokyo*)

Cargo packaging into protein capsids enables cargo delivery and bioreactor construction. Recently, a nonviral nucleocapsid (NC-4) packaging its own mRNA was developed from bacterial protein cage, but its cargo versatility remains unclear. Moreover, heterogeneous NC-4 structures lacking RNA-binding sequences suggest its potential for cargo-templated morphological control. To investigate this, NC-4 was engineered to enable in vitro assembly with diverse cargos including RNA, DNA and protein. Notably, packaging of structured DNA origamis altered the size and shape of nucleocapsids. These results demonstrate broad cargo compatibility and morphological flexibility mediated by electrostatic interactions.

1Pos035 Model screening of an epitope-tag peptide from a random library consisting of a reduced set
of amino acids using PL display

Shingo Ueno, Fumi Toshioka, Takanori Ichiki (*iCONM, Kawasaki Inst. Industry. Promo.*)

Peptide ligase-mediated display (PL display) is an originally developed bead surface protein display method that uses peptide ligase to link proteins and their DNA on magnetic beads with a minimal peptide spacer. Previously, we achieved complete enrichment of an epitope tag gene with a 1 in 10,000 presence rate in a single FACS selection. Here we present a model screening of an epitope tag peptide from a random library with a reduced set of amino acids. Consensus sequences of the epitope tag peptide were enriched in two rounds of selection from a 1.7e6 diversity library with six amino acid alphabets. The enrichment rate of the consensus sequence, as estimated by NGS analysis, was up to 686-fold.

1Pos036 分子進化によるウイルス模倣粒子の構造多様化と機能化
Functionalization and structural diversification of artificial nucleocapsids by laboratory evolution

Naohiro Terasaka (*Earth-Life Sci. Inst., Inst. Future Sci., Inst. Sci. Tokyo*)

Viruses use protein shells to package genetic material and hijack host cells. Inspired by this, we engineered artificial virus-like mRNA-encapsulating protein capsules (nucleocapsids) via directed evolution of bacterial lumazine synthase. Cryo-EM and X-ray footprinting confirmed structural evolution in both RNA and protein, enabling efficient mRNA packaging into 240-mer capsules. Surface modifications through genetic fusion and posttranslational methods allowed peptide display for targeted delivery. Another circular permutation and additional evolution of mutant libraries yielded diverse structures. These nucleocapsids offer functional and structural versatility, serving as models for primitive evolution and safe viral alternatives.

1Pos037 細胞内タンパク質結晶エンジニアリングによる刺激応答固相転移
Engineering in-cell protein crystals for the stimuli-responsive solid-solid phase transitions

Kosuke Kikuchi¹, Misaki Nagama¹, Junko Tanaka¹, Haonan Kong¹, Satoshi Abe², Takafumi Ueno^{1,3} (¹*Sch. of Life Sci. and Tech., Science Tokyo*, ²*Grad. Sch. of Life and Env. Sci., KPU*, ³*IIR-ASMat, Science Tokyo*)

Solid-solid phase transitions underpin drastic structural and functional changes in materials, yet their design and control in protein assemblies remain largely unexplored. In this study, we engineer intracellular protein crystals that undergo lattice-level transformations in response to external stimuli. Leveraging in-cell crystallization to bypass conventional bottlenecks, we identify crystals exhibiting reversible, diffusion-less transitions—reminiscent of martensitic behavior. This work establishes a framework for constructing dynamic protein-based materials with architected phase transitions.

1Pos038 アクティブ・ラーニングによる ATP 合成酵素の阻害タンパク質 IF₁ の再設計
Redesign of the inhibitor protein IF₁ for ATP synthase via an active-learning framework

Ryohei Kobayashi^{1,2}, Constantin Guyot^{2,3}, Jun Ohnuki^{2,3}, Hiroyuki Noji^{1,4}, Kei-ichi Okazaki^{2,3} (¹*Dep. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, ²*Institute for Molecular Science*, ³*SOKENDAI*, ⁴*RIPH, Univ. Tokyo*)

Recent advances in computational power and machine learning have significantly progressed protein science. However, the design of proteins involving large structural changes remains limited. To overcome this problem, we aim to establish an active-learning framework that integrates computational prediction with experimental validation. As a test case, we redesign IF₁, a regulator protein of mitochondrial ATP synthase to prevent ATP hydrolysis. Although no enhancement was observed when the entire sequence was predicted using ProteinMPNN, we successfully identified several mutants with 5-fold higher affinity than IF₁(WT), by modifying the sequence prediction strategy. For further improvement, we are now incorporating machine learning models and AlphaFold3 into our workflow.

1Pos039 高速 AFM・生化学手法による E6AP/E6/p53 複合体の構造動態の統合的解析
Integrated analysis of structural dynamics of E6AP/E6/p53 complex by HS-AFM and biochemical methods

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Ubiquitin conjugation to target proteins (ubiquitination) is a post-translational modification that regulates numerous cellular processes. E6AP (E6-associated protein), a type of ubiquitin ligase (E3) with a role in adding ubiquitin to substrates, is known to acquire cancer suppressor protein p53-specific ubiquitination activity by binding to Human Papilloma Virus (HPV)-derived tumor protein E6. It is now also clear that ubiquitination of p53 by E6AP and E6 is a major factor in cervical cancer. Therefore, we aim to elucidate the structural dynamics of the detailed E6AP/E6/p53 complex including the IDR (intrinsically disordered region) and how E6 activates the p53 ubiquitination activity of E6AP using HS-AFM and biochemical methods.

1Pos040 MAP7 は微小管結合を介して FUS の相分離を制御する：ALS 関連変異体との相互作用比較からの示唆
MAP7 Regulates FUS Condensate Formation via Microtubule Binding: Insights from ALS-Linked Mutant Interactome Analysis

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Fused in sarcoma (FUS) forms pathological condensates via aberrant phase separation in ALS. Using photoactivated proximity crosslinking, we identified candidate interactors differentially associated with wild-type and ALS-related mutant FUS (e.g., R521C). Among them, MAP7, a microtubule-binding protein, showed reduced interaction with the mutant form. Functional analysis revealed that MAP7 overexpression suppresses FUS granule formation by decreasing both granule size and the number of granule-positive cells. This suppression required the microtubule-binding domain of MAP7. These results suggest that MAP7 negatively regulates FUS phase separation and that altered FUS-MAP7 interactions may contribute to ALS pathogenesis.

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The nucleosome is the basic unit of chromatin and essential for DNA storage and gene regulation. Histone tails, mostly at N-termini, are key for gene regulation but are intrinsically disordered region, their dynamics are hard to analyze by cryo-EM or X-ray crystallography. Here, we show that their dynamics can be tracked using tail-conjugated proteins and high-speed atomic force microscopy, which offers nanometer and sub-second resolution. We used *E. coli* to overexpress both wild-type and Spytag-modified histone proteins to prepare reconstituted nucleosomes. Spycatcher-sfGFP were attached to visualize tail dynamics. The results indicate that histone tails exhibit flexible dynamics around the histone core. These findings give new insight into chromatin and epigenetics.

Aya Ogino¹, Yumiko Ohhashi², Hideki Taguchi², Hiroki Konno³ (¹*Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ.*, ²*Inst. of Integ. Res., Science Tokyo.*, ³*WPI Nano Life Sci. Inst. (WPI-Nano LSI), Kanazawa Univ.*)

The yeast prion protein Sup35 forms amyloid fibrils that cause the prion phenotype [PSI⁺]. In addition to the amyloid formation, the intrinsically disordered domain of Sup35 drives the reversible phase separation under stress conditions. However, the mechanism of the phase transition process remains unknown.

In this study, we elucidate the droplet formation process of Sup35 using high-speed atomic force microscopy (HS-AFM), which has nanometer spatial resolution and sub-millisecond temporal resolution and can observe the structural dynamics of proteins in real time.

Naoya Shibayama (*Div. Biophys., Jichi Med. Univ.*)

Structural changes underlying protein allostery are often modeled using a two-state framework, involving transitions between tense (T) and relaxed (R) states, with hemoglobin as a classical example. However, even for hemoglobin, the relationship between its crystal structures and functional behavior in solution remains not fully understood. In this study, we directly measured the O₂ equilibrium curves of various hemoglobin crystal forms and further examined the structural and functional properties of individual equilibrium conformers of hemoglobin trapped in silica gels that prevent conformational interconversion within hydrated pores. This integrated approach allowed us to uncover previously unrecognized structure-functional relationships in hemoglobin.

Kazumasa Muramoto, Kyoko Shinzawa-Itoh (*Grad. Sch. Sci., Univ. Hyogo*)

Respiratory chain generates proton motive force coupled to electron transfer at high energy efficiency. Mitochondrial respiratory terminal enzyme (cytochrome c oxidase: CcO) pumps protons coupled to the oxygen reduction.

Previous studies reported that carbon dioxide (CO₂) and nitrous oxide (N₂O) affect the function of CcO. In this study, we determined the crystal structure of CO₂-, N₂O-, and Xe-bound bovine CcO in the oxidized and reduced states at resolutions of 1.75–1.85 Å. Binding of Xe in a hydrophobic channel supported the proposed O₂ transfer pathway. CO₂, N₂O, and Xe were all bound to a common site in another hydrophobic channel that branched from the O₂ transport channel. The role of another hydrophobic channel formed by nuclear DNA-coded subunit is discussed.

1Pos045 海洋性ビブリオ菌におけるプロトン駆動べん毛モーターのストマチン様タンパク質 FliL と MotAB 固定子複合体の相互作用
Association of stromatin-like protein FliL and MotAB stator complex of proton-driven flagellar motor in marine *Vibrio*

Michio Homma^{1,2}, Kazuki Yokoyama³, Norihiro Takekawa⁴, Tatsuro Nishikino⁵, Hajime Nakatani¹, Seiji Kojima³ (¹*Dep. Biomol. Eng., Grad. Sch. Eng., Nagoya Univ.*, ²*Dep. of Physics, Grad. Sch. Sci., Nagoya Univ.*, ³*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, ⁴*Dep. Macromol. Sci., Grad. Sch. Sci., Osaka Univ.*, ⁵*Dep. Life Sci. Appl. Chem., Nagoya Inst. Tech.*)

A flagellar protein FliL, which is a single transmembrane (TM) protein with a large periplasmic region has been found to be important for the motor function at high load condition, such as highly viscous environments. It has been speculated that FliL and the stator complex, which is ion channel, associate to support the ion conductance. Marine *Vibrio* has two kinds of FliL for polar(pof) and lateral(laf) flagella. We had shown that pof-FliL formed a homo decamer ring and seemed to surround the flagellar stator to support the structure. Pof-FliL is not essential for motility but laf-FliL is. In this study, we purified the lateral flagellar motor of MotAB and laf-FliL using the expression vector in *E. coli*. The interaction between them were investigated.

1Pos046 ATR-FTIR による環状ヌクレオチド依存性カリウムチャネル SthK のリガンド選択の分子機構研究
Investigation of molecular mechanisms of ligand selection in a cyclic nucleotide dependent potassium channel SthK by using ATR-FTIR

Taisei Maeda¹, Tatsuro Nishikino^{1,2}, Hiroki Ogasawara³, Hiroto Fukuda³, Yuji Furutani^{1,2} (¹*Graduate School of Engineering, Nagoya Institute of Technology*, ²*Optobiotechnology Research Center*, ³*Nagoya Institute of Technology*)

Cyclic nucleotide-dependent ion channels (CNG channels) are activated by cyclic nucleotides such as cAMP and cGMP. Physiologically, they play an important role in signal transduction in vision and olfaction.

SthK is a CNG potassium channel from the bacterium *Spirochaeta thermophila*.

The aim of this study is to elucidate the molecular mechanism of ligand selection in SthK by acquiring difference spectra before and after ligand binding using total reflection infrared spectroscopy (ATR-FTIR), which is sensitive to minute structural changes.

The ligand-selection and gate-opening/closing mechanisms of SthK are discussed based on a comparison of the conformational changes and the binding affinities of cAMP and cGMP upon ligand binding.

1Pos047 Visualization and analysis of P-glycoprotein dynamics by using HS-AFM
Visualization and analysis of P-glycoprotein dynamics by using HS-AFM

Yui Kanaoka¹, Takeshi Murata², Takayuki Uchihashi^{1,3} (¹*Grad. Sch. Sci., Univ. Nagoya*, ²*Grad. Sch. Sci., Univ. Chiba*, ³*ExCELLS*)

P-glycoprotein (P-gp) is an ATP-dependent transporter that exports various drugs from cells and contributes to multidrug resistance in cancer. Its overexpression reduces chemotherapy efficacy. Structural studies, including cryo-EM, show P-gp cycles between Open and Closed conformations via ATP hydrolysis: the NBDs capture substrates in the Open state and dimerize in the Closed state for transport. However, its real-time dynamics remain unclear. Using high-speed atomic force microscopy (HS-AFM), we visualized conformational changes in P-gp reconstituted in nanodiscs. Surprisingly, under nucleotide-free conditions, NBDs showed dynamic opening/closing, likely from intrinsic flexibility. With 2 mM ATP, NBDs stayed nearly closed, showing reduced opening angles.

1Pos048 異種タンパク質結合 OmpG ナノポアの開閉挙動観察
Observation of gating behavior of OmpG nanopore conjugating other protein

Kazuha Endo, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Nanopore sensing is one of the most powerful method of a single molecule detection monitoring the change of ionic current caused by protein translocation through a nanopore. OmpG, that is a monomeric β -barrel protein with 14 β -strands, is used as biosensor detecting antibodies. However, an intersection of long amino acid sequences into loops of OmpG may inhibit the pore formation. Therefore, the detection of the protein-protein interactions using OmpG is difficult. In this study, we observed gating behavior of OmpG conjugating other protein using a tag/catcher system that enables the proteins to bond spontaneously. We report that a dwell time of close states is distinguished between OmpGs conjugating proteins with different molecular weights.

1Pos049 近接した標的 DNA 配列のタンデムリピートに集積する Dof 転写因子の 1 分子観察
Single-molecule observation of Dof transcription factor accumulating to neighboring tandem repeats of target DNA sequences

Hayato Yamashita¹, Akihiro Tsuji¹, Hirotake Furihata², Zhangliang Zhu^{2,3}, Takuya Miyakawa^{2,3}, Masayuki Abe¹ (¹Grad. Sch. Eng. Sci., Univ. Osaka, ²Grad. Sch. Agr. Sci., Univ. Tokyo, ³Grad. Sch. Bio., Kyoto Univ.)

DNA-binding with one-finger (Dof) proteins are a family of plant-specific transcription factors and play crucial roles in diverse plant biological processes, such as photoperiodic flowering and seed germination. However, it remains unclear how the Dof domain recognizes a restricted set of promoters for gene regulation by binding to just four nucleotides, AAAG/CTTT.

We investigated the single-molecular dynamics of the interaction between Dof and DNA using high-speed atomic force microscopy (HS-AFM). The binding of Dof molecules to the target DNA was visualized by HS-AFM. Analysis of the data revealed that the binding affinity of the Dof domain increases depending on the number of coupled sequences within the tandem repeat [1].

[1] H. Furihata et al, *Nature plants* (2025)

1Pos050 UvrD ヘリカーゼの野生型と C 末端欠失変異体間の DNA を介した相互作用
DNA-mediated interaction between wild-type and C-terminal deletion mutants of UvrD helicase

Hiroaki Yokota (*Grad. Sch. New Photon. Indust.*)

Escherichia coli UvrD is a non-hexameric superfamily I DNA helicase essential for DNA repair pathways. To elucidate the role of the C-terminal amino acids crucial to dimerization and helicase activity, single-molecule direct visualization has been performed for UvrD mutants lacking the C-terminus. Our previous studies have shown that multiple UvrD molecules simultaneously participated in DNA unwinding, both in mutants lacking the C-terminal 40 amino acids (Biophys. J. 2020) and the entire C-terminus (Biophys. J. 2013). In this study, I present data on the association and dissociation dynamics between wild-type UvrD and the C-terminal deletion mutants on DNA, and discuss how the C-terminal region affects the interaction between the first and second bound UvrD molecules.

1Pos051 液液相分離により形成するナノスケール凝縮体の蛍光寿命相関解析
Fluorescence lifetime correlation analysis on nanoscale liquid condensates formed through liquid-liquid phase separation

Rene Toyama, Miyuki Sakaguchi, Shoichi Yamaguchi, Takuhiro Otsu (*Grad. Sch. Sci. Eng., Saitama Univ.*)

Liquid-liquid phase separation (LLPS) of biomolecules has attracted much attention due to its biological relevance, and various experimental techniques have been applied to understand the physicochemical properties of biomolecules in liquid condensates. However, most of the works focused on large condensates with the diameter larger than the optical limit of microscope (typically larger than 5 micrometers). Here, we applied fluorescence lifetime correlation analysis to aim at elucidating the molecular properties of nanoscale condensate. The application on the LLPS of histone H1 protein and DNA reveals the drastic conformational change of DNA upon the formation of the nanoscale condensate.

1Pos052 Folding of Frameshift-Stimulating RNA Pseudoknots Is Modulated by the Upstream Structures

Jin-Der Wen (*National Taiwan University*)

The RNA genome of SARS-CoV-2 contains a pseudoknot (PK) that stimulates -1 ribosomal frameshifting, essential for viral protein synthesis. The PK comprises three stems (S1, S2, S3) and typically folds in the S1-S3-S2 order. A recent study found that the first half of S1 can form an alternative stem (AS1) with an upstream sequence, altering PK formation. Using optical tweezers, we show that without the upstream sequence, folding follows the usual S1-S3-S2 order with high conformational heterogeneity. A loop-truncated AS1 slightly reduces heterogeneity, while a stabilized AS1 yields more homogeneous PK conformations. Upstream structures can thus modulate PK folding pathways. Biological implications remain under study.

1Pos053 自己複製を目指した成長する DNA 液滴の設計
Design of Growing DNA Droplets Toward Self-Replication

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DNA droplets, formed through liquid-liquid phase separation of self-assembling DNA nanostructures, are attracting attention as artificial cell models with dynamic information processing capabilities due to their responsiveness to external environments. This research aims to establish growth mechanisms for DNA droplets that could potentially enable self-replication functions. To achieve DNA droplet growth, amplifying the component DNA nanostructures is necessary. We proposed a novel isothermal amplification mechanism for single-stranded DNA that forms these nanostructures and verified whether amplification occurs. By establishing a growth mechanism for DNA droplets, it becomes possible to provide self-replication functionality to these artificial cell models.

1Pos054 miRNA の濃度を認識する DNA 液滴コンピュータ構築を目指した化学反応シミュレーション
Chemical reaction simulation for development of DNA droplet computers which recognize concentration of miRNAs

Chisa Kato¹, Yuko Yoshida¹, Masahiro Takinoue^{1,2,3} (¹*Sch. Comp. Sci., Inst. Sci. Tokyo*, ²*Sch. Life Sci. Tech., Inst. Sci. Tokyo*, ³*ASMat, Inst. Sci. Tokyo*)

Molecular computing is the research field that challenges the potential of molecules to conduct information processing. In recent years, studies have shown that neural networks can be realized utilizing molecular. We reported a new type of molecular computer composed of DNA droplets. The computational DNA droplets recognize the presence of miRNAs to compute AND operation. In this research, we propose DNA droplets that recognize not only the presence but also the concentration of miRNAs to perform more complex operations. Simulations were conducted, and our numerical models were confirmed to successfully describe the DNA droplet computer output. As a prospect, we plan to make the DNA droplet computers in the experiment.

1Pos055 自動分注ロボットと機械学習を用いた DNA 論理回路の自動設計
Automated design of DNA logic circuits using automated pipetting robots and machine learning

Yuko Yoshida¹, Kanta Takagi¹, Masahiro Takinoue^{1,2,3} (¹*School of Computer Science, Institute of Science Tokyo*, ²*School of Life Science and Technology, Institute of Science Tokyo*, ³*Research Center for Autonomous Systems Materialogy (ASMat), Institute of Science Tokyo*)

In recent years, wet experiments involving solutions have become increasingly complex and are becoming a heavy task for experimenters. To solve this problem, we constructed an experiment system that does not require humans by realizing a cycle of “experiment with robot → classify results by learning model → determine next experimental condition → experiment with robot → ...”. We also realized the construction of logical operations by DNA droplet computing using this experimental system. In this study, we realized AND, OR computation by DNA droplet computing by using an automated experimental system to search for conditions in appropriately designed DNA sequences.

1Pos056 DNA ナノミウラ折り：力学的に変形可能なナノ折り紙構造
DNA-Based Miura-ori: A Mechanically transformable Nano-Origami Architecture

Daisuke Ishikawa¹, Ibuki Kawamata², Masahiko Hara³, Masashi Ikeuchi¹ (¹*LBB, Science Tokyo*, ²*Grad. Sch. Sci., Kyoto Univ.*, ³*Sch. Mater. Chem. Technol., Tokyo Tech*)

Origami engineering, which folds flat structures geometrically, holds industrial promise. Japanese researchers have made major contributions, especially the Miura-ori fold by Dr. Miura, enabling compact folding of large surfaces for maps and satellite panels. However, applying reversible folding to the nanoscale remains unexplored. DNA origami, though well known, differs as it fixes DNA strands rather than using mechanical folds. This study proposes a design method for nano-origami by constructing a nanoscale Miura-ori fold using DNA nanotechnology to achieve reversible, mechanical folding at the nanoscale.

1Pos057 CRISPR Cas13a システムを用いた *Salmonella* RNA のデジタル検出
Digital Detection of *Salmonella* RNA with CRISPR Cas13a system

Svitlana Kovalchuk¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Graduate School of Engineering, The University of Tokyo*, ²*Research Institute of Planetary Health (RIPH), The University of Tokyo*)

A new *Salmonella* detection technology has been developed merging Cas13-based RNA detection system and digital bioassay technology (d-Sal assay), addressing the requirement for swift and efficient on-site detection of *Salmonella*. In our system, we use multi-site targeting. Accordingly, the simultaneous use of 7 crRNAs complementary to different regions of the target RNA generates 7 LwaCas13a-crRNA-tgRNA molecules from a single target RNA molecule. To enhance the catalytic efficiency of Cas13a trans-cleavage, we use chemical enhancers (DDT and PVA). The sensitivity of the method has increased 2 fold. The LOD calculation is approximately 1.02fM. The developed d-Sal assay has the potential to become a method for the rapid, sensitive detection of *Salmonella*.

1Pos058 静電相互作用により誘起された不均一な DNA 溶液中の力の伝搬
Force propagation in heterogeneous DNA solution induced by electrostatic interactions

Miku Nakao¹, Saki Matsuyama¹, Akinori Miyamoto², Yoshihiro Murayama^{1,2} (¹*Dep. Biomedical Engineering., Grad. Sch. Engineering., Tokyo University of Agriculture and Technology*, ²*Dep. Applied Physics., Grad. Sch. Engineering., Tokyo University of Agriculture and Technology*)

Deformation of cell nucleus by external forces affects gene expression. DNA in cell nucleus is heterogeneous, as in heterochromatin and euchromatin, where electrostatic interactions play an important role. To identify the effect of heterogeneity on the force propagation in DNA solution, we observed force acting on probe particle due to the external force produced by moving particle, using dual trap optical tweezers. We added polylysine to the DNA solution to induce the heterogeneity of DNA solution. It was observed that the polylysine produced a heterogeneous structure, as the fluctuations of the beads were distinctly different depending on the location. We discuss the propagation of tangential and normal forces in solutions with such heterogeneous structures.

1Pos059 分子動力学シミュレーションを用いたインターカレーションした DNA とヌクレオソームの構造ダイナミクス解析
The conformation and dynamics of intercalated DNA and nucleosome analyzed by molecular dynamics simulation

Hisashi Ishida¹, Hidetoshi Kono^{1,2} (¹*Inst. Quantum Life Science, QST*, ²*cQUEST, Chiba Univ.*)

Intercalators modulate DNA structure through direct molecular interactions, influencing replication and transcription. Using molecular dynamics simulations with 18-mer DNA, we investigated binding mechanisms of SYBR Gold, YOYO-1, and DOXO (doxorubicin). Two primary intercalation patterns were observed: insertion between adjacent base pairs (RISE-type) and insertion via base-pair opening (OPEN-type). These interaction modes distinctly altered DNA contour length and stiffness. Further investigating DOXO in a nucleosome system revealed preferential binding to nucleosomal DNA, which reduced atomic contacts between DNA and histone arginine residues, potentially destabilizing nucleosome structure and facilitating histone eviction.

1Pos060 Unveiling the centromere/kinetochore structure in chicken DT40 cells using expansion microscopy and fluorescence correlation spectroscopy

Yasuhiro Hirano^{1,2}, Akira Kitamura³, Toru Hirota², Tatsuo Fukagawa¹ (¹*Graduate School of Frontier Biosciences, The University of Osaka*, ²*Cancer Institute of JFCR*, ³*Faculty of Advanced Life Science, Hokkaido University*)

The kinetochore is a crucial structure for chromosome segregation, yet how over hundred of related proteins assemble on the centromere remains unclear. Here, using expansion microscopy, we found that CCAN, proteins constitutively associated with centromere forms a cartwheel-like structure on interphase centromere in chicken DT40 cells. Knockout of CENP-C, whose oligomerization is essential for kinetochore function, reduced the wheel size, suggesting that CENP-C is involved in the clustering of CCAN. Fluorescence correlation spectrometry estimated 43.4 ± 27.6 CENP-C molecules per kinetochore, approximately 2-fold more than other CCAN components. These results suggest that CENP-C-mediated CCAN clustering in interphase precedes functional kinetochore formation.

1Pos061 凝縮体形成と共役した転写動態の粒子ベース反応動力学モデリング
Particle-based modeling of reactive dynamics of transcription coupled with condensate formation

Daiki Sugata, Shoji Takada (*Grad. Sch. Biol., Univ. Kyoto*)

Transcriptional dynamics are closely linked to transcriptional condensates, which consist of RNA polymerase II, Mediators, and other transcription factors. Recent studies suggest that the formation and dissolution of these condensates may be regulated by charge balance, particularly involving nascent RNA and elongating transcripts, which could drive transcriptional bursts. To gain a comprehensive understanding of these phenomena, particle-based simulations incorporating transcriptional reactions may be necessary. In this study, we explicitly model not only the binding of Pol II to DNA but also its translocation along the DNA and the generation of RNA particles. We attempt to reproduce the reentrant behavior observed in transcriptional condensates.

1Pos062 エネルギー準位統計によるペプチドの分類
Classification of peptides by energy level statistics

Masanori Yamanaka (*CST, Nihon Univ.*)

Peptides play a variety of roles in the body. The classification of these peptides is biological and chemical. In this study, we focused on the electronic state of peptides to classify them. Peptide structures were taken from molecular dynamics trajectories, and quantum chemical calculations were performed on individual structures to obtain molecular orbitals and their energies. By applying the method of energy level statistics of random matrix theory to these electronic states, the statistical distribution function of molecular orbital energy level intervals was calculated, and peptides were classified according to the shape of the distribution function. The calculations were performed by both ab initio and density functional methods, and the consistency was checked.

1Pos063 物理学の知識を組み込んだ AI 創薬の開発
Development of drug discovery AI incorporating physics-based knowledge

Yuuka Ogawa¹, Tatsuki Kawauchi², Tomohiko Hayashi² (¹*Faculty of Engineering, Niigata Univ.*, ²*Grad. Sch. Sci. and Tech., Niigata Univ.*)

This study presents the development of a comprehensive drug discovery AI incorporating physics-based knowledge to design innovative drugs with fewer side effects. We aim to develop a method to simultaneously predict drug-target affinity and side effects by integrating binding free energy (BFE) calculations based on statistical thermodynamics with side effect predictions based on bioinformatics. Affinity prediction uses our BFE method, which estimates drug-target affinity in seconds on a standard workstation by accelerating hydration free energy calculations. By dividing the BFE into physically meaningful terms, we can identify the physical factors that drive binding. we try to apply such “physics-based knowledge” to side effect prediction.

1Pos064 トレハロース水溶液を用いた AQP 過剰発現 CHO 細胞の凍結保存
Cryopreservation of AQP4-overexpressing CHO cells using trehalose aqueous solution

Sumire Matsuo¹, Masato Yasui², Youichiro Abe², Tsutomu Uchida³ (¹*Graduate school of engineering, Hokkaido University*, ²*School of Medicine, Keio University*, ³*Faculty of Engineering, Hokkaido University*)

Cryopreservation of cells is used in several industrial applications, and further improvements in this technology are needed. Dehydration is considered an important factor in viability in cell cryopreservation. In our previous study, we have conducted research using Chinese hamster ovary cells overexpressing aquaporin-4 (AQP4 overexpressing CHO) and have shown that excessive dehydration during slow freezing reduces viability. Therefore, in this study, we performed cryopreservation experiments using a trehalose aqueous solution, which is expected to have protective effects at lower osmolarities. The results showed that viabilities of the trehalose aqueous solution equivalent to or higher than those in trehalose-containing medium were achieved with the trehalose solution.

Kiyoshi Ohnuma¹, Chihiro Takeuchi¹, Hazuki Tsuboi¹, Ryo Kojima¹, Tsuji Shota¹, Emilio Macias Estrada Raul¹, Hayashi Yohei², Miyu Mori¹ (¹Nagaoka University of Technology, ²RIKEN)

Human gastrulation, organized as 2D layers, is a critical stage related to implantation and malformations. While human iPS cells (hiPSCs), corresponding to pre-gastrulation stage cells (epiblast), enable in vitro differentiation studies, migration and pattern formation remain unclear.

We engineered a human embryo model by co-culturing hiPSCs and mesoderm on sub-millimeter adhesion surfaces. Both cell types exhibited random movements daily, suggesting suitability for 2D layer formation. Over 3 days, mesoderm cells aggregated centrally while hiPSCs positioned peripherally, suggesting early gastrulation-like pattern formation.

Our engineered model will reveal physical principles governing human gastrulation inaccessible in vivo.

Hiroshi Koyama^{1,2}, Toshihiko Fujimori^{1,2} (¹Div. Embryology, NIBB, ²SOKENDAI (Graduate University for Advanced Studies))

To quantitatively assess mechanical forces of cell-cell interactions in multicellular systems, we developed an image-based method for statistically inferring mechanical forces of cells (Koyama et al., 2023). We have applied this method to early embryos of the mouse and *C. elegans*, and to epithelial cells including MDCK cells. The inferred forces of pairwise cell-cell interactions were approximated as functions dependent on cell-cell distances. These functions were related to subcellular mechanical components such as cell-cell adhesive forces. The profiles of these functions, acting as local rules, gave rise to the emergent properties of morphogenesis in early embryogenesis. Our framework quantitatively links cellular forces to morphogenetic events.

Kenshiro Kaneko, Tomoki P. Terada (Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.)

Muscle contraction is caused by shortening of sarcomeres driven by actin and myosin filaments. The lever arm model has generally been considered to explain the muscle fiber experiment. On the other hand, the single molecule experiment have suggested the existence of biased Brownian motion of myosin heads along actin filament. Motivated by this, we have been constructing a simulation model that incorporates both lever arm model and biased Brownian motion to elucidate the contribution of the effect of biased Brownian motion on the macroscopic properties of muscle contraction. By improving the model using the results of both types of experiments, we discuss the contribution of the biased Brownian motion in the muscle contraction.

Masayuki Hoshida^{1,2}, Takumi Toji², Tatsuya Iwata³, Noriko Takeuchi¹, Hajime Honda², Ikuko Fujiwara² (¹School of Health Sciences, Kitasato University, ²Materials Sci. & Bioeng., Nagaoka Univ. of Tech., ³Faculty of Pharmaceutical Sciences, Toho University)

Cellular actin polymerizes into filaments and forms branched or bundled structures. Fascin, an actin-bundling protein, uniquely generates tightly aligned bundles that serve as rigid cytoskeletal structures, particularly in filopodia. Like other actin-based structures, these bundles must undergo disassembly to enable cytoskeletal remodeling and recycling during cell migration. However, the mechanism underlying the disassembly of fascin-induced bundles remains poorly understood. In this study, we directly observed the disassembly of fascin-mediated actin bundles over time using an *in vitro* motility assay. Through spatiotemporal analysis, we aim to clarify the mechanical properties of the bundles and the mechanism governing their disassembly.

1Pos069 **バクテリア鞭毛モーターにおける MotAB の駆動機構：理論モデルによるアプローチ**
Exploring the Driving Mechanism of MotAB in the Bacterial Flagellar Motor via Theoretical Modeling

Shintaro Kubo^{1,2}, Yasushi Okada³, Shoji Takada⁴ (¹Wako, RIKEN, ²Dept. of Applied Chem., the Univ. of Tokyo, ³Dept. of Med., the Univ. of Tokyo, ⁴Grad. Sch. Sci., Kyoto Univ.)

Bacterial flagellar rotation is powered by the MotAB stator complex via proton transfer. Cryo-EM revealed a 5:2 MotAB structure, suggesting MotA rotation around MotB. To explore the mechanism, we built a structure-based model of *Campylobacter jejuni* MotAB and ran MD simulations under various protonation states. We found that when two MotA chains remain deprotonated, the MotA pentamer rotates ~36° per proton transfer. Our results propose a plausible model of proton-coupled rotation and offer insight into ion-driven molecular motors.

1Pos070 **ADP-Pi ミオシン S1 と F-actin 間駆動力の物理原理について**
On the physical principle of the driving force between myosin S1 with ADP-Pi and F-actin

Makoto Suzuki (Tohoku University)

The driving force on S1 is thought to be due to the interaction between S1 and the HMW around F-actin, which could be an interfacial tension effect as in Cytoskeleton (2017) & Springer book(2018). Here, the gradient of the squared strength of the electric field near the front or rear side of S1 along F-actin should induce a driving force on S1 due to the polarization coefficient of each partial side domain. Since solvent ions gather on the charged residues on the S1 surface within nanoseconds, it takes longer to increase the time-averaged polarizability of the side chains on the partial surfaces of the S1. (1) Suzuki M. et al. Cytoskeleton 74:5 12-527 (2017) & The Role of Water in ATP Hydrolysis Energy transduction by Protein Machinery, Springer (2018).

1Pos071 **キネシン 1 の協調的運動における情報ラチェット機構**
Information ratchet mechanism for the coordinated unidirectional movement of kinesin-1

Michio Tomishige¹, Hiroshi Isojima², Kohei Matsuzaki¹ (¹Dept. Phys. Sci., Aoyama Gakuin Univ., ²Dept. Appl. Phys., Univ. Tokyo)

Kinesin-1 is a dimeric motor protein that moves along microtubules in a hand-over-hand manner. Its movement has traditionally been explained by the neck linker's power stroke, which directs the Brownian motion of the tethered head forward. However, recent studies of synthetic molecular motors suggest that kinetic asymmetry is essential for catalysis-driven movement, while power strokes mainly affect efficiency. Here, we present experimental evidence that kinesin-1's preferential forward stepping arises from kinetic asymmetry in microtubule binding between forward and backward sites, and the ATP hydrolysis energy primarily drives the preferential detachment of the trailing head, making the system function as an information ratchet.

1Pos072 **動的水チャネルを介したべん毛モーターの回転運動の全原子分子動力学解析**
All-atom molecular dynamics analysis of rotational motion of flagellar motor mediated by dynamic water channels

Yukinari Kamiyama, Takumi Matsumoto, Tsubasa Nakai, Mitsunori Takano (Grad. Sch. Adv. Sci. & Eng., Waseda Univ.)

MotAB complex of bacterial flagellar motor is composed of MotB dimer and ring-like MotA pentamer. Recent studies suggest that MotA rotates around MotB, coupling with proton flow from outside of membrane. To elucidate the rotational mechanism of MotAB, we conducted all-atom MD simulation using recent cryo EM structure of MotAB. We observed the unidirectional Brownian rotation of MotA, depending on protonation state of conserved aspartate in MotB (bD). In addition, we observed that water channels, which would mediate the proton transfer, are formed and disrupted as the protonation state of bD and the rotational angle of MotA change. We discuss the coupling mechanism of the rotational motion and the proton transfer, both of which are mediated by the dynamic water channels.

Takanori Harashima^{1,2}, Akihiro Otomo^{1,2}, Ryota Iino^{1,2} (¹*Institute for Molecular Science*, ²*Graduate Institute for Advanced Studies, SOKENDAI*)

DNA nanoparticle (DNA-NP) motor moves on an RNA monolayer surface as a burnt-bridge Brownian ratchet driven by enzymatic RNA hydrolysis. However, its speed is only a few nm/s and far lower than those of motor proteins. Here, we performed high-precision single-particle tracking and developed geometry-based kinetic simulation to identify bottleneck limiting motor performance. We found that both enzyme binding and DNA/RNA hybridization are the bottlenecks, and increased enzyme concentration and redesigned DNA/RNA sequence to improve the bottlenecks. The engineered motor achieved a speed of 30 nm/s and a run length of 3 μ m. Furthermore, to improve unidirectionality, we developed 1D RNA/DNA nanotube rail and visualized unidirectional motion of DNA-NP motor along the rail.

Akihiro Fukuda, Yohei Nakayama, Shoichi Toyabe (*Grad. Sch. Eng., Tohoku Univ.*)

Biological molecular motors are high-performance nanomachines that convert chemical energy into mechanical motion through chemomechanical coupling. Some motors have intermediate states within a reaction cycle. The coupling is often described by reaction-diffusion models with aligned potential. The alignment of potential is expected to affect motor performance. In this study, we investigate how intermediate states influence kinetics, focusing on their role in enhancing motor speed. We found that the speed is increased when the intermediate states lower the barrier height. Our findings provide insights into the design of natural motors and guide the development of efficient artificial molecular motors.

Kenta Toshino, Taro Q.P. Uyeda (*Dept. Pure. & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

Actin filaments exhibit structural polymorphism, adopting different conformations depending on bound actin-binding proteins (ABPs) or nucleotides. We analyzed submicron-scale inhomogeneity in fluorescence intensity along filaments labeled with sub-stoichiometric rhodamine-phalloidin (RhPh). Simulation analysis assuming random binding and colocalization of RhPh and Alexa488-phalloidin along the filaments indicated that structural polymorphism of the filaments contributes to the inhomogeneous staining. The fluorescence inhomogeneity was reduced by Pi or ATP + myosin II. Given that these conditions reduce cofilin affinity of actin, the observed fluorescence inhomogeneity may reflect structural states that influence ABP interactions.

Shingo Fukuda¹, Akihiro Otomo^{2,3}, Ryota Iino^{2,3}, Toshio Ando¹ (¹*WPI NanoLSI, Kanazawa Univ.*, ²*Inst. for Mol. Sci., NINS*, ³*SOKENDAI*)

F₁-ATPase is a molecular motor that rotates the γ shaft in the $\alpha_3\beta_3$ stator ring. The β s sequentially undergo conformational changes to drive the γ rotation by hydrolyzing ATP. Many studies have used optical microscopy to observe probes attached to the rotating γ , revealing the coupling of rotation and catalysis based on the γ angles. However, the conformational dynamics of catalytic β s have remained elusive. Here, we used our fastest high-speed AFM to visualize the rotor-less F₁-ATPase ($\alpha_3\beta_3$ subcomplex). This imaging has enabled the identification of previously unidentified intermediate structures, thereby establishing the coupling scheme based on the β s' conformations. This highlights the coordination between β subunits during the chemomechanical cycle.

1Pos077 テザーの改変によるキネシン-1 モータードメインの基本的運動機構の解明
Tether-dependent regulation reveals core motility mechanism of the kinesin-1 motor domain

Rieko Sumiyoshi¹, Masahiko Yamagishi^{1,2}, Junichiro Yajima^{1,2,3} (¹*Grad. Arts & Sci., Univ. Tokyo*, ²*Komaba Inst. Sci., Univ. Tokyo*, ³*RCCSB, UBI, Univ. Tokyo*)

Kinesin is a motor protein that walks along microtubules, but the precise molecular mechanism of its motility remains unclear. Dynamics of N- and C-terminal tethers have been proposed as essential for motor activity. Here, we show that motility can arise from the motor core itself. We performed *in vitro* gliding assays using kinesin monomers tethered via various surface loops with different artificial tethers. All tested loop-tethered kinesin exhibited unidirectional motility, and tether properties significantly affected behavior. Surprisingly, some showed minus-end-directed motility, and one even reversed its direction depending on tether type. We propose a model in which the kinesin motor core generates force in response to external forces and local electrostatic cues.

1Pos078 *C.elegans* キネシン BMK-1 と有糸分裂キネシン Eg5 阻害剤の生化学的特性と相互作用
Biochemical Characterization and Interaction of *C.elegans* kinesin BMK-1 with Mitotic Kinesin Eg5 Inhibitors

Fofou Yonta Tostani, Shunsuke Kumagai, Nur Fatin Liyana Binti Salwadi, Shinsaku Maruta (*Grad.Sch., Soka Univ.Tokyo*)

Kinesin Eg5 hydrolyzes ATP to power crosslinking of anti-parallel microtubules during mitosis and overexpressed in cancer cells. Inhibitors like STLC and monastrol bind a pocket formed by helices $\alpha 2$, $\alpha 3$, and an extended L5. We previously developed photoresponsive Eg5 inhibitors for light-controlled ATPase activity *in-vitro*. To adapt this *in vivo*, we focused on *C. elegans*, which expresses BMK-1 (KLP-16) with an elongated L5 like Eg5. BMK-1's biochemical traits, however, remain unclear. We expressed its motor domain in *E. coli* and analyzed biochemical features and STLC response. Varying L5 length altered sensitivity to STLC, suggesting a shared allosteric site. Our findings indicate that despite functional differences, BMK-1 shares key biochemical properties with Eg5.

1Pos079 KIF6 による鞭毛運動とエネルギー調節の分子メカニズム
KIF6's Role in Ciliary Motility and Energy Regulation

Tsukasa Makino¹, Chizuru Ito², Takeshi Masuda³, Kazuho Ikeda¹, Daisuke Takao^{1,4}, Yasushi Okada^{1,5}, Kiyotaka Toshimori², Masahide Kikkawa¹ (¹*Univ. Tokyo*, ²*Chiba Univ.*, ³*Keio Univ.*, ⁴*Huazhong Agricultural Univ.*, ⁵*RIKEN BDR*)

Cilia and flagella are essential for movement *in vivo*, driven by dynein and ATP. Mutations in the KIF6 gene, a kinesin protein, are linked to ciliopathies, but its role in motility remains unclear. This study investigates KIF6's function using KIF6 knockout (KO) and EGFP-KIF6 transgenic mice. KIF6 KO mice exhibited male infertility, immotile sperm, and abnormal ciliary structure. In transgenic mice, KIF6 localized from spermatocyte cytoplasm to the manchette (a microtubule structure involved in flagellar elongation) and to the flagellum's midpiece. KIF6's interaction with energy metabolism-related proteins suggests its role in ATP regulation, crucial for flagellar motility. These findings reveal the molecular mechanisms of motility and energy regulation.

1Pos080 歯周病菌の線毛の先端蛋白質 FimD の X 線結晶構造解析
Structure of FimD, a tip protein of the pili of gum disease bacterium *Porphyromonas gingivalis*

Norihiro Takekawa, Yusuke Ando, Rei Kojima, Katsumi Imada (*Grad. Sch. Sci., Osaka Univ.*)

Fim pili of *P. gingivalis* consist of five pilin proteins, FimA/B/C/D/E. The single pilus is formed by approximately 40–200 FimA molecules, with one FimB at the base and one of the tip pilins (FimC/D/E) at the tip. The tip pilins share conserved N-terminal domains and unique C-terminal regions. In this study, we determined the X-ray crystal structure of the C-terminal region of FimD. This region contains two domains: one resembling the BACON domain, which binds to glycoproteins such as mucin, and another resembling the Lcl_C domain, which forms a trimer to bind glycans. These findings suggest that pili with FimD at the tip form a bundle of three, and the bundle interacts with glycoproteins secreted by host epithelial cells via both the BACON and trimeric Lcl_C domains.

1Pos081 細胞形態切り替え材料による細胞周期の進行速度操作への試み
Modulating Cell Cycle Progression by Dynamic Control of Cell Shape Using Stimuli-Responsive Substrates

Sayaka Masaike, Satoru Kidoaki (*IMCE, Univ. Kyushu*)

Cell synchronization is essential for studying cell-cycle phase-specific phenomena, but chemical methods such as DNA or microtubule inhibitors can impair viability and induce genomic instability. We propose a drug-free strategy based on the link between the cell cycle and cell shape: interphase cells are spread, mitotic cells are rounded. Disrupting adhesion states appropriate for each cell-cycle phase alters the duration of that phase. Cells also adapt their shape in response to mechanical cues. We hypothesized that mimicking the mechanical adhesion environments of specific cell-cycle phases enables drug-free synchronization via intrinsic mechano-responsiveness. We investigated whether shape-induced cues delivered via tunable substrates modulate cell-cycle progression

1Pos082 巨大纖毛虫 *Spirostomum ambiguum* の細胞伸長に関わる表層微小管束間の滑り運動
Active sliding between microtubule ribbons extending from the ciliary basal bodies elongates the giant ciliate *Spirostomum ambiguum*

Kosuke Nakamura¹, Seiji Sonobe¹, Kazuhiro Oiwa^{1,2} (¹Grad. Sch. Sci., Univ. Hyogo, ²Adv. ICT Res. Inst., NICT, Kobe)

Spirostomum ambiguum snaps short on mechanical cue and then slowly regains length. EM shows its cortex is built from parallel microtubule ribbons issuing from ciliary basal bodies; ribbon overlap is high in the contracted state and low in the elongated one, suggesting re-extension is produced by ribbon sliding. Demembrated cells swell slightly when Mg-ATP is locally applied. Isolated basal-body + ribbon complexes (Oregon-green-taxol-labelled) assemble comb-like arrays with 1.9 μm ciliary spacing; 5 μM ATP expands this to 2.8 μm , supporting a telescope-like, dynein-driven elongation mechanism. This reset readies the cell for repeated contract-elongation cycles. (Supported by JSPS KAKENHI, Grant Numbers JP25K00974, JP21H02455, JP17K07376 to K.O.)

1Pos083 時間情報を用いたアメーバ細胞の牽引力場測定
Inference of cellular traction forces using temporal information

Kazuko Hamaoka, Hirokazu Tanimoto (*Grad. Sch. Nanobiosci., Yokohama City Univ.*)

Traction force is a mechanical force that cells exert on the substrate. Estimating traction force from gel displacement data using traction force microscopy is an ill-posed inverse problem, and it is difficult to estimate accurately due to the influence of measurement noise.

In this study, we developed a new method for estimating traction force using a Kalman filter, which differs from conventional spatial filtering and regularization methods. The proposed method incorporates a dynamical model of cell movement into a state equation, temporally smoothes noise, and sequentially estimates traction force at high temporal resolution. In this presentation, we report numerical simulations and experimental data applications, including comparisons with other methods.

1Pos084 CheY Phosphorylation-Mediated Turning Enables Polarity Alignment at the Swarming Front in *Vibrio alginolyticus*

Kakeru Sumitomo, Ikuro Kawagishi, Masatoshi Nishikawa (*Grad. Sch. Sci., Univ. Hosei*)

Vibrio alginolyticus cells exhibit collective migration on agar surfaces, with elongation and numerous lateral flagella that drive movement along the long axis. Orientation at the leading edge is key for collective migration. We previously reported that leading cells align perpendicularly to the spread, but how this polarity forms are unclear. Here, we show that leading cells turn over, moving to and from the rear in about 50 sec. Tracking showed about five times higher curvature in trajectories than in swarm-deficient cells, which accumulate with perpendicular polarity. This suggests frequent turning aids alignment and smooth leading-edge movement. We found that the phosphorylation/dephosphorylation cycle of CheY is essential for low-persistency motion and swarming.

[1Pos085](#) Mechanosensitive adhesion complexes that lead to complex cell crawling behaviors in a one-dimensional track.

Hsuan-Yi Chen (*National Central University*)

We present an active gel model with mechanosensitive adhesion complexes that exhibit simple moving behaviors, such as rest and constant velocity motion, and complex cell crawling behaviors, such as stick-slip and back-and-forth movements. In this model, adhesion complexes are modeled as elastic objects that sense the total force and the gradient of force acting on them by the active gel. We find that adhesion complexes sensing force are less likely to exhibit complex moving patterns than adhesion complexes sensing force gradient. A result that future quantitative mechanobiological experiments can test.

[1Pos086](#) 制御された局所外力印加により明らかにする細胞境界の変形と分子応答の因果関係
Reveal the causal relationship between tissue deformation and molecular response through optical manipulation

Kenji Nishizawa¹, Shao-Zhen Lin³, Claire Chardès², Jean-François Rupprecht³, Pierre-François Lenne² (¹*Graduate School of Engineering, Tohoku University*, ²*CNRS, Centre de Physique Théorique*, ³*CNRS, The Institute of Developmental Biology of Marseille*.)

Tissue morphogenesis during embryonic development relies on the dynamic remodeling of cell-cell junctions. In this study, we developed a 2-point optical manipulation technique to apply distinct mechanical patterns to junctions in the early epithelium of *Drosophila* embryos. By employing two optical traps, we deform the tissue significantly. Notably, direct manipulation of both ends of a junction led to complete contraction of the junctional segment. Furthermore, real-time imaging of Myosin-II dynamics demonstrated a deformation-mode-dependent molecular feedback mechanism. These findings underscore the pivotal role of Myosin-II in the mechanical remodeling of cell-cell junctions and highlight the significance of mechanical feedback in tissue morphogenesis.

[1Pos087](#) リアルタイムフィードバック機構を用いたサブストレイトの硬さによる機械刺激への拍動応答
Modulation of Beating Response to Mechanical Stimulation by Substrate Stiffness Using Real-Time Feedback Control

Ayaka Namiki, Arisa Mizutani, Yuuta Moriyama, Toshiyuki Mitsui (*Dept. Phys. Sch. Sci., Aoyamagakuin Univ.*)

Substrate stiffness influences cell behavior such as differentiation, proliferation, and alignment, playing a key role in replicating *in vivo* conditions. We examined the beating response of cardiomyocytes on PDMS substrates with different stiffnesses (400 kPa and 80 kPa) under mechanical stimulation. Cardiomyocytes were isolated from chick embryos at embryonic day 5 and cultured on linearly patterned collagen-coated PDMS to promote 1D alignment. A custom device enabling phase-controlled mechanical stimulation via real-time prediction of spontaneous beating was used. Significant modulations in beating response were observed between the two stiffness conditions, suggesting that substrate elasticity critically affects cardiomyocyte mechanical responsiveness and function.

[1Pos088](#) Integrative Spatiotemporal Analysis of Collective Cell Migration and ERK Dynamics in Epithelial MDCK Wound Healing

Lisna Hidayati¹, Kazuhiro Aoki², Yuichi Sakumura¹ (¹*Graduate School of Science and Technology, Nara Institute of Science and Technology*, ²*Graduate School of Biostudies, Kyoto University*)

How ERK signaling regulates collective cell migration by coordinating neighboring cells during wound healing remains unclear. We developed an integrative workflow combining time-lapse imaging, image preprocessing, manual cell segmentation, ERK quantification, cell tracking, and Motion-Triggered Average (MTA) to dissect MDCK scratch wound healing. About 70% of the inner cells migrated below 1.5 pixels/frame, while cells near the wound edge moved faster. We found that the movement of each cell is related not only to its own ERK activity but also to the time derivative of those activities in surrounding cells. Our cell-centered MTA revealed how neighboring cells align their motion, providing fine-scale insights into collective migration dynamics.

1Pos089 破骨細胞融合における membrane-cortex attachment と BAR タンパク質の機械的制御
Mechanical control of cell-cell fusion during osteoclastogenesis by membrane-cortex attachment and BAR proteins

Yuri L. Nemoto^{1,2}, Yumeng Wan², Tsukasa Oikawa³, Kazunori Takano⁴, Takahiro K. Fujiwara⁵, Kazuya Tsujita^{1,2}, Toshiki Itoh^{1,2}
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Cell-cell fusion, a fundamental biological phenomenon, is mediated by membrane protrusion driven by actin reorganization. However, the role of membrane mechanics in this process remains to be elucidated. We revealed that a decrease in plasma membrane (PM) tension is a mechanical prerequisite for cell-cell fusion during osteoclastogenesis. Osteoclast differentiation causes the reduction in ezrin expression, a member of ERM protein, resulting in a decrease in PM tension. Mechanistically, reduced PM tension leads to membrane protrusive invadosome formation driven by membrane curvature-inducing/sensing BAR proteins, thereby promoting cell-cell fusion. The findings of this study offer insights into the mechanism of cell-cell fusion under the control of membrane mechanics.

1Pos090 幅広い細胞種に適応した中心体単離手法の開発
Development of centrosome isolation methods adaptable to various cell types

Momoko Miyazawa, Shohei Yamamoto, Daiju Kitagawa (*Grad. Pharm., Univ. Tokyo*)

The centrosome is an evolutionarily conserved organelle among many animal cells and contributes to the formation of the mitotic spindle and cilia. It is a membrane-less organelle composed of centrioles surrounded by a pericentriolar matrix. Its unique physical properties are suggested to play a role in maintaining its structure and function. However, the physical properties of the centrosomes remain poorly understood. We have been developing methods to isolate centrosomes from human cells to directly measure their physical properties. In this presentation, we will report our new centrosome isolation method applicable to various cell types, aiming to establish a system for analyzing differences in the physical properties of centrosomes across different cell types.

1Pos091 TIRF 解析によるアクチン重合ダイナミクスにおける His161 の役割解明
Elucidating the role of His161 in actin polymerization dynamics using TIRF analysis

Kota Onozato¹, Mitsusada Iwasa², Shuichi Takeda², Toshiro Oda³, Hajime Honda¹, Ikuko Fujiwara¹ (¹Materials Sci. & Bioeng., Nagaoka Univ. of Tech., ²Grad. Sch. Info., Nagoya Univ., ³Faculty of Health and Welfare, Tokai Gakuin University)

Actin polymerization is coupled with ATP hydrolysis, and the nucleotide state critically regulates filament dynamics. The ADP-Pi state is the most stable within filaments, and release of Pi promotes turnover. We focused on His161, whose side chain flips toward ATP upon polymerization, rearranging water molecules to regulate hydrolysis. Using recombinant human β -actin, which shares the active-site sequence with skeletal α -actin, our TIRF assay found that the H161D mutant polymerized at a rate comparable to wild type (8.2 vs. 8.7 / μ M/s) but showed no depolymerization (0.0 vs. 0.9 /s). In bulk assay, this mutant showed slow Pi release. Together with X-ray crystallographic data, we discuss how the H161 mutation impairs actin ATP hydrolysis and polymerization dynamics.

1Pos092 アクチン重合制御における古細菌ゲルソリン各ドメインの TIRF および構造解析による機能解明
Dissecting Domain Functions of Archaeal Gelsolin in Actin Assembly by TIRF and Structural Analyses

Houryou Mizuki¹, Shuichi Takeda^{2,3}, Robert Robinson^{3,4}, Ikuko Fujiwara¹ (¹Materials Sci. & Bioeng., Nagaoka Univ. of Tech., ²Grad. Sch. Info., Nagoya Univ., ³RIIS, Okayama Univ., ⁴VISTEC, Thailand.)

Actin and gelsolin, essential proteins in eukaryotes, are also found in Asgard archaea, close relatives of eukaryotes. We studied a gelsolin from *Lokiarchaeota*, 3DGel, composed of D0, D1, and D2 domains. TIRF assays revealed that full-length 3DGel severs actin filaments in a Ca^{2+} -dependent manner, similar to eukaryotic gelsolins. As in eukaryotes, minimal severing activity resides in D1 but is detectable only at high concentrations. This activity was restored by connecting D2, indicating cooperative actin interactions. D0 did not affect actin depolymerization but partially inhibited barbed end elongation, suggesting a leaky cap function. Crystal structures showed that D1 and D2 bind actin like eukaryotic gelsolins, while D0 engages barbed end subunits via a unique mode.

1Pos093 TIRF 顕微鏡と構造解析により明らかになった Cytochalasin D のアクチンフィラメント作用機構
Cytochalasin D Inhibits Actin Dynamics through Transient Capping and Severing

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Cytochalasin D (CytoD) is widely used as a barbed-end capper of actin filaments; however, its molecular mechanism remains unclear. Using TIRF microscopy, we demonstrated that CytoD inhibits actin polymerization by transiently capping barbed ends, with a capping half-life of approximately 80 seconds. This suggests that CytoD caps actin filaments through a rapid association and dissociation cycle. Interestingly, CytoD severs filaments at commonly used concentrations, while cofilin and inorganic phosphate suppress this severing activity. We discuss CytoD's regulatory mechanism on actin, drawing on kinetic data from TIRF observations and structural insights from the CytoD-bound actin complex.

1Pos094 初期胚における一過的な核の物性変化と転写のバーストの促進
Changes in the physical properties of early embryonic nuclei promote a transcriptional burst

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The nucleus regulates gene expression and genome organization, but its physical properties in embryonic cells remain poorly understood. We investigated nuclear mechanics during early mouse development and found that nuclei at the 2-cell stage undergo marked softening and deformation coinciding with zygotic gene activation (ZGA). Softer nuclei correlated with higher developmental potential. Mechanistically, lamin B1 was transiently cleared from the nuclear envelope via autophagy, while other lamins remained. Disrupting this process stiffened nuclei and impaired ZGA transcription. Artificial stiffening also suppressed ZGA transcription. Thus, nuclear softening driven by autophagy-mediated lamin B1 removal is essential for transcriptional activation and normal development.

1Pos095 The mechanical properties of cells grown at the interface of ferroelectric domain walls

Alexis Borowiak, Takeshi Shimi, Yohei Kono, Takeshi Fukuma (*NanoLSI, Kanazawa University*)

In this work, we aim to establish a new method for investigating the mechanical properties of living cells with an AFM nanoneedle for cells grown on field gradients that occur between opposite ferroelectric polarization domains and study the electromechanical properties of living cells. Our results suggest that the field gradient created at the interface of opposite ferroelectric domains affects the mechanical properties of the cell and nucleus membranes. The penetration of the cell membrane is more straightforward as almost no force is needed to penetrate its cell membrane. These results open new possibilities for understanding, studying, and modulating the inner part of cells under a field gradient at the interface of 180° ferroelectric domain walls.

1Pos096 1 分子 SuperPAINT 法による細胞膜全体にわたる動的ナノスケール不均一性の可視化
SuperPAINT visualization of dynamic nanoscale heterogeneity of the entire plasma membrane

Maoji Wang¹, Bo Tang¹, Takahiro Fujiwara², Taka-Aki Tsunoyama¹, Akihiro Kusumi¹ (¹Okinawa Institute of Science and Technology, ²Institute for Integrated Cell-Material Sciences, Kyoto University)

In this presentation, I will introduce the use of superPAINT, a single-molecule super-resolution PAINT method (see the presentation by Bo Tang et al.), for time-dependent mapping of molecular concentrations (hotspots) and local diffusion properties in the live-cell plasma membrane (PM). We examined CD59, a GPI-anchored protein, which is considered enriched in nanoscale lipid raft domains. Our newly developed analysis software enables direct visualization and measurement of CD59 cluster lifetimes, spatial organization, and rapid molecular exchange. This analysis is extended to other raft-associated and non-associated proteins, providing an entirely new method for visualizing the time-dependent changes of the nanoscale heterogeneities of the entire PM at a glance.

Takemasa Nakamura¹, Hiroyuki Noji^{1,2}, Kazuhito Tabata^{1,2} (¹*Department of Applied Chemistry, School of Engineering, University of Tokyo*, ²*Research Institute of Planetary Health (RIPH), The University of Tokyo*)

Escherichia coli is considered to possess a robust ability to maintain intracellular Ca^{2+} concentration ($[\text{Ca}^{2+}]_{\text{in}}$) homeostasis within two orders of magnitude from its physiological concentration (300 nM). In this study, we constructed *E. coli* BL21-AI expressing the calcium sensor protein NEMOer-c and quantified $[\text{Ca}^{2+}]_{\text{in}}$ at 0–100 mM extracellular Ca^{2+} concentrations ($[\text{Ca}^{2+}]_{\text{ex}}$) by fluorescence imaging. As a result, the $[\text{Ca}^{2+}]_{\text{in}}$ in BL21-AI increased to the millimolar level, becoming comparable to $[\text{Ca}^{2+}]_{\text{ex}}$. Further, similar single-cell experiments of *E. coli* C43 revealed strain-dependent variability in the population of cells exhibiting $[\text{Ca}^{2+}]_{\text{in}}$ fluctuations. These results suggest that the $[\text{Ca}^{2+}]_{\text{in}}$ homeostasis of *E. coli* can possess heterogeneity.

Amine Aladag¹, Taka-Aki Tsunoyama¹, Irina Meshcheryakova¹, Maoji Wang¹, Jun-Seok Lee¹, Bo Tang¹, Hiroko Hijikata³, Takahiro K Fujiwara³, Sawako Yamashiro², Akihiro Kusumi¹ (¹*Okinawa Institute of Science and Technology*, ²*Kyoto University Graduate School of Biostudies*, ³*Kyoto University Institute for Integrated Cell-Material Sciences, KULAS*)

How the neuronal inhibitory synapse (NIS) is generated is a central issue in neuronal network regulation. Gephyrin is a major protein in the NIS, but does not directly interact with another key NIS component actin, whereas actin-polymerizing proteins, Ena/VASP family proteins, particularly VASP, Evl, and Mena (VEM), which contain extensive intrinsically disordered regions, exist in the NIS. Here, we found that gephyrin and individual VEM proteins alone can undergo liquid-liquid phase separation (LLPS) both in vitro and in cultured cell lines, and that they also form co-condensates, which induce actin polymerization. These results suggest that co-condensation of gephyrin with VEM proteins and actin polymerization on the co-condensates may be key steps for NIS formation.

Gen Honda^{1,2}, Satoshi Sawai^{1,3}, Miho Yanagisawa^{1,2,3} (¹*Department of Basic Science, Graduate School of Arts and Sciences, University of Tokyo*, ²*Komaba Institute for Science, Graduate School of Arts and Sciences, University of Tokyo*, ³*Research Center for Complex Systems Biology, Graduate School of Arts and Sciences, University of Tokyo*)

How molecular diffusion is controlled in fluidic membranes remains largely unclear. Using a reconstitution approach, we found that cell extracts reduce fluidity of artificial lipid bilayers. Pharmacological, genetic and enzymatic studies indicated that lipid-modifying enzyme phospholipase D (PLD) is responsible for the reduced fluidity. In live cells, over-expression of PLD specifically reduced diffusivity of the myristoylated kinase PKBR1. The reduction in PKBR1 diffusivity depends on its polybasic region near the lipidated end, supporting a direct interaction with anionic phospholipids. PLD over-expression suppressed the size and lifetime of PIP3 patches. Our results suggest that "myristoyl-electrostatic switch"-like mechanism plays in PIP3 patch formation.

Dan Horonushi¹, Souta Suzuki¹, Maiha Ando¹, Haruka Yuki¹, Shinya Kato¹, Kenji Yasuda^{1,2} (¹*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, ²*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

To elucidate the mechanism limiting macrophage phagocytosis, we assessed the phagocytic capacity using IgG-opsonized non-digestible microneedles, microcapillary tubes, and microbeads. Macrophages backtracked their membrane to expel the microneedle at the engulfment limit. The maximum internalized volume correlated with membrane expansion in a 5.0 μm region surrounding the attached needle. In contrast, macrophages reached the phagocytic limit prior to maximum membrane expansion, and no membrane backtracking was observed in bead phagocytosis. These findings indicate two distinct mechanisms for limiting macrophage phagocytosis: membrane backtracking at the physical limit of engulfment, and inhibition of phagocytosis initiation to prevent over-phagocytosis and cell damage.

1Pos101 神経細胞による心筋細胞集団間の興奮伝導接続
Excitatory Connection Between Cardiomyocyte Populations Mediated by Neurons

Ayuri Sakaguchi, Kentaro Kito, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ., Tokyo, Japan*)

In the treatment of myocardial infarction, cardiac cell sheet applications have been progressing as a promising regenerative therapy. Since neurons, like cardiomyocytes, are excitable cells, we hypothesized that they could also be a means of reconstructing electrical conduction. To test this hypothesis, we used agarose microchamber (AMC) to connect two cardiomyocyte populations via neurons and recorded their activity using a multi-electrode array (MEA) system. As a result, synchronized beating was observed between the two populations. For the next study, we are preparing detachable neuronal cell sheets using PEI-coated dishes and transplanting them to connect cardiomyocyte populations, to evaluate whether functional neural networks can mediate excitation conduction.

1Pos102 複数微粒子貪食数に対する細胞膜最大伸長量の応答変化計測からの最大貪食機能の解明
Determining Maximum Macrophage Phagocytosis by Measuring Membrane Extension
Response During Sequential Particle Uptake

Shinya Kato¹, Dan Horonushi¹, Haruka Yuki¹, Kei Shibata², Syunya Morikawa², Kenji Yasuda^{1,2} (¹*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, ²*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

Phagocytosis by macrophages consumes their membrane, leading to the assumption that the phagocytic limit is determined by the extent of membrane depletion. To investigate this hypothesis, we quantified the maximum membrane extension of macrophages using opsonized microneedles after the cells had engulfed multiple opsonized beads. The results demonstrated that the degree of membrane extension remained constant regardless of the number of beads internalized. Macrophages that had ceased phagocytosis after consecutive engulfment were still capable of extending their membranes in response to external stimuli. These findings suggest that the limit of phagocytosis capacity is governed not solely by total membrane consumption but also by an alternative regulatory mechanism.

1Pos103 オブソニン化マイクロニードルに対するマクロファージ応答の極性を明らかにする貪食膜伸長と細胞運動の相関解析
Coupled coordination of phagocytic membrane extension and cell migration reveals polarity in macrophage response to opsonized microneedles

Haruka Yuki¹, Dan Horonushi¹, Maiha Ando¹, Sinya Kato¹, Kenji Yasuda^{1,2} (¹*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, ²*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

Phagocytosis and migration in macrophages are both regulated by GTPases, yet their interaction remains unclear. We investigated how cell motility regulates spatial phagocytosis using opsonized microneedles. During single-needle phagocytosis, migration accompanied phagocytic membrane extension but stopped during retraction. When two microneedles were applied sequentially from opposite sides, phagocytosis of the second needle was suppressed during extension toward the first needle. Initiation of retraction from the first needle triggered phagocytosis of the second needle and reversed migration. These findings indicate that directional migration limits local phagocytic ability, producing spatial polarity on the macrophage surface.

1Pos104 単一細胞レベルにおける直線状心筋細胞ネットワークの伝導速度
Conduction Velocity of Linear Cardiomyocyte Networks at single-cell level

Shinnosuke Mori, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

The conduction velocity of cardiomyocytes in dispersed culture is slower than that of the living heart. This is because the direction of potential propagation is not constant and tends to diffuse. In this study, we measured the conduction velocity of linear cardiomyocyte networks at the single-cell level using an agarose microchamber (AMC) and the Multi-Electrode Array (MEA) system. As a result, we could construct a linear cardiomyocyte network with a minimum width of 20 μm on MEA with AMC. The conduction velocity is currently being analyzed. In order to measure the conduction velocity at narrower widths, we are currently investigating processing techniques and analysis methods.

Chiho Watanabe (Grad. Sch. Int. Sci. Life, Hiroshima Univ.)

Tau protein is a major aggregation-prone protein implicated in various neurodegenerative diseases. The cellular environment in which tau aggregation occurs in vivo is typically crowded with both macromolecules and membranes. In this study, we investigated the interactions between tau protein and lipid membranes using model lipid membranes (large unilamellar vesicles, LUVs) and environment-sensitive fluorescent probes such as Laurdan and Prodan, which shift their fluorescence spectra depending on the polarity of their surroundings. Fluorescence shifts were observed upon addition of tau proteins to LUVs with certain lipid compositions. These shifts also appeared to differ depending on whether the tau protein was wild-type or mutant.

Phonphiphat Bamrung (คณะวิทยาศาสตร์ มหาวิทยาลัยเกษตรศาสตร์)

The spread of antibiotic-resistant bacteria is a serious global health threat. Coco-glucoside, a natural surfactant derived from coconut oil, shows antibacterial activity by disrupting bacterial membranes. However, its mechanism remains unclear. This study uses molecular dynamics (MD) simulations to investigate how different types of coco-glucoside (C8, C10, C12, and C14) affect the membrane of *Escherichia coli*. The results reveal that each variant disrupts the membrane via distinct pathways, with C8 interacting most rapidly. Additionally, coco-glucosides tend to form micelles prior to membrane disruption. These insights can guide the development of natural antibacterial agents and support innovations in pharmaceuticals and hygiene products.

Emika Matsumoto¹, Michael Postrado², Hiroshi Takahashi² (¹Sch. Sci. Tech. Gunma Univ., ²Grad. Sch. Sci. Tech. Gunma Univ.)

Recent studies show that high doses of sucralose can impair immune responses in mice. To explore its interaction with cell membranes, we investigated model membranes of dipalmitoylphosphatidylcholine (DPPC) bilayers in sucralose solutions. Calorimetry revealed a biphasic effect: pre-transitions and main transition temperatures decreased at low concentrations, while the main transition increased at higher levels. Pre-transitions disappeared above the concentration where this reversal occurred. X-ray diffraction showed that sucralose above 0.2 M induces the interdigitated gel (LβI) phase below the main transition. Prodan fluorescence indicated that sucralose solutions are slightly more hydrophobic than sucrose, possibly explaining LβI phase formation.

Ai Nakagawara¹, Takafumi Shimoaka¹, Toshiyuki Takagi², Hiroshi Takahashi¹, Takashi Kikukawa³, Hideki Amii^{1,4}, Masashi Sonoyama^{1,4,5} (¹Grad. Sch. Sci. & Tech., Gunma Univ., ²AIST, ³Fac. Adv. Life. Sci., Hokkaido Univ., ⁴GIAR, Gunma Univ., ⁵GUCFW, Gunma Univ.)

Phospholipids with partially fluorinated double hydrophobic chain ends (FnFn-DMPC) are reported to be useful in studies of the membrane protein bR. In this study, we developed novel FnF0-DMPC phospholipids, of which only one of the hydrophobic chains is partially fluorinated. By calorimetric measurements of F4F0-DMPC bilayer membranes, the phase transition temperature of F4F0-DMPC is found to be lower than that of F4F4-DMPC. This means a wider temperature range of the liquid crystalline phase F4F4-DMPC, which is suitable for the study of membrane proteins. In addition, spectroscopic measurements of the proteoliposome composed of bR and F4F0-DMPC (bR/F4F0-DMPC) revealed that the quaternary structure and photocycle of bR are different from those of bR/F4F4-DMPC.

1Pos109 表層糖鎖が関与する細菌の細胞外膜小胞形成
Involvement of the surface carbohydrates in bacterial membrane vesicle formation

Jun Kawamoto¹, Taiku Tsudzuki¹, Tomoya Imai², Takuya Ogawa¹, Tatsuo Kurihara¹ (¹*Institute for Chemical Research, Kyoto University*, ²*Research Institution for Sustainable Humanosphere*)

A Gram-negative bacterium, *Shewanella vesiculosa* HM13, produces a large number of extracellular membrane vesicles (MVs). MVs of this strain harbor a single major cargo protein, P49, and are coated with a unique surface polysaccharide that consists of a repeating unit of pentasaccharides containing an acetyl-rich amino sugar. The defect in the surface polysaccharide-synthesis genes resulted in the loss of cargo loading of P49 and a significant reduction in MV production. This mutant showed abnormal balloon-like structure on the membrane surface, indicating that the exterior sugar component might be involved in MV formation in this bacterium.

1Pos110 Giant Plasma Membrane Vesicle の膜粘度測定
Viscosity of Giant Plasma Membrane Vesicles

Tatsuya Itoi (*Dept. of Physics, Tohoku University*)

Membrane viscosity is a key parameter to understanding cellular functions, as it governs the transport of functional molecules in the membrane. We recently developed a method to evaluate membrane viscosity by inducing vortex flow in a model membrane and comparing the flow patterns with a theoretical prediction. Using this method, we found that the viscosity of model membranes composed of only lipids varies significantly with lipid composition. In this study, we measured the viscosity of giant plasma membrane vesicles (GPMVs), which retain the lipid diversity and protein content of the plasma membrane but lack the actin cytoskeleton. We report how structural features of living cells regulate membrane viscosity by comparing GPMVs with model membranes.

1Pos111 自動化技術による膜粘度の顕微鏡画像データ解析の精度向上
Improving accuracy of microscopic image data analysis for membrane viscosity measurement using automation technique

Kenya Haga, Yuka Sakuma, Masayuki Imai (*Grad. Sch. Sci., Tohoku Univ.*)

Membrane viscosity plays a crucial role in the transport of biomolecules responsible for cellular functions. Therefore, membrane viscosity is a key parameter for understanding cellular functions. We recently developed a method for quantitative measurement of membrane viscosity by inducing vortex flow in a model biomembrane and analysing the flow pattern based on theoretical predictions. In this measurement, it is essential to accurately track the position of embedded tracer particles. Here, we used the image analysis software Fiji to automate the detection of tracer positions and the visualization of membrane flow. We report the results and demonstrate the effectiveness of this automated approach.

1Pos112 パターン化人工膜と光ピンセットによる人工生体膜分子の時空間操作
Spatiotemporal Manipulation of Membrane Molecules in Artificial Membranes Using Membrane Patterning and Optical Tweezers

Yasushi Tanimoto¹, Shunya Moriyama¹, Kyoko Masui¹, Fumio Hayashi², Kenichi Morigaki^{3,4}, Chie Hosokawa¹ (¹*Grad. Sch. Sci., Osaka Metropolitan Univ.*, ²*Grad. Sch. Sci., Kobe Univ.*, ³*Biosignal Res. Center, Kobe Univ.*, ⁴*Grad. Sch. Agri., Kobe Univ.*)

Artificial membranes are widely used to investigate the molecular behavior of biological membranes, which are structurally and compositionally complex. In this study, we developed complementary techniques for controlling membrane organization across multiple scales. We achieved microscale spatial confinement of membrane proteins such as rhodopsin and lipids by patterning photopolymerized membranes and demonstrated spatiotemporal manipulation of lipid mobility dynamics with high spatial precision using optical tweezers. These approaches provide controllable environments for studying the diffusion, localization, and interactions of membrane molecules. They also offer new possibilities for the implementation of functional membrane systems in biosensing and drug screening.

1Pos113 電位依存性プロトンチャネル活性化の N 末端制御
N-terminal control of voltage-gated proton channels

Ryuya Nawata, **Akira Kawanabe**, Yuichiro Fujiwara (*Grad. Sch. Biomed. Health Sci., Hiroshima Univ.*)

The voltage-gated proton channel (Hv1) enables proton transport in response to membrane voltage, and is regulated by factors like pH, metal ions, lipids, and ATP. Hv1 has a topology with four transmembrane domains and both N- and C-termini located in the cytoplasm. Mammalian Hv1 activates more slowly than invertebrate Hv1, possibly due to its long, unstructured N-terminal region. This study used electrophysiology to examine mouse Hv1 expressed in HEK293T cells, focusing on the N-terminus. Truncation experiments showed that removing more than 32 residues accelerates activation, while deleting only the first 21 residues slows it down. These findings suggest that the N-terminus has a defined interaction with the transmembrane region, influencing activation kinetics. COI:No

1Pos114 高速原子間力顕微鏡による非競合阻害剤結合状態の AMPA 受容体ナノダイナミクスの解明
High-speed atomic force microscopy reveals nano-dynamics of AMPARs with the non-competitive inhibitors

Keisuke Sato¹, Yimeng Zhao², Motoyuki Hattori², Mikihiro Shibata^{3,4} (¹*Grad. Sch. NanoLS, Kanazawa Univ.*, ²*Sch. Life Sci., Fudan Univ.*, ³*WPI-NanoLSI, Kanazawa Univ.*, ⁴*InFiniti, Kanazawa Univ.*)

AMPA receptors (AMPA) are crucial in drug discovery for epilepsy due to their central role in neuroexcitation. Recent studies have shown that non-competitive inhibitors of AMPARs, such as perampanel (PER), are effective therapeutic agents for epilepsy. However, the nano-dynamics of AMPARs upon inhibition by PER remain unknown. Here, we used high-speed atomic force microscopy [A. Sumino *et al.* *ACS Nano* 2024] to visualize the nanoscale dynamics of AMPARs in the presence of PER. Our findings indicate that the dimeric structure of the flexible extracellular domain of AMPARs frequently splits into monomers upon binding with PER. We will discuss the molecular inhibition mechanism of AMPARs resulting from PER binding.

1Pos115 油中水滴接触膜を用いた膜張力定量下でのアクアポリンの水透過性測定
Measuring aquaporin water permeability using pressure-determined droplet interface bilayers with defined membrane tension

Misuzu Ueki, Takahisa Maki, **Masayuki Iwamoto** (*Dep. Mol. Neurosci., Facul. Med. Sci., Univ. Fukui*)

We evaluated the water permeability of lipid bilayers reconstituted with *Escherichia coli* aquaporin Z (AqpZ) using a droplet interface bilayer (DIB) system in which bilayer tension is quantified from droplet internal pressure (pressure-determined DIB, PDIB). Water permeability increased in an AqpZ concentration-dependent manner under bilayer tensions of 2.2–3.0 mN/m. The AqpZ-induced permeability was inhibited by mercury, with an IC_{50} of 340 μ M. Fluorescence microscopy enabled quantification of AqpZ molecules within the bilayer, allowing estimation of unitary water permeability. These results validate the PDIB method as a platform for analyzing aquaporin activity under defined mechanical conditions.

1Pos116 Ion translocation mechanism of Na⁺-pumping NADH-quinone oxidoreductase from molecular dynamics simulations

Takehito Seki^{1,2}, Moe Ishikawa-Fukuda^{3,4}, Jun-ichi Kishikawa⁵, Masatoshi Murai³, Takahiro Masuya³, Hideto Miyoshi³, Danielle McFee⁴, Blanca Barquera⁴, Kei-ichi Okazaki^{1,2} (¹*SOKENDAI*, ²*Institute for Molecular Science*, ³*Graduate School of Agriculture, Kyoto University*, ⁴*Department of Biological Science, Rensselaer Polytechnic Institute*, ⁵*Department of Applied Biology, Kyoto Institution of Technology*)

The Na⁺-pumping NADH-ubiquinone oxidoreductase (Na⁺-NQR) is a respiratory enzyme that utilizes NADH-mediated reduction as a driving force to generate a Na⁺ gradient. Although cryo-electron microscopy has revealed the complex structures of Na⁺-NQR, the pathway and mechanism of Na⁺ translocation remain unclear. In this study, we performed redox-switched atomistic molecular dynamics (MD) simulations and revealed the redox-state-dependent Na⁺ binding to the iron-sulfur cluster buried in the transmembrane region. Then, targeted MD simulation showed that the alternating-access mechanism of the transmembrane helices mediates Na⁺ translocation. Furthermore, we developed a Markov state model to explore the energetics and kinetics underlying Na⁺ translocation by Na⁺-NQR.

1Pos117 糖脂質 MPlase が関与する膜タンパク質輸送機構の物理化学的解析
Exploring the Role of a Glycolipid MPlase in Membrane Protein Transport through
Physicochemical Studies

Shoko Mori¹, Kaoru Nomura¹, Kohki Fujikawa¹, Tsukiho Osawa¹, Ken-ichi Nishiyama², Keiko Shimamoto^{1,3} (¹Bioorg. Res. Inst., *Suntory Fdn. Life Sci.*, ²Fac. Agric., *Iwate Univ.*, ³Grad. Sch. Sci., *Osaka Univ.*)

For synthesized proteins to function properly, their correct localization is essential. A glycolipid called MPlase (Membrane Protein Integrase), located in the inner membrane of *Escherichia coli*, contributes to the integration of nascent proteins into the cell membrane. We analyzed the interactions between MPlase and molecules involved in these membrane integration events using physicochemical methods such as SPR. It was suggested that substrate proteins and ribosomes interact with MPlase, indicating that MPlase plays a role in membrane transport through these interactions. These analyses will provide new insights into the molecular mechanisms underlying membrane protein transport and highlight the crucial role of MPlase in maintaining cellular function.

1Pos118 コレラ菌アミノ酸走性受容体の広範かつ特異的な検知プロファイル
The versatile and specific sensing profiles of *Vibrio cholerae* amino-acid chemoreceptors

So-ichiro Nishiyama¹, June Minaki¹, Taisei Kumakura¹, Yuta Nogami¹, Fuga Omori^{2,3}, Katsumi Imada⁴, Ikuro Kawagishi^{2,3} (¹Fac. App. Life Sci., *Niigata Univ. Pharm. Med. Life Sci.*, ²Grad. Sch. Sci. and Engin., *Hosei Univ.*, ³Res. Cen. Micro-Nano Tech., *Hosei Univ.*, ⁴Dep. MacroMol. Grad. Sch. Sci., *Osaka Univ.*)

Vibrio cholerae, the causative agent of cholera, exhibits chemotaxis toward various amino acids. It possesses over 40 chemoreceptor homologs, which we call MCP-like proteins (MLPs). Among them, we identified Mlp24 and Mlp37, and the recently Mlp6 as amino-acid chemoreceptors. While their sensing profiles overlap, each also detects distinct ligands. In this study, we examined non-proteinogenic amino acids to further explore these sensing profiles. Mlp37 mediated no response, whereas Mlp24 sensed wide variety of non-proteinogenic amino acids as attractants. Mlp6 displayed a complex profile, sensing some as attractants and others as repellents. The versatility and specificity of these receptors, along with their physiological insights will be discussed.

1Pos119 Abnormal differentiation of olfactory sensory neurons in ATF5 upstream open reading frame mutant mice

Haruo Nakano, Sanetoki Koide, Shuya Yoshida, Mariko Umemura, Shigeru Takahashi, Yuji Takahashi, Yasuhiro Shinkai (*Environ. Biol., Life Sci., Tokyo Univ. Pharm. Life Sci.*)

Activating transcription factor 5 (ATF5) is a stress-responsive transcription factor and is essential for the differentiation and survival of sensory neurons in murine olfactory organs. ATF5 mRNA has two upstream open reading frames (uORF1 and uORF2) in its 5' untranslated region, which confer stress-regulated ATF5 protein translation. In this study, we introduced a mutation into nearby AUG codon of uORF2 to examine the effect of uORF2 translation efficiency on the differentiation of olfactory sensory neurons. We found that mutant olfactory sensory neurons displayed reduced ATF5 protein expressions and less developed into mature neurons. Our results suggest an interplay of uORF2 and ATF5 on the maturation of olfactory sensory neurons.

1Pos120 飢餓状態における線虫 *C. elegans* の低温耐性獲得機構と人工進化解析による新規因子の探索
Mechanism of acquisition of cold tolerance in *C. elegans* during starvation and search for novel factors by artificial evolution analysis

Seiya Kamino¹, Miina Fuzisawa¹, Atsushi Doi², Hideki Doi², Akane Ohta¹, Atsushi Kuhara^{1,3} (¹Institute for Integrative Neurobiology, *Konan University*, ²Kinki University · School of Agriculture Medical Institute of Bioregulation, ³PRIME, AMED)

Adaptation to changing temperatures physiologically is an essential ability for animals on the earth, because temperature is one of uneliminated environmental factors. *C. elegans* has a tolerance mechanism to cold temperatures, 'cold tolerance'. Cold tolerance depends on rearing temperature: worms reared at 15°C can survive at 2°C, while those reared at 25°C die. Unfortunately, we found that starved *C. elegans* enhances resistance to cold temperatures. We now investigate molecular and genetical mechanisms to make starved nematodes more resistant to cold temperatures. In other approach, we are investigating accumulated mutations in the genome to reveal how animals have adapted and evolved over generations against temperature change.

1Pos121

C. elegans の低温耐性に関わる転写伸長因子 TCEB の機能細胞の絞り込み

Narrowing down the functional cells of TCEB, a transcription elongation factor involved in cold tolerance in *C. elegans*

Sho Yabuuchi^{1,2}, Hiroaki Teranishi^{1,2}, Toshihiro Iseki^{1,2}, Natsune Takagaki^{1,2}, Yohei Minakuchi³, Atsushi Toyoda³, Akane Ohta^{1,2}, Atsushi Kuhara^{1,2,4} (¹Dept. Biol. Grad. Sch. Sci. Konan Univ, ²Inst. of Integral NeuroBiol. Konan Univ, ³National Institute of Genetics, Japan, ⁴PRIME AMED)

We are using cold tolerance of *C. elegans* as a model for temperature response (Ohnishi et al., *Nat commun*, 2024). We show here that *tceb-3* gene encoding transcription elongation factor positively regulates cold tolerance. *tceb-3* mutant showed defective cold tolerance which was caused by neural malfunction. Transcriptome analysis with transgenic *tceb-3* mutants determined that a glycerol phosphatase regulates cold tolerance. Combination with single cell transcriptome database and cis-element analysis of *tceb-3* promoter, we narrowed down the number of candidates TCEB-3 functional cells to 6. Ca²⁺ imaging suggested that one of the six neurons showed temperature responsiveness under cooling. We are testing cold tolerance of mutants lacking genes expressed in this neuron.

1Pos122

カエル神経筋接合部シナプスにおけるカゼインキナーゼ阻害剤の効果: 単発刺激放出の抑制と連続刺激での放出増大短期可塑性の強化

Investigation of effect of a casein kinase 2 inhibitor at the frog NMJ: EPP was reduced and short-term plasticity was intensified

Naoya Suzuki (Grad.Sch.Sci., Nagoya Univ.)

It was reported that syntaxin-1A was phosphorylated by casein kinase 2. I studied effect of a casein kinase 2 inhibitor, tetrabromobenzotriazole (TBB), on EPP at the frog NMJ and its short-term presynaptic plasticity, two components of facilitation (fast and slow facilitation) induced by 8 stimuli with 15 msec interval, and augmentation & potentiation induced by 300 stimuli at 20 Hz. The effects of TBB were irreversible. Data before and after a treatment of TBB (bath application of 0.01mM TBB for 30 min then wash out it for 30 min) were compared. After the treatment of TBB, EPP was reduced to about 50-60 %. The amplitudes of slow facilitation, augmentation and potentiation were enhanced to about 1.5 times. The amplitude of fast facilitation did not change.

1Pos123

Thermosensory signal processing by multiple thermoreceptors within a single thermosensory neuron in *C. elegans*

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Sensing environmental information and respond appropriately is essential for organisms to survive and proliferation. We analyzing cold tolerance of *C. elegans* as one of the model for studying thermosensory mechanisms. We have identified ASG, ADL and ASJ, as thermosensory neurons in cold tolerance. Electrophysiological analysis identified that Degenerin/Epithelial Sodium Channel DEG-1 and UNC-8 which are mechanoreceptors act as thermo-receptor. TRP channels and GPCR are thermoreceptors in ADL, and here we found that DEG-1 and UNC-8 are expressed in ADL. We are then investigating whether DEG/ENAC is the third thermoreceptors in ADL, and how triple thermosensory signaling from three types of thermo-receptors is processed within single cell.

1Pos124

クロライドイオンを対イオンとしてもつサンゴオプシンの分光研究

Spectroscopic studies of a coral opsin with chloride ion as a counterion

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Rhodopsins are light-sensitive proteins that initiate vision in animals by covalently binding retinal via a protonated Schiff base linkage, which is stabilized by a counterion, typically a negatively charged amino acid. In the coral opsin Antho2c, however, a chloride ion uniquely functions as the counterion instead of an amino acid residue. In this study, we investigated structural changes associated with chloride ion binding in Antho2c. ATR-FTIR spectroscopy revealed that substitution with different monovalent anions produced broadly similar spectra with subtle variations. Furthermore, spectral changes correlated with the ionic radius, suggesting that environmental effects, rather than differences in binding affinity, modulate the chromophore environment.

1Pos125 アプソモナドが持つ新奇紫外・青色光受容アニオンチャネルロドプシン ApuRs の分光学的特性
Spectroscopic characterization of ApuRs, novel UV- and blue-absorbing anion channel rhodopsins from Apusomonads

Takashi Nagata¹, Luis Javier Galindo², Shunki Takaramoto¹, Andrey Rozenberg³, Hiroto Takahashi¹, Oded Bějá³, Keiichi Inoue¹
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Apusomonads are heterotrophic protists branching deeply within the eukaryotic tree. Apusomonad rhodopsins (ApuRs) constitute a newly discovered microbial rhodopsin group forming a distinct phylogenetic clade, separate from previously known rhodopsins. We characterized the absorption spectra of multiple ApuRs and demonstrated that most act as UV-absorbing anion channels, representing the first microbial rhodopsins known to exhibit absorption maxima in the UV region. We also identified unique retinal photoisomerization pathways triggered by illumination. Site-directed mutagenesis revealed key residues critical for spectral tuning between UV- and blue-absorbing ApuRs. In the presentation, we will discuss potential molecular mechanisms underlying spectral tuning.

1Pos126 固体 NMR によるヘリオロドプシンのアミノ酸残基特異的なダイナミクスとプロトン化状態の解析
Residue-Specific Characterization of Heliorhodopsin Dynamics and Protonation States by solid-state NMR

Yuki Samatsu¹, Sari Kumagai¹, Kota Katayama², Hideki Kandori², Izuru Kawamura¹ (¹*Grad. Sch. Eng. Sci., Yokohama Natl. Univ.*, ²*Grad. Sch. Eng., Nagoya Inst. Tech.*)

Heliorhodopsin (HeR) is a membrane protein with a retinal chromophore, forming a new rhodopsin family with unique topology and a long photocycle [1]. The function of *Thermoplasma* archaeon HeR (TaHeR) is unclear, but the long photocycle implies a signaling role. His23 and His82 are suggested to be involved in M and O intermediate formation [1-3]. Using solid-state NMR, we estimated the pKa values of His23 and His82 from ¹⁵N₂-His labeled mutant samples. In addition, we analyzed the dynamics of the long loop of TaHeR through relaxation time measurements using ¹⁵N-Pro labeled sample.

[1] A. Pushkarev et al. (2018) *Nature*, **558**, 595.

[2] W. Shihoya et al. (2019) *Nature*, **574**, 132.

[3] M. Tsujimura et al. (2022) *Commun Biol*, **5**, 1336.

1Pos127 Time-resolved crystallography reveals structural transitions of a bifunctional cryptochrome bearing a light-harvesting antenna chromophore

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Cryptochromes (CRYs) belong to photolyase/cryptochrome superfamily (PCSF), acting as regulatory blue-light photoreceptors when a light-absorbing chromophore flavin adenine dinucleotide is bound. Recently, we have successfully captured light-activated intermediate structures of a bifunctional animal-like CRY from *Chlamydomonas reinhardtii* (CraCRY), which works both as CRY and DNA repairing photolyase (PL), via time-resolved serial femtosecond X-ray crystallography (TR-SFX), providing structural insights of the signaling states as CRY.

Here, we performed TR-SFX of CraCRY bearing an auxiliary light-harvesting antenna chromophore, 8-hydroxydeazariboflavin (8-HDF), showcasing the molecular basis how CraCRY shifts its bifunctionality toward PL upon 8-HDF binding.

1Pos128 短波長シフトした光駆動内向きプロトンポンプロドプシンの波長制御機構の研究
Study on the color-tuning mechanism of a blue-shifted light-driven inward proton-pumping rhodopsin

Yoshitaka Kato¹, Borja Aldegue-Riquelme², Oded Bějá^{3,4}, Josefa Antón², Keiichi Inoue¹ (¹*ISSP, Univ. Tokyo*, ²*Department of Physiology, Genetics and Microbiology, University of Alicante*, ³*Faculty of Biology, Technion—Israel Institute of Technology*, ⁴*The Nancy and Stephen Grand Technion Energy Program, Technion—Israel Institute of Technology*)

Xenorhodopsins (XeR) are a subgroup of microbial rhodopsins that functions as light-driven inward proton pumps. Although several inward proton pumps have been identified, their absorption spectra are less diverse than those of outward proton pumps. Recently, we discovered a novel XeR, EltXeR, from the extracellular virome of a saltern pond near Eilat, Israel, which may also contain vesicles and other viral-like particles. Interestingly, the absorption maximum wavelength of EltXeR is 525 nm, which is 25–52 nm shorter than those of previously reported XeRs (550–577 nm). In this study, we performed mutational analyses to elucidate the color-tuning mechanism of EltXeR and identified several amino acid residues that contribute to its spectral properties.

Kazuki Ohmichi¹, Tomoki Kawaguchi¹, Keita Sato², Hideyo Ohuchi², Hisao Tsukamoto¹ (¹*Grad. Sch. Sci. Kobe Univ.*, ²*Okayama Univ.*)

Opsins are photoreceptive G protein-coupled receptors (GPCRs) and responsible for photoreception in animals. When opsins receive external light signals, they activate trimeric G proteins. Trimeric G proteins are divided into four subtypes, Gs, Gi/o, Gq, and G12, and Gs-, Gi/o-, and Gq-coupled opsins have been identified and characterized. On the other hand, recent studies revealed that many GPCRs including some opsins are more promiscuously coupled with multiple G protein subtypes than expected. For example, we reported that a ciliary opsin in a fan worm is primarily coupled with Gi/o but also weakly coupled with G12 [Fukuzawa et al., 2025]. In this study, we analyzed G protein-coupling specificity (or promiscuity) of various invertebrate ciliary opsins.

Masae Konno, Takashi Nagata, Keiichi Inoue (*ISSP, Univ. Tokyo*)

Engineering of protein variants is essential for understanding molecular mechanisms and creating advanced protein tools. Although AI-based algorithms predict residues critical for protein functions, manual production of all proposed variants is impractical. We have constructed a new automated liquid-handling platform to address this issue. As a test case, spectral-tuning mutants of *Gloeobacter* rhodopsin were produced by 19 mutations at each of three key residues. *E. coli* transformants carrying mutant genes were isolated by limiting dilution, and their absorption maximum wavelengths were determined in parallel using a microplate reader. This platform facilitates high-throughput and scalable protein variant production, thereby accelerating next-generation protein design.

Rei Abe-Yoshizumi¹, Hideki Kandori^{1,2} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*OptoBio., Nagoya Inst. Tech.*)

Heliorhodopsin (HeR) is a photoreceptor protein discovered in 2018 as the third family of rhodopsins[1], and light-driven ion transport ability was first reported in 2022[2]. However, compared to microbial rhodopsin, which has diverse functions, its physiological function remains unclear. In this study, we focused on actinomycetes as a bacterium that encodes a large number of HeR and attempted to analyze their genetic expression in natural cells. Comparison of HeR gene expression in *Rhodococcus* sp. at different growth stages showed that the HeR gene was expressed at all stages. We will also perform similar analyses using other actinomycetes and discuss the physiological role of HeR.

[1] Nature, 558, 595, 2018, [2] Elife, e78416, 2022

Koyo Yamada¹, Rei Abe-Yoshizumi¹, Tatsuro Nishikino^{1,2}, Hideki Kandori^{1,2} (¹*Grad. Sch. of Eng., Nagoya Inst. of Tech.*, ²*OptoBio Tech. Res. Cent., Nagoya Inst. of Tech.*)

Rhodopsins are retinal-binding proteins with seven transmembrane segments and perform various functions initiated by photoisomerization of retinal. In 2018, functional metagenomics analysis discovered the third family of rhodopsin, heliorhodopsins (HeRs). HeR is not homologous to microbial rhodopsins but the mechanism of the conformational change by the retinal isomerization is similar to that of microbial rhodopsins. Its function has not been well understood, particularly in native cells. In this study, we focused on *Streptomyces alkaliphilus* (*S. alkaliphilus*), who is cultivatable and contains a HeR gene (SaHeR). We would like to discuss the physiological function of SaHeR, based on the qRT-PCR results from *S. alkaliphilus* cells cultured in various conditions.

1Pos133 中温性細菌 *Modestobacter muralis* 由来のロドプシンの発現と光反応
Expression and photoreaction of rhodopsin from the mesothermal bacterium *Modestobacter muralis*

Haruna Matsumura¹, Shota Takahashi¹, Takafumi Shimoaka¹, Fumio Hayashi², Takashi Kikukawa³, Masashi Sonoyama^{1,4,5}

(¹Grad. Sch. Sci. Tech., Gunma Univ., ²Ctr. Inst. Analysis, Gunma Univ., ³Fac. Adv. Life. Sci., Hokkaido Univ., ⁴GIAR, Gunma Univ., ⁵GUCFW, Gunma Univ.)

Our recent bioinformatic work has identified a novel clade of microbial rhodopsins (ActR I) characterized by a long C-terminus from *Actinomycetes* and mainly a DTE functional motif in helix C. We expressed ActR I from the mesophilic bacterium *Modestobacter muralis* (MmActR I) using *E. coli* strain Lemo21(DE3). The photoreaction of purified MmActR I was investigated by laser flash photolysis. In the neutral to weakly alkaline pH range, the decay of the M intermediate was pH-dependent, suggesting that the pKa of the proton donor (E104) of MmActR I is acidic. The feature of the pKa of MmActR I contrasts with that of proteorhodopsin (PR), the most common microbial rhodopsin with a DTE motif, in which the pKa of the proton donor is neutral.

1Pos134 最先端の蛍光顕微分光法による細胞内の多様な光合成超複合体を観る
Capturing *in vivo* dynamic photosynthetic supercomplexes using state-of-the-art fluorescence excitation-emission microscopy

Xianjun Zhang^{1,2}, Ryutaro Tokutsu³, Jun Minagawa⁴, Shen Ye¹, Yutaka Shibata¹ (¹Tohoku University, ²Massachusetts Institute of Technology, ³School of Veterinary Science, Kitasato University, ⁴National Institute for Basic Biology)

The energy conversion with high efficiency in photosynthetic supercomplexes during photosynthesis relies on the exquisite organization of their light-harvesting antennae. Although the structures of supercomplexes have been resolved by Cryo-EM, the antenna-protein composition within cells remains largely elusive. A state-of-the-art fluorescence spectral microscope enables the simultaneous acquisition of excitation and emission spectra at a subcellular scale. This technological advancement allows us to access the dynamic antenna system of photosystem I (PSI) *in vivo* at 80 K. We uncover a mega-scale PSI supercomplex whose size exceeds that of the structures reported by Cryo-EM so far. These mega-complexes are accumulated in a intracellular characteristic area.

1Pos135 光化学系 II 結晶を用いた Mn₄CaO₅ クラスターの構築機構の時間分解赤外分光解析
Time-resolved infrared study of the photoassembly process of the Mn₄CaO₅ cluster using photosystem II crystals

Yuki Kato¹, Kazuki Ogura¹, Yoshiki Nakajima², Jian-Ren Shen², Takumi Noguchi¹ (¹Grad. Sch. Sci., Nagoya Univ., ²Res. Inst. Interdiscip. Sci., Okayama Univ.)

The water-oxidizing Mn₄CaO₅ cluster in PSII is known to assemble via photooxidation of Mn²⁺, but its detailed mechanism remains elusive. In this study, we investigated the photoassembly mechanism of the Mn₄CaO₅ cluster using time-resolved FTIR spectroscopy by comparing Mn-depleted PSII in solution and in crystals, with the latter mostly retaining the protein structure upon Mn depletion. In solution, bands in the carboxylate stretching and amide I regions changed markedly within milliseconds to seconds, whereas no such changes were observed in crystals. These results indicate that the band changes arise from protein conformation changes concomitant with Mn³⁺ relocation, occurring during the dark rearrangement process that follows the initial photooxidation of Mn²⁺.

1Pos136 Spectral Shifts in Chromophore Absorption Wavelengths Caused by Three Linkers in the Phycobilisome Rod of *Synechocystis* PCC 6803

Hiroto Kikuchi (Dept. Phys., Sch. Med., Nippon Med. Sch.)

In the phycobilisome rod of *Synechocystis* sp. PCC 6803, several linker proteins connect phycocyanin hexamer units to form a larger supramolecular structure. Although typically regarded as structural scaffolds, our electronic-state calculations suggest that these proteins also induce spectral shifts in the absorption wavelengths of chromophores. These shifts likely contribute to an energy gradient along the rod, which may facilitate efficient excitation energy transfer toward the reaction center. Thus, linker proteins may serve a dual role: maintaining supramolecular architecture and optimizing light-harvesting efficiency through spectral tuning. Our results, based on theoretical calculations, reveal the functional role of linker proteins in the phycobilisome rod.

1Pos137 紅色光合成細菌 *Phaeospirillum molischianum* の LH2 タンパク質の再構築：カロテノイドと界面活性剤の影響

Reconstruction of LH2 protein from a purple photosynthetic bacterium *Phaeospirillum molischianum*: effects of carotenoids and detergents

Taiga Miura, Yoshitaka Saga (*Grad. Sch. Sci. Eng, Kindai Univ.*)

Purple photosynthetic bacteria have peripheral light-harvesting antenna protein termed LH2. LH2 protein from a purple bacterium *Phaeospirillum molischianum* has an octameric ring structure. This structure is formed by assembly of α - and β - polypeptides, bacteriochlorophyll *a* and carotenoids. To gain insights into the formation of the LH2 ring structure and the photofunctions, we studied reconstruction of LH2 from the pigments and polypeptides. Polypeptides were obtained by decomposition of native LH2. The polypeptides were dissolved in buffer containing detergents and LH2 complex was reconstructed by adding the pigments. In this presentation, we mainly report the effects of carotenoids and detergents on reconstruction of the LH2 complex.

1Pos138 光合成酸素発生系における翻訳後アミノ酸修飾によるシステインスルホン酸配位子の形成
Formation of a cysteine sulfonate ligand via post-translational modification in the photosynthetic oxygen-evolving complex

Kazuha Nakamura¹, Takehiro Suzuki², Hatsune Mizue¹, Tomomi Kitajima-Ihara¹, Minako Hirano¹, Yuki Kato¹, Naoshi Dohmae², Takumi Noguchi¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*RIKEN, CSRS.*)

The oxygen-evolving Mn₄CaO₅ cluster in photosystem II is stabilized by six carboxylate ligands. We recently found that amino acids with a sufficient number of carbon atoms, when mutated from Asp/Glu, were post translationally converted to Asp/Glu, restoring O₂ evolution. In this study, we examined the properties of the D1-D170C mutant, in which Asp was substituted with Cys, with fewer carbon atoms. It was shown that this mutant exhibited ~10% O₂ activity, and Cys was post-translationally modified to cysteine sulfonate (Cys-SO₃⁻). The S-state transitions advanced up to the second flash, with further transitions significantly inhibited. These results indicate that Cys-SO₃⁻ in this mutant functions as a ligand to the Mn₄CaO₅ cluster, enabling low-efficiency O₂ evolution.

1Pos139 遠赤色利用可能な光化学系IIの光捕集機能におけるカロテノイドの役割
Light-harvesting functions of carotenoids in the far-red light utilizing photosystemII from *Acaryochloris marina*

Vasco Joris¹, Naoki Suenaga², Miki Bando-Uotani^{1,3}, Kyoko Shinzawa-Ito⁴, Natsuko Inoue-Kashino⁴, Yasuhiro Kashino⁴, Keisuke Kawakami⁵, Koji Yonekura⁵, **Daisuke Kosumi**⁶ (¹*Grad. Sch. Sci. and Tech., Kumamoto Univ.*, ²*Facul. Sci., Kumamoto Univ.*, ³*Dev. Tech., Kumamoto Univ.*, ⁴*Grad. Sch. Sci, Hyogo Univ.*, ⁵*RIKEN, SPring-8*, ⁶*IINa, Kumamoto Univ.*)

Photosystem II (PSII) is an essential membrane-protein complex that drives the water-splitting reaction using sunlight in oxygenic photosynthesis. The cyanobacterial PSII from *Acaryochloris marina* contains chlorophyll *d*, a photosynthetic pigment utilizing far-red light. This PSII also includes two types of carotenoids, zeaxanthin and alpha-carotene, which absorb light energy in the blue-green region of the spectrum. In this study, we performed femtosecond pump-probe spectroscopic measurements on the PSII-chlorophyll-binding protein from *Acaryochloris marina* to clarify the energy transfer dynamics from carotenoids to chlorophyll *d*.

1Pos140 光化学系I超複合体の高分解能AFM観察
High-resolution AFM imaging of photosystem I supercomplex in thylakoid membrane

Azusa Owada¹, **Daisuke Yamamoto**² (¹*WDB Co., LTD.*, ²*Fac. Sci., Fukuoka Univ.*)

Photosystem I (PSI) intrinsic in the thylakoid membranes is a fundamental protein in the light reaction of photosynthesis. PSI supercomplex consists of one reaction center and four peripheral light harvesting complexes (LHCI). The structures of supercomplex extracted from the thylakoid membrane have been obtained in atomic detail by cryo-EM. However, the structural analysis of the complexes embedded in the native membrane is still challenging. Here, the structure of PSI-LHCI supercomplex in the membrane was directly visualized at a single molecule level using HS-AFM. The reaction center and the associated LHCI were clearly visualized. The AFM structure and the molecular organization of PSI-LHCI within the membrane will be discussed.

1Pos141 光合成酸素発生系における脂肪族アミノ酸の非天然カルボキシラート配位子への翻訳後変換
Post-translational conversion of aliphatic amino acids to non-natural carboxylate ligands in the
photosynthetic oxygen-evolving complex

Hatsune Mizue¹, Takehiro Suzuki², Takumi Matsubara¹, Tomomi Kitajima-Ihara¹, Minako Hirano¹, Yuichiro Shimada¹, Yuki Kato¹, Naoshi Dohmae², Takumi Noguchi¹ (¹*Department of Physics, Graduate School of Science, Nagoya University*, ²*Biomolecular Characterization Unit, RIKEN Center for Sustainable Resource Science*)

Photosynthetic oxygen evolution occurs at the Mn-CaO₄ cluster in the oxygen-evolving complex (OEC) of photosystem II (PSII). We recently showed that certain aliphatic amino acids, introduced by mutation of the D1-D170 ligand, were post-translationally converted into Asp and its derivatives, restoring O₂-evolving activity. Here, we further examined the structures and properties of these non-natural amino acids in OEC. Val in D170V and Leu in D170L were converted into (3S)-β-MeAsp and (4S)-γ-MeGlu, respectively. Quantum chemical calculations and delayed luminescence measurements showed that these non-natural amino acids act as ligands to the Mn-CaO₄ cluster, supporting a normal S-state cycle. We additionally report the results of analyses of the new D1-E189V/L/I mutants.

1Pos142 カリウムチャネルロドプシン B1ChR2 の K⁺選択性メカニズムの解明と応用に向けて
Towards a mechanistic understanding and application of K⁺ selectivity of potassium
channelrhodopsin B1ChR2

Ryotaro Shimamura¹, Shoko Hososhima^{1,2}, Hideki Kandori^{1,2}, Satoshi Tsunoda^{1,2} (¹*Grad. School of Engineering, Nagoya Institute of Technology*, ²*Opto Bio Technology Research Center*)

Channelrhodopsins are light-gated ion channels, constituted of seven transmembrane-helices that involve a retinal as a chromophore. The cation-conducting ChRs are widely applied as optogenetics tools for neuronal excitation, whereas the anion-conducting ChRs are used for optical neuronal silencing. The discovery of a K⁺ selective ChR (KCR) has been long-awaited, because K⁺ efflux is involved in neuronal hyperpolarization.

In this study, we focus on B1ChR2, a high K⁺ selective KCR with a faster channel closing kinetics than the other KCRs (e.g. HcKCR1). We performed electrophysiological analysis of B1ChR2 and its variants. In B1ChR2, the composition of amino acid residues involved in K⁺ selectivity and their functional contributions may differ from those in HcKCR1.

1Pos143 PYP を用いた光可逆的タンパク質性液液相分離形成の解析
Analysis of photo-reversible proteinaceous liquid-liquid phase separation formation using PYP

Yoichi Yamazaki¹, Ranmaru Shirahama¹, Kento Yonezawa^{1,2}, Hironari Kamikubo^{1,2} (¹*NAIST MS*, ²*NAIST CDG*)

Photoactive Yellow Protein (PYP) and its interacting protein, PYP Binding Protein (PBP), form oligomeric complexes in a light-dependent manner. The fusion protein of the N-terminal region of FUS protein (FUS_{LC}) and PBP (PBP-FUS_{LC}) shows a liquid-liquid phase separation in photoreaction with PYP. To clarify the process of PYP and PBP-FUS_{LC} droplet formation, the oligomeric complexes states and the salt concentration dependence on droplet formation were measured. The results showed that PBP-FUS_{LC} exhibits droplet formation even by itself as the salt concentration increases, and that in complex formation with PYP, droplet formation at lower salt concentrations becomes possible as the degree of PBP-FUS_{LC} multimerization increases.

1Pos144 Disordering of cell membrane lipids induced by THz irradiation

Hiromichi Hoshina (*RIKEN RAP*)

This study investigates how THz radiation non-thermally affects living organisms. Using fluorescence recovery after photobleaching, we measured lipid molecule diffusion in HeLa cell membranes under THz irradiation at 0.10, 0.29, and 0.48 THz. Temperature calibration with an ultrathin thermocouple eliminated heating effects. Irradiation at 0.10 and 0.29 THz increased diffusion constants below cell growth temperature, showing enhanced membrane fluidity. Laurdan fluorescence imaging revealed red shifting, indicating THz radiation induces order-disorder phase transition in membrane lipids by affecting bound water molecules. These findings have implications for THz radiation safety standards and potential cell manipulation methods.

1Pos145

H⁺輸送活性の低いナトリウムポンプロドプシンにおけるプロトン化レチナル塩基周辺の水素結合ネットワーク

Hydrogen-Bonding Network Around the Protonated Retinal Schiff Base in a Sodium-Pumping Rhodopsin with Low H⁺ Transport Activity

Hiroto Takizuka¹, Yuma Ito¹, Akiko Ito¹, Hideki Kandori^{1,2}, Yuji Furutani^{1,2} (¹Graduate School of Engineering, Nagoya Institute of Technology, ²Optobiotechnology Research Center, Nagoya Institute of Technology)

Microbial rhodopsins have seven transmembrane α -helices with an all-trans retinal chromophore linked via a Schiff base to Lys on helix 7. Light triggers the retinal isomerization to 13-cis, inducing formation of several intermediates and thermally reverting to all-trans. KR2 is a well-known light-driven Na⁺ pump that transports H⁺ in the absence of Na⁺. However, FdNaR from *Flagellimonas* sp. DIK exhibits minimal H⁺ transport. To clarify the structural difference, we measured low-temperature FTIR difference spectra of FdNaR upon K intermediate formation: (i) O–D stretches of strongly hydrogen-bonded waters and (ii) N–D stretches of the protonated Schiff base differ from those in KR2, indicating an altered hydrogen-bonding network near the Schiff base in FdNaR.

1Pos146

チャネルロドプシン GtCCR3 の波長制御とチャネル開閉機構

Color tuning and channel gating mechanism of cation-channelrhodopsin GtCCR3

Jinichiro Tabé¹, Shoko Hososhima^{1,2}, Hideki Kandori^{1,2}, Satoshi Tsunoda^{1,2} (¹Graduate School of Engineering, Nagoya Institute of Technology, ²Opto Bio Technology Research Center)

Recent studies have identified five cation channelrhodopsins (GtCCR1–5) from the cryptophyte alga *Guillardia theta*. Although these proteins share high amino acid sequence homology, they exhibit distinct spectral properties: GtCCR3 shows maximal light-induced activity at 470 nm, whereas GtCCR1, 2, 4, and 5 peak at 510–530 nm, indicating a spectral separation of ~50 nm. To investigate the mechanism of this color tuning, we constructed a homology model of GtCCR3 and compared it with cryo-EM structures of GtCCR2 and 4. Guided by structural insights, we performed site-directed mutagenesis and patch-clamp recordings. This analysis revealed that several residues such as Ser228 in transmembrane helix 7 play a pivotal role in the blue-shifted absorption of GtCCR3.

1Pos147

Unveiling Calcium's Role in the Emergence of Molecular Chirality

Chen Chen¹, Ruiqin Yi², Tony Z. Jia³ (¹Biofunctional Catalyst Research Team, RIKEN Center for Sustainable Resource Science (CSRS), ²Guangzhou Institute of Geochemistry, Chinese Academy of Sciences, ³Earth-Life Science Institute, Institute of Future Science, Institute of Science Tokyo)

Understanding how prebiotic molecules gave rise to homochiral polymers is central to the origin of life. α -Hydroxy acids (α HAs) can undergo dehydration polymerization into polyesters that form membraneless droplets. We focused on tartaric acid (TA), a chiral α HA, to explore stereoselective polymerization. Enantiopure D-TA or L-TA polymerize efficiently, while racemic DL-TA does not due to stereochemical mismatch. Ca²⁺ ions affect this process in two ways: (1) enriching enantiomeric excess by selectively crystallizing racemic TA, and (2) switching polymerization behavior—suppressing enantiopure TA polymerization while enabling racemic polymerization. This suggests inorganic ions helped guide early chiral selection and protocell formation in prebiotic environments.

1Pos148

緑藻類の光応答に及ぼす細胞数と細胞分化の影響

Effects of cell number and cell differentiation on the photo-response of green algae

Daito Seito, Yoshihiro Murayama (Tokyo University of Agriculture and Technology, Faculty of engineering, Department of Biomedical Engineering)

The green algae of the *Volvox* species have evolved through an increase in cell number and state of cell differentiation. The purpose of this study is to clarify the effects of cell number and cell differentiation on photo-response of *Volvox* species. We compared the photo-responses of two species of green algae, *Pleodorina* (64, 128 cells) and *Volvox* (2000 cells), which differ in cell number and state of cell differentiation. The results showed that *Pleodorina* could achieve phototaxis almost equal to that of *Volvox*, even with a smaller number of cells. On the other hand, photosensitive cells of *Pleodorina* are more widely distributed than that of *Volvox*, suggesting that *Volvox* has gained functional differentiation of somatic cells instead of losing photosensitive cells.

1Pos149 **最小ゲノム細菌の実験室適応進化**
Adaptive laboratory evolution of minimal genome bacterium

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Minimal cell (JCV1-syn3B) has the artificial minimal genome constructed by essential genes for cell growth. Here, we adapted minimal cell to low temperature. Minimal cell was passaged cultured at 30°C and then at 25°C. The passaged strains showed faster growth speed than the original strain at low temperatures. To investigate the mechanism for adaptation, genome sequencing analysis and proteomics analysis were performed. The detected mutations did not explain but the expression level changes of several proteins indicate important functions for adaptation. The genome of adapted strain was transplanted into the original strain. The transplanted strain showed similar growth to the adapted strain, indicating that the mutations are responsible for low temperature adaptation.

1Pos150 **短いランダムな RNA 集団に創発する遺伝の解析**
Exploring emergent heritability in short random RNA pools

Jiro Kakizaki¹, Alike Andjani Widada¹, Norikazu Ichihashi², Ryo Mizuuchi¹ (¹*Fac. Sci. Eng., Waseda Univ.*, ²*Grad. Sch. Arts and Sci. Univ. Tokyo*)

The RNA world hypothesis proposes that the first self-reproducing system emerged from prebiotically accessible short random RNA pools (primordial RNA pools). However, how such a system could appear remains unclear. To explore this, we investigated compositional changes in multiple primordial RNA pools over two-month serial transfer experiments. High-throughput sequencing revealed temporal shifts in two-nucleotide patterns (2-mers) in the RNA products over time. Notably, 2-mer frequencies tended to remain similar across successive rounds, while gradually changing over the entire experimental timescale, suggesting a primordial form of heritability. These findings offer insights into how heritable, self-reproducing systems could emerge from primordial RNA pools.

1Pos151 **膜結合アクトミオシンネットワークによる人工細胞の形態変化**
Morphological modification of artificial cell encapsulating membrane-bound actomyosin system

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Reconstituting the behavior of motor proteins interacting with cell membranes and cytoskeletal filaments within a cell-sized space reveals insights into essential cellular functions. In this study, we aimed to reconstitute actomyosin motility in Water-in-Oil droplets using membrane-bound myosin I that anchors to and exerts force on both the cell membrane and actin cytoskeleton. Membrane-bound myosin I caused gliding of actin filaments on the inner surface of the droplet. Furthermore, we also added myosin II to the droplets. The contractile force of the actomyosin network caused deformation of the droplet. Our reconstituted artificial cell system containing membrane-bound actomyosin provides insight into cell deformation and intracellular mechanical processes.

1Pos152 **DNA で操る合成細胞のアクチン骨格：DNA とタンパク質の橋渡しによる機能拡張**
DNA-Regulatable Actin Cytoskeleton in Synthetic Cells: Bridging DNA and Proteins toward Enhanced Functionality

Daichi Nakajima¹, Keita Abe¹, Satoshi Murata¹, Shinichiro M. Nomura¹, Hideaki Matsubayashi² (¹*Department of Robotics, Graduate School of Engineering, Tohoku University*, ²*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*)

DNA-regulated synthetic cells have been developed by leveraging the programmability of DNA, but their functionality remains limited by the four-letter nucleotide code. Here, integrating DNA with functionally diverse "proteins", we developed a DNA-regulatable actin cytoskeleton reconstituted in cell-sized liposomes. Our DNA signal transduction system 'Chabashira' detects external DNA, accumulates DNA-tagged pVCA (an actin nucleation factor) on the inner membrane, thereby drives actin assembly. We demonstrate the versatility of this system by achieving localized actin assembly in 50% of liposomes using streptavidin–biotin or SNAP–benzylguanine DNA-tagging of pVCA. This generalizable approach lays the foundation for robust DNA–protein hybrid systems in synthetic cells

1Pos153

人工分子の化学修飾による微小管のプログラム可能な配列制御

Programmable Microtubule Arrangement via Synthetic Molecular Modification

Kenta Tamaki¹, Hiroto Morita¹, Ryota Iino², Takayuki Uchihashi¹ (¹*Grad. Sch. of Sci., Nagoya Univ.*, ²*IMS, NINS*)

Chemical modification of proteins with synthetic molecules enhances native functions and creates novel ones. We applied this approach to control microtubule arrangement and explore new functionalities. We previously showed that mixing microtubules with artificial hexameric kinesins prepared by SpyTag-SpyChatcher cross-linking resulted in microtubule bundling. Although the bundling may improve kinesin transport, analyzing its dynamics remains difficult. Thus, we focused on direct microtubule modification. Microtubules functionalized with complementary DNA strands are expected to bundle *via* hydrogen bonding, while azobenzene-modified ones should allow reversible bundling and dispersion under light. We will synthesize these systems and analyze kinesin transport efficiency.

1Pos154

翻訳因子の持続的な再生産による *in vitro* 自己増殖系の構築

Sustainable regeneration of translation factors toward *in vitro* self-regeneration

Kentaro Shoji¹, Katsumi Hagino¹, Norikazu Ichihashi^{1,2,3} (¹*Department of Life Science, Graduate School of Arts and Science, The University of Tokyo*, ²*Komaba Institute for Sciences, University of Tokyo*, ³*Universal Biology Institute, University of Tokyo*)

Reconstructing the self-reproduction ability of living systems *in vitro* is a major challenge in bottom-up synthetic biology. To achieve this, it is essential to regenerate all molecular components involved in translation. In this study, we successfully demonstrated the sustainable regeneration of each of four essential translation factors (IF2, IF3, EF-G, and EF-Tu) directly from their DNA templates over 10 rounds of 2.5-fold serial dilutions, using a reconstituted transcription/translation system (PURE system). These factors were continuously regenerated without the need for external supplementation. This result represents a significant step toward the realization of self-replicating artificial systems.

1Pos155

A Hybrid *In Silico*/In-Cell Controller for Robust Optimization of Microbial Bioprocesses

Katsuyuki Kunida^{1,2}, Tomoki Ohkubo², Yuichi Sakumura¹ (¹*Department of Computational Biology, School of Medicine, Fujita Health University*, ²*Data-Driven Biology, Division of Biological Science, Nara Institute of Science and Technology*)

Engineered microorganisms are valuable platforms for producing compounds such as fuels and pharmaceuticals. However, overexpressing bottleneck enzymes, crucial for high yields, can impair microbial growth. This issue can be addressed using model-based *in silico* controllers or in-cell feedback controllers with genetic circuits. *In silico* controllers optimize enzyme expression via predictive models but are vulnerable to process-model mismatches. In-cell controllers sense intracellular signals and adjust enzyme levels in real time. In this study, we propose a hybrid *in silico*/in-cell controller (HISICC) that integrates both strategies to maintain high productivity. We validated this concept through two computational case studies using engineered *Escherichia coli* strains.

1Pos156

生体制御モジュールを用いたリボソームの人工制御

Artificial regulation of ribosomes using the trans-acting engineered regulatory module

Maho Fujino, Yoshikazu Tanaka, Takeshi Yokoyama (*Grad. Sch. Life Sci., Tohoku Univ.*)

Translation control is an essential process for gene regulation. Therefore, the development of highly-operable modules for controlling translation *in situ* is beneficial. In this study, we aimed to control translation by the designed trans-acting regulatory module bind to ribosomes and designing a supramolecular complex, the ribosome, freely. Cryo-EM single-particle analysis of the regulatory module-bound ribosome complex revealed that the regulatory module bound to the ribosome as expected manner. In this presentation, we show the recent our achievement of regulatory module design and future investigation of artificial translation control.

1Pos157 マイクロ流路内での水/水相分離が創り出す細胞サイズ液滴の規則配列
Spontaneous generation of linearly-arranged uniform microdroplets through phase separation in microfluidic channel

Mayu Shono¹, Ken Hirano², Akihisa Shioi³, Kenichi Yoshikawa⁴ (¹*Komaba Institute for Science, Graduate School of Arts and Sciences*, ²*Health and Medical Research Institute, National Institute of Industrial Science and Technology (AIST)*, ³*Department of Chemical Engineering and Materials Science, Doshisha University*, ⁴*Faculty of Life and Medical Sciences, Doshisha University*)

We report a novel methodology for generating uniform cell-sized microdroplets that mimic the crowded environments similar to living cells. Uniformly sized DEX-rich droplets spontaneously entrapping DNA were generated by injecting a homogeneous polyethylene glycol (PEG)/dextran (DEX) mixture containing DNA below the critical concentration, through microphase separation inside a polydimethylsiloxane (PDMS) microfluidic channel. The numerical calculation using the Cahn-Hilliard equation, which includes the effect of dehydration from PDMS, successfully reproduced the experimental results. The methodology holds promise as a smart and scalable approach to real-world cell modeling, with potential implications for drug delivery systems.

1Pos158 多細胞様液滴による翻訳と共役した RNA ゲノム複製の空間的分離
Multicell-like communicating droplets enabling spatial control of translation-coupled genomic RNA replication

Hidekazu Sono¹, Keiji Murayama², Kensuke Ueda³, Norikazu Ichihashi^{3,4,5}, Ryo Mizuuchi^{1,6} (¹*Dept. Elect. Eng. & Biosci., Fac. Sci. & Eng., Waseda Univ.*, ²*Dept. Biomol. Eng., Grad. Sch. Eng., Nagoya Univ.*, ³*Komaba Inst. for Sci., Univ. Tokyo*, ⁴*Dept. Life Sci., Grad. Sch. Arts & Sci., Univ. Tokyo*, ⁵*Universal Biol. Inst., Univ. Tokyo*, ⁶*FOREST, JST*)

Liquid-liquid phase-separated (LLPS) droplets are membraneless, cell-like structures. Using droplets composed of polyethylene glycol (PEG) and dextran (DEX), we developed stable, multicell-like structures that retain key LLPS properties such as selective molecular enrichment and permeability. These droplets can exchange not only small molecules but also macromolecules over 100 kDa. By encapsulating two distinct artificial genomic RNAs along with a cell-free translation system in separate droplets, we demonstrated the synthesis and inter-droplet exchange of an encoded RNA replication enzyme and NTP, inducing RNA replication. Such droplet-droplet cooperation could lead to artificial multicellular models with spatiotemporal control of gene expression and replication.

1Pos159 Organization of multicellular-like liposome structures with specific shapes

Shun Okada, Kan Shoji (*Nagaoka University of Technology*)

Living tissues offer complex functions through precise spatial organization and regulated cell-to-cell communication. Thus, multicellular-like liposome structures (MILSs), which are assembled with multiple liposomes, are expected to be applied as artificial cell tissues. Although DNA-based adhesion and communication between liposomes were achieved, controlling liposome alignment within MILSs is challenging. If MILSs can be formed with spatially aligned liposomes, the information transfer in tissues can be mimicked with MILSs. Recently, we reported a microrail channel for aligning multiple liposomes in specific shapes. Here, we demonstrated the formation of specific-shaped MILSs by adhering each aligned liposome via DNA-based adhesive molecules under the microrail.

1Pos160 構造揺らぎを想定した変異体タンパク質のアンサンブルドッキングによる相互作用解析
Interaction analysis by ensemble docking of mutant proteins assuming structural fluctuations

Nobuyuki Uchikoga¹, Yuri Matsuzaki² (¹*Dept. Network Design, Sch. Interdisip. Math. Sci., Meiji Univ.*, ²*Acad. Leadership, Sci. Tokyo*)

Protein interactions are important for conformational fluctuations. In this study, in order to evaluate mutants for allosteric inhibition release, we created mutants to increase conformational fluctuations of proteins and performed ensemble docking. Multiple conformational structures were created by molecular dynamics for each mutant protein, and rigid body docking was performed for each structure to obtain interaction pattern information considering the conformational fluctuation. By applying these analyses to ATP phosphoribosyltransferase, the relevance of structural fluctuations and interaction pattern information to the effects of allosteric inhibition release will be discussed.

1Pos161 Towards automation in HS-AFM data analysis and interpretation**Romain Amyot**, Holger Flechsig (*NanoLSI, Kanazawa University*)

High-Speed Atomic Force Microscopy (HS-AFM) allows the visualisation of the dynamics of biomolecules at non-equilibrium and near-physiological conditions. A typical HS-AFM experiment leads to a large collection of images to be analysed and interpreted. However, the low resolution of images coupled with the lack of automation make the analysis and the interpretation tough, time consuming and subject to experimentalist biases.

In this communication, we are going to show our attempts for automated analysis of HS-AFM images based on Computer Vision methods and our collaboration with the Tama's lab at Nagoya University for the implementation of the Normal Mode Flexible Fitting (NMFF-AFM) method into the BioAFM viewer software to support the interpretation of HS-AFM images.

1Pos162 乳がん組織における TP53 ホットスポット変異と発現変動の関連機構
Association between TP53 hotspot mutations and expression alterations in breast cancer tissues**Takaharu Naito**, Takanori Sasaki (*Fac. Adv. Math. Sci., Meiji Univ.*)

Hotspot missense mutations in the tumor suppressor TP53 often lead to oncogenic gain-of-function, but the mechanism of variation in TP53's own expression upon introduction of these mutations is unknown. We investigated expression patterns of TP53 hotspot mutants (HS-MT) and the functions of genes highly correlated with these patterns. Using TCGA breast cancer data, we extracted differentially expressed genes (DEGs) among wild-type (WT), HS-MT, and other mutant (MT) groups. We then identified genes strongly correlated with changes in TP53 expression. TP53 levels were significantly higher in HS-MT than in WT and MT. Among 1525 DEGs, 10 showed strong positive correlation with HS-MT ($r > 0.5$). HS-MT may upregulate their own expression through G1/S cell cycle-related genes.

1Pos163 RNA-seq を用いた相関分析による転移性乳がんの miRNA 予後予測因子の選出
Selection of miRNA Prognostic Factors for Metastatic Breast Cancer by Correlation Analysis Using RNA-seq**Sota Kageyama**, Takanori Sasaki (*I. Fac. Adv. Math. Sci., Meiji Univ.*)

Many mRNA biomarkers have already been put into practical use in breast cancer (BR). In addition, miRNAs, which are a type of non-coding RNA, are also expected to be utilized as biomarkers. The purpose of this study was to select miRNA prognostic factors in metastatic BR. As a research method, we detected differentially expressed miRNAs from the RNA-seq data of metastatic BR patients and calculated the correlation coefficients between the expression patterns of these miRNAs and known mRNA biomarkers. As a result, 17 miRNAs with particularly high correlations were selected as candidate prognostic factors. Among these candidates, four miRNAs have also been proposed as metastatic BR-related miRNAs in other reports, which confirms the validity of our research method.

1Pos164 内分泌療法による乳がんの予後に関与する効果修飾遺伝子と PPI network 領域の予測
Prediction of effect modifiers and PPI network regions involved in endocrine therapy-induced breast cancer prognosis**Shoya Oba**, Takanori Sasaki (*I. Fac. Adv. Math. Sci., Meiji Univ.*)

Endocrine therapy (ET), which targets hormone receptors, significantly reduces recurrence and mortality in breast cancer. This study aimed to identify effect modifiers of ET and their Protein-Protein interaction (PPI) network regions. In practice, we constructed a PPI network of 366 genes potentially affected by ET and performed survival analysis using breast cancer samples with and without ET application based on gene expression. As a result, 34 genes were identified as effect modifiers whose prognosis is reversed by ET status. In particular, the 17 effect modifiers that promote poor prognosis with the application of ET formed a PPI network and were involved in hormone signaling, indicating that these genes may be involved in endocrine resistance.

1Pos165 大規模なデータセットで学習した事前学習モデルを利用したタンパク質・リガンド結合親和性の予測

Predicting protein-ligand binding affinity using pre-trained models on large-scale dataset

Sei Inoue, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

Evaluating the binding affinity between proteins and ligands is a fundamental task in computer-aided drug design. In recent years, various deep learning models have been developed to predict binding affinity. While PDBbind is commonly used as a training dataset in this field, its limited size (~20,000 complexes) is insufficient for deep learning applications. We propose a transfer learning model leveraging two large-scale pre-trained models—GearNet, trained on 800,000 protein structures, and GROVER, trained on 11,000,000 molecular graphs—as feature extractors. We evaluated our model on the PDBbind core set (281 complexes). Our model predicted the negative logarithm of the inhibition constant (pK_i) with a RMSE of 1.23 and a Pearson Correlation Coefficient of 0.834.

1Pos166 蛋白質リガンド相互作用の pIC50 の機械学習予測
pIC50 Prediction Using Protein–Ligand Interactions

Shuji Endo, Masanori Yamanaka (*Grad. Sch. Sci. & Tech., Nihon Univ*)

This study aims to build a machine learning model to predict pIC50 values using integrated data from FMODB and ChEMBL. Ligand–protein interaction parameters computed by the Fragment Molecular Orbital (FMO) method were extracted from FMODB, and experimental pIC50 values were obtained from ChEMBL. These datasets were merged to construct a training set. After preprocessing and removing duplicates, regression models were trained using XGBoost. To address high dimensionality, singular value decomposition (SVD) was applied, showing that reducing features to 7 dimensions yielded optimal R^2 . Further optimization with Optuna improved prediction performance beyond $R^2 = 0.5$. Our results show the potential of combining quantum chemical data with bioactivity for drug discovery.

1Pos167 深層学習モデル gr Predictor を用いたタンパク質 2 量体界面の水和分布予測
Predicting the Hydration Structures at the Protein-Protein Interfaces of Dimers using a Deep-Learning Model “gr Predictor”

Yuki Ito, **Takashi Yoshidome** (*Dep. of Appl. Phys., Tohoku Univ.*)

Computing the hydration structures around proteins in a short time will enable explicit consideration of hydration for investigating amino acid mutations, ligand–binding processes, and protein conformational changes. Previously, we proposed a deep-learning model named “gr Predictor” that successfully reproduced hydration structures obtained using the 3D-RISM theory within approximately one minute [1]. Here, we demonstrated that the gr Predictor can also successfully predict the hydration structures at the protein–protein interface of dimers, and the prediction performance was essentially the same as that of the hydration structures in the whole protein.

[1] K. Kawama, Y. Fukushima, M. Ikeguchi, M. Ohta, and T. Yoshidome, *J. Chem. Inf. Model.*, 62, 4460 (2022).

1Pos168 Analysis of water dynamics around antifreeze proteins by molecular dynamics simulations

Naο Abe¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)

Antifreeze proteins (AFPs) are functional proteins that prevent the freezing of body fluids and cells under low-temperature conditions, thereby enabling the survival of organisms. AFPs possess an ice-binding site (IBS) and a non-ice-binding site (NIBS), and it is known that the translational motion of hydration water is significantly more restricted around the IBS compared to the NIBS. In this study, molecular dynamics simulations are performed on eight types of AFPs, followed by analyses of solute and hydration dynamics to evaluate the dynamic interactions between AFPs and surrounding water molecules. The results aim to provide atomic-level insights into the relationship between AFP structure and antifreeze activity.

1Pos169 QM/MM Study of the Reaction Mechanism of a SAM-Dependent 3-Amino-3-Carboxypropyl Transferase in Nocardicin Biosynthesis

Masayuki Karasawa¹, Takayoshi Awakawa², Takahiro Mori^{3,4,5}, Ikuro Abe^{3,4}, Tohru Terada^{1,4} (¹*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*RIKEN Cent. Sustain. Res. Sci. (CSRS)*, ³*Grad. Sch. of Pharm. Sci., Univ. of Tokyo*, ⁴*Collab. Res. Inst. Innov. Microbiol. (CRIIM)*, ⁵*JST PRESTO*)

Nocardicin A is a monocyclic β -lactam antibiotic produced by an actinomycete, *Nocardia uniformis* subsp. *tsuyamanensis*, and its 3-amino-3-carboxypropyl (3-ACP) moiety is essential for antimicrobial activity. This 3-ACP group is transferred from *S*-adenosylmethionine (SAM) by a SAM-dependent enzyme, NAT, to the phenolic hydroxy group of nocardicin G via an S_N2 reaction. To explore the detailed mechanism, we performed MD simulations and QM/MM calculations using a model of NAT in complex with SAM and nocardicin G, based on the crystal structure with SAH and nocardicin G. Our results revealed that a proton relay between SAM and protein residues establishes the appropriate protonation states, thereby facilitating the subsequent S_N2 reaction to complete the 3-ACP transfer.

1Pos170 Elucidating the Binding Pathway of Abltide to Abl Kinase through Enhanced 2D Replica Exchange Molecular Dynamics Simulations

Yichao Wu, Ai Shinobu (*Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka*)

Abl kinase plays essential roles in cell-cycle regulation, growth arrest and apoptosis, and its aberrant activation drives cancers such as chronic myeloid leukemia. To guide inhibitor design, we utilize two-dimensional (2D) replica exchange MD simulations (gREST/REUS) to investigate the binding of substrate-mimicking peptide, abltide, with Abl kinase. We identified the binding states, intermediate states and encounter states in our simulation. In the intermediate states, the Abl-136D-abltide-4Y and Abl-174F-abltide-5A contacts break and a transient Abl-174F-abltide-2A interaction can form. Given the instability of the binding state, we will employ Free Energy Perturbation (FEP) in future work to explore potential single-point mutations that enhance binding affinity.

1Pos171 Free energy analysis of drug inclusion in polymeric micelles using molecular dynamics simulation

Mai Ukawa¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)

Drug delivery systems are technologies and methods to deliver drugs to specific disease sites for safe and efficient treatment. In the design of drug nanocarriers, it is important to understand the behavior of the carrier and drug molecules. We perform molecular dynamics simulations to pull drug molecules out of micelles composed of sodium dodecyl sulphate, which is treated as a model for biological systems. The potential of mean force during the process is calculated. The morphological changes of the micelle during the withdrawal process and the interactions between the micelle and the drug molecule are observed.

1Pos172 BEMM-GEN: A Toolkit for Generating a Biomolecular Environment-Mimicking Model for Molecular Dynamics Simulation

Takunori Yasuda, Rikuri Morita, Yasuteru Shigeta, **Ryuhei Harada** (*CCS, Univ. of Tsukuba*)

Understanding the cellular environment effects on protein conformations is crucial for elucidating functions. In molecular dynamics simulations, carbon nanotubes and hydrophobic cages have been widely used to mimic the cellular environments such as ribosome tunnels and chaperones. However, recent studies suggest that these simple models may not adequately capture the environmental effects. Thus, it is necessary to generate cellular environmental models that mimic target biomolecules. For this issue, we have developed a biomolecular environment-mimicking model generator (BEMM-GEN) that generates cylindrical and spherical models, integrating arbitrary proteins into the generated models. BEMM-GEN provides model and protein complexes. (<https://github.com/y4suda/BEMM-GEN>).

1Pos173 Effects of Phosphorylation in the Naturally-Denatured Region of TGIF-1 on Functional Regulation

Madoka Nakatani¹, Simon Hikiri², Junichi Higo³, Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*, ³*Grad. Sch. Info. Sci., Univ. Hyogo*)

5'TG3' interacting factor 1 (TGIF-1) inhibits the function of Transforming Growth Factor β by interacting with the Smad complex. An experimental study (Guca et al., 2018) shows that the intrinsically disordered region (IDR) of phosphorylated TGIF-1 binds more readily to the DNA recognition helix of the positively charged homeodomain than the unphosphorylated IDR, forming an autoinhibitory structure. In this study, we use multi-dimensional virtual-system coupled molecular dynamics to examine the binding of DNA recognition helix and IDR and the formation of self-inhibiting structures, as in the experiment. We analyze the interaction with the DNA recognition helix in the N-terminal region of the homeodomain, which is involved in binding to DNA minor groove.

1Pos174 Binding Free Energy Analysis of PD-L1 and Macrocyclic Peptide Inhibitors

Hyunji Kim¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)

Monoclonal antibodies targeting PD-L1 have demonstrated clinical success, but their limitations in tissue penetration have prompted interest in macrocyclic peptides as alternative inhibitors. This study aims to computationally evaluate the binding free energies of such peptides using molecular simulations. Molecular dynamics simulations generate conformational ensembles, and the three-dimensional reference interaction site model is applied to calculate solvation free energies. By combining solvation and internal energy components, the study estimates the binding free energies of peptide-protein complexes. The calculated affinities are compared to experimental trends, and energy decomposition reveals dominant energetic and entropic contributions to binding.

1Pos175 Elucidation of the binding mechanism between botulinum toxin and antibodies through binding free energy analysis

Yuka Maeda¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)

To assess the impact of structural diversity among multiple subtypes of botulinum neurotoxin type A (BoNT/A) and monoclonal antibody variants on binding affinity, we calculated the binding free energies of their complexes as a measure of stability. Molecular dynamics simulations and the three-dimensional reference interaction site model are employed to calculate the binding free energy and identify critical interactions governing complex formation. Binding free energy differences among toxin-antibody combinations are analyzed to reveal subtype-specific binding characteristics.

This presentation compares multiple BoNT/A-antibody complexes to identify binding energy components and interaction features relevant to affinity optimization.

1Pos176 アクチンの分子揺らぎに内在する複数の機能運動
Multiple functional motions of actin are embedded in its intrinsic molecular fluctuation

Ryotaro Koike¹, Kei Moritsugu², Motonori Ota¹ (¹*Grad. Sch. Info., Nagoya Univ.*, ²*Grad. Sch. Sci., Osaka Metro. Univ.*)

Actin is one of the most abundant proteins in a cell. It polymerizes into a filament, hydrolyses ATP and depolymerizes back into the monomeric form, and this cycle is essential for the cytoskeleton dynamics. During the process of polymerization and depolymerization, actin interacts with other proteins and changes its structure. Actin has at least four forms: G, F, C and O forms, and the GF, FC, CG and GO transitions are functional structural changes. We performed molecular dynamics simulations of actin in each form, extracted its major fluctuations using principal component analysis, and compared them with functional structural changes. We will present the relationship between multiple functional motions of actin and its structural fluctuation.

1Pos177**MD シミュレーションを用いた膜の伝熱性解析****Analysis of the Thermal Insulation Properties of Lipid Bilayers Using Molecular Dynamics (MD) Simulations****Ayaka Kiyota¹**, Yuichi Togashi^{1,2} (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*RIKEN*)

It has been reported that the nuclear temperature is about 1 °C higher than the cytoplasm [1]. One possible reason is thermal insulation by lipid bilayers, but its mechanism is unclear. We used Molecular Dynamics (MD) simulations, which model molecular motion, to analyze this. Lipid bilayers and water were alternately arranged. A central region was heated, and temperature changes were measured at both ends. We compared thermal responses when the number of bilayers between heated and measured regions was five, one, or zero (only water). Results showed how lipid bilayers affect thermal conductivity. This study helps clarify intracellular temperature control and may support biomimetic or cell engineering system design.

[1] K. Okabe et al., *Nat. Commun.* 2012, 3, 705.

1Pos178**Molecular Simulation Study on the Conformational Dynamics and Activation Pathway of Melanopsin****Ruisi Zou¹**, Kohe Obayashi², Hisao Tsukamoto², Toshifumi Mori^{1,3} (¹*Grad. Sch. Integr. Sci. & Eng., Univ.kyushu*, ²*Grad. Sch. Sci., Kobe Univ.*, ³*Inst. Mater. Chem. & Eng., Kyushu Univ.*)

Melanopsin belongs to the GPCR family which is essential for non-visual photoreception in mammals. A competitive antagonist AA92593 has been reported to inhibit its function, but the molecular details remain unclear. Furthermore, the activation mechanism of melanopsin has not been explored in detail. In this study, we used AlphaFold2(AF2)-predicted structures and molecular docking to model the melanopsin-AA92593 complex, followed by MD simulations to identify key residues interacting with AA92593. Based on these insights in simulations, we validated functionally important mutants experimentally. We also studied the possible activation pathway of melanopsin using the AF2 guided structure modeling, and the key features associated with the activation will be discussed.

1Pos179**Investigating Protein Condensation and Ion Contributions with Explicit Solvent Coarse-Grained Models****Yangyang Zhang¹**, Cheng Tan¹, Yuji Sugita^{1,2} (¹*RIKEN R-CCS, Kobe, Japan*, ²*RIKEN PRI, Wako, Japan*)

Protein condensates are central to biological function and disease. Physicochemical factors such as ions critically influence their formation. To probe protein–ion interplay, we performed MD simulations of TDP-43 LCD condensates using two explicit-solvent CG models MARTINI and SPICA. We rebalanced interactions to match atomistic condensate concentrations at 0.15 M NaCl, then simulated across a wide salt range. The scaled MARTINI model reproduced experimental reentrant phase separation. Differences in ion distributions between SPICA and MARTINI revealed how different electrostatic treatments affect ion partitioning and intermolecular contacts. These results demonstrate the capability of explicit-solvent CG models to describe salt-dependent protein condensation.

1Pos180**Neuropsin (KLK8)の触媒活性に対する金属添加効果の計算化学的検討****Effect of metal ion addition on the catalytic activity of Neuropsin (KLK8): a computational study****Masami Lintuluoto¹**, Mari Fujimoto¹, Humika Nakamura¹, Souma Kai¹, Yoshifumi Fukunishi², Hideki Tamura³, Jua Mikael Lintuluoto⁴ (¹*Graduate School of Life and Environmental Sciences, Kyoto Prefectural University*, ²*Cellular and Molecular Biotechnology Research Institute, National Institute of Advanced Industrial Science and Technology (AIST)*, ³*Laboratory of Biofunctional Science, Hoshi University School of Pharmacy and Pharmaceutical Sciences*, ⁴*Graduate School of engineering, Kyoto University*.)

Neuropsin is a serine protease highly expressed in the central nervous system, where it contributes to cognitive functions via its proteolytic activity. It cleaves specific substrates such as neuregulin-1, but the enzymatic mechanism and regulation of its catalytic activity remain unclear. Our previous molecular dynamics (MD) studies suggested four key factors that affect substrate specificity and catalytic function. Crystal structures also indicate that metal ions such as Ca²⁺ and Zn²⁺ may modulate enzymatic activity. In this study, we investigate the effects of metal ion binding on the catalytic mechanism of neuropsin using MD simulations. Based on the MD results, we plan to perform quantum mechanical (QM) calculations to explore the electronic-level mechanisms.

1Pos181 分子動力学シミュレーションを用いた多剤排出輸送体 MdfA の基質特異性と排出機構の解析
Analysis of substrate specificity and efflux mechanism of the multidrug transporter MdfA using MD simulations

Hodaka Tanabe, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ of Tokyo*)

Multidrug resistance transporters are characterized by their remarkably broad substrate specificity including diverse antibiotics. MdfA is one of these transporters derived from *E. coli*. Although MdfA effluxes many compounds, it does not efflux some compounds. To elucidate the mechanism of the substrate specificity, we constructed structural models binding various compounds using the inward-open crystal structure of MdfA and performed MD simulations for the models. We found that transition to the occluded conformation occurred when a transported compound bound to the substrate-binding cavity of MdfA. In contrast, an untransported compound did not induce the conformational transition and were ejected from the cavity, which results in failure of the transport.

1Pos182 阻害剤の柔軟性がレセプタータンパク質への結合に与える影響の拡張アンサンブルによる検証
Verification of the effect of ligand and receptor flexibility on inhibitory activity by generalized-ensemble algorithms

Suzuka Saitou¹, Simon Hikiri², Junichi Higo³, Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*, ³*Grad. Sch. Info Sci., Hyogo Univ.*)

In computational drug discovery, few studies have quantitatively demonstrated the relationship between ligand flexibility and inhibitory activity. For example, a previous study used three ligands against mSin3B, a protein associated with medulloblastoma and suggested that increased ligand flexibility leads to increased binding affinity (increased inhibitory activity) of the target protein and ligand [1], but more examples need to be examined to know whether such a relationship is universal.

In this study, we perform docking simulation of protein-ligand complexes against SARS-Cov-2 papain-like protease, one of the proteases of the novel coronavirus, and its ligands, including a candidate inhibitor derived from GRL0617.

1. Hayami et al. *Scientific Reports* 11, 6178 (2021).

1Pos183 計算化学を用いた 2-オキソグルタル酸依存性ジオキシゲナーゼによるオロバンコール環拡大反応の触媒機構の解明
Computational study on the catalytic mechanism of 2-oxoglutarate-dependent dioxygenase in the ring expansion of orobanchol

Hanting Jiang¹, Takatoshi Wakabayashi², Hajime Sato¹, Yoshitaka Moriawaki^{1,4}, Masato Homma³, Yukihiro Sugimoto³, Tohru Terada¹ (¹*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ²*Dept. of Appl. Biol. Chem., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, ³*Dept. of Biochem., Grad. Sch. of Agri. and Life Sci., Kove Univ.*, ⁴*Med. Res. Inst., Inst. of Integr. Res., Science Tokyo*.)

Orobanchol is a plant hormone with a six-membered ring, while its derivative, medicaol, features a rare seven-membered ring. The enzyme catalyzing this ring expansion, medicaol synthase (MOS), a 2-oxoglutarate-dependent dioxygenase, has recently been identified, but its catalytic mechanism remains unclear. In this study, we applied computational chemistry approaches, including MD simulations and QM/MM calculations, to investigate the reaction mechanism. We constructed a reasonable enzyme-substrate complex model and elucidated the catalytic pathway of the ring expansion. Furthermore, we investigated key residues involved in substrate recognition, complex stabilization, and catalysis, providing insights into the substrate specificity and reactivity of MOS.

1Pos184 薬剤設計のための AQP7 チャネルへの阻害剤侵入に関するインシリコ解析
In silico analysis of inhibitor intrusion into the AQP7 channel for efficient drug design

Koryo Obata¹, Yasuteru Shigeta², Ryuhei Harada² (¹*Grad. Sch. degree programs in life and earth sciences, University of Tsukuba*, ²*Center for Computational sciences, University of Tsukuba*)

Aquaporins (AQPs) are channel proteins that promote water transport across biological membranes. Among them, AQP7 has been identified as a regulator of breast cancer, and its inhibitor has been investigated. An intensive screening work identified a small molecule, Z433927330, which inhibits water transport through AQP7. However, this inhibitor failed to improve overall survival rate of cancer model mouse. Thus, to gain insights into the development of AQP7 inhibitors, we investigated how Z433927330 intrudes the channel of AQP7 and approaches its binding site using molecular dynamics simulation. Our results suggested that the binding site is difficult to access from the extracellular side and Z433927330 exhibits a low inhibitive activity in the extracellular side.

1Pos185 分子動力学を用いた 超音波誘導性の piezo 1 立体構造変化解析
Analysis of ultrasound-induced structure changes in piezo1 using Molecular Dynamics

Yoshio Nakano, Kazuki Arita, Satoka Kasai, Kazumi Yoshizawa, Tsugumi Yamauchi, Daisuke Yamada, Akiyoshi Saitoh, Satoru Miyazaki (*Fac. Pharm. Tokyo Univ. Sci.*)

Ultrasound stimulates cells through piezo1 protein, which is expressed on cell membrane. However, the mechanism remains unclear. To clarify the mechanism, we focused on the three-dimensional structure of piezo1. Recent research has shown that piezo1 is expected to move in conjunction with the cell membrane. In this study, we analyzed that ultrasound waves influence piezo1 structure using Molecular Dynamics. In this presentation, we will introduce the details of the simulation results.

1Pos186 分子動力学計算による脂質スクランブラーゼ Atg9 の開閉運動における脂質及び水分子の挙動解析
Lipid and Water Dynamics during the Functional Cycle of the Lipid Scramblase Atg9: A Molecular Dynamics Study

Ayaka Shimbo, Takaharu Mori (*Grad. Sci., Tokyo Univ. of Sci.*)

Atg9, the only transmembrane protein among autophagy-related proteins, facilitates lipid transport and water influx into autophagosomes. Atg9 forms a homotrimeric complex with pores and transits between the closed and open state. To investigate the molecular mechanisms of Atg9 function, we performed targeted molecular dynamics simulations focusing on the transition from the closed to open state. We analyzed the behavior of water and lipid molecules during this process. Our results reveal that the number of water molecules that entered the pore increased by about 20% and the lipid molecules near Atg9 exhibited a tendency to enter the pore. The membrane undulation caused by this transition of Atg9 may contribute to the curvature of autophagosomal membranes.

1Pos187 拡散モデルによる全原子シミュレーションからの粗視化力場の学習
Learning coarse-grained force fields from all-atom simulations via diffusion models

Ryounosuke Kouriki, Tsuyoshi Terakawa (*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)

We present a framework for learning coarse-grained (CG) force fields from all-atom molecular dynamics (MD) simulations using a denoising diffusion model. This approach enables unsupervised learning of CG force fields directly from structural ensembles. We construct Ca-level CG force fields and show that the resulting models reproduce thermodynamic and dynamic features of reference MD trajectories. These force fields can be used in CG MD simulations via Langevin dynamics. We also explore applications to proteins such as GCN4, where folding is coupled to multimerization, as a testbed for modeling interaction-driven structural transitions. This approach may provide a path toward simulating phenomena like liquid-liquid phase separation.

1Pos188 AlphaFold と MD シミュレーションによるコラーゲン三重らせん構造の解析
Structural Analysis of Collagen Triple Helices Using AlphaFold and Molecular Dynamics Simulations

Rikuto Noguchi¹, Taiyo Eguchi¹, Aimi Yamashita¹, Kohsuke Adachi², Masato Kinoshita³, Yuuta Moriyama¹, Toshiyuki Mitsui¹
(¹Grad. Sch. Sci. and Eng., Aoyamagakuin Univ., ²Fac. Agr. and Mar. Sci., Kochi Univ., ³Grad. Sch. Agr., Kyoto Univ.)

Collagen is the most abundant repeat-structured protein in the human body, and the stability of its characteristic triple-helical structure is known to be highly dependent on its amino acid sequence. Traditionally, the large size and repetitive nature of collagen have posed significant challenges for structural analysis, limiting the application of molecular dynamics (MD) simulations to evaluate its structural stability. Recently, the advent of AlphaFold, an AI tool capable of highly accurate protein structure prediction, has opened new avenues for tackling this challenge. In this study, we utilized collagen structures predicted by AlphaFold as initial coordinates and performed MD simulations using NAMD to investigate their structural stability and dynamics.

1Pos189 細胞の剥離を含む頂点モデルにおける破壊パターンの解析
Analysis of fracture patterns in a vertex model including detachment of cells

Nozomi Fujita¹, Yuichi Togashi^{1,2} (¹Grad. Sch. Life Sci., Ritsumeikan Univ., ²BDR, RIKEN)

Organs are composed of cells, and analyzing cell clusters helps understand tissue behavior. The vertex model is a mathematical approach to simulate such multicellular systems, where each cell is represented as a polygon, and shape changes are driven by forces on shared vertices. This model allows us to simulate transitions in processes like alignment, apoptosis, and adhesion. However, standard transitions cannot model detachment of cells since edges are shared. To address this, Chen et al. proposed the T4 transition, which introduces new vertices and edges to simulate detachment when stress exceeds a critical threshold. While previous studies fixed most parameters, we explored a wider range and simulated diverse environments, revealing qualitatively different behaviors.

1Pos190 粗視化格子モデルによるタンパク質の進化とアロステリック制御
Coarse-Grained Lattice Modeling of Protein Evolution and Allostery

Jin Kousaka^{1,2}, Radek Erban³, Yuichi Togashi¹ (¹Graduate School of Life Sciences, Ritsumeikan University, ²Kobe Inst., Riken, ³Mathematical Institute University of Oxford)

While elastic network models and Go-like models capture small-scale elastic responses, they fail to reproduce large-scale evolutionary transitions involving domain rearrangement and function acquisition. We propose a 3D lattice-based, coarse-grained model in which volume elements are uniformly placed around protein backbone atoms and connected by elastic edges. This framework preserves network flexibility while enabling local structural perturbations to propagate over long distances. Under evolutionary selection acting on network geometry, our model reproduces allosteric transitions involving domain rearrangement and function acquisition. We demonstrate its robustness to thermal fluctuations and show how these fluctuations can be harnessed to explore functional space.

1Pos191 Boosting weak signals with incorrect ligands in the sensory system

Yan-Ru Chen (Department of Physics, National Central University)

Biological cells can detect the presence of a small number of ligands. For example, T cell receptors can respond to a few agonist peptides among many self-peptides with large signals. We show that a minimal model that includes kinetic proofreading and the generic binding-state coupling of neighboring receptors in a receptor cluster has receptor activation in the absence of correct ligands inhibited, but even one correct ligand can induce receptor activation due to receptors binding to many incorrect ligands, resulting in strong signal amplification. This mechanism is distinct from the existing theoretical models for T cell receptor activation; it also has potential application in the design of sensitive micron-scale detectors.

1Pos192 グリオブラストーマ細胞の移動メカニズムを解明するための数理モデリングと解析
Mathematical modeling and analysis to elucidate the migration mechanism of glioblastoma cells

Hauna Tagawa¹, Daisuke Kanematsu², Asako Katsuma², Yonehiro Kanemura², Yuichi Sakumura¹ (¹Graduate School of Science and Technology, Nara Institute of Science and Technology, ²National Hospital Organization Osaka National Hospital)

Glioblastoma is a highly invasive brain tumor that resists complete surgical removal, making the control of cell migration crucial. In this study, we analyzed cell images and developed a quantitative mathematical model of glioblastoma cell migration with protrusions to elucidate the underlying motility mechanisms. The analysis of the time-lapse images revealed extracellular matrix-dependent differences in cell motility. Based on these data, we estimated model parameters and reproduced the observed motility differences. We are conducting a parameter sensitivity analysis to identify key factors influencing motility. This approach may facilitate the identification of potential therapeutic targets and enhance our understanding of glioblastoma cell migration.

1Pos193 Modeling hysteresis in protrusion mechanics during neuronal polarization

Akane Uchida, Naoyuki Inagaki, Yuichi Sakumura (*Graduate School of Science and Technology, Nara Institute of Science and Technology*)

Neuronal polarization is the process by which a neuron establishes asymmetry among its neurites while its axon extends. In cell morphological changes—including neuronal polarization—stress with history-dependent properties acts at sites of deformation. However, few mathematical models incorporate such history dependence. In this study, we formulated a stress function whose stress-strain curve traces a hysteresis loop and integrated it into an existing polarization model. The history-dependent stress term reduces stress during the retraction phase in a strain-rate-dependent manner, thereby promoting the accumulation of elongation factors. Consequently, the modified model's timing of polarization more closely matched experimental data than that of the original model.

1Pos194 シグナル伝達系における時間符号化の進化
Evolution of temporal encoding in signaling network

Thoma Itoh^{1,2}, Yohei Kondo³, Kazuhiro Aoki⁴, Nen Saito² (¹*Dept. Basic Biol., Grad. Sch. Life Sci., SOKENDAI*, ²*Grad. Sch. Integrated Sciences for Life, Univ. Hiroshima*, ³*Grad. Sch. Med., Univ. Nagoya*, ⁴*Grad. Sch. Biostudies., Univ. Kyoto*)

Cells process information via signaling pathways. The MAPK signaling pathway, essential for cell fate decisions, receives various inputs, induces input-specific MAPK dynamics, and drives diverse gene expression. This mode of information transmission through temporal dynamics is known as temporal encoding. However, why such complex signaling evolved remains unclear.

To explore this, we constructed an abstract model of a signaling system consisting of an encoder (a nonlinear network generating dynamics) and a decoder (predicting inputs from the dynamics). We conducted evolutionary simulations to maximize the mutual information between inputs and predictions. Through this approach, we investigate the conditions under which temporal encoding with complex dynamics can evolve.

1Pos195 Mathematical Modeling and Simulation of Epithelial Wound Closure Dominated by Fingering Instability

Hikaru Emoto, Nen Saito (*Graduate School of Integrated Sciences for Life, Hiroshima University*)

Epithelial wound healing restores tissue integrity through cell migration and contraction by cell-cell adhesion. In large wounds, local cell movement induces epithelial fingering, a morphological instability where tissue boundaries form finger-like protrusions. While this has been experimentally observed, its role in healing remains unclear. We constructed a continuum model using the phase-field method to simulate rough wound closure governed by epithelial fingering. The model captures tissue shape changes by incorporating stress balance and spatially dependent migration. This approach enables future comparison with experiments and may clarify the functional significance of epithelial fingering in healing.

1Pos196 Mechanical balance of adhesions mediates chiral collective rotation induced by cell chirality

Ryohei Nishizawa^{1,2}, Tomoki Ishibashi¹, Goshi Ogita¹, Tatsuo Shibata^{1,2} (¹*BDR, Riken*, ²*Grad Sch. of FBS., Osaka Univ.*)

Chiral properties of living systems are observed as asymmetric structures. Recently, cell chirality has been implicated in LR-asymmetric morphogenesis, but how it generates asymmetric organs remains unknown. We found a cultured epithelial cell that shows chiral rotation in both single-cell and multicellular colonies. Pharmacological treatment reverses the collective rotation, suggesting involvement of not only intrinsic cell chirality but also mechanical interactions. A vertex-based mechanical model reproduces collective rotation from cell chirality, and its direction is determined by mechanical balance between cell-cell and cell-substrate adhesions. We will present results and discuss theoretically how chiral collective rotation emerges from cell chirality.

1Pos197 Multiphase chemistry of bio-related molecules in microdroplets studied aerosol optical tweezers

Yuan-Pin Chang (*Dept. of Chem., National Sun Yat-sen Univ., Taiwan*)

The multiphase mass transport or reaction of single aqueous microdroplets containing ascorbic acid, cysteine or nicotine was investigated by means of aerosol optical tweezers with Raman spectroscopy. The oxidation of ascorbic acid or cysteine in microdroplets via gaseous O₃ is exploited as a model system to elucidate the oxidation damages of antioxidants or amino acids in biosurfaces, such as airway-lining fluid, and exhaled bioaerosols. The evaporation kinetics of nicotine in microdroplet is exploited as a model system of aerosols released from e-cigarette. The other main advantage of this technique is the manifestation of cavity-enhanced Raman scattering which can provide the microphysical properties of each microdroplet, such as droplet radius, in high accuracies.

1Pos198 非平衡ナノ逆ミセルのテラヘルツ振動凝縮
Terahertz vibrational condensation in out-of-equilibrium nanoscale reverse micelles

Hiroshi Murakami (*QST*)

Over half a century ago, Fröhlich showed that the population number of the lowest-frequency mode of the terahertz (THz) vibrational band becomes a macroscopic value, which is called vibrational condensation, if the energy (e.g., metabolic energy in cells) input rate exceeds a critical value, and proposed that the coherent vibration induced by that condensation in biomolecules is crucial in their reactions in cells. Extensive theoretical studies based on a quantum theory have validated the model. No experimental studies, however, have observed the spectral transition due to that condensation. Nanoscale reverse micelles (RMs) are used with in-situ THz spectroscopy under the energy input of microwave at 2.45 GHz. The results agree with those derived from the model.

1Pos199 ナノ内視鏡 AFM 法を用いた上皮間葉転換による細胞内核膜硬さ変化測定
Nanoendoscopy-AFM based nanomechanical measurements reveal changes in nuclear elasticity during epithelial-mesenchymal transition

Takehiko Ichikawa, Yohei Kono, Makiko Kudo, Takeshi Shimi, Takeshi Fukuma (*NanoLSI, Kanazawa Univ.*)

The assessment of nuclear structural changes is considered a potential biomarker of metastatic cancer. However, accurately measuring nuclear elasticity remains challenging. Traditionally, nuclear elasticity has been measured by indenting the cell membrane with a bead-attached atomic force microscopy (AFM) probe. However, this method is influenced by the cell membrane and cytoskeleton. In this study, we employed Nanoendoscopy-AFM, a technique in which a nanoneedle probe is inserted into a living cell to directly measure nuclear elasticity. Our findings show that nuclear elasticity decreases when treated with TGF- β , which induces epithelial-mesenchymal transition (EMT). The findings suggest that nuclear structure changes during cancer progression.

1Pos200 ナノスケール構造・化学変化ダイナミクス分析のための高速 AFM・顕微ラマン複合装置
High-speed AFM/micro-Raman multimodal system for studying nanoscale conformational and chemical dynamics

Keishi Yang¹, Feng-Yueh Zhan², Verma Prabhat¹, Takayuki Uchihashi^{2,3}, Takayuki Umakoshi^{1,4} (¹*Grad. Sch. Eng., Univ. Osaka*, ²*Grad. Sch. Sci., Univ. Nagoya*, ³*ExCELLS*, ⁴*Inst. Adv. Co-creation Studies, Univ. Osaka*)

High-speed atomic force microscopy (HS-AFM) can observe various dynamics of proteins including conformational changes. By combining it with Raman spectroscopy, one can study both conformational changes and chemical-bond dynamics simultaneously, which enhances the analytical ability to reveal biological functions more in details. In this study, we developed the HS-AFM/micro-Raman multimodal system that can acquire one Raman spectrum per one HS-AFM image at the same area, enabling a correlation between conformational and chemical changes. We show some demonstrations of multimodal measurements with several types of samples, where the system successfully acquires Raman spectra from the HS-AFM observation area.

1Pos201 機械学習画像解析を活用した 3 次元バクテリアバイオフィルムの In vivo マイクロレオロジー計測
In vivo microrheological measurement for 3D bacterial biofilm with machine learning image analysis

Takuya Ohmura¹, Dominic J. Skinner², Konstantin Neuhaus^{3,4}, Gary P.T. Choi⁵, Jörn Dunkel⁶, Knut Drescher³ (¹*RIES, Hokkaido Univ.*, ²*Cent. Comput. Biol., Flatiron Instit.*, ³*Biozentrum, Univ. of Basel*, ⁴*Dept. Phys., Univ. of Marburg*, ⁵*Dept. Math., Chinese Univ. of Hong Kong*, ⁶*Dept. Math., MIT*)

Bacterial biofilms cause disadvantages in our lives such as clogging industrial pipes, forming dental plaque and contributing to human infections. The cell-to-cell interactions within biofilms are mediated by extracellular matrixes, which gives them high resistance to antibiotics and makes them mechanically difficult to remove.

We performed measurements of local material property within *Vibrio cholerae* by combining microfluidic system, 3D live-cell imaging and machine learning image analysis. The fitting the measured values with the multi-spring model clarified the localization of biofilm stiffness. The spatial distribution of stiffness correlates to the particular component of the extracellular matrix.

1Pos202 レーザーマニピュレーション法を用いた超微量ナノポア計測の開発
The development of the ultralow concentration detection using laser manipulation method and nanopore sensing

Masaya Yokono (*Nagaoka Univ. of Tech.*)

Nanopore measurement plays an important role in the medical field as a tool for measuring biomolecules because it does not require modification of the biological molecules. However, the short capture radius from a pore and to detect target samples in the presence of foreign substances are major issues. To solve these problems, we propose an ultra-trace nanopore measurement method with high selectivity. In this method, we use magnetic beads and laser manipulation technique to carry target samples to the specific position. In this presentation, we show experimental results as proof of the principle of the proposed method, allowing to detect RNA and GFP at low concentration. Also, we show our demonstration of Amyloid β detection for its application to the medical field.

1Pos203 酸化物/a-Si:H 積層薄膜による光触媒の作製とフラバン分子を用いた水素生成量の検出システム
Fabrication of photocatalysts based on oxide/a-Si:H stacked thin films and detection system of hydrogen production using flavan molecules

Yuki Sato¹, Kohei Saito¹, Akiko Hinoguchi¹, Hiroshi Masumoto², Yutaka Tsujiuchi^{1,2} (¹*Mat. Sci., Akita UNIV.*, ²*FRIS, Tohoku UNIV.*)

To enable the use of visible light energy for the photocatalytic function of titanium dioxide, we have fabricated a device based on titanium manganese oxide thin film/hydrogenated amorphous silicon thin film (a-Si:H).

With this device, the photocatalytic function of hydrogen production occurs in the ultraviolet to visible light region. In this study, we will formulate a formulation to calculate the amount of hydrogen production by directly calculating the transition between two states of a solution containing flavane molecules as the pH changes from the spectral measurement data, and investigate a measurement system that enables continuous measurement.

1Pos204 ゲル, 紫外可視光変換物質, FLAVAN 分子, 半導体, を用いた光照射ダイオード特性制御システム
Light irradiation diode characteristic control system using gels, UV-Visible light converting materials, FLAVAN molecules, semiconductors

Yutaka Tsujiuchi^{1,2}, Hiroshi Masumoto², Yuto Takayama¹, Kohei Saito¹, Akiko Hinoguchi¹ (¹*Mat. Sci., Akita UNIV.*, ²*FRIS, Tohoku UNIV.*)

We will study the control of light-irradiated diode characteristics using phenomena such as pH changes in ionic equilibrium states of FLAVAN molecules and other substances in biological systems, ion pair formation and annihilation inside hydrogels, and exciton generation at hydrogen-rich sub-surfaces in hydrogenated amorphous silicon as a system. Various, gels, UV/Visible light converting materials, FLAVAN molecules, semiconductors, will be used to analyze the interaction of light, molecules, and ions and applied to the study of sensor devices.

1Pos205 分子混雑効果が誘起する HIV-1 グアニン四重鎖 RNA の構造不均一性の単一分子レベルの解析
Analysis of structural heterogeneity in HIV-1 G-quadruplex RNA induced by molecular crowding at the single-molecule level

Miyuki Sakaguchi¹, Atsuki Harada¹, Kunihiro Ishii^{2,3}, Tahei Tahara^{2,3}, Takuhiro Otsu¹, Shoichi Yamaguchi¹ (¹*Grad. Sch. Sci. Eng., Saitama Univ.*, ²*Molecular Spectroscopy Lab., RIKEN*, ³*RIKEN Center for Advanced Photonics*)

G-quadruplex of HIV-1 RNA (G4) is a promising therapeutic target. To evaluate its stability in a cellular crowding environment, we examined the structural changes of G4 induced by polyethylene glycol (PEG), which mimics the molecular crowding effect. We applied independent fluorescence component analysis (IFCA) (bioRxiv, 2025.03.04.641393), a recently developed model-free method based on independent component analysis for unmixing multiparameter fluorescence signals, to the photon data of G4 labeled with a FRET dye pair. The results demonstrated the sensitive separation of 3% impurity and the detection of two looser G4 conformations induced by PEG, indicating increased structural heterogeneity under the crowding condition.

1Pos206 Single power-law rheology of crowded cytoplasm in living cells

Hiroyuki Ebata, **Daisuke Mizuno** (*Department of Physics, Kyushu University*)

The dynamic shear modulus, $G(\omega)$, has been reported to vary considerably without consistent rules even within the same cell. Thus, uncovering the physical basis of cytoplasmic rheology remains a major challenge. Here, we employed microrheology with a 3D feedback technique to minimize laser phototoxicity and examined cytoplasmic viscoelasticity across varied mechanical environments, cell types, and cytoskeletal disruptions. Unlike previous studies, a single power-law rheology $G(\omega) \propto (-i\omega)^{0.5}$ was observed over a broad frequency range for all conditions except ATP depletion. Cytoskeletal disruptions had only a minor effect on locally measured viscoelasticity. These findings demonstrate that molecular crowding governs the observed universality.

1Pos207 抗血清由来プローブを使った IRIS 多色超解像顕微鏡法による内在性の分子複合体の構成
The composition of endogenous molecular complexes by IRIS, multiplexed super-resolution imaging using antiserum-derived probes

Tai Kiuchi¹, Ryouhei Kobayashi², Shuichiro Ogawa¹, Louis Elverston², Dimitrios Vavylonis³, Naoki Watanabe² (¹*Grad. Sch. Med., Kyoto Univ.*, ²*Grad. Sch. Bio., Kyoto Univ.*, ³*Dept. Phys., Lehigh Univ.*)

To visualize molecular complexes by IRIS multiplexed super-resolution imaging, we developed antiserum-derived fluorescent probes that can associate with and dissociate from the target protein. The use of the antiserum-derived probes enables high-density labeling beyond the maximum density of antibody and about 2-fold improvement in resolution by averaging localization of a long-binding probe. Furthermore, we developed an image analysis PC-coloring to evaluate the correlation of molecular localization. By these techniques, we found laminar complex formation of eight endogenous proteins including EGFR and Grb2 at the rim of a clathrin-coated structure (CCS). The composition of the complex suggests that Grb2 and CCS component complexes locally recruit EGFR to the CCS rim.

1Pos208 Fluorescence lifetime imaging for quantification of subcellular GTP/GDP ratios in mammalian cells

Loan Thi Ngoc Nguyen¹, Cong Quang Vu², Satoshi Arai^{1,2} (¹*Div. NanoLSI, Univ. Kanazawa*, ²*WPI-NanoLSI, Univ. Kanazawa*)

Real-time quantification of guanosine triphosphate/guanosine diphosphate ratio (GTP/GDP), a key indicator of cellular metabolic status, provides valuable insights into cellular activity. Here, we developed a fluorescence lifetime biosensor, named FLIM-GTP/GDP, for quantifying GTP/GDP using fluorescence lifetime imaging microscopy (FLIM). We incorporated a GTP/GDP-binding domain into a circularly permuted enhanced yellow fluorescent protein. Through screening 3,000 mutants, we identified a mutant that exhibited a 0.7 ns change in response to different GTP/GDP ratios. We validated FLIM-GTP/GDP in HEK293T cells treated with inhibitors. We observed distinct GTP/GDP ratios across different cellular compartments of different cells and heterogeneity at the plasma membrane

1Pos209 Development of Organelle Heating Technology to Study the Spatiotemporal Dynamics of HSP Expression

Hettimudalige Dilini Nisansala¹, B.M.K.D. Basnayake¹, Takeru Yamazaki², Kayoko Nomura², Satoshi Arai^{1,2} (¹*Grad. Sch. of Frontier Science Initiative, Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

Heat shock protein (HSP) is essential for maintaining cellular homeostasis under heat stress. Still, their expression under heat stress at the subcellular level remains unclear. Key questions include: which organelles are highly sensitive to heat for HSP expression? what is the optimal temperature for inducing HSPs in each organelle? How long should each organelle be heated to trigger HSP expression? To address these, we developed “Organelle heating technology” with organelle-targeted heating dyes to enable localized heating in the mitochondria, nucleus, and ER. This technology allows the specific heating of target organelles by up to 10 °C. We first focused on mitochondrial heating, studying cellular temperature gradients and HSF1 nuclear granule formation.

1Pos210 酵素のナノスケール運動観察を目指したラベルフリー高精度一分子イメージングシステムの開発
Label-free high-precision single-molecule imaging system for nanoscale enzyme motion

Masato Sawa¹, Yasushi Okada^{1,2,3,4,5} (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*Grad. Sch. Med., Univ. Tokyo*, ³*Kobe Inst., Riken*, ⁴*WPI-IRC, Univ. Tokyo*, ⁵*UBI, Univ. Tokyo*)

The intracellular environment is inherently out of equilibrium, with cells using non-thermal fluctuations to fluidize their densely packed cytoplasm. Theoretical models predict that cytoplasmic enzymes undergo transient directional movements (ballistic motion) during catalytic cycles, thereby generating such non-thermal fluctuations. However, direct observation of the ballistic motion of enzymes remains challenging due to technical limitations. We are developing a label-free single molecule imaging system capable of tracking single enzymes and detecting ballistic motion directly. Here, we present our progress in constructing this system and demonstrate its capability to track nanometer-sized particles.

1Pos211 EMCCDの高精度ノイズモデルを用いた機械学習による細胞の高倍率生物発光イメージングのためのデノイジング
Denoising for high-magnification bioluminescence imaging of cells through machine learning with precise noise modeling of EMCCD

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Bioluminescence imaging (BLI) depends on luciferase-luciferin luminescence emission without excitation light. Although BLI allows for microscopy observation of cells with little phototoxicity, its lower luminescence intensity than fluorescence gives rise to images of lower quality, which restricts the scope of its application, especially at high magnification. In this study, we report a denoising technique for BLI with EMCCD camera. We established the noise model of EMCCD to simulate low-light images from ground truth clear images, which were used to train a neural network for denoising. The trained neural network successfully computed clear images from low-light bioluminescence images. The present technique is likely to push the limit of high-magnification BLI.

1Pos212 高速 AFM を用いた PfDYN2 の膜構造認識に基づくマラリア原虫分裂機構の探究
Investigation of Plasmodium division mechanisms based on membrane recognition by PfDYN2 using high-speed AFM

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Malaria causes many deaths, and drug-resistant strains highlight the need for new treatments. PfDYN2, essential for membrane constriction during the division, is a promising drug target, but its mechanism is unclear. EM showed PfDYN2 forms C-shaped. HS-AFM visualized PfDYN2 wrapping lipid nanotubes and forming spirals, supporting this role. Yet, its membrane assembly dynamics remained unknown. We hypothesized that PfDYN2 responds to membrane curvature. To test this, we created curved substrates using PDMS. PfDYN2 wrapped substrates at curvatures similar to lipid nanotubes, while other shapes appeared at different curvatures. These results suggest curvature-dependent polymerization of PfDYN2 and offer insight into membrane remodeling during parasite division.

1Pos213 ミオシン分子に結合したアクチン線維の超解像顕微像解析

Super-resolution images of actin filaments bound to myosin molecules using a microscope with a home-built illumination system

Daichi Kobayashi, Taiki Tsujimoto, Kuniyuki Hatori (*Graduate School of Science and Engineering, Yamagata University*)

To determine the nanometer-scale structural behavior of actin filaments in vitro, we used a dSTORM with a fluorescence microscope equipped with a high-power laser illumination system. We analyzed the super-resolution images of actin filaments bound to S1, HMM, and full-length myosin molecules fixed to a collodion-coated glass surface. The full width at half maximum of single filament images was calculated to be at 40 nm, 55 nm, and 61 nm in the presence of S1, HMM, and full-length myosin, respectively. This result indicates the possibility of detecting the difference in configuration of actin filaments as a function of the size of the myosin fragments. In addition, we demonstrate the availability of inexpensive home-built super-resolution microscope.

1Pos214 一分子蛍光イメージングを用いた分子シャペロンによるアミロイド脱凝集過程のメカニズムの解明
Amyloid conformation-dependent disaggregation of chaperone revealed by single molecule fluorescent imaging

Yoshiko Nakagawa¹, Shingo Tamai¹, Takashi Nomura¹, Takahiro Nakayama², Motomasa Tanaka¹ (¹*RIKEN, CBS*, ²*WPI Nano Life Science Institute, Kanazawa University*)

Several neurodegenerative diseases, such as Parkinson's and Alzheimer's, are characterized by the pathological accumulation of amyloid fibrils composed of disease-related proteins. These disorders may progress via cell-to-cell transmission of misfolded aggregates, promoted by intracellular fragmentation of amyloid. Molecular chaperones disaggregate amyloids by extracting monomers from fibril ends or internal sites. Structural differences among fibrils affect transmission efficiency, highlighting the importance of conformation. We analyzed amyloid structures by cryo-EM and established real-time imaging using super-resolution microscopy and HS-AFM. Our study reveals structure-dependent disaggregation, offering insight into new therapeutic strategies.

1Pos215 温度ジャンプ高速原子間力顕微鏡の開発と性能評価

Development and characterization of a temperature jump high-speed atomic force microscopy

Mai Tambo, Ayumi Sumino (*Grad. Sch. of biostudies, Kyoto univ.*)

To understand temperature responding structural changes for various temperature-sensitive biomolecules, we developed a temperature jump high-speed atomic force microscopy. We used an infrared laser to heat liquid water around the sample. By optimizing the wavelength of the laser and the optical system, the infrared light was irradiated only near the AFM tip, and the sample was heated locally, thereby successfully raising the sample temperature above 55°C within 10 ms and rapidly cooling it to room temperature by stopping the irradiation. Using this system, the phase transition of lipid membranes at 55°C was observed with almost no displacement. We expect that this system will be a useful tool for studying the temperature response mechanisms of biomolecules.

1Pos216 Load-induced remodeling of mechanosensing proteins in suspended cell sheets

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Two-dimensional cell assemblies, or cell sheets, are important tissue materials used in regenerative medicine and tissue engineering. The cell sheets are subjected to mechanical stimuli during handling. Therefore, understanding how the cells in the cell sheet respond to these stimuli is crucial for maintaining its properties under control. Here, we report a dual-color confocal fluorescence microscopy equipped with a pair of glass micro-needles to sustain and stretch a fibroblast cell sheet above the glass substrate. We find that mechanosensing protein complexes are formed at the cell-cell junctions under stretching, through which the cells sense the mechanical stress. Our method can serve as a 2D tissue model providing insights into cell state during implantation.

1Pos217

金ナノ粒子を用いる酸化還元蛋白質の電子移動制御と電気バイオものづくり

Efficacy of uncapped gold nanoparticles for electron transfer to redox proteins and its application for bioproduction

Yasuhiro Mie¹, Chitose Mikami¹, Kentaro Akiyama², Yoshiaki Yasutake¹ (¹*Biomanufacturing Production Res. Ctr., AIST*, ²*Molecular Biosystems Res. Inst., AIST*)

Redox proteins are promising in production of valuable chemicals for up-coming SDGs society. However, the requirement of electron transfer system to activate these proteins is a bottleneck in practical uses. Recently, we have prepared “pure” gold nanoparticle without any additives (uncapped gold nanoparticle), which makes the use (application) of gold nanoparticle more easily. In the present study, we have prepared the electrode using the gold nanoparticle and examined the electron transfer reactions to redox proteins such as cytochrome c and P450. The efficacy of the present electrode for rapid electron transfer was demonstrated, which is expected to result from the nanoporous structure composed of nanoparticles.

1Pos218

ARTIFICIAL CONTROL OF A HIGHLY ACTIVATED PLASTIC DEGRADING ENZYME BY PHOTOCHROMIC NANODEVICES

Ateke Yanick Besong, Shota Nishida, Shinsaku Maruta (*Grad.Sch.Sci.Eng., Soka Univ*)

Cutinase is a serine esterase in the α/β hydrolase superfamily, secreted by fungi to hydrolyze ester bonds including PET. Cut190 from *Saccharomonospora viridis* AHK190 has three functional sites; activity increases with Ca^{2+} binding at site 1. We created Cut190 mutants with high activity and photoswitch ability. F77 was mutated to tryptophan (F77W), showing 15-fold higher activity than wild type using p-nitrophenyl butyrate. F77C was made for photochromic compound incorporation and showed increased activity, but PAM was not incorporated, likely as F77 is buried. Thus, surface-exposed mutants S75C, S76C, and S79C were prepared. S75C was purified and showed higher activity. PAM covalently bound S75C, indicating successful photoswitch introduction.

1Pos219

異常拡散系の初期通過問題における系の総数依存性とその役割

The role of population for first passage time problem with anomalous diffusion

Yuta Sakamoto, Takahiro Sakaue (*Aoyama Gakuin University*)

First passage time problem, which is a stochastic process problem for a random walker to arrive at the setting goal, underlies a wide range fields such as biology, chemical reaction and so on. On these fields, we sometimes encounter the situation where a tremendous number of random walkers exist for a few of goals. Fertilization, in which many sperms ($\sim 10^8$) exist for a single ovule, is a good example for the situation. Germ cells have lifetime to fertilize, and it is considered that a tremendous number of sperm plays an important role in arriving at a goal within their lifetime. Our purpose is to construct the population theory for anomalous diffusion, which is complex diffusion often observed in vivo, and reveal the role of population for biological phenomena.

1Pos220

2点MSD解析の基礎と応用

Two-Point MSD Analysis for Eliminating External Motion

Naoya Katayama, Takahiro Sakaue (*Dept. of Phys. Aoyama Gakuin Univ.*)

In three-dimensional experimental observations of chromatin loci and similar structures, global translational and rotational movements of the nucleus may contaminate the observed data. In such cases, the standard Mean Square Displacement (MSD) reflects not only the intrinsic diffusion of internal movement but also external translational and rotational diffusion, potentially leading to inaccurate interpretations of the internal dynamics. In this study, we propose physics quantities based on the relative distance between two internal points, which allows us to eliminate the influence of external motion and extract the intrinsic diffusion behavior.

2Pos001 マウスノロウイルスカプシドと細胞レセプター sCD300lf の結合様式の解明
Elucidation of the binding mechanism between murine norovirus capsid and sCD300lf receptor

Kentaro Hiraka^{1,2}, Reiko Todaka³, Kei Haga³, Kazuhiko Katayama³, Kazuyoshi Murata^{1,2} (¹*ExCELLS, NINS*, ²*NIPS, NINS*, ³*Grad. Sch. Infection Control Sci., Kitasato Univ.*)

Norovirus causes epidemic nonbacterial gastroenteritis in animals. Recently, our group elucidated the capsid structure of murine norovirus using Cryo-EM and discovered that the protruding (P) domain structure of the capsid drastically changes before infection [1].

In this study, the complex structure of murine norovirus capsid and its cellular receptor, the soluble domain of CD300lf (sCD300lf), was investigated by Cryo-EM in two different capsid states. As a result, sCD300lf bound to the P domain of murine norovirus capsid in the infectious state but did not bind to the capsid in the non-infectious state. This result suggests a sophisticated mechanism of murine norovirus infection to target organs.

[1] Song et al., *PLoS Pathog.* 16(7) (2020)

2Pos002 細菌の細胞分裂に関与するタンパク質 FtsZ の構造遷移機構の解析
Structural transition mechanism of Bacterial cell division protein FtsZ

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FtsZ is a prokaryotic tubulin homolog and is essential in bacterial cell division. FtsZ bound with GTP polymerizes into tubulin-like protofilaments, accompanied by the conformational change of the subunit from relaxed to tense states. However, only FtsZs derived from a few bacterial strains have been observed to undergo the conformational change using the structural biology technique, suggesting that the conformational stability may depend on their amino acid sequences. To clarify the sequence dependency on the conformational stability, we determined the crystal structures of the chimeric FtsZ conjugated from different strains and discussed the conformational stability.

2Pos003 溶液 NMR による自然免疫シグナルタンパク質 MyD88 の多量化および相互作用解析
NMR analysis of the interactions of the MyD88 TIR domain in innate immune signaling

Shiho Nukui, Yudai Ito, Kazuki Kasai, Hidehito Tochio (*Dept. of Biol. Sci., Grad. Sch. of Sci., Kyoto Univ.*)

In innate immune signaling, Toll-like receptors (TLR) dimerize on the cell membrane upon recognition of the pathogen, allowing their cytosolic region to interact with MyD88, an adaptor protein that mediates downstream signaling. MyD88 then oligomerizes to transmit the signal. Several gain-of-function mutations of MyD88 have been identified in patients with diffuse large B-cell lymphoma, where spontaneous multimerization of MyD88 without TLR activation was triggered, leading to constitutive activation of downstream signals, resulting in tumor malignancy and resistance to treatment.

In this study, we analyzed the multimerization patterns of MyD88-TIR and how these patterns are affected by the gain-of-function mutation using solution NMR spectroscopy.

2Pos004 ATR-FTIR 分光法によるアデノシン A2a 受容体のリガンド誘起構造変化解析
Ligand-induced conformational changes in the adenosine A2a receptor probed by ATR-FTIR spectroscopy

Shuma Tajima¹, Kento Watanabe¹, Shota Nakamura², Mika Hirose², Akitoshi Inoue³, Takayuki Kato², Ryoji Suno³, Hideki Kandori^{1,4}, Kota Katayama^{1,4} (¹*Nagoya Institute of Technology Graduate School of Engineering*, ²*Institute for Protein Research, Osaka University*, ³*Kansai Medical University*, ⁴*Nagoya Institute of Technology OptoBioTechnology Research Center*)

Adenosine receptors are a class of GPCRs that recognize the neurotransmitter adenosine and are of great interest as drug target for sleep-related disorders. We have established a method to detect receptor conformational changes upon ligand binding using attenuated total reflection Fourier-transform infrared (ATR-FTIR) spectroscopy. This technique has previously been applied to muscarinic and opioid receptors to elucidate their ligand-binding mechanisms. In this study, we successfully obtained infrared difference spectra reflecting conformational changes in the mouse A2a receptor upon binding of adenosine its endogenous agonist. In future work, we aim to analyze structural changes and binding affinities in response to antagonist and Na⁺ binding.

Naito Ishimoto^{1,2,3}, Joshua Wong², Shan Heb², Sally Shirranc⁴, Olivia Paramio², Chloe Seddon^{2,3}, Nanki Singha^{2,3}, Carlos Balsalobre⁵, Ravi Sonanie⁶, Abigail Clements³, Edward Egelman⁶, Gad Frankel², Konstantinos Beis^{2,3} (¹*Grad. Sch. Life Sci., Yokohama City Univ.*, ²*Department of Life Sciences, Imperial College London*, ³*Rutherford Appleton Laboratory, Research Complex at Harwell*, ⁴*Biomedical Sciences Research Complex Mass Spectrometry & Proteomics Facility, University of St Andrews*, ⁵*Department de Genètica, Universitat de Barcelona*, ⁶*Department of Biochemistry and Molecular Genetics, University of Virginia*)

The high resolution cryo-EM structure of the conjugative H-pilus from IncHI1 plasmid R27 reveals that TrhA pilin subunits make a cyclisation through a covalent bond between Gly1 and Asp69, following cleavage of five C-terminal residues. Mutagenesis confirms this cyclisation is essential for pilus biogenesis and conjugative transfer. TrhA assembles into a helical structure with phospholipids at 1:1 stoichiometry. This novel cyclic structure enhances structural stability, potentially explaining the efficient dissemination of antimicrobial resistance genes via IncH plasmids among bacterial pathogens.

Jie Ma¹, Masahiro Fukuda², Seiwa Nakamura³, Seiya Tajima¹, Koichiro Kishi³, Suhyang Kim², Hideaki Kato^{1,2,3} (¹*Graduate School of Science, The University of Tokyo*, ²*Research Center for Advanced Science and Technology, The University of Tokyo*, ³*Graduate School of Arts and Sciences, The University of Tokyo*)

Channelrhodopsins are light-gated ion channels widely used in optogenetics to control neuronal activity. Engineered variants with enhanced ion selectivity have expanded their utility, including the Ca²⁺-selective channel CapChR2, which exhibits significantly improved calcium permeability. Here, we report cryo-EM structures of CapChR2 in both calcium-free and calcium-bound states. Structural comparison reveals side chain-level rearrangements in the presence of Ca²⁺, suggesting a potential mechanism for calcium selectivity. These findings provide a structural basis for understanding and further engineering channelrhodopsins with customized ion selectivity for advanced optogenetic applications.

Sakura Homma¹, Seri Nishimoto², Tomoya Tendo³, Kanata Warisaya², Hiroki Minami², Issei Tanaka², Ryuya Toyooka³, Takashi Horiyama⁴, Tomohiro Tachi³, Yasuhiro Matsunaga^{1,5} (¹*Grad. Sch. Sci. & Eng., Saitama Univ.*, ²*Grad. Sch. Eng., Univ. Tokyo*, ³*Grad. Sch. Arts & Sci., Univ. Tokyo*, ⁴*Grad. Sch. Fac. Inf. Sci. & Tech., Hokkaido Univ.*, ⁵*RIKEN*)

While Caspar-Klug (CK) theory classifies capsid sizes, subunit shape variations are poorly understood, especially for non-CK structures. We aim to identify subunit shapes forming icosahedral interfaces beyond CK theory. Previously, we classified T=1 subunit shapes via "dihedron-unfolding tiling". We investigated this approach for non-CK T=2 structures. For T=2, exhaustive search yielded three subunit shapes: rhombic triacontahedron, rhombic enneacontahedron, and a pentagon-triangle combination. These can be formed by bisecting a T=1 dihedron-folding tile into two congruent shapes. Theoretical analysis revealed one further bisection case, not observed in existing T=2 structures. Detailed tile shapes will be given in the poster.

Zecheng Zhang¹, Qianyan Tang¹, Weitong Ren², Jun Wang³ (¹*Hong Kong Baptist University, HKSAR, China*, ²*Wenzhou Institute, Univ. Chin. Acad. Sci, China*, ³*Nanjing University, China*)

Protein folding and functional dynamics are interconnected concepts in biophysics. Analyzing an extensive dataset of AlphaFold2-predicted structures, we identify a fundamental scaling law linking contact order (protein folding) to fluctuation entropy (functional dynamics). This law persists across protein lengths and taxonomic boundaries, revealing a robust negative correlation: long-range contacts stabilize structures while constraining flexibility. Cross-organism comparisons show proteins from complex organisms exhibit lower contact order and higher entropy at similar chain lengths. These findings integrate AI-driven models with statistical physics, offering a quantitative framework to study folding-function relations, proteome evolution, and biomolecular design.

2Pos009 クライオ電子顕微鏡を用いた V-ATPase の構造機能解析
Structural and Functional Analysis of V-ATPase Using Cryo-Electron Microscopy

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V-ATPase is an ATP-driven proton pump involved in organelle acidification and implicated in cancer cell survival, proliferation, and metastasis, making it a promising target for drug development. We determined the high-resolution cryo-EM structure of rat brain-derived V-ATPase in complex with Bafilomycin A1, a potent V_o-specific inhibitor. For purification, we utilized the interaction between the A subunit and SidK, a Legionella-derived effector protein. To explore its native conformation, we purified synaptic vesicles (SVs) from rat brain and visualized them by cryo-EM. We have tried to improve the purification step of SVs from a brain to determine high resolution structure of V-ATPase in the native biological membranes.

2Pos010 酵母プリオンタンパク質の構造・細胞表現系相関解析
Structural and Phenotypic Correlation Analysis of Yeast Prion Proteins

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The yeast prion protein Sup35 forms structurally diverse amyloid fibrils, each of which corresponds to a distinct prion strain with unique phenotypic features. Here we analyzed four Sup35 fibrils derived from WT and a S17R mutant using cryo-EM, revealing differences in amyloid core structures, stabilization energies and interactions with the molecular chaperones required for prion propagation. These findings establish a direct link between structural polymorphism of amyloid and its propagation efficiency, providing new insights into the molecular basis of prion strain phenotypes. The structural framework not only elucidated yeast prion biology but also provided broader implications for pathophysiology of neurodegenerative disorders.

2Pos011 放線菌由来新規プレニル基転移酵素の構造-機能相関の解明
Structure-function relationship of novel prenyltransferase from *Streptomyces* sp. KS84

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Terpenoids represent the most widely distributed family of natural products and play significant physiological roles in nature. The diverse terpene scaffolds are biosynthesized by the enzymes in the prenylsynthase superfamily. Indole prenyltransferase (IPT), one of the enzymes in the prenylsynthase superfamily, catalyzes the condensation of an isoprene to an indole compound, consequently producing an indole terpene scaffold. Therefore, IPT plays a crucial role in generating a variety of terpene scaffolds. However, the three-dimensional structure and catalytic mechanism of IPT have been unclear. In this study, we determined the X-ray crystal structure of a novel IPT derived from *Streptomyces* sp. KS84, and discussed its catalytic mechanism.

2Pos012 Protein Language Models Capture Evolutionary Trends via Embedding Variation

Yuxiang Zheng, Zecheng Zhang, Qian-Yuan Tang (*Hong Kong Baptist Univ*)

Protein language models (PLMs) capture key patterns in protein sequences, enabling large-scale analysis. We applied ESM-2, a typical PLM, to proteomes of 48 diverse organisms, analyzing protein embeddings at the residue level. Natural protein sequences exhibit distinct embedding patterns compared to shuffled or mutated variants, with residues of similar physicochemical properties clustering along sequences. PLM-derived features correlate with AlphaFold-predicted structural properties, including surface accessibility. For proteins of given chain lengths, embedding variation correlates with organismal complexity, reflecting a robust statistical trend. These findings highlight PLMs' potential for high-throughput analysis of protein dynamics and evolution.

2Pos013 時間分解真空紫外円二色性による SDS ミセル結合過程における β -ラクトグロブリンの構造ダイナミクス観測
Observing structural dynamics of β -Lactoglobulin Binding to SDS Micelle by Time-Resolved Vacuum-Ultraviolet Circular Dichroism

Satoshi Hashimoto¹, Koichi Matsuo^{1,2} (¹*Grad. Sch. Adv. Sci. Eng., Hiroshima Univ.*, ²*HiSOR*)

Membrane-bound proteins change their native structure upon interacting with the membrane to express various biological functions. The structural alternations of β -lactoglobulin (bLG) binding to sodium dodecyl sulfate (SDS) micelles were observed by time-resolved vacuum-ultraviolet circular dichroism (TR-VUVCd) (178–260 nm) in the range of 0.2–120 s. Kinetic analysis showed the presence of two types of intermediates and secondary structure analysis revealed the step-by-step increments of numbers of helices from native to micelle-bound states. The affinity of these helices with the micelle surface was evaluated by molecular dynamics simulations, revealing the mechanism by which bLG wraps micelles via electrostatic and hydrophobic interactions.

2Pos014 ペプチド結合の折り目効果の強化による黄色蛍光タンパク質 Venus の収量増加の試み
Attempts to increase the yield of the yellow fluorescent protein Venus by enhancing the ORIME effect of a peptide bond

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Venus, a yellow fluorescent protein, has been utilized in many studies due to its high fluorescence intensity. Based on our relaxation model of the main-chain peptide bond in proteins (Chiba et al., *Protein Science*. 2023), we produced E90D Venus by replacing Glu90 in a loop, to increase the biosynthetic yield of Venus. The yield of E90D Venus obtained using *E. coli* was found to be significantly higher than that of Venus, as in the case of YFPuv, prepared by replacing five amino acids in GFPuv. On the other hand, fluorescence intensity of E90D YFPuv was almost the same as that of YFPuv, whereas fluorescence intensity of E90D Venus was decreased. Comparison of 2D NMR (¹H-¹⁵N HSQC) showed that more peak positions were changed in E90D Venus than in E90D YFPuv.

2Pos015 トリプシン様蛋白質分解酵素のプロ領域による立体構造形成の解明
Propeptide-Mediated Folding of a Trypsin-Like Protease

Kairi Ogawa¹, Nana Sakata¹, Orika Ashida¹, Mitsuhiro Miyazawa², Shigeru Shimamoto¹, Yuji Hidaka¹ (¹*Grad. Sch. Sci. Eng., Univ. Kindai*, ²*PrevenTec Inc.*)

Cocoonase (CCN), produced by *Bombyx mori*, is a trypsin-like enzyme that is synthesized as a precursor, proCCN. Recently, we reported that the propeptide region plays an important role in the folding of mature CCN. However, the detailed folding mechanism of proCCN remains unclear. Therefore, to investigate the propeptide-mediated folding of CCN, a degradation-suppressed CCN mutant protein was used, as CCN exhibits significant protease activity during the folding reaction. Refolding experiments of the reduced mature CCN were performed in the presence and absence of the synthetic propeptide. Additionally, we also performed a reaction in which the propeptide was added exogenously during the folding process. The refolding process was monitored by RP-HPLC.

2Pos016 変性状態下における BDPA の non-local 相互作用とフォールディング機構の再検討
Revisiting the Folding Mechanism of BDPA through non-local interactions in the Denatured State

Seiichi Hayashi¹, Saeko Yanaka^{1,2,3}, Maho Yagi^{1,2,4}, Yukiko Isono^{1,2}, Koichi Kato^{1,2,4}, Kunihiro Kuwajima⁵ (¹*Institute for Molecular Science, National Institutes of Natural Sciences*, ²*Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences*, ³*Materials and Structures Laboratory at Institute of Integrated Research, Institute of Science Tokyo*, ⁴*Graduate School of Pharmaceutical Sciences, Nagoya City University*, ⁵*Department of Physics, School of Science, University of Tokyo*)

Residual structures in denatured proteins are crucial for understanding folding mechanisms. Here, we applied our developed DMSO-quenched H/D exchange NMR method to examine how a single-point mutation affects the denatured state of the B domain of protein A (BDPA). In the wild-type, specific regions showed significant protection from exchange, which was markedly reduced in the L20A mutant. Despite the sequence distance between Leu20 and the affected region, the results suggest that non-local hydrophobic interactions help stabilize residual secondary structures. Our findings support a framework folding model, where persistent tertiary contacts guide stepwise structure formation, contrasting with the traditionally proposed nucleation-condensation model.

2Pos017 構造に基づく単純な統計力学モデルを用いた骨形成タンパク質2のフォールディング反応過程の予測
Prediction of the folding process of bone morphogenetic protein 2 using a simple structure-based statistical mechanical model

Yusaku Hirata¹, Koji Ooka², Munehito Arai^{1,2,3} (¹*Department of Physics, The University of Tokyo*, ²*College Arts and Sciences, The University of Tokyo*, ³*Department of Life Sciences, The University of Tokyo*)

Recent machine learning models can accurately predict protein structures formed after folding. However, even these models cannot predict the dynamics of the folding process, especially for proteins with complicated structures called "cystine knots". Here, we used the WSME-L(SS) model, which is a simple, structure-based statistical mechanical model, to predict the folding of a bone morphogenetic protein 2 (BMP-2) monomer with a cystine knot. The model predicted that a "window" of the cystine knot forms at the earliest stage of folding, followed by an α -helix, β -sheets and a disulfide bond running through the window. Thus, our approach can also be used to predict the folding process of proteins with complicated structures.

2Pos018 RNAによるタウ凝集の速度論的解析
Kinetics of RNA-induced Tau Aggregation

Hiyori Araki, Hide Miyaguchi, Hideyuki Komatsu (*Department of Bioscience and Bioinformatics, Faculty of Systems Engineering and Computer Science, Kyushu Institute of Technology*)

The abnormal aggregation of a microtubule-binding protein tau is related to Alzheimer's disease and other dementias. Analysis of aggregation process is important for understanding their pathology. Extracellular heparin has been used as an exogenous aggregation-promoting polyanion in *in vitro* aggregation analysis using fluorescent dyes such as thioflavin T. Although intracellular RNA is another candidate for the aggregation-promoting polyanion, RNA-induced aggregation kinetics has hardly been reported because of RNA-binding by the dyes. Thus, some fluorescent dyes will be tested for the kinetic analysis in the presence of RNA, and the aggregation process of wild-type tau and a disease-associated P301L mutant will be analyzed using a selected appropriate fluorescent dye.

2Pos019 がん抑制タンパク質 p53 のアセンブリ形態制御法の確立
Control of the assembly morphology of the tumor suppressor protein p53

Emi Hibino¹, Reiji Hijikata¹, Haruna Yoshida¹, Hidekazu Hiroaki^{1,2,3} (¹*Grad. Sch. Pharm. Sci., Nagoya Univ.*, ²*BeCellBar*, ³*COMIT*)

The tumor suppressor protein p53 prevents oncogenesis. The DNA binding domain of p53 (p53-DBD) is aggregation-prone, leading to loss of p53 function. However, research on aggregation pathways is complicated because p53-DBD simultaneously generates at least two types of aggregates: amorphous aggregates and amyloid aggregates. Our aim is to produce distinct aggregates and inhibit both types of aggregation. First, we discovered reagent X suppressed amorphous aggregation and promoted amyloid aggregation of p53-DBD. Second, we successfully identified reagent Y that inhibits both types of aggregation. Interestingly, reagent Y induced the formation of higher-order multimers of p53-DBD. In conclusion, we have demonstrated that the form of p53 can be controlled.

2Pos020 Molecular Shape Evolution of the Clock Protein KaiC

Shuji Akiyama^{1,2}, Yoshihiko Furuike^{1,2} (¹*NINS, IMS*, ²*SOKENDAI*)

The core oscillator of the cyanobacterial circadian clock can be reconstructed by mixing the three kinds of clock proteins KaiA, KaiB, and KaiC in the presence of ATP. Our previous study suggests that the establishment of the self-sustained protein-based oscillator occurred in a most recent common ancestor of cyanobacteria long after the emergence of a primitive photosynthetic system. In this study, we studied the molecular shapes of extant and ancestral KaiCs using small-angle x-ray scattering. The results indicate that ancestral KaiCs have evolved along two pathways distinguished in terms of compactness: one pathway toward losing compactness as adaptive time-measuring systems, and the other toward gradually acquiring compactness as the autonomous oscillators.

2Pos021

オワンクラゲ由来蛍光タンパク質における二量体形成の比較

Comparison of Dimerization Behavior of Fluorescent Proteins from the Jellyfish *Aequorea Victoria*

Yuna Kinoshita, Haruko Hosoi (*Grad. Sch. Sci., Toho Univ.*)

Fluorescent proteins (FPs) have been developed and used for visualizing living cells. Oligomerization of FPs can be a serious problem in living cells because it affects the intracellular environment. In this study, we focused on the most common FPs: enhanced green fluorescent protein (eGFP) and enhanced yellow fluorescent protein (eYFP). We performed picosecond time-resolved fluorescence anisotropy measurements and found that the dimerization tendency of eGFP is much weaker than that of eYFP. Furthermore, these quaternary structures are different, although eGFP and eYFP differ in only 5 out of 239 amino acids. We clarify that we identified the amino acid responsible for dimer formation, which allows us to control the quaternary structures of FPs.

2Pos022

グライコプロテオミクスのための O-glycoprotease IMPa 活性部位付近の相互作用解析

Analysis around the Active Site of O-glycoprotease IMPa for Glycoproteomics

Hiromitsu Shimoyama, Tomoaki Tamano, Issaku Yamada (*The Noguchi Institute*)

As glycans are sensitive to inner cell situations, such as, a disease and youth, an analysis of glycoproteins provides much helpful information for our health. To analyze the glycoproteins, an enzyme with high cleavage activity for glycoproteins is needed.

IMPa is O-glycoprotease with high activity, however, for some peptide sequence, IMPa cannot work as for others. In this study, the interactions and structures of IMPa and cleavable/non-cleavable glycopeptide complex systems using molecular dynamics simulations. A distribution of contact map showed differences between IMPa and the cleavable/non-cleavable glycopeptides. We would like to discuss about the relationship between the differences and IMPa's activities.

2Pos023

Functional and Structural Analyses on Clock Protein KaiC to Identify the Essential Step for the Temperature Compensation

Kanta Kondo^{1,2}, Yoshihiko Furuike^{1,2}, Kota Horiuchi^{1,2}, Yasuhiro Onoue², Shuji Akiyama^{1,2} (¹SOKENDAI, ²IMS)

A cyanobacterial clock protein KaiC undergoes the ATP hydrolysis and the phosphorylation cycle (P-cycle) in a circadian manner. The ATPase activity and the period of P-cycle are almost constant at a wide range of physiological temperature. To elucidate the temperature compensation mechanism, we screened temperature-dependent KaiC mutants based on their ATPase activities and investigated their functional properties. Through a series of biochemical experiments, we identified several mutants whose ATPase activities decrease by half and P-cycles get slightly longer as temperature increases. In this meeting, we will discuss these results together with the structural analysis we are working on to identify the essential step for the temperature compensation.

2Pos024

シトクロム P450 還元酵素におけるフラビン補因子の還元によるアロステリック応答の分子動力学解析

Molecular dynamics analysis of the allosteric response to reduction of flavin cofactors in cytochrome P450 reductase

Mikuru Iijima, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)

Cytochrome P450 reductase (CPR) supplies electrons from NADPH to downstream heme proteins via two flavin cofactors FAD and FMN. CPR has two flavin-containing domains, FAD domain and FMN domain, and it is considered that the electron transfer is regulated by open-closed interdomain motion. In this study, keeping in mind our previous finding that the closed state is intrinsically stable (Iijima et al., 2019), we analyzed the coupling between the redox and structural states of CPR by longer MD simulations using higher-resolution X-ray structures. We then found a redox-state-dependent interdomain twisting, which is suited for electron transfer to downstream proteins and is likely caused by the dielectric allostery of CPR due to the net-charge change in the flavin cofactors.

2Pos025**一本鎖抗体の活性に対する大腸菌外膜タンパク質 OmpF の効果**

Effect of *Escherichia coli* outer membrane protein, OmpF, on the activity of single-chain variable fragments

Keiko Okano, Anna Ogi, Takao Izuka, Toshiyuki Okano (*Department of Electrical Engineering and Bioscience, School of Advanced Science and Engineering, Waseda University*)

We previously obtained C13 monoclonal antibody whose antigen binding activity changes depending on temperature; the C13 antibody dissociates from the antigen as the temperature increases. We expressed a single-chain variable fragment (scFv) of the C13 antibody in *E. coli*, and purified it from the insoluble fraction by denaturation and refolding. Utilizing the feature of the C13 scFv, we developed a temperature-dependent protein purification system termed THETA system. Here we found that the C13 scFv was efficiently expressed and purified in the presence an *E. coli* outer membrane protein, OmpF. To reveal the mechanism of the action by OmpF, we further generated OmpF-deficient *E. coli* and evaluated the effect on the expression and refolding efficiencies of the C13 scFv.

2Pos026**時計タンパク質 KaiC における第三の周期調節部位**

The third period-regulating site in the clock protein of KaiC

Kota Horiuchi^{1,2}, Yoshihiko Furuike^{1,2}, Kumiko Ito-miwa³, Shuji Akiyama^{1,2} (¹*Institute for Molecular Science, SOKENDAI*, ³*Nagoya University*)

In the presence of KaiA and KaiB, the cyanobacterial clock protein KaiC is repeatedly auto-phosphorylated and then auto-dephosphorylated (P-cycle) with a period of approximately 24 h. There are multiple sites in KaiC at which the period length of the P-cycle is affected by amino acid substitutions. Among these, only S157 and Y402 are known as the period-regulating sites, because the mutations even at the same site result in either shorter and longer period of the P-cycle depending on the type of post-substitution residue. In this study, we newly identified the third period-regulating site of KaiC and investigated the properties of the mutants obtained by replacing the site with 19 different amino acid residues.

2Pos027**Time-Resolved Study of Light Intensity-Dependent Clustering Dynamics of TePixD**

Chihiro Aramoto¹, Yusuke Masuda¹, Shunro Tokonomi², Masahide Terazima¹, Yusuke Nakasone¹ (¹*Grad. Sch. Sci., Kyoto University*, ²*Grad. Sch. Sci., Gakushuin University*)

We discovered that TePixD, a blue light sensor protein from the thermophilic cyanobacterium, forms large, visually observable clusters in response to intense blue light, which revert to the initial soluble state in the dark. Although the underlying mechanism remains unclear, this phenomenon may provide insights into novel regulatory systems in biology. To elucidate this unique clustering mechanism, we measured reaction dynamics using the transient grating (TG) method. Under strong light, we observed multi-step changes in the diffusion coefficient, which likely reflect the initial steps of clustering. We are now conducting a detailed analysis of the light intensity dependence on the TG signal to develop a reaction model for this process.

2Pos028**細菌膜内切断プロテアーゼ RseP の基質結合構造と光架橋解析から提案する基質ドッキング機構
Substrate docking mechanism of intramembrane protease RseP revealed by the substrate-bound cryoEM structure and photocrosslinking analysis**

Yosuke Shimizu¹, Tatsuya Kobayashi¹, Kikuko Asahi², Terukazu Nogi², Yoshinori Akiyama¹, **Yohei Hizukuri**¹ (¹*Inst. Life Med. Sci., Kyoto Univ.*, ²*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

RseP, the S2P family intramembrane protease of *E. coli*, is involved in regulating transmembrane signaling, including the extracytoplasmic stress response, and in maintaining membrane proteostasis. We previously proposed a model in which a gate structure within RseP controls substrate access to its proteolytic active site. In this study, we explored the substrate-gate interactions using a gate-targeted *in vivo* photo-crosslinking approach. We also determined the cryo-EM structure of the substrate-bound state of a bacterial RseP orthologue and performed the structure-guided photo-crosslinking analysis. Based on the results, we propose a revised substrate docking model, in which the substrate passes through the gate via a threading mechanism (Asahi *et al.*, 2025, *Sci. Adv.*).

2Pos029

ナノ秒蛍光相関分光法を用いたタンパク質とRNAの高速ダイナミクスの観測
Ultrafast dynamics of protein and RNA investigated by nanosecond fluorescence correlation spectroscopy

Yuji Itoh^{1,2}, Yutaka Sano^{1,2}, Ibuki Soshino^{1,2}, Shrutarshi Mitra^{1,2}, Divya Rajendran³, Athi N. Naganathan³, Satoshi Takahashi^{1,2} (¹Grad. Sch. Sci., Tohoku Univ., ²IMRAM, ³IIT Madras)

Nanosecond fluorescence correlation spectroscopy (ns-FCS) is a powerful method to detect the dynamics of biomolecules such as proteins and nucleic acids. We aim to characterize the ultrafast chain dynamics of proteins and short RNA strands. We first measured B domain of protein A (BdpA), and 4 M of GdmCl caused the appearance of a chain dynamics, demonstrating the very fast dynamics of the unfolded BdpA. We further conducted the ns-FCS measurements with short RNA strands and found that their chain dynamics is extremely sensitive to the salts and denaturant in the buffer solutions. We are currently trying to investigate the chain dynamics of DNA binding domain of cytidine repressor (CytR) in the presence of DNA strands and under the high ionic strength.

2Pos030

酸化 LDL の高感度検出を目指したバイオセンサーの合成研究
Synthetic study of biosensors for measurement of oxidized LDL

Takahisa Hiruma, Ryota Kumakura, Seiji Takeda (*Pharm. Sci., Hokkaido Univ. of Sci.*)

LOX-1 has a potential to bind modified LDLs such as oxidized LDL. The modified LDLs recognized by LOX-1 have been attention because LOX-1 is related to macrophage foaming and developing inflammation. Currently, modified LDL can be measured by immunoassay using oxidized LDL antibodies or recombinant LOX-1 but there is room for improvement in selectivity and sensitivity for modified LDL. Interaction of the LOX-1 with modified LDL is not strong, suggesting that multiple LOX-1s might be involved to interact with modified LDL. Therefore, we designed a molecule with two affinity sites for the LOX-1 to increase density of the LOX-1. We will present our study on the synthesis of the molecule and analysis of binding properties to LDLs by using bio-layer interferometry.

2Pos031

酵素反応を用いたタンパク質の部位特異的蛍光色素ラベル化法の開発
Development of site-specific fluorophore labeling to target protein by using enzymatic reactions

Ai Hanano^{1,2}, Saori Kanbayashi¹, Cassidy Schmitt¹, Hiroyuki Oikawa³, Tateki Suzuki⁴, Takao Hashiguchi⁴, Yuji Itoh^{1,2}, Satoshi Takahashi^{1,2} (¹Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, ²Graduate School of Life Sciences, Tohoku University, ³Molcure Inc, ⁴Institute for Life and Medical Sciences, Kyoto University)

Labeling of fluorophores to specific locations of target proteins is an essential step in the single-molecule fluorescence spectroscopy. To enable the labeling, we first used transglutaminase (TG), an enzyme that conjugates primary amines linked to a fluorophore to the six-residue Q3 tag inserted into the target protein. However, TG caused the crosslinking of the target, lowering the efficiency of the labeling. To further seek other enzymatic reactions, we next adopted Sfp phosphopantetheinyl transferase, which transfers fluorophores to an S6-tag fused to the protein. We demonstrated that Sfp can label the target protein even at the very low concentration. This approach may support single-molecule FRET investigations of viral proteins.

2Pos032

分子動力学計算とニューラルネットワークの連携による生体分子小角散乱プロファイルの解析
Interpretation of small-angle scattering profiles of biomolecules by molecular dynamics simulation and neural networks

Masahiro Shimizu (*KURNS, Kyoto Univ.*)

Small-angle scattering profiles of biomolecules reflect their dynamics. Because the profiles are not very informative, help with molecular dynamics (MD) simulation is often required to interpret their molecular motions. While this is valid, the results depend on parameters of MD force fields. Therefore, visualizing possible molecular motions based on a scattering profile requires MD simulations with various parameter sets, which is computationally expensive. Here, we present an approach for reducing the computational costs. Instead of sampling conformation distribution for each force field, short elemental motions are obtained from MD simulations, which are then used to construct a neural network that outputs molecular motions from a scattering profile.

[2Pos033](#) AlphaFold3 を用いた AFM 画像から 3 次元立体構造の高速な再構築手法
Rapid Reconstruction of Atomic 3D Configurations from an AFM image by AlphaFold3

Tsuyoshi Kawai, Yasuhiro Matsunaga (*Grad. School. Sci. Eng., Univ. Saitama*)

Atomic force microscopy (AFM) captures biomolecular dynamics under biological conditions, but the observable information is limited to surface geometries. Here, we propose a rapid reconstruction method by utilizing AlphaFold3. Specifically, we impose height restraints extracted from the image on the diffusion process within AlphaFold3, steering the sampling toward structures consistent with the measurement. Existing rigid-body or flexible fitting approaches often require hours or days of computation, but our strategy leverages AlphaFold3's co-evolutionary priors to narrow the conformational search and finish in minutes. We evaluate reconstruction accuracy across a range of image noise levels and discuss the applicability to real AFM images.

[2Pos034](#) The development of AMP-based antibiotics for drug-resistant Gram-negative bacteria

Wei Chun Weng, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo*)

Antimicrobial resistance is one of the critical health threats of this century. Antimicrobial peptides (AMPs) offer a promising alternative by killing bacteria through membrane disruption, reducing the likelihood of resistance development. However, high concentrations of AMPs may still cause undesirable side effects. To address this challenge, we explored the synergy effect between different types of biomolecules. In our preliminary experiments using representative Gram-negative bacteria, we observed that certain AMP combinations significantly lowered the minimum inhibitory concentrations (MICs). This approach may represent a potential strategy for combating drug-resistant Gram-negative pathogens.

[2Pos035](#) Development of red-color fluorescence lifetime biosensors for quantification of ATP levels in living cells

Tri Minh Phan¹, B.M.K.D Basnayake¹, Quang Vu Cong², Satoshi Arai^{1,2} (¹*Graduate School of Frontier Science Initiative, Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

Fluorescence lifetime-based biosensors enable robust quantification of target molecules through fluorescence lifetime imaging microscopy (FLIM). We previously developed a green FLIM biosensor, qMaLioffG, for quantifying adenosine triphosphate (ATP), the cellular energy currency. Here, we extend this approach to the red spectrum by incorporating a circularly permuted red fluorescent protein into an ATP-binding domain. Through linker optimization, we identified two mutants: qMaLionR, which exhibited an increase $\Delta\tau = +0.4$ ns, and qMaLioffR, which showed a decrease $\Delta\tau = -1.3$ ns in response to ATP between 0 and 10 mM. Using qMaLionR and qMaLioffR, we performed multiplex imaging with qMaLioffG to simultaneously quantify ATP levels in both cytoplasm and mitochondria.

[2Pos036](#) タンパク質工学を利用した人工セルロソームの構築とセルロース分解の効率化
Construction of an artificial cellulosome using protein engineering toward improvement of cellulose degradation

Momoka Takazawa, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Cellulose is the most abundant organic substance on Earth, and its effective utilization can help address the depletion issue of fossil fuels. However, cellulose decomposition is difficult because the cellulose has a robust structure and cellulases are easily inactivated. In this study, to realize efficient cellulose decomposition, we form a cellulase complex using a Catcher/Tag system and a Cohesin-Dockerin interaction. The cellulase complex is composed of endoglucanase and scaffolding protein that can bind to cellulose. The formation of scaffolding proteins was identified by SDS-PAGE as a molecular weight of more than 250 kDa. Binding of endoglucanase to the scaffolding protein through Cohesin-Dockerin interaction was observed using a confocal microscope.

2Pos037 De novo design of sensor proteins: calcium-binding protein**Rie Tatsumi**, Nobuyasu Koga (*IPR, Univ. Osaka*)

The creation of sensor proteins that change conformations upon binding to various molecules will enable to visualize various molecules. In this study, we aim to develop a general method for creating biosensors that recognize a variety of molecules. By using diverse designed protein structures as building blocks and linking them with naturally occurring protein linkers known to have conformational change ability, we attempted to design sensor proteins that change conformations upon binding to the ligand of interest. As a proof of concept, we have set out to design calcium-binding sensor proteins. In this poster, we will talk about the design concept of sensor proteins and the progress of the calcium-binding protein design.

2Pos038 遺伝子にコードされた蛍光バイオセンサーのためのモジュール型設計戦略: VEGF 検出への応用
Modular design strategy for genetically-encoded fluorescent biosensors: Application to VEGF Detection**Momoko Oya**^{1,2}, Ryohei Ozaki-Noma¹, Tetsuichi Wazawa¹, Kazunori Sugiura¹, Mitsuru Hattori¹, Masataka Michigami³, Daisuke Fujiwara³, Ikuro Fujii³, Takeharu Nagai¹ (¹*SANKEN, The Univ. of Osaka*, ²*Grad. Sch. Pharm. Sci., The Univ. of Osaka*, ³*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

Protein-based fluorescent biosensors are engineered to detect specific target molecules by exhibiting fluorescence changes upon binding. Traditionally, the development of such biosensors has required extensive effort, as each biosensor is typically custom-designed for its target. Here, we present a modular and generalizable design strategy for fluorescent biosensors, comprising distinct domains for target recognition and signal transduction. As a proof of concept, we constructed a biosensor for vascular endothelial growth factor (VEGF), whose fluorescence was successfully shown to respond to VEGF binding. This modular biosensor architecture holds promise for the streamlined development of a wide range of biosensors.

2Pos039 FUS タンパク質の天然変性領域と RNA の相互作用機構の解明
Unveiling the Interaction Mechanism between a FUS Intrinsically Disordered Region and RNA by Molecular Dynamics Simulation**Yoshie Iijima**, Soichiro Kijima, PhuocDuy Tran, Akio Kitao (*Grad. Sch. Life Sci. and Tech., Science Tokyo*)

Fused in sarcoma (FUS) is an RNA-binding protein involved in neurodegenerative disorders, such as amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). However, the molecular mechanisms of how ALS-linked mutations alter FUS-RNA interactions remain elusive. To address this gap, we conducted molecular dynamics simulations of the RGG1 domain of wild-type FUS and ALS-linked mutant, each in complex with RNA. We examined the impact of the mutations on RNA-binding behavior by analyzing differences in interaction dynamics observed during the simulations. These results will be reported in the presentation.

2Pos040 TIA1 の自己集合における核酸の寄与の解明
Investigating the contribution of nucleic acids to the self-assembly of TIA1**Anupap Chauyjaroen Suk**¹, Naotaka Sekiyama¹, Aya Ogino², Hiroki Konno³, Hidehito Tochio¹ (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ.*, ³*WPI Nano Life Sci. Inst. (WPI-Nano LSI), Kanazawa Univ.*)

Under cellular stress, proteins and mRNAs coalesce through protein-RNA and protein-protein interactions to form stress granules (SGs). However, how these interactions contribute to SG assembly remains not fully understood. A major SG component, T-cell intracellular antigen 1 (TIA1), contains three RNA-recognition motifs (RRMs) and an intrinsically disordered prion-like domain. In this study, we investigated the molecular mechanism of TIA1 self-assembly using atomic force microscopy (AFM) and complementary approaches. AFM showed that in the presence of single-stranded DNA substrates bearing multiple TIA1-binding motifs, TIA1 self-assembled into nanoscale clusters that grew over time. This finding suggests nucleic acid-protein interaction is a key driver of TIA1 assembly.

2Pos041 実験とシミュレーションによる Hero 蛋白質のヘリックス形成の研究
The α -Helix Formation of Hero Proteins Studied by Experiments and Simulations

Takao Yoda¹, Ai Niitsu², Cheng Tan³, Naoya Tochio², Haeri Im^{3,4}, Takanori Kigawa², Jaewoon Jung^{3,4}, Yuji Sugita^{3,4}
(¹Nagahama Institute of Bio-Science and Technology, ²RIKEN IMS, ³RIKEN R-CCS, ⁴RIKEN PRI)

The heat-resistant obscure (Hero) proteins are intrinsically highly disordered proteins with activity that inhibits the irreversible aggregation of other proteins (clients). Here, we studied their helix formation using CD, NMR, and molecular simulations. Experiments revealed helix formation of several Hero-derived peptides. We also explored the conformations of these peptides using state-of-the-art force fields for proteins and the gREST method for efficient sampling. We found that Amber99SBws-STQ reproduces the helix formation of the peptides well. Our simulation data suggested that interactions of hydrophilic residues increase with the helix formation of Hero9, suggesting the possibility that the helix formation helps Hero9 to interact with its client proteins.

2Pos042 超音波照射を用いた夾雑環境下における α -シヌクレインシードの高感度検出
Ultrasonic Cavitation Enhances Selective Detection of α -Synuclein Amyloid Fibrils from a Crowded Environment

Tomoki Ota, Kichitaro Nakajima, Keiichi Yamaguchi, Yuji Goto, Hirotsugu Ogi (*Grad. Sch. Eng., Osaka Univ.*)

Amyloid fibrils of α -synuclein (α Syn) are implicated in Parkinson's disease. Detecting α Syn seeds is key for the early diagnosis, but protein-rich biological fluids hinder seed detection. Here, we show that ultrasonication enables reliable detection of α Syn seeds even in the presence of 40 mg/mL serum albumin. Seeded and unseeded samples were clearly distinguished, with a detection limit as low as 10 pg/mL, unattainable by conventional shaking. Notably, amyloid formation kinetics correlated with seed concentration only under ultrasonication, suggesting selective amplification of seed-dependent growth and suppression of nonspecific aggregation. These findings demonstrate that ultrasonication provides a powerful tool for detecting amyloid seeds.

2Pos043 脱窒タンパク質超分子複合体の可溶化条件の最適化
Optimization of Solubilization Conditions for supramolecular complex of denitrification proteins

Sara Tanibayashi (*Grad. Sch. Sci., Univ. Hyogo*)

Denitrification, a part of global nitrogen cycle, involves four consecutive reduction reactions which are catalyzed by metalloenzymes such as nitric oxide reductase (NOR). These enzymes are thought to form a supramolecular complex to improve efficiency by preventing loss of intermediates. Here, we aimed to isolate such a complex. His-tagged NOR was expressed in *Pseudomonas aeruginosa*, and membranes were solubilized using 1% Digitonin. SDS-PAGE of the solubilized fraction purified by Ni-affinity chromatography and gel filtration showed that purified high-molecular-weight fraction contained a protein with molecular weight of ~70 kDa in addition to NOR. This indicates that NOR forms a supramolecular complex with other proteins.

2Pos044 オリゴマー型アロステリック蛋白質の機能に於ける両親媒性溶質の影響 - 疎水性相互作用の役割
Effect of Amphipathic Solutes on the Function of an Oligomeric Allosteric Protein - Role of Hydrophobic Interactions

Antonio Tsuneshige^{1,2}, Takehiko Haga² (¹Frontier Bioscience, HOSEI UNIVERSITY, ²Micro-Nano Tech. Ctr., HOSEI UNIVERSITY)

We have studied the effect of two amphipathic solutes on the allosteric function of tetrameric Hb, under non-denaturing conditions. These solutes were, in increasing order of hydrophobicity, (1) betaine, and (2) 3-(1-Pyridino)-1-propane sulfonate. Both solutes are characterized by having a hydrophilic cationic, hydrophilic anionic, and hydrophobic moieties. Contrasting with betaine, results from oxygenation experiments and size-exclusion chromatography suggested that solute (2) was able to "dissolve" the tetrameric Hb into dimers, which still exhibited cooperativity typical of a "two-binding site" system. These results contrast with the accepted knowledge that allosteric function can be exhibited only in the complete oligomeric (tetrameric) state.

2Pos045 オレキシン受容体 2 の C 末端 IDR と受容体コアドメインとの分子内相互作用に関する溶液 NMR 解析

Solution NMR Analysis of the Intramolecular Interaction between the C-terminal IDR and the Receptor Core Domain of Orexin Receptor 2

Riki Kato¹, Yuki Kanazaki¹, Ken-Ichi Akagi², Yohei Miyanoi², Kayo Imamura¹, Hidehito Tochio¹ (¹Grad. Sch. Sci., Univ. Kyoto, ²Inst. Protein Research, Univ. Osaka)

Orexin receptor 2 (OX2R) plays a pivotal role in the promotion of wakefulness and is a critical drug target for sleep disorders. Although the intrinsically disordered C-terminus of OX2R has been reported to be essential for effective signaling, the structural mechanisms underlying its signaling transduction remain poorly understood. To investigate potential interactions between the OX2R C-terminus and the receptor core, we first assessed intramolecular interactions in a model protein using NMR spectroscopy, in which ¹⁵N-labeled OX2R C-terminus was ligated to unlabeled maltose-binding protein (MBP). The 1H-¹⁵N HSQC spectrum indicated that the OX2R C-terminus did not interact with MBP. At the meeting, data for the C-terminus ligated to the receptor core will be discussed.

2Pos046 抗体を用いた膜結合型 CLIC1 を標的としたモノクローナル抗体の作製と機能解析 Development of Monoclonal Antibodies Specifically Targeting Membrane-bound CLIC1 and Their Functional Characterization

Kazuki Imai^{1,2}, Ayana Yamagishi^{1,2}, Masumi Iijima³, Chikashi Nakamura^{1,2} (¹Grad. Sch. Eng., Tokyo Univ. Agric. Technol., ²CMB, AIST, ³Fac. Appl. BioSci., Tokyo Univ. of Agri.)

CLIC1 is a metamorphic protein existing in both soluble and membrane-bound forms. In highly malignant cancers, its membrane expression increases, promoting invasiveness via chloride ion efflux. To specifically target the membrane-bound form, we generated monoclonal antibodies and evaluated their interaction using AFM. Two clones binding to CLIC1 on live cell surfaces were obtained. Chloride efflux assays revealed distinct inhibitory effects between the clones. Moreover, immunostaining showed membrane localization for one clone and nuclear localization for the other. These clones will help clarify the unknown structure and function of CLIC1.

2Pos047 多剤排出トランスポーター EmrE の pH 依存的基質結合駆動力変換には Asp84 が関与する Asp84 Is Involved in the pH-Dependent Driving Force Conversion for Substrate Binding in the Multidrug Efflux Transporter EmrE

Kazumi Shimono¹, Daisuke Takahashi¹, Shuichi Miyamoto¹, Seiji Miyauchi² (¹Fac. Pharm. Sci., Sojo Univ., ²Fac. Pharm. Sci., Toho Univ.)

The higher the pH, the greater the entropic effect on substrate binding by the multidrug transporter EmrE. This conversion occurs near a pK_a of 6.9, attributing to a reduction in conformational entropy loss. Thermodynamic studies were performed on EmrE mutants (E14D, E25Q and D84N) to elucidate the role of acidic residues in this shift. E14D retained ΔH -driven binding even when D14 was ionized at pH 6.0. The binding driving force of E25Q shifted similarly to that of the wild type. D84N remained ΔH -driven at pH 7.4. These suggest that Asp84 contributes to driving force conversion. Given the 3D structures and the pK_a of His110 at 6.8, a salt bridge between D84 and H110 could stabilize the high-entropy structure at high pH by regulating the conformational entropy.

2Pos048 Allosteric Effects of Sodium Binding on the κ -Opioid Receptor Revealed by FTIR Spectroscopy

Ryo Nishikawa¹, Seiya Iwata¹, Shun Yokoi², Ryoji Suno³, Chiyo Suno-Ikeda³, Ayori Mitsutake², Takuya Kobayashi³, Hideki Kandon^{1,4}, **Kota Katayama**^{1,4} (¹Grad. Sch. Eng. Univ. Nagoya Inst., ²Grad. Sch. Phys. Univ. Meiji, ³Grad. Sch. Med. Univ. Kansai Med., ⁴OptBioTech. Res. Cent. Univ. Nagoya Inst.)

Opioid analgesics such as morphine act via opioid receptors (GPCRs), but their use is limited by side effects, highlighting the need for safer alternatives. Recent studies show that Na^+ binds to GPCR allosteric sites, distinct from orthosteric sites, modulating receptor activity and offering new drug design strategies. We used FTIR spectroscopy to analyze Na^+ -induced structural changes in the κ -opioid receptor (KOR). Na^+ binding caused a downshift in the amide-I band across all ligand-bound states, indicating receptor inactivation. Notably, band intensity decreased only with KOR-selective ligands, suggesting distinct Na^+ binding modes. These findings offer insights into allosteric modulation and support rational drug design targeting Na^+ sites.

2Pos049 分子動力学シミュレーションを用いた CRISPR Type I-C における DNA 切断前後のダイナミクスの違い
Molecular dynamics simulation study of the differences in dynamics before and after DNA cleavage in CRISPR Type I-C

Ryusei Haruna¹, Yoshihiro Kashiyama¹, Ryota Kiyooka¹, Shota Shimogoochi¹, Naoyuki Miyashita^{1,2} (¹*Grad. Sch. BOST, KINDAI Univ.*, ²*BOST KINDAI Univ.*)

The CRISPR system is an adaptive immune system in prokaryotes. It recognizes and eliminates viral DNA. CRISPR Type I-C, a subtype of CRISPR, consists of multiple Cas modules. The gRNA bound to Cas7 recognizes target DNA based on its sequence. Subsequently, Cas3 binds to the Type I complex and cleaves the DNA.

To elucidate the atomic-level differences in dynamics before and after target DNA cleavage by Cas3, we performed molecular dynamics simulations for the pre- and post-DNA cleavage states of CRISPR Type I-C and analyzed the differences in dynamics between them in detail.

2Pos050 Advancing Biophysical Protein-DNA Interaction and Dynamics Studies Through Enhanced Sampling

Mohamed Marzouk Sobaih, Ai Shinobu (*Premium Research Institute for Human Metaverse Medicine (WPI-PRIME), The University of Osaka*)

Biophysical interactions between DNA-binding proteins and DNA are crucial for regulating gene expression but challenging to study due to slow dynamics and transient interactions. Here, we performed 1 μ s conventional molecular dynamics simulations of the SAC7D-DNA complex, a model for non-specific binding. We conducted analyses including contact maps and binding free energy calculations (MM/PBSA) to identify key interface residues. Recognizing significant challenges in extending two-dimensional replica-exchange molecular dynamics (2D-REMD) from protein-ligand to protein-DNA systems, we aim to optimize this method for capturing DNA-protein unbinding dynamics, addressing complexities in distance definition and sampling efficiency.

2Pos051 高速 AFM を用いた ATP 依存的な Smc5/6 の構造ダイナミクスの可視化
ATP dependent dynamics of Smc5/6 by high-speed atomic force microscopy

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The structural maintenance of chromosomes (SMC) complexes are ring-shaped ATPase assemblies that topologically encircle DNA strands to form physical links between distantly separated DNA segments. However, how these proteinaceous rings bind to and manipulate DNA at the sub-molecular level remains elusive. Here, we applied high-speed atomic force microscopy (HS-AFM) to directly visualize ATP-dependent structural changes in individual Smc5/6 molecules. In the absence of ATP, a stable I-form was observed, whereas in the presence of ATP, frequent transitions between the I- and O-forms occurred. Furthermore, when bound to DNA, Smc5/6 preferentially interacted with the twist regions of the DNA, resulting in DNA compaction.

2Pos052 NMR による α -シヌクレインと G4RNA の相互作用メカニズム解析
NMR study of the interaction between α -Synuclein and G4RNA

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The aggregation of α -synuclein is a hallmark of Parkinson's disease. Increasing evidence suggests that G-quadruplex RNA (G4RNA) actively promotes this process, but the underlying mechanism remains unclear. Here, we demonstrate that the N-terminal of α -synuclein directly binds G4RNA. Deletion of the electronegative C-terminal enhances this interaction, while hydrophobic-to-hydrophilic mutations in the N-terminal weaken it, suggesting the contribution of electrostatic and hydrophobic interactions. Importantly, α -synuclein preferentially interacts with G4RNA oligomers, as identified by NMR and native PAGE. These findings reveal that G4RNA topology modulates α -synuclein aggregation, offering mechanistic insights into RNA-driven pathology in Parkinson's disease.

2Pos053 Valosin-containing protein behaved like an ATPase for FUS granules

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Fused in sarcoma (FUS), an RNA-binding protein, condensate through liquid-liquid phase separation. FUS granules contain a multifunctional AAA ATPase, valosin-containing protein (VCP) *in cell*. It was reported that VCP colocalized to the FUS granules regulated the residence time of the FUS granule by consuming ATP. We investigated the function of VCP on the FUS granules *in vitro*. FUS granules stability was dependent on ATP concentration, and disappeared at high ATP concentration. However, when ATP inhibitor was added to the FUS granules that had disappeared with high concentrations of ATP, the FUS granules formed again. FUS granules formed similarly when VCP was added instead of ATPase. This result suggested that VCP behaves like an ATPase for the FUS granules *in vitro*.

2Pos054 DNA 液滴の個数制御された分裂を実現する酵素カスケード反応
Enzymatic cascade reactions for number-controlled division of DNA droplets

Tatsumi Sakuma¹, Tomoya Maruyama², Masahiro Takinoue^{1,2,3} (¹*Department of Life Science and Technology, Institute of Science Tokyo*, ²*Research Center for Autonomous Systems Materialogy, Institute of Integrated Research, Institute of Science Tokyo*, ³*Department of Computer Science, Institute of Science Tokyo*)

Constructing artificial cells that mimic key functions of living cells, such as growth and division, contributes to our understanding of the origin of life. In particular, the division which can control cell number is a crucial reaction involved in self-replication. DNA droplets have attracted attention as a new compartment for constructing artificial cells since their dynamics can be easily realized by designing sequences. Although previous studies demonstrated the division of DNA droplets, the control of the number of DNA droplets has not been achieved. Here, we report an enzymatic cascade reaction system that induces multi-step dynamics in DNA droplets, including two-phase separation followed by division, thereby enabling number-controlled DNA droplets division.

2Pos055 核酸増幅システムの特性検証
Characterization of Responsive Nucleic Acid Amplification systems

Ken Komiya¹, Chizuru Noda¹, Takashi Nakakuki² (¹*X-star, JAMSTEC*, ²*Faculty of Comp. Sci. & Sys. Engi., Kyutech*)

We had developed a cascaded DNA generation reaction system [1], that is applicable to automatic nucleic acid testing [2]. Short single-stranded DNA molecules generated in the reaction system can be regarded as the signals from the viewpoint of molecular robotics to drive the reactions, including the structural change of a DNA probe or a DNA nanomachine and the modified sandwich ELISA assay. In the present study, we experimentally characterized the signal amplification performance along with numerical simulation and extended the reaction driven by sssDNA for achieving the DNA-based autonomous molecular systems.

[1] K. Komiya, C. Noda, M. Yamamura, *New Gener Comp*, 2024, Vol. 42, pp. 237-252

[2] M. Komori, K. Komiya, *et al.*, *Anal Bioanal Chem*, 2019, Vol. 411 pp. 3789-3800

2Pos056 酵素反応によって活性化された DNA 凝集体
Active DNA condensates coupled with enzymatic reactions

Tomoya Maruyama¹, Masahiro Takinoue^{1,2} (¹*Research Center for Autonomous Systems Materialogy, Institute of Integrated Research, Institute of Science Tokyo*, ²*Department of Computer Science, Institute of Science Tokyo*)

Intracellular biomolecular condensates, as phase-separated droplets, show dynamic behaviors depending on chemical energy such as ATPs, but these behaviors and their underlying mechanisms remains poorly understood. Synthetic condensates serve as the models of intracellular condensates to elucidate their mechanism. In this study, we report that active DNA condensates, which are synthetic condensates formed by the self-assembly of DNA nanostructures, exhibited dynamic behavior activated by enzymatic reaction using chemical energy. We believe that this system will help to elucidate the dynamic nature of intracellular biomolecular condensates.

2Pos057 PEG-mediated regulation of DNA droplets: Stabilization with bulk PEG and transition to vesicle-like structures via DNA-PEG conjugates

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Establishing a programmable polymeric droplet system advances our understanding of its functional mechanism in biology and facilitates the development of artificial cells and molecular robots. DNA-based droplets (DNA droplets) are formed by self-assembly of DNA nanostructures, and the physical properties and functions of DNA droplets can be designed based on sequence information. However, the physicochemical properties of DNA as a material are limited; therefore, integrating features from other polymers is a promising approach. This study focused on PEG, a hydrophilic soft polymer. Under a PEG-based crowding environment, the thermal stability of DNA droplets increased. In addition, PEG-modified DNA induced a spontaneous transition to vesicle-like DNA liquids.

2Pos058 サブテラヘルツ波照射が DNA 塩基対の形成に与える影響の溶液 NMR 研究
Investigation of sub-terahertz irradiation effects on DNA base pair formation by solution NMR

Yuji Tokunaga¹, Koh Takeuchi¹, Hiromichi Hoshina², Masahiko Imashimizu³ (¹*Grad. Sch. Pharm. Sci., UTokyo*, ²*RIKEN Center for Advanced Photonics*, ³*CMB, AIST*)

Formation and breaking of double-strand DNA (dsDNA) are fundamental to physiological roles of DNAs. Formation of dsDNA is mediated by base pairs, which are stabilized by ionic hydration. We previously revealed that irradiation of sub-terahertz (sub-THz) electromagnetic waves accelerates the protein hydration process. Here, we investigated how the sub-THz irradiation affects the formation of DNA base pairs. We analyzed time-dependent increase of imino-group NMR signals from a pool of random sequence DNAs after hydration, which reflects the formation and stability of base pairs. Surprisingly, sub-THz irradiation accelerated the slow equilibration process of the base pair formation, suggesting that sub-THz perturbed the hydrogen bond networks in the DNA hydration layer.

2Pos059 ポリアミンによる遺伝子発現活性の温度依存性
Temperature dependence of gene expression activity in the presence of polyamines

Shotaro Kato¹, Takashi Nishio^{1,2}, Yuko Yoshikawa¹, Koichiro Sadakane¹, Kenichi Yoshikawa¹ (¹*Grad. Sch. Life and Med. Sci., Doshisha Univ.*, ²*MolBis, AIST*)

Naturally occurring polyamines have various biological functions including marked effects on the structure and function of genomic DNA molecules. Changes in the higher-order structure of DNA caused by polyamines are expected to be related to genetic activity. Here, we examined the effect of temperature on gene expression in the presence of various concentrations of a trivalent polyamine, spermidine (SPD(3+)), by adapting an in vitro cell-free luciferase assay. In this presentation, details of the changes in expression activity induced by SPD(3+) at each temperature condition will be presented, along with the results of measurements of DNA conformational changes in the presence of SPD(3+), and the mechanism of the temperature effect on expression will also be discussed.

2Pos060 Hi-C コンタクトマップのスペクトル分解解析
Spectral decomposition analysis of Hi-C contact maps

Ai Ito, Takahiro Sakaue (*Aoyama Gakuin University*)

Chromatin structure plays a crucial role in regulating gene expression. Hi-C (high-throughput chromosome conformation capture) is a widely used technique for investigating the three-dimensional organization of chromatin, generating contact maps that represent genome-wide contact frequencies in the form of a matrix. In this study, we employ the spectral decomposition method to analyze rich information embodied in Hi-C contact maps. In parallel, we also analyze contact maps generated by coarse-grained molecular dynamics simulations of sequence-defined polymers. Comparing thus obtained spectral analysis results from various natural and artificial contact maps in a broad range of length scales, we aim to clarify features in contact maps associated with genome organization.

2Pos061 クロマチンドメインの熱力学的サイズ制限について
Thermodynamic size limits in chromatin domains

Fujishiro Shin (*FIFC, Kyoto Univ.*)

Nucleosomal interactions give rise to chromatin domains. Inactive nucleosomes condense to form the core of a domain, and active, acetylated nucleosomes act as the shell, exposing promoters and enhancers. When the radius of a domain is R , the masses of the core and the shell scale with R^3 and R^2 , respectively. Therefore, the fraction of active chromatin in the domain, ϕ , must follow $\phi \sim R^2/R^3 = 1/R$, or the radius of the domain must scale with $R \sim 1/\phi$. This explains why domains are smaller in active regions (high ϕ) and larger in inactive regions (low ϕ). In this poster presentation, we discuss a free energy model based on this idea in detail, and how well the model describes the chromatin domain sizes in various species.

2Pos062 複製依存的ヒストン標識 (Repli-Histo 標識) を用いて明らかにする, ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい
Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells

Katsuhiko Minami^{1,2}, Kako Nakazato^{1,2}, Satoru Ide^{1,2}, Kazunari Kaizu^{3,4}, Koichi Higashi^{2,5}, Sachiko Tamura¹, Atsushi Toyoda⁶, Koichi Takahashi³, Ken Kurokawa^{2,5}, Kazuhiro Maeshima^{1,2} (¹*Genome Dynamics Laboratory, NIG*, ²*SOKENDAI*, ³*Laboratory for Biologically Inspired Computing, RIKEN BDR*, ⁴*Cell Modeling and Simulation Group, ExCELLS*, ⁵*Genome Evolution Laboratory, NIG*, ⁶*Comparative Genomics Laboratory, NIG*)

Chromatin in living cells serves not only as a repository of genome sequence but also significantly influences cellular functions through its physical properties. We have recently identified unique physical properties of euchromatin (more liquid-like) and heterochromatin (more gel-like), using live-cell single-nucleosome imaging with a novel euchromatin/heterochromatin-specific labeling method (replication-dependent histone labeling, or Repli-Histo labeling). Chromatin is replicated from regions with greater nucleosome motion, suggesting that local chromatin motion can influence replication timing by regulating chromatin accessibility to replication initiation factors. We will further discuss how various factors influence the motion of euchromatin and heterochromatin.

2Pos063 水中でのタンパク質分子間結合の高速計算に向けた GBSA 陰溶媒モデルの精査
Scrutiny of GBSA implicit solvent model for fast simulation of protein-protein binding in water

Fangqian Wei, Yukinari Kamiyama, Wataru Moriya, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)

GBSA implicit solvent model is based on the generalized Born (GB) and surface area (SA) models and accelerates MD simulation of biomolecules in water. However, GBSA model has not yet been fully exploited to study protein-protein binding. In this study, taking barnase-barstar binding as an example, we first scrutinize SA model by referring to the van der Waals (vdW) energies obtained from MD simulation with explicit water. We show that SA model well reproduces the explicit-water MD data but care must be taken for the surface-tension coefficient to account for the accumulated vdW attractions due to buried atoms. We then scrutinize GB model and show the importance of considering the entropic term arising from the temperature-dependent dielectric constant of water.

2Pos064 長距離静電相互作用のカットオフ計算で生じる水の層状構造: 格子スピン模型による検証
The electrostatic problem of water revisited: Strange layer structure emerging from the truncated long-range interactions

Yoshiteru Yonetani (*National Institutes for Quantum Science and Technology (QST)*)

In 2005, our MD study of water [Chem. Phys. Lett. 406, 49 (2005)] showed that increasing cutoff length does not improve the simulation result necessarily; on the contrary, it makes the result worse. In the extreme situation, a strange layer structure appears, which is far from real water. Nonetheless, this cutoff-induced phenomenon remains largely unexplained. We here explored the underlying mechanism by the Monte Carlo simulations on a lattice model with dipolar spins. The cutoff calculations produced similar layers. The layer width varied with the cutoff length. These features are certainly consistent with the water case, indicating that the layer formation is the general behavior of dipolar systems whose interactions are truncated at a finite distance.

2Pos065 機械学習による過冷却水のローカル構造と水素結合エネルギーの解析
Machine-Learning Analysis of Local Structural Motifs and Hydrogen-Bond Energetics in Supercooled Water

Taku Mizukami¹, Nguyen Viet Cuong³, Dam Hieu Chi² (¹Japan Advanced Institute of Science and Technology, Materials Science, ²Japan Advanced Institute of Science and Technology, Knowledge Science, ³HPC Systems)

Water is not only a ubiquitous liquid but also known for a variety of anomalies. The mechanisms underlying these anomalies are believed to be closely related to those governing the functional expression of biomacromolecules, and have attracted research interest. We investigated the behavior of water molecules by integrating MD simulations with machine learning techniques. As a result, we identified several distinct local structural motifs in supercooled water, and found that their population ratios and network connectivity vary depending on temperature and pressure. Furthermore, these structures were found to correlate with the potential energy landscape associate with hydrogen bonding. We are currently investigating how these structures relate to the phase diagram.

2Pos066 *Atoh1* 依存的な遺伝子ネットワーク構築に向けたドライ解析
In silico prediction of *Atoh1*-dependent gene networks using target genes of *lin-32*, a homolog of *Atoh1*, in *Caenorhabditis elegans*

Saki Imamura¹, Sayaka Hori² (¹Graduate School of Humanities and Sciences, Nara Women's University, ²Faculty Division of Natural Sciences, Nara Women's University)

Atoh1 is a bHLH transcription factor essential for the development of neurons involved in hearing and respiration in *Mus musculus*. However, the gene regulatory network controlled by *Atoh1* remains unclear, especially with respect to its direct targets in the brain and central nervous system. In this study, we employed a computational approach to predict potential *Atoh1* target genes. As a model, we focused on *Caenorhabditis elegans* *lin-32*, a homolog of *Atoh1* that similarly regulates neuronal development. We used *lin-32* target genes as a reference to help predict the target genes of *Atoh1*. Our analysis provides insight into key directions for future experimental validation.

2Pos067 高速 AFM による Afamin-Wnt3a 相互作用と動態の解明
Unveiling Afamin-Wnt3a interactions and dynamics using high-speed AFM

Hikaru Ichida¹, Kosuke Mizuno^{1,3}, Amyot Romain², Flechsig Holger², Satoshi Toda³, Noriyuki Kodera² (¹Grad. Sch. NanoLS., Kanazawa Univ, ²WPI-NanoLSI, Kanazawa Univ., ³Institute for Protein Research, Osaka Univ.)

Wnt3a is a secreted protein essential for morphogenesis and homeostasis. Due to post-translational lipidation, Wnt3a cannot exist as a monomer and instead forms homotrimers or heterodimers with Wnt-related molecules to conceal the hydrophobic lipid, which otherwise lowers solubility. A stable Afamin/Wnt3a complex was recently reported to preserve Wnt3a activity. However, how this complex maintains structural stability in solution remains unclear. In this study, Afamin and Afamin/Wnt3a complex were observed by high-speed AFM. Afamin showed flexible conformations, including open and closed forms. Furthermore, Wnt3a binds to the N-terminal domain of Afamin and suppresses its dynamics. These findings suggest how Afamin contributes to complex formation with Wnt3a.

2Pos068 神経分化における細胞内の発熱が関与する転写機構の解明
Elucidation of the Transcriptional Mechanisms Involving Intracellular Heat Generation in Neural Differentiation

Yukiho Shimazaki^{1,2}, Kohki Okabe³, Yoshie Harada^{4,5} (¹Grad. Sch. Sci., Univ. Osaka, ²IPR, Univ. Osaka, ³Grad. Sch. Pharm. Sci., Univ. Tokyo, ⁴WPI-PRIME, Univ. Osaka, ⁵QIOB, Univ. Osaka)

In neuronal differentiation, neural stem cells elongate their projections and differentiate into neurons under the induction of nerve growth factors and other factors. Previously, we revealed that this process is accelerated by heating the nucleus, and the temperature of the entire cell increases 24 hours after induction of differentiation. Furthermore, intracellular introduction of polymers that inhibit the temperature increase impaired neuronal differentiation, which was partially rescued by heating the nucleus. In this study, by performing transcriptome analysis in cells in which neuronal differentiation is inhibited by the introduction of the polymer, we plan to elucidate the mechanism of neuronal differentiation that requires heat produced in the cell.

2Pos069

赤血球可視化ゼブラフィッシュを用いた血液循環における物理量評価

Quantitative Analysis of Hemodynamic Parameters in Blood Circulation Using Red Blood Cell-Visualized Zebrafish

Yusei Inoue, Mana Okada, Toshiyuki Mitsui, Yuuta Moriyama (*Grad. Sch. Sci. and Eng., Aoyamagakuin Univ*)

The circulatory system is essential for supplying oxygen and nutrients and removing waste in multicellular organisms. In teleosts, the most diverse group of vertebrates, the heart features a unique structure called the *bulbus arteriosus*, rich in smooth muscle and elastin, which helps regulate blood pressure and flow. The *bulbus arteriosus* is formed with the contribution of *elastin b*, a teleost-specific gene important for its development. Despite its evolutionary significance, the in vivo function of this structure remains poorly understood. Here, we use high-speed imaging of fluorescently labeled red blood cells in transgenic zebrafish and an *elastin b* knockout line to quantify hemodynamic parameters and clarify its role in circulation.

2Pos070

重合阻害物質を用いた短いアクチンフィラメントの構造解析

Structural analysis of short actin filaments using polymerization inhibitors

Yuta Arimura, Takuo Yasunaga (*Grad. Sch. Comp. Sci. & Eng., Kyutech*)

Actin is a highly conserved protein that forms filaments and is essential in various cellular processes. While structural differences between the middle and end segments of actin filaments have been reported, comprehensive analyses remain limited. Observing relatively short filaments offers an efficient means to capture the structural characteristics of filament ends, which are otherwise less accessible in long filaments. We try to generate short filaments suitable for detailed structural analysis of filament termini by controlling filament length using specific polymerization-inhibiting drugs. Here we will report the dynamics of the segmentation of actin filaments and the possibility of length control.

2Pos071

アミロライド誘導体フェナミルがビブリオ菌べん毛モーター固定子のナトリウムイオン輸送を阻害する分子機構

Inhibition mechanism of phenamil, an amiloride derivative of sodium channel inhibitor, for the rotation of the *Vibrio* flagellar stator

Tatsuro Nishikino^{1,2}, Norihiro Takekawa³, Jun-ichi Kishikawa⁴, Mika Hirose⁵, Seiji Kojima⁶, Michio Homma⁷, Takayuki Kato⁵, Katsumi Imada³
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The bacterial flagellar motor consists of the rotor and stator, and their interaction is essential to generate torque. The stator in marine *Vibrio* is made up of five PomA and two PomB molecules and functions as a sodium ion channel. Phenamil, a derivative of amiloride known as a sodium channel blocker, inhibits the sodium driven stator. To clarify the inhibition mechanism, we purified the *Vibrio* stator and performed single particle analysis by cryo electron microscope. A phenamil molecule binds at the PomA-PomB interface and inhibits conformational changes of the stator rather than directly blocking the channel [1]. We will discuss the mechanism underlying phenamil-mediated inhibition of the stator.

[1] Nishikino et al. **122**, *Proc Natl Acad Sci U S A*. e2415713122 (2025).

2Pos072

Design and Development of a Novel Photoswitchable Inhibitor Targeting Mitotic Kinesin Eg5

Nur Fatin Liyana Binti Salwadi¹, Islam Md Alradzi², Shinsaku Maruta² (¹Grad. Sch. Sci. Eng., Soka Univ., ²Sch. Sci. Eng., Soka Univ.)

In this study, we designed and synthesized a novel photochromic compound, SP-SAB-SP, comprising azobenzene and two spiropyran units as a photoswitchable Eg5 inhibitor. This compound can adopt multiple isomeric states via combinations of each photochromic unit, enabling reversible control of its bioactivity. Upon illumination with specific wavelengths of light, SP-SAB-SP undergoes structural transitions, allowing spatially and temporally precise modulation of Eg5 inhibition. Structural and biochemical compound revealed its binding to the Eg5 motor domain and demonstrated its inhibitory efficacy. These findings provide insights into the design of light-controllable molecular inhibitors.

[2Pos073](#) Loop-tethered kinesin-14 reveals factors underlying motility and directionality

Taisei Sano, Rieko Sumiyoshi, Masahiko Yamagishi, Junichiro Yajima (*Grad. Arts & Sci., Univ. Tokyo*)

Kinesin-14 is a unique member of the kinesin superfamily that moves toward microtubule minus end. The N-terminal neck-helix region of the motor domain is considered essential for its directional motion. However, the detailed mechanisms of directional motion remain unknown. In this study, we anchored the specific loop region within the kinesin-14 motor domain using artificial tethers in an in vitro gliding assay. We observed unidirectional movement of the microtubules even when anchored within the motor domain, indicating that conformational changes in the terminal region alone are not sufficient for kinesin-14 motility. By comparing their motility based on anchoring locations, we show the possibility of directional determinants within the kinesin-14 motor domain.

[2Pos074](#) 混雑環境下におけるキネシンの動態解析のためのマイクロレオロジー計測 Micro-rheology measurement for dynamic analysis of kinesin in crowded environments

Gai Ohashi¹, Takeshi Yokoyama², Takayuki Ariga¹ (¹*Graduate School of Frontier Biosciences, Osaka University*,
²*Graduate school of life science, Tohoku University*)

Metabolism-dependent stirring observed inside cells (nonthermal fluctuations) has been suggested to enhance cytoplasmic fluidity and influence intracellular molecular dynamics and rheology. In addition, nonthermal fluctuation is observed to accelerate kinesin, a molecular motor operating within cells. However, this acceleration has only been observed in low-viscosity *in vitro* solutions, so it remains unclear whether this acceleration phenomenon is also observed in crowded intracellular environments.

To investigate this, we constructed optical-tweezers-based micro-rheology measurement system, evaluated the viscosity experienced by vesicle-mimicking probe particles in crowded environments, and analyzed the effects on kinesin.

[2Pos075](#) 変異体解析による海洋性ビブリオ菌側ベン毛固定子 MotA/MotB 複合体活性化の探求 Mutational analysis to explore activation of the *Vibrio alginolyticus* lateral flagellar stator, MotA/MotB complex

Kazuki Yokoyama¹, Michio Homma², Norihiro Takekawa³, Seiji Kojima¹ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Grad. Sch. Eng.*, ³*Grad. Sch. Sci.*)

Vibrio alginolyticus swarms or moves in highly viscous environments using numerous lateral flagella. The proton-driven lateral flagellar stator is composed of two proteins MotA and MotB. The activation mechanism of MotAB complex has been solved for homologous proteins through structure-based analyses. Here we aimed to explore the functions of *Vibrio* MotAB by mutational approaches. Based on the predicted structure of MotB by AlphaFold2, we mutated residues in putative helix $\alpha 1$ of the peptidoglycan binding domain which are involved in the stator activation. Furthermore, we isolated suppressor mutants that can swarm in the absence of FlhL, which seems to support the active form of MotAB. We'd like to clarify what is happened by the mutations of helix $\alpha 1$ or suppressors.

[2Pos076](#) 細菌ベン毛モーターにおける固定子 MotB の N 末端へのタンパク質融合はローター-固定子相互作用を阻害する Inhibition of rotor-stator interaction by protein fusion to the N-terminus of the stator protein MotB in the bacterial flagellar motor

Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)

The torque of bacterial flagellar motors is generated through rotor-stator interactions. The studies by Cryo-EM tomography suggest that structural rearrangements of the rotor occur during changes in rotational direction. In this study, we provide results that functionally support this model. The GFP fused to the N-terminus of MotB strongly inhibited rotor-stator interactions during clockwise (CW) rotation, but not during counterclockwise (CCW) rotation. This inhibition for CW rotation was reduced by extending the linker between GFP and MotB. These results suggest that GFP prevents structural changes in the rotor and that the rotor adopts different structures in the CW and CCW states.

2Pos077

バクテリアべん毛モーターの回転データにおける揺らぎ評価手法の開発

Development of a method for evaluating fluctuations in rotational data of bacterial flagellar motors

Kenta Takemori, Yusuke V. Morimoto (*Grad. Sch. Comput. Sci. and Syst. Eng., Kyushu Inst. Tech*)

Bacteria rotate the flagellar motors by utilizing electrochemical potentials. However, the role of the fluctuations in the input and output of the flagellar motor is not clear. In this study, a new evaluation method for the fluctuations in the rotation data measured by the bead assay was investigated. As a result, the fluctuation had periodicities with a frequency slower than the rotation speed. Also, the FFT analysis showed that the property of decreasing power with increasing frequency was similar to the characteristics of pink noise. This suggests that bacterial cells may utilize the properties of pink noise.

2Pos078

微小管 C 末端 Tail の伸長と単量体 KIF1A の微小管結合の分子動力学解析

Molecular Dynamics Analysis on the Extension of C-terminal Tail of Tubulin and Monomeric KIF1A Binding to Microtubule

Koki Adachi, Mitsunori Takano (*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*)

Microtubule (MT) provides the rail for MT-based molecular motors. C-terminal tail (CTT) of tubulin is negatively-charged disordered region, which modulates functions of MT through posttranslational modification. However, the structural state of CTT and the interaction with the molecular motors remain unclear because of the intrinsically disordered nature of CTT. In this study, by all-atom MD simulation of MT consisting of 15 $\alpha\beta$ tubulin dimers, we show that β CTT (β tubulin CTT) distributes above MT due to electrostatic repulsion whereas α CTT distributes on MT due to electrostatic attraction. β CTT further extends outward in the presence KIF1A and attracts K-loop of KIF1A. We further investigate the longitudinal and lateral movements of KIF1A on MT during the binding.

2Pos079

Unveiling the N-type ATPase: A Hidden Player in the Rotary ATPase Family

Hiroshi Ueno, Atsuki Nakano, Tatsuki Matsui, Hiroyuki Noji (*Grad. Sch. Eng., Univ. Tokyo*)

Rotary ATPases are classified into several families: F-type, V-type, A-type, and N-type ATPases, among which the N-type ATPase remains the least characterized. We recently engineered an F-type ATPase/synthase with multiple peripheral stalks, uncovering design principles for constructing such architectures. Building on this insight, we focused on the N-type ATPase as a naturally occurring rotary ATPase with multiple peripheral stalks. Here, we present the structural features and functional implications of the N-type ATPase from *Burkholderia thailandensis*, shedding light on this lesser-known member of the rotary ATPase family.

2Pos080

ミオシンの 2D 投影像の深層学習による構造分類に関する研究

Deep Learning-Based Structural Classification of Myosin from 2D Projection Images

Hikaru Iwasaki, Hitomi Wada, Takuo Yasunaga (*Grad. School. Comp. Sci. Syst., KIT*)

We developed a machine learning approach to classify protein structural states from electron microscopic (EM) projections at various angles. We evaluated our method on the myosin S1 motor domain, which has two principal conformations (power-stroke/recovery-stroke states). We trained a CNN-based variational autoencoder (VAE) to learn a 16-dimensional latent space from the images. Using these latent encodings, we trained two supervised classifiers (CNN and MLP) and could distinguish the conformations. Furthermore, Latent space showed partial separation of the two states. Projections from each angle overlapped in latent space, depending on the projection directions. We will further examine how the projection angle affects classification to integrate cryo-EM data.

2Pos081 蛍光顕微鏡と AFM を併用した細胞-基質接着間構造の解析
Analysis of cell-substrate adhesion structures by combined fluorescence microscopy and atomic force microscopy

Shun Sato, Shinji Deguchi (*Grad. Sch. Eng. Sci., The Univ. of Osaka*)

Focal adhesions (FAs) are specialized cellular structures that mediate attachment to the extracellular matrix and are essential for mechanical stability, cell migration, and cell morphology. Super-resolution fluorescence microscopy has revealed that FAs exhibit a stratified nanoscale architecture composed of various protein layers. However, detailed structural and mechanical characterization has remained limited due to the invasiveness of conventional sample preparation and limited spatial resolution. In this study, cellular architecture was preserved during FAs extraction, enabling high-resolution analysis of FAs organization and mechanics through combined fluorescence microscopy and atomic force microscopy (AFM).

2Pos082 高速原子間力顕微鏡を用いた液中における Notch レセプターと Delta リガンドの構造解析
Structural analysis of Notch receptor and Delta ligand in solution using high-speed atomic force microscopy

Shigetaka Nishiguchi (*Kansai Center, National Institute of Advanced Industrial Science and Technology*)

Notch signaling is important for embryogenesis, tissue homeostasis, and diseases, triggered by binding of extracellular domains (ectodomains) of Notch receptors and ligands on cell membranes. Structural analysis of the Notch receptors and ligands is important for understanding the Notch signaling mechanisms. Here, high-speed atomic force microscopy analysis of thirteen EGF ectodomains of Notch receptor (NOTCH1) revealed a string-like structure which contains three kinked portions. Full-length ectodomains of Delta ligand (DLL4) showed a flexible string-like portion mainly composed of eight EGF ectodomains. The different flexibility of EGF ectodomains of NOTCH1 and DLL4 may be important for binding specificity and physiological functions.

2Pos083 微小管結合 RhoGEF である GEF-H1 の *in vitro* 動態解析
In vitro kinetic analysis of microtubule-binding RhoGEF, GEF-H1

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Directional migration requires the precise regulation of the actin cytoskeleton, orchestrated in part by microtubules. Previous studies have demonstrated that the activity of GEF-H1 in stimulating the RhoA-actomyosin axis is modulated by its association with microtubules. However, the mechanism underlying GEF-H1's microtubule binding remains largely elusive. We utilized an *in vitro* reconstitution system to examine the interaction between GEF-H1 and microtubules in detail. Our findings reveal that GEF-H1 directly associates with microtubules and that the presence of RhoA-GDP and GTP significantly enhances this interaction. These results suggest that nucleotide exchange on RhoA promotes conformational changes that increase GEF-H1's affinity for microtubules.

2Pos084 細菌べん毛モーターにおける固定子ユニットへの FliL 結合の定量化
Characterising the stoichiometry of FliL binding to stator units in bacterial flagellar motors

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Many motile bacteria possess flagellar motors composed of multiple stators and a rotor, and the number of stators varies in response to external load. We focused on FliL, a membrane protein involved in stator stabilization, and analyzed its interaction with the stator. Using GFP-tagged FliL (GFP-FliL), we confirmed that it forms a complex with the stator, although its incorporation into the motor was inefficient. We quantified the number of GFP-FliL molecules per stator by analyzing the intensity of diffusing fluorescent spots on the membrane, and found that about nine FliL molecules associate with a single stator. We are currently analyzing a variant of FliL fused with mCherry in the periplasmic region, which shows higher incorporation efficiency into the motor.

2Pos085

単一微生物の活発な運動を追跡するための広視野顕微鏡法

Wide-field microscopy for tracking active locomotion of single microorganisms

Kaname Kuroda, Seichiro Kinoshita, Masayoshi Nishiyama (*Grad. Sch. Sci. Eng., Kindai Univ.*)

Many microorganisms move toward favorable habitats. Optical microscopy has been used for monitoring their motions. It was technically difficult to track their active locomotion for a long time. This is because many microorganisms move out of view in a short time. Here, we show a wide-field microscope for tracking active locomotion of single microorganisms. We constructed a relay optics inserting between a microscope body and camera. The developed system allowed us to acquire images of long, narrow areas in a single shot. By using the system, we could track the movement of a *Paramecium* over a long time. The present techniques could be extended to study a variety of samples moving in one direction.

2Pos086

多孔質培地中における周毛性細菌の運動性

Motility of peritrichous bacteria in porous media

Naoki Kanda, Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)

Salmonella swim by rotating multiple flagella. When the bacterium swims smoothly, all the flagella rotate in the same direction and form a bundle. Unraveling the flagellar bundle by the flagellar reversal causes the cell to tumble, allowing the cell to reorient its swimming direction. The *Salmonella* motility is affected by environmental factors such as viscosity, which is believed to be significant for thriving and pathogenicity. Here, we investigated the *Salmonella* motility in porous gel. The cell tracking revealed that the bacteria show intermittent swimming with frequent pausing. The pausing contained the tumbling and trapping by the gel. The swimming speed in porous media exceeds three times that in water. We will discuss the mechanisms underlying these phenomena.

2Pos087

サルモネラにおける cAMP 濃度と運動能の相関の計測

Measurement of the correlation between cAMP levels and motility in *Salmonella* cells

Keisuke Sakai, Yusuke V. Morimoto (*Grad. Sch. Comp. Sci. and Syst. Eng., Kyushu Inst. Tech.*)

Techniques have been developed to control cellular activity by expressing photoactivated proteins in target cells and modulating the behavior through light stimulation. This study aims to develop a method for controlling the dynamics of *Salmonella* cells using light. In bacteria, including *Salmonella*, cAMP is known to regulate the expression of motility-related genes. This study focuses on how light-induced increases in intracellular cAMP levels affect *Salmonella* motility. Two photoactivated adenylyl cyclases (PACs), bPAC and LprA, which are activated by light, were expressed in *S. Typhimurium*. Swarm assays and single-cell swimming analyses using microscopy revealed that increase in intracellular cAMP levels lead to reduced bacterial motility.

2Pos088

高圧力下にある哺乳類精子細胞の鞭毛運動の直接観察

Direct observation of flagellar motility in mammalian sperm cells at high pressure

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Masayoshi Nishiyama⁵ (¹Okayama Univ. Sci., ²Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ., ³Gunma Univ.,
⁴Pref. Univ. Hiroshima, ⁵KINDAI Univ.)

Eukaryotic flagella and cilia generate rhythmical beating motions. Here, we report the swimming motility of non-motile sperm cells in a knockout mouse model. The cells lacked the entire radial spoke 1 in sperm flagella, due to the deletion of *Iqub*. At 0.1 MPa and 37 °C, the sperm cells were unable to swim in solution with weak flagellar motility. At 60 MPa, a certain number of the cells started to swim unidirectionally in solution. After the pressure release, all the cells stopped swimming. This is consistent with previous results in *Chlamydomonas* non-motile mutants. Furthermore, the swimming speed of human sperm cells was also increased by ~10 % at 5 MPa. Thus, the application of pressures could activate the flagellar motility across species.

2Pos089

イオンチャネル領域に変異を持つキメラ固定子複合体 PomA/PotB の機能解析
Mutational analysis of the ion channel region of PomA/PotB, a chimeric stator of bacterial flagellar motor

Kaito Nagano (*Grad.Sch.Sci., Osaka Univ.*)

The bacterial flagellar motor consists of a rotor and a stator and is driven by specific ion flow through the stator. Most flagellar motors are driven by proton or sodium ions (Na^+). However, the amino acid residues responsible for determining ion selectivity remain unclear. Here, we prepared PomAPotB, a chimeric Na^+ -type stator that can drive the flagellar motor in *E. coli*, introduced mutations in the putative ion pathway of the chimeric stator, and analyzed the cell motility and ion conductivity of the stator. Although the mutations did not convert the ion selectivity of the chimeric stator, we isolated stator variants that show motility under very low Na^+ concentration. We will discuss the possible mechanism of the high motility of the mutant stators.

2Pos090

Spiroplasma 由来の MreB を発現した Syn3B 破砕液を内包したリボソームの形態変化
Deformation of Liposomes by Encapsulation of Syn3B expressing *Spiroplasma* MreB

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MreB, a bacterial actin, typically forms static filaments that maintain rod-like cell shape by organizing the cell wall synthesis machinery. In contrast, the wall-less bacterium *Spiroplasma* has a helical cell shape and exhibits unique swimming motility. Among its five MreB isoforms, MreB4 and MreB5 are essential for generating this motility, although the underlying mechanism remains unclear. We encapsulated cell extracts from a synthetic nonmotile minimal bacterium (JCVI-syn3B) expressing both MreBs into liposomes. Light microscopy revealed that the fraction of deformed liposomes increased with extract concentration, suggesting that MreB4 and MreB5 alone can induce membrane deformation. We discuss implications for the minimal motility machinery.

2Pos091

Regulation of Epithelial Homeostasis by Stretch and Cell Density

Rosario Ibanez¹, Honghan Li², Shinji Deguchi¹ (¹*Osaka University, Graduate School of Engineering Sciences, Deguchi Laboratory*, ²*University of Science and Technology Liaoning, School of Computer Science and Software Engineering*)

Mechanical forces are known regulators of epithelial behavior. When mechanical reciprocity between cells and their environment is lost, an inflammatory response may be triggered, leading to adaptation or disease. In this study, we applied uniaxial and biaxial stretching to MCF10A epithelial cells and analyzed NF- κ B activation, actin cytoskeleton remodeling, and morphological changes under varying mechanical and density conditions. Stretch primed NF- κ B activation, but cell density was the gatekeeper of nuclear translocation. These results highlight the synergistic interplay between mechanical stress and epithelial organization in regulating inflammatory signaling.

2Pos092

直接の力学摂動に対する微小管とアクチン骨格の構造応答
Structural response of microtubule and actin cytoskeletons to direct intracellular load

Ryota Orii, Hirokazu Tanimoto (*Yokohama City Univ.*)

Microtubule and actin are the two major cytoskeletal polymers that form organized functional structures in the interior of eukaryotic cells. How microtubule and actin cytoskeletons respond to the loads is poorly understood. In this study, we directly applied perturbing intracellular forces to microtubule and actin cytoskeletons and quantitatively evaluated how these cytoskeletons structurally respond to the loads. The strain fields of the microtubule complex and actin meshwork follow the same scaling. Single microtubule analysis revealed that the individual microtubules are enclosed by the elastic medium of actin. Our results suggest that microtubule and actin cytoskeletons act as an integrated continuum in the cytoplasm in response to intracellular loads.

2Pos093

機械的ストレス下における微小管束の粘弾性応答

Viscoelastic Behavior of Microtubule Bundles Under Mechanical Stress

Syeda Rubaiya Nasrin¹, Marie Tani¹, Gadiel Saper², Masatoshi Ichikawa¹, Ibuki Kawamata¹, Henry Hess², Akira Kakugo¹ (¹Grad. Sch. Sci., Kyoto Univ., ²Dept. Biomed. Engg. Columbia Univ.)

Microtubules (MTs) are essential cytoskeletal filaments that support cell structure and enable intracellular transport. In neurons, MTs are crosslinked into bundles, but their mechanical properties are not fully understood. We investigated how tensile and compressive forces affect MT bundles versus individual MTs using in vitro assays with a custom-built micro-stretcher and fluorescence microscopy. MT bundles showed enhanced buckling resistance and increased fragmentation under tension. Unlike individual MTs, they exhibited strain rate-dependent behavior, indicating viscoelasticity. We interpret these findings from a viscoelastic viewpoint. This study provides biophysical insight into cytoskeletal mechanics and may aid biomimetic design or disease modeling.

2Pos094

Actin Network Morphogenesis: From Spots to Rings and Interconnected Bundles

Vivek Semwal, Biplab Bhattacharjee, Tatsuo Shibata (RIKEN Center for Biosystems Dynamics Research Laboratory for Physical Biology)

Formation of actomyosin network and generated forces play crucial roles in various biological phenomena like cellular migration, cell shape control etc. Using a simplistic coarse-grained model in a 2d space with actin filaments, myosin motors and crosslinking proteins, we depict self-organisation of actomyosin network into various structures like spots, ring and stripes observed in various biological systems. Myosin generated contractile force, crosslinking mediated stability and treadmilling force found to play crucial role in determining the shape and dynamics of the actomyosin network.

2Pos095

電子顕微鏡による細胞性粘菌の多細胞体における細胞間構造の可視化

Intercellular structures in the multicellular body of *Dictyostelium discoideum* visualized by electron microscopy

Yuki Gomibuchi, Yusuke V. Morimoto, Takuo Yasunaga (Grad. Sch Comp. Sci and Sys. Eng., Kyushu Inst. Tech.)

When starved, *D. discoideum* cells aggregate to form a multicellular body. These multicellular bodies were resin-embedded, and ultrathin sections were prepared for observation using TEM. Wild-type, *csaA*⁻ and *tgrB1/CI*⁻ cells exhibited similar cadherin-like intercellular structures, which decreased upon exposure to EGTA. Enlarged tubular structures were also observed, suggesting Ca²⁺-dependent intercellular structures. *CadA*⁻ cells had uneven intercellular spacing, with vesicles and enlarged tubular structures between cells. The organization resembled that of EGTA-treated cells, and the thread-like structure was suggested to be DdCAD-1. Ca²⁺-dependent intercellular structures are thought to contribute to cell-cell adhesion in multicellular bodies but are not essential.

2Pos096

膜リモデリングを介した TRPV4-GPCR のクロストーク

TRPV4-GPCR crosstalk mediated by membrane remodeling

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The plasma membrane contains cholesterol-rich domains where GPCRs accumulate. However, the role of membrane domain recruitment in GPCR signaling remains unclear. Here, we show that TRPV4 regulates GPCR signaling via membrane remodeling. Using AT1R as a model, we performed four-color single-molecule imaging of TRPV4, AT1R, β -arrestin (β arr), and the cholesterol probe D4H in HEK293 cells. TRPV4 activation reduced inner leaflet cholesterol, increased AT1R diffusivity, and suppressed β arr recruitment upon angiotensin stimulation. A NanoBiT split-luciferase assay confirmed that TRPV4 activation suppresses GPCR-mediated Gq and β arr signaling. These findings provide a membrane-dependent spatial control mechanism for TRPV4-GPCR crosstalk.

2Pos097 ATP 濃度は CBASS 応答の活性化と抑制を調節する
ATP levels modulate the activation and suppression of CBASS responses

Yoshiaki Kinoshita, Rikiya Watanabe (*RIKEN, PRI*)

Bacterial defense systems rely on two components: (i) sensors detecting phages and (ii) effectors eliminating them. We examined how autoimmune responses are suppressed in CBASS (Cyclic oligonucleotide-Based Antiphage Signaling System). Cell assays showed that phage infection lowers intracellular [ATP], triggering activation. To further dissect the mechanism, we reconstituted the signaling cascade *in vitro*, from recognition to DNA degradation. Using purified CBASS components, we monitored the ATP-dependent synthesis of the second messenger (cA3) and its downstream activation of a cA3-responsive DNase in real time, utilizing fluorescent digital readouts. Thus, ATP levels serve as a key regulatory switch, modulating both the activation and suppression of CBASS responses.

2Pos098 Thermal regulation on EML4-ALK condensates dynamics and signaling activation

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Anaplastic lymphoma kinase (ALK) becomes oncogenic through fusion with echinoderm microtubule-associated protein-like 4, forming EML4-ALK, which is found in 3–7% of non-small-cell lung cancers (NSCLC). Patients with variant 1 (V1) respond well to tyrosine kinase inhibitors, while those with variant 3 (V3) show greater disease progression. These variants form distinct condensates—V3 exhibits liquid-like phase separation like properties, whereas V1 forms Hsp90-dependent stable, solid structures. How these potentially heat-sensitive condensates respond to thermal stress remains unclear. Here, we investigate how heat affects the localization, signaling, and molecular organization of EML4-ALK condensates by the optically controlled local heating method for the first time.

2Pos099 細胞膜脂質による上皮成長因子受容体の活性制御機構の解析
Bilateral regulation of EGFR activity and local PI(4,5)P₂ dynamics in mammalian cells observed with single-molecule microscopy

Mitsuhiro Abe¹, Masataka Yanagawa^{1,2}, Yasushi Sako¹ (¹*RIKEN PRI*, ²*Grad. Sch. Pharm. Sci., Kyoto Uni.*)

We visualized both EGFR and PI(4,5)P₂ nanodomains in the plasma membrane of HeLa cells using single-molecule microscopy. The EGFR and PI(4,5)P₂ nanodomains aggregated before stimulation with EGF through transient visits of EGFR to the PI(4,5)P₂ nanodomains. The degree of coaggregation decreased after EGF stimulation and depended on phospholipase C γ , the EGFR effector hydrolyzing PI(4,5)P₂. Artificial reduction in the PI(4,5)P₂ content of the plasma membrane reduced both the dimerization and autophosphorylation of EGFR after stimulation with EGF. Inhibition of PI(4,5)P₂ hydrolysis after EGF stimulation decreased phosphorylation of EGFR-Thr654. Thus, EGFR kinase activity and the density of PI(4,5)P₂ around EGFR molecules were found to be mutually regulated.

2Pos100 2 回の忌避刺激に対する大腸菌忌避応答と受容体脱メチル化酵素 CheB 動態
Repellent response of *Escherichia coli* to twice repellent stimuli and kinetics of the receptor demethylase CheB

Yugo Tomoda, Yoichi Kuroki, Yumiko Uchida, Akihiko Ishijima, **Hajime Fukuoka** (*Grad. Sch. Front. Biosci., Univ. Osaka*)

E. coli swims toward favorable and escapes from unfavorable conditions. We recently showed the polar localization of CheB represents the active level of chemotaxis system in a cell. In this study, by high-throughput imaging, we quantified the repellent response of *E. coli* to first and second stimuli. The response to first stimulus increased depending on the concentration of L-isoleucine from 1 to 10 mM and remained constant above 10 mM. The response to second stimulus, which was increased by 5 mM to first stimulus, decreased depending on the concentration from 6 to 15 mM and remained constant above 15 mM. We are now constructing the model to explain these phenomena and we will discuss how the cell responds to a wide range of repellent concentrations in the meeting.

2Pos101

心筋細胞集団間の線維芽細胞接続における心筋細胞同期

Synchronization of Cardiomyocytes in Fibroblasts Connections between Cardiomyocyte Clusters

Mayu Yamada, Tomoyuki Kaneko (*LaRC.FB.Hosei Univ.*)

In the heart, Cardiomyocytes (CMs) are responsible for beating, and the surrounding fibroblasts (Fibs) are thought to act as insulators that do not propagate the potential. However, Fibs can propagate the potential of CMs within a short distance or range. In this study, by combining agarose microchamber (AMC) and multi-electrode array (MEA), CMs were placed on MEA in two separate regions, which were connected by the Fib region. As a result, we successfully bridged the two CM regions with a 250 μ m-square Fibs region and recorded electrical signals from both the two CM regions. In future studies, we will vary the width and length of the Fib region to examine the conditions under which the beating of the two CM regions becomes synchronized.

2Pos102

溶液中の細胞性粘菌多細胞体への薬物添加

Drug addition to multicellular bodies of *Dictyostelium discoideum* in solution

Sotaro Fukuda¹, Tomohiro Shima², Yusuke V. Morimoto³ (¹*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech,* ²*Grad. Sch. Sci, Univ. Tokyo,* ³*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech*)

Elucidating the functions of multicellular organisms, including humans, is a major objective in both life sciences and medical research. However, most *in vitro* pharmacological experiments are conducted on single cells, and it remains challenging to perform such experiments on multicellular systems *in vitro* such as organoids derived from stem cells. This study established experimental conditions for drug administration to multicellular bodies of *Dictyostelium discoideum* in solution, a task previously considered challenging, in order to enable the observation of multicellular organisms in solution. The aim is to elucidate their developmental processes and signaling activities under these conditions.

2Pos103

海洋性バクテリア *Vibrio alginolyticus* の情報伝達タンパク質 CheY 動態の 1 細胞観察

Observation of CheY-GFP dynamics in a single *Vibrio alginolyticus* cell

Eito Kawamura, Ryoya Takase, Yumiko Uchida, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front. Biosci., Univ. Osaka*)

V. alginolyticus swims in liquid environment by flagella and its rotational direction is controlled by binding of signaling molecule CheY to a motor. In this study, we are attempting to observe the dynamics of CheY-GFP in a single *Vibrio* cell. Most of CheY proteins was localized at the cell pole where the polar flagellum is located. The intensity of polar fluorescent spot by CheY-GFP was much higher than that by GFP-FlhG, one of the motor components, indicating most of CheY molecules probably bind to components other than the polar flagellum such as receptor array. We are now trying to measure the dynamics in CheY localization in a single *Vibrio* cell when the external signal is applied. We want to discuss these quantitative parameters of CheY dynamics in the meeting.

2Pos104

心筋細胞クラスターサイズによる薬剤応答の違いの解析

Effect of Cardiomyocyte Cluster Size on Drug Response

Chinatsu Fujita, Kentaro Kito, Tomoyuki Kaneko (*LaRC.FB.Hosei Univ*)

Conventional cardiotoxicity assays are time-consuming and costly, which has created a strong demand for high-throughput testing methods. In this study, we used agarose microfabrication technology to create agarose microchambers (AMCs) for culturing cardiomyocytes derived from 7-day-old chick embryos into clusters. These clusters were formed on a multi-electrode array (MEA) system, enabling the formation of independently beating cardiomyocyte populations. Using extracellular field potential recordings, we calculated the Inter-Spike Interval (ISI), Field Potential Duration (FPD), and the Short-Term Variability (STV) of FPD. For the next study, we aim to investigate how varying the size of cardiomyocyte clusters affects their pharmacological responses.

2Pos105

細胞性粘菌における新規細胞巨大化法による細胞内高分解能計測

High-resolution intracellular measurements using a novel cell enlargement method in *Dictyostelium discoideum*

Yukihisa Hayashida¹, Yuki Gomibuti², Chikoo Oosawa², Takuo Yasunaga², Yusuke V Morimoto² (¹Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech., ²Dept. Phys. and Info. Eng., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech)

To understand sequential signal transduction, it is essential to visualize how information is processed within a single cell. However, the size of many model organisms, including the cellular slime mold *Dictyostelium discoideum*, is too small relative to the speed of signal transmission. We therefore developed a method to generate giant cells by partially inhibiting cytokinesis in *Dictyostelium*. Using fluorescence microscopy, we observed cAMP relay and associated Ca²⁺ dynamics in these giant cells. This revealed phenomena not detectable in normal-sized cells. Giant cells retaining intercellular signaling enabled observation of intracellular signal transduction with over tenfold higher spatiotemporal resolution.

2Pos106

スフィンゴミエリンのナノドメイン形成に対するコレステロールの影響

Cholesterol assists gel-like nanodomain formation of biologically relevant sphingomyelins

Masanao Kinoshita¹, Koki Yamane², Nobuaki Matsumori² (¹Grad. Sch. Sci. Tech., Gunma Univ., ²Grad. Sch. Sci. Tech., Kyushu Univ.)

Sphingomyelin (SM) is a major constituent of functional membrane domains termed lipid rafts. Recently, we proposed that SM molecules of the same type preferentially assemble to form nanodomains, which in turn cluster to form lipid rafts. However, the effect of cholesterol (chol) on the nanodomain formation remains unknown though chol is an essential component of lipid rafts. In this study, we examined the effect of chol on the domain-formation ability of SM and its dihydro analog. As a result, both SMs (0–20 mol%) form nanodomains in the chol-containing membrane while did not in the chol-free membrane. Electron diffraction revealed that both SMs form gel-like packing in the nanodomains. These results indicate that chol assists gel-like nanodomain formation of SM.

2Pos107

DPPH アッセイとハイパースペクトル顕微鏡を用いた炎症性腸疾患に対する抗酸化ナノザイムの評価

Evaluation of Antioxidant Nanozymes for Inflammatory Bowel Disease Using DPPH Assay and Hyperspectral Microscopy

Ami Saito (Institute of Industrial Science, The University of Tokyo)

Inflammatory bowel disease (IBD), such as Crohn's disease and ulcerative colitis, is a chronic intestinal disorder with unclear pathogenesis and limited treatment options. Oxidative stress, caused by imbalance between reactive oxygen species (ROS) and antioxidant enzymes, contributes to IBD and increases colorectal cancer risk. We developed biocolloid-based nanozymes with antioxidant activity. Their radical-scavenging ability is evaluated by DPPH assay based on spectral change. Hyperspectral microscopy enables real-time tracking of nanozyme activity and localization in cells and organoids. We also assess synergistic effects with antimicrobial peptides (AMPs), innate immune molecules involved in chronic inflammation. This study may help develop novel therapies for IBD.

2Pos108

アシル鎖長の異なるスフィンゴミエリンは脂質ラフト様秩序膜ドメイン内で異なるナノドメインを形成する

Sphingomyelins with varying acyl chain lengths form segregated nanodomains within lipid raft-like ordered membrane domains

Akane Nakamoto¹, Masanao Kinoshita², Nobuaki Matsumori¹ (¹Grad. Sch. Sci., Kyushu Univ., ²Grad. Sch. Sci. & Tech., Gunma Univ.)

Sphingomyelin (SM)-rich ordered membrane domains, known as lipid rafts, contain SM species with diverse acyl chain lengths. Previously, we reported that the structure of SM acyl chains regulates their partitioning between the raft-like ordered phase and surrounding fluid matrix. In this study, we investigated domain formation by C16:0SM and C22:0SM using their fluorescent analogues. Fluorescence correlation spectroscopy (FCS) analysis showed that C16:0SM and C22:0SM exhibit different diffusion coefficients within the liquid-ordered (Lo) domain. Moreover, high-resolution fluorescence imaging showed that these SM species form nanodomains, with each SM segregating within the Lo domain. These findings support the homophilic interaction model proposed by our group.

2Pos109

パターン化モデル膜における電気泳動を用いた膜タンパク質の分離

Separation of membrane proteins by electrophoresis in a patterned model membrane

Keigo Kitayama¹, Kenichi Morigaki² (¹Grad. Sch. Agr., Kobe University, ²Biosignal Research Center, Kobe University)

Many functions of biological membranes are achieved by membrane proteins. To analyze their functions, it is necessary to separate them while preserving their native state. However, conventional protein separation techniques frequently involve denaturing conditions. Thus, supported lipid bilayers (SLBs), used as model membranes, serve as a platform for membrane protein separation. In particular, electrical manipulation is effective for separating membrane components in SLBs. In our study, we achieved electrophoretic separation of charged lipids and membrane-bound proteins in SLBs confined by patterned polymeric bilayers. Furthermore, we analyzed molecular transport and steady-state concentration gradients under an electric field using a theoretical model.

2Pos110

両親媒性モデルペプチド 18A の改変による脂質膜曲率を認識するペプチドの開発

Development of curvature sensitive peptides based on the amphipathic model peptide 18A

Kazuna Ikeuchi, Keisuke Ikeda, Hiroyuki Nako, Minoru Nakano (*Fac. Pharm. Sci. Univ. Toyama*)

We have developed a peptide capable of recognizing lipid membrane curvature. We have added two charged amino acids residues at each end of an amphipathic model peptide 18A, which mimics α -helix of apolipoprotein A-I. Liposomes with different particle sizes were prepared and added to the peptide solution, and the tryptophan fluorescence spectrum was recorded. The liposomes with smaller particle size, i.e., with higher curvature, showed a significant increase fluorescence in intensity and blue shift of maximum wavelength. This suggested that the peptide had curvature recognition ability.

2Pos111

F₁F₀-ATP 合成酵素の複合体状態によるミトコンドリア形態と機能の制御機構

Regulatory mechanism of mitochondrial dynamics and function via the complex state of F₁F₀-ATP synthase

Aoi Ichikawa¹, Takaya Ishihara^{1,2}, Naotada Ishihara¹ (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., ²Dept. Life Sci., Faculty of Med., Shimane Univ.)

Mitochondria dynamically change their morphology by membrane fusion and fission. And the balance between fusion and fission is crucial for maintaining respiratory function. We previously reported that mitochondrial fission deficient HeLa cells (Drp1 KO cells) have elongated mitochondria with impaired respiratory function. Based on these findings, we performed RNAi screening for genes that recover mitochondrial structures and function in Drp1 KO cells, and identified one of the subunits in F₁F₀-ATP synthase. And from detailed analysis, we found that dimeric ATP synthase promotes mitochondrial fusion activity, independent with enzyme activity. Thus, we found that complex state of ATP synthase has a key role for regulating mitochondrial membrane dynamics and function.

2Pos112

長さ分布を調整したアクチン封入リボソームの形態変化

Morphological changes in actin-encapsulated liposomes with adjusted length distribution

Yuki Mizutani, Mahito Kikumoto, Ken Bessho, Kingo Takiguchi (*Grad. Sch. Sci., Univ. Nagoya*)

As one of the constitutive approaches to elucidate the mechanism of cell morphogenesis by the cytoskeleton, studies have focused on liposome deformation. It has found that when the concentration of encapsulated F-actin exceeds 50 μ M, nematic liquid crystals are formed even within liposomes, and liposomes are deformed into a spindle shape. In this study, the effect of the length distribution of actin filaments on liposome deformation was examined.

The results showed that preparation of the length distribution produced differences in the frequency of deformation. We also examined the effect of encapsulation of Light Meromyosin filaments as rod-shaped materials other than actin filaments.

2Pos113 脂質二重膜小胞の安定性に対するアクチンの影響
Effect of Actin on the Stability of Lipid Bilayer Vesicles

Ken Bessho, Mahito Kikumoto, Yuki Mizutani, Kingo Takiguchi (*Grad. Sch. Sci., Nagoya Univ.*)

The liposome is the simplest model of cell, has long been used to research the dynamics of lipid membranes. Liposomes stressed by osmotic pressure are known to show various responses depending on the magnitude of the stress, and we have constructed an observation system suitable for quantitative analysis of liposomes. As the first attempt, the effect of the encapsulation of F-actin on the liposomal responses was examined, and the results showed that the encapsulation of F-actin prevented liposome breakdown or prolonged the time required for these responses. In addition, also F-actin outside the liposome, i.e., it was not encapsulated, was more strongly interacted with the liposome than other proteins, suggesting that F-actin is spontaneously strengthening the membrane.

2Pos114 Reconstitution of actin cytoskeleton into artificial membranes

Yosuke Senju^{1,2}, Feng-Ching Tsai³, Zack Jarin⁴, Ilpo Vattulainen¹, Gregory Voth⁴, Patricia Bassereau³, Pekka Lappalainen¹ (¹*Univ. Helsinki*, ²*Okayama Univ.*, ³*Institut Curie*, ⁴*Univ. Chicago*)

The actin cytoskeleton powers membrane deformation during many cellular processes, such as migration, morphogenesis, and endocytosis. Phosphoinositides regulate the activities of many actin-binding proteins (ABPs). Here, we applied a combination of biophysical assays and atomistic molecular dynamics simulations to uncover the molecular principles by which ABPs interact with phosphoinositide-containing membranes. Our results reveal that these proteins show large differences in the dynamics of membrane interactions and in the ranges of phosphoinositide densities that they sense. Furthermore, we successfully reconstituted the formation of membrane protrusions driven by ABPs into artificial membranes (GUVs), and unraveled their mechanisms.

2Pos115 細胞質側とペリプラズム側の張力センサーの異なる役割により明らかになった MscL の非対称な機械刺激感受性
Asymmetric Mechanosensitivity of MscL Channel Revealed by Differential Roles of Cytoplasmic and Periplasmic Tension Sensors

Takeshi Nomura¹, Yasuyuki Sawada², Masahiro Sokabe³ (¹*Sch. Human Sci. Environ., Univ. Hyogo*, ²*Institute of Materials Innovation, Nagoya Univ.*, ³*Human Information Systems Labs, Kanazawa Institute of Technology*)

The bacterial mechanosensitive channel MscL opens in response to membrane tension, with two key residues, F7 and F78, located near the cytoplasmic and periplasmic faces, respectively. However, their relative contributions to channel gating are unclear. To investigate this, we generated *E. coli* MscL mutants by substituting either F7 or F78 with 19 different amino acids and measured their activation thresholds using the patch-clamp technique. We found that F7 mutations altered mechanosensitivity 1.53 times more than F78 mutations, indicating that the cytoplasmic side has a greater influence on gating. These findings reveal asymmetric tension sensing across the bilayer, suggesting distinct mechanosensitivity between the inner and outer membrane leaflets in MscL function.

2Pos116 点突然変異によるクラミドモナス TRP チャネル TRP11 の機能解析
Functional analysis of a TRP channel in *Chlamydomonas*, TRP11, by point mutagenesis

Takanao Miyake, Miyu Kimura, Kenjiro Yoshimura (*Col. Sys. Engineer. Sci., Grad. Sch. Engineer. Sci., Shibaura Inst. Technol.*)

TRP11 is a transient receptor potential (TRP) channel of *Chlamydomonas reinhardtii* and is involved in mechanoresponses, such as avoiding reaction and shear-induced deciliation. The molecular mechanism of TRP11, however, has not been elucidated. In this study, we performed alanine scanning mutagenesis by generating mutants of the residues facing the ion conducting pore of TRP11. The mutant TRP11 was expressed in a TRP11 knock-out cell and the cells were subjected to shear force. The mutants with mutations at residues predicted to comprise the channel gate and ion-selectivity filter were defective in showing shear-induced deciliation. This result shows that the TRP11 is an ion conducting unit that triggers mechanoresponses.

2Pos117

MscL での二箇所での張力感受：F7 と F78 の間にある機能的関連性
Dual-Site Tension Sensing in MscL: Functional Link Between F7 and F78

Yasuyuki Sawada¹, Takeshi Nomura², Masahiro Sokabe³ (¹*Inst. Materials, InFuS, Nagoya Univ.*, ²*Sch. Human Sci and Env., Univ. Hyogo*, ³*Human Information Systems Labs, Kanazawa Inst. Tech.*)

The bacterial mechanosensitive channel MscL is a homopentamer composed of subunits with two transmembrane helices, TM1 and TM2. A key gating residue, F78 on TM2's periplasmic side, transmits membrane tension to TM1. Meanwhile, the F7N mutant, with a substitution on TM1's cytoplasmic side, shows a loss-of-function phenotype, suggesting that F7 is also involved in gating. To explore this, we performed molecular dynamics simulations of the F7N mutant. The results indicate that N7 weakens lipid interactions at F78, implying that F7 and F78 are functionally coupled in tension sensing and essential for proper MscL opening.

2Pos118

DNA チャネル内部の官能基修飾とイオン輸送特性の相関の分子論的解析
Molecular analysis of the correlation between functional group modifications inside DNA channels and ion transport properties

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DNA channels that mimic the function of ion channels have attracted much attention. While size-dependent selective transport and open/close control mechanisms have been realized in DNA channels, internal functionalization for transport control has not yet been achieved. To control ion transport by internal functionalization, it is important to understand the correlation between structural properties of channel and ion transport properties. However, it is difficult to experimentally investigate ion transport phenomena at the nanoscale. In this study, we investigate the effects of hydrophobicity and length of functional group on ion transport by modifying the inside of DNA channels with ethyl and hexyl groups using molecular dynamics simulations.

2Pos119

ストレス応答センサーキナーゼ BaeS のマルチリガンド認識機構
Multiple ligand recognition mechanisms of the membrane stress sensor kinase BaeS

Hirotaka Tajima^{1,2}, Riku Takei³, Kentaro Yamamoto⁴, Ikuro Kawagishi^{1,2,3} (¹*Dept. Frontier Biosci., Hosei Univ.*, ²*Res. Cen. Micro-Nano Tech., Hosei Univ.*, ³*Grad. Sch. Sci. Eng., Hosei Univ.*, ⁴*Dept. Mycobacteriol., Lepr. Res. Ctr., NIID*)

The sensor kinase BaeS, via its response regulator BaeR, regulates expression of genes such as *acrD* in response to stimuli including indole and tungstate. Although BaeS was previously thought to detect membrane stress, our recent findings suggest that it senses intracellular indole. This study aimed to elucidate the stress-sensing mechanisms of BaeS. ITC measurements revealed that tungstate binds directly to its periplasmic domain. In contrast, a BaeS variant lacking this domain retained indole-sensing ability. Mutagenesis of the cytoplasmic domain identified a mutant specifically defective in indole sensing. We conclude that BaeS employs distinct mechanisms to sense tungstate and indole.

2Pos120

動物と植物間で保存された miRNA 合成分子に関わる遺伝子によって制御される温度耐性機構
Temperature tolerance regulated by a miRNA processing molecule conserved between animals and plants

Sakura Sengoku^{1,2}, Akane Ohta^{1,2}, Teruaki Taji³, Atsushi Kuhara^{1,2,4} (¹*Graduate School of Natural Science, Konan University*, ²*Institute for Integrative Neurobiology, Konan University*, ³*Department of Bioscience, Tokyo University of Agriculture*, ⁴*AMED-PRIME, Japan Agency for Medical Research and Development*)

Adaptation to temperature changes is an essential for animals and plants to survive and proliferate. Taji et al. found responsible gene, *SE*, for diversity of heat tolerance in *Arabidopsis* (Unpublished). Here we found that its *C. elegans* homolog SRRT regulating miRNAs processing promotes temperature tolerance. SRRT is expressed in many cells containing neuron and localized at nucleus. We are attempting to examine (1) whether heat stimulus alters the expression level and localization of SRRT, (2) at which developmental stage SRRT is required for heat tolerance, and (3) which types of miRNA are processed via SRRT using RNA-seq analysis.

2Pos121 神経ネットワークを構成する細胞数がバースト発火に与える影響
Effect of Number of Cells in Neural Network on Burst Firing

Takumi Yamaguchi, Kentaro Kito, Tomoyuki Kaneko (*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

The Excitatory/Inhibitory (E/I) balance is properly regulated in the central nervous system, however in epilepsy this balance is disrupted, and abnormal excitation is induced. In this study, we fabricated Agarose Micro Chambers (AMCs) using agarose microfabrication technology to form neural cell colonies consisting of a small number of neurons. Furthermore, we measured the extracellular potential of each neural cell colony using a Multi-Electrode Array (MEA) system. As a result, we observed a tendency for colonies with longer burst durations to appear as the size of the neural cell colony decreased in burst firing. For the next study, we will observe the behavior of glutamate administration when it promotes abnormal excitation.

2Pos122 方位選択性を備えた深層ニューラルネットワークモデルによるハーマン格子錯視の定量解析
Quantitative analysis of the Hermann grid illusion using a minimal deep neural network with orientation-specific edge detection

Masayo Inoue¹, Izumi Ohzawa^{2,3}, Kazufumi Hosoda^{2,3,4} (¹*Grad. Sch. Eng., Kyutech*, ²*Grad. Sch. Frontier Biosciences, Osaka Univ.*, ³*CiNet, NICT*, ⁴*Kobe Univ. Grad. Sch. Health Sciences*)

The straightness of grid line edges is essential for the Hermann grid illusion because the illusory effect is reduced significantly when the grid lines are distorted. A new explanation for the importance of orientation selectivity in the primary visual cortex has been proposed. However, whether this new hypothesis can explain the illusion has not been quantitatively verified. This study aimed to demonstrate the validity of the new hypothesis using a simple deep neural network model with a mechanism to detect straight edges. Our model computes an illusory output for the straight grid input. Our results suggest that the detection of straight edges is both necessary and sufficient for the Hermann grid illusion.

2Pos123 ミミズ古典的条件づけの神経メカニズムの解明
Molecular mechanism of associative learning in earthworm, *Eisenia fetida*

Yoshihiro Kitamura¹, Sukehiro Kabayama² (¹*Dept. Math. Sci. Phys., Col. Sci. Eng., Kanto Gakuin Univ.*, ²*Appl. Matl. Life. Sci., Grad. Sch. Eng., Kanto Gakuin Univ.*)

Molecular mechanism of associative learning in earthworms was investigated. We previously reported that NO signaling is involved in memory acquisition in worms conditioned in paired trials of a weak vibration and a bright light. Administration of NO synthase inhibitor L-NAME before conditioning fully inhibited acquisition of short- and long-term memory. When L-NAME was administered after acquisition of short-term memory, worms did not acquire long-term memory. Furthermore, administration of L-NAME to worms that had acquired long-term memory had no effect on memory acquisition. From these results, we concluded that NO production is essential for both short- and long-term memory formation, and that long-term memory begins to form within hours of the end of conditioning.

2Pos124 牧羊犬はどのように羊を追いつてるのか？：視覚情報に基づく誘導方法
How Do Shepherd Dogs Herd Sheep? – A Visual Perception-Based Guiding Rule

Kosuke Miyoshi¹, Nen Saito^{1,2} (¹*Graduate School of Integrated Science for Life, Hiroshima University*, ²*Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences*)

Guiding a group of agents to a destination using repulsive forces from fewer external agents is called the herding problem. In this problem, we propose a simple control rule only based on visual perception, instead of relying on coordinate information as in previous approaches.

The control rule determines the shepherd's direction by using only angular information. It requires no complex parameter tuning to achieve effective control, making it easy to implement. Despite its simplicity, the method succeeds even under challenging conditions where existing methods often fail.

We outline the design principles and geometric basis of the visual control rule and present simulation-based quantitative evaluations.

2Pos125

発光プローブを用いた哺乳類メラノプシンとアレスチンとの相互作用解析

Analyses of the interaction between mammalian melanopsin and arrestin using bystander BRET probes

Kento Takano, Hisao Tsukamoto (*Grad. Sch. Sci., Kobe Univ.*)

Melanopsin is a photoreceptive GPCR that functions in mammalian retinal ganglion cells and mediates non-visual photoreception such as circadian photoentrainment and pupillary reflex. Unlike visual pigments, melanopsin is inactivated by beta-arrestins but not visual-arrestins. The details underlying the melanopsin-arrestin interaction are still unclear. In this study, we analyzed the binding dynamics of beta-arrestin to melanopsin using bystander BRET (bioluminescence resonance energy transfer) probes. Our BRET analyses successfully detected the interaction of beta-arrestin with melanopsin. In particular, C-terminal region of melanopsin dynamically regulates the binding mode of beta-arrestin.

2Pos126

光依存的シグナル伝達に関する新奇ロドプシンの分子特性

Molecular properties of novel microbial rhodopsins with a photosensory function in light-dependent signal transduction

Qianfan Zhou, Masae Konno, Keiichi Inoue (*ISSP, Univ. Tokyo*)

Microbial rhodopsins are photoreceptive membrane proteins using retinal chromophore. In this study, we identified new rhodopsins that exhibit structural similarities with the rhodopsin sensor domain of histidine kinase rhodopsins (HKRs). The molecular properties of these rhodopsins were investigated by ion-pumping assays, transient absorption spectroscopy, pH titration, and retinal configuration analysis. While they did not exhibit ion-pumping activity, a formation of a long-lived photointermediate was observed upon light illumination, suggesting their sensory function for light-dependent signal transduction. In the presentation, their molecular properties will be compared with those of HKRs to elucidate structural and functional similarities and differences.

2Pos127

PYP と PBP の光依存的多量化反応における PBPC 末端領域の寄与

Contribution of the PBP C-terminal region to the light-dependent multimerization reaction of PYP and PBP

Yusuke Kuwahara¹, Youichi Yamazaki¹, Kento Yonezawa^{1,2}, Sachiko Toma-Fukai¹, Hironari Kamikubo^{1,2} (¹NAIST, MS, ²NAIST, CDG)

Photoactive yellow protein (PYP) binds to the interacting protein, PYP-binding protein (PBP), in a light-dependent manner to form various multimerized complexes. The C-terminal region of PBP stabilizes these complexes, but its detailed role is unknown. In this study, we generated two PBP mutants (PBPΔC126 and PBPΔC118) with deletions after residues 126 and 118, respectively, and their complex formation was analyzed. In PBPΔC126, complex formation with PYP caused an absorption shift to 445 nm. However, PBPΔC118 showed no shift, maintaining the original PYP absorption at 438 nm. SAXS measurements confirmed complex formation in both mutants. These results indicate that the C-terminal region of PBP stabilizes the complex and generates an absorption shift of PYP.

2Pos128

ラマン分光およびアミノ酸置換体を用いたシアノバクテリオクロム RcaE の光変換機構の研究

Photoconversion mechanism of cyanobacteriochrome RcaE studied by Raman spectroscopy and Mutagenesis

Taisei Koga¹, Masako Hamada², Yuu Hirose², Tomotsumi Fujisawa¹, Masashi Unno¹ (¹Fac. Sci. Eng., Saga Univ., ²Dept. Appl. Chem. Life Sci. Toyohashi Univ. of Tech.)

Cyanobacteriochrome (CBCR) belongs to the phytochrome superfamily of photoreceptors and uses a linear tetrapyrrole (bilin) as a chromophore. RcaE is a representative member of the green/red CBCR subfamily. This protein undergoes a reversible photoconversion between green-absorbing (Pg) and red-absorbing (Pr) states, where the bilin chromophore adopts a deprotonated C15-Z_{anti} and a protonated C15-E_{syn} structures, respectively. However, the details of the photoreaction remain unknown. In this study, we have used K261E mutant of RcaE, since this mutant has a structure that is similar to an intermediate state. We investigated the structure of this mutant using a combined approach of Raman spectroscopy and computational chemistry.

Chihiro Fujiyabu¹, Gyoja Fuji², Keita Sato³, Emi Kawano-Yamashita⁴, Hideyo Ohuchi³, Takehiro Kusakabe²,
Takahiro Yamashita¹ (¹Grad. Sch. Sci., Kyoto Univ., ²Grad. Sch. Nat. Sci., Konan Univ., ³Fac. Med., Dent. & Pharm.
Sci., Okayama Univ., ⁴Fac. Sci., Nara Women's Univ.)

Opsins are universally responsible for visual and non-visual photoreceptions in animals. Among these opsins, pinopsin functions as a blue-sensitive pigment mainly in the pineal gland and its related organs of birds, reptiles, amphibians and non-teleost fishes. However, the pinopsin gene has not been identified in the genomes of teleost fishes. In this study, we identified a pinopsin gene in the genome of a teleost fish. Our analysis revealed that this pinopsin gene functions in the pineal gland and has two specific mutations that result in a unique green sensitivity of the pinopsin protein. Based on the comparison of rhodopsin and pinopsin genes, we would like to provide a model for the diversification of visual and pineal opsins in teleost fishes.

Tomotsumi Fujisawa¹, Nozomi Tanaka¹, Jun Tamogami², Masashi Unno¹ (¹Fac. Sci. Eng., Saga Univ., ²Coll. Pharm. Sci., Matsuyama Univ.)

Sensory rhodopsin II (SRII) is a prototype photosensor that binds the retinal Schiff base chromophore. Upon photoabsorption, SRII is transformed into the signaling state, where two long-lived photointermediates are known to contribute. One is the M intermediate containing the deprotonated 13-*cis* chromophore, and the other is the O intermediate that is believed to have the protonated all-*trans* chromophore. The chromophore in the O intermediate is also thought to have the atypical 15-*syn* (C=N *cis*) configuration about the Schiff base moiety. Here, we study SRII from *Natronomonas pharaonis* using Raman spectroscopy and find that the retinal chromophore configuration in the O intermediate is the 13-*cis*, 15-*anti* (C=N *trans*).

Kazumi Sakai¹, Kengo Fujii¹, Chihiro Fujiyabu¹, Yasuhiro Shiga², Takahiro Yamashita¹ (¹Grad. Sch. Sci., Kyoto Univ., ²Tokyo Univ. of Pharm. and Life Sci.)

In general, animals have a variety of opsins for visual and non-visual photoreceptions. Most non-visual opsins bind 11-*cis* retinal and have the bistable property, that is, the photo-reversibility between the dark state and the active state. Arthropsin is a protostome-specific non-visual opsin and belongs to the Gq-coupled opsin group together with mollusk and arthropod rhodopsins and vertebrate Opn4. Our analysis revealed that arthropsin have unexpected spectral diversity ranging from the UV to the red region. Moreover, several arthropsin have characteristic molecular properties, such as the binding preference of retinal isomers and the photoreaction property. We would like to discuss the molecular basis underlying the diversity of arthropsin.

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Takahiro Yamashita⁴, Yuki Sudo², Keiichi Kojima² (¹Grad. Sch. Med. Dent. & Pharm. Sci., Okayama Univ., ²Fac. Med.
Dent & Pharm Sci., Okayama Univ., ³Grad. Sch. Sci., Kobe Univ., ⁴Grad. Sch. Sci., Kyoto Univ.)

Opsins are universal photoreceptive proteins that serve as the molecular basis of photoreception in animals, and are phylogenetically classified into several subfamilies, including Opn5, that correspond well with functional characteristics, such as G protein selectivity and photochemical properties. While most Opn5 proteins exhibit UV sensitivity, we recently identified a unique subgroup of Opn5 in crustaceans that shows visible-light sensitivity. In this study, we characterized molecular properties of these visible-light sensitive opsins and compared them with those of UV-sensitive Opn5. Our analysis revealed that these opsins preferentially activate Gq-type G proteins. Based on the results, we discuss their physiological functions and potential as optogenetic tools.

2Pos133 幅広い時間スケールでの時分割結晶構造解析により明らかになったクリプトクロムのシグナル伝達機構
Cryptochrome signal transduction mechanism revealed by time-resolved crystallography across broad timescales

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Time-resolved crystallography has emerged as a powerful tool for revealing how biological macromolecules function in real time and at atomic resolution. By combining time-resolved serial femtosecond crystallography (TR-SFX) and time-resolved serial oscillation crystallography (TR-SOX), we investigated structural changes in *CraCRY*, a photoreceptive flavoenzyme (an animal-like cryptochrome from *Chlamydomonas reinhardtii*), over a broad timescale ranging from nanoseconds to seconds. The resulting 3D molecular movie captured a cascade of structural transitions initiated by the reduction and subsequent protonation of the FAD cofactor, ultimately leading to *CraCRY*'s signaling state characterized by unfolding of the C-terminal α -helix.

2Pos134 緑色硫黄細菌の光合成反応中心複合体のカロテノイド配糖体を介する三重項エネルギー移動
Energy transfer pathway forming triplet-excited state of carotenoid in the photosynthetic reaction center of green sulfur bacteria

Tomomi Inagaki¹, Masatoshi Kida², Daisuke Kosumi³, Chihiro Azai⁴ (¹*Graduate School of Life Sciences, Ritsumeikan University*, ²*Graduate School of Science and Technology, Kumamoto University*, ³*Institute of Industrial Nanomaterials, Kumamoto University*, ⁴*Faculty of Science and Engineering, Chuo University*)

The major carotenoids of green sulfur bacteria are chlorobactene and γ -carotene, while some of which are glycosylated with glucose. These carotenoid glycosides are specifically bound to the photosynthetic reaction center (RC) complex and quench the electronically excited Bchl *a*. In this study, we tracked excitation energy transfer (EET) reactions in the GsBRC complex of *Chlorobaculum tepidum* using transient absorption spectroscopy. We observed formation of a carotenoid triplet state (Car-T₁) under photoaccumulation conditions, which is a culture under high-light illumination. We inferred the EET scheme leading to the Car-T₁ formation and a function of the carotenoid glycosides contributing to the Bchl *a* quenching that occurs in the RC complex of *C. tepidum*.

2Pos135 Evaluating the mobility of LHCII in plant thylakoid membrane using high-speed AFM

Nami Yamano, Yudai Nishitani, Daisuke Yamamoto (*Fukuoka University*)

In plant photosynthesis, excitation valance between photosystem I and II is tuned through the migration of light harvesting complex II (LHCII) in response to the solar irradiance. However, the molecular mechanisms underlying the excitation-tuning remain unclear due to the lack of single-molecule information on LHCII mobility. Here, we aimed to visualize LHCII within the thylakoid membrane from spinach using HS-AFM. Mobility of LHCII in membrane patch was evaluated by analyzing the relaxation curve of correlation-coefficient between HS-AFM images. The granum LHCII exhibited relatively static behavior. By contrast, LHC-pool in stroma lamella showed quite diffusive mobility. This result indicates the functional difference between LHCII located in grana and stroma lamella.

2Pos136 モデル植物苔類ゼニゴケ由来の光化学系Ⅰ二量体のクライオ電子顕微鏡単粒子構造解析
Cryo-EM structures of dimeric PSI-LHCI supercomplex from the model organism *Marchantia polymorpha*

Pi-Cheng Tsai¹, Romain La Rocca¹, Hiroyasu Motose², Jian-Ren Shen¹, Fusamichi Akita¹ (¹*Adv. Res., Univ. Okayama*, ²*Grad. Sch. Envir. Life, Nat. Sci. & Tech., Univ. Okayama*)

Photosystem I (PSI) is a conserved light-energy converter from cyanobacteria to vascular plants, while its light-harvesting complex (LHC) varies among species. The liverwort *Marchantia polymorpha*, an early land plant model, provides insights into photosynthetic evolution during terrestrial adaptation. We determined high-resolution (1.94 Å and 2.52 Å) structures of monomeric and dimeric PSI-4 LHCI supercomplexes from *M. polymorpha* without cross-linking. Our results reveal that PsaB-PsaM and PsaG-PsaH interactions are key to PSI-LHCIs dimerization, shedding light on structural evolution of PSI in land plants.

2Pos137 光化学系 II の Mn 高親和性サイトの配位環境
Coordination environment of Mn high-affinity site in Photosystem II

Naohiko Nakamura, Shinya Kosaki, Hiroyuki Mino (*Grad. Sch. Sci., Univ. Nagoya*)

Photosystem II (PSII) is a photosynthetic protein complex, which evolves molecular oxygen in the catalytic center, manganese cluster. The manganese cluster consists of four Mn, one Ca, five O, and surrounding amino acid residues. Weak chemical reduction releases three Mn is easily removed, but one Mn is tightly binding. The tightly binding Mn has possibly a role of reconstruction Mn cluster from apo-PSII. We investigated the properties and location of the tightly binding Mn. Pulsed EPR measurements show that the tightly binding Mn is located on the specific site, labelled 'Mn2', which is an original position of Mn cluster in mature PSII.

2Pos138 The most stable LH1-RC architecture from a thermophilic purple sulfur bacterium,
Caldichromatium japonicum

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Ccm.japonicum is a newly described thermophilic purple sulfur phototrophic bacterium isolated from a microbial mat of Nakabusa hot springs in Japan. This bacterium is phylogenetically related to *Tch.tepidum*, which grows phototrophically at the highest temperature (58°C) among purple bacteria and contains Ca²⁺ as an indispensable cofactor. Here, we report the effects of Ca²⁺ on the structural and functional properties of the LH1-RC from *Ccm. japonicum* and its highly resolved cryo-EM structure. It was demonstrated that the *Ccm. japonicum* LH1-RC exhibits the highest thermal stability among purple bacteria in the presence of Ca²⁺. Based on the structural information, the origins responsible for the highest thermal stability of the *Ccm. japonicum* LH1-RC are discussed.

2Pos139 Spectroscopic characterization of the light-harvesting 1 reaction center complexes from
psychrophilic photosynthetic purple bacteria

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Rhodofex (*Rfx.*) *antarcticus* strain AB and strain Fryx1 are psychrophilic purple phototrophic bacteria isolated from a microbial mat or water column under the ice of the permanently frozen lake in Antarctica. These organisms grow at a temperature range of 0 – 25°C (optimally at 15-18°C), the lowest growth temperatures among purple phototrophs ever reported. To understand mechanisms for this unique psychrophilic photosynthesis, we purified LH1-RC complexes from *Rfx. antarcticus* strain AB and strain Fryx1 and characterized them spectroscopically. Intriguingly, these psychrophiles exhibited the minimal uphill energy gap and the fastest energy transfer rate. Based on these findings, the strategy of psychrophiles to survive under extreme environments is discussed.

2Pos140 Spectroscopic and structural characterization of purple bacterial LH1-RC complexes containing
bacteriochlorophyll b

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The bacteriochlorophyll (BChl) *b*-containing purple bacteria are rare species and grow phototrophically with the lowest energy of light (longer than 1000 nm) among phototrophic organisms. Although recent Cryo-EM analyses have revealed the 3D structures of the LH1-RCs from several species containing BChl *b* (*Blc. viridis*, *Blc. tepida*, *Hcs. halochloris*), their photosynthetic functions including light-harvesting abilities and uphill energy transfer mechanisms are not fully understood. In this study, we report spectroscopic and structural characterization of the LH1-RC complexes from BChl *b*-containing species, including purple sulfur bacterium, *Hcs. abdelmalekii*.

赤色光にตอบสนองするアニオンチャネルロドプシンのイオン輸送機構 Ion transport mechanism of channel rhodopsin in response to red light

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Microbial rhodopsins are reactive to blue or green light which does not effectively penetrate through biological tissues. A1ACR1 is an anion channelrhodopsins (ACRs) from *Labyrinthula*. A1ACR1 exhibits spectral sensitivities with maxima at 610 nm, the most red-shifted ChRs known. However, A1ACR1 shows significant inactivation of the activity and is not the best tool for neuronal silencing. In this study, we measured the photocurrent of the A1ACR1 by using a whole-cell patch-clamp. Site-directed mutagenesis study showed that the specific charged residues affect the inactivation and the ion selectivity. The mutants R232A and H235A, located on the extracellular side, showed a decrease in inactivation. Here we propose the ion transport mechanism of A1ACR1.

新規内向きプロトンポンプ, PhXeR の分光学的解析 Spectroscopic Analysis of a Novel Inward Proton Pump, PhXeR

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Microbial rhodopsins exhibit various functions, such as ion transport and sensor for signal transduction, through structural changes induced by retinal photoisomerization. We found a microbial rhodopsin from a marine bacterium *Pseudalkalibacillus hwajinpoensis*, which is a homolog of an inward proton-pumping xenorhodopsin (PhXeR). Its amino acid sequences of the motif in the third transmembrane helix contain aspartic acid, serine and serine (DSS). Here we measured the ion transport activity in *E.coli* cells, and confirmed inward proton pump. We applied various spectroscopic analysis to PhXeR, including transient absorption and FTIR spectroscopy. We would like to discuss the molecular mechanism of PhXeR based on our spectroscopic results.

Photoregulation of Ras Function Using Photoresponsive Protein

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The small GTPase Ras functions as a molecular switch in signal transduction, regulated by conformational changes in nucleotide-binding motifs. While its switching is well studied, optogenetic control remains limited. We previously showed HRas activity can be photoreversibly modulated by fusion with the light-responsive protein Photozipper (PZ). Here, we engineered a photoresponsive Ras variant, PA (photoactivatable analogue)-Ras, by fusing the LOV2-Ja domain from *Avena sativa* phototropin1 to Ras's catalytic domain. PA-Ras underwent reversible conformational changes under blue light and darkness. Its GTPase activity, regulated by GEFs and GAPs, was controllable via light-induced photoisomerization. These findings support optogenetic control of Ras signaling.

Autonomous Multicolor Bioluminescence Imaging in Bacteria, Mammalian, and Plant Hosts

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Bioluminescence imaging offers advantages over fluorescence, including no phototoxicity, minimal photobleaching, and high signal-to-noise ratios. Yet, conventional systems require exogenous luciferin, limiting long-term use. While promising, the lack of color diversity has restricted its broader application to multiplexed imaging. I addressed this by developing Nano-lanternX (NLX), a five-color autonomous system based on the bacterial *lux* operon. NLX enables multicolor imaging in bacteria, mammalian cells, and plants via spectral unmixing. I visualized multicolor signals in *E. coli*, HEK293T, cardiomyocytes, and *Nicotiana benthamiana*, demonstrating applications in gene expression, protein localization, and real-time cellular dynamics without external substrates.

2Pos145 Na⁺ポンプから Cl⁻ポンプに変異させた光駆動イオンポンプロドプシンの時間分解赤外分光に関する研究
Time-resolved FTIR study of light-driven ion pump rhodopsin mutants converted from Na⁺ to Cl⁻ pump

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Krokinobacter rhodopsin 2 (KR2) is a light-driven outward sodium ion pump rhodopsin. A previous report showed a functional conversion to an inward chloride pump by mutating the NDQ motif to the NTQ motif like in a chloride ion pump with one or two additional mutations at F72 and D102 (K. Inoue et al., J. Biol. Chem. 2016). It was reported that KR2 NTQ D102N/F72G triple mutant exhibited robust inward chloride ion pumping activity. In this study, we studied the molecular mechanism underlying the functional conversion of the KR2 mutants by using time-resolved infrared spectroscopy, which resolves the dynamics in the microsecond to millisecond range. We investigated structural changes important for the ion selectivity and pumping mechanisms of sodium and chloride ion pumps.

2Pos146 環状ヌクレオチド依存性チャネルを用いた光活性化アデニル酸シクラーゼの活性測定系の開発
Development of a system to measure activity of photoactivated adenylyl cyclase using cyclic nucleotide-gated channels

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We have developed an activity measurement system for photoactivated adenylyl cyclase (PAC) using cyclic nucleotide-gated (CNG) channels. PAC is a unique protein that produces cAMP in response to blue light. Although several types of PACs have been identified, their detailed properties have not yet been compared. To compare the properties of PACs, we are developing a system that detects changes in cAMP concentration produced by PAC as changes in CNG channel current with high temporal resolution. So far, we have confirmed a positive correlation between cAMP concentration and the open probability of CNG channels. Additionally, we have integrated an illumination system into a typical channel current measurement system.

2Pos147 Structural and functional analysis of Heimdallarchaeaota tubulin reveals the origin of eukaryotic microtubules

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The microtubule is essential for eukaryotic cellular processes, and its emergence was a key event in eukaryogenesis. Asgard archaea are the closest known prokaryotic relatives of eukaryotes. BLAST searches of the Heimdallarchaeaota metagenome identified two genes predicted to encode alpha and beta tubulin, but their properties remain unknown. Here, we report the formation of a Heim alpha-beta tubulin heterodimer and analyze its dynamics using biophysical and biochemical methods. We also investigate the individual features of monomers to explore the origin of microtubule-forming tubulins. Moreover, encapsulating filament-forming Heim tubulins in a synthetic cell system offers a simplified model to study the potential roles of Asgard tubulins in cellular morphogenesis.

2Pos148 古生代ミオグロビンによる高酸素環境への適応
Adaptation of Paleozoic Myoglobins to the Oxygenized Environments

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Myoglobins (Mbs) and hemoglobins (Hbs) originated about 500 million years ago from the common-ancestor globin and had adapted vertebrate animals to the oxygenized environments newly appeared on the earth. Here we have resurrected ancestral Mbs (aMbs) of earlier bony fish, amphibia and reptile in the Paleozoic era, and of their descendants, and investigated their biochemical properties to find the evolutionary traces. The O₂-binding affinities of the early reptile and mammal aMbs were found to lower significantly in comparison with both their precedent and descendant Mbs of various animals. The functional changes appeared to follow the atmospheric O₂ increase, suggesting that these animals adapted the environments by changing the O₂ affinity of Mb and possibly Hb.

2Pos149

数千種の細菌における走化性遺伝子群の組み合わせ進化ダイナミクス

Combinatorial evolutionary dynamics of chemotaxis genes across thousands of bacterial species

Takao Suzuki (*Juntendo Univ. Grad. Sch. Med.*)

The bacterial chemotaxis system has long been considered a tightly integrated signaling network, where each gene plays a critical role. However, comparative genomic analyses across thousands of bacterial species have revealed a diversity of chemotaxis gene combinations. Here, I used a novel phylogenetic comparative method, *pathwayPCM*, to reconstruct macroevolutionary pathways of gene combinations. We found that many species possess unexpected combinations of chemotaxis genes, and even genes traditionally regarded as essential are frequently absent. This approach identifies which signaling components are evolutionarily labile and which genes tend to co-evolve across bacterial lineages. The results illuminate the flexible architectures of bacterial signaling networks.

2Pos150

PURE system 内における翻訳阻害効果の解消

Relieving Translation Repression Caused by Inhibitory DNA Sequences in the PURE System

Akari Sakurai (*Graduate School of Arts and Sciences, The University of Tokyo*)

In vitro construction of self-reproducible artificial systems is a major challenge in bottom-up synthetic biology. Such systems must synthesize all components required for replication, transcription, and translation. This demands a high level of protein synthesis capacity, so we need to get the best performance out of the PURE system.

We developed an assay to quantitatively evaluate the protein synthesis capacity of the PURE system. Using this assay, we found that the capacity decreased when expressing a particular translation factor. We saw the same effect with several other translation factor genes. Further investigation indicated that this reduction occurs not at the transcription stage but during translation, most likely due to ribosome stalling.

2Pos151

タンパク質集積による脂質-タンパク質非対称膜小胞内膜での効率的な酵素反応

Protein accumulation enhances enzymatic reactions on inner leaflet of asymmetric lipid-protein vesicles

Masato Suzuki, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Liposomes have been widely used as model systems for creating artificial cells. Recently, vesicles formed from amphiphilic proteins have also been reported. In this study, we formed the asymmetric vesicles composed of phospholipids in the outer leaflet and amphiphilic proteins and phospholipids in the inner leaflet. First, two types of proteins were accumulated to the inner leaflet in response to external stimuli using a protein dimerization system. Second, the conjugation of two types of proteins to an amphiphilic protein molecule was confirmed by a total internal reflection fluorescence (TIRF) microscopy. Finally, we demonstrated that the enzyme accumulation on the inner leaflet of the asymmetric vesicles enhanced the efficiency of enzymatic reactions.

2Pos152

組織再構築を目指したリポソーム内細胞培養系の開発

Development of Cell Culture System in Liposomes for Tissue Reconstruction

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Three-dimensional (3D) cell culture offers significant potential in regenerative medicine. To develop 3D tissues using liposomes, this study encapsulated fibroblasts which isolated from chick-embryo heart into liposomes made by emulsion transfer method and attempted long-term culture while encapsulated. We tested liposome formation with culture medium without cells. Adding negatively charged phospholipids (DOPG, DOPS) suppressed aggregation and enhanced formation efficiency. The largest radius was observed at DOPC:DOPS=1:4, and the highest number density was achieved at DOPC:DOPG=3:2. After encapsulation of cells in lipid monolayers (liposome precursors), the cells maintained their shape for approximately 3 days. The next goal is cell encapsulation within liposomes.

2Pos153 ポリリン酸–塩水溶液の液–液相分離における一価イオンの影響
Monovalent Ion Effect on Liquid–Liquid Phase Separation of Aqueous Polyphosphate–Salt Mixtures

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Polyphosphate (polyP) can form aggregates in living cells, such as polyP granules in bacteria, through liquid–liquid phase separation (LLPS). The mechanism of polyP aggregation has been examined using LLPS systems of polyP solutions induced by multivalent ions. Although the typical concentrations of monovalent ions in living cells are much higher than those of multivalent ions, the effects of monovalent ions are little known. This study demonstrated that submolar NaCl induces LLPS of polyP solutions. Small-angle X-ray scattering measurements revealed that NaCl significantly stabilizes the intermolecular association of polyP. These findings suggest that the modulation of monovalent ion concentrations is an underlying mechanism of polyP aggregation within living cells.

2Pos154 Retrofitting of antibiotic target sites on ribosomes: A synthetic approach to reveal the molecular basis of antimicrobial resistance

Ryo Muramatsu, Yoshikazu Tanaka, Takeshi Yokoyama (*Grad. Sch. Life Sci., Univ. Tohoku*)

The global spread of drug-resistant bacteria urgently requires understanding how current antibiotics work and how resistance arises, to enable rational development of new drugs. However, due to infection risks, drug-resistant strains can only be handled in specialized facilities. We focused on ribosomes, the one of main targets of antibiotics, to understand antimicrobial resistance mechanism. To enable drug resistance studies in general labs, we provided new approach to reconstitute the drug-resistant ribosomes into the cell-free translation system by transplanting the antibiotic target site on ribosomes of pathogenetic *Mycobacterium* into those of *E. coli*. This system provides a safe and accessible platform for studying antibiotic resistance mechanisms.

2Pos155 細胞サイズ空間への閉じ込めがもたらすタンパク質の遅い拡散と反応拡散波による緩和効果
Enhanced repulsive interactions suppress protein diffusion in membrane-confined systems, alleviated by propagating protein waves

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Living cells are characterized by the confinement of high concentrations of macromolecules into micrometer-sized spaces by membranes. This confinement affects molecular diffusion. Using an artificial cell system, we found that the diffusion of negatively charged protein, BSA, slows down with cell size. This is attributed to enhanced electrostatic repulsion due to competition for cations between negatively charged membranes. Remarkably, propagating waves of Min proteins dynamically counteract these repulsive forces, restoring diffusion rate. These findings provide new insights into how intracellular environments regulate molecular transport, emphasizing the delicate balance of forces that govern biomolecular dynamics within cell-sized space.

2Pos156 クラミドモナス封入リボソームの遊泳速度決定要因の解析と光スイッチング
Analysis of Swimming Velocity Determinants and Optical Switching of Chlamydomonas-Encapsulated Liposomes

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Bio-hybrid swimmers are made by combining biological and synthetic materials. In this study, we investigated the swimming mechanism of our own bio-hybrid swimmer, the Chlamydomonas-encapsulated liposome (CL). CLs were prepared by the water-in-oil emulsion-transfer method, after which high-frame-rate imaging was used to obtain parameters such as deformation frequency f , the cell-to-liposome size ratio αCL , dimensionless membrane deformation p^* , and dimensionless swimming velocity U^* . We observed a positive correlation ($r = 0.63$) between p^* and U^* , consistent with the scaling $U^* \propto p^{*2}$. Additionally, to control membrane deformation, we prepared CLs with a photo-responsive phospholipid, successfully achieving reversible, light-triggered switching of their motility.

2Pos157 細菌べん毛と Rbody により誘導されるリポソームの能動的変形
Active deformation of liposomes induced by bacterial flagella and R-bodies

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In this study, we aimed to induce active deformation of liposomes using bacterial flagella and R-bodies. Flagella function as rotary propellers and undergo transitions between different helical conformations in response to environmental conditions such as pH. Similarly, R-bodies exhibit pH-triggered transitions from a coiled to an extended state, generating forces sufficient to disrupt lysosomal membranes. We fluorescently labeled these proteins, encapsulated them within liposomes, and manipulated the internal pH. Both proteins showed conformational changes inside the liposomes. Notably, liposomes containing R-bodies underwent dynamic transformations from spherical to lemon-like shapes, suggesting their potential application as actuators in molecular robotic systems.

2Pos158 異なるリポソーム表面で作動する DNA 回路をつなぐ「DNA シナプス」
"DNA Synapse" Wiring DNA Circuits Operating on Separate Liposome Surfaces

Masahito Hayashi, Taro Toyota (*Grad. Sch. Arts Sci., Univ. Tokyo*)

Molecular control networks require error-free wiring between reactive units. We built a "DNA synapse" in which computing and reporter liposomes interact only upon membrane contact. Liposome A bears a polymerase-driven DNA AND gate (Nat Commun 2019) anchored on its outer surface; liposome B carries dual-color beacons. After mixing A and B, we introduced two Boolean input DNAs with dNTPs and DNA polymerase to the external medium. A 30 min incubation at 37°C made liposome B display green or red fluorescence corresponding to the logical AND of the two inputs. These results show that DNA circuits operating on separate liposome surfaces can be specifically linked through membrane contact, offering a high-fidelity route toward large-scale DNA logic circuit implementation.

2Pos159 Pfam ドメイン AlphaFold 構造の特徴探索
Features of Pfam domain in Alpha Fold DB

Yamato Nakaya, Ryotaro Koike, Motonori Ota (*Graduate School of Informatics, Nagoya University*)

With the advent of AlphaFold2, the prediction of protein 3D structures from amino acid sequences has reached near experimental accuracy, enabling studies that utilize these structures to predict protein functions. Some of these investigations refer to Pfam to segment AlphaFold structures into functional domains. In this study, we explored the features of Pfam domain in Alpha Fold DB. Specifically, we extracted structures unique to Pfam domains that are not currently registered in the structural domain databases and evaluated their characteristics such as structural variation within individual domains.

2Pos160 タンパク質参照構造との立体構造比較に基づくタンパク質と結合分子の変形構造のモデリング
Deformation Modeling of Proteins and Ligands Based on Structural Comparison with Reference Protein Structures

Takeshi Kawabata, Kengo Kinoshita (*Grad. Sci. Info. Sci., Tohoku Univ.*)

Proteins often perform their functions by transitioning among multiple structural states. While some proteins have many experimentally determined conformations, others have only a few available structures, even using AlphaFold2. We developed a method to deform an available structure by comparing it to a desired target structure. Given a structure X and a homologous reference structure R* of the target state, by aligning X to R*, we derive residue-wise rigid transformations. For side chains, insertions, and bound molecules, rigid transformations are smoothly interpolated in 3D space, ensuring consistency among covalently bonded atoms. To evaluate accuracy, we constructed a benchmark from the PDB consisting of triplets: X, an alternative conformation X*, and R*.

2Pos161 水と構造を考慮したタンパク質-基質結合親和性予測機械学習モデル
Machine learning prediction model of protein-ligand binding affinity considering hydration structures

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Aiming at improving the accuracy of protein-ligand binding affinity prediction, we developed a GCN-based prediction model that explicitly considers the change in the hydration structure around the protein upon ligand binding. This model was trained with a dataset composed of a total of 8,861 hydrated structural models of protein-ligand complexes and their ligand-free structures. The complex structures were obtained from the PDBBind database and the ligand-free structures were generated by removing the ligands from the complex structures. The hydration structures were predicted by the 3D-RISM theory and the MOFT program. Preliminary results suggest that the prediction accuracy can be improved by considering the hydration structures.

2Pos162 AlphaFold3 の予測構造に基づく Type-51 R-body 構造変化機構の解明
Mechanism of Type-51 R-body conformational change based on structural predictions using AlphaFold3

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Type51 Refractile-body (R-body) is a roll-shaped giant protein complex composed of RebA and RebB, found in the endosymbiotic bacterium *Caedibacter taeniospiralis* in *Paramecium*. It reversibly changes its structure between a rolled form (230 nm) and a needle-like form (20,000 nm) in response to pH changes.

Although the large-scale structural transformation of the R-body is thought to arise from subtle conformational changes in RebA and RebB, no structure-based model has been proposed that can rationally explain the underlying mechanism of this structural change. In this study, we predicted the polymerization pattern of RebA and RebB using AlphaFold3 and interpreted the resulting structures based on experimental data.

2Pos163 深層学習でリガンド結合状態の RNA 構造を生成する
Generate RNA Conformations in Ligand-binding States with Deep Learning

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Due to the vital roles in diverse biological processes, RNA is drawing much attention as potential drug target. Structure Based Drug Design (SBDD) is a promising approach while its prediction accuracy critically depends on how similar RNA conformations tested are to ligand-binding ones. We employed a generative deep learning model (DL) for HIV-1 Transactivation Response Element (TAR) and succeeded to generate conformations with the known cryptic binding cavity without *a priori* knowledge of the cavity. They show binding scores similar to those calculated for experimentally-resolved complexes. To our best knowledge, no prior theoretical simulation studies have succeeded in generating the pocket. Our finding shows new application of DL to promote SBDD for RNA.

2Pos164 インシリコ解析による RseP 阻害剤候補のスクリーニングと構造予測をベースとした基質選択の分子基盤の解明
In Silico Screening of RseP Inhibitor Candidates and Elucidation of the molecular basis of substrate selectivity by Structure Prediction

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The bacterial site-2 protease RseP hydrolyzes substrates within the membrane and contributes to homeostasis through stress signaling and signal peptide degradation. Although the *E. coli* RseP structure has been reported (Imaizumi et al., Sci. Adv., 2022), its mechanism of substrate selectivity remains poorly understood. RseP-selective inhibitors are promising antibacterial candidates because RseP is essential for the bacterial cell growth. In this study, we screened ~200,000 compounds using docking and AlphaFold3-based modeling, selecting 240 candidates based on docking and membrane permeability scores. Also, AlphaFold3 modeling of RseP complexes with known substrates such as RseA predicted that the cleavage sites of some substrates were close to the catalytic zinc ion.

2Pos165

ESM 埋め込みのアテンションプーリングを用いたタンパク質機能同一性予測
Protein Functional Identity Prediction Using Attention-Pooling of ESM Embeddings

Kotaro Ukai, Tohru Terada, Suguru Fujita (*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

We present a deep learning model that predicts functional identity of a pair of proteins based on their sequence embeddings derived from ESM-3, a state-of-the-art protein language model. Each protein's embedding matrix was processed with an attention-based pooling mechanism to extract a fixed-length vector representation. The absolute difference between the vectors of the two proteins was used as the input to a multilayer perceptron classifier. Training evaluation, and test were conducted using a dataset composed of 50,000 positive (identical functions) and 50,000 negative (different functions) examples. Our model achieved high accuracy (over 98%) on the test set, demonstrating the effectiveness of attention pooling in capturing informative features from the embeddings.

2Pos166

AlphaFold3 versus AlphaFold2 in Sampling Alternative Conformational States of Transporter Proteins

Jun Ohnuki, Kei-ichi Okazaki (*Institute for Molecular Science*)

AlphaFold (AF) is the most successful protein-structure-prediction AI. We previously reported that a perturbation on multiple sequence alignment given to AF2 remedies bias in structure prediction of transporter proteins and enables it to sample alternative conformational states indispensable for their function. While the latest AF3 can predict structures with bound ligands, facilitating further understanding of protein function, its ability to sample alternative conformations remains unclear. In this study, we compare the conformational sampling ability of AF3 to that of AF2 for transporter proteins. We also discuss the possible application of AF-predicted structures for accelerating the efficiency of rare-event sampling molecular dynamics simulation.

2Pos167

インフルエンザウイルス・ノイラミニダーゼの薬剤耐性機構に関する理論的研究：酵素反応の自由エネルギープロファイル解析
Computational study of the drug resistance mechanism of influenza virus neuraminidase: Free energy profile analysis of enzyme reaction

Ryotaro Katsumata¹, Manabu Igarashi², Norifumi Yamamoto¹ (¹*Chiba Tech*, ²*Hokkaido University*)

Influenza virus neuraminidase (NA), a key target for antiviral drugs, is an enzyme exhibiting sialidase activity. Certain mutations in NA have been linked to NA inhibitor resistance. While these mutations may influence its enzymatic reaction mechanisms, the precise details are still unclear. In this study, we employed molecular simulations to analyze the NA reaction in drug-resistant variants of NA, aiming to elucidate the detailed mechanism of NA inhibitor resistance. We utilized the residue interaction network (RIN) analysis method to investigate alterations in intra-enzyme interactions resulting from drug-resistant mutations. Additionally, the QM/MM free energy perturbation method was applied to examine the free energy profiles associated with the NA reaction.

2Pos168

ネットワーク解析による 3α-HSD の二量体間における信号伝達機構の解明
Signal transduction mechanism between the subunits of 3α-HSD by network analysis

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3α-Hydroxysteroid dehydrogenase (3αHSD) is a homodimeric enzyme that catalyzes reversible redox reactions of hydroxy and carbonyl groups at the C3α position of steroids, using NAD(P)(H) as a coenzyme. Among these, the bacterial 3αHSD from *Pseudomonas* sp. B-0831 (Ps3αHSD) is clinically used to measure bile acid levels. Previous studies have shown that Ps3αHSD has negative cooperativity in the NADH binding: binding of the first NADH induces a conformational change that lowers the affinity for the second. Although this signal is thought to be transmitted across the dimer interface, the mechanism remains unclear. In this study, the residue interactions of Ps3αHSD were investigated by network analysis to elucidate the signal transduction mechanism across the dimer interface.

2Pos169 Prediction of Cross-Species Binding Affinities of GPCR-Targeting Drugs

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A part of drugs people take is excreted without being metabolized and is discharged into wastewater. Because about 40% of drugs target G protein-coupled receptors (GPCRs), the drugs flowing into rivers and seas should affect aquatic lives via disrupting their intracellular signaling involving GPCRs. Recent experiments demonstrate that some drugs more strongly inhibit GPCRs from zebrafish than those from human. In this study, we developed a method to predict the binding affinities of GPCR-targeting drugs to GPCRs from various species. We used HelixFold 3 to predict the GPCR-drug complex structures and performed free energy perturbation calculations on them. The calculated values well agreed with the experimental ones for the H1 and beta1 inhibitors and their receptors.

2Pos170 FtsZ 重合ダイナミクスの 10 分規模にわたるメソスコピック反応動力学シミュレーション
Mesoscopic Reactive Dynamics Simulation of FtsZ Polymerization Dynamics on the order of 10 minutes

Yoshiki Bessho, Shoji Takada (*Grad. Sch. Sci., Kyoto Univ.*)

The bacterial tubulin homolog protein, FtsZ, is thought to contribute to determining bacterial division sites and generating contractile forces by polymerization and depolymerization. To investigate cell division, an event occurring on the order of tens of minutes, studies have been conducted using 2D Monte Carlo simulations and 3D rigid body models, but 3D molecular dynamics simulations have not been performed. To study the dynamics of FtsZ, where the chemical reaction is rate-limiting rather than diffusion, we develop models for reactive molecular dynamics simulations at the biological timescale by combining reactions and diffusion, and compare the simulation results with existing experimental data.

2Pos171 全ての側鎖の動きを含めた AI を用いたタンパク質の構造変化モーフィング手法の開発: MOVE-DM 3.0
Development of a Protein Structural Change Morphing method with All Side-Chain Consideration using an AI-based approach: MOVE-DM 3.0

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Large structural changes in proteins such as enzymes are crucial for their functions. Morphing methods have been very useful and one of the simplest methods to elucidate structural changes between two states. However, many commonly used linear morphing methods are difficult to reproduce the order of domain movements. Furthermore, conventional methods could not reproduce side-chain movements in the protein. We previously developed a nonlinear morphing method for protein main chain structural changes using molecular dynamics (MD) simulations and AI, and improved its accuracy by refining the AI (MOVE-DM 2.5). In this study, we developed a nonlinear morphing method for protein structural changes with side-chain movements using AI and MD simulations (MOVE-DM 3.0).

2Pos172 Aβ 凝集における相互作用ダイナミクスの解明: Aβ40/Aβ42 各種会合状態の比較
Unraveling the Role of Interaction Dynamics in Aβ Aggregation: A Comparative Study of Aβ40/Aβ42 Monomers, Homodimers, and Heterodimers

Ayumu Koike, Norifumi Yamamoto (*ChibaTech*)

Aβ42 aggregation is key in Alzheimer's. We studied Aβ40-Aβ42 heterodimer aggregation using MD, compared to Aβ40/Aβ42 monomers and homodimers. Aβ40-Aβ42 heterodimer, despite β-sheet propensity, showed poor intermolecular β-sheet network formation needed for stable aggregates. PCA showed Aβ40-Aβ42 had frequent transient contacts, limited β-sheet evolution. Aβ40 systems (monomer/homodimer) had more β-sheet but fewer persistent interactions; Aβ42 systems (monomer/homodimer) efficiently built stable contacts and β-sheet rich aggregates. Interaction persistence and stability, not count/transience, are critical for Aβ amyloidogenesis. This yields insights on Aβ isoform interplay and structural basis of Aβ42 pro-aggregation vs. Aβ40 attenuation.

2Pos173 pH一定の分子動力学シミュレーション由来のトラジェクトータに基づく結合自由エネルギー計算：FabI 酵素での検証
Binding free energy calculation based on constant-pH molecular dynamics simulation-derived trajectory: application to FabI enzyme

Shin-ichi Fujiwara (*Fac. Med., Tottori Univ.*)

Binding free energy is crucial for understanding protein-ligand interactions. For more accurate binding free energy calculations, we introduced the constant-pH molecular dynamics (CpHMD) simulations, in which protonation states of amino acid side chains can be changed during the simulations. Binding between enoyl-ACP reductase (FabI) and 16 compounds was investigated, in which experimental binding affinity was measured at pH 8.0. When the CpHMD simulation-derived trajectory data were used, the experimental and calculated binding free energies showed a higher correlation than those in the conventional MD simulations, in which protonation states of amino acid side chains are fixed during the simulations. More detailed results will be discussed in the presentation.

2Pos174 分子シミュレーションを用いた PET トレーサー PBB3 と TMEM 繊維の結合と安定性
Binding and Stability of PET Tracer PBB3 with TMEM Fibrils using molecular simulations

Nanami Matsumoto¹, Yoshitaka Tadokoro¹, Naoyuki Miyashita^{1,2} (¹*Grad. Sch. of BOST, KINDAI Univ.*, ²*BOST, KINDAI Univ.*)

Amyloids of Transmembrane protein (TMEM) 106B (TMEM fibrils) are commonly observed in patients with various neurodegenerative diseases, such as Alzheimer's disease and Parkinson's disease. TMEM106B is a protein associated with neurodegenerative diseases and may serve as a potential target for PET radiopharmaceutical development. TMEM106B is a transmembrane protein located on the lysosomal membrane, and a portion of it is known to form TMEM fibrils within lysosomes. Currently, these TMEM fibrils are considered an important target protein for understanding the progression of neurodegenerative diseases. In this study, to elucidate the detailed binding mechanism of PBB3 to TMEM106B fibrils, we performed docking simulations and molecular dynamics simulations.

2Pos175 Markov state Model に基づいた環状ペプチド膜透過過程の多次元の反応座標における速度論的な解析
Kinetic analysis of membrane permeation processes of cyclic peptides on multiple reaction coordinates based on the Markov state model

Masatake Sugita^{1,2}, Kei Terakura¹, Takuya Fujie^{1,2}, Keisuke Yanagisawa^{1,2}, Yutaka Akiyama^{1,2} (¹*Sch. Computing, Science Tokyo*, ²*MIDL, Science Tokyo*)

We have developed methods based on extended ensemble molecular dynamics to simulate the membrane permeation process of cyclic peptides and to predict membrane permeation coefficients. However, previous studies have analyzed the membrane permeation process based only on one-dimensional reaction coordinates in the direction across the membrane, making it difficult to clarify the relationship between changes in peptide conformation and orientation with respect to the membrane and membrane permeability. In this study, the membrane permeation process of cyclic peptides was projected onto multidimensional reaction coordinates and analyzed based on the Markov state model (MSM) to determine what kind of motion could be the rate-limiting factor for membrane permeation.

2Pos176 Molecular dynamics simulations of peptide aggregation properties

Joe Mori^{1,2,3}, Satoru G Itoh^{1,2,3}, Hisashi Okumura^{1,2,3} (¹*SOKENDAI*, ²*IMS*, ³*ExCELLS*)

Protein aggregation, including the formation of amyloid fibrils, can abolish native protein function and is implicated in severe disorders such as Alzheimer's disease. However, many aspects of aggregation kinetics, mechanisms, and the molecular pathways leading to amyloid fibril formation remain poorly understood. To address these gaps, we employ molecular dynamics simulations, which allow direct observation of dynamic structural changes at atomic resolution, to investigate the aggregation behavior of peptides. In this presentation, we will report the results obtained from these simulations.

2Pos177 Implementation of Modeling Employing Limited Data in GENESIS

Azuki Mizutani¹, Alberto Perez², Yuji Sugita^{1,3} (¹Riken, ²Dept. of Chem., Univ. Florida, ³Riken, R-CCS)

Integrating experimental data with molecular dynamics (MD) simulations helps overcome force field and sampling limitations, providing guiding power and enhancing the realism of the simulations. However, incorporating experimental data can be challenging because of inherent noise or incomplete information.

In this study, we used “Modeling Employing Limited Data (MELD),” a structured sampling method developed by Perez et al. This method utilizes Bayesian inference to select constraint conditions generated from experimental data based on energy, facilitating highly accurate sampling from noisy data. We introduced this method to GENESIS for application in multiscale models. Additionally, this method can be applied to predicting the structure of protein-DNA complexes.

2Pos178 メチル化ヒストン断片と LEDGF の結合安定性に関する分子動力学シミュレーション
Molecular dynamics simulations of the binding stability of methylated histone fragments to LEDGF

Hinako X. Suzuki⁴, Hisashi Okumura^{2,3,4}, Satoru Itoh^{1,2,3} (¹IMS, ²ExCELLS, ³SOKENDAI, ⁴Dept. Sci., Shinshu Univ.)

Lens epithelium-derived growth factor (LEDGF) is a chromatin-binding protein involved in gene transcription. It plays a mediating role in the interaction between various proteins and chromatin. The chromatin-binding region of LEDGF is the PWWP domain, which is known to specifically recognize histone H3 when lysine 36 (H3K36) is dimethylated or trimethylated.

To elucidate details of this methylation-dependent binding affinity, we performed molecular dynamics simulations of the PWWP domain with histone fragments. Our results indicate that both hydrophobic and electrostatic interactions play essential roles in the binding between the PWWP domain and H3K36. Furthermore, we found that water molecules also contribute to the binding.

2Pos179 Atomic-Level Analysis of pH-Dependent Switchable Binding in Ipilimumab-CTLA-4 Complex for Designing Therapeutic Antibodies

Wanda Destiarani^{1,2}, Kowit Hengphasatporn², Yasuteru Shigeta², Ryuhei Harada² (¹Grad. Sch. Sci. Tech., Univ. Tsukuba, ²CCS, Univ. Tsukuba)

Therapeutic antibodies face challenges like on-target/off-tumor toxicity, causing cardiotoxicity and inflammation. To address this, switchable antibodies that activate only in cancerous cells are needed. Ipilimumab variants (Ipi95, Ipi105, Ipi106) with charged amino acid mutations in their CDRs showed improved binding to CTLA-4 in acidic conditions. We performed molecular dynamics simulations on these variants under neutral and acidic conditions to study their pH dependency. Alanine scanning identified key residues involved in binding. Our computational results, radius of gyration, number of contacts, and binding affinity show a positive correlation with experimental data ($R^2=0.7818$), highlighting the potential of designing pH-dependent therapeutic antibodies.

2Pos180 タンパク質の形状を考慮した粗視化モデル分子動力学シミュレーションを用いた ECMO 中空糸膜モデル中の血漿と酸素・二酸化炭素の浸透機構
Permeation Mechanism of Plasma, O₂ and CO₂ in ECMO Hollow Fiber Membrane model Using CG MD Simulation Considering Protein Shape

Ryota Shibasaki¹, Makoto Hukuda^{1,2}, Naoyuki Miyashita^{1,2} (¹Grad. Sch. BOST, KINDAI Univ., ²BOST KINDAI Univ.)

Extracorporeal membrane oxygenator (ECMO) is used for the treatment of severe respiratory failure, substituting the role of the lung by exchanging carbon dioxide(CO₂) and oxygen(O₂) in the blood through a hollow fiber membrane (HFM). Since this treatment often lasts 6h or more, plasma leakage from the HFM has become an issue during ECMO support. Therefore, improving the durability of ECMO to prevent such failures is an urgent issue. In this study, we performed Coarse-Grained Molecular Dynamics(CG MD) simulations for the HFM made from polypropylene and polymethylpentene which are representative materials of ECMO. The transport mechanisms for O₂, CO₂ and plasma are investigated by using the CG MD Simulation that takes into account the shapes of the albumin molecule.

2Pos181

N 結合型糖鎖修飾による Neuropsin (KLK8) の触媒活性の調節機構
Modulation of enzymatic activity in Neuropsin (KLK8) by N-glycosylation

Mai Fujiwara¹, Masami Lintuluoto¹, Yoshifumi Fukunishi², Hideki Tamura³, Juha Lintuluoto⁴ (¹Grad. Sch. Life and Env. Sci., Univ. Kyoto Pref, ²CMB, AIST., ³Lab. Biofunc. Sci., Univ. Hoshi Sch. of Pharm. Sci., ⁴Grad. Sch. Eng., Univ. Kyoto)

Kallikrein 8 (KLK8, also known as Neuropsin) is an extracellular serine protease involved in the modulation of synaptic plasticity. KLK8 selectively hydrolyzes neuropeptide precursors into their active forms during signal transduction. This function is believed to be regulated by post-translational modifications such as glycosylation, as well as by metal ions like calcium and zinc. Our previous studies demonstrated that the optimal formation of the catalytic triad is a key factor for KLK8 activity, and that molecular dynamics (MD) simulations can predict substrate reactivity. In this study, we investigated the effects of different glycan patterns -including bisecting GlcNAc and sialylated structures- on the catalytic activity of KLK8 using MD simulations.

2Pos182

Theoretical study of competitively ligands binding to AMP-activated protein kinase

Taiga Murakami, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Natu. Sci. Tech., Univ. Kanazawa*)

AMP-activated protein kinase (AMPK) acts as an energy sensor that monitors intracellular ADP/ATP and AMP/ATP ratios. When ADP or AMP increases, ATP bound to AMPK is replaced by ADP (or AMP) and AMPK is activated and promotes the ATP production pathway. The purpose of this study is to qualitatively examine the competitive binding of ATP and ADP to inactivated AMPK. The tendency of excessive self-aggregation of ATP that had occurred in previous studies was improved by adjusting the charge. For MD simulations, we will use systems containing water, the AMPK, ATP, and ADP (ATP/ADP ratios are 30/70, 50/50, and 90/10). The relationship between the ATP/ADP ratio and the binding affinity of the two ligands will be presented at the conference based on the simulation results.

2Pos183

分子シミュレーションを用いた p53N 末端天然変性領域の結合におけるリン酸化と結合相手の影響
Investigating Binding Modes of p53 N-terminal IDR by dPaCS-MD: Impact of Phosphorylation and Partners

Yoshito Hasegawa, Duy Phuoc Tran, Akio Kitao (*Life Science and Technology, Science Tokyo Univ.*)

The intrinsically disordered N-terminal region of p53 protein controls its binding through specific phosphorylation sites and partner selection. This region typically forms an α -helix upon binding to other proteins, but it takes an extended shape when it is doubly phosphorylated and binds to the p62 PH domain. To understand the differences in binding, we constructed four protein complex models as combinations of phosphorylated or non-phosphorylated p53 bound to either p62 PH or its TFB1 counterpart, and performed dissociation parallel cascade selection molecular dynamics (dPaCS-MD). The results show how phosphorylation and different partners affect binding modes and strength, providing insight into the design of anticancer drugs that target p53.

2Pos184

KaiC におけるリン酸化状態変化により誘起されるアロステリック応答の全原子分子動力学解析
All-atom molecular dynamics analysis of allosteric response in KaiC induced by phosphorylation state change

Riki Ueno¹, Yudai Terui¹, Koki Adachi¹, Toshifumi Mori², Shuji Akiyama^{3,4}, Mistunori Takano¹ (¹Grad. Sch. Adv. Sci. Eng., Waseda Univ., ²Inst. Mat. Chem. Eng., Kyushu Univ., ³CIMos, IMS, NINS, ⁴SOKENDAI)

KaiC is a cyanobacterial circadian clock protein, exhibiting a phosphorylation cycle coupled with ATP hydrolysis. Recent crystal structures indicated that the phosphorylation site in the CII domain and the ATPase site in CI domain are allosterically linked, and the phosphorylation and dephosphorylation of S431 play the essential role in the allostery. To elucidate the physical mechanism of the allostery, we conducted long (25- μ s) all-atom molecular dynamics simulations of KaiC and investigated how KaiC responds to the phosphorylation state change at S431. We show that the net-charge change accompanying the phosphorylation state change at S431 induces a rearrangement of the hydrogen bond network and affects the hydration state in the ATPase site.

2Pos185 フラグメント分子動力学を用いたニューロセリン新規阻害剤の研究開発
Development of Novel Inhibitors for Neuroserpin Using Fragment Molecular Dynamics

Nanase Sakashita¹, Hiroto Terada¹, Daiki Akai¹, Bunzo Mikami^{2,3}, Maki Onda¹, Kei Moritsugu¹ (¹*Grad. Sch. Sci. OMU*, ²*RISH Kyoto Univ.*, ³*IAE Kyoto Univ.*)

Neuroserpin, a serine protease inhibitor predominantly expressed in the cerebrum, has been implicated in neurodegenerative diseases such as Alzheimer's disease. In this study, we aimed to develop a computational approach for inhibitor discovery targeting a newly identified binding pocket that were revealed by recent crystallographic analysis. We first applied a method that combines fragment molecular dynamics using small molecular fragments with diverse chemical properties and an enhanced ensemble technique to efficiently explore hidden crypt sites. Furthermore, we attempted to investigate an approach to develop lead compounds based on the calculated binding affinity results of the fragments.

2Pos186 部位選択的 Gaussian accelerated Molecular Dynamics の開発
Development of site-selective Gaussian accelerated Molecular Dynamics

Hiraku Oshima (*Grad. Sch. Sci., Univ. Hyogo*)

The Gaussian accelerated Molecular Dynamics (GaMD) method accelerates changes in molecular structure by biasing dihedral potentials of the molecule. However, even if we want to accelerate the motion of only a local portion, it is necessary to bias the entire structure. In this study, we developed a site-selective GaMD method (ssGaMD) that can selectively accelerate a part of a molecule. The ssGaMD method accelerates molecular motion by selecting a region of interest and biasing only the potential energy associated with that region. We applied it to the binding of β -Cyclodextrin (CD) to aspirin. In normal MD, aspirin and CD rarely dissociate once bound, but we improved the binding/dissociation frequency by biasing only the CD-aspirin interaction with the ssGaMD method.

2Pos187 gREST-ABMD 法によるマルチスケールな自由エネルギー地形探索
New enhanced conformational sampling method for multi-scale molecular dynamics simulations

Shingo Ito¹, Hiraku Oshima², Yuji Sugita^{1,3} (¹*RIKEN Center for Computational Science*, ²*Graduate School of Life Science, University of Hyogo*, ³*Cluster for Pioneering Research, RIKEN*)

Due to high computational costs, conventional multidimensional enhanced conformational sampling methods, such as gREST/REUS, make it challenging to perform long-time MD simulations. Here, we developed a new enchanted conformational sampling method, named gREST-ABMD, which integrates generalized replica-exchange with solute tempering (gREST) with the adaptively biased molecular dynamics (ABMD) method. Using the time-dependent biasing potentials with the parallel tempering, our method achieved low-cost and highly accurate free energy calculation in multi-scale MD simulations, including coarse-grained (CG), all-atom (AA), and QM/MM models. We show the performance of free energy calculations of three different systems in the CG, AA, and QM/MM models.

2Pos188 Predicting structural and functional properties of albumins from pets and economic animals by molecular modeling and machine learning

Darunee Traiphophon (*Grad. Sch. Sci., Univ. Kasetsart*)

Serum albumin (SA) is the most abundant plasma protein and shows structural similarities across species. Human serum albumin (HSA) functions as a transport protein and serves as a clinical biomarker. In addition, animal serum albumins have been identified as cross-reactivity allergens, which are particularly relevant in allergology and immunology. Albumin structures and functions affect allergies. Thus, in this work, molecular dynamics (MD) simulations were performed to explore the structural and dynamic properties of pet and economic animals. Furthermore, the machine-learning (ML) method will be used to predict the albumin properties of species with unknown structure and function. This approach aids understanding of albumin functions and supports allergy screening.

2Pos189

シミュレーションによる細菌べん毛周辺の正電荷分布の動態解析

Analysis of the Dynamics of Charged Particle Distributions near a Bacterial Flagellum

Suguru Ushioda, Masashi Tachikawa (*Grad. Sch. Nanobio., Yokohama City Univ.*)

Recent studies revealed that (i)bacterial flagella are negatively charged, and (ii)efficiency of bacterial motion increases in high viscous fluid. Here, we hypothesize that the charged flagella increase the viscosity of the surrounding fluid through electrostatic interactions with positive charges to enhance motility. We modeled the rotating flagellum as a negative charge undergoing circular motion. We developed a 2D model in which the distribution of positive charges is determined by the balance between Coulomb interactions and thermal diffusion. We revealed that the positive charges distribution is changed by **the angular velocity of negative charge**. We also discuss the impact of flagellar electrostatic properties on bacterial motility.

2Pos190

Cryo-EM and MDSPACE Reveal Continuous Conformational Heterogeneity in Glutamate Dehydrogenase

Tingting Wang¹, Osamu Miyashita¹, Hideki Shigematsu², Masaki Yamamoto³, Florence Tama^{1,4} (¹*R-CCS, RIKEN, JASRI, SPring-8*, ³*RIKEN SPring-8 Center*, ⁴*Department of Physics and ITbM, Nagoya Univ.*)

The continuous conformational heterogeneity of the GDH hexamer was studied by a hybrid method combining cryo-EM single-particle analysis with biased MD simulations. We applied the MDSPACE method (Vuillemot et al., *JMB* 2023) to large-scale particle image datasets. RELION analysis was performed for selection of high-quality single-particle images and accurate pose estimations. MDSPACE, implemented in GENESIS, was used for flexible fitting to reconstruct unique conformational states embedded in each image. Ensemble-level analysis revealed the underlying structural variability.

2Pos191

A tension gradient in a nonconserved cell membrane generates a divergent pattern of cell shape and motility

Valentina Tyukosova¹, Satoru Okuda² (¹*Kanazawa University, Division of Nano Life Science*, ²*Kanazawa University, Nano Life Science Institute*)

Cells exhibit various shapes and motions, mainly governed by cell membrane dynamics. During these behaviors, cells actively distribute tension along the membrane, while its components are dynamically remodeled. However, little is known about how such tension distributions in non-conserved membranes regulate cell shape and motion. We performed numerical simulations of non-conserved cell membranes under a tension gradient. The results demonstrate a variety of cell shapes and motions arising from interplay between the strength of the tension gradient, environmental friction, and membrane viscosity—features not observed in conserved membrane dynamics. These findings highlight the impact of active and dynamic properties of cell membranes on regulation of cellular behavior.

2Pos192

「細胞死」の理論

Theoretical Basis for Cell Death

Yusuke Himeoka¹, Shuhei A. Horiguchi^{2,3}, Tetsuya J. Kobayashi^{1,3} (¹*Universal Biology Institute, The University of Tokyo*, ²*Nano Life Science Institute, Kanazawa University*, ³*Institute of Industrial Science, The University of Tokyo*)

Understanding deaths and life-death boundaries of cells is a fundamental challenge in biological sciences. Here, we present a theoretical framework for investigating cell death. We conceptualize cell death as a controllability problem within dynamical systems, and developed an efficient method to compute the controllability of cellular metabolic states. By applying the method to the kinetic model of *E. coli* central carbon metabolism, we successfully revealed the life-death boundary that we term "SANZ hypersurface". The formulation of cell death through mathematical principles provides a foundation for the theoretical study of cellular mortality.

2Pos193

物理と生物の統一理論；公平な増幅と崩壊による自律的最適化

A Unified Theory of Biology and Physics; Self-Optimization by Martingale Turnover with Amplification

Tomoyuki Yamaguchi (*Research Institute, Nozaki Tokushukai Hospital*)

Adaptation mechanism in living systems remains unclear. Here, I show that the number of cells of two types converges to target ratio by repeating the processes of increase and decrease in stochastic simulation and analyze this process using stochastic differential equations. Even if each cell, regardless of its type, had the same probability of division or death, cell ratio approached a ratio where decay rate was low. This process was described by a modified Langevin equation, in which the mass is a variable. The process was a type of random walk with smaller step size in better states, and the derived probability density function was well fitted to the distribution of cell ratios in the stochastic simulation. Thus, we mathematically formalized the principle of livings.

2Pos194

脱分化の力学系モデリング

Dynamical Systems Modeling of Dedifferentiation

Kansuke Sasamori¹, Yusuke Himeoka¹, Chikara Furusawa^{1,2} (¹*Sch. Sci., Univ. Tokyo*, ²*BDR, Riken*)

There is a principle of irreversibility in multicellular development: cell differentiation potential declines as development proceeds [1]. On the other hand, dedifferentiation, which breaks this irreversibility, occurs, for instance, in plant callus tissue [2] and lens regeneration in newts [3], and its likelihood varies among species. No general principle currently explains this diversity. Here, we compare the dedifferentiation potential across species by modeling the process in a dynamical systems view. We also examine how gene-regulatory-network structure and cell-cell interactions shape dedifferentiation potential.

[1] Wolpert (2015). [2] Steward et al., *Dev.* (1975). [3] Madhavan et al., *PNAS* (2006).

2Pos195

空間変化を伴う反応拡散系

Reaction-diffusion system with spatial deformation

Naoto Yonekura, Shinji Deguchi (*Grad. Sch. Eng. Sci., Univ. Osaka*)

A reaction-diffusion system describes how the concentration of one or more substances changes over space and time due to two processes: local chemical reactions and diffusion. While reactions create or consume substances, diffusion spreads them through space. These systems are known for producing complex patterns, such as stripes or spots, in biological and chemical contexts. Conventional reaction-diffusion models do not take into account spatial deformation, an important mechanical factor, even though biological structures are constantly subjected to deformation and stretching in space. To apply reaction-diffusion systems to biological structures, we will develop a new theoretical framework that incorporates spatial deformation into the reaction-diffusion model.

2Pos196

Changes of microbial interactions among core members are one of major driving force to induce community succession

Reika Mimoto¹, Takashi Okada², Yasuhisa Saito³, Hiroyuki Futamata^{1,4,5} (¹*Grad. Sch. Integr. Sci. Tech., Shizuoka Univ.*, ²*Inst. Med. Biol. Kyoto Univ.*, ³*Grad. Sch. Sci. Eng. Shimane Univ.*, ⁴*Grad. Sch. Sci. Tech. Shizuoka Univ.*, ⁵*Res. Inst. Green Sci. Tech., Shizuoka Univ.*)

Soil microbiota was enriched with chemostat culture using phenol as sole carbon and energy source because it is important to manage functional homeostasis. Amplicon sequence analysis targeting 16S rRNA genes showed that the community structure became different equilibrium states via succession. Mathematical model based on real data succeeded to predict not only the two major equilibrium states but also others, suggested that microbiota is capable of assembling different communities. Spearman analyses indicated that microbial interactions among core members consisted of major and minor populations changed dynamically. These results suggested that the dynamic changes of interactions among core members is one of major driving force to induce community succession.

2Pos197 Effects of combined period-modulating mutations on circadian rhythm in a cyanobacterial clock protein system

Eri Hiraiwa, Yuji Nishimura, Kosuke Maki (*Grad. Sch. Sci., Univ. Nagoya*)

Cyanobacterial three clock proteins, i.e., KaiA, KaiB, and KaiC, exhibit circadian rhythms in the presence of ATP even in vitro. The circadian rhythms are observed in several aspects including the ATPase activity and the phosphorylation state of KaiC, which has two phosphorylation sites. Our previous study showed that a variant with a single phosphorylation site exhibited oscillation with approximately half a day period at appropriate concentrations of KaiA and KaiB. In addition, several short-period KaiC variants, with modulation in their ATPase activities, have been reported. In this study, we introduced an amino acid replacement associated with short-period ATPase activity into a single phosphorylation-site variant. We will present the results in the presentation.

2Pos198 Polydiacetylene biosensor detecting different binding affinities

Niklas Urs Brenner, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo*)

Polydiacetylene is a mechanochromic polymer that detects forces by twisting its conjugated backbone and changes its color or emits fluorescence. Various biosensors have been demonstrated for detecting temperature, ions, biomolecules etc. using this blue-to-red transition of polydiacetylene.

In this work, we tried to detect differences in binding affinities of two biomolecules, streptavidin and traptavidin. They possess a ten-fold difference in binding affinity towards biotin. Binding affinities can play a crucial role in medical conditions, for example, in heparin-induced thrombocytopenia, where the binding of an antibody can lead to a severe condition. Therefore, it is important to develop a quick and cheap method that can detect affinity differences.

2Pos199 Selective IR measurement of only the chromophore part in fluorescent proteins by resonance IR method

Konoka Mifune¹, Hirona Takahashi^{1,2}, Minori Yamakawa¹, Makoto Sakai^{1,2} (¹*Graduate school of Science and Engineering, Okayama University of Science*, ²*Faculty of Science, Okayama University of Science*)

It is known that absorb or emit wavelengths of fluorescent proteins vary with the structure of the chromophore and interaction with the amino acids around the chromophores. In this study we applied the resonance IR spectroscopy to fluorescent proteins (turboGFP, phiYFP, eCFP and so on). The obtained resonance IR spectra were compared, and the characteristics of the resonance IR spectra of turboGFP and phiYFP, which have the same chromophore but different fluorescence wavelengths, are quite different. This result may be due to differences in the local structure of chromophores affected by surrounding proteins. In the presentation, the interaction between chromophores and proteins will also be discussed based on the results of vibrational relaxation measurements.

2Pos200 Direct observation of single integrin-mediated forces on soft substrates using a DNA-based force sensor

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Cells sense mechanical forces via integrin–ECM, affecting biological states including cell behavior and fate. However, quantifying them remains technically difficult. Biologically relevant measurements require soft and tunable substrates, as cellular forces depend on substrate stiffness. Traction force microscopy is widely used to estimate cellular forces on such substrates, but estimates forces from substrate deformation, requiring complex analysis and limiting accuracy. Recently developed DNA-based force sensors enable direct force measurements via fluorescence changes, but background noise hinders detection on soft substrates. We developed a system reducing background for direct force measurement on soft substrates. This poster presents our method and applications.

2Pos201 低温ラマン光学活性分光装置の開発及び光受容タンパク質への応用
Development of low-temperature Raman optical activity spectrometer and its application to photoreceptor proteins

Naoya Sasaki, Tomotsumi Fujisawa, Masashi Unno (*Fac. Sci. Eng., Saga Univ.*)

In various chemical reactions that occur in proteins, molecules react by changing their structures in three dimensional manner. Raman optical activity (ROA) spectroscopy has a unique capability to accurately observe the conformational changes of such molecules. In this study, we developed a spectrometer that combines ROA spectroscopy and low temperature trapping. The application of this cryo-ROA spectrometer to photointermediates of biological photoreceptors and the current challenges are presented.

2Pos202 Analysis of *Alcanivorax borkumensis* biofilm on binary oil mixtures

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Spilled oil poses a serious threat to marine environments. Bacteria such as *Alcanivorax borkumensis* (*Alca*) aid in oil degradation by forming biofilms on the oil–water interface. Although *Alca* biofilms are known to degrade oil, prior studies focused on single-component oils, leaving *Alca*'s response to complex crude oil unclear.

To investigate this, we examined biofilm formation on drops containing both degradable and non-degradable components (binary oil mixtures with varying ratios). We find that the oil composition plays an important role in biofilm behavior, suggesting interfacial tension may be a key factor. Using a capillary-based microfluidic device, we measure the *in situ* active interfacial tension of *Alca* biofilms.

2Pos203 光ファイバ型蛍光相関分光法によるヒト血清中の細胞外小胞の定量計測
Measurement of extracellular vesicles in human serum using fiber-optic fluorescent correlation spectroscopy

Johtaro Yamamoto (*Health & Med. Res. Inst., AIST*)

Extracellular vesicles (EVs) are nanoscale particles secreted by cells. EVs can be isolated from various bodily fluids such as blood, saliva, and urine. These vesicles carry molecular components including proteins and nucleic acids that reflect the characteristics of their parent cells. EVs released by cancer cells often contain cancer-specific proteins, and thus, quantitative analysis of EVs obtained from body fluids has the potential to enable non-invasive cancer diagnosis by assessing the proportion of EVs derived from cancer cells.

In this poster, we present results of a Fiber-optic Based Fluorescence Correlation Spectroscopy (FB-FCS) measurement of EVs in human serum, demonstrating its potential utility in EV analysis.

2Pos204 ソリッドステートナノポアによる tRNA の柔軟性の評価
Flexibility Evaluation of tRNA by Solid State Nanopore

Gaku Ogino¹, Kazuki Nagashima¹, Hikaru Nozawa¹, Artem Lysenko¹, Tatsuhiko Tsunoda¹, Tsutomu Suzuki², Sotaro Uemura¹ (¹*Graduate School of Science, The University of Tokyo*, ²*Graduate School of Engineering, The University of Tokyo*)

Post-transcriptional modification, Mg²⁺, spermidine and pentamidine, are known to influence the structural stability of tRNA *in vivo*. The flexibility of tRNA is essential for molecular recognition during translation on the ribosome. In this study, we investigated the effects of modifications, MgCl₂ and poly amines on tRNA flexibility by measuring tRNA translocation signals through a nanopore. Nanopore technology enables direct single-molecule analysis by detecting ionic current blockades as molecules pass through nanometer-scale pores. Our data showed that translocation times through the nanopore varied in response to modification or ligands such as spermidine and pentamidine indicating that these factors affect the conformational flexibility of tRNA.

2Pos205 Contactless Stiffness Measurement of Biomolecular Condensates through Acoustic Trapping**Kichitaro Nakajima**, Hirotosugu Ogi (*Graduate School of Engineering, Osaka University*)

Biomolecular condensates formed through liquid-liquid phase separation are associated with cellular biological functions and the onset of diseases. Their material properties are likely related to their roles in the cellular environment. Thus, it is important to measure their material properties at single-particle resolution. However, this remains challenging. In this study, we propose a framework to measure the stiffness of biomolecular condensates at single-particle resolution by utilizing acoustic trapping. We develop an acoustofluidic device that allows us to trap condensates in a microscale space. We analyze the Brownian motion of trapped condensates to extract bulk moduli of biomolecular condensates in a contactless manner.

2Pos206 癌の生体ナノイメージングを指向した遠赤色発光性白金ナノクラスターバイオナノプローブの開発
Far red-emitting Pt nanoclusters based bio-nanoprobes for *in vivo* tumor-targeted imaging**Shin-ichi Tanaka**^{1,2}, Hiroki Wadati^{3,4}, Kazuhisa Sato^{5,6} (¹*National Institute of Technology (KOSEN), Kure College*, ²*NHO Kure Medical Center and Chugoku Cancer Center*, ³*Department of Material Science, Graduate School of Science, University of Hyogo*, ⁴*Institute of Laser Engineering, Osaka University*, ⁵*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*, ⁶*Division of Materials and Manufacturing Science, Graduate School of Engineering, Osaka University*)

Biomedical imaging has become an indispensable tool in the fields of cancer diagnosis and therapy. Fluorescent Pt nanoclusters (NCs) are promising nanomaterials for biomedical applications, because Pt NCs exhibit the excellent optical property and possess ultrasmall size (0.8 ± 0.2 nm in diameter), highly photostability and biocompatibility. Herein, we report the biomedical application of far red-emitting (Em/Ex=680/580 nm) Pt NCs based bio-nanoprobes (Pt nanoprobes) and demonstrate that the Pt nanoprobes acts as a *in vivo* magnifier for precise fluorescent imaging of expressed marker protein (Protease-activated receptors 1 (PAR1)) at metastatic breast cancer. Our Pt nanoprobes have successfully been accumulated in tumor tissues and have specifically detected the PAR1.

2Pos207 ルーピング期心臓形成にエタノールが与える影響の SS-OCT 観測
Swept-source OCT analysis of ethanol effects on embryonic heart looping**Aimi Yamashita**, Taiyo Eguchi, Rikuto Noguchi, Ryuichiro Yamazaki, Yuuta Moriyama, Toshiyuki Mitsui (*Dept. Phys. Sch. Sci., Aoyamagakuin Univ.*)

Alcohol intake during pregnancy is a known environmental risk for congenital heart defects, yet the underlying mechanisms remain unclear due to difficulties in continuous embryonic observation.

Here, we combined shell-less chick embryo culture with swept-source OCT to noninvasively track cardiac development under ethanol exposure.

OCT images revealed characteristic changes in heart rate and wall motion, including loss of contraction synchrony and reversed pulsation between ventricle and outflow tract. Structural changes such as outflow tract narrowing and endocardial cushion reduction were also observed. In addition, we discuss on cardiac morphology based on 3D reconstructions obtained by machine learning-based segmentation of the heart.

2Pos208 Recent Updates to Post-acquisition Super Resolution for Cryo-electron Microscopy**Ray Burton-Smith**, Kazuyoshi Murata (*National Institute of Physiological Sciences*)

Since the introduction of super resolution acquisition for cryo-EM, it has been used to improve the clarity of cryo-EM reconstructions. Recent reports have demonstrated achieving resolutions beyond the physical Nyquist limit using super resolution data acquisition. This shows the power of modern direct electron detectors, but the data was still acquired with super resolution acquisition enabled. Here, we demonstrate exceeding this limitation by pre-processing the raw micrograph movies from counting mode data which reached physical Nyquist. It is possible to exceed the physical Nyquist limit with what we call “post-acquisition super resolution”, or PASR; it can also be applied to data acquired with super resolution to push resolution further still.

2Pos209 生体分子機能の増強に向けた分子局所加温技術の開発
Development of Molecular Heating Technology toward the Enhancement of Biomolecular Functions

Yuya Matsuda¹, Kayoko Nomura², Cong Quang Vu², Takeru Yamazaki², Satoshi Arai^{1,2} (¹*Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

Biomolecular reactivity increases with temperature, typically doubling every 10 °C as described by the Arrhenius equation. However, since cellular damage occurs above 42 °C, the available temperature range for activating reactivity is quite limited. Here, we propose a method for directly heating individual biomolecule. In this approach, photothermal dye is covalently bound to a target protein via the HaloTag, enabling the delivery of heat generated by near-infrared (NIR) illumination. To test the concept, we used a photothermal dye-labeled fluorescent protein and examined how heat influences its fluorescence in a temperature-dependent manner. This local heating has the potential to enable precise control of cellular functions through thermal manipulation.

2Pos210 Ensemble of Deep Neural Network Models for Drug Screening Using 3D Images of *Drosophila* Larvae

Md Al Mehedi Hasan¹, Jean-Emmanuel Clement², Walker Peterson³, Tsubasa Kobayashi³, Soichiro Hata⁴, Takuya Otsuka⁴, Koji Tabata^{1,2}, Masahiro Sonoshita⁴, Keisuke Goda^{3,5}, Tamiki Komatsuzaki^{1,2} (¹*Research Institute for Electronic Science, Hokkaido University, Sapporo, Japan*, ²*Institute for Chemical Reaction Design and Discovery, Hokkaido University, Sapporo, Japan*, ³*Department of Chemistry, Graduate School of Science, The University of Tokyo, Tokyo, Japan*, ⁴*Institute for Genetic Medicine, Hokkaido University, Sapporo, Japan*, ⁵*Department of Bioengineering, University of California, Los Angeles, California 90095, USA*)

Drosophila serves as a powerful model to study cancers and plays a significant role in advancing drug screening efforts due to its genetic and molecular similarities with humans. Determining drug efficacy by monitoring drug-induced cellular changes is the primary concern in the drug screening process. Manual dissection based comprehensive screening is labor-intensive, time-consuming and requires specialized skills, which limits both the scalability and accuracy of the process. To address these challenges, we ensemble deep transfer learning-based tumor screening models that utilize 3D fluorescence images of *Drosophila* larvae to enable automated drug screening. Our findings aligned with existing literature and validated the proposed image-driven drug screening strategy.

2Pos211 オプティカル光熱赤外分光法 (O-PTIR) の液-液相分離分析への応用可能性についての考察
Consideration of the applicability of optical photothermal infrared spectroscopy (O-PTIR) to liquid-liquid phase separation analysis

Naoki Baden (*Nihon Thermal Consulting Co.*)

Optical photothermal infrared spectroscopy (O-PTIR) is a new microscopic infrared spectroscopy that can perform infrared analysis with submicron spatial resolution. By utilizing photothermal conversion, O-PTIR can suppress the overlap of absorption by water, which has a large heat capacity, compared to FTIR, and since measurements can be performed without contact, cells in water and liquid samples can also be measured. Taking advantage of these features, we measured the phase separation structure of water/olive oil and cells in water by using O-PTIR reflection mode, and investigated the applicability of O-PTIR to liquid-liquid phase separation (LLPS) analysis.

2Pos212 生物発光による多色同時観察法の開発
A method for simultaneous observation of multiple bioluminescence colors

Mitsuru Hattori¹, Tetsuichi Wazawa¹, Yuki Hiruta², Takeharu Nagai¹ (¹*SANKEN, The University of Osaka*, ²*Faculty of Science and Technology, Keio University*)

Identifying individual cells within a population is a fundamental aspect of cellular observation. Fluorescent labels have limitations in multiple detection simultaneously due to their dependence on excitation light. Bioluminescence offers the potential to overcome these limitations, enabling the simultaneous detection of multiple targets.

In this study, we present a method to expand the color of bioluminescence by introducing dual-receptor bioluminescence resonance energy transfer (BRET). Using this approach, we achieved simultaneous multi-color cell imaging with a color CMOS camera. This method provides a simple and effective means for the simultaneous observation of multiple biological molecules and phenomena.

2Pos213 Development of X-ray fluorescence microscope toward non-destructive nanoscale investigation of phase-separated structures in cell nucleus

Yosuke Tomioka¹, Yukako Oma¹, Masahiko Harata^{1,2}, Yuki Takayama^{1,2} (¹*Graduate School of Agricultural Science, Tohoku University*, ²*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*)

For the functions of the cell nucleus, various non-membranous structures, including chromatin domains, are formed by condensation of macromolecules. X-ray scattering microscopy (XSM) is a promising method for non-destructive, nanoscale investigation of these structures. However, identifying their molecular components is challenging. To address this, we are developing a combined system of XSM and X-ray fluorescence (XRF) microscopy, where specific macromolecules can be visualized using XRF labels. As a first step, we built an XRF microscope with 2 μm resolution at the synchrotron facility NanoTerasu. Using this setup, we visualized chromatin domains in hydrated HeLa cells as a Br-XRF intensity map by staining with Br-DAPI and enclosing them in a custom-built enclosure.

2Pos214 黄金の蝶々型ナノ粒子を用いた液液相分離液滴の生成消滅制御テクノロジー
Regulatory nanotechnology of liquid-liquid phase separated condensates formation/
deformation dynamics by using gold nano-butterflies

Tomohiro Nobeyama¹, Koji Takata³, Tatsuya Murakami³, Yoichi Yamada², Kentaro Shiraki² (¹*Institute for Advanced Study iCeMS, Kyoto University*, ²*Pure and Applied Physics, University of Tsukuba*, ³*Graduate School of Engineering, Toyama Prefectural University*)

Liquid-liquid phase separated (LLPS) droplets are attracting attention as fundamental reaction fields in a living cell. The manipulation of LLPS droplet formation/deformation dynamics has emerged as a target in nanobiotechnology. Herein, we provide butterfly-shaped gold nano-butterflies (GNBs) as the first nanodevices for LLPS droplet dynamics regulation. The concave surface of GNBs interacts with the droplet precursors to facilitate LLPS droplet formation. Near-infrared laser irradiation to the GNBs causes droplets with GNB to disperse. GNBs activated the enzymatic reaction of lysozyme in droplets with weak laser irradiation. The innovative design of GNBs represents a promising strategy for manipulating LLPS dynamics and offers exciting prospects for the future.

2Pos215 発蛍光プローブを用いた入れ替わり可能なタンパク質ラベル化システムの開発
Development of Exchangeable Protein Labeling System Using Fluorogenic Probe

Masafumi Minoshima¹, Shahi Imam Reja², Kohei Iijima¹, Kazuya Kikuchi^{1,2} (¹*Grad. Sch. Eng. The University of Osaka*, ²*IFReC, The University of Osaka*)

Protein labeling is an indispensable tool to investigate protein dynamics inside living cells using fluorescence imaging technology. However, it is still challenging to monitor the dynamics of proteins for a long time because of the photobleaching of fluorophores. Herein, we develop a new protein labeling method that continuously exchanges the fluorophores. This system can maintain apparent labeling state regardless of the photobleaching. The labeling strategy relies on a protein tag that reversibly binds to the chemically designed fluorogenic probes. These probes largely increased the fluorescence intensity upon binding to the protein tag. We demonstrated the exchangeability of the protein labeling system in vitro and in live cells.

2Pos216 CaM-M13 システムを用いたイオンによる生体分子機械の組み立て制御
Controlling the Assembly of Biomolecular Machines by Ions Using the CaM-M13 System

Ziyun Zhang¹, Nobuyuki Nishibe¹, Shinsaku Maruta^{1,2} (¹*Grad. Sch. Sci., Univ. Soka*, ²*Sch. Sci., Univ. Soka*)

We developed a calcium-responsive system to modulate the assembly and activity of the small GTPase Ras by fusing calmodulin (CaM) and the M13 peptide to its N- and C-termini. In the presence of Ca^{2+} , CaM-Ras-CaM and M13-Ras-M13 underwent conformational changes that promoted their association into higher-order complexes, as verified by SEC-HPLC and native PAGE. The fusion of CaM to Ras reduced its intrinsic GTPase activity by 70%, which was subsequently restored upon calcium-induced interaction with M13-Ras-M13. Additionally, kinetic analysis in the presence of GAP and GEF revealed changes in K_d and V_{max} values, confirming the regulatory mechanism. This strategy provides a novel means for dynamic control of protein function via calcium-dependent structural rearrangement.

2Pos217 大気圧プラズマによるマウス筋芽細胞 C2C12 の成長促進

Growth promotion of murine myoblast cells C2C12 by non-thermal atmospheric pressure plasma exposure

Takeru Kobayashi, **Miho Tsuji**, Kumagai Shinya (*Meijo University*)

We used non-thermal atmospheric pressure plasma to control growth of murine myoblast cells C2C12. Briefly, plasma is a 4th state of matter and is a system that consists of positively and negatively charged particles including electrically neutral atomic/molecular species. These particles are thermally agitated and collide with each other generating active species such as radicals, ions/electrons, and photons. These active species can be used to affect cells. After proliferation of C2C12 cells using DMEM (10% FBS), differentiation was induced using DMEM (2% HS). We found that moderate plasma exposure enhanced growth of C2C12 cells but excessive plasma exposure suppressed it. Then, we applied electrical stimulation and observed contractions of differentiated C2C12 cells.

2Pos218 An enzyme discovery approach based on microbial growth in water-in-oil microdroplets

Fumika Hemmi, Kazuma Kouno, Sotaro Uemura, **Ryo Iizuka** (*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

Uncultured environmental microbes are promising sources of novel enzymes. However, more than 99% of these microbes are difficult to culture using conventional techniques, making the discovery of enzymes challenging. To tackle this, we developed an approach using Fluorescent Nucleic Acid Probe, an indicator of microbial growth, to screen microbes capable of assimilating specific substrates within water-in-oil microdroplets. Using agarose as a substrate, we successfully isolated agarolytic bacteria, allowing us to identify genes encoding agarolytic enzymes. We are now extending this approach to screen for enzymes that degrade other polysaccharides, demonstrating the versatility for discovering diverse enzyme genes from previously inaccessible microbial resources.

2Pos219 インクジェットパターン植菌法による大腸菌のコロニー成長の評価

Evaluation of microbial colony growth of *Escherichia coli* inoculated via bioprinting

Mikiko Tsudome^{1,2}, Shigeru Deguchi¹, Yutetsu Kuruma^{1,2} (*¹Jamstec, ²Yokohama City Univ.*)

High-throughput screening of environmental microorganism is crucial for harnessing their potential in novel biotechnological applications, including enzyme and antibiotic production. In this study, we developed a patterned inoculation technique for microbial cells using bioprinting. The newly developed technique enables precise control of inoculation positions with a spatial resolution of a few micrometers, allowing high-density inoculation on agar media. Employing this method, we successfully cultivated one hundred *Escherichia coli* colonies within a 20 × 20 mm agar medium. Furthermore, quantitative analysis of colony size using optical profilometry revealed that colony spacing significantly influences colony growth.

2Pos220 膜のゆらぎを制御した膜面上の相分離

Phase separation on a membrane surface with controlled membrane fluctuations

Naoki Iso¹, Takahiro Sakaue¹, Shunsuke Yamazaki², Tsutomu Hamada² (*¹Department of Physical Sciences, Aoyama Gakuin University, ²School of Materials Science, Japan Advanced Institute of Science and Technology*)

Biological membranes, though composed of lipid bilayers that are only a few nanometres thick, exhibit properties essential for cellular functions. In membranes containing multiple lipid species, lateral organization and domain formation arise and phase separation is thought to be involved in these processes. Due to the quasi-two-dimensional nature of membranes, their undulations and structural transitions are intrinsically coupled with phase behaviour, resulting in phenomena distinct from those observed in bulk systems. In this study we investigate the mechanism of phase separation mediated by the suppression of membrane fluctuations under osmotic stress, employing an integrated theoretical-experimental approach.

3Pos001 ミオシン II の化学反応と力学反応との共役の分子メカニズムに関する進捗報告
Progress report on the molecular mechanism of the conjugation of chemical and mechanical reactions of myosin II

Riho Sato, Takuo Yasunaga (*Grad. Sch. Comput. Sci. Syst. and Eng. Kyushu Inst. Tech*)

Muscles are vital for both voluntary and involuntary movements, like walking and breathing. These actions are induced by proteins, mainly actin and myosin. In muscle tissue, myosin II forms thick filaments that slide against actin filaments, generating contraction. It is known that the myosin head plays a central role by converting ATP energy into mechanical movement through structural changes. However, the flexibility of the myosin head was also reported. Here, by electron microscopy, we observed myosin head structures under various nucleotide conditions. We are challenging to clarify the molecular mechanism behind muscle motion.

3Pos002 ファージの宿主認識の構造解析
Structural analysis of phage host recognition

Shuji Kanamaru (*Department of Life Science and Technology, Institute of Science Tokyo*)

The first and crucial step in bacteriophage host recognition is the binding to its host receptor by the phage's receptor-binding protein (RBP); this interaction dictates specificity. As host receptor proteins are generally integral membrane proteins, it is very difficult to purify and structurally analyze their complexes with phage RBPs under membrane protein solubilisation conditions, which often affect native states. To overcome this problem, we developed UV cross-linking coupled with sensitive LC-MS/MS analyses to map interacting sites. The resultant proximity data were then incorporated into distance-constrained structure prediction to produce an experimentally-supported binding model of the RBP-receptor complex, yielding new insights into this key recognition.

3Pos003 HOIL-1L による HOIP の活性制御機構の構造生物学的解析
Structural biology of the regulation of HOIP activity by HOIL-1L

Marina Koga¹, Kazuki Kasai², Kayo Imamura¹, Kazuhiro Iwai³, Takayuki Kato⁴, Mika Hirose⁴, Keiichi Namba², Tomoko Miyata², Rie Motohashi¹, Hidehito Tochio¹ (¹*Grad. Sch. of Sci., Kyoto Univ.*, ²*Grad. Sch. of Fro., Osaka Univ.*, ³*Grad. Sch. of Med., Kyoto Univ.*, ⁴*inst. for pro., Osaka Univ.*)

Ubiquitination is a widely found protein modification mechanism in cells. Among the different types of ubiquitin chains, linear ubiquitin chains play an essential role in immune responses and inflammation. LUBAC (linear ubiquitin chain assembly complex), a ubiquitin ligase specific for linear chains, comprises three subunits: HOIP, HOIL-1L and SHARPIN. HOIP contains the catalytic center, and the remaining two are involved in HOIP regulation. The details of how the individual domains work together in ubiquitin conjugation are still unknown. In this study, we prepared an active subcomplex (mini-LUBAC) involving a portion of HOIP and HOIL-1L and attempted to elucidate the ubiquitination mechanism using solution NMR and cryo-electron microscopy.

3Pos004 AcrB による薬剤排出の分子基盤の解析
Analysis of the molecular basis of drug efflux by AcrB
Analysis of the molecular basis of drug efflux by AcrB

Wataru Sakaguchi¹, Yuto Muto¹, Atsuki Nakano¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Department of Molecular Biosciences, Kyoto Sangyo University*, ²*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*)

AcrB, multidrug efflux transporter in *Escherichia coli*, uses the proton motive force to expel drugs from the cytoplasm to the outside. While the structure of solubilized AcrB has been reported, its structure under proton motive force remains unknown. In this study, AcrB was reconstituted into liposomes to mimic physiological conditions, allowing structural analysis in a substrate-bound and energized state. We determined the structure at 3.25 Å resolution. To validate these findings, we are currently measuring the transport activity of the substrate doxorubicin to uncover the molecular basis of AcrB-mediated drug efflux.

3Pos005 Liposome に再構成した LRRC8A の構造解析
Structural analysis of LRRC8A reconstituted into liposome

Ryuga Teramura¹, Atsuki Nakano¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Life, Sci., KSU*, ²*Research Center, Univ. Osaka*)

LRRC8 family are membrane proteins that function as channels allowing the passage of Cl⁻ across cell membranes. However, the gating mechanism of the LRRC8A channel remains unclear. To analyze the mechanism in natural, we need to mimic natural conditions. Using detergents and nanodiscs are commonly used to solubilize membrane proteins for structural analysis, but they cannot replicate osmotic stress or cell expansion. Therefore, we reconstituted the LRRC8A channel into liposomes and analyzed the structure using cryo-electron microscopy (cryo-EM). To enable structural analysis, we established an expression and purification system. As a result, we successfully observed reconstituted LRRC8A channels into the liposomes.

3Pos006 ウシ心筋ミトコンドリアの SMP における ATP 合成酵素のオリゴマー構造
Structure of ATP synthase oligomer in SMP membranes of bovine heart mitochondria

Atsuki Nakano¹, **Katsuya Matsuki**¹, Shunsuke Akisada¹, Kaoru Mitsuoka², Ken Yokoyama¹ (¹*Department of Molecular Biosciences, Kyoto Sangyo University*, ²*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*)

To understand the native structure of membrane protein complexes functioning on biological membranes, it is essential to determine their structures in the natural membrane environment. Here, we employed single-particle analysis to elucidate the structures of ATP synthase FoF1 and respiratory chain complexes on sub-mitochondrial particles (SMPs) isolated from bovine heart mitochondria. On SMPs, the most of FoF1 was identified as dimers bound by the regulatory factor dimeric IF1. In addition, the tetrameric structure formed by the association of FoF1 IF1 dimers and the linear arrangement of the F1 head were also identified. These structures induced a membrane curvature of ~120°, indicating the presence of a structure on SMP similar to the tips of mitochondrial cristae.

3Pos007 人工赤色蛋白質 AzamiRed1.0 に復帰変異を導入した変異体シリーズの構造と分光学的性質
Structures and spectroscopic properties of a series of revertant mutant proteins of AzamiRed1.0, an engineered red fluorescent protein

Isamu Nagatomi¹, Hiromi Imamura², Norihiro Takekawa¹, Katsumi Imada¹ (¹*Grad. Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Biost., Kyoto Univ.*)

Red fluorescent proteins (RFPs) are suitable for deep-tissue imaging due to reduced absorption and scattering. However, conventional RFPs show low brightness and limited sequence diversity. We recently succeeded in conversion of a green fluorescent protein AzamiGreen (AG) to RFP (AR1.0) by introducing 29 mutations. However, the geometric arrangement of the residues essential for red chromophore formation remains unclear. Here, we made a series of mutant proteins by introducing reverted mutations in AR1.0 to the AG sequence and analyzed their absorption spectra and structures. We report the structures of AR1.3 (9 mutations), AR1.4 (12 mutations), and AR1.7 (19 mutations) and discuss the relation between the structure and the spectroscopic properties.

3Pos008 HeLa S3 細胞内のヒト UCHL3 の立体構造解析
In-cell NMR study of human UCHL3 in HeLa S3 cells

Hikari Sato¹, Moeka Nagamine¹, Yuiri Akae¹, Shigeharu Kubota¹, Hiroki Miyata¹, Haruka Sugawara¹, Kohsuke Inomata^{1,2,3}, Teppei Ikeya¹, Yutaka Ito¹ (¹*Department of Chemistry, Tokyo Metropolitan University*, ²*Institute for Molecular Science, National Institutes of Natural Sciences*, ³*Okazaki Collaborative Platform, National Institutes of Natural Sciences*)

We found that yeast ubiquitin C-terminal hydrolase (YUH1) exhibits dynamic conformational polymorphisms in two functionally significant loop regions, which are critical for its enzymatic activity. A similar polymorphism is predicted to exist in UCHL3, the human homologue of YUH1. NMR analysis of UCHL3 in live HeLa S3 cells was initiated to identify the effect of the intracellular crowding environment on the dynamic behaviour of YUH1/UCHL3. Stable isotope-labelled UCHL3 was introduced into cells by electroporation, and 2D ¹H-¹⁵N and ¹H-¹³C correlation spectra were successfully observed. The side-chain resonance assignments as well as collecting NOE/PCS/PRE-derived structural restraints are in progress aiming at identify the dynamic structure of UCHL3 in cells.

Shuto Kubo, Seito Kato, Ryouma Tagishi, Akio Horikawa, Sayeesh P.M., Kousuke Inomata, Teppei Ikeya, Yutaka Ito
(*Department of Chemistry, Tokyo Metropolitan University*)

Proteins in cells function under a crowding environment with various macromolecules. In our previous in-cell NMR study performed in Sf9 cultured insect cells, we succeeded in visualising the intracellular 3D structures of proteins, which are clearly different from those in dilute solution.

In order to investigate in detail which interactions in the intracellular crowded environment cause these structural changes, analyses were carried out in artificial crowded environments using various crowders. The tilt of a helix-loop region of protein G B1 domain away from the beta-sheet found in Sf9 cells could be reproduced by adding BSA, while Ficoll PM70 provided a 3D structure similar to that in dilute solution. The analysis on a ubiquitin mutant will also be presented.

Hiroyasu Koteishi¹, Akihiro Kawamoto¹, Ginga Shimakawa³, Hiroaki Matsui², Yoshinori Tsuji², Yusuke Matsuda², Genji Kurisu¹ (¹*IPR, Osaka Univ.*, ²*Dept. Biosci., Sch. Biol. & Environ. Sci., Kwansei Gakuin Univ.*, ³*Grad. Sch., Agri. Sci., Kobe Univ.*)

In water, low CO₂ levels and its auto-conversion to bicarbonate (HCO₃⁻) limit photosynthesis. To adapt, algae have evolved CO₂-concentrating mechanisms (CCMs) to efficiently utilize HCO₃⁻. Interestingly, diatoms alone are responsible for approximately 20% of global CO₂ fixation, yet the underlying molecular mechanisms remain unclear. In this study, we analyzed the structure of PtBEST1, a candidate bicarbonate channel recently identified in the diatom *Phaeodactylum tricornutum*. PtBEST1 was overexpressed and purified from insect cells (Sf9), and its structure has been determined at about 2.0 Å resolution at pH 6.0, 8.0, and 9.0 by Cryo-EM single particle analysis. We compare it with the homologous anion channel bestrophin and discuss the structural changes induced by pH.

Ren Nakanishi (*kyoto sangyo university*)

Iota toxin produced by *C. perfringens* type E is a binary toxin consisting of Ia and Ib, which acts as an enterotoxin. Ia acts as an ADP-ribosyltransferase, while Ib forms a heptameric pore on the cellular membrane and allows Ia to pass through into the cell. In anthrax toxin protective antigen (PA), mutations around the ϕ -clamp, which is a common constriction site as well as Ib, have been suggested to form an intermediate structure for membrane pore formation. In this study, we mutate the residues around the ϕ -clamp of Ib and ought to analyze the structure by cryo-EM to clarify the pore formation process of Ib. The detailed results will be presented in the poster.

Toshiaki Ueda¹, Aiko Hasegawa², Yozo Nakazawa^{1,2}, Koji Umezawa¹ (¹*Grad. Sch. of Sci. & Tech., Shinshu Univ.*, ²*Sch. of Med., Shinshu Univ.*)

The extracellular region of interleukin-3 receptor subunit alpha (IL3R α) consists of two fibronectin III-like domains and an N-terminal domain (NTD). It has been suggested that the NTD conformational fluctuation is regulated by binding with higher affinity IL-3 mutant (K116W) than wild-type IL-3.

To investigate the effects of the IL3R α NTD fluctuations on IL-3 binding affinities, we performed all-atom molecular dynamics simulations for IL-3/IL3R α complex, IL-3K116W/IL3R α complex and IL3R α without the ligand. The ten 1- μ s trajectories for each system were analyzed by RMSF and MMGBSA methods. The results showed no significant differences in the NTD fluctuations between wild-type and K116W complexes. Further analysis will be applied to confirm the same conclusion.

3Pos013 分泌発現量に関わる α 接合因子プレプロリーダー配列の動的構造特性
Dynamical structural property of α -mating factor pre-pro-leader sequence and relationship with the expression yield

Kazumasa Sakurai (*Inst. Adv. Tech., Kindai Univ.*)

A major secretory expression system is the methylotrophic yeast *Pichia pastoris* with the α -factor prepro-leader sequence (ppaMF). Although the expression yield is dependent on the target protein and the amino acid sequence of ppaMF, the underlining mechanism has not been fully understood. We hypothesized that the dynamical structure of ppaMF is relevant to the expression efficiency.

We constructed an expression system of ppaMF and performed NMR signal assignment. 100% assignment of ppaMF residues have been achieved. We then performed chemical shift analysis, relaxation measurements, and hydrogen exchange measurements to understand the dynamic structure of the ppaMF region. Based on the results, we discuss the residual structure of the ppaMF region.

3Pos014 The relationship between initial structure and polymorphism of amyloid fibrils from SARS-CoV-2 spike peptide

Manami Yamaguchi¹, Emi Hibino¹, Natsuko Goda¹, Takeshi Tenno^{1,2}, Hidekazu Hiroaki^{1,2,3} (¹*Grad. Sch. Pharm. Sci., Nagoya Univ.*, ²*BeCellBar, LLC*, ³*COMIT*)

The S192 peptide (residues 192–211) from the SARS-CoV-2 spike protein was previously reported to form amyloid fibrils, potentially causing to brain fog. We investigated the factors influencing S192 amyloid fibril formation, because we observed polymorphic fibril structures under different conditions. Lyophilized S192 peptide was dissolved in hexafluoro-2-propanol (HFIP) or dimethyl sulfoxide (DMSO), diluted, and incubated at 37 °C. The lag time and morphology of fibrils differed depending on the solvent used. Fourier transform infrared spectroscopy revealed that the S192 monomer adopted distinct secondary structures in HFIP and DMSO. We will discuss the amyloid fibril formation mechanism, including the influence of its secondary structure on the seeding process.

3Pos015 GFPuv の発色団形成反応におけるカルボニル基の役割
Role of carbonyl groups in the chromophore formation of GFPuv

Tomoya Adachi¹, Masaru Hoshino², Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*Kyoto Univ. Pharm.*)

The chromophore of the green fluorescent protein GFP is formed by a spontaneous main chain cyclisation reaction. Such a reaction of the main chain never occurs in normal proteins, so it is thought that the GFP provides a special intramolecular environment for this reaction to occur. To clarify the intramolecular environment of GFPuv, we produced a mutant in which Glu222, which interacts with the chromophore, was replaced by Gln, weakening the negative electrostatic potential in the molecule. This was used to compare 2D-NMR (¹H-¹⁵N HSQC) spectra to investigate how the environment around the amide of individual peptide bonds in the molecule was changed, based on the site-specific relaxation model of peptide bonds (Chiba et al., *Protein Science*, 2023).

3Pos016 GFP 様タンパク質 mCherry が分子の内部にもつ酸性アミノ酸の役割
Role of acidic Amino Acids inside the molecule of GFP-like Proteins

Pattarisa Rerganan¹, Masaru Hoshino², Nobuhiro Suzuki³, Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*Kyoto Univ. Pharm.*, ³*NARO*)

mCherry is a red GFP-like protein based on tetrameric DsRed. We have been investigating how the environment surrounding the amide in each main chain peptide bond is altered by amino acid substitution by 2D-NMR (¹H-¹⁵N HSQC) to study the difference in the nature of the individual peptide bonds in the mCherry molecule. In the process, we found that some peak positions shifted significantly when mCherry was incubated at 37 °C. We hypothesized that this phenomenon might be an extreme example of site-specific relaxation of peptide bonds (Chiba et al., *Protein Science* 2023) caused by negative electrostatic potentials formed in the molecule, resulting in cleavage of the main chain peptide bonds, and performed a series of amino acid substitution experiments.

3Pos017 E222DGFPuv は中性 pH で acidic form の発色団のみを持つ
E222DGFPuv has only chromophores in acidic form at neutral pH

Yutsuki Mimura¹, Masaru Hoshino², Kaori Chiba¹ (¹*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll. Japan*, ²*Kyoto Univ. Pharm.*)

GFP-like proteins, including GFPuv, have an acidic amino acid on the 11th β -strand with side chains pointing towards the inside of the molecule. The chromophore is formed by spontaneous main-chain cyclisation, which does not occur within normal protein molecules, and the local negative electrostatic potential formed by the acidic amino acids is thought to be essential for this unusual reaction. Therefore, based on the site-specific relaxation model of the main chain peptide bond (Chiba et al., *Protein Science*. 2023), a mutant was produced in which Glu222 was replaced by Asp with a shorter side chain to alter the intramolecular environment of GFPuv. The results show that the absorption peak at 478 nm observed for GFPuv in neutral pH solutions disappears.

3Pos018 タンパク質をモデルとした生物の超高压力耐性のラマン分光研究
Raman Spectroscopic Study on Ultra-High Pressure Resistance in Small Organisms Using Proteins as a Model

Kantaro Iwasa¹, Toshiki Nakao¹, Minoru Kato^{1,2} (¹*Grad. Sch. of Life Sci. Univ. Ritsumei*, ²*Col. of Life Sci. Univ. Ritsumei*)

Certain small organisms, such as tardigrades in a desiccated dormant state, are known to be able to survive even when subjected to pressures of up to 7.5 GPa. This suggests that the origin of in vivo protein resistance to ultra-high pressure may be due to the low intracellular water content and/or the accumulation of trehalose, which increases significantly during desiccated dormancy. In this study, we used bovine serum albumin (BSA) as a model protein and examined structural changes induced by pressure using Raman spectroscopy. We examined how water content and trehalose concentration affect BSA structural changes and discussed the origin of ultra-high-pressure resistance in the desiccated dormant state.

3Pos019 部位特異的変異体を用いた α -イソプロピルリンゴ酸合成酵素(IPMS)のロイシン認識メカニズムの解明
Elucidation of the leucine recognition mechanism of α -isopropylmalate synthase (IPMS) using site-directed mutants

Hanane Nakamura¹, Yuto Miura¹, Hana Kitazume¹, Kanon Sugao², Yoko Akazawa³, Shigeru Shimamoto⁴, Takayuki Ohnuma², Atsushi Kurata², Koichi Uegaki² (¹*Grad.Sch.Agric.Kindai univ.*, ²*Agric.Kindai univ.*, ³*AIST*, ⁴*Fac.Sci. & Eng.Kindai univ*)

In the leucine biosynthesis of *Saccharomyces cerevisiae*, α -isopropylmalate synthase (IPMS) is a rate-limiting enzyme regulated via feedback inhibition by leucine. We focused on the interaction between IPMS and leucine with the aim of identifying the factors responsible for allosteric inhibition. Y538 and T549, the residues predicted to interact with the leucine methyl group based on structural modeling, were substituted with other amino acids. The mutants were analyzed using isothermal titration calorimetry (ITC) and IPMS activity measurements. As a result, mutants that enhance hydrophobic interactions have an order-of-magnitude increase in leucine sensitivity. Based on these findings, we discuss the mechanisms underlying leucine recognition and allosteric inhibition.

3Pos020 α -イソプロピルリンゴ酸合成酵素のロイシン感受性とリンカードメインの構造変化
Leucine Sensitivity and Structural Changes in the Linker Domain of α -Isopropylmalate Synthase

Yuto Miura¹, Hanane Nakamura¹, Hana Kitazume¹, Kanon Sugao², Yoko Akazawa³, Kazuki Mitani⁴, Shigeru Shimamoto⁴, Kazuki Kawahara^{5,6}, Hiroya Oki⁷ (¹*Grad. Sch. Agric., Kindai Univ.*, ²*Agric., Kindai Univ.*, ³*AIST*, ⁴*Fac. Sci. & Eng., Kindai Univ.*, ⁵*Grad. Sch. Pharm. Sci., Osaka Univ.*, ⁶*CiDER, Osaka Univ.*, ⁷*Res. Inst. Microbial Dis., Osaka Univ.*)

α -Isopropylmalate synthase (IPMS), a rate-limiting enzyme in leucine biosynthesis, is regulated allosterically by L-leucine. IPMS is a homodimer comprising regulatory, linker, and catalytic domain, with leucine binding and active sites 50 Å apart. *S. cerevisiae* has two IPMS isozymes, leucine-sensitive Leu4p and less sensitive Leu9p, despite >80% sequence identity. We investigated allosteric inhibition using wild-type and domain-swapped chimeras. Isothermal titration calorimetry showed exothermic binding of leucine to Leu4p, but not Leu9p. A Leu4p chimera with Leu9p's linker domain showed thermodynamic properties similar to Leu9p, suggesting the linker domain modulates leucine sensitivity through structural rigidification.

3Pos021 均一基質バインダーのダイナミクスと進化
Dynamics and Evolution of Uniform Substrate Binder

Yusran Abdillah Muthahari¹, Yovin Sugijo¹, Paola Laurino^{1,2} (¹*Protein Engineering and Evolution Unit, Okinawa Institute of Science and Technology*, ²*Institute for Protein Research, Osaka University*)

An enzyme needs to acquire both binding and catalysis to function. However, it is unclear how enzymes with similar catalytic cores could adapt different binders to evolve distinct functions and kinetics. The haloalkanoic dehalogenase superfamily (HADSf) utilizes modular substrate binders to diversify functions. Here, we focus on revealing how nature fine-tuned the open/closed dynamics of the substrate binding domain of Phosphoglucosyltransferase B (PgmB). Compared to its phosphatase orthologs, PgmB has a broader opening of the substrate binding to enable bi-substrate ping-pong kinetics with substrate inhibition. Our preliminary findings showed that open/closed dynamics of PgmB determined the formation of productive Enzyme-Substrate (ES) complexes.

3Pos022 ヘイムダルアクチンは短いフィラメントを形成し、骨格筋トロポミオシントロポニン複合体と共沈する
Heimdall actin forms short filaments and coprecipitates with the muscle tropomyosin-troponin complexes

Kaoru Takahashi¹, Tomoharu Matsumoto², Akihiro Narita², Taro Q.P. Uyeda¹ (¹*Dept. Pure. & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, ²*Dept. Physics, Grad. Sch. of Science, Nagoya Univ.*)

Heimdall archaeota is an Asgard archaeon, and its actin is closely related to eukaryotic actin. Characterizing Heimdall actin should shed light on the evolutionary origin of eukaryotic actin functions. Here, we expressed Heimdall actin (~42 kDa) fused with a GST tag in *E. coli*, purified it by affinity chromatography and removed the tag with PreScission protease. The protein precipitated upon ultracentrifugation in F-buffer of pH 6.0, and the precipitate was redissolved in G-buffer of pH 8.0. Precipitation also occurred in the presence of Loki profilin. Heimdall actin in F buffer formed only short filaments of about 70-100 nm as examined by TEM. Moreover, it coprecipitated with the muscle tropomyosin-troponin complex.

3Pos023 EPR 法による南極海および深海細菌由来無機ピロフォスファターゼの低温適応機構の解明
EPR Spectroscopy Reveals the Cold Adaptation Mechanism for Di-Mn²⁺ Inorganic Pyrophosphatase

Ren Sugawara, Yuri Kusu, Kantaro Sakamoto, **Masaki Horitani** (*Fac. Agri., Saga Univ.*)

Inorganic pyrophosphatase (PPase) catalyzes the hydrolysis reaction of inorganic pyrophosphate into two inorganic phosphates. Ginting and co-workers have reported that the activity of Mn²⁺ bound PPase from *Shewanella* sp. AS-11, which lives in the Antarctic Ocean. We have recently characterized the activity and thermal stability PPase from *Shewanella benthica*, which lives in the deep sea. Both PPases were cold adapted enzymes with relatively high thermal stability. In general, enzyme activity increases at higher temperatures until the enzyme is denatured. However, both PPases were inconsistent with this theory. To elucidate the cold adaptation mechanism, we present here electron paramagnetic resonance (EPR) spectroscopic studies of both PPases.

3Pos024 ヒト H 鎖フェリチン内部に形成される鉄コアに対するリン酸の影響
Effect of phosphate on the iron core formed in human H-ferritin

Katsuaki Hanabusa¹, Takumi Kuwata², Haruki Sakakibara¹, Kazuo Fujiwara¹, Masamichi Ikeguchi^{1,2} (¹*Department of Biosciences, Graduate School of Science and Engineering, Soka University*, ²*Department of Science and Engineering for Sustainable Innovation, Soka University*)

Ferritin is a protein that stores iron in the cavity formed by shell-like assembly of 24 subunits. Mammals have hetero 24-meric ferritins composed by heavy and light chains, whereas bacterial ferritins are composed by solely heavy chain-like subunits. We have previously shown that phosphate affects the shape of the iron core reconstituted in *E. coli* ferritin. In this study, we reconstituted the iron cores in *Chlorobaculum tepidum* ferritin and human heavy chain ferritin in the presence and absence of phosphate, and the core size and shape were analysed by ultracentrifugation and small-angle X-ray scattering. For both ferritins, phosphate led to formation of cores with relatively uniform size and shape, whereas the core formed in the absence of phosphate was variable.

3Pos025 NMR による Ubiquitin C-terminal Hydrolase (UCHL3)のユビキチンとの相互作用とダイナミクス解析
NMR analysis of the intermolecular interaction between Ubiquitin C-terminal Hydrolase (UCHL3) and ubiquitin, and their molecular dynamics

Shigeharu Kubota, Hiroki Miyata, Haruka Sugawara, Yutaka Ito, Teppei Ikeya (*Department of Chemistry, Tokyo Metropolitan University*)

Ubiquitin C-terminal Hydrolase L3 (UCHL3) is a human deubiquitinating enzyme that hydrolyzes small molecule adducts attached to the C-terminus of ubiquitin (Ub), regenerating free Ub. Our previous studies on its yeast homolog, YUH1, revealed the presence of multiple conformational states and highly dynamic regions, namely the gating and crossover loops, which are essential for enzymatic activity. Although similar structural flexibility has been suggested for UCHL3, its multi-state three-dimensional structures and the detailed mechanism of Ub recognition remain unclear. Here, we present a solution NMR analysis of the interaction between UCHL3 and Ub and provide insights into their molecular dynamics across different time scales.

3Pos026 Purification and functional analysis of Loki archaea actin

Haruka Tatsuta¹, Gaku Sakai¹, Yuta Yanase¹, Tomoharu Matsumoto², Akihiro Narita², Taro Uyeda¹ (¹*Grad. Sch. Adv. Sci. Eng., Univ. Waseda*, ²*Grad. Sch. Sci., Univ. Nagoya*)

Asgard archaea, such as Lokiarchaeota are considered the closest prokaryotic relatives of eukaryotes and possess primitive versions of eukaryotic cytoskeletal components, including actin homologs. In this study, we expressed and purified soluble Loki actin fused to a GST tag in E.coli, and subsequently removed the tag to obtain native protein. The purified Loki actin was pelleted by ultracentrifugation in the presence of Mg-ATP and 50 mM KCl at pH 7.4. Notably, the pellet regained solubility when resuspended in G-buffer for eukaryotic actin. Co-sedimentation assays indicate that Loki actin interacts with eukaryotic actin-binding proteins (ABPs) such as tropomyosin. Structural characterization using transmission electron microscope is planned.

3Pos027 A high-performance software suite for 3D reconstruction from single-particle X-ray scattering

Wenyang Zhao¹, Osamu Miyashita¹, Florence Tama^{1,2,3} (¹*RIKEN Center for Computational Science*, ²*Institute of Transformative Bio-Molecules, Nagoya University*, ³*Graduate School of Science, Nagoya University*)

X-ray free-electron laser (XFEL) single-particle analysis (SPA) enables 3D structure determination of biological macromolecules under near-physiological conditions. We are developing a high-performance software suite for 3D reconstruction from XFEL data. Its first package, xmatch3d, assembles 2D images into a 3D diffraction intensity distribution using our slice-matching algorithm. The second, xphase3d, performs phase retrieval to restore a 3D molecular electron density map. A machine learning-based tool for analyzing phase retrieval results is also under investigation. The suite has been deployed on the supercomputer Fugaku, where it efficiently uses high-performance computing resources to run numerous reconstruction trials in parallel and process large 3D volumes.

3Pos028 CaMKII と GluN2B ペプチドの結合を可視化する高速 AFM 基板の開発
Development of a HS-AFM substrate to visualize the binding between CaMKII and GluN2B peptides

Kodai Hasegawa¹, Taiki Kobayashi², Hiroki Konno^{3,4}, Yusuke Miyanari^{3,4}, Mikihiro Shibata^{3,4} (¹*Grad.Sch.NanoLS., Kanazawa Univ.*, ²*Sch.Math.&Phys., Kanazawa Univ.*, ³*WPI-NanoLSI, Kanazawa Univ.*, ⁴*InFiniti, Kanazawa Univ.*)

High-speed atomic force microscopy (HS-AFM) is a powerful technique for visualizing the dynamics of single proteins at nanometer resolution. However, the sample must be immobilized on the AFM substrate, and overly strong immobilization can inhibit free protein-protein interactions. In this study, we aimed to observe the direct binding of CaMKII to the C-terminal peptides of GluN2B (GluN2Be), which play a critical role in the induction of long-term potentiation (LTP) in neurons. We used a Tamavidin2-coated AFM substrate to reduce undesirable protein immobilization. Additionally, SpyCatcher/Tag was applied to immobilize GluN2Be on the Tamavidin-2 substrate. In the poster, we will present biochemical analysis and HS-AFM imaging of the optimized AFM substrate.

3Pos029 高速 AFM 用超微小カンチレバーの変位検出レーザーの自動位置アライメント
Automatic position alignment of the deflection detection laser to ultra-small high-speed AFM cantilever

Taiyo Ogawa¹, Noriyuki Kodera², Kenichi Umeda² (¹*Grad.Sch.Math. & Phys., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*)

In recent years, we have been working to improve the temporal resolution of high-speed AFM (HS-AFM). As part of this effort, we have developed an ultra-small cantilever with a resonance frequency of 3 MHz in liquid and a spring constant of 0.3 N/m, making it suitable for gentle imaging of biological samples. However, the cantilever size was significantly reduced, leading to difficulties in aligning the position of deflection detection laser to the cantilever. To solve this issue, here we designed a new cantilever stage and automated the laser position alignment using computer-controlled inertial piezo motors. As a result, we achieved automatic alignment of the laser position to cantilever with the help of image recognition methods.

3Pos030 蛍光明滅を併用した TDP-43-核酸相互作用の定量性向上
Improving quantitative detection of TDP-43-nucleic acid interactions by combining fluorescence blinking analysis

Haruki Kawai¹, Akira Kitamura² (¹*Grad. Sch. of Life Sci., Hokkaido Univ.*, ²*Fac. of Adv. Life Sci., Hokkaido Univ.*)

TAR DNA/RNA-binding Protein 43 kDa (TDP-43) regulates transcription and splicing by binding nucleic acids. To quantify the binding affinity between TDP-43 and nucleic acids, we purified recombinant TDP-43 from *E. coli* and measured its dissociation constant (Kd) using fluorescence correlation spectroscopy (FCS) with fluorescently labeled single-stranded DNA (ssDNA). In addition to monitoring diffusion changes upon TDP-43-ssDNA binding, we analyzed alterations in fluorescence blinking behavior during FCS measurements. By combining both diffusion and blinking information, we established a method that improves the accuracy of Kd quantification. Furthermore, we detected complex conformation change across different concentration ranges by blinking behavior.

3Pos031 磁気コンパスの機構解明に向けた共焦点顕微鏡による FAD-Trp 系の蛍光測定
Fluorescence measurement of the FAD-Trp system by confocal microscopy to elucidate the mechanism of the magnetic compass

Akihiro Tateno¹, Toru Kondo^{1,2} (¹*ExCELLS*, ²*NIBB*)

The ability to sense the geomagnetic field, known as a magnetic compass, has been reported in many animals, including the European robin. Radical pair mechanism has been proposed as a mechanism for the magnetic compass. ErCry4, which is a type of avian cryptochrome, is a potential candidate protein for a magnetic compass because it forms a radical pair consisting of FAD and tryptophan (Trp) upon photoexcitation. Although studies of FAD-Trp radical pairs in proteins have revealed details of their spin dynamics, the anisotropy of the magnetic field effect and subsequent signal propagation mechanisms remain unresolved. Here, we performed fluorescence measurements of FAD-Trp radical pairs using the confocal microscopy. The detailed results will be discussed on the day.

3Pos032 Tag/Catcher システムを用いたタンパク質構造体への異種タンパク質の取り込みの検討
Incorporation of heterologous proteins into protein structures using the Tag/Catcher system

Yume Kosuge, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

In living cells, biopolymers are densely packed in a state known as molecular crowding, which facilitates efficient enzymatic reaction by promoting enzyme proximity. To mimic that state, we focused on the polymerization Cry3Aa, a protein derived from the soil bacterium *Bacillus thuringiensis* (Bt). Co-expression of Cry3Aa and a target enzyme enables efficient passive entrapment of the enzyme in the nanoporous channels of Cry3Aa crystals. However, it takes approximately 72 hours to form Cry3Aa crystals in *Bt*. Cry3Aa expressed in *E. coli* undergoes crystallization and polymerization at low pH. We formed a protein complex of Cry3Aa and a target, protein using the Tag/Catcher system in a test tube. The polymerization was investigated using SDS-PAGE and a microscope.

3Pos033 耐熱性酵素を用いた無細胞アルカン合成
Cell-free alkane synthesis using thermostable enzymes

Kaisei Nagao¹, Shunji Suctaka¹, Munechito Arai^{1,2} (¹*Dept. Life Sci., Univ. Tokyo*, ²*Dept. Phys., Univ. Tokyo*)

Cyanobacteria can produce alkanes corresponding to diesel oil using aldehyde-deformylating oxygenase (ADO). However, the alkanes are not released outside the cells, which limits production. To address this issue, we developed a cell-free alkane synthesis system that first converts fatty acids to aldehydes with carboxylic acid reductase (CAR) and then converts the aldehyde to alkanes with ADO. We used thermostable variants of CAR and ADO, expressing them separately in *Escherichia coli* and mixing them after crude purification and heat treatment, respectively. This enzyme mixture successfully produced alkanes from fatty acids, suggesting that cell-free alkane synthesis using thermostable enzymes is a promising method for mass-producing biofuels.

3Pos034 大腸菌における翻訳促進ペプチドの機械学習による予測と実証
Machine learning-guided identification and validation of translation-enhancing peptides in *Escherichia coli*

Chie Motono¹, Yokoyama Gentaro², Hideo Nakano³, Teruyo Ojima-Kato³, Michiaki Hamada² (¹*Cellular and Molecular Biotechnology Research Institute, AIST*, ²*Graduate School of Advanced Science and Engineering, Waseda University*, ³*Graduate School of Bioagricultural Sciences, Nagoya University*)

Fusion of specific four-amino-acid peptides to a protein's N-terminus can enhance expression by improving translational efficiency¹. We built Random Forest and XGBoost models using experimental data of 158 peptides in *E. coli*, then predicted expression levels for ~160,000 possible sequences. Top candidates were experimentally validated and added for model retraining, repeating this cycle three times. This approach enabled efficient discovery of translational enhancer peptides and demonstrated the utility of machine learning for optimizing microbial protein production.

1) Ojima-Kato et al., *J Biosci Bioeng.* 2017, **123**, 540. doi: 10.1016/j.jbiosc.2016.12.004.

3Pos035 タンパク質ファミリー 2 種の配列を深層学習により混合させた新規タンパク質の特性
Deep Learning-Guided Generation of "Marble-Type" Hybrid Transcription Factors Bridging Two Subfamilies

Michio Aiko, Atsushi Minami, Sota Okuda, Kazumasa Ohtake, **Daisuke Kiga** (*Waseda U, Dept. Elect Eng and Biosci*)

Many protein families, such as quorum sensing regulators, include multiple subfamilies, yet the properties of proteins with intermediate sequences remain unclear. We used a deep generative model, a variational autoencoder (VAE), to design "marble-type" transcription factor variants blending two parental proteins. The synthesized genes were tested in *E. coli* for their activity. About 50% of the variants were functional; notably, one mutant activated both parent-specific promoters, indicating dual specificity. This study addresses the question: "Does residue-level blending of proteins yield functional intermediates between the parents?" Our approach enables fine-grained recombination beyond conventional engineering, offering a new strategy for synthetic biology.

3Pos036 A platform for developing thermogenetic tools to control protein function

Quang Cong Vu, Satoshi Arai (*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

Thermogenetics uses temperature-sensitive proteins to regulate cellular activities, offering a promising alternative to optogenetics. While thermogenetic approaches have primarily focused on ion channel regulation via transient receptor potential channels, tools for controlling intracellular protein function through heat activation remain limited. Here, we developed a heat-activated human caspase 8 (CASP8) using a temperature-sensitive domain (TSD) for controlling programmed cell death. By fusing TSD with CASP8, heating above 35 °C induced coactivation of the TSD, bringing two CASP8 molecules into proximity to trigger dimerization-induced activation and promotes cell death. This platform introduces a new class of thermogenetic tools for controlling cellular processes.

3Pos037 **SOS1 天然変性領域(IDR)の GRB2 との多価相互作用と液液相分離形成機構の溶液 NMR 解析**
NMR analysis of the multivalent interaction between SOS1 intrinsically disordered region and GRB2 and its liquid–liquid phase separation

Rina Kamimura¹, Sangya Yu¹, Maho Watanabe¹, Toshifumi Hayashi¹, Haruka Sugawara¹, Tsutomu Mikawa², Yutaka Ito¹, Teppei Ikeya¹ (¹*Department of Chemistry, Graduate School of Science, Tokyo Metropolitan University*, ²*RIKEN Center for Biosystems Dynamics Research*)

SOS1 is a guanine nucleotide exchange factor recruited by GRB2 in response to upstream signals, where it activates RAS by catalyzing the exchange of GDP to GTP. Recent studies have shown that SOS1 and GRB2 can also act as scaffolds of liquid–liquid phase separation (LLPS), thereby modulating the intensity of cell signaling pathways. Although this condensed condition is believed to be driven by multivalent interactions between the intrinsically disordered region (IDR) of SOS1 and the two SH3 domains of GRB2, the underlying molecular mechanisms remain poorly understood. Here, we present a solution NMR analysis of the interaction between the SOS1 IDR and GRB2 within LLPS droplets and discuss its recognition mechanisms and potential contribution to signal transduction.

3Pos038 **Kinetic Study on LLPS of Pbp1 by Combining Stopped-Flow and Transient Grating Methods**
Ryo Taniguchi, Masahide Terazima, Yusuke Nakasone (*Grad. Sch. Sci., Kyoto Univ.*)

Pbp1 is an intrinsically disordered protein that undergoes liquid-liquid phase separation (LLPS) in response to environmental changes and plays a role in autophagy regulation. However, the mechanisms of LLPS, particularly the reaction kinetics, remain unclear due to the disordered nature of the protein.

To address this, we have developed a method that combines stopped-flow and transient grating techniques (SF-TG), allowing time-resolved observation of structural changes and molecular assembly via diffusion coefficient measurements. For Pbp1, we examined solvent conditions to drive LLPS and labeled the protein with a photochromic molecule. Using SF-TG, we detected preliminary signals indicative of early-stage assembly, demonstrating the potential of this approach.

3Pos039 **SAXS-guided prediction of animal-like cryptochrome from green alga *Chlamydomonas reinhardtii* structure via coarse-grained MD simulations**

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Animal-like cryptochrome from the green alga *Chlamydomonas reinhardtii* (CraCRY) is a bi-functional protein that can perform light-induced gene regulation of the biological clock (cryptochrome function) as well as light-induced DNA repair. CraCRY consists of a structured N-terminal domain known as photolyase homology region (PHR), and intrinsically disordered C-terminal extension (CTE), which is highly flexible and makes it hard to predict the structures experimentally. In this research, we integrated computational approaches —AlphaFold modeling and coarse-grained molecular dynamic simulations— with experimental small-angle x-ray scattering (SAXS) data to obtain detailed structural information of CraCRY and gain insights into the mechanism behind its functions.

3Pos040 **高速 AFM による結核菌休眠制御タンパク質 MDP1 のサブ分子観察**
Sub-molecular imaging of MDP1, a dormancy-regulating intrinsically disordered protein in *Mycobacterium tuberculosis*, by high-speed AFM

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MDP1 is a histone-like protein responsible for dormancy, growth suppression and acquiring drug tolerance in *Mycobacterium tuberculosis*. Understanding the structural dynamics of MDP1 is important for developing drugs to eradicate tuberculosis. However, this has been difficult due to the presence of an intrinsically disordered region (IDR). Here, we succeeded in high-speed AFM observations of full-length MDP1 at the sub-molecular level in which the structured HU-region and the rapidly fluctuating flexible IDR were visualized. To quantify the structural dynamics of MDP1 molecule, AI-driven auto-tracking was used. Furthermore, we quantitatively analyzed the structural changes induced by drugs that potentially inhibit the functions of MDP1.

3Pos041 Modification of intramolecular electron transfer membrane protein for photo-induced iron reduction

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Cytochrome *b*₅₆₁D2 (CYB561D2) is an endoplasmic reticulum-localized membrane protein encoded by the human tumor suppressor gene *101F6*. This protein, a constituent of the cytochrome b561 family, transfers electrons from cytosolic ascorbate through two *b*-type heme cofactors to ferric iron present in the endoplasmic reticulum lumen, inducing its reduction. However, the detailed mechanism of the electron transfer remains unclear. In this study, we aimed to photo-reduction of the iron instead of ascorbate by attaching a photosensitizer to CYB561D2 in order to elucidate the mechanism using spectroscopy. Cys residues were mutated in CYB561D2 suitable for chemical modification with sensitizer and evaluated their iron-reduction activity.

3Pos042 Analysis of the Transport Mechanism in the ABC transporter Based on Spectroscopic Tracking of Heme

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ABC transporters are membrane proteins that transport allocrites upon ATP binding and hydrolysis. Based on structural analysis, it has been proposed that the conformational changes induce allocrite transport. However, the question how allocrite transport is coupled to the chemical changes in ATP remains unclear. We focused on the ABC heme importer BhuUV-T, which transports heme as an allocrite, expecting its spectral changes along the translocation. Titration of BhuUV with heme-bound BhuT monitored by UV-vis absorption spectroscopy estimated the dissociation constant between BhuUV and heme to ~30 nM. In addition, a stepwise transport process was observed, where heme was first transferred from BhuT to BhuUV, followed by incorporation into the channel upon ATP binding.

3Pos043 QM/MM シミュレーションを用いたハロロドプシンの光活性化状態に関する理論的研究
Theoretical studies on halorhodopsin photoactivation using QM/MM simulations

Tomo Ejiri, Shigehiko Hayashi (*Grad. Sci., Univ. Kyoto*)

Halorhodopsin (NpHR) from *Natronomonas pharaonis* is a light-driven chloride pump containing a retinal protonated Schiff base. We investigated the atomic-level photoactivation mechanism using QM/MM simulations and umbrella sampling to analyze chloride transport within the protein. Our simulation results suggested that the ground-state conformation appears to require two chloride ions per monomer. In the photoactivated states, chloride transport is facilitated by both retinal's positive charge and Arg123 orientation. Importantly, Arg123 side-chain movements induce extracellular helix conformational changes, shifting residues like Met120 to create structural barriers preventing chloride backflow.

3Pos044 全長構造から読み解く KcsA の構造ダイナミクスと機能
Structural dynamics and function of KcsA revealed by the full-length structures

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KcsA, a potassium channel from *Streptomyces lividans*, forms a minimal tetrameric channel and serves as a model for K⁺ channels.

Diffraction X-ray Tracking (DXT) suggests that gating in its cytoplasmic domain (CPD) may involve global twisting motions. However, flexibility of the CPD has hindered full-length structure determination. Recently, multiple full-length KcsA structures including the CPD were resolved by single-particle cryo-EM. We performed molecular dynamics simulations using these structures and analyzed inter-subunit correlated motions. Our results suggest potential conformational transitions associated with channel gating dynamics.

3Pos045 脂質過酸化能の評価に向けた BRIL 融合型シトクロム b561D2 のナノディスク化
Preparation of BRIL-fused cytochrome b561D2 in nanodisc to evaluate its peroxidation activity for lipid membrane

Haruka Yoshimura¹, Motonari Tsubaki¹, Hisroshi Sugimoto^{2,3}, Tetsunari Kimura^{1,4} (¹*Graduate School of Science, Kobe University*, ²*Spring-8 Center, RIKEN*, ³*Graduate School of Science, University of Hyogo*, ⁴*Molecular PhotoScience Research Center, Kobe University*)

Cytochrome b561D2 (CYB561D2) is a membrane protein encoded by a tumor suppressor gene found in human lung cancer cells. CYB561D2 is known to reduce intracellular ferric ions to ferrous ions, which have been proposed to peroxidize lipid membranes with oxygen molecules, resulting in the cancer-cell death called “ferroptosis.” However, there is no direct evidence that the ferrous ions reduced by CYB561D2 peroxidize the lipid membrane. To investigate the peroxidation activity of CYB561D2 in the similar conditions to those *in vivo*, CYB561D2 was incorporated into nanodisc. For the stable expression of CYB561D2 in *E. coli*, BRIL structure was introduced into C-terminal of CYB561D2, increasing the yield by 4.7 times compared to the expression of wild type in *Pichia* system.

3Pos046 Affinity between of the ABC transporter BhuUV and the periplasmic binding protein BhuT, investigated by biolayer interferometry

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ABC transporters are membrane proteins that couple ATP hydrolysis to the trans-membrane translocation of substrates. One of the ABC transporters, BhuUV, is involved in heme uptake, where the periplasmic binding protein, BhuT, captures the free heme, followed by its delivery to BhuUV. However, the specificity between BhuUV and holo-BhuT is unclear because of the lack of the affinity data between BhuUV and apo/holo-BhuT. In this study, the quantitative analyses using biolayer interferometry were performed, and the binding rates between BhuUV and apo/holo-BhuT were estimated to $5.5/7.5 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$, respectively, indicating that the recognition of BhuUV to BhuT is independent of the existence of heme.

3Pos047 Molecular Simulations Reveal Phase Separation Mechanisms of Pluripotency Transcription Factor Combinations

Samuel Blazquez Fernandez, Yutaka Murata, Shoji Takada, Tsuyoshi Terakawa (*Department of Biophysics, Graduate School of Science, Kyoto University, Kyoto, Japan*)

Transcriptional condensates formed via liquid-liquid phase separation (LLPS) play key roles in gene regulation by clustering transcription factors. In pluripotent cells, core factors such as Nanog, Oct4, Sox2, and Klf4 show LLPS behavior, but the mechanisms underlying their assembly remain unclear. Here, we use coarse-grained Molecular Dynamics simulations to study their phase behavior in various combinations—including single proteins, pairs, and triplets—with and without DNA. We show that multivalent interactions and DNA binding cooperatively drive condensate formation, and that different combinations exhibit distinct phase separation propensities. These results offer insights into how selective condensate assembly contributes to pluripotency regulation.

3Pos048 高速 AFM による形状測定とナノ力学測定を用いた DNA-MDP1 複合体の薬剤応答解析
Structural and nano-mechanical analysis of drug effects on DNA-MDP1 complexes using high-speed AFM

Kaho Nakamoto¹, Yuna Goto¹, Kenichi Umeda², Akihito Nishiyama³, Sohkiichi Matsumoto³, Noriyuki Kodera² (¹*Grad. Sch. Math. & Phys., Kanazawa Univ.*, ²*WPI-NanoLSI, Kanazawa Univ.*, ³*Dept. Bacteriol., Niigata Univ. Sch. Med.*)

Mycobacterial DNA-binding protein 1 (MDP1) is a protein that promotes dormancy in *Mycobacterium tuberculosis* (Mtb) by compacting its chromosomal DNA. The dormant state of Mtb has drug tolerance, so current anti-TB chemotherapy is less effective to dormant Mtb. Therefore, new drugs are being developed to inhibit the function of MDP1. In this study, we used high-speed AFM to observe how candidate drugs react with the DNA-MDP1 complexes at high spatiotemporal resolution. We found that the addition of drugs relaxed the compacted DNA structure formed by MDP1. Furthermore, we analyzed the effects of drugs on the nano-mechanical properties of the DNA complexes, including Young's modulus, hydrophobic forces, and electrostatic interactions.

3Pos049 Slippage Dynamics of Trinucleotide Hairpins and Their Disruption of the Genome-Maintaining Function of Human Replication Protein A (hRPA)

I-Ren Lee, Yu-Chi Kuang, Cheng-Wei Ni, Szu-Yu Chen (*Department of Chemistry, National Taiwan Normal University*)

Abnormal expansion of trinucleotide repeats (TNRs) is linked to neurodegenerative diseases. TNRs form noncanonical structures that may cause slippage during replication, recombination, or repair, leading to genomic instability. Using single-molecule FRET, we examined TNR hairpins of varying lengths and found that, despite high thermodynamic stability, they undergo repeat-dependent slippage driven by local instability. This behavior likely extends to longer disease-associated repeats. Moreover, slippage interferes with the genome-maintaining function of human replication protein A (hRPA), highlighting DNA slippage reconfiguration as a key factor in TNR-mediated instability.

3Pos050 グルタミン tRNA 合成酵素の分子機構に関する理論的研究
Theoretical study on a molecular mechanism of the glutamyl-tRNA synthetase

Ayaka Matsuyama¹, Masahiko Taguchi², Shigehiko Hayashi¹ (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*IMRAM, Tohoku Univ.*)

Aminoacyl-tRNA synthetases (aaRSs) are essential enzymes in the protein translation process, synthesizing aminoacyl-tRNA which selectively binds tRNA to the amino acid that corresponds to the tRNA. It may be possible to synthesize aaRSs that are compatible with non-canonical amino acids by modifying substrate recognition site of canonical aaRSs. In this study, we analyzed the reaction mechanism of glutamyl-tRNA synthetase, one of the 20 types of canonical aaRS, using ab initio QM/MM free energy geometry optimizations. As a result, our study revealed that proton transfers occur via a water molecule between the nucleophilic OH group of tRNA and the O atom of the phosphate of Glu-AMP during the binding between glutamate and tRNA.

3Pos051 紫外線損傷 DNA の低分子化合物による光修復
Photorepair of UV-damaged DNA by small molecules

Tatsuya Iwata, Rina Fuchigami, Risa Inomata, Manato Okabe, Yumika Ochiai, Fumio Takahashi, Mineo Iseki (*Fac. Phar. Sci., Toho Univ.*)

In the process of attempting spectroscopic analyses against a deoxyribozyme (DNAzyme) binding 5-hydroxytryptamine (5-HT) as an antenna (Thorne et al., *J. Mol. Biol.* 2009), that functions as photorepair of UV-damaged DNA (cyclobutane pyrimidine dimer (CPD) without phosphodiester bond), we found that 5-HT photorepairs UV-damaged DNA even without the DNA oligonucleotides. To investigate mechanisms of 5-HT photorepair of damaged DNA, photorepair of CPD with phosphodiester bond by 5-HT, and photorepair by a 5-HT analog (5-chlorotryptamine, 5-CT) were conducted. We also did not obtain results that the DNA oligonucleotide would increase the effect of 5-HT. Possible photorepair mechanisms of 5-HT and its analog will be discussed.

3Pos052 A Systematic Approach for Integrating DNA Aptamers and DNA-Responsive Nanosystems via Strand Displacement Reactions

Satofumi Kato¹, Masahiro Takinoue², Hiroaki Onoe¹ (¹*Graduate School of Science and Technology, Keio University*, ²*Department of Computer Science, Institute of Science Tokyo*)

DNA aptamers are efficient molecular recognition probes and have been combined with nanosystems functionalized by DNA molecular reactions to construct complex and autonomous sensing systems. However, conventional sensing systems often require direct modifications to the aptamer sequence, which can potentially compromise aptamer affinity. In this research, we propose a systematic approach to integrate DNA aptamers and DNA-responsive nanosystems via DNA strand displacement reactions. Aptamers are incorporated into the system without modification, and the entire system is constructed based on designable DNA molecular reactions. We believe this approach allows the application of aptamers to various DNA-based systems for constructing functional sensing systems.

3Pos053 Self-limited assembly of shape-adjustable DNA origami modules into desired polygonal shapes

Ayu Sakamoto, **Yuki Suzuki** (*Grad. Sch. Eng., Mie Univ.*)

Self-assembly is a ubiquitous mechanism for generating diverse biological structures and complex systems. One of the fundamental principles underlying the formation of fixed-size assemblies of identical molecules is the polymerization of slightly distorted monomers, which limits growth due to strain accumulation. Inspired by this, we propose a modular DNA origami building block whose geometry is tunable by external molecular signals. This nanostructure assembles via shape complementarity at its ends, while the size of the homomultimer is constrained by its internal bending angle, which is predetermined by signal DNAs. The modular design enables self-limiting and programmable assembly into polygonal rings with defined side numbers.

3Pos054 DNA 超らせん構造のねじれと伸長による力学的制御
Mechanical control of DNA supercoils by torsion and extension

Shinnosuke Inui, Anzu Kawamura, Yoshihiro Murayama (*Department of Biomedical Engineering, Faculty of Engineering, Tokyo University of Agriculture and Technology*)

In vivo, the topological state of DNA is altered by various enzymes. Using magneto-optical tweezers, we examined the extent to which the higher-order structures of DNA can be mechanically controlled by torsion and extension. The experimental results showed that loops in a supercoil are exchanged between plectonemes and solenoids in response to changes in tension, indicating that the DNA supercoiling structure is dynamically controlled. This suggests that sequence-dependent DNA mechanical properties regulate gene expression.

3Pos055 ESR 分光学で捉えた液液相分離中のヘテロクロマチンタンパク質 1(HP1)のダイナミクス
Dynamics of heterochromatin protein 1 (HP1) during phase separation, as studied by ESR spectroscopy

Isao Suetake², Kazunobu Sato¹, Toshiki Takei³, Tomoaki Sugishiata³, Yuichi Mishima³, Yoh Matuski³, Toshimichi Fujiwara³, Takeji Takui¹, Makoto Miyata¹, Hironobu Hojo³, **Toshiaki Arata**^{1,3} (¹*Grad. Sch. Sci., Osaka Met. Univ.*, ²*Grad. Sch. Home Economics, Kobe Women's Univ.*, ³*Inst. Protein Res., Univ. Osaka*)

HP1 has a structure of N-tail-CD-HR-CSD-C-tail, with the CSD forming a dimer, and the hinge region (HR) and two tails are IDRs. Nanosecond motions of phosphomimic SD- or SP-HP1 regions labeled with the nitroxyl spin label MSL at LLPS state were measured by ESR spectroscopy, and all restricted, and no spin-spin interaction (<2 nm) was observed in either case. For the IDRs, >50% of label was clearly divided into slow (1-2 ns) and very slow (10-100 ns) modes, while the remaining the same as that (0.7 ns) in 0.3 M NaCl. Interestingly, similar restrictions, especially two modes at IDRs, were observed to low extents even at non-LLPS state, suggesting that LLPS is mediated by dynamic dimers and multimers existing in solutions outside droplets.

3Pos056 Mechanical Insights into Nucleosome Remodeling by divalent Cations: A Single-molecule study

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Nucleosome remodeling dynamics regulate genome accessibility via unstacking and unwrapping. These highly dynamic processes are critical for transcription and replication. Using dual-trap optical tweezers, we studied 4-mer and 12-mer nucleosomal arrays (Widom-601 repeats) under divalent cations (Mg²⁺, Ca²⁺). Without Mg²⁺, outer and inner DNA turns unwrap at low (0–10 pN) and high (10–40 pN) forces, respectively, with rupture events matching nucleosome counts. Mg²⁺ lowers unwrapping forces and induces large disruptions, suggesting nucleosome unstacking. Rupture frequency stays unchanged, indicating Mg²⁺ enhances stacking while easing DNA removal. Overall, Mg²⁺ modulates chromatin mechanics, balancing accessibility, and compaction.

3Pos057 スクレオソーム DNA 引き剥がしダイナミクスの解読：ナノポアが明らかにするヒストン N 末端テイルの役割
Decoding Nucleosomal DNA Unwrapping Dynamics: The Role of Histone N-Terminal Tails Revealed by Nanopores

Satoshi Oghihara¹, Hikaru Nozawa¹, Takumi Oishi², Fritz Nagae³, Munetaka Akatsu², Shoji Takada³, Hitoshi Kurumizaka², Sotaro Uemura¹ (¹*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, ²*Institute for Quantitative Biosciences, The University of Tokyo*, ³*Department of Biophysics, Graduate School of Science, Kyoto University*)

At the single-molecule level, we examined the collective impact of N-terminal histone tails on the complex process of nucleosomal DNA unwrapping, which plays a pivotal role in gene regulation. Utilizing solid-state nanopores to compare canonical nucleosomes with those entirely devoid of N-terminal tails (tailless), we uncovered profound differences in their unwrapping behaviors. Tailless nucleosomes exhibited a markedly more heterogeneous landscape of current blockade pathways, indicating diverse and less constrained unwrapping trajectories compared to canonical nucleosomes. This study highlights the power of nanopore platforms to dissect complex epigenetic regulatory mechanisms.

3Pos058 回折 X 線明滅法を用いた不凍液中の再結晶過程に伴う水分子動態解析
Molecular dynamics analysis of the recrystallization behavior of water in antifreeze solutions by Diffracted X-ray Blinking

Daisuke Sasaki¹, Umena Yasufumi², Yuji C. Sasaki¹ (¹*Department of Advanced Materials Science, Graduate School of Frontier Sciences, The University of Tokyo*, ²*Synchrotron Radiation Research Center, Nagoya University*)

The recrystallization of intracellular water is closely related to biological function and freeze tolerance under low temperatures. This study analyzed the molecular dynamics of water in antifreeze solutions during recrystallization to gain new insights into its behavior. We used Diffracted X-ray Blinking (DXB), which quantifies intensity fluctuations in time-resolved wide-angle diffraction images using pixel-wise autocorrelation. Experiments were conducted at Aichi SR BL2S1. Images were acquired at 300 ms/frame at eight temperatures from 115 K to 205 K. Analysis of the amorphous water region revealed ice rings at 155–185 K, and despite increased thermal fluctuations at higher temperatures, decay constants decreased in this range, indicating reduced molecular motion.

3Pos059 サブテラヘルツ波照射による DNA 塩基対形成の非熱的促進
Non-thermal acceleration of DNA base-pair rearrangement using sub-THz irradiation

Masahiko Imashimizu, Johtaro Yamamoto, Tomoya Inose (*AIST*)

We investigated the effects of sub-THz irradiation on the rearrangement of hydrogen bonds involved in DNA base pairing. We developed a system combining UV absorption and fluorescence correlation spectroscopy (FCS) with sub-THz irradiation to enable in situ monitoring of base-pair formation in aqueous solutions of DNA oligomers with a random sequence. Our results show that sub-THz irradiation markedly accelerates base-pair formation, while equivalent heating does not. This effect depends on the presence of DNA counterions, suggesting a non-thermal mechanism. In this presentation, we summarize our findings and propose a model for the sub-THz irradiation effects on biomacromolecules through modulation of hydration dynamics.

3Pos060 ショウジョウバエ胚の後腸の捻転と伸長は異なる集団細胞移動によって独立して制御される
Distinct collective cell behaviors independently regulate the rotation and elongation of the embryonic gut in *Drosophila*

Mikiko Inaki^{1,2}, Satoru Okuda³, Kenji Matsuno² (¹*Grad. Sch. Sci., Univ. Hyogo*, ²*Grad. Sch. Sci., Univ. Osaka*, ³*Nano LSI, Kanazawa Univ.*)

This study explores how distinct shape changes in epithelial cells are coordinated during organ morphogenesis, focusing on the *Drosophila* embryonic hindgut. The hindgut shows left-right asymmetric rotation and anteroposterior elongation, driven by cell sliding and intercalation, respectively. Genetic analysis and live imaging reveal that Myosin1D and E-cadherin regulate cell sliding, while Par-3 controls intercalation, both requiring MyosinII activity. A mathematical model further demonstrates that these independently regulated cellular dynamics can concurrently drive shape changes via anisotropic edge contraction. This suggests a general strategy where independently controlled cellular behaviors share a common apparatus to shape complex tissues.

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- [3Pos061](#) 細胞性粘菌における細胞分化・脱分化と細胞内 Ca^{2+} 動態の相関分析
Correlative analysis of intracellular Ca^{2+} dynamics with cell differentiation and dedifferentiation in *Dictyostelium*

Rintaro Aono, Yusuke V. Morimoto (*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech.*)

A comprehensive understanding of the mechanisms of cell differentiation and dedifferentiation is essential for the advancement of regenerative medicine and cancer therapy. In this study, we utilized *Dictyostelium discoideum* as a model organism for investigating developmental processes. By comparing intracellular Ca^{2+} signal fluctuations under conditions of induced differentiation and dedifferentiation, we aim to elucidate the underlying mechanisms governing these cellular transitions.

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- [3Pos062](#) 人工ヒト胚モデルにおけるサイズ依存的なパターン形成：胚葉形成のダイナミクスに関する考察
Size-Dependent Pattern Formation in Engineered Human Embryo Models: Insights into Gastrulation Dynamics

Miyu Mori¹, Hazuki Tuboi¹, Ryo Kojima¹, Chihiro Takeuchi¹, Yohei Hayashi², Kiyoshi Ohnuma¹ (¹*Nagaoka University of Technology*, ²*BioResource Research Center, RIKEN*)

Human gastrulation begins with the epiblast, a single-layered disc that forms the three germ layers. To mimic and understand cell movement in human gastrulation, we plated human iPS cells (epiblast-like) with iPS-derived mesoderm cells on a 0.5 mm circular microprint area, roughly comparable to the human epiblast before gastrulation. Mesodermal cells accumulated centrally, forming an early gastrulation-like single-cored pattern, which we reported at the last meeting. Here, when we increased the microprint diameter to 6 mm, mesoderm cells formed islands, creating a multiple-cored pattern, indicating that embryonic size is crucial for gastrulation. These findings advance our understanding of human embryogenesis dynamics unobservable in vivo.

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- [3Pos063](#) 昆虫飛翔筋の回転平均化された2次元X線回折像からサルコメアの3次元構造を復元する
Restoration of the 3D structure of insect flight muscle from a rotationally averaged 2D X-ray diffraction pattern

Hiroyuki Iwamoto (*SPRING-8 · JASRI*)

The contractile machinery of muscle has a very regular array of contractile protein filaments, and gives rise to a complex and informative diffraction pattern when irradiated with X-rays. However, analyzing these diffraction patterns is often challenging mainly because only rotationally averaged diffraction patterns can be obtained. We solved this problem by using coherent diffractive imaging. Using this technique, the real-space 3-D structure of the contractile machinery can be effectively restored from a single rotationally averaged 2-D diffraction pattern. In this calculation, we used the model of insect flight muscle. We also extended this technique to a diffraction pattern experimentally recorded from *Lethocerus* flight muscle.

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- [3Pos064](#) Cilia-like Beating of Clamped Microtubules Driven by Kinesin Motors

Jane Wanja Karanja, Douglas K. Ng'ang'a, Takahiro Nitta (*Applied Physics Course, Faculty of Engineering, Gifu University, Gifu 501-1193, Japan*)

Cilia are prevalent in a myriad of cell types and play vital roles in various cellular activities, including motility and fluid transportation. These activities are fulfilled by cilia beating motion driven by molecular proteins. However, the intricate architecture of natural cilia makes their beating mechanism challenging to understand. Working with simplified, reconstituted systems is beneficial in investigating these fundamental principles. Here, we present a Brownian Dynamics simulation investigation into cilia-like beating of clamped microtubules driven by kinesin motors. Our model captures the buckling deformations and cilia-like beating which offers an enhanced understanding of the underlying mechanism.

3Pos065 Buckling and Trajectory Deflections of Microtubules Driven by Kinesin Motors

Douglas Kagoiya Ng'ang'a, Takahiro Nitta (*Applied Physics Course, Faculty of Engineering, Gifu University*)

Microtubules (MTs) driven by kinesins on solid surfaces function as active polymers, drawing interest as active matter and as means of transport in biosensors. These MTs occasionally get pinned, causing buckling and spiraling. Subsequent depinning may cause deflections of MT trajectories, reducing transport efficiency in biosensors. While defective kinesins are a presumed cause, the mechanisms behind buckling and deflections remain unclear. We present a simulation study on pinning and depinning in kinesin-driven MTs. We observed force-induced depinning with minimal deflection soon after pinning. Without depinning, MTs either get stuck or buckle and spiral. Our findings would improve understanding of MT buckling and deflections and enhance utilization in biosensors.

3Pos066 Cryo-EM visualization of the conformational states of G_1 -ATPase, a rotary motor driving *Mycoplasma mobile* gliding

Takuma Toyonaga¹, Daisuke Unabara¹, Tasuku Hamaguchi¹, Koji Yonekura^{1,2} (¹*IMRAM, Tohoku Univ.*, ²*RIKEN SPring-8 Center*)

Mycoplasma mobile, a fish pathogenic bacterium, exhibits a unique gliding motility powered by a motor that evolved from F_1F_0 -ATPase, a rotary ATPase conserved across most organisms. This motor, designated as G_1 -ATPase, has been identified as a novel member of the rotary ATPase family and assembles into a chained supercomplex within the cell. In the present study, single-particle cryo-EM analysis of isolated G_1 -ATPase in the presence of ATP revealed three distinct conformational states, suggesting that the central shaft rotates in 120° steps—a rotational mechanism conserved among all rotary ATPases. To further investigate the detailed mechanism, we are conducting cryo-EM analysis of G_1 -ATPase in the presence of ATPγS, a slowly hydrolyzing ATP analog.

3Pos067 Development of gold nanoparticle-based optical switches for reversible artificial muscles driven by kinesin motor proteins

Kensei Hori¹, Taiyo Sato¹, Yuich Hiratsuka², Keisuke Morishima⁴, Takahiro Nitta³ (¹*Grad. Sch. Nat. Sci. & Tech., Univ. Gifu*, ²*JAIST*, ³*Univ. Gifu*, ⁴*Univ. Osaka*)

Kinesin motor protein and microtubule can form active networks and have been used to build artificial muscles (AM) for soft robots. However, a major drawback of the AM is that they contract only once and cannot be used repeatedly. To overcome this drawback, we aim to develop a gold nanoparticle-based optical switch that controls the contraction and relaxation of the AM. For this purpose, we created gold nanoparticles modified with thermos-responsive polymers and kinesin motor proteins. With dynamic light scattering and fluorescent observation, we confirmed bindings of the polymer and protein to gold nanoparticles and their reversible thermal response. These results indicate the potential of the modified gold nanoparticles for use as optical switches for the AM.

3Pos068 二重オプトジェネティックツールによるキネシン 14 のアンカー位置制御を介した微小管運動方向の光制御
Light-controlled directional reversal of microtubule motility via dual optogenetic switches regulating kinesin-14 anchoring

Masahiko Yamagishi^{1,2}, Junichiro Yajima^{1,2,3} (¹*Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo*, ²*Komaba Institute for Science, The University of Tokyo*, ³*Research Center for Complex Systems Biology, Universal Biology Institute, The University of Tokyo*)

Force generation by molecular motors on the microtubule is essential for biological processes such as cell division. *In vitro* gliding assays have been used as the reconstitution of these processes, and also have developed for nanotechnological application such as bio-computing. Previous studies using optogenetic tools that control protein–protein interactions have enabled light-regulated start/stop control of microtubule motility. However, direction-control is also critical both in cells and for applications. In this study, we achieved light-controlled reversal of microtubule gliding by combining kinesin-14 monomers, whose motility direction depends on the anchoring point, with two optogenetic tools that exhibit different light-dependent binding/unbinding patterns.

3Pos069 LOV トロポニンによるアクトミオシンの光制御
Light control of myosin-actin based motility by LOV-Troponin

Koki Yasuda (*JAIST*)

In this study, we aim to create an optical control system for the myosin actin movement. Muscle contraction is controlled by regulatory proteins, troponin and tropomyosin, which bind to actin filaments. The myosin-binding site on the actin filaments is masked by Tropomyosin, but Ca^{2+} binding to the calcium-binding domain of troponin (TnC) causes a conformational change, shifting the position of Tropomyosin and activates the muscle. We designed an artificial Troponin that switches from Ca^{2+} control to a blue-light response by fusing portion of TnC with the light-sensitive protein LOV. We will evaluate the light responsiveness by measuring ATPase activity and in vitro motility assay.

3Pos070 脂質二重膜中で機能する ATP 合成酵素のクライオ電子顕微鏡構造解析
Cryo-EM structures of ATP synthases functioning in lipid bilayers

Atsuki Nakano¹, Jun-Ichi Kishikawa², Christoph Gerle⁵, Hideki Shigematsu⁴, Kaoru Mitsuoka³, Ken Yokoyama¹ (¹*Fac. of Life Sci., Kyoto Sangyo Univ.*, ²*Applied Biology, Kyoto Institute of Technology*, ³*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*, ⁴*JASRI*, ⁵*RIKEN SPring-8 Center*)

In this study, the structure of V_0V_1 reconstituted in liposomes during ATP synthesis was determined by structural analysis in the presence of proton motive force (pmf). For V_0V_1 to rotate to synthesize ATP, it is necessary to store energy for every 30° rotation of the c12-ring and then release energy for the 120° rotation of the DF rotor in the V_1 domain. Structural analysis of V_0V_1 presence of pmf revealed that the rotational energy is stored in the rotor and stator subunits by 30° rotation. Furthermore, we have successfully applied this structural analysis method to various membrane proteins and used liposomes and biomembranes to analyze the structures of various membrane proteins under more physiological conditions.

3Pos071 骨格筋の収縮原理を細胞外で模倣したアクトミオシン-フィブリンゲル混合アクチュエータ
Actomyosin-fibrin gel composite actuator mimicking contraction mechanism of skeletal muscle extracellularly

Takuro Kawasumi¹, Koki Yoshida², Yuichi Hiratsuka³, Hiroaki Onoe¹ (¹*Keio University*, ²*Shibaura Institute of Technology*, ³*Japan Advanced Institute of Science and Technology*)

This study proposes actuation system of fibrin gel-actomyosin composite gel actuator, fabricated by embedding reconstituted actomyosin—biomolecular motor proteins derived from chicken skeletal muscle tissue—into a fibrin gel matrix. The actuator contracts upon exposure to adenosine triphosphate, without requiring cell culture processes. This system translates the self-organizing mechanism of the actomyosin molecular motor system into macroscopic motion using only biologically derived proteins. We succeeded in fabricating the first actomyosin gel actuator using fibrin gel. Furthermore, we evaluated the performance of the actuator in terms of Young's modulus, contractility, and contractility force, and discussed the superiority of the actuator over previous studies.

3Pos072 情報熱力学による F_1 -ATPase 内の相互作用の実験的評価
Experimental evaluation of interactions within F_1 -ATPase based on information thermodynamics

Ken Takagi¹, Yohei Nakayama¹, Chun-Biu Li², Stefano Bo³, Takahiro Sagawa⁴, Shoichi Toyabe¹ (¹*Department of Applied Physics, Tohoku University, Japan*, ²*Department of Mathematics, Stockholm University, Sweden*, ³*Department of Physics, King's College London, United Kingdom*, ⁴*Department of Applied Physics, The University of Tokyo, Japan*)

The biological molecular motor F_1 -ATPase is known to efficiently convert mechanical and chemical work, but the mechanism underlying this high efficiency remains unclear. In this work, to elucidate this mechanism, we focused on the interaction between the rotating shaft and the stator that drives the shaft rotation by exploiting the framework of information thermodynamics. In particular, we quantified the information and energy flows between subunits by analyzing single-molecule trajectories, allowing us to discuss the thermodynamics of each subsystem. We observed asymmetrical flow patterns between ATP hydrolysis and synthesis. We discuss the implications of these results, with a particular focus on the relation between energy conversion efficiency and information flow.

3Pos073

Enterococcus hirae V-ATPase の Na⁺能動輸送を支える a サブユニットの 2 つのハーフチャネルの非対称な Na⁺結合親和性
Asymmetric Na⁺ binding affinities of two half-channels in a-subunit support active Na⁺ transport of *Enterococcus hirae* V-ATPase

Akihiro Otomo^{1,2}, Yuan-E Lee^{3,4}, Juliette Lahore⁵, Raymond Burton-Smith^{2,3,4}, Kano Suzuki⁶, Takeshi Murata⁶, Kazuhoshi Murata^{2,3,4}, Ryota Iino^{1,2} (¹*Institute for Molecular Science*, ²*SOKENDAI*, ³*ExCELLs*, ⁴*National Institute for Physiological Sciences*, ⁵*Chmie ParisTech*, ⁶*Grad. Sch. Sci., Univ. Chiba*)

Enterococcus hirae V-ATPase actively transports Na⁺ across the membrane. To understand mechanism of active transport, we investigated Na⁺ affinities of two half-channels in stator a-subunit of V_o using cQ651 mutant in which Na⁺ binding site of rotor c-ring was modified. Detergent-solubilized cQ651 showed no clear Na⁺ densities at ion binding sites of the rotor c-ring in cryo-EM structural analysis, even at 100 mM Na⁺. Furthermore, cQ651 reconstituted into liposome transported H⁺ and was competitively inhibited by Na⁺ outside the liposome (entrance half-channel side) but not by Na⁺ inside (exit half-channel side). These results demonstrate largely different Na⁺ binding affinities between two half channels and an essential structural basis supporting active Na⁺ transport.

3Pos074

Elucidating Dynein Velocity Enhancement via Binding Affinity Modulation

Haruki Kawase^{1,2}, Kenta Ishibashi², Akane Furuta², Ken'ya Furuta^{1,2} (¹*The university of Osaka*, ²*National institute of information and communications technology*)

Biomolecular motors are proteins that convert chemical energy to physical force. Although their various velocities are important in playing their various roles, it is not revealed how to determine the velocities. Previous studies have shown the myosin's binding affinity contributes to the velocity. Therefore, we substituted several amino acids in the microtubule-binding domain of dynein to reduce this binding affinity. As a result, one of the modified dyneins exhibited an 18-fold increase in velocity compared to the wild type. Although Affinity is defined as the ratio of the association rate constant to the dissociation rate constant, there is no study monitoring them. This study aims to clarify them and elucidate how to determine the velocity of biomolecular motors.

3Pos075

アクチン架橋タンパク質による細胞間境界の力安定性維持機構
Actin Crosslinking Proteins Maintain Force Stability at Cell-Cell Boundaries

Hiroki Katsuta¹, Satoru Okuda², Nobutomo Fujimoto³, Duc Doan Manh¹, Hiroaki Hirata⁴, Keiji Naruse¹ (¹*Faculty of Med. Dent. and Pharm Sci., Okayama Univ.*, ²*Nano LSI, Kanazawa Univ.*, ³*Dept. Med., Okayama Univ.*, ⁴*Dept. Life Sci. and Biotech., KIT*)

The actomyosin system serves as a force generator in adherent cells, contributing to adhesion to neighboring cells and substrates. Previously we have found that stress fibers become more heterogeneous when actin crosslinking proteins (ACPs) are depleted. However, how ACPs affect adherens junctions (AJs) remains unclear. Time-lapse imaging of fluorescently labeled AJ proteins revealed that AJ displacement significantly increased upon ACP depletion in a force-dependent manner. Our results suggest that ACPs contribute to force stability at cell-cell boundaries, which might be essential for regulating cell density and proliferation.

3Pos076

Scale-dependent mechanobiological responses of focal adhesions

Gento Takeshima, Takumi Saito, Shinji Deguchi (*Grad. Sch. Eng. Sci. Univ. Osaka*)

Focal adhesions (FAs) are protein complexes that anchor cells to the extracellular matrix and mediate signaling. Beyond their adhesive role, FAs regulate cellular functions through force-dependent signaling pathways. Paxillin, an adaptor protein located in FAs, is essential for maintaining FA stability, which is modulated by its phosphorylation-dephosphorylation state. However, the relationship between paxillin phosphorylation and mechanical forces within FAs remains unclear. Here, we investigated this relationship by pharmacologically modulating endogenous force generation. Interestingly, different experimental approaches revealed opposing responses at the subcellular and whole-cell levels, suggesting distinct mechanobiological responses of FAs depending on the scale.

3Pos077 歯周病菌の Fim 線毛先端タンパク質 FimE の C 末端領域の構造
Structure of the C-terminal region of FimE, a tip protein of the Fim pili from *Porphyromonas gingivalis*

Hikaru Tanizaki¹, Norihiro Takekawa², Katsumi Imada² (¹Sch. Sci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ.)

Porphyromonas gingivalis is a major pathogen for periodontal disease and has the Fim pili, an adherence factor for infection. The Fim pili consists of five types of proteins: the anchor pilin, the stalk pilin, and three tip pilins (FimC, FimD, and FimE). Though the tip pilins are essential for cell adhesion, their roles in adhesion and target molecules remain unclear. Here, we determined the structure of the C-terminal region of FimE at 1.9 Å resolution. The structure comprises two domains: an N-terminal BACON domain and a C-terminal domain. The BACON domain is known as a glycoprotein-binding domain. The C-terminal domain exhibits structural resemblance to DNA or disaccharide-binding domains in eukaryotes, suggesting FimE is involved in DNA or disaccharide binding.

3Pos078 Light-Guided Actin Dynamics Drives Protocell Migration

Hideaki Matsubayashi¹, Shiva Razavi², Daichi Nakajima³, Hideki Nakamura⁴, Tomoaki Matsuura⁵, Shin-ichiro Nomura³, Takanari Inoue² (¹Frontier Research Institute for Interdisciplinary Sciences (FRIS), Tohoku University, ²School of Medicine, Johns Hopkins University, ³Graduate School of Engineering, Tohoku University, ⁴Hakubi Center for Advanced Research, Kyoto University, ⁵Earth-Life Science Institute, Science Tokyo)

Cell migration emerges from cytoskeletal protein dynamics, with actin polymerization as the primary force-generating mechanism. To investigate the minimal requirements for directional motility, we engineered a light-controlled system enabling spatiotemporal control of actin polymerization within giant unilamellar vesicles (GUVs). This reconstituted system generated actin-driven membrane protrusions and sustained unidirectional movement at 0.43 micron/min. Analysis reveals that cooperative mechanics between branched and linear actin networks drive force generation and membrane deformation. This platform provides quantitative insights into cytoskeletal force transduction and a reductionist approach for investigating cellular motility.

3Pos079 Elucidating the role of *Spiroplasma* fibril protein using synthetic bacterium, JCVI syn3

Ali Ahsan, Hana Kiyama, Makoto Miyata (Grad. Sch. Sci., Osaka Metropolitan Uni.)

Spiroplasma swims by switching the handedness of the internal ribbon structure composed of fibril, and five MreB proteins. The role of fibril in *Spiroplasma* swimming is still unclear. To clarify the function of fibril, we incorporated syn3 cells with Fibril alone, as well as with individual MreB4 and MreB5 proteins, and their combination. The cells with fibril alone, and fibril with MreB4 exhibited non-motile and left-handed helical phenotype, MreB5 alone was right-handed, and fibril with MreB5 showed both configurations. The swimming syn3 cell with fibril exhibited better swimming processivity and stabler helicity switching compared with MreB54 cells lacking fibril. This suggests a possible role of the fibril as a frame for *Spiroplasma* swimming.

3Pos080 Manipulation of rotational direction of the archaeal flagella motor in *Halobacterium salinarum* by light modulation

Jumpei Segal¹, Masaki Mizutani¹, Daisuke Nakane², Takayuki Nishizaka¹ (¹Gakushuin University, ²University of Electro-Communications)

H. salinarum, a halophilic archaeon, moves forward and backward by rotating its archaeal flagella (archaella) in a clockwise and counter-clockwise manner, respectively. Photoreceptor called 'sensory rhodopsin I' detects light of specific wavelength, 587 nm in peak, and modifies the rotation with CheY through its phosphorylation. We illuminated orange light to a cell anchoring to the glass through a single archaellum under an optical microscope. Unexpectedly, repetitive 3-second illumination with 3-s intervals induced continuous changes in rotational direction, which was contradictory to the previous report in terms of phototaxis. Using this manipulation method in a tethered-cell assay, we will address the rotational dependency of torque powered by the archaeal motor.

3Pos081

クラミドモナス鞭毛におけるマスティゴネマ線維の構造と機能

Strucutre and function of mastigoneme filaments in *Chlamydomonas* cilium

Toshiki Yagi, Ryuta Yoshizawa, Kakeru Komori (Dept. Life and Env. Sci, Pref. Univ. Hiroshima)

Chlamydomonas possesses lateral filaments, mastigonemes, on the distal two-thirds region of the cilium. The filaments are thought to enhance ciliary force generation by increasing the surface area during the cilia motion. Recently, they have been found to be anchored to the mechano-sensitive channel PKD2. Interestingly, the wild type exhibited 10% increase in swimming speed after mechanical agitation, whereas the *mst1* mutant, which loses all the mastigonemes, showed no increase in swimming speed. The increase was abolished in the absence of extracellular Ca^{2+} , suggesting that mastigonemes function not only physical structures to increase ciliary surface area for more effective force generation, but also sensory structures for mechanical stimuli via PKD2 channel.

3Pos082

マイクロ構造体を用いた運動性を持つ微生物の運動方向の操作

Manipulation of the direction of movement of motile microbes using microstructures

Masaru Kojima¹, Mitsuhiro Horade² (¹Grad. Sch. Eng.Sci., The Univ. of Osaka, ²Fac. of Sci. and Eng., Setsunan Univ.)

In recent years, research on bio-hybrid systems that utilize organisms and biomolecules as actuators has attracted much attention. In such research, methods have been proposed to control and apply the motion of microscopic organisms by applying microstructures. Restricting the movement of a moving microorganism has many advantages, such as making it possible to observe the organism for a longer period of time and facilitating the measurement of its movement characteristics. Therefore, in this study, we proposed a wall-shaped microstructure that can be used to control the direction of movement of microorganisms and to immobilize them, and confirmed its effectiveness.

3Pos083

機械的な力の付加による細胞集団運動の変化から機械走性メカニズムに迫る

Approaching the Mechanism of Mechanotaxis via Collective Cell Migration Induced by Mechanical Force Loading

Chihori Asano¹, Keitaro Shibata², Shigenobu Yonemura² (¹Grad. Sch. Med., Tokushima Univ., ²Grad. Sch. Biomed. Sci., Tokushima Univ.)

Cells exhibit mechanotaxis, the ability to sense mechanical forces as signals and determine the direction and speed of their migration. In monolayer sheets formed by epithelial cells, individual cell movements propagate to surrounding cells as mechanical stimuli, forming complex mechanical networks. However, due to difficulties in visualizing and quantifying forces, the mechanisms of mechanotaxis remain poorly understood. In this study, we applied localized mechanical forces to epithelial cell sheets using magnetic tweezers and laser ablation. We observed a distinct migratory polarity in response to specific external forces. By analyzing the relationship between force and the direction of migration, we aim to elucidate the detailed mechanism underlying mechanotaxis.

3Pos084

Phototaxis and light-driven accumulation in wild isolates of *Heterosigma akashiwo*

Naoki Uemura¹, Shoko Ueki², Daisuke Nakane¹ (¹Dept. Eng. Sci., Univ. Electro-Communications, ²Inst. Plant Sci. Res., Univ. Okayama)

Heterosigma akashiwo causes harmful algal blooms (HABs), but the mechanism underlying its rapid growth and accumulation remains unclear. Here, we visualized blue-light-dependent phototaxis and the resultant accumulation characteristic in wild isolates from HABs. Phototaxis was synchronized with a 12-h light/dark cycle, moving positively at noon and negatively at dusk. Cells propelled straight with rotation at 1 Hz, presumably essential to recognize light direction. To test this, we exposed the cells to modulated light at the same frequency as their rotation, which disrupted phototaxis. This study demonstrates that wild isolates of HABs exhibit light-driven accumulation, which can be artificially controlled through periodic light irradiation.

3Pos085 Dynamic response of keratin assemblies to thermal stress in mutant keratinocytes implicated in Epidermolysis bullosa simplex

Doyin Rachael Abiola¹, Tetsuya Kitaguchi², Birgitte E. Lane³, Madoka Suzuki¹ (¹*Inst. Protein Res., Univ. Osaka*, ²*Inst. Integr. Res., Sci. Tokyo*, ³*SRIS, Singapore*)

Epidermolysis bullosa simplex (EBS) is a genetic skin blistering disorder primarily caused by mutations in keratin intermediate filament protein genes *KRT5* or *KRT14*. Patient symptoms are often reported to grow with increased heat. In cultured mutant cells, keratin forms condensates as well as the normal filaments. To gain mechanistic insights, we examined keratin dynamics under thermal stress in real time using optically controlled localized heating. Condensates are predominantly localized at the cell periphery, but upon heating, the condensates appeared broadly throughout the cell cytoplasm and their number increased significantly. We quantitatively analyze the characteristic parameters such as the number and size of the condensates under varying thermal stresses.

3Pos086 植物左右ねじれ伸長創発メカニズムの解明
Elucidating the mechanisms of plant chiral growth

Eiki Meguro¹, Masayoshi Nakamura², Toshifumi Mori³ (¹*Grad. Sch. Sci., Nagoya Univ.*, ²*Grad. Sch. Sci. and Eng., Saitama Univ.*, ³*Institute for Materials Chemistry and Engineering, Kyushu Univ.*)

Chirality is a characteristic observed in plant growth. While such chirality is thought to be genetically regulated, the mechanisms for determining left-right handedness are unknown. In prior research, twisting mutants of *Arabidopsis thaliana* had been isolated. Most of these twisting mutants were found to have a single amino acid substitution in a tubulin gene, which encodes a component of microtubules. However, the mechanism by which this microscopic phenomenon at the amino acid level leads to the macroscopic changes in plant twisting remains poorly understood. In this research, two *Arabidopsis* twisting mutants, TUB2^{P287L}, which exhibits right-handed growth, and TUB4^{E388K}, which exhibits left-handed, were analyzed using live cell imaging and molecular simulations.

3Pos087 出芽酵母アクチンフィラメントの in situ 構造解析に向けた取り組み
Towards in situ Structural Analysis of Actin Filaments in Budding Yeast

Hiroyo Takazaki¹, Kana Shimamoto^{1,2}, Stephen Mwaniki¹, Misaki Arie¹, Akira Shinohara¹, Takayuki Kato¹ (¹*IPR, Univ. Osaka*, ²*Grad. Sch. Sci., Univ. Osaka*)

Recent advances in cryo-LM and cryo-FIB have enabled in situ structural analysis of cellular proteins by cryo-EM. Here, we focus on actin filament structures in *Saccharomyces cerevisiae*, which, despite containing a single actin isoform, forms three distinct structures—patches, cables, and rings—exclusively in cells. To selectively visualize these structures, we use yeast strains expressing Abp140-GFP, an actin filament-binding protein, and Myo1-RFP, a marker for actin-myosin rings. The 3D cryo-CLEM is used to localize regions of interest (ROI), followed by cryo-FIB milling to prepare thin lamellae including ROI. Subsequent cryo-ET imaging is performed to gain insights into the organization and function of distinct actin filament assemblies in yeast.

3Pos088 ケモメカニカルモデルによる焦点接着斑とアクトミオシン動態の解析
Chemomechanical Model of Focal Adhesion–Actomyosin Dynamics

Eiji Matsumoto, Shinji Deguchi (*Graduate School of Engineering Science, The University of Osaka*)

In this work, we present a chemomechanical approach to focal adhesion–actomyosin dynamics. Specifically, this approach focuses on two variables—focal adhesion area and actomyosin-generated tension—which form a mutual feedback loop based on major signaling pathways (e.g., RhoA and Rac1). To capture the inherent timing of these pathways, we use delay differential equations to explicitly model their response times as delays. As a result, our findings indicate that the presence of a time delay and changes in the activation states of these signaling pathways capture the diverse adhesion dynamics observed experimentally, unifying them in a single phase diagram.

3Pos089

分子シャペロン α B-クリスタリンはチューブリン凝集を抑え微小管会合活性を維持する
The molecular chaperone α B-crystallin delays thermal aggregation of tubulin and maintains microtubule polymerization activity

Shinya Horinouchi^{1,2}, Daisuke Inoue³, Shohei Yamamoto⁴, Eri Fujita⁵, Miho Shimizu², Toshiyuki Watanabe¹, Yoriko Atomii² (¹Grad. Sch. of Eng., Tokyo Univ. Agric. and Technol., ²ACRO, Teikyo Univ., ³Faculty of Design, Kyushu Univ., ⁴Grad. Sch. of Pharmaceutical Sci., The University of Tokyo, ⁵Faculty of Medical Tech., Teikyo Univ.)

Tubulin is unstable and prone to aggregation, limiting long-term in vitro observation. α B-crystallin acts as a molecular chaperone to suppress aggregation and maintain proteostasis. We previously showed that α B-crystallin inhibits tubulin aggregation and enhances microtubule resistance to depolymerizing stress, though the process remained unclear. In this study, we monitored temporal changes in tubulin aggregation and polymerization activity at 37 °C over 6 h by fluorescence imaging. α B-crystallin delayed both the formation and growth of aggregates during the early phase (0.5–3 h) and preserved polymerization activity. Moreover, α B-crystallin deficiency impaired neuronal differentiation, suggesting its potential dynamic chaperone role in microtubule regulation.

3Pos090

生細胞内における力伝播
Force propagation inside a living cell

Ayama Tokuyasu, Hirokazu Tanimoto (Graduate School of Nanobioscience., Univ. Yokohama city)

Mechanical forces produced in living cells are essential in various cell-biological processes including cell motility and division. However, it is difficult to map the propagation of forces inside the cell. We established a new approach for mapping the propagation of mechanical stresses in the cytoplasm of adherent cells. By combining intracellular magnetic tweezers with traction force microscopy, we investigated how mechanical forces applied to the cell propagated in the cell to the cell-substrate boundary. We found that the mechanical force partly spreads in the cytoplasm during propagation. In the presentation, we will show these results and discuss about the feature of the propagated forces and the roles of cytoskeletons in the forces propagation.

3Pos091

High Hydrostatic Pressure Regulates the TGF- β Signaling Pathway

Xinxuan Li (Okayama University)

Transforming growth factor- β (TGF- β) is a key regulator of articular cartilage anabolism and plays a critical role in cartilage development and homeostasis. However, how high hydrostatic pressure modulates this pathway remains unclear. In this study, we investigated the response of chondrocyte TGF- β signaling to high hydrostatic pressure stimulation. We found that high hydrostatic pressure (>20 MPa) induced nuclear translocation of Smad 3 molecules from the cytoplasm. This translocation was also inhibited by blocking the TGF- β type I receptor (ALK-5). These results suggest that high hydrostatic pressure activates the TGF- β signaling pathway in chondrocytes through ALK-5, facilitating the nuclear translocation of Smad 3 and cartilage-specific genes.

3Pos092

大腸菌のアレイブリンキングにおける活性伝搬の役割
The role of signal transduction in *E. coli* array blinking

Kaho Yoshinari, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka, Yumiko Uchida (Grad. Sch. Frontier Biosci. Univ. Osaka)

In *E. coli*, flagellar motors switch the rotational direction coordinately without external signals. Recently, we proposed the fluctuation in CheYp concentration derived from the spontaneous array blinking of receptor array activity controls multiple motors. We hypothesized this blinking is triggered by the cooperative spread of activation across the array, originating from the activation of a single receptor molecule. To test this, we measured the strength of switching coordination in cells co-expressing wild-type Tar and mutant Tsr lacking cooperative response to serine. The strength of coordination decreased with increasing the ratio of mutant Tsr to Tar. Based on results, we discuss the relation of cooperativity in the array and the array blinking.

Satomi Itoki¹, Naoki Hidaka³, Ikuro Kawagishi^{1,2,3}, Yoshiyuki Sowa^{1,2,3} (¹*Grad. Frontier Biosci., Hosei Univ.*, ²*Res. Cent. Micro-nano Tech., Hosei Univ.*, ³*Dept. Frontier Biosci., Hosei Univ.*)

E. coli cells swim by rotating their flagellar motors and control rotation direction to navigate toward favorable environments. Chemotaxis, a response to chemical stimulation, has been extensively studied as a model for intracellular signal transduction. In contrast, the molecular mechanisms of phototaxis remain poorly understood. Here, we use FRET to observe how *E. coli* cells exhibit a repellent response to blue light at the molecular level. To minimize interference between blue light exposure and fluorescence excitation, we chose to use long-wavelength fluorescent proteins fused to the response regulator CheY and its phosphatase CheZ. We are currently establishing a FRET-based analysis to detect CheY-CheZ interactions in response to blue light stimulation.

Moeno Furuya¹, Momo Akada², Tomoyuki Kaneko^{1,2} (*1**FB, Hosei Univ.*, *2**FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

Reentry is one of the main causes of fatal arrhythmias. To clarify the detailed mechanisms of the reentry, we aim to elucidate the mechanism by reproducing reentry *in vitro*. In this study, we used a Multi-Electrode Array (MEA) system, which allows simultaneous multi-point recording of extracellular potentials, combined with agarose microfabrication to control cell shape and adhesion on the MEA system. By irradiating with a near-infrared laser to locally raise temperature, we could arbitrarily set the active firing origin and analyze conduction velocity at each electrode. We attempted to measure the conduction delays and induce reentry caused by changing the width of part of a circular cardiomyocyte network and inducing the beating initiation near that region.

Kanan Tominaga, Takaaki Nishikawa, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

Irradiation of cardiomyocytes with near-infrared laser is known to induce beating. We used this phenomenon to calculate the refractory period of cardiomyocytes. In this study, cardiomyocytes isolated from the hearts of 7-day-old chick embryos were seeded onto multi-electrode array probe, and the refractory period was calculated from the extracellular potential recordings obtained through periodic irradiation with near-infrared laser. As a result, the refractory period was found to be a reasonable value for cardiomyocytes of chick embryos. In the future, we will derive the refractory period of cardiomyocytes under various conditions, since the refractory period depends on the cell condition, temperature, and the original beating cycle.

Yuna Honda, Kentaro Kito, **Tomoyuki Kaneko** (*LaRC, FB, Hosei Univ.*)

Fibrosis with myocardial infarction is known to cause arrhythmia and heart failure. We are developing a model system to reproduce the cardiomyocyte network of such a fibrotic model of the heart and to verify the treatment or the side effects of drugs. Striped cardiomyocyte networks were created by combining a Multi-Electrode Array (MEA) system for extracellular potential measurement and agarose microchambers for controlling cell adhesion sites. Fibroblasts proliferating from the cardiomyocyte network bridged between the cardiomyocyte networks, creating striped cardiomyocyte-fibroblast networks. Extracellular potential measurements with MEA system revealed fast conduction within the cardiomyocyte network and slow conduction through the fibroblasts.

3Pos097 環状心筋細胞ネットワークにおける発火起点からの細胞外電位の振幅の変化
Variation of Extracellular Potential Amplitude in Circular Cardiomyocyte Network from Active Firing Origin

Momo Akada, Kentaro Kito, Tomoyuki Kaneko (*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

Cardiac arrhythmias often result from abnormal conduction. To artificially reproduce such phenomena, we investigated the effects of near-infrared laser irradiation on the circular cardiomyocyte network. In this study, we utilized a combination of multi-electrode array (MEA) technology and an advanced agarose micro-patterning technique. Analysis of peak-to-peak amplitudes revealed that near-infrared laser irradiation significantly modulates extracellular potential amplitudes. Specifically, a reduction in amplitude was observed near the active firing origin, with amplitude progressively increasing farther from the origin. This understanding is vital for controlling conduction and reconstructing reentry in vitro, thereby advancing arrhythmia research.

3Pos098 高フレーム撮影による2つの心筋細胞の拍動同期解析
Analysis of two Cardiomyocytes beating synchronization with high-frame-rate imaging

Sasa Shimizu, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

Cardiomyocytes (CMs) possess automaticity and adjacent CMs are connected by gap junctions to synchronize their beating. The purpose of this study is to control CMs derived from chick embryos at the single-cell level and clarify the mechanisms of beat synchronization and its fluctuations between adjacent CMs. The beating was quantified by seeding agarose micro chambers (AMCs) with CMs and recording changes in cell surface brightness caused by contractions using a high-frame-rate camera. Dumbbell-shaped AMCs were fabricated, and cells with beat initiation were identified by comparing the starting point of intensity change when two CMs connect and synchronize their beating. In the future, we will examine the mechanisms of beat synchronization by connecting multiple CMs.

3Pos099 近赤外線レーザー照射による心筋細胞のFPD評価
Variation in Field Potential Duration of cardiomyocytes induced by near-infrared laser irradiation

Yuka Motoyama, Tomoyuki Kaneko (*FB, Hosei Univ.*)

The QT interval in the ECG is known to correlate with the beating interval of the heart. This corresponds to field potential duration (FPD) in the extracellular potential of cardiomyocytes *in vitro*. In this study, we controlled the beating interval of cardiomyocytes cultured on Multi-Electrode Array (MEA) probe using near-infrared laser irradiation and clarified the correlation with FPD. FPD was calculated from the change in extracellular potential of cardiomyocytes on MEA probe in response to the near-infrared laser irradiation interval. As a result, the relationship between the beating cycle and FPD was clarified. For future study, we would like to investigate the FPD of cardiomyocyte by varying the interval of laser irradiation.

3Pos100 Single-molecule imaging analysis of mutual inhibition and positive feedback for Ras excitability in eukaryotic migrating cells

Satomi Matsuoka, Koji Iwamoto, Masahiro Ueda (*Grad. Sch. Frontier Biosciences, Univ. Osaka*)

Mutual inhibition and positive feedback compose a core of an excitable mechanism for anterior-posterior polarity formation in eukaryotic migrating cells. Such signaling molecules like Ras small G-protein, RasGEF, phosphoinositide kinase/phosphatase and phosphoinositides exhibit co-localizing or mutually exclusive domain-like accumulations on the cell membrane spontaneously. Quantitative analysis of membrane-association/dissociation kinetics and lateral diffusion of them by single-molecule imaging revealed the molecular basis of the excitable mechanism. Here, the reconstitution of the spatiotemporal dynamics by single-particle simulations will be discussed, which provides a mechanistic insight into the spontaneous generation of anterior-posterior polarity.

3Pos101 脂質凝集体の脂質分子パッキングに対するスクラロースとスクロースの効果の比較
Comparison of the effects of sucralose and sucrose on the lipid molecular packing in lipid aggregates

Yuki Homma, Hiroshi Takahashi (*Grad. sch. Sci. Tech. Gunma Univ.*)

Sucralose (SCL), obtained by chlorinating sucrose (SCR), was believed to have no impact on physiological functions. However, it has recently been found to affect the immunity of mice, presumably due to its effect on lipid membranes. To clarify how SCL interacts with lipid membranes, we studied the structural changes of three types of lipids. Studies of lipid systems that can adopt a cubic or inverted hexagonal phase revealed that adding SCL stabilized the lamellar phase, whereas adding SCR did not. These results suggest that SCL increases the occupied area per lipid molecule at the membrane surface. Furthermore, to compare the effect of SCL with that of SCR, we estimated the occupied area per lipid molecule by analyzing X-ray diffraction data.

3Pos102 ハイドロゲルで被覆されたモデル生体膜アレイ
Model membrane array sealed with a hydrogel layer

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Model lipid bilayer membranes provide a platform to study the interactions and mechanics of natural cellular membranes. We have developed a supported lipid bilayer (SLB) array in a framework of polymeric lipid bilayer in which the SLBs are covered beneath a hydrogel. The microchannel was produced from lithographically polymerized diacetylene phospholipid DiynePC. The continuous SLBs were generated by self-spreading of lipid bilayer from condensed reservoir. The hydrogel acted as a sealing film on top of the SLB. It suppressed the bulk flow and allowed selective observation of biomolecules on the SLBs. This microchannel system can be applied for fundamental biophysical studies and biomedical applications such as high-throughput screening and biosensors.

3Pos103 バイオフィーム脱離因子 Dspl が関連する膜リモデリングは緑膿菌バイオフィームにおける細胞外小胞形成を誘発する
Membrane remodeling by a biofilm dispersion factor Dspl enhances vesicle formation in *Pseudomonas aeruginosa* biofilms

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A broad range of bacterial species release membrane vesicles (MVs), nano-sized spherical structures (20–400 nm), and MV formation is activated under biofilm conditions. In *Pseudomonas aeruginosa*, deletion of *dspl*, which encodes an enzyme for the biosynthesis of a biofilm dispersal signal *cis*-2-decenoic acid (CDA), significantly repressed MV production. The aim of this study was to unravel the mystery of the relationship between Dspl and enhanced MV production in biofilms. In the *dspl* mutant, decreased outer membrane permeability and alteration of the fatty acid composition in MV were observed. Our study demonstrated the involvement of a biofilm dispersion factor in enhancing MV production with membrane remodeling in *P. aeruginosa* biofilms.

3Pos104 人工膜とナノ空間を用いた生体分子・膜小胞解析技術の開発
Analyzing biomolecules and vesicles using model membranes and nanometric gap junction

Yu Yoshimura¹, Nanami Nagatsuka¹, Taisei Higashihara¹, Rinshi S. Kasai², Kenichi G.N. Suzuki^{2,3}, Kenichi Morigaki⁴ (¹*Grad. Sch. Agri., Kobe Univ.*, ²*National Cancer Center Japan*, ³*iGCORE., Gifu Univ.*, ⁴*Biosignal Research Center., Kobe Univ.*)

Extracellular vesicles (EVs) are secreted by all cells and selectively transport biomolecules such as proteins, lipid, and nucleus among cells. However, the methodology for EV purification has not been definitively established. In this study, we will introduce a model nanometric gap junction on a patterned supported lipid bilayer for separating EVs by the affinity to the lipid membrane and EV size distribution. As a model of EVs, Quantum dots and phospholipid vesicles were bound to the SLBs and introduced into the nanometric gap junction with different thickness. In the future, separation of EVs using the nanometric gap on the SLBs will be conducted to explore the relationship between EV size and molecules they contain.

3Pos105 粗視化分子動カモデルによる SARS-CoV-2 エンベロープ膜の構造と形成の探索
Exploring SARS-CoV-2 envelope structure and formation by coarse-grained molecular dynamics simulation

Ryo Urano, Wataru Shinoda (*Okayama Univ. RIIS*)

Development of virus-like particle (VLP) can provides a safe way to investigate replication cycle of virus without nucleic materials, and consists of viral proteins and various lipids molecules. On the otherhand, the structural function of each component of the proteins and lipids to build viral envelop remains unclear. SARS-CoV-2 (CoV2) envelope has three membrane proteins: Spike(S), Envelope(E), and Matrix(M) protein. We performed the molecular dynamics simulations for different membranes with various compositions changing the type of proteins and lipids to compare the shape and orientation of molecules to investigate that how protein-protein or protein-lipid interactions affect the structure of the envelope required for VLP design.

3Pos106 Curcumin and its derivatives modulate membrane domains and induce IL-6 receptor shedding in monocytes

Toshiyuki Murai¹, Yoshikazu Masaki², Kazuma Yasuhara² (¹*Grad. Sch. Med., Osaka Univ.*, ²*Grad. Sch. Sci. Tech., NAIST*)

Proteolytic cleavage and release of single-spanning transmembrane receptors, a process called shedding, is vital for normal physiological functions and pathological responses, including inflammation and cancer. IL-6 receptor is one of the principal single-spanning transmembrane receptors localized in membrane rafts in leukocytes. Herein, we report that turmeric curcumin and its amphiphilic derivatives induce IL-6 receptor shedding in human monocytic cells via ADAM10 proteinase, and altered the membrane domains formed on cell-sized giant vesicles. These findings offer a novel strategy to develop therapeutic intervention using membrane-active compounds, such as curcuminoids, for diseases such as inflammation and cancer.

3Pos107 微細穴にマニピレートしたヒト培養細胞と基板支持脂質膜間の脂質移行の促進
Enhanced Lipid Transfer Between Micropore-Manipulated Human Cells and Supported Lipid Bilayers

Asahi Gono¹, Takayuki Nakaya², Reibun Sakane², Naoki Shimura², Takashi Okuno^{3,4} (¹*Grad. Sch. Sci., Univ. Yamagata*, ²*Orbray CO., Ltd.*, ³*Fac. Sci., Univ. Yamagata*, ⁴*CID, Univ. Yamagata*)

We are developing a supported cell membrane system by fusing cultured cells with a supported lipid bilayer (SLB) to simplify membrane protein purification. Previously, we showed that phospholipid transfer from SLB to cell membranes increased from ~5% to ~80% with PEG (Mw = 8,000). In this study, as a PEG-free method, HeLa cells were manipulated by suction into micropores ($\phi 2, 4, 6 \mu\text{m}$) formed on SLBs containing N-Rh-PE. Even without PEG, about 80% of HeLa cells manipulated into micro-wells showed transfer of fluorescent phospholipids. This efficient lipid mixing is likely due to tight contact between the cell membrane and the SLB within the wells. We will also report transfer of cell-derived glycosphingolipids to the SLB.

3Pos108 反応拡散方程式に基づく真核細胞の小胞体におけるタンパク質ドメイン形成に関する数理モデル
Modeling the formation of protein domains on the endoplasmic reticulum in eukaryotic cells with reaction-diffusion equations

Tomoyo Nishigaki, Masashi Tachikawa (*Grad. Sch. of Nanobiosci., Yokohama City Univ.*)

Elucidating the mechanism of membrane traffic, a system for transporting macromolecules by wrapping them in vesicles, is essential for understanding the various cellular functions. In membrane traffic, vesicles bud from a source organelle and fuse with a destination organelle to deliver their contents. Although the transport between the endoplasmic reticulum (ER) and the Golgi apparatus is well-studied, formation and stabilization mechanisms of ER exit site (ERES) remain unrevealed. Focusing on two components of ERES, Sar1p and Sec23/24p, we constructed two mathematical models for ERES formation and evaluated them. Model 1 reproduced Sec23/24p accumulation, while Model 2 showed Sar1p behavior but failed to support Sec23/24p clustering.

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- 3Pos109** 無細胞合成されたタンパク質における疎水領域の長さとアミノ酸配列が引き起こすリポソームのエンドサイトーシス様の分裂
Endocytosis-like fission of liposomes induced by the length of hydrophobic domains in cell-free synthesized proteins

Aika Yamamoto, Yuki Nagai, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

Endocytosis is one of the important biological functions. Endocytosis-like fission in liposomes of artificial cell membranes has been reported under osmotic pressure or high salt concentration, but the frequency was low. We demonstrate highly efficient endocytosis-like fission of liposomes induced by the proteins. When membrane-interacted oleosins were expressed in liposomes encapsulating a cell-free protein synthesis system, modified I-shaped oleosins were observed to trigger endocytosis-like fission as insertion into the vesicle membrane. However, the mechanism of action of this membrane deformation remains unclear. In this study, we investigate the effects of the length and amino acid sequence of the hydrophobic region of oleosin on the membrane deformation activity.

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- 3Pos110** Development of a simple method for the reconstitution of ion channels using agarose gel beads

Mami Asakura^{1,2}, Kohta Takagi³, Miho Ohnishi³, Minako Hirano², Toru Ide² (¹*Dept. of Comp. Tech. Soln., Okayama Univ.*, ²*Grad. Sch. Health Sys., Okayama Univ.*, ³*Fac. Eng., Okayama Univ.*)

We have developed a simple and efficient method for the formation of artificial lipid bilayers and the incorporation of channel proteins using agarose gel beads. Channel currents were measured more efficiently using the beads on which liposomes containing channels were immobilized than beads on which channels were directly immobilized. Liposome-immobilized beads enabled rapid and reproducible current measurements. Furthermore, our technique allows for the measurement of untagged channels by reconstituting them into liposomes that contain affinity-tagged lipids. Using this platform, we have successfully recorded various ionic currents, including channels derived from biological tissues, demonstrating its versatility and practical utility for electrophysiological studies.

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- 3Pos111** 脂質-オレオシン非対称膜小胞の内膜湾曲による機械刺激依存性チャネルを介した物質輸送
Molecular transportation via mechanosensitive channel in response to membrane curvature of the asymmetric lipid-oleosin vesicles

Kotaro Baba, Koki Kamiya (*Grad. Sch. Sci & Tech, Gunma Univ.*)

Asymmetric lipid-oleosin vesicles contain a phospholipid and an amphiphilic protein (oleosin) monolayer in the outer and inner leaflet, respectively. These vesicles allow other proteins to accumulate on the oleosin leaflet and enable to transport molecules via mechanosensitive channel of large conductance (MscL) in response to membrane pressure changes. In this study, to activate MscL on the vesicles by the membrane curve controlled by the other proteins accumulation and dissociation on the inner leaflet, we observed the MscL reconstitution into the asymmetric vesicles with fluorescent proteins (FP)- fused oleosins in the inner leaflet. The presence of FP-fused oleosin in the inner leaflet increased the amount of MscL reconstitution compared to the vesicles without FP.

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- 3Pos112** 脂質膜で隔てられた DNA 振動子の結合に関する研究
Coupling of DNA oscillators separated by lipid membranes

Kazumo Takahashi¹, Keita Abe¹, Hideaki Matsubayashi², Shinichiro Nomura¹, Ibuki Kawamata³, Satoshi Murata¹
(¹*Department of Robotics, Graduate School of Engineering, Tohoku University*, ²*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*, ³*Division of Physics, Graduate School of Science, Kyoto University*)

Chemical oscillations driven by biomolecules are essential for maintaining cellular activity. Between multiple cells, there is a synchronization of oscillations called entrainment, which is closely related to such biological activities. Inspired by the biological chemical oscillations, artificial chemical oscillators have been engineered such as the Predator-Prey DNA ecosystem (Fujii & Rondelez, ACS Nano, 2013). Previous studies have shown that the amplitude and frequency of this oscillator vary with temperature, DNA concentration, and the enzymatic activity. However, the effects of the interaction of multiple oscillators remain unexplored. Therefore, we report microscopic observations of two oscillators in contact across lipid membranes under temperature control.

3Pos113 Membrane Translocation of Nucleic Acids via Cholesterol-modified DNA Hybridization

Rinka Aoki, Satoshi Murata, Hideaki Matsubayashi, Keita Abe, Shin-ichi M. Nomura (*Grad. Sch. Eng., Univ. Tohoku*)

Research on molecular robotics using artificial molecular circuits across membrane compartments is progressing, but most approaches require pore formation, causing uncontrollable leakage. We propose a novel strategy achieving sequence-specific membrane crossing via hybridisation without membrane disruption using cholesterol-modified DNA strands. Cholesterol-labelled DNA strands (drivers) partially hybridise with ssDNAs near giant unilamellar vesicle (GUV) membranes, enabling selective crossing through the membrane. Pre-encapsulating fully complementary DNA into GUVs confirmed internal transport of target sequences. This system represents the first example of sequence-specific DNA molecular pumping and provides a platform for programmable molecular device integration.

3Pos114 コレラ菌セロトニン走性受容体の同定および機能解析
Identification and characterization of the serotonin chemoreceptor in *Vibrio cholerae*

Fuga Omori¹, Sotaro Asaoka¹, Hirotaka Tajima^{2,3}, Ikuro Kawagishi^{1,2,3} (¹*Grad. Sch. Sci. and Engin., Hosei Univ.*, ²*Fac. of Biosci. and Appl. Chem., Hosei Univ.*, ³*Res. Cent. for Micro-Nano Tech., Hosei Univ.*)

Vibrio cholerae, the etiological agent of cholera, exhibits chemotactic responses toward various chemicals. We found that it senses serotonin, a biogenic amine derived from tryptophan and primarily produced in the intestine. A screen of methyl-accepting chemotaxis proteins (MCPs) identified Mlp29 as the one responsible for serotonin sensing. Deletion of the *mlp29* gene abolished serotonin taxis. ITC measurements demonstrated that the periplasmic region of Mlp29 binds serotonin. Mutagenesis studies indicated that the membrane-distal CACHE domain is essential for serotonin sensing. Immunoblot analysis revealed that the quorum-sensing regulator HapR enhances *mlp29* expression. As host serotonin levels rise with bacterial density, serotonin taxis may contribute to infection.

3Pos115 GPCR-mediated signaling in heat tolerance of *C. elegans*

Shiori Mototake^{1,2}, Yuki Sato^{1,2}, Kohei Ohnishi^{1,2,3}, Tohru Miura^{1,2,3}, Akane Ohta^{1,2,3}, Atsushi Kuhara^{1,2,3,4} (¹*Dept. Biol., Facul. Sci. & Engineer. Konan Univ.*, ²*Dept. Biol. Grad. Sch. Sci. Konan Univ.*, ³*Inst. of Integral NeuroBiol. Konan Univ.*, ⁴*PRIME AMED*)

We are studying GPCR-mediated thermosensation in *C. elegans*. We previously reported thermo-sensitive GPCR regulating cold tolerance (Ohnishi et al., *Nat. Commun.*, 2024). We began analyzing heat tolerance, where animals grown at 25°C can survive at 31°C, unlike those grown at 15°C. We identified a cGMP-gated channel mutant *tax-4* with enhanced heat tolerance. This phenotype was rescued by expressing the wild-type *tax-4* gene in specific sensory neurons, ASJ and ASI. Similar phenotypes were found in *Ga* subunit mutants expressed in the same neurons. Since *Ga* is GPCR-activated, we screened GPCR mutants and identified SRH gene whose mutation caused enhanced heat tolerance. We are now testing combinations of GPCR mutations to examine possible redundancy in thermosensation.

3Pos116 培地中 Na⁺上昇による神経活動変化
Neural Activity by Increasing Concentration of Sodium Ion in Culture Medium

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In cases of hypernatremia, the sodium concentration in the blood increases, central nervous system abnormalities have been reported to be induced. In this study, extracellular potentials were measured by increasing the sodium ion concentration in neuronal cell culture medium using a multielectrode array(MEA) system. As a result, it was found that the inter-burst interval(IBM) became shorter and the amplitude decreased compared to normal conditions. For the next study, we aim to clarify the differences in activity under high sodium conditions when altering the size of neuronal cell populations, by constructing an agarose micro chamber(AMC) using agarose microfabrication technology.

3Pos117 The synaptic vesicle cluster restricts the diffusion of cytosolic α -Synuclein via boundary confinement

Kye Kudo¹, Adekunle T. Bademosi¹, S. Sean Millard², Frédéric A. Meunier^{1,2} (¹*Queensland Brain Institute, The University of Queensland*, ²*School of Biomedical Sciences, Faculty of Medicine, The University of Queensland*)

Cytosolic proteins typically display high mobility through Brownian motion, resulting in the tendency to evenly distribute within cells. α -Synuclein, a small cytosolic protein which regulates neurotransmitter release, uniquely forms clusters at the presynaptic terminal via mechanisms that remain elusive. Using single-particle tracking photoactivatable localization microscopy (sptPALM) at the *Drosophila* neuromuscular junction, we tracked the movement of individual α -synuclein molecules, revealing the highly dynamic clustering restricted to the synaptic vesicle cluster. The movement of α -Syn was confined by a boundary defined by the synaptic vesicle cluster, as evidenced by measuring a bouncing phenotype from single molecule trajectories.

3Pos118 ヨーロッパモノアラガイの味覚嫌悪学習に関係する CGC の mGluR を介した抑制作用
Metabotropic glutamate receptor-mediated inhibition of CGCs associated with conditioned taste aversion memory in *Lymnaea*

Yoshimasa Komatsuzaki¹, Samui Chiba¹, Ayaka Itoh², Ken Lukowiak³, Minoru Saito² (¹*Grad. Sch. Sci. and Tech, Nihon Univ.*, ²*Grad. Sch. Integ. Basic. Sci., Nihon Univ.*, ³*Univ of Calgary, Calgary*)

The cerebral giant cells (CGCs) in the pond snail *Lymnaea stagnalis*, key modulators of feeding behavior, show altered GABAergic responses after CTA. Here, we examined how glutamatergic and GABAergic signaling to CGCs changes with learning. In naïve animals, GABA increased CGC firing via both GABA_A and GABA_B receptors, while this response was diminished after CTA learning. Glutamate suppressed CGC firing in both groups; this inhibition was blocked by MCPG, indicating a metabotropic glutamate receptor (mGluR)-dependent mechanism. In contrast, AMPA and NMDA increased firing. DNQX failed to block the inhibition, further confirming mGluR involvement. This is the first evidence that mGluR-mediated inhibition of CGCs is a key component of memory-related plasticity in *Lymnaea*.

3Pos119 mGluR1 と GHS-R1a のクロストークによる小脳シナプス可塑性の制御
Cross-talk between mGluR1 and GHS-R1a signaling modulates cerebellar synaptic plasticity

Moritoshi Hirono¹, Boyang Zhang¹, Hiroshi Hosoda², Masanori Nakata¹ (¹*Dept. Physiol., Wakayama Med. Univ.*, ²*Dept. Mol. Pathophysiol., Shinshu Univ.*)

Ghrelin, an endogenous orexigenic peptide, and its functional receptor, growth hormone secretagogue receptor 1a (GHS-R1a) are expressed in the cerebellar cortex. To elucidate whether ghrelin-GHS-R1a signaling modulates induction of cerebellar long-term depression (LTD), which requires the activation of type 1 metabotropic glutamate receptor (mGluR1), we investigated the cross-talk between GHS-R1a and mGluR1 in Purkinje cells of the anterior lobules. We found that ghrelin increased the amplitude of mGluR1-mediated excitatory inward currents, and a GHS-R1a antagonist JMV3002 attenuated LTD induction. Thus, the activation of GHS-R1a could facilitate LTD induction and may contribute to cerebellar motor learning required during feeding behavior.

3Pos120 流れ刺激に対するハルテリアの逃避遊泳行動
Flow-induced escape behavior of *Halteria* sp.

Koki Kanda¹, Yukinori Nishigami^{1,2}, Takuya Ohmura^{1,2}, Katsuhiko Sato³, Toshiyuki Nakagaki^{1,2} (¹*Graduate School of Life Science, Hokkaido University*, ²*Research Institute for Electronic Science, Hokkaido University*, ³*Faculty of Science, University of Toyama*)

Ciliates are unicellular eukaryotes that swim with ciliary beating. *Halteria* is a ciliate with a body length of 20–30 μ m. It exhibits characteristic high-speed swimming (~100 body lengths/second) by reversing its ciliary beating. This behavior is hypothesized to function as an escape response to predators. Some predators larger than *Halteria* generate suction flows during feeding. We investigated how *Halteria* sp. responds to the suction flow. *Halteria* sp. showed more frequent high-speed swimming both in suction flow generated by the ciliate *Stentor* sp. and in artificial flow produced with a syringe pump. These findings suggest that *Halteria* sp. enhances escape efficiency by modulating high-speed swimming in response to extracellular fluid stimuli.

3Pos121 Uncovering light-sensitive mechanism of non-visual opsins

Seiwa Nakamura¹, Asato Kojima¹, Kazuhiro Kobayashi², Masahiro Fukuda², Koki Kawakami², Suhyang Kim², Takashi Nagata³, Kota Katayama^{4,5}, Hideki Kandori^{4,5}, Keiichi Inoue³, Hideaki E. Kato^{2,6} (¹*Grad. Sch. Art. Sci., Univ. Tokyo*, ²*RCAST, Univ. Tokyo*, ³*ISSP, Univ. Tokyo*, ⁴*Life Sci. Appl. Chem., Grad. Sch. Eng., Nagoya Inst. Tech.*, ⁵*OptoBio Tech. Res. Cent.*, ⁶*Grad. Sch. of Sci, Univ. Tokyo*)

Opsins are photoreceptive proteins essential for visual and non-visual light responses. Visual opsins, like rhodopsin, are mainly expressed in retinal photoreceptors and are structurally well-characterized, revealing G-protein activation mechanisms. In contrast, non-visual opsins are found in various tissues (e.g., brain, liver, muscle) and regulate diverse physiological processes such as circadian rhythms and thermoregulation. Their functional diversity reflects differences in spectral properties and G-protein specificity. However, low expression and thermal instability hinder structural studies. This study conducted structural and functional analyses of human non-visual opsins to clarify their light-responsive mechanisms.

3Pos122 A Structural Approach to the Potassium-Selective Channelrhodopsin HcKCR1 for Its Development as an Optogenetic Tool

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HcKCRs are the first identified potassium-selective channelrhodopsins and are expected to serve as a novel optogenetic tool for neuronal silencing. Recently, the structures of KCR have been elucidated, and we have successfully enhanced its properties through mutagenesis. These promising features have attracted considerable interest from neuroscientists as a next-generation optogenetic tool. However, the underlying mechanisms driving these improvements remain unclear, preventing the optimal design of future variants. In this study, we investigate the mechanisms underlying the enhanced properties with structural analysis and explore further applications of KCR variants.

3Pos123 低温ラマン分光法による Cl⁻ポンプロドプシン(*Mastigocladopsis repens* 由来)の発色団構造変化の解明 Cryogenic Raman Study of Chromophore Structural Changes during the Photocycle of a Light-Driven Cl⁻ Pump from *Mastigocladopsis repens*

Kana Miyazaki¹, Takashi Kikukawa², Masashi Unno¹, Tomotsumi Fujisawa¹ (¹*Fac. Sci. Eng., Saga Univ.*, ²*Fac. Adv. Life Sci., Hokkaido Univ.*)

A light-driven Cl⁻ pump (*MrHR*) from the cyanobacterium *Mastigocladopsis repens* is known as a novel type of retinylidene photoreceptor. Because the structural motif of *MrHR* for the Cl⁻ transport is different from the representative archaeal Cl⁻ pump, the mechanism of its photocycle has been considered distinctive. However, the structural changes of chromophore during the photocycle are not well understood. Thus, we used cryogenic Raman spectroscopy to study the chromophore structural changes of *MrHR*. We observed five photointermediates exhibiting the different chromophore structures and specified the transient states that mediate the release and uptake of Cl⁻.

3Pos124 細胞性粘菌の発生と細胞骨格に対するレチナールの影響 Effect of retinal on development and cytoskeleton in *D. discoideum*

Shuhei Tsuchihashi¹, Kazuki Akiyama¹, Yusuke V. Morimoto² (¹*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech.*, ²*Grad. Sch. Comput. Sci. Syst. and Eng, Kyushu Inst. Tech.*)

Retinal is involved in light sensing via rhodopsins, but its role in *Dictyostelium discoideum* lacking rhodopsin families remains unclear. We previously showed that retinal delays the developmental transition from unicellular to multicellular forms in *D. discoideum*. Here, we found that retinal induces cell rounding and inhibit pseudopod formation, suggesting that retinal may act directly or indirectly on actin. Furthermore, the addition of retinal to multicellular bodies altered fruiting body morphology, suggesting effects on late-stage development. However, phototaxis remained unchanged, indicating that retinal has little effect on the phototaxis of *D. discoideum*.

3Pos125**有機溶媒中における微生物ロドプシンの物理化学的特性の解析****Comparative analysis of the physicochemical properties of microbial rhodopsins in organic solvents****Miyu Inokuchi¹, Keiichi Kojima², Yuki Sudo²** (¹*Grad. Sch. Med. Dent. & Pharm. Sci., Okayama Univ.*, ²*Fac. Med, Dent & Pharm Sci., Okayama Univ.*)

Microbial rhodopsins are membrane proteins that convert light-energy into molecular functions such as ion transport. From the perspective of green chemistry, rhodopsins hold potential for applications in biocatalysts, biosensors, and bioelectronic devices. For such applications, protein stability in organic solvents is essential. Here, we investigated the physicochemical properties of various rhodopsins in organic solvents. Several rhodopsins retained their visible colors and exhibited photocyclic reactions, including the formation of M and O intermediates, in solutions containing 30% (v/v) ethanol or methanol. Based on these findings, we discuss the key factors that regulate rhodopsin functionality in organic solvents and their potential as tools for green chemistry.

3Pos126**微生物ロドプシンによる光駆動型有機アニオン輸送の発見****Discovery of light-powered organic anion transport by microbial rhodopsins****Simiao Shen¹, Kaisei Ohno², Takashi Tsukamoto^{1,2,3}, Kwang-Hwan Jung⁴, Yuki Sudo⁵, Takashi Kikukawa^{1,2,3}** (¹*Grad. Sch. Life Sci., Hokkaido Univ.*, ²*Sch. Sci., Hokkaido Univ.*, ³*Fac. Adv. Life Sci., Hokkaido Univ.*, ⁴*Dept. Life Sci. & Bionano Cent., Sogang Univ.*, ⁵*Fac. Med., Dent. & Pharm. Sci., Okayama Univ.*)

Microbial rhodopsins are membrane proteins that primarily function as light-driven ion transporters. They have long been thought to transport only small inorganic ions such as H⁺, Cl⁻, and Na⁺. Here, we report that several anion-pumping rhodopsins can also transport organic anions. In particular, a cyanobacterial rhodopsin is capable of translocating bulky organic ions, including those containing a benzene ring. These anions are transported via the same fundamental mechanism as Cl⁻: binding in the dark state and translocation upon photoactivation. Organic ions with pK_a above 2 are not transported, despite having an appropriate size. This study provides the first evidence that naturally occurring proteins can use light to transport organic compounds across membranes.

3Pos127**一分子蛍光 in situ hybridization 法によるメダカ組織におけるオプシン発現細胞の解析****Single-Molecule FISH Analysis of Opsin-Expressing Cells in Medaka****Keita Sato, Hideyo Ohuchi** (*Fac. Med, Dent & Pharm Sci., Okayama Univ.*)

Opsins are light-sensitive GPCRs. Besides nine visual opsins, the medaka genome encodes 25 non-visual opsins whose functions remain unclear. Because medaka are small, genetically tractable, and easy to rear, they provide an ideal system for dissecting opsin biology. Identifying the cells that express each non-visual opsin is essential for clarifying their roles. Classic radioactive or enzymatic in situ hybridization lacks resolution and multiplexing capacity. We thus adopted the single-molecule fluorescence ISH technique with SABER (Kishi et al., 2019), optimizing conditions to cut costs and suppress nonspecific staining. Using this protocol, we mapped non-visual opsin-positive cells across multiple medaka tissues and discuss their putative physiological functions.

3Pos128**Light Intensity-Dependent Reaction Dynamics of the Photoresponsive Enzyme MsLadC****Dai Takeuchi, Masahide Terazima, Yusuke Nakasone** (*Grad. Sch. Sci., Kyoto Univ.*)

MsLadC is a photoresponsive dimeric enzyme composed of a LOV domain and a GGDEF domain. While it is known to undergo conformational changes and show a marked increase in diguanylate cyclase activity upon blue light illumination, the detailed reaction dynamics remain unclear.

In this study, we used the transient grating (TG) method to investigate the photoreaction dynamics of MsLadC. Protein structural changes were detected as changes in the diffusion coefficient. Notably, the reaction yield depended on the excitation light intensity, with pronounced structural changes observed only when both monomer units in the dimer were simultaneously excited.

Furthermore, analysis of the time evolution of the TG signal allowed us to determine the reaction rate constants.

3Pos129

センサリーロドプシン II (SRII) からトランスデューサー (HtrII) への情報伝達におけるシグナリング中間体の同定

Identification of signaling states of sensory rhodopsin II (SRII) in the signal transduction to its cognate transducer protein (HtrII)

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Identification of signaling states in HtrII-complexed SRII is a crucial issue for understanding of the signal transduction. The results of a previous *in vivo* behavioral assay suggested that the photocycle intermediates M and O (especially O) are putative signaling states. In the previous study, varying artificial retinal analogues-binding SRIIs were used for examining the relationship between the relative signaling efficiency and the relative time-averaged concentrations of respective photoproducts. Here, we performed motion analysis using various SRII mutants, which have different lifetimes of M and O, and investigated the correlation between the photoresponse time and the mean residence time (MRT) of each state. Our results implied that the main signaling state is M.

3Pos130

高速原子間力顕微鏡を用いた植物光合成膜におけるタンパク質複合体のダイナミクス解析 Analysis of protein complex dynamics in plant photosynthetic membranes by high-speed atomic force microscopy

Yudai Nishitani, Daisuke Yamamoto (*Fac. Sci., Fukuoka Univ.*)

Regulation of higher-order structures of photosynthetic protein complexes in thylakoid membrane is essential for light adaptation. However, the molecular dynamics of the complexes associated with the regulation of photosynthetic reaction remain poorly understood. In this study, we employed high-speed atomic force microscopy (HS-AFM) to visualize protein complexes within the thylakoid membrane from spinach. The analysis of the lateral diffusion of intramembrane PSII demonstrated that the diffusion rate depends on salt condition in the buffer. Furthermore, we compared the PSII diffusion in light- and dark-adapted thylakoid membranes. The intramembrane dynamics of PSII under various environmental conditions will be discussed.

3Pos131

機械学習を用いた光合成タンパク質複合体における環境適応アミノ酸残基の推定 Estimating environmentally adaptive residues in photosynthetic complexes using machine learning

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Photosynthetic organisms, from land plants through cyanobacteria, thrive in diverse environments worldwide. While protein evolution is key to their adaptation, the specific sequence features enabling this remain unknown. As a first step to address this question, we explored the link between growth temperature and the evolution of photosynthetic proteins using machine learning. We created multiple sequence alignments of photosynthetic protein complexes such as Photosystem I and II, Light harvesting complex from more than 1,800 species using BLAST and MAFFT. We then gathered growth temperature and habitat data via the Köppen classification using GPT-4. Random Forest Regression was applied to identify key residues as effective estimators of the environmental parameter.

3Pos132

暗発酵および光発酵による最適化 Optimization by dark and photo fermentation

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Hydrogen is renewable carrier and considered to be a clean fuel for future. However, the current methods of producing hydrogen are based on fossil fuels and then emit greenhouse gases that cause global warming. A promising method from biomass using microorganisms has been favored because it contributes to the production of renewable and carbon-neutral hydrogen, referred to as “biohydrogen”, and is environmentally friendly. Among the methods for biohydrogen production, two-stage processes of dark and photo fermentation have the potential to achieve high hydrogen production and high conversion efficiency of hydrogen by using the renewable resources and industrial and agricultural wastes as substrate. In dark fermentation, substrate, such as

3Pos133 光合成タンパク質超複合体の空間分解分光にむけた超解像吸収顕微鏡の開発
Super-resolution absorption microscopy toward spatially-resolved spectroscopy of photosynthetic protein supercomplexes

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Photosynthetic excitation energy transfer (EET) from light-harvesting systems to reaction centers takes place within their supercomplexes. These protein supercomplexes are considered to have spatially heterogeneous conformations, likely leading to the functional robustness.

However, it is still unclear how the conformational heterogeneity affects the EET process. To clarify this point, super-resolution spectroscopy is needed, particularly with absorption detection that enables observation of intermediate states during the EET.

In this study, we developed a super-resolution absorption microscope using a STED-like approach. We will discuss spatially resolved spectroscopy, for EET within the supercomplexes and supramolecular antennas of green sulfur bacteria.

3Pos134 網羅的単一分子分光を用いた光阻害修復途上光化学系IIの観測
Observation of photosystem II under repair from photoinhibition by exhaustive single-molecule spectroscopy

Kyosuke Watanabe, Shen Ye, Yutaka Shibata (*Graduate school of science, Tohoku Univ.*)

Photosystem II (PSII), a large photosynthetic pigment-protein complex, are constantly damaged by excessive light. PSII is maintained by a rapid repair cycle *in vivo*, but its details have not been well understood. This is mainly because PSII under repair are transient and scarce, making its purification impractical. In this study, we perform exhaustive single-molecule spectroscopy to detect fluorescence spectra of the PSII under repair.

Solubilized proteins were extracted from pea leaves after photoinhibition and recovery treatment. The sample containing 10 pM particles was excited with a 630 nm laser in the cryogenic microscope. We compared spectra of bright spots to those of known photosynthetic proteins and identified spectra of the transient molecular species.

3Pos135 Localization of auxiliary proteins of LHC assembly during its insertion into thylakoid membrane

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Light-harvesting complex (LHC) proteins of green algae are encoded by the nuclear genome. They are translated in the cytosol and imported to the chloroplast across the chloroplast envelope. cpSRP43 binds to LHC to prevent their aggregation in the chloroplast and Alb3.1 recognizes the cpSRP43-LHC complex to mediate its insertion into thylakoid membrane. Although chlorophylls (Chls) are associated with LHC during this process, when and where it occurs remain unclear. To reveal this, we use venus-fused cpSRP43 and Alb3.1 in a green alga *Chlamydomonas reinhardtii* to examine their localization by cryo-confocal microscope. Furthermore, we analyze purified venus-fused cpSRP43 and Alb3.1 complexes by single molecule spectroscopy to confirm binding of Chls to them.

3Pos136 重合脂質膜鋳型法による再構成チラコイド膜のタンパク質込み合いの評価
Evaluation of protein crowding in reconstituted thylakoid membrane supported by polymerized lipid membranes

Hayata Sakai¹, Koki Takagi², Kenichi Morigaki³, Shen Ye¹, Yutaka Shibata¹ (¹*Graduate School of Science Tohoku Univ.*, ²*Agricultural Science, Graduate School of Kobe Univ.*, ³*Graduate School of Biosignal Research Center Kobe Univ.*)

Photosynthetic proteins are embedded in the thylakoid membranes within chloroplasts. To analyze functional membrane proteins outside of living cells, we have developed a method to reconstruct planar thylakoid membranes supported by UV-polymerized lipid bilayers. This technique, overcoming the problem of edge-instability, achieves both membrane stability at room temperature and preservation of its fluidity.

This study evaluates how closely the reconstituted thylakoid membranes mimic native systems by conducting the time-resolved fluorescence measurements. From the dynamics of singlet-singlet annihilation under various excitation intensities, the degree of protein crowding was estimated. The results were compared between the reconstituted and native Thylakoid Membranes.

3Pos137

一分子時間分解蛍光分光測定による光合成光捕集アンテナ複合体のエネルギー移動解析
Single-molecule time-resolved fluorescence spectroscopy of energy transfer in photosynthetic antenna complex

Shinnosuke Masuda^{1,2,3}, Mai Watanabe⁴, Toru Kondo^{1,2,3} (¹SOKENDAI, ²NIBB, ³ExCELLS, ⁴Dept. of Science, Tokyo Metropolitan Univ.)

Photosynthetic antenna complexes mediate the excited energy transfer (EET) to reaction centers. Their structures, optimized at the atomic level to carry out the efficient EET, are known to fluctuate under physiological conditions. However, it is still unclear how the conformational dynamics affect the EET. Single-molecule spectroscopy (SMS) is often used to directly observe dynamic behaviors through fluorescence detection, but it is still challenging to analyze the whole EET processes because of the broad wavelength range of fluorescence. In this study, we develop a Michelson interferometer with time correlated single photon counting and perform single-molecule time-resolved fluorescence spectroscopy of photosynthetic antenna complexes.

3Pos138

Oscillatoria acuminata 由来の光活性化アデニル酸シクラーゼのC末端領域による活性制御機構の解明
The role of the C-terminal region in regulating the activity of the photoactivated adenylyl cyclase from *Oscillatoria acuminata*

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Our study aims to elucidate how the C-terminal region regulates the activity of OaPAC, a photoactivated adenylyl cyclase derived from *Oscillatoria acuminata*. We have previously shown that the 18 amino acids in the C-terminal region affect OaPAC activity. However, the role of this region remains unclear. This study identified the key amino acids in the C-terminal region that are essential for activity. Additionally, we are investigating which amino acids interact with the C-terminal region using molecular dynamics (MD) simulations and examining how the C-terminal region is involved in activity. At the meeting, the regulatory mechanism of OaPAC activity will be discussed.

3Pos139

光活性化アデニル酸シクラーゼの活性調節機構の解明
Regulatory mechanism of photoactivated adenylyl cyclase activity

Hinase Kondo¹, Masahiko Taguchi^{2,3}, Syun Sakuraba^{4,5}, Masumi Takebe⁶, Koki Shimomae¹, Mei Kawamoto¹, Mami Asakura^{1,7}, Akiya Hukuda², Eriko Nango^{2,3,8}, Hidetoshi Kono^{4,5}, Toru Ide¹, Minako Hirano¹ (¹Grad. Sch. Health Sys., Okayama Univ., ²Graduate School of Science, Tohoku Univ., ³IMRAM, Tohoku Univ., ⁴QLS, QST, ⁵cQUEST, Chiba Univ., ⁶Hamamatsu Photonics K.K., ⁷Dept. of Comp. Tech. Soln., Okayama Univ., ⁸SRIS, Tohoku Univ.)

This study aims to clarify the mechanism regulating the activity of photoactivated adenylyl cyclase (PAC). Several types of PACs have been identified so far, and each of these PACs exhibits distinct enzyme activity in response to blue light illumination: the activity of PAC from *Oscillatoria acuminata* (OaPAC) is low, whereas that of PAC from *Beggiatoa sp.* (bPAC) is high. In this study, we identified the region that characterizes PAC activity by measuring the activity of OaPAC and bPAC chimeric mutants. Additionally, we are investigating the structural dynamics of the two PACs and their mutants using molecular dynamics (MD) simulations. The regulatory mechanism elucidated will be discussed at the meeting.

3Pos140

リジン主鎖同位体標識ロドプシンの赤外分光解析
FTIR Analysis of microbial rhodopsins with ¹⁵N-labeled lysine backbone

Mako Ooka¹, Tatsuro Nishikino^{1,2}, Teppei Sugimoto¹, Yuma Ito¹, Yuji Furutani^{1,2}, Hideki Kandori^{1,2} (¹Graduation school of Engineering, Nagoya institute of technology, ²OptoBio Technology Research Center, Nagoya institute of technology)

Light-induced difference FTIR spectroscopy probes vibrational changes of photoreceptive proteins upon their perturbation. Among the various vibrations, amide bands reflect backbone changes, although they involve collective vibrations and lack site-specificity. In this study, we leveraged two key features of rhodopsins: only one lysine residue in the transmembrane region (binding retinal on TM7), and structural changes localized near the retinal at 77 K. By labelling α -position of lysine with ¹⁵N, we aimed to detect site-specific structural changes of the backbone. This approach enabled the detection of vibrations involving the backbone nitrogen in various microbial rhodopsins. We will discuss the implications of these signal changes.

3Pos141 低温赤外分光法によるウイルス由来カチオンチャネルロドプシンの構造解析
Structural analysis of viral cation channelrhodopsin using low-temperature FTIR spectroscopy

Mako Aoyama^{1,2}, Kota Katayama^{1,2}, Hideki Kandori^{1,2} (¹*Grad. Sch. Eng., Nagoya Inst. Tech.*, ²*Nagoya Inst. Tech., OptoBioTechnology Research Center*)

OLPVR1 is a light-gated cation channelrhodopsin from viruses. Recent X-ray crystallographic study showed that the water-containing hydrogen-bonding network in OLPVR1, similar to that of a light-driven proton-pump bacteriorhodopsin (BR), is collapsed in the open state of OLPVR1. In this study, we investigated structural changes during the photocycle of OLPVR1 by low-temperature FTIR spectroscopy, and the data obtained for the wild type were compared with those of mutants. The FTIR results showed that OLPVR1 does not possess strongly hydrogen-bonded water molecules commonly observed in light-driven proton pumps, but contains a unique hydrogen-bonding network that may be characteristic of viral channel function.

3Pos142 短波長応答チャネルロドプシン KnChR の分子機能
Unraveling the Functional Mechanism of KnChR: A Short-Wavelength Absorbing Cation Channelrhodopsin

Satoshi Tsunoda^{1,2}, Koki Natsume¹, Yuzhu Wang³, Tatsuki Tanaka³, Shoko Hososhima^{1,2}, Wataru Shihoya⁴, Osamu Nureki³, Hideki Kandori^{1,2} (¹*Grad. Sch. Eng., Nagoya Institute of Technology*, ²*OptoBio Technology Research Center, Nagoya Institute of Technology*, ³*Grad. Sch. Sci., The University of Tokyo*, ⁴*Keio University School of Medicine*)

KnChR is a cation channelrhodopsin composed of a rhodopsin domain followed by a large soluble cytoplasmic domain. It exhibits two unique properties: regulation of channel gating by the C-terminal domain and absorption of short-wavelength visible light at 430 and 470 nm, among the most blue-shifted channelrhodopsins. We performed electrophysiological recordings and solved its molecular structure. The results revealed that the unique architecture of the C-terminal region plays a key role in allosteric modulation of channel kinetics. We also engineered KnChR for a further blue shift to 420 nm. Finally, we demonstrate that UV or deep-blue light can trigger action potentials in KnChR-expressing neurons, expanding its utility in optogenetic applications.

3Pos143 Photocontrol of GTPase Cycle of the small G-protein H-Ras using its regulator RASGRF1 with photochromic molecular devices

Isra Lilatul, Nobuyuki Nishibe, Shinsaku Maruta (*Grad.Sch.Sci.Eng., Univ.Soka*)

Small G-protein Ras functions as a molecular switch in cellular signaling. Activation requires binding guanosine-5'-triphosphate (GTP), whereas inactivation follows guanosine diphosphate (GDP) binding. Guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs) mediate this GTP-GDP cycle. Here we photoregulated Ras by engineering RASGRF1, a GEF, with Photozipper (PZ), a blue-light-responsive Aureochrome1 variant, fused to its C-terminus. The RASGRF1-PZ chimera underwent reversible photoisomerization, enabling blue-light-dependent modulation of GEF activity in vitro. These results support the use of light-responsive proteins as modular devices for optically switching small GTPase enzymatic activity.

3Pos144 ペプチド液滴による原始的な自己区画の確立
Establishment of Primitive Self-Compartments with Peptide-Droplets

Yota Tabata, Tomoyuki Kaneko (*FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

Self-compartments are necessary for the origin of life because they accumulate substances at higher concentrations than in the external environment and promote chemical reactions. In this study, we considered the droplets as primitive self-compartments and found that peptide-droplets were formed by heating a mixture of glycine, alanine, aspartic acid, glutamic acid, and valine and dissolving it in an aqueous solution simulating the primordial ocean (mock primitive seawater). The formation of the peptide-droplets depended on the type of amino acid, heating time, and salt concentration of the mock primitive seawater. In the future, we would like to investigate whether it concentrates biomolecules and show that it functions as primitive self-compartments.

3Pos145

ベイズ学習と統計力学による進化の理論：タンパク質を例に

An Evolutionary Theory Based on Bayesian Learning and Statistical Mechanics: The Case of Proteins

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The concept of "robustness of the phenotype to environmental perturbations across generations" is essential for natural selection. However, it has not been formalized. This study formalizes robustness in the lattice protein model using Bayesian learning and statistical mechanics, focusing on the stability of the posterior distribution of amino acid sequences against perturbations in the chemical potential of water surrounding proteins. In a 36-residue two-dimensional square lattice protein model, we found that proteins with higher robustness tend to have a higher proportion of α -helices and a lower proportion of β -sheets. This finding is confirmed by empirical validation using a protein database with larger proteins.

3Pos146

微生物進化実験を用いた進化可能性ランドスケープと増殖-死滅トレードオフの定量
Quantifying Evolutionary Landscapes and the Growth-Death Trade-off in Microbial
Experimental Evolution

Atsushi Shibai¹, Riku Kamiura¹, Shumpei Sato¹, Shigeyuki Kakizawa³, **Chikara Furusawa^{1,2}** (¹*BDR, RIKEN*, ²*UBI, Univ. Tokyo*, ³*AIST*)

We quantitatively analyze properties of evolutionary dynamics using high-throughput evolution experiments in *E. coli*. This talk presents two studies: (1) Quantification of evolvability landscapes by simultaneously measuring resistance to multiple antibiotics, allowing estimation of a potential landscape describing evolutionary trajectories; (2) Analysis of a growth-death trade-off in *Mycoplasma syn3B*, where serial transfer during log phase increased growth rate but also elevated death rate. We discuss the underlying mechanisms of this trade-off.

3Pos147

ミニマル合成細菌 syn3B のゲノムサイレンシング

Silencing a genome of minimal synthetic bacterium syn3B

Hana Kiyama¹, Sohkichi Matsumoto², Makoto Miyata^{1,3} (¹*Grad. Sch. Sci., Osaka Metropolitan Univ.*, ²*Grad. Sch. Med., Niigata Univ.*, ³*OCARINA, Osaka Metropolitan Univ.*)

A minimal synthetic bacterium, syn3B has a synthetic genome consisting only of 489 genes essential for survival. Thus, most of its cellular functions are directly related to maintenance of life. MDP1 is an intrinsically disordered protein that induces dormancy in *Mycobacterium tuberculosis* (not "*Mycoplasma*") by aggregating the genome. In this study, we aim to discuss the conditions necessary for cells to "live" by studying the effects of silencing the genome of syn3B by MDP1 on their growth and survival. When MDP1 expression was induced in syn3B, growth of 99% of the cells was inhibited. In addition, aggregation of the genome of MDP1-induced syn3B was observed under a fluorescence microscope. We would like to discuss the revival of syn3B from inhibited growth state.

3Pos148

ミニマル合成細菌 syn3B のゾンビと生き返り

Zombie cells and revival of minimal synthetic bacterium syn3B

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To discuss the boundary between life and materials, we focused on a minimal synthetic bacterium syn3B, which is capable of genome transplantation. We previously succeeded in producing zombie cells by inducing a restriction enzyme in syn3B, leading to genome degradation. By transplanting genome to zombie cells, we got colonies of transplants, which was confirmed to contain the donor genome by colony PCR, suggesting that the zombie cells revived. We improved the efficiency of zombification by combining two restriction enzymes, resulting in the final surviving ratio of 0.0003%, with a 100-fold improvement. RNA-seq analysis revealed significant differences in gene expression between uninduced cells and zombie cells. We will discuss the boundary based on these results.

3Pos149 Myosin distribution and the deformation and behavior of the droplets formed by phase separation

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(¹Grad. sch. Sci., Univ. Nagoya, ²Grad. Sch. Arts and Sci., Univ. Tokyo, ³Grad. Sch. Eng., Univ. Mie, ⁴Sci Ctr. Self-Organization., Univ. Doshisha)

Liquid-liquid phase separation (LLPS) is considered to be involved in the creating highly compartmentalized spaces in cells. A mixed solution of PEG (polyethylene glycol) and DEX (Dextran), which causes LLPS, is used as constructive approach mimicking the crowded environment inside a cell. Myosin has been well known to be monomer or thick filamentous polymer depending on the salt condition. Previously, we found that myosin, as well as its fragments, can affect the behavior of droplets causing them to deform. Here, using fluorescent labeled myosin, we clarified the localization of myosin in PEG/DEX solution. We will discuss what causes the deformation of the droplets, and the effect of the polymerization state of myosin on LLPS.

3Pos150 Scalable preparation of GUVs using freeze-dried gelatin gel

Takumi Furusawa¹, Keita Abe¹, Hideaki Matsubayashi², Satoshi Murata¹, Shin-Ichiro Nomura¹, Richard James Archer³ (¹Department of Robotics, Graduate School of Engineering, Tohoku University, ²Frontier Research Institute for Interdisciplinary Sciences, Tohoku University, ³Department of Computer Science, School of Computing, Institute of Science Tokyo)

Giant unilamellar vesicles (GUVs) are widely utilized as biomimetic membranes for artificial cells. Existing GUV preparation methods are difficult to scale up, especially in high ionic strength solutions. Here we demonstrate the production of a high concentration of GUVs under physiologically relevant conditions on a mL scale by using freeze-dried gelatin as a high surface area substrate. Gelatin coated with thin lipid layers is shown to promote formation of GUVs in a range of conditions by swelling and partial dissolution of the substrate. We believe this cheap, simple and biologically compatible production method will facilitate access to GUVs for artificial cells and lead to further development of macro-scale artificial multicellular systems.

3Pos151 巨大リボソーム内でのクラミドモナスの片腕変異株の運動解析
Motion Analysis of Uniflagellate *Chlamydomonas* Mutants inside Giant Liposomes

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Biohybrid swimmers (BHSs) combine biological and synthetic components. We developed a BHS, liposomes encapsulating *Chlamydomonas* (CLs), and investigated its swimming mechanism. However, the complex 3D swimming behavior of the wild-type complicates motion analysis. In this study, we analyzed a uniflagellate *Chlamydomonas* mutant exhibiting rotational motion. Cells were encapsulated in liposomes via an emulsion transfer method. We measured the membrane deformation and rotation frequency, among other parameters. Two periodic deformations were observed: small (~50 Hz) from flagellar beating and larger (~4.5 Hz) from cell body rotation. Two rotational modes appeared: one along the inner membrane and another near the liposome center.

3Pos152 クラミドモナス封入リボソームの運動能力の解明に向けた微小物質の共封入
Co-encapsulation of Micro-objects in *Chlamydomonas*-Encapsulated Liposomes for Motility Characterization

Hiromasa Shiraiwa¹, Koichiro Akiyama¹, Shunsuke Shiomi¹, Masahito Hayashi^{1,2}, Tomoyuki Kaneko¹ (¹LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ., ²Dept. Biotech. Life Sci., Tokyo Univ. Agri. Tech.)

Liposomes have applications at the microscale, including targeted drug delivery and assisted fertilization. Our laboratory previously developed “Chlamy-lipo,” which encapsulates live *Chlamydomonas* and is driven by its swimming ability. For substance transport, Chlamy-lipo must contain other substances that are the substances to be transported, however this point has not been clarified.

In this study, we attempted co-encapsulation of micro-objects. We successfully encapsulated polystyrene beads or *E. coli*, each with 5 to 20 particles per vesicle, and controlled Chlamy-lipo’s direction by the cells’ phototaxis. We plan to study how cargo type and number affect motility to explore the potential of Chlamy-lipo as a microcarrier.

Sota Miura, Koichiro Sadakane (*Grad. Sch. Life and Med Sci., Doshisha Univ.*)

When polyethylene glycol (PEG), a water-soluble polymer, is mixed with dextran (DEX) at certain concentrations, cell-sized droplets form. Adding lecithin, a key component of cell membranes, causes it to self-assemble at droplet interfaces and interiors, forming cell-like structures. This model is promising for studying cellular phenomena and for use as a safe sample in drug testing. To better mimic real cellular conditions, stability is essential. Droplet size and stability can be controlled by adjusting the concentrations of PEG, DEX, and lecithin. In this study, we focused on interfacial tension, a key factor in droplet behavior, and evaluated its changes due to lecithin, based on fusion relaxation time and droplet viscosity.

Wancheng Zhang¹, Aileen Cooney², Lorenzo Di Michele³, Yuval Elani², Tomoaki Matsuura¹ (¹*Earth-Life Science Institute, Institute of Science Tokyo*, ²*Department of Chemical Engineering, Imperial College London*, ³*Department of Chemical Engineering and Biotechnology, University of Cambridge*)

Giant unilamellar vesicles (GUVs) have been widely utilized as models for artificial cells. However, GUVs exhibits obvious limitations for its compositional simplicity and low stability under complex conditions to mimic natural cells. In this study, we presents a gel-in-GUV system (GiG), in which a polyethylene glycol (PEG) hydrogel is encapsulated as artificial inner cellular environment [1] and covalently linked to the membrane. This GiG system exhibits enhanced stability against detergents and mechanical stress, while maintaining benign ability to incorporate membrane proteins. This system offers valuable insights for the design of more robust and complex artificial cell models.

References

[1] *Chem. Commun.* 2014, 50 (44), 5895–5898.

Ryuya Bamba, Koichiro Sadakane (*Grad. Sch. Life and Med Sci., Doshisha Univ.*)

It is known that a mixed solution of PEG and DEX can take three states depending on its composition. A phase diagram can be drawn. It has been shown that droplets spontaneously form at concentration compositions near the boundaries of these regions, and these droplets are used as cell models for research on intracellular phenomena. The conditions of phase separation and the boundaries of the regions can be related. However, the phase diagram so far has been drawn subjectively. Light scattering can provide more accurate conditions for cell model formation.

In this study, we will obtain data on the change of scattering intensity with temperature in the PEG/DEX system and discuss the effects of phospholipids and surfactants on the phase separation.

Riki Haida¹, Makiko Suwa^{1,2}, Kenji Echuya² (¹*Biological Science Course, Graduate School of Science and Engineering, Aoyama Gakuin University, Kanagawa, Japan*, ²*Chem. Biological Science Course, Department. Science and Engineering, Aoyama Gakuin University, Kanagawa, Japan*)

The mechanism of membrane insertion during protein translation differs between eukaryotes, with complex internal membranes, and simpler prokaryotes. Previous work showed that synonymous codon bias regulates translation speed and structure formation (*Cell Rep.* 42, 2023). Then we focused on codon usage in membrane proteins and compared yeast and *E. coli*. We evaluated relative synonymous codon usage (RSCU) by mapping DNA and amino acid sequences of transmembrane(TM) and extramembrane(ETM) regions, and compared these with experimental tRNA abundance data. The results revealed region-specific RSCU differences in both species, with particularly wide gap in Arg codons. Codons with high tRNA abundance were enriched in the ETM region of *E. coli* and the TM region of yeast.

[3Pos157](#) Evaluating Protein Generative AI for Exploring Uncharted Sequence Space

Hafumi Nishi^{1,2,3} (¹*Grad. Sch. Info. Sci., Tohoku Univ.*, ²*Fac. Core. Res, Ochanomizu Univ.*, ³*ToMMo, Tohoku Univ.*)

Protein generative AI promises novel biodesigns, yet its coverage of sequence space and reliability of fold retention remain unclear. I evaluated the sequence-diffusion model EvoDiff-38 M/100 M by generating 100 variants of T4 lysozyme, RNase H and GFP. A UMAP projection of ESM-2 embeddings placed the sequences largely outside natural and Pfam clusters; a few bridged families but most formed isolated islands, showing limited traversal. AlphaFold2 predictions showed that many outputs lost the target fold, confirming that naïve generation rarely preserves structure. Conditional runs of ESM-3-1.4 B/7 B and Chroma prompted with InterPro IDs behaved similarly. This benchmark underscores the need for steerable, fold-aware pipelines before large-scale protein design.

[3Pos158](#) Structure prediction of protein complexes using cross-linking mass-spectrometry data with the estimated error rate

Hiroto Matsubara, Takaharu Mori (*Tokyo University of Science*)

Structure determination of large protein complexes is one of the challenging issues in structural biology. X-ray crystallography and cryo-EM have been widely used for structure determination. Cross-linking mass-spectrometry (XL-MS) is also useful for identifying nearby amino-acid sequences. However, XL-MS data contain many errors originated from aggregation of the target protein in solution, making it difficult for determining the complex structure using XL-MS data. Here, we develop a rigid-body docking algorithm based on a score function that combines the atomic interaction energies and XL-MS restraint energy with the estimated error rate. Considering the error rate could automatically discard the errors, and thereby, improve the structure prediction accuracy.

[3Pos159](#) EpiLoop : 説明可能なグラフ・トランスフォーマーによる細胞特異的クロマチンループのストライプ型／ドット型識別と分類

EpiLoop: explainable graph transformer for identifying and classifying cell-specific chromatin loops into stripe or dot structures

Bingxin Xie^{1,2}, Yuichi Taniguchi^{1,2,3} (¹*Grad. Sch. Biostudies, Kyoto Univ.*, ²*iCeMS, Kyoto Univ.*, ³*Inst. for Advanced Study, Kyoto Univ.*)

Chromatin loops shape 3D genome organization to regulate gene expression, yet Hi-C provides only 5–10 kb resolution and Micro-C remains expensive and scarce. We present EpiLoop, an explainable graph-transformer framework that identifies chromatin loops at near-kilobase resolution using routine epigenetic data. Loop anchors are derived from high-resolution reference maps, and the model is trained and validated on held-out data to deliver accurate loop calls with confidence scores. Unlike existing methods, EpiLoop provides per-loop explanations of the key epigenetic marks and genomic contacts driving each prediction. The fully automated pipeline enables precise loop mapping, targeted validation, and accelerated discovery in gene regulation and disease.

[3Pos160](#) 金属イオン結合部位を予測する機械学習モデルの開発 Development of Machine Learning Models for Predicting Metal Ion-binding Sites

Yamato Machara, **Masafumi Shionyu** (*Grad. Sch. Biosci, Nagahama Inst. Bio-Sci. and Tech.*)

Many metal ions bound to proteins play key roles in enzymatic reactions and structural stabilization. Thus, identifying the binding sites of metal ions may provide clues to the functions of uncharacterized proteins. Although methods based on structural data have been developed, those relying on precise atomic coordinates may perform poorly with the predicted structures. To address this, we developed a machine learning model using a graph neural network (GNN) to predict the metal ion-binding sites on the predicted structures. In our approach, protein structures are represented as graphs, with amino acids as nodes. The predictive performance of the trained models for Zn²⁺, Mg²⁺, Na⁺, and Ca²⁺ binding sites, and a comparison with existing methods are discussed.

3Pos161 アルツハイマー病特異的タウ線維構造の Inverse folding
Inverse folding of Alzheimer disease-specific tau filaments

Motoharu Tajitsu¹, Maria Kano², Taeko Kimura², Sakura Homma¹, Taisuke Tomita², Yasuhiro Matsunaga^{1,3} (¹*Grad. Sch. Sci. Eng., Saitama Univ.*, ²*Grad. Sch. Pharm. Sci., Tokyo Univ.*, ³*RIKEN*)

Replicating Alzheimer disease (AD)-specific tau PHF fold in vivo is vital for AD mouse models and tau-targeted therapeutics. This PHF fold is found only in patient-derived tau, with recombinant wild-type (WT) tau failing to form such structures in vitro. To address this, we use an inverse folding approach to redesign sequences promoting assembly. We redesigned tau sequences focusing on retaining the ability to induce WT tau assembly. The redesigned sequences computationally predicted structures close to the target. Notably, several unconstrained residues were preserved from the WT sequence, indicating their potential role. These findings offer insights into tau aggregation determinants, aiding development of tauopathy models replicating AD-relevant conformations.

3Pos162 環境変化と損傷に対するロバストネスの進化
Evolution of Robustness to Environmental Change and Damage

Mao Sakae (*Ritsumeikan LifeScience*)

This research uses the Evogym simulator to explore how robust soft robot designs evolve, allowing them to maintain function despite environmental shifts and physical damage. I aim to uncover the engineering principles behind biological organisms' incredible adaptability and resilience. By co-evolving robot morphology and neural networks under various terrains and damage scenarios, we seek to understand how dynamic, self-organizing robustness emerges. My findings will offer insights into biological mechanisms like redundancy and plasticity, contributing to the development of bio-inspired robots for disaster response, self-healing materials, and prosthetics, while deepening our understanding of life's evolutionary robustness.

3Pos163 The Impact of Environmental Factors on the Predatory Behavior of Marine Organisms

Haruki Kawakami (*Ritsumeikan university*)

This study investigates how environmental constraints affect marine predator behavior using an extended Boid-based agent simulation. The model includes oxygen level, body temperature, and a rush behavior triggered near prey. Simulation results show that while acceleration boosts prey capture early on, increased oxygen consumption shortens dive times and lowers overall efficiency. Models with oxygen- or temperature-based constraints produced more realistic behavior. This framework offers a foundation for linking physiological limits with predator-prey dynamics in future ecological modeling.

3Pos164 深層学習を用いた筋小胞体形態と Ca^{2+} 濃度の関係の解析
Analysis of the relationship between sarcoplasmic reticulum morphology and Ca^{2+} concentration using deep learning

Katsuya Saito¹, Kenji Etchuya², Jun Nakamura³, Chikara Sato^{1,3,4,5}, Makiko Suwa^{1,2} (¹*Biol. Sci., Grad. Sch. Sci. Eng., Aoyama Gakuin Univ.*, ²*Chem. Biol. Sci., Dept. Sci. Eng., Aoyama Gakuin Univ.*, ³*Natl. Inst. Adv. Ind. Sci. Techno. (AIST)*, ⁴*Div. Immune Homeostasis, Dept. Pathol. Microbiol., Nihon Univ. Sch. Med.*, ⁵*Div. Microbiol., Dept. Pathol. Microbiol., Nihon Univ. Sch. Med.*)

Sarcoplasmic reticulum (SR) is involved in skeletal muscle diseases. The morphological changes of SR are considered to be affected by the configurations of calcium pumps (Ca^{2+} -ATPase) present on the membrane. To elucidate the molecular mechanism of SR, it's necessary to investigate the morphologies of isolated SR vesicles using a lot of electron microscope (EM) images. Previous studies detect the SR vesicles automatically by deep learning because manual classification requires a long time, and machine learning was found to be effective. However, since there are differences in detection accuracy between each morphology. In the future we aim to improve the accuracy for each specific morphologies and identify the three-dimensional structure of the calcium pump.

3Pos165 **ヌクレオチド三リン酸の長時間結合は細胞質中の蛋白質間相互作用を抑制する**
Prolonged Bindings of Nucleoside Triphosphates Reduces Protein-Protein Interaction in Cytoplasm

Isseki Yu¹, Michael Feig², Yuji Sugita³ (¹*Maebashi Institute of Technology*, ²*Michigan State Univ.*, ³*Riken*)

ATP, one of the most abundant metabolites in cytoplasm, has recently been found to prevent the formation of LLPS in vitro. To obtain molecular-level insights into this effect, we performed MD simulations of bacterial cytoplasm. It was indicated that the presence of metabolites clearly reduces the protein-protein interactions. Notably, nucleoside triphosphates (ATP, GTP, CTP, and UTP), showed prolonged (more than microseconds) binding with protein surfaces. In contrast, other metabolites and ions diffused rapidly to the bulk phase. Such prolonged binding of nucleotide triphosphates enhances the electrostatic repulsion between macromolecules. Remarkably, these effects were not reproduced by the simulation of high-ion-concentration aqueous solutions.

3Pos166 **光応答性膜モジュレータ分子の分子動力学シミュレーション**
Molecular Dynamics of Light-Responsive Twistable Membrane Modulators

Reo Kadowaki¹, Huo Wenting², Koji Miki², Kouichi Ohe², Wataru Shinoda³ (¹*Grad. Sch. Env. Life and Nat. Sci., Univ. Okayama*, ²*Grad. Sch. Eng. Sci., Univ. Kyoto*, ³*Res. Inst. Interdiscip. Sci., Univ. Okayama*)

To improve the delivery of drugs with low membrane permeability, light-triggered membrane-modulator molecule such as TPE-C-N have been developed. These molecules adsorb onto cell membranes and, upon light irradiation, undergo a structural transition from a planar to a twisted conformation, temporarily disrupting the membrane and enhancing permeability. However, the underlying molecular mechanisms remain poorly understood. In this study, we use coarse-grained molecular dynamics simulations to investigate the effects of TPE-C-N on a POPC lipid bilayer. Our simulations suggest that light-induced conformational changes in multiple TPE-C-N molecules act cooperatively to deform the membrane, providing mechanistic insights into how these molecules may facilitate drug delivery.

3Pos167 **Binding free energy shift of Barnase-Barstar complex due to single and double mutations**

Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

Protein-protein and interactions promote/inhibit protein functions in living cells and play a key role in many biological processes, including signal transduction, enzyme regulation, immune responses, and even viral infection. Amino acid mutations can significantly change the binding free energy and cause functional effects such as protein stability, disruption of signal transduction pathways, and even disease development. In this study, we propose a simple approach to estimate the binding free energy shift due to single and double mutations for Barnase-Barstar complex. We have succeeded in obtaining calculation results for single and double mutants of Barnase-Barstar complex and these values are in good agreement with experimental values.

3Pos168 **Molecular Dynamics Study of Potential Inhibitors Targeting VP28 from White Spot Syndrome Virus in Tiger Shrimp**

Fachruddin Hari Anggara Putera, Kazutomo Kawaguchi, Hidemi Nagao (*Graduate School of Natural Science and Technology, Kanazawa University*)

The tiger shrimp (*Penaeus monodon*) is a key aquaculture species threatened by White Spot Syndrome Virus (WSSV). VP28, a major envelope protein of WSSV, facilitates the virus's entry into host cells, making it an important target for antiviral intervention. This study aimed to identify potential VP28 inhibitors using molecular docking, 100 ns molecular dynamics simulations, and MMPBSA binding energy analysis. Five potential inhibitors were tested: EGCG, betasitosterol, emodin, cuminaldehyde, and eugenol. EGCG showed the strongest binding (−23.01 kcal/mol) via multiple hydrogen bonds. Betasitosterol showed strong hydrophobic interaction. Emodin had moderate stability, while cuminaldehyde and eugenol were weaker. EGCG emerged as the most promising inhibitor.

3Pos169 MD シミュレーションによる脂質フリッパーゼ MurJ の構造変化とイオン相互作用の解析
Analysis of Structural Changes and Ion Interactions of the Lipid Flippase MurJ by Molecular Dynamics Simulations

Keina Murata, Takaharu Mori (*Tokyo Univ. of Science*)

MurJ plays a key role in cell wall biosynthesis in Gram-negative bacteria by flipping Lipid II, a peptidoglycan precursor, across the inner membrane. Its structural cycle involves not only the binding and releasing of Lipid II but also the coordination of Na⁺ and Cl⁻ ions within a hydrophobic groove. However, the relationship between conformational changes, ion coordination, and substrate transport remains unclear. In this study, we investigated the transition from the inward-closed to inward-open state using MD simulations under varying ionic conditions. The results showed that Na⁺ is more stably coordinated to the binding site of MurJ in the presence of Cl⁻, and that structural transitions may be influenced by other factors, not limited to ion coordination.

3Pos170 Investigation of the Reason Why Ornithine Was Excluded from the Proteinogenic Amino Acids by Quantum Chemical Calculations

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The chemical structure of ornithine (Orn) is similar to that of lysine, but Orn is not a constituent of proteins. When Orn is incorporated into a peptide chain, an irreversible non-enzymatic lactamization occurs, which is known to inhibit peptide chain synthesis. The detailed reaction mechanisms have not been sufficiently elucidated. In this study, quantum chemical calculations were performed on reaction pathways of Orn lactamization using the model compound Ac-Orn-NMe (Ac = acetyl, NMe = methyl-amino). The activation energies for the lactamization of Orn were lower than that for the typical non-enzymatic reactions. This suggests that the high reactivity of Orn may contribute to its exclusion from standard amino acids.

3Pos171 MD 計算によるタンパク質透過チャネル SecY と分泌モニタータンパク質 VemP との相互作用解析
Elucidating the interactions between the protein-conducting channel SecY and translocating VemP via steered MD simulations

Shunsuke Muraoka¹, Hiroyuki Mori², Takaharu Mori¹ (¹*Tokyo University of Science*, ²*Kyoto University*)

In bacterial cells, newly synthesized proteins are transported across the membrane through the SecYE channel. Recently, a monitor protein VemP was found to sense its own protein transport activity and stop translation when its membrane permeability is reduced. The stability during secretion involves hydrophobic interactions between VemP and the SecYE complex. However, the specific location and the detailed mechanism of the interaction have not been elucidated. Here, we analyze the interaction between VemP and SecY by investigating the process of VemP permeation through the SecYE channel using steered MD simulation. Our results reveal that VemP interacts with two highly hydrophobic sites near pouring on the cytoplasmic side of the SecYE.

3Pos172 分子動力学シミュレーションによる HaloKbp1a₆₃₅ 蛍光タンパク質の理論研究
Theoretical Study of HaloKbp1a₆₃₅ Fluorescence Protein Sensor by Molecular Dynamics Simulations

Natthanan Kongchu, Shigehiko Hayashi (*Grad. Sch. Sci., Kyoto Univ.*)

We theoretically studied HaloKbp1a₆₃₅, a K⁺-sensing fluorescent protein, which exhibits substantial fluorescence by largely shifting the JF635-HTL fluorophore moiety's equilibrium from the neutral lactone (L) form towards the charged zwitterionic (Z) form upon K⁺ ion binding. After modifying the protein by covalently linking the fluorophore to the Halo-Tag domain, MD simulations were performed for both L/Z forms. It is found that the L form was buried inside the protein's cavity, whereas the Z form was exposed to water due to the opening movement by relative motions between the ion binding domain and the Halo-Tag one. We interpreted that hydrophobic interactions of side chains are prominent to stabilize the L form, and the Z form prefers exposure to water solvation.

3Pos173 Analysis of water dynamics around antifreeze proteins by molecular dynamics simulations

Shinnosuke Nakamura¹, Nao Abe¹, Simon Hikiri², Takuya Takahashi² (¹*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ²*Coll. Life Sci., Ritsumeikan Univ.*)

Biswas et al. calculated that the density within hydration shell around the ice-binding surface of antifreeze proteins is lower than that around the non-binding surface, and proposed a hypothesis to explain its function [1].

In this study, we developed a unique program to calculate the water density around the entire protein and each residue using the Monte Carlo method, aiming to elucidate its detailed function. Specifically, we applied a multiplicatively weighted Voronoi division using the van der Waals radius of the atom as a weight, and estimated the volume contained in each cell. The hydration shell density of each residue was then evaluated by counting the number of water molecules inside.

[1] A. Biswas et al. *J. Phys. Chem. Lett.* **12**, 8777 (2021).

3Pos174 カーボンドットとがん細胞膜脂質との相互作用に関する Steered 分子動力学シミュレーション
Steered Molecular Dynamics Study of Carbon Dot Interactions with Cancer Cell Membrane Lipids

Atsunori Yuki (*Grad. Sch. Bioinformatics. Ritsumeikan University. Shiga*)

Carbon dots (CDs) are emerging nanomaterials with great potential for cancer therapy and have recently attracted attention as drug delivery carriers and bioimaging probes. This study focuses on the membrane permeability of CDs, a key factor in their efficient intracellular delivery, and aims to elucidate the underlying molecular mechanisms.

Based on previous research, we constructed combinations of a simple CD with biomembrane models mimicking both cancer cell membranes and normal cell membranes. We then performed molecular dynamics (MD) simulations and quantitatively evaluated the energy barriers associated with membrane permeation of CDs using the umbrella sampling method.

3Pos175 水中およびクロロホルム中における鎖状と環状のグリシンペプチドに関する立体構造集団解析
Conformational ensembles of linear and cyclic glycine peptides in water and chloroform

Koji Umezawa^{1,2}, Yoshiyuki Yamaoka¹, Yuzuki Takase¹, Rei Kitajima¹, Jumpei Morimoto³, Shinsuke Sando³ (¹*Agri., Shinshu Univ.*, ²*Grad. Sch. of Sci. & Tech., Shinshu Univ.*, ³*Grad. Sch. of Eng., Univ. of Tokyo*)

Peptides are functional and useful amino-acid oligomers. Glycine is the simplest amino acid, which has a wide range of conformations in peptide. The conformational space of glycine polymers might cover the whole of peptide-conformation world. Then, in this study, we have investigated the conformational ensembles of glycine peptides in the range from 6 to 15 residues by the enhanced-sampling molecular dynamics simulations with all-atom models. The effects of solvent conditions (water or chloroform) and peptide shapes (linear or cyclic) on the ensembles were clarified. We will present the hydrogen bonding patterns and the free-energy landscapes.

3Pos176 Thermal Modulation of NOMPC Gating Springs in *Aedes aegypti*: Insights from Comparative Modeling and MD Simulations

Roberto Carlos Pestana Nobles¹, Martin Pavlovich¹, YuMin M. Loh^{1,2}, Matthew P. Su^{1,2,3}, Azusa Kamikouchi^{1,2}, Osamu Miyashita⁴, Florence Tama^{1,2,4} (¹*Institute of Transformative Bio-Molecules (ITbM), Nagoya University, Nagoya, Japan*, ²*Graduate School of Science, Nagoya University, Nagoya, Japan*, ³*Institute for Advanced Research, Nagoya University, Nagoya, Japan*, ⁴*RIKEN Center for Computational Science, Kobe, Hyogo, Japan*)

Male *Aedes aegypti* mosquitoes locate conspecific females using hearing. Improved knowledge of the molecular basis of mosquito hearing, could help generate novel methods of control. Mosquito auditory mechanotransduction relies on mechanosensory transduction channels, such as NOMPC, whose opening is mediated via mechanical gating springs and it is unclear whether temperature modulates this process. Here, we aim to characterize the *Aedes aegypti* NOMPC homolog through comparative sequence analysis, structural modeling, and molecular dynamics simulations at 18°C and 40°C to evaluate gating mechanics and thermal modulation of mechanotransduction. Clarifying temperature effects on the gating spring will refine mechanosensation models and inform vector control strategies.

3Pos177 Analysis of the Interconversion Mechanisms of “CO-in” and “CO-out” Conformations of Ferredoxin Using Molecular Dynamics Simulations

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Plant-type ferredoxin (PtFd) is a type of electron transfer protein that contains a [2Fe–2S] cluster as an active center. PtFd takes two redox states, *i.e.*, oxidized and reduced forms, and the interconversion between the two plays crucial roles in efficient electron transfer. Changes in the redox forms of PtFd cause peptide-bond flips near the active center and can affect affinity for electron acceptor. Based on the peptide-bond orientation, the conformations adopted by oxidized and reduced forms are called “CO-in” and “CO-out”, respectively. In this study, the molecular dynamics simulations were performed to analyze the extensive conformational sampling and interconversion mechanisms between “CO-in” and “CO-out” conformations of both oxidized and reduced PtFd.

3Pos178 Distinct Structural Responses of CRY1 and CRY2 to Small Molecule Binding: A Coarse-Grained Molecular Dynamics Simulation Study

Ajeet Kumar Yadav¹, Florence Tama^{1,2,3} (¹*Department of Physics, Nagoya University*, ²*ITbM, Nagoya University*, ³*Riken Center for Computational Science*)

Cryptochrome 1 and 2 (CRY1/2) are responsible for the circadian clock in mammals and are emerging targets for the therapeutic modulation of sleep disorders. Despite increasing interest, their conformational and ligand-induced structural changes remain inadequately characterized. In this study, we employ coarse-grained molecular dynamics to investigate the structural dynamics of CRY1 and CRY2 in both apo and complexes with a range of biologically relevant small molecules. In particular, we will characterize the conformational ensembles of the C-terminal regions of both CRY1 and CRY2 to identify potential conformations that align with data suggesting possible interaction sites with the PHR domain.

3Pos179 Multiscale modeling of spatiotemporal heterogeneity in biomolecular condensates

Eiji Yamamoto¹, Kento Fujita², Yusuke Takagi², Youtaro Takeda² (¹*Dept. Sys. Des. Eng., Keio Univ.*, ²*Grad. Sch. Sci. Tech., Keio Univ.*)

A variety of proteins and nucleic acids can form biomolecular condensates via phase separation. The presence of intrinsically disordered proteins (IDPs) imparts highly dynamic and complex behaviors to the condensates, which exhibit liquid-like properties and viscoelasticity. Here, we investigate the heterogeneous nature of biomolecular condensates using multiscale molecular dynamics simulations. Particle-based simulations reveal heterogeneity, intermolecular interactions, and molecular dynamics within condensates formed by multiple types of IDPs and polyadenylated RNA. In addition, mesoscale simulations employing a continuous concentration field model elucidate spatiotemporal heterogeneity within multicomponent droplets and its impact on droplet morphology.

3Pos180 High-throughput virtual screening and *de novo* design of functionalised nanographenes targeting the FAD binding site of CRY clock proteins

Ben Cree¹, Manami Hayashi², Masaya Hagai², Kazuhiro J. Fujimoto², Hideya Kono⁴, Kazuma Amaike⁴, Takeshi Yanai^{2,3}, Kenichiro Itami⁴, Florence Tama^{1,2,3} (¹*Computational Structural Biology Research Team, RIKEN R-CCS*, ²*Graduate School of Science, Nagoya University*, ³*Institute of Transformative bioMolecules, Nagoya University*, ⁴*Molecule Creation Laboratory, RIKEN*)

Traditional drug discovery spans a small region of chemical space, vast swathes of which remain unexplored. In this study, we employ the high-throughput virtual screening of a unique library of DFT optimised fused-ring nanographenes - flexible, π -conjugated structures with nonplanar and three-dimensional geometries not commonly found in conventional drug-like molecules. These nanographenes were screened against the circadian clock proteins CRY1 and CRY2, with promising structures subsequently being optimised in a *de novo* inhibitor design campaign - utilising a bespoke computational pipeline informed by crystallographic fragments. These functionalised designs will be subsequently synthesised using novel chemistries, in order to be experimentally validated.

3Pos181 Temperature-Dependent Conformational Changes of Dengue Virus Envelop protein

Dokainish Hisham, Yoshimasa Takahashi (*Research Center for Vaccine Development, NIID, Japan Institute for Health Security*)

Dengue virus (DENV) poses a major global health concern with limited therapeutic options. At physiological temperature, DENV adopts a bumpy viral surface morphology that exposes cryptic epitopes critical for immune recognition. To investigate how these hidden epitopes become accessible to the immune system, we performed enhanced sampling molecular dynamics (MD) simulations using generalized replica exchange with solute tempering (gREST) and umbrella sampling (US), expanded open state in which the E protein lifts, exposing conserved epitopes. These findings provide critical insights for the rational design of vaccines and antibody-based therapeutics.

3Pos182 シスチン/グルタミン酸アンチポーター xCT 輸送体の基質輸送過程の分子シミュレーション Molecular Simulation of Substrate Transport Mechanisms in the Cystine/Glutamate Antiporter xCT

Ikumi Mizuno, Kei Moritsugu (*Grad. Sch. Sci., OMU*)

The cystine/glutamate antiporter xCT (SLC7A11) is highly expressed in cells of the nervous and immune systems and is crucial for cellular stress resistance. This study aims to evaluate the substrate transport process coupled with the conformational changes between the inward-facing (IF) and outward-facing (OF) structures through molecular simulations, assessing the transport efficiency of substrates and the inhibitory potency of inhibitors. After modeling the uncharacterized OF structure, we performed multiple targeted molecular dynamics (MD) simulations to quantify the transport efficiency of substrates and inhibitors like erastin during the conformational transition between IF and OF. Additionally, we analyzed molecular mechanisms such as interaction with substrates.

3Pos183 ALSにおけるSOD1の構造動態・金属結合部位の反応性・毒性機構に関する理論的解析 Computational Insights into SOD1 Conformational Dynamics, Metal Site Reactivity, and Toxic Mechanisms in ALS

Shun Fujimaki¹, Shinya Tahara², Takakazu Nakabayashi², Norifumi Yamamoto¹ (¹*Chiba Tech*, ²*Tohoku Univ*)

Superoxide dismutase 1 (SOD1), a Cu/Zn-binding antioxidant enzyme, is implicated in the pathogenesis of amyotrophic lateral sclerosis (ALS). Although metal ion dissociation and disulfide bond cleavage in SOD1 are associated with ALS, the detailed mechanisms remain unclear. To investigate conformational changes, we performed molecular dynamics (MD) simulations on wild-type SOD1 (SOD1-SS), its apo form (apoSOD1-SS), and the disulfide-reduced apo form (apoSOD1-SH). Metal loss reduced α -helix formation in the electrostatic loop, while disulfide bond cleavage caused no major structural changes. Residue interaction network analysis revealed shifts in intramolecular interactions, and QM/MM methods will be used to study the reactivity of abnormal metal-binding sites.

3Pos184 D30N/L90M 変異を持つ HIV-1 プロテアーゼにおける薬剤耐性メカニズムの解明：残基間相互作用ネットワーク解析 Unveiling Drug Resistance Mechanisms in HIV-1 Protease with D30N and L90M Mutations: Residue Interaction Network Analysis

Keidai Yamase (*Chiba Tech*)

Background

HIV-1, the causative agent of AIDS, readily develops drug resistance due to its high mutation rate. While protease inhibitors are a cornerstone of therapy, mutations such as D30N and L90M can compromise their efficacy. To elucidate the mechanisms underlying this resistance, we performed molecular dynamics (MD) simulations of wild-type, D30N, and D30N/L90M HIV-1 protease.

Method

We conducted 1 μ s MD simulations for each system. Dynamic residue interaction network (dRIN) analysis was employed to identify conformational changes associated with resistance.

Results

Our dRIN analysis revealed that the D30N mutation weakens residue interactions within the protease flap region. Consequently lowers drug-binding affinity by altering the internal interaction network.

3Pos185

D2-L29/卵白リゾチーム複合体の変異による親和性向上メカニズム

Molecular Dynamics Elucidation of Mutation-Induced Affinity Enhancement in the D2-L29 VHH/ Hen Egg Lysozyme Complex

Rika Munakata, Motoki Inoue, Takefumi Yamashita (*Univ. Hoshi*)

Single-domain antibodies (VHHs) are promising therapeutic agents. Recently, it was reported that designed mutations enhance the affinity of D2-L29 VHH for hen egg lysozyme (HEL). To understand the affinity enhancement, we performed molecular dynamics (MD) simulations and MM-PBSA calculations for the wild-type (WT) and mutants of the HEL-VHH complex. The calculated binding free energies are consistent with the previous experimental results. The A107R mutant newly forms a stable salt bridge between HEL and VHH, strengthening electrostatic interactions, whereas the A107Y mutation introduces additional hydrogen bonds and hydrophobic contacts. These results demonstrate that MD analysis yields mechanistic insights, thus guiding future antibody design.

3Pos186

ニューラルネットワークを用いた溶液系の adaptive QM/MM 法の改善

Enhancement of Adaptive QM/MM Approaches for Solution-Phase Systems via Neural Networks

Hiroshi Watanabe, Takuma Ikeda, Haruyuki Nakano (*Dep. Chem., Fac. Sci., Kyushu Univ.*)

To incorporate quantum chemical effects of solvents into simulations of solution systems, a quantum mechanical (QM) model is needed. However, applying QM to the entire system is computationally expensive. The QM/MM method addresses this by combining QM for the solute and molecular mechanics (MM) for the solvent, but it struggles with molecular dynamics (MD) simulations due to solvent diffusion. To solve this, adaptive QM/MM methods were developed to switch solvent models on-the-fly based on solute distance. However, they often cause unphysical solvation structures and dynamics. We propose a new method that integrates neural network-based machine learning into the adaptive QM/MM framework to overcome these challenges.

3Pos187

Engineering Epithelial Layer Structures via Cell Surface Tension Using a 3D Vertex Model

Chayanit Thiticharoentam¹, Satoru Okuda² (¹*Division of Nano Life Science, Kanazawa University*, ²*WPI Nano Life Science Institute, Kanazawa University*)

The precise arrangement of cells is crucial for engineering three-dimensional (3D) tissues. However, the dynamic interactions between cells present a significant challenge in controlling their organization. In this study, we used a 3D Vertex model to engineer epithelial layer structures by considering the mechanical forces at cell surfaces. We generated a variety of layered structures comprising varying numbers of cell types, further demonstrating the possibility for cell sorting. Our findings contribute to the field of bioengineering by introducing a novel method for predicting engineered tissue structures, thereby addressing the current challenge of designing complex, multi-cellular architectures with controlled precision.

3Pos188

Discovery of novel inhibitor candidate compounds using accurate *in silico* screening protocol

Hiroto Terada, Kei Moritsugu (*Grad. Sch. Sci., OMU*)

Structure-based *in silico* screening is widely used as an important tool in drug discovery. It is problematic that a single crystal structure has been used as a receptor in conventional studies. Questions arise about how suitable receptor structures are chosen for a diverse compound library and whether the structures obtained from molecular dynamics (MD) simulations are useful for improved docking prediction accuracy. In this study, using a protein kinase MEK1 cocrystal structures as a test case, we developed accurate screening protocol by examining appropriate methods to take structural ensembles and to evaluate the affinity using associated docking scores. Furthermore, the derived protocol was then applied to other drug discovery targets such as EGFR and so on.

3Pos189 Structural dynamics analysis of actin filament formation using molecular dynamics simulation

Kenta Omoto (*Grad. Sch. Sci., OMU*)

Actin is a protein that forms filaments within cells and plays a significant role in cellular transport and cytokinesis. During the filament formation, actin undergoes structural changes that are dependent on the position (barbed/pointed ends or the center) and bound nucleotide (ATP/ADP+Pi/ADP). In this study, we conducted several molecular dynamics simulations of ATP/ADP+Pi/ADP-bound 5-mer actin filaments to analyze the structural variations of the five actins. The resulting structural changes and fluctuations were analyzed by calculating residue contacts between adjacent actin subunits and associated subunit interactions. We also examined the actin binding affinities of barbed/pointed ends and their association and dissociation processes.

3Pos190 変動環境下での代謝恒常性を支える Bowtie 型代謝ネットワーク
Bowtie-Structured Metabolic Networks Maintain Homeostasis under Fluctuating Environments

Yudai Iyoda¹, Chikara Furusawa^{1,2}, Yusuke Himeoka¹ (¹*Grad. Sch. Sci., Univ. Tokyo*, ²*BDR, Riken*)

Metabolic networks have a so-called “Bowtie” or “Core–Periphery” structure, where a variety of nutrient inputs converge on a few hub metabolites and then diverge toward multiple growth-factor outputs. It remains an open question in theoretical biology whether such a Bowtie structure possesses adaptive properties or merely reflects a by-product of metabolic evolution.

We construct an artificial class of hypothetical metabolic networks to explore both Bowtie and non-Bowtie structures. We show that Bowtie structures confer homeostatic maintenance of growth-factor production under nutrient fluctuations. In this talk, I will discuss how these homeostatic benefits may have driven the evolutionary selection of Bowtie structures in metabolic systems.

3Pos191 一細胞と組織における力学応答の矛盾を統合する張力ホメオスタシスモデルの構築
Tension homeostasis model integrating contradictory mechanical responses in a single cell and tissues

Yoshihito Sawazaki¹, Yohei Kondo², Naoki Honda^{1,2} (¹*Grad. Sch. Integr. Life Sci., Univ. Hiroshima*, ²*Grad. Sch. med., Univ. Nagoya*)

Tissues containing contractile cells, such as fibroblasts, exhibit a phenomenon called tensional homeostasis. This refers to the ability of cells to maintain the mechanical tension of the tissue at a set point in response to external perturbations. However, the response of fibroblasts to external perturbations exhibits seemingly contradictory behavior depending on the spatial scale. Traction force increases in a single cell in response to external tensile forces, while it decreases at the tissue scale. We aim to reveal the mechanism of tensional homeostasis in tissues by mathematically modeling cell-cell interactions via substrate strain.

3Pos192 代謝動力学モデルを用いた細胞の低温ストレス応答解析
Analysis of Cellular Responses to Cold Stress Using a Metabolic Kinetics Model

Atsuki Hishida¹, Yusuke Himeoka², Chikara Furusawa^{2,3} (¹*Grad. Sch. Sci., Kyoto Univ.*, ²*Univ. Biol. Inst., Grad. Sch. Sci., Univ. Tokyo*, ³*BDR, Riken*)

Using a kinetic model of *E. coli*'s central metabolism, this study showed system-wide temperature effects on dynamics of cellular metabolism. When reaction parameters were reduced temperature-dependently, a steady state stable at room temperature destabilized under cold stress, driving the network into alternative state where metabolic activity slowed dramatically. An ATP/ADP imbalance emerged as the key destabilizing factor; adding ATP/ADP-homeostatic reactions restored stability. Further analysis showed that tuning enzyme concentrations can preserve the original steady state at low temperature. These findings indicate the complexity and potential compensability of the temperature effect on intracellular metabolic states.

3Pos193 液滴勾配による遺伝子誘導の数値モデル
Gene Guidance by Droplet Gradients: A Theory

Takeshi Sugawara (*Center for Data Science, Kochi Univ.*)

Enhancers regulate gene activity by forming phase-separated droplets with transcription factors, capturing target genes near promoters. However, gene mobility is constrained in the crowded nucleus, and how enhancers find distant targets remains unclear. Inspired by axon guidance, we propose a hypothesis: "Gene Guidance." Promoters detect droplet concentration gradients and move toward enhancers via a chemotaxis-like mechanism, "droplet taxis," enabling efficient interactions. While prior MD models struggle to simulate droplets genome-wide, we present a phenomenological model coupling DNA with droplet fields. It explains gene capture by enhancer condensates and aligns with experimental findings. We introduce the concept, progress, and future directions.

3Pos194 回帰的な無機膜ダイナミクスで歩行するソフトロボット
A Walking Soft Robot Actuated by Recursive Inorganic Membrane Dynamics

Ryusei Kubota, Muneyuki Matsuo (*Graduate School of Integrated Sciences for Life, Hiroshima University*)

Self-propelled inorganic objects with structural asymmetry from material rigidity, such as Janus particles, have been widely studied. In contrast, objects that exploit softness to spontaneously break symmetry and generate self-propulsion have not been reported. We present a walking inorganic soft robot actuated by non-equilibrium dynamics through recursive formation and dissolution of an $\text{Al}(\text{OH})_3$ membrane. When AlCl_3 solution in a bottom-holed container was floated on NaOH solution, a membrane formed at the AlCl_3 aq./NaOH aq. interface and gradually dissolves due to complexation with OH^- . This process generates rhythmic foot-like protrusions, enabling autonomous walking. A model coupling membrane dynamics with water flow will be discussed to explain the walking.

3Pos195 擬二次元環境下における繊毛虫テトラヒメナの疎密波形成と伝播
Formation and propagation of the density wave by Ciliate *Tetrahymena* under a Quasi-2D Environment

Ryuhei Itoh¹, Kohei Okuyama¹, Ibuki Kawamata¹, Marie Tani¹, Akira Kakugo¹, Masatoshi Ichikawa^{1,2} (¹*Grad. Sch. of Sci., Kyoto Univ.*, ²*Grad. Sch. Integ. Sci. Life, Hiroshima Univ.*)

In nature, there are many collective motion by self-propelled organisms that convert external energy into movement, such as fish schooling and bacterial pattern formation. Understanding these phenomena experimentally is the key to developing a unified physical framework for collective motion.

In this study, we report the emergence of a propagating density wave in a quasi-2D suspension of ciliate-*Tetrahymena*. We investigate how motility, local density, chamber height, and cell concentration influence the wave's emergence and propagation speed. These findings offer valuable experimental insights into nonequilibrium collective behavior in biological systems.

3Pos196 Development of a Micro-Acoustic Resonator for Micro-Rheological Measurement of Biomolecular Condensates

Taichi Yoshikawa, Hirotsugu Ogi, Kichitaro Nakajima (*Graduate School of Engineering, Osaka University*)

Biomolecular condensates are mesoscale viscoelastic bodies formed via liquid-liquid phase separation in cells. Analyzing their rheological properties is essential for understanding their roles in cellular function and malfunction. However, current methods are limited by their invasiveness due to the use of probe particles and/or laser irradiation. Here, we present a novel, non-invasive analytical platform based on a micro-acoustic resonator to dissect the micro-rheology of condensates. Our resonator can trap and deform single microscale condensates using acoustic radiation force. By applying amplitude modulation to the acoustic field, we evaluate the frequency-dependent viscoelastic properties of biomolecular condensates.

3Pos197**光学的手法を用いた選択的 DNA 増幅技術の開発**

Development of selective DNA amplification technology by optical method

Ren Saito¹, Hironori Sugiyama³, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Dep. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, ²*RIPH., Univ. Tokyo*, ³*ELSI., Science Tokyo*)

Screening using microchamber arrays, based on digital quantification, enables protein expression from single-molecule DNA templates, thereby allowing the efficient recovery of highly active mutants with high enrichment efficiency. However, conventional DNA recovery methods rely on microcapillaries that require contact-based manipulation, leading to issues such as non-specific amplification due to contamination and the need for large equipment for integration with microscopy. This research developed an optical DNA amplification method that works in defined micro-regions, which aimed to achieve non-contact DNA recovery. In the future, the system will be further optimized and established as a reliable screening method.

3Pos198**硫酸アンモニウム混合液で加工したナノポアを用いた高解像度一分子構造解析**

High-resolution single-molecule structural analysis of nanopore sensing using ammonium sulfate assisted fabrication

Wataru Tsuchiya¹, Lin Liu², Kyosuke Matsuda¹, Fan-Yan Wei³, Hirohito Yamazaki⁴ (¹*Grad.Mech., Nagaoka Univ. of Tech.*, ²*Grad.Sch.Med, Tohoku Univ.*, ³*IDAC, Tohoku Univ.*, ⁴*Mech., Nagaoka Univ. of Tech.*)

In this study, we demonstrate single molecule measurement using nanopore fabricated under condition of an ammonium sulfate contained buffer and investigate its effect. Our streaming potential measurement revealed that the interaction between DNA and ammonium ions was strengthened, leading to a slower translocation speed. Nanopore measurement made it possible to detect the difference in secondary structure between polyC and polyA in poly(dC)50(dA)50(dC)50 without unzipping DNA duplex. Next, we investigated the structural stability of mouse RNA modification-deficient tRNA using developed method. Our nanopore measurements of modification-deficient proline tRNA and wild-type proline tRNA using the same pore showed different structural stability.

3Pos199**Vibrational relaxation process of flavin compounds measured by resonance IR method****Minoru Yamakawa¹**, Hirona Takahashi^{1,2}, Konoka Mifune¹, Makoto Sakai^{1,2} (¹*Graduate School of Science and Engineering, Okayama University of Science*, ²*Faculty of Science, Okayama University of Science*)

We used resonance IR spectroscopy to measure the resonance IR spectra of flavin compounds (flavin mononucleotide; FMN, flavin adenine nucleotide; FAD and lumiflavin), and successfully observed vibrations in the skeleton of the flavin. In addition, the measurement of resonance IR intensities as a function of the delay time between the IR and visible lasers was performed to shed light on the vibrational relaxation. It was observed that the signal rises and then beats. This indicates dissipation of vibrational energy. A characteristic beat was observed only for certain IR vibrations (around 1545 cm⁻¹) of FMN, FAD and lumiflavin. Therefore, because no side chains effect was observed, the characteristic beat is thought to be due to the flavin skeleton.

3Pos200**Design of nanodiamonds for subcellular thermal manipulation****Daisuke Watanabe¹**, Yoshie Harada^{1,2} (¹*WPI-PRiME, Univ. Osaka*, ²*IQIB, Univ. Osaka*)

Temperature is a fundamental parameter in biological systems. Recent studies have shown that even small changes in intracellular temperature can affect cellular functions. While micrometer-scale laser heating has demonstrated that localized temperature increases influence cellular behavior, it remains insufficient to evaluate the significance of submicron heating at the organelle level. This study aims to develop a nanoscale local heating technique targeting specific organelles using heater-thermometer hybrid diamond nanosensors which combine temperature-sensitive fluorescent nanodiamonds and photothermal polydopamine. This approach offers a technological platform for manipulating biological functions, different from traditional molecular biology-based methods.

3Pos201 液性相分離を用いたオイルフリーデジタルバイオアッセイ
Oil-free Digital Bioassay with Aqueous Two-Phase Separation

Yoshihiro Minagawa¹, Kai Matsumoto¹, Hiroyuki Noji^{1,2} (¹Dept. App. Chem., Univ. Tokyo, ²RIPH., Univ. Tokyo)

Digital bioassays, stochastically confining targets in microreactors for "1"/"0" signal detection, are highly sensitive systems. However, the LOD in digital bioassays requiring oil sealing is restricted by total reactor volume. To address this, we introduce an oil-free digital RNA detection method using an aqueous two-phase system (DEX/PEG). This method concentrates SARS-CoV-2 RNA, Cas13, and Dextran Binding Domain (DBD)-conjugated probes in DEX droplets within a femtoliter reactor array device (FRAD). This enables multiple RNA loadings for continuous enrichment and improved sensitivity. Component immobility was confirmed by FRAP analysis. Multiple sample loadings achieved sub-femtomolar sensitivity.

3Pos202 プログラム可能な DNA 応答型発光センサープラットフォーム：スプリット Cas12a とルシフェラーゼ再構成に基づくシステム
Programmable DNA-responsive bioluminescent sensor platform based on split Cas12a and luciferase reconstitution

Figueiredo Diogo^{1,2}, Mitsuru Hattori², Takeharu Nagai^{1,3} (¹Graduate School of Frontier Biosciences, Osaka University, Suita, Osaka, ²Department of Biomolecular Science and Engineering, SANKEN, Osaka University, Ibaraki, Osaka, ³Trans dimensional Life Imaging Division, Institute for Open and Transdisciplinary Research Initiatives, Osaka University, Suita, Osaka)

CRISPR-Cas12a has emerged as a powerful nucleic acid detection tool. Here, we present a novel molecular sensing platform that integrates Cas12a with split luciferase technology for programmable, bioluminescent detection of DNA. Cas12a is divided into two inactive fragments, each fused to a split luciferase component. Upon target recognition by a guide RNA, the fragments reassemble, restoring luciferase activity and producing light only when the specific DNA is present. This method is robust, background-free, and easily reconfigurable, allowing broad adaptation for diverse DNA targets. Beyond point-of-care diagnostics, it enables DNA-responsive bioluminescent imaging in biological systems, expanding molecular sensing in biophysics.

3Pos203 細胞内温度変動を支配する非伝導性熱散逸
Non-conductive heat dissipation governs intracellular temperature variations

Masaharu Takarada¹, Takashi Funatsu², Kohki Okabe¹ (¹Graduate School of Pharmaceutical Sciences, The University of Tokyo, ²Graduate School of Integrated Sciences for Life, Hiroshima University)

Recently, it has been discovered that intracellular temperature variations (~1°C) by spontaneous heat generation exist in cells. However, calculations based on commonly accepted heat conduction models in cells indicated that spontaneous heat generation can only increase intracellular temperature by 10⁻⁵°C. We hypothesized that overlooked mechanism of heat dissipation exists in cells other than heat conduction and measured heat dissipation in cells. From observation of the relaxation process after stopping intracellular heating by infrared laser, we revealed that non-conductive mode of heat dissipation exists in cells more than 1000 times slower than the calculated value of heat conduction model.

3Pos204 Development of a Homo-FRET-Based Approach to Monitor Protein Conformational Changes

Tomoya Mukai^{1,3}, Yasushi Okada^{1,2,3} (¹Grad. Sch. Sci., Univ. Tokyo, ²Grad. Sch. Med., Univ. Tokyo, ³Kobe Inst., Riken)

Visualization of conformational changes of proteins in living cells is essential for understanding their functions. Förster Resonance Energy Transfer (FRET) is widely used for this purpose. In particular, Homo-FRET, which involves energy transfer between identical fluorophores close together, causes changes in fluorescence anisotropy. This allows the detection of relative positional changes of fluorophores using a single fluorescence channel. In this study, we aimed to apply Homo-FRET to probe conformational changes of a mechanosensitive ion channel. We report our current progress in establishing this method and aim to discuss its potential utility for investigating structural dynamics of proteins in cellular contexts.

3Pos205 蛍光多重イメージングのための、青色と緑色光で光スイッチングする緑色蛍光タンパク質の開発
A green fluorescent protein reversibly photoswitched by blue and teal light for multiplexed imaging

Ryohei Ozaki-Noma, Tetsuichi Wazawa, Kazunori Sugiura, Takeharu Nagai (*SANKEN, The Univ. of Osaka*)

Reversible photoswitching fluorescent proteins (rsFPs) can reversibly transition between fluorescently bright and dark states with specific wavelengths of light. rsFPs offer powerful tools for multiplexed imaging within a single optical window for fluorescence emission. Here, we report a green rsFP reversibly photoswitched by blue (~460 nm) and teal (~520 nm) light. This unique spectrum of photoswitching allows for distinction from all previously known rsFPs, and therefore, increases the number of distinguishable FPs in multiplex fluorescence imaging. We successfully decomposed green fluorescent signals into four rsFP components. Our results highlight its potential for complex spatiotemporal imaging applications in cell biology.

3Pos206 鶏卵の孵卵中のレーザースペckル法による血管の可視化に適した露光時間の探索
Searching for Optimal Exposure Time for Visualization of Blood Vessel of Chicken Egg During Incubation Using Laser Speckle Imaging Method

Hiroyuki Tamura^{1,2,3}, Tetsuhito Suzuki⁴, Keiichiro Shiraga^{1,5}, Naoshi Kondo¹, Yuichi Ogawa⁶ (¹Graduate School of Agriculture, Kyoto University, ²Distinguished Doctoral Program of Platforms (WISE), Kyoto University, ³JSPS Research Fellowship for Young Scientists DCI, ⁴Graduate School of Bioresources, Mie University, ⁵PRESTO, JST, ⁶Department of Medicine, Hyogo Medical University)

Laser speckle imaging (LSI) is emerging as a promising, non-invasive method for visualizing blood vessels in developing chicken embryos, which is crucial for the sex prediction in the early incubation stage. In this study, we focused on determining the optimal exposure time that maximizes the contrast between blood vessels and the yolk. Model-based analysis indicated that when multiple particle dynamics coexist, a single exposure time maximizes contrast differentiation. Experiments using both white- and brown-shelled eggs—widely distributed egg types—confirmed that an exposure time of 5 to 10 ms is optimal for enhancing vessel visibility under standard LSI conditions.

3Pos207 XY クロストークを低減した高速 AFM スキャナーの開発
Development of a high-speed AFM scanner with reduced XY crosstalk

Sora Nishida¹, Kenichi Umeda², Noriyuki Kodera² (¹Grad. Sch. Math & Phys., Kanazawa Univ., ²WPI-NanoLSI, Kanazawa Univ.)

High-speed AFM (HS-AFM) is a unique microscopy that allows direct real-time visualization of the shape and dynamics of biomolecules without any chemical labeling. It has contributed to uncovering the functional mechanisms of various proteins. However, the current HS-AFM scanner has a problem that the images are distorted by displacement of about 4.5 nm in the X direction per 100 nm in the Y direction. This leads to reduced accuracy in distance measurements in HS-AFM observations. Here, we developed a HS-AFM scanner with reduced XY crosstalk. As a result, the new scanner successfully reduces the image distortion caused by crosstalk to about 90% compared to the conventional scanners, without deteriorating high-speed scanning performance.

3Pos208 Correlation Analysis of Intracellular Temperature Heterogeneity and Subcellular Structures

Keisuke Fujita¹, Yoshie Harada^{1,2} (¹WPI-PRIME, Univ. Osaka, ²QIQB, Univ. Osaka)

We used a multiplexed immunofluorescence technique to overlay 30 types of stained images, generating 30-dimensional pixel-level data for each cell. These data were clustered using self-organizing maps and further grouped into dozens of clusters, enabling systematic characterization of organelle-dependent cellular heterogeneity. We are currently developing an experimental system to investigate how this heterogeneity relates to intracellular temperature distribution. Although various sensors have been used to measure temperature distribution in cells, its physiological significance remains unclear. This presentation introduces an approach that combines multiplexed imaging with intracellular thermometry to explore the biological functions underlying thermal heterogeneity.

3Pos209 急速凍結ディープエッチングレプリカ電子顕微鏡を用いた滑走細菌のペプチドグリカン層の可視化
Visualization of peptidoglycan layer of gliding bacteria by using quick-freeze deep-etch replica electron microscope

Yuhei Tahara^{1,2}, Makoto Miyata² (¹Grad. Sch. Eng., Osaka Metropolitan Univ., ²Grad. Sch. Sci., Osaka Metropolitan Univ)

Myxococcus xanthus and *Flavobacterium johnsoniae* are diderm bacteria that adhere to solid surfaces and perform a unique gliding motility. This motility mechanism transmits the force generated inside the cell to external adhesive proteins across the rigid cell wall (peptidoglycan: PG). In this study, to clarify the structural differences of the cell walls, the isolated PG was visualized by using a quick-freeze deep-etch replica electron microscope. *M. xanthus* showed larger PG holes and hole area ratios than *E. coli* and *F. johnsoniae*. This is consistent with a model in which a complex mediated by PG transmits force in *M. xanthus* gliding complex, while a complex penetrating PG transmits force in *F. johnsoniae*.

3Pos210 電子顕微鏡における複素観測：シェルツァー限界を超える
Complex Observation in Electron Microscopy : Surpassing the Scherzer Limit

Kuniaki Nagayama (*Science Communication Laboratory LLC*)

Complex observation was first published a quarter century ago. Its objective was to surpass the Scherzer limit, which had been a resolution limit since Scherzer's 1947 paper. It combines conventional and Zernike phase plate experiments in a complex manner to break the limit. However, there were challenges with the two-experiment setup. These were recently resolved by generating an extended CTF (the squared absolute value of the CTF) using a Wiener filter, resulting in a single-experiment method. This paper reports on how the extended CTF improves electron microscopy performance in terms of resolution and sensitivity. This is demonstrated using simulations of four phase-contrast methods (Scherzer, Zernike, Hilbert, Foucault) when applied to green fluorescent protein.

3Pos211 Non-invasive Evaluation of iPSC-derived Cardiomyocytes Using Deep Learning

Taishi Kakizuka^{1,2}, Taro Ichimura², Takeharu Nagai^{1,2} (¹SANKEN, Univ. Osaka, ²OTRI, Univ. Osaka)

We developed deep learning-based methods to non-invasively assess iPSC-derived cardiomyocytes. Monolayer cardiomyocyte sheets containing tens of thousands of cells were imaged using our ultra wide-field imaging system, AMATERAS, followed by immunostaining to label cardiac subtypes. A convolutional neural network trained on beating dynamics successfully classified atrial and ventricular subtypes with ~90% accuracy. We also applied self-supervised representation learning and computed anomaly scores, revealing rare abnormal cells (< few %) with distinct morphology. Calcium imaging showed these cells had spontaneous calcium sparks, suggesting arrhythmic potential. These methods are expected to contribute to robust quality control of iPSC-derived cardiomyocytes.

3Pos212 赤外 STED と共焦点顕微鏡の組み合わせによる、細胞周期と細胞内の構造の同時計測
Observation of cell cycle and fine structures by using the combination of confocal and Infrared STED microscopy

Kaoru Katoh^{1,2,3}, Totai Mitsuyama^{1,2} (¹ExCELLS, National Institutes of Natural Sciences, ²AIRC, AIST, ³SIGMA, Univ Tsukuba)

Fluorescent cell cycle markers, such as Fucci, enabled easy identification of cell cycles using green and red fluorescence and facilitated biochemical analysis. However, the use of red and green fluorescence of the cell cycle markers restricts wave length of the dyes for labeling proteins and structures in the cell.

In this study, we combined confocal and infrared STED microscopy to establish an experimental system that confirms the cell cycle using visible light and records super resolution images of intracellular fine structures using infrared. We identified cell cycles and observed structures of intracellular organella with super resolution level. Detail of the images and experiments should be discussed in the presentation.

3Pos213 High-speed in-line force mapping - imaging of mechanical properties from microtubules to bacteria

Christian Ganser¹, Shigetaka Nishiguchi², Feng-Yueh Chan³, Takayuki Uchihashi^{1,3} (¹*National Institutes of Natural Sciences, Exploratory Research Center on Life and Living Systems*, ²*National Institute of Advanced Industrial Science and Technology, Department of Life Science and Biotechnology*, ³*Nagoya University, Department of Physics*)

High-speed atomic force microscopy (HS-AFM) has been immensely successful in revealing biological mechanisms from the single-protein scale to the scale of cells. Recently, we have developed a new imaging mode called high-speed inline force mapping (HS-iFM), which combines the measurement of mechanical properties with topography measurements at high spatiotemporal resolutions. In contrast to conventional force mapping, where the force map resolution dictates the topography resolution, HS-iFM allows for setting the resolutions independently by rapidly switching between force and topography measurements. In order to demonstrate the flexibility of HS-iFM, applications of mechanical property measurements of microtubules and *Escherichia coli* bacteria will be presented.

3Pos214 Fabrication of Periodic Inorganic Nanoparticles Using a Fusion Protein of Dps and Nanofiber-Forming Peptide

Mitsuhiro Okuda^{1,2,3}, Gabriela Pretre^{2,3} (¹*Meiji Univ.*, ²*CIC nanoGUNE*, ³*Komie Corp.*)

The cage-shaped protein Dps (DNA-binding protein from starved cells) from *Listeria innocua* can accumulate iron as iron oxide within its internal cavity *in vivo*. This cavity has potential as a template for the synthesis of artificial metal nanoparticles (NPs), with the protein shell regulating their size. In our previous study, we developed a fusion protein composed of Dps and a nanofiber-forming peptide to form ordered Dps crystals. In the present study, we synthesized artificial iron and cobalt oxide nanoparticles within this fusion protein. Crystallization of the fusion protein including these NPs led to the formation of a periodic NPs structure.

3Pos215 淘汰圧制御に向けた溶液交換技術の開発
Development of Solution Exchange Technology for Controlling Selection Pressure

Nanato Takaso¹, Yoshihiro Minagawa¹, Hiroyuki Noji^{1,2} (¹*Graduate School of Engineering, The University of Tokyo*, ²*Research Institute of Planetary Health (RIPH), The University of Tokyo*)

Microchamber arrays, using a cell-free protein expression system, confine and express various DNA sequences in separate chambers, allowing simultaneous observation of many mutants. However, some enzymes are not active under expression conditions and require solution exchange with suitable buffer to observe their activity. Without such exchange, only enzymes active under expression conditions can be evaluated. However, both DNA and enzymes typically flow out by buffer exchange, making it impossible to assess their activity. In this study, enzymes and DNA were immobilized in the chambers to test whether they could remain functional after buffer exchange. Enzymes were fixed via covalent bond between a SNAP-tag and benzylguanine, while DNA was trapped in the same chamber.

3Pos216 キネシン-微小管系を内包したゲル人工筋肉の収縮特性評価
Characterization of contractile behavior of artificial muscle gel incorporating Kinesin-Microtubule networks

Shuichi Ishino (*JAIST*)

In recent years, the development of artificial muscles based on motor proteins has progressed, with reports of millimeter-scale contraction and light-controlled actuation using the kinesin-microtubule system. This study focuses on fibrin gel, which can be easily formed, aiming to develop an artificial muscle gel with stable contractile force and localized light-controlled contraction. This is achieved by embedding kinesin-microtubule filaments into fibrin fibers formed through the fibrinogen-thrombin reaction. Ultimately, we aim to create an artificial muscle gel capable of locally modulating contraction states by leveraging the relaxation properties of kinesin.

3Pos217

油気界面における生体分子からなる膜状構造の形成とその応用

Film-like biomolecular structures at the oil-air interface and their potential application

Daichi Tominaga¹, Shogo Hamada², Yusuke Sato¹ (¹*Grad. Sch. Com., Kyushu. Inst. Tech.*, ²*Grad. Sch. Com., Inst. Sci. Tokyo*)

Techniques for constructing thin films are widely employed in surface modification and sensor/actuator development. Employing biomolecules offers a promising route to highly biocompatible film-like structures. However, conventional methods are often unsuitable for biomolecules due to their fragility.

In this study, we present a novel technique to forming film-like biomolecular structures at the oil-air interface. In this method, Water-in-oil (W/O) droplets containing biomolecules were prepared and dropped onto a glass substrate, resulting in the spontaneous formation of film-like structures at the oil-air interface. We will discuss underlying mechanism of this process, and its potential application.

3Pos218

The Role of Fluid Dynamics in Active Phase-Separating Systems

Charu Datt^{1,3}, Jonathan Bauermann^{2,3}, Nazmi Burak Budanur³, Frank Julicher³ (¹*Department of Mechanical Engineering, Keio University*, ²*Department of Physics, Harvard University*, ³*Max Planck Institute for the Physics of Complex Systems, Dresden*)

The role of hydrodynamic flows in cellular organisation by liquid-liquid phase separation remains relatively unexplored. As living cells are inherently out of thermodynamic equilibrium, phase-separation phenomena inside them occur under non-equilibrium conditions. Using theoretical and numerical calculations, we study phase-separating liquid mixtures that are maintained out of equilibrium through chemical reactions. We find that Marangoni forces and active fluid flows generated by the chemical reactions lead to interesting dynamics and diverse patterns; in general, we explore the interplay of phase-separation physics, active chemical reactions and hydrodynamics, an exploration which we believe is essential for a physical understanding of intracellular organisation.

3Pos219

OptoChaperone – A biohybrid tool for regulating protein condensates in cells and *in vitro*

Thanh Tuan Do, Motonori Matsusaki, Soichiro Kawagoe, Hiroyuki Kumeta, Tomohide Saio (*Division of Molecular Science (Saio's Lab), Institute of Advanced Medical Sciences, Tokushima University, Tokushima, Japan*)

Here, we propose OptoChaperone, a biohybrid tool that enables manipulation of condensation *in vitro* and in cells using light irradiation. Our results validated that the activity of OptoChaperone is switchable: blue light turns on its activity to suppress droplet formation, while UV light turns off the activity, allowing droplet formation. We demonstrated that OptoChaperone efficiently modulates several disease-related protein condensates, including fused in sarcoma, TAR DNA-binding protein 43, and heat shock factor 1. Given the reversibility and efficiency of OptoChaperone in manipulating protein condensates, this tool offers a new approach for understanding both physiological and pathological protein condensates and aggregation.

3Pos220

Attenuation of TDP-43 proteinopathy by graphene quantum dots in amyotrophic lateral sclerosis

Yunseok Heo, Yuxi Lin, Young-Ho Lee (*Korea Basic Science Institute*)

Aberrant phase separation- and stress granules (SGs)-mediated cytosolic aggregation of TDP-43 in motor neurons is the hallmark of amyotrophic lateral sclerosis (ALS). In this study, we found that graphene quantum dots (GQDs) potentially modulate TDP-43 aggregation during the SGs dynamics and phase separation. The intrinsically disordered region in the C-terminal of TDP-43 exhibited amyloid fibril formation; however, the GQDs inhibited the formation of amyloid fibrils through direct intermolecular interactions with TDP-43. These effects were accompanied by attenuating the ALS phenotype in animal models. We expect that the GQDs could offer a new therapeutic approach for proteinopathy-associated ALS.

Name Index (索引)

名字 (Family Name) のアルファベット順にソートしています。すべて、オンラインで入力されたデータのま
ま、表示しています。

Abe, Ikuro (阿部 郁朗)	1Pos169	Akada, Momo (赤田 萌々)	3Pos094
Abe, Keietsu (阿部 敬悦)	1GC001		3Pos097
Abe, Keita (安部 桂太)	1Pos152	Akae, Yui (赤江 唯里)	3Pos008
	3Pos112	Akagi, Ken-Ichi (赤木 謙一)	2Pos045
	3Pos113	Akagi, Ken-ichi (赤木 謙一)	3SEA-2
	3Pos150	Akai, Daiki (赤井 大輝)	2Pos185
Abe, Kimihiro (安部 公博)	1MSF-4	Akai, Hiromu (赤井 大夢)	1EB004
Abe, Masayuki (阿部 真之)	1SEA-5		2Pos118
	1Pos049	Akamatsu, Kanako (赤松 香奈子)	1GB001
Abe, Mitsuhiro (阿部 充宏)	2Pos099	Akatsu, Munetaka (赤津 綜隆)	3Pos057
Abe, Nao (阿部 なお)	1Pos168	Akazawa, Yoko (赤澤 陽子)	3Pos019
	3Pos173		3Pos020
Abe, Ryoji (安部 稜士)	1GG001	Akeda, Yukihiro (明田 幸宏)	1MSF-4
	1GG003	Akimoto, Seiji (秋本 誠志)	2SGP-3
Abe, Satoshi (安部 聡)	1Pos037		2Pos139
Abe, Youichiro (阿部 陽一郎)	1Pos064	Akisada, Shunsuke (秋定 駿佑)	3Pos006
Abe-Yoshizumi, Rei (吉住 玲)	2SJA-3	Akita, Fusamichi (秋田 総理)	2Pos136
	1Pos131	Akita, Ryo (秋田 嶺)	3SGA-5
	1Pos132	Akiyama, Hidefumi (秋山 英文)	3SBA-9
Abiola, Doyin Rachael	3Pos085	Akiyama, Kazuki (秋山 一樹)	3Pos124
Acharya, Saahil	2SGA-3	Akiyama, Kentaro	1Pos217
Adachi, Kohsuke (足立 亨介)	1Pos188	Akiyama, Kentaro (秋山 健太郎)	1MSG-4
Adachi, Koki (足立 航輝)	2Pos078	Akiyama, Koichiro (秋山 浩一朗)	2Pos156
	2Pos184		3Pos151
Adachi, Kyosuke (足立 景亮)	1SDA-2		3Pos152
Adachi, Makoto (足立 誠)	2SBA-2	Akiyama, Shuji (秋山 修志)	1Pos023
Adachi, Taiji (安達 泰治)	1SEA-6		1Pos024
	2SFA-7		2Pos020
	1GG005		2Pos023
Adachi, Tomoya (安達 友弥)	3Pos015		2Pos026
Afroze, Farhana	1EA004		2Pos184
Afzal, Bilal M.	3SAA-4	Akiyama, Yoshinori (秋山 芳展)	2Pos028
Agarwal, Krishna	3SAA-2		2Pos164
Ageta-Ishihara, Natsumi (上田(石原) 奈津実)	1SDA-3	Akiyama, Yutaka (秋山 泰)	2Pos175
Aguilar, Perez Gerard	2SGA-3	Akizuki, Saiko (秋月 彩子)	3Pos138
Ahluwalia, Balpreet S.	3SAA-4	Aladag, Amine	1Pos098
Ahmad, Azeem	3SAA-4	Aladag, Amine (Aladag Amine)	1SHA-4
Ahsan, Ali (Ahsan Ali)	2Pos090	Alastair, Stewart (Alastair Stewart)	1GE009
	3Pos079	Aldeguer-Riquelme, Borja (Aldeguer-Riquelme Borja)	
Aiko, Michio (相子 美智雄)	3Pos035		1Pos128
Aizawa, Tomoyasu (相沢 智康)	1MSG-1	Algiffari, Muhammad	1GJ002
	1GA011	Ali, Samson	2Pos147
	1GG009	Altieri, Fabiano	1GF003
	1Pos021	Amaike, Kazuma	3Pos180

Amakawa, Kahoru (天川 薫)	2Pos168	Arikawa, Keisuke (有川 敬輔)	1Pos033
Amalla, Bon Leif Dominguez	1GF009	Arimura, Yuta (有村 悠太)	2Pos070
Amari, Toshiki (甘利 俊樹)	1SDA-4	Arita, Kazuki (有田 和生)	1Pos185
Amii, Hideki (網井 秀樹)	1Pos108	Ariyoshi, Shiori (有吉 志千里)	1Pos022
Amyot, Romain	1Pos161	Artem, Lysenko	3SGA-5
Andini, Nadya	3Pos122	Asada, Hidetsugu (浅田 秀基)	2SBA-2
Ando, Maiha (安藤 舞羽)	1Pos100	Asahi, Kikuko (旭 紀久子)	2Pos028
	1Pos103	Asakura, Mami (朝倉 真実)	3Pos110
	3SBA-4	Asakura, Mami (朝倉 真美)	2Pos146
Ando, Tomohiro (安東 智大)	1Pos076		3Pos138
Ando, Toshio (安藤 敏夫)	1Pos080		3Pos139
Ando, Yusuke (安藤 優介)	1Pos128	Asano, Chihori (浅野 千帆莉)	2SFA-2
Antón, Josefa (Antón Josefa)	1Pos128		3Pos083
Aoki, Kana (青木 佳南)	2SFA-6	Asano, Yuka (浅野 友香)	2Pos088
Aoki, Kazuhiro (青木 一洋)	3SHA-5	Asanuma, Daisuke (浅沼 大祐)	1GG011
	1Pos088	Asaoka, Sotaro (浅岡 草太朗)	3Pos114
	1Pos194	Ashida, Orika (芦田 織歌)	1Pos025
Aoki, Rinka (青木 凜夏)	3Pos113		2Pos015
Aoki, Toma (青木 斗真)	1GH003	Atomi, Yoriko (跡見 順子)	2SCP-3
Aoki, Wataru (青木 航)	2SHA-1		3Pos089
Aono, Rintaro (青野 麟太郎)	3Pos061	Auer, Florian (Auer Florian)	1MSG-5
Aoyama, Mako (青山 真子)	3Pos141	Awakawa, Takayoshi (淡川 孝義)	2SCA-3
Aoyama, Risako (青山 理紗子)	1Pos023		1GH006
Aoyama, Tomohiro (青山 知裕)	1Pos029		1Pos169
Arai, Makiko (荒井 万喜子)	2SFA-4	Awazu, Toshikuni (粟津 敏邦)	1MSF-3
Arai, Munchito (新井 宗仁)	2SCA-6	Azai, Chihiro (浅井 智広)	2SGP-2
	1GC009		2Pos134
	1GC010		3Pos133
	2Pos017	Baba, Akiko (馬場 晶子)	1GG001
	3Pos033	Baba, Kotaro (馬場 康太朗)	3Pos111
Arai, Satoshi	1Pos208	Bademosi, Adekunle T.	3Pos117
	1Pos209	Baden, Naoki (馬殿 直樹)	2Pos211
	2Pos035	Bae, Jiwan (ベ ジワン)	2SKP-2
	3Pos036	Balsalobred, Carlos (Balsalobred Carlos)	2Pos005
Arai, Satoshi (新井 敏)	1EB001		1YK1030
	2Pos209	Bamba, Ryuya (馬場 琉矢)	3Pos155
Arai, Sora (新井 想空)	1GI001	Bamrung, Phonphiphat	1Pos106
Arai, Tatsuya (新井 達也)	1MSG-1	Bando-Uotani, Miki (板東 (魚谷) 未季)	1Pos139
	1GA011	Bang, Kyuhyeon	2SKA-1
	1GG009	Barquera, Blanca (Barquera Blanca)	1Pos116
	1Pos021	Basnayake, B.M.K.D	2Pos035
Araki, Hiyori (荒木 陽好)	2Pos018	Basnayake, B.M.K.D.	1Pos209
Araki, Mitsugu (荒木 望嗣)	2SFP-1	Bassereau, Patricia	2Pos114
Araki, Yuka (荒木 優香)	1GB011	Bauermann, Jonathan	3Pos218
Aramoto, Chihiro (荒本 智大)	2Pos027	Bayliss, Richard (ベイリス リチャード)	2Pos098
Arata, Toshiaki (荒田 敏昭)	3Pos055	Beckstein, Oliver	1EE002
Arayama, Miyu (荒山 みゆ)	1GB002	Beis, Konstantinos (Beis Konstantinos)	2Pos005
Archer, Richard James	1EA004		1YK1030
Archer, Richard James (アーチャー ジェームズリ チャード)	3Pos150	Beppu, Kazusa (別府 航早)	2SEP-6
Arie, Misaki (有江 弥咲)	3Pos087	Bertocchi, Cristina	2SIP-3
Ariga, Takayuki (有賀 隆行)	1GE012	Bessho, Ken (別所 賢)	2Pos112
	2Pos074		2Pos113

Bessho, Yoshiki (別所 芳樹)	2Pos170	1GB007	
Bhatt, Sunil	3SAA-2	Chauyjaroenusuk, Anupap (Chauyjaroenusuk Anupap)	2Pos040
Bhattacharjee, Biplab	2Pos094	Che, Yong-Suk (蔡 榮淑)	2Pos084
Bhattacharjee, Biplab (Bhattacharjee Biplab)	2SEP-7		3Pos092
Bielecki, Michael (Bielecki Michael)	1MSG-5	Chen, Chen (陳 辰)	1Pos147
Binti Salwadi, Nur Fatin Liyana	1Pos078	Chen, Hsuan-Yi (陳 宣毅)	1Pos085
	2Pos072	Chen, Jiali (陳 佳麗)	1GF011
Blazquez Fernandez, Samuel	3Pos047	Chen, Szu-Yu (陳 思妤)	3Pos049
Bo, Stefano	3Pos072	Chen, Yan-Ru (陳 彥茹)	1Pos191
Boroevich, Keith	3SGA-5	Chen, Yiran (陳 伊然)	2Pos052
Borowiak, Alexis	1Pos095	Chen, Yu-Chia (Chen Yu-Chia)	1Pos094
Boyer, David (Boyer David)	2Pos010		1YK1100
Brachet, Anna	1SHA-3	Chen, Zibo	1MSI-3
Brandani, Giovanni (ブランドーニ ジョバンニ)		Cheng, Tat Cheung (鄭 達翔)	1MSG-5
	1MSG-6	Chi, Dam Hieu (ダム ヒョウ チ)	2Pos065
Brandani, Giovanni Bruno	2SAA-2	Chi, Peter (冀 宏源)	2SBP-2
Brenner, Niklas Urs	2Pos198	Chiba, Genta (千葉 元太)	1GG004
Budanur, Nazmi Burak	3Pos218	Chiba, Kaori (千葉 かおり)	1MSH-5
Burton-Smith, Ray	2Pos208		1GA002
Burton-Smith, Raymond (Burton-Smith Raymond)			3HL1115
	3Pos073		3HL1130
Burton-Smith, Raymond N. (Burton-Smith Raymond N.)			2Pos014
	1Pos010		3Pos015
Bustamante, Carlos (Bustamante Carlos)	2Pos010		3Pos016
Butola, Ankit	3SAA-2		3Pos017
Byrne, Eamon F. X.	3Pos122	Chiba, Samui (千葉 祥生)	3Pos118
Béjà, Oded	1GI002	Chiba, Shuntaro (千葉 峻太朗)	2SFP-6
Béjà, Oded (Béjà Oded)	2SJA-3	Chien, Yi-Sian (Chien Yi-Sian)	1SCA-5
	1Pos125	Chikenji, George (千見寺 浄慈)	3Pos145
	1Pos128	Chimura, Takahiko	1EA003
C. Sasaki, Yuji (佐々木 裕次)	3Pos058	Choi, Gary P.T.	1Pos201
Camilli, Pietro De (ピエトロ デカミリ)	1EC001		1YK1000
Canela, Andres (Canela Andres)	1SIA-2		1GF004
Caramello, Nicolas	2Pos133	Chow, Siu Yu Angela	1MSG-1
	1YK1115	Chrisnanto, Jeremia Oktavian	3SJA-6
Carver, John A. (Carver John A.)	1GB006	Chuma, Shunsuke (中馬 俊祐)	2Pos210
Cattarius, Savannah	1MSF-2	Clement, Jean-Emmanuel	2Pos005
Chadou, Kaito (茶堂 快渡)	1GA006	Clements, Abigail (Clements Abigail)	1YK1030
Chan, Feng-Yueh	3Pos213		2Pos035
Chan, Justin (ジャスティン チャン スオン)	1MSJ-4	Cong, Quang Vu	3Pos154
Chang, Chia-en	2SHP-4	Cooney, Aileen (Cooney Aileen)	3Pos180
Chang, Huan-Cheng (張 煥正)	2SJP-3	Cree, Ben	
Chang, Yuan-Pin	1Pos197	Cuong, Nguyen Viet (グエン ヴィエット クーン)	
Chanhyuk, Min	2SKA-5		2Pos065
Chao-Cheng, Cho	1Pos004	D'Ascenzi, Jacopo (D'Ascenzi Jacopo)	2SJA-3
Chardès, Claire (Chardès Claire)	1Pos086	Daeho, Park	2SKA-5
Chatake, Toshiyuki (茶竹 俊行)	1MSH-4	Dai, Liqiang (戴 立強)	1EE005
	1MSH-6	Daitoku, Hiroaki (大徳 浩照)	1GA003
	1GA002	Dalmo, Roy A.	3SAA-4
	3HL1115	Das, Bratati	1ED002
Chatani, Eri (茶谷 絵理)	1SCA-5	Das, Rakesh	1EA004
	1GB006	Date, Koki (伊達 弘貴)	2Pos162

Datt, Charu	3Pos218	Erban, Radek	1Pos190
David, A. Simpson	2SJP-4	Essen, Lars-Oliver	2Pos133
Debbarma, Naithok Khachuk	1Pos011		1YK1115
Deguchi, Shigeru (出口 茂)	2Pos219	Etchuya, Kenji (越中谷 賢治)	3Pos156
Deguchi, Shinji (出口 真次)	2SIP-7		3Pos164
	2Pos081	Evangelista, Nathan	1EA003
	2Pos091	Faessler, Reinhard	1SHA-2
	2Pos195	Fainsod, Shai	1G1002
	3Pos076	Fan, Hsiufang (范 秀芳)	1EA002
	3Pos088	Fan, Linlin Z.	3Pos122
Deguchi, Takahiro (出口 隆宏)	1MSF-2	Fan, Shujie	1EE002
Deisseroth, Karl	3Pos122	Fangjia, Luo (Fangjia Luo)	2SJA-3
Destiarani, Wanda	2Pos179	Fedosov, Dmitry (Dmitry Fedosov)	1GH009
Dilini Nisansala, Hettimudalige	1Pos209	Feig, Michael (フアイグ マイケル)	3Pos165
Diogo, Figueiredo (ディオゴ フィグイレド)	3Pos202	Flechsig, Holger	1Pos161
Do, Thanh Tuan	3Pos219	Flechsig, Holger (Holger Flechsig)	1Pos039
Dohmae, Naoshi (堂前 直)	1Pos138	Fong, Meng-lao (Fong Meng-lao)	1Pos127
	1Pos141	Frankel, Gad (Frankel Gad)	2Pos005
Dohmen, Rosalie (Dohmen Rosalie)	1G1003		1YK1030
Doi, Atsushi (土井 淳)	1Pos120	Frick, Tobias (Frick Tobias)	1GJ011
Doi, Hideki (土井 英樹)	1Pos120	Fuchigami, Rina (渕上 里奈)	3Pos051
Dontschuk, Nikolai	2SJP-1	Fuchigami, Sotaro (渕上 壮太郎)	1SAA-3
Doura, Tomohiro (堂浦 智裕)	2SBA-3	Fuji, Gyoja (行者 落)	2Pos129
Drescher, Knut	1Pos201	Fujie, Takuya (藤江 拓哉)	2Pos175
	1YK1000	Fujii, Ikuo (藤井 郁雄)	2Pos038
Drescher, Knut (Drescher Knut)	2SGA-4	Fujii, Kengo (藤井 研吾)	2Pos131
Drinnenberg, Antonia	3Pos122	Fujii, Masako (藤井 真子)	3Pos102
Dror, Ron O.	3Pos122	Fujii, Ritsuko (藤井 律子)	2SGP-5
Dudon, Théo	1SHA-3		2SGP-6
Dunkel, Jörn	1Pos201	Fujikawa, Kohki (藤川 紘樹)	1Pos117
	1YK1000	Fujikawa, Ryosuke (藤川 良祐)	1GG006
Dunkel, Jörn (Dunkel Jörn)	2SGA-4	Fujimaki, Shun (藤卷 竣)	3Pos183
E, Chao (鄂 超)	1EE005	Fujimori, Toshihiko (藤森 俊彦)	1Pos066
Ebata, Hiroyuki	1Pos206	Fujimoto, Kazuhiro (藤本 和宏)	1SGA-5
Egelman, Edward (Egelman Edward)	2Pos005	Fujimoto, Kazuhiro J.	3Pos180
	1YK1030	Fujimoto, Mari (藤本 麻里)	1Pos180
Eguchi, Taiyo (江口 太陽)	1Pos188	Fujimoto, Nobutomo (藤本 信智)	3Pos075
	2Pos207	Fujimoto, Ryutaro (藤本 竜太郎)	2SDA-4
Eisenberg, David (Eisenberg David)	2Pos010	Fujinami, Daisuke (藤浪 大輔)	1SJA-4
Ejiri, Tomo (江尻 智森)	3Pos043	Fujino, Maho (藤野 真帆)	1Pos156
Ekimoto, Toru (浴本 亨)	2Pos162	Fujisaki, Hiroshi (藤崎 弘士)	1SBA-4
	2Pos164	Fujisawa, Tomotsumi (藤澤 知績)	1G1003
Elani, Yuval (Elani Yuval)	3Pos154		2Pos128
Elverston, Louis	1Pos207		2Pos130
Emoto, Hikaru (江本 光)	1Pos195		2Pos201
Endo, Kazuha (遠藤 多葉)	1Pos048		3Pos123
Endo, Motomu (遠藤 求)	3SJA-1	Fujise, Kenshiro (藤瀬 賢志郎)	1EC001
Endo, Nobuyuki (遠藤 伸幸)	1GA003	Fujishima, Kosuke	1GC006
Endo, Shuji (遠藤 修仁)	1Pos166	Fujishima, Kosuke (藤島 皓介)	3SFA-6
Engelhardt, Tobias	1MSF-2		1GG001
Engilberge, Sylvain	2Pos133		1GG003
	1YK1115	Fujishiro, Shin (藤城 新)	1MSJ-7

Fujita, Chinatsu (藤田 千夏)	2Pos104	Fukuda, Masahiro	3Pos122
Fujita, Eri (藤田 恵理)	3Pos089	Fukuda, Masahiro (福田 昌弘)	1GI004
Fujita, Hideaki (藤田 英明)	1Pos216		1GI005
Fujita, Keisuke (藤田 恵介)	1GJ006		2Pos006
	3Pos208		3Pos121
Fujita, Kento (藤田 健人)	1GH011	Fukuda, Shingo (福田 真悟)	1Pos076
	3Pos179	Fukuda, Sotaro (福田 颯太郎)	2Pos102
Fujita, Nozomi (藤田 希実)	1Pos189	Fukuma, Takeshi	1Pos095
Fujita, Suguru (藤田 卓)	2SCA-1	Fukuma, Takeshi (福岡 剛士)	2SHP-7
	1Pos009		1Pos199
	2Pos165	Fukumoto, Akihisa (福本 晃久)	1GD009
Fujita, Yuichi (藤田 祐一)	2SGP-1	Fukunaga, Hiroki (福永 裕樹)	2Pos200
Fujita, Yuya (藤田 雄也)	1Pos006	Fukunishi, Yoshifumi (福西 快文)	1Pos180
Fujitsuka, Kenji (藤塚 健次)	1GB006		2Pos181
Fujiwara, Daisuke (藤原 大佑)	2Pos038	Fukuoka, Hajime (福岡 創)	1GJ008
Fujiwara, Ikuko (藤原 郁子)	1Pos068		2Pos076
	1Pos091		2Pos084
	1Pos092		2Pos100
	1Pos093		2Pos103
	2Pos090		3Pos092
Fujiwara, Kazuo (藤原 和夫)	3Pos024	Fukushima, Shun-ichi (福島 俊一)	1GG012
Fujiwara, Kei (藤原 慶)	2SKP-3	Fukute, Jumpei (福手 淳平)	1SEA-6
	2Pos155	Funahashi, Toshiya (船橋 俊也)	3SBA-4
Fujiwara, Koki (藤原 弘貴)	1GG006	Funatsu, Takashi (船津 高志)	1EB005
Fujiwara, Mai (藤原 麻衣)	2Pos181		3Pos203
Fujiwara, Satoru (藤原 悟)	1MSH-4	Furihata, Hirotake (降旗 大岳)	1Pos049
Fujiwara, Shin-ichi (藤原 伸一)	2Pos173	Furuike, Yoshihiko (古池 美彦)	3SAA-5
Fujiwara, Takaaki (藤原 孝彰)	1Pos001		1Pos024
	1Pos011		2Pos020
	2SGA-3		2Pos023
Fujiwara, Takahiro	1Pos096		2Pos026
Fujiwara, Takahiro (藤原 敬宏)	1Pos098	Furukawa, Sachika (古川 幸佳)	1GA010
Fujiwara, Takahiro K	1EC003	Furuki, Tomohiro (古木 智大)	2Pos153
Fujiwara, Takahiro K (藤原 敬宏)	1SHA-4	Furumoto, Hiroko (古元 礼子)	1GE012
Fujiwara, Takahiro K. (藤原 敬宏)	1GF002	Furusawa, Chikara (古澤 力)	2SHA-4
	1Pos089		2Pos194
	1Pos113		3Pos146
Fujiwara, Yuichiro (藤原 祐一郎)	1Pos123		3Pos190
	2Pos129		3Pos192
Fujiyabu, Chihiro (藤藪 千尋)	2Pos131	Furusawa, Takumi (古澤 拓実)	3Pos150
	2SGA-6	Furuta, Akane (古田 茜)	3Pos074
Fujiyoshi, Satoru (藤芳 暁)	2SBA-4	Furuta, Ken'ya (古田 健也)	3Pos074
Fujiyoshi, Yoshinori (藤吉 好則)	1Pos002	Furutani, Yuji (古谷 祐詞)	2SJA-3
	3Pos055		1GG007
Fujiwara, Toshimichi (藤原 敏道)	1Pos060		1GI004
Fukagawa, Tatsuo (深川 竜郎)	2SAP-2		1GI006
Fukai, Yohsuke T	2SFA-4		1GI010
Fukamachi, Shuya (深町 崇耶)	1GA003		1Pos046
Fukamizu, Akiyoshi (深水 昭吉)	1Pos149		1Pos145
Fukatsu, Takema (深津 武馬)	1Pos074		2Pos142
Fukuda, Akihiro (福田 朗大)	2SJA-5		2Pos145
Fukuda, Ayaka (福田 彩華)	1Pos046		3Pos122
Fukuda, Hiroto (福田 大士)			

Furutani, Yuji (古谷 裕司)	3Pos140	Hamaguchi, Tasuku (濱口 祐)	3Pos066
Furuya, Moeno (古谷 萌乃)	3Pos094	Hamaoka, Kazuko (浜岡 加寿子)	1Pos083
Fusamae, Sawa (房前 佐和)	1Pos017	Hanabusa, Katsuaki (英 克明)	3Pos024
Futamata, Hiroyuki (二又 裕之)	2Pos196	Hanano, Ai (花野 愛)	2Pos031
	3Pos103	Hara, Masahiko (原 正彦)	1Pos056
Fuzisawa, Miina (藤沢 みいな)	1Pos120	Harada, Atsuki (原田 淳生)	1Pos205
Fässler, Reinhard	1EC003	Harada, Kosei (原田 康生)	1GG008
Galindo, Luis Javier (Galindo Luis Javier)	1Pos125	Harada, Ryuhei (原田 隆平)	1GH003
Ganser, Christian	3Pos213		1Pos020
Gentaro, Yokoyama (横山 源太郎)	3Pos034		1Pos172
Gerle, Christoph (ゲーレ クリストフ)	3Pos070		1Pos184
Giannone, Gregory	1SHA-3		2Pos179
Gibo, Shingo (儀保 伸吾)	3SJA-5	Harada, Yoshie (原田 慶恵)	1SCA-3
Gingeleit, Lukas (Gingeleit Lukas)	1MSG-5		3SJA-6
Ginter, Taren (ギンター テーレン)	1GG001		1GG006
	1GG003		2Pos068
	2Pos210		3Pos200
Goda, Keisuke	3SGA-2		3Pos208
Goda, Keisuke (合田 圭介)	3Pos014	Harada, Yoshihisa (原田 慈久)	1GD012
Goda, Natsuko (合田 名都子)	2Pos095	Haraguchi, Takeshi (原口 武士)	1Pos151
Gomibuchi, Yuki (五味渕 由貴)	2Pos105	Harashima, Takanori (原島 崇徳)	2SEP-3
Gondhalekar, Riddhi Prashant	1GC006		1Pos073
Gong, Ya-Chen (龔 亞晨)	2SBP-2	Harata, Masahiko (原田 昌彦)	2Pos213
Gono, Asahi (郷野 朝日)	3Pos107	Haruna, Ryusei (春名 竜征)	2Pos049
Goto, Yuhei (後藤 祐平)	3SHA-5	Hasan, Md Al Mehedi	2Pos210
Goto, Yuji (後藤 祐児)	2Pos042	Hasegawa, Aiko (長谷川 藍子)	3Pos012
Goto, Yuna (後藤 優菜)	3Pos040	Hasegawa, Kodai (長谷川 航大)	3Pos028
	3Pos048	Hasegawa, Yoshito (長谷川 義人)	2Pos183
	1SIA-2	Hashiguchi, Takao (橋口 隆生)	2Pos031
Grenci, Gianluca (Grenci Gianluca)	1GA008	Hashimoto, Satoshi (橋本 聡)	2Pos013
Gu, Yuzhong (顾 羽中)	2Pos014	Hastewell, Alasdair (Hastewell Alasdair)	2SGA-4
Gunji, Erika (軍司 絵里佳)	1Pos038	Hasunuma, Tomohisa (蓮沼 誠久)	1MSG-7
Guyot, Constantin (Guyot Constantin)	2SKA-5	Hata, Soichiro	2Pos210
Gwangrog, Lee	1GA007	Hatakeyama, Jumpei	3SBA-1
Ha, Trong Thang	1SEA-4	Hatakeyama, Tetsuhiro S. (畠山 哲央)	3SFA-4
Hada, Masashi (羽田 政司)	2Pos001	Hatanaka, Ryo (畑中 涼)	1GA001
Haga, Kei (芳賀 慧)	1Pos111	Hatazawa, Suguru (畠澤 卓)	2SAP-3
Haga, Kenya (芳賀 健也)	2Pos044	Hatori, Kuniyuki (羽鳥 晋由)	1Pos213
Haga, Takehiko (芳賀 剛彦)	3Pos180	Hatsuda, Tetsuo (初田 哲男)	3SJA-5
Hagai, Masaya	1Pos154	Hattori, Mitsuru (服部 満)	1GJ005
Hagino, Katsumi (萩野 勝己)	3Pos156		2Pos038
Haida, Riki (灰田 吏毅)	2Pos138		2Pos212
Hall, Malgorzata (Hall Malgorzata)	2Pos128		3Pos202
Hamada, Masako (濱田 雅子)	2Pos163	Hattori, Motoyuki (服部 素之)	1Pos114
Hamada, Michiaki (浜田 道昭)	3Pos034	Hattori, Nanako (服部 七奈子)	2Pos142
	3HL1100	Hayakawa, Masayuki (早川 雅之)	2SEP-7
Hamada, Riku (濱田 理公)	1EA004	Hayashi, Fumio (林 史夫)	1Pos133
Hamada, Shogo	3Pos217	Hayashi, Fumio (林 文夫)	3SIA-7
Hamada, Shogo (浜田 省吾)	3HL1015		1Pos112
Hamada, Shota (濱田 勝太)	2Pos220	Hayashi, Gosuke (林 剛介)	2SHA-3
Hamada, Tsutomu (濱田 勉)	2SGA-1	Hayashi, Kumiko (林 久美子)	2SIP-1
Hamada, Yuta (濱田 悠太)	2Pos156		1GD012
Hamaguchi, Sota (濱口 蒼太)			

Hayashi, Manami	1GE012	Hijikata, Reiji (土方 礼嗣)	2Pos019
Hayashi, Masahito (林 真人)	3Pos180	Hikiri, Simon (肥喜里 志門)	1Pos168
	2Pos090		1Pos171
	2Pos152		1Pos173
	2Pos156		1Pos174
	2Pos157		1Pos175
	2Pos158		1Pos182
	3Pos151		3Pos173
	3Pos152	Himeoka, Yusuke (姫岡 優介)	2SKP-7
Hayashi, Seichiro (林 成一郎)	1SJA-4		2Pos192
	2Pos016		1YK0915
Hayashi, Shigehiko (林 重彦)	3SBA-4		2Pos194
	1GH010		3Pos190
	3Pos043		3Pos192
	3Pos050	Hinoguchi, Akiko (樋之口 耀子)	1Pos203
	3Pos172		1Pos204
Hayashi, Taiyo (林 泰瑠)	1GC003	Hinuma, Shuji (日沼 司)	1GF001
Hayashi, Tomohiko (林 智彦)	1Pos063	Hirai, Fumi (平井 美実)	1MSG-1
Hayashi, Toshifumi (林 俊文)	3Pos037	Hiraiwa, Eri (平岩 恵理)	2Pos197
Hayashi, Yohei (林 洋平)	3Pos062	Hiraiwa, Tetsuya	1EA004
Hayashida, Yukihisa (林田 幸久)	2Pos105	Hiraizumi, Masahiro (平泉 将浩)	1MSF-3
Hazama, Takayoshi (畚 隆喜)	3HL0930	Hiraka, Kentaro (平賀 健太郎)	2Pos001
Heb, Shan (Heb Shan)	2Pos005	Hirano, Atsushi (平野 篤)	2Pos153
	1YK1030	Hirano, Ken (平野 研)	1Pos157
Heidebrecht, Christopher	1MSF-2	Hirano, Minako (平野 美奈子)	1Pos138
Hemmi, Fumika (逸見 文香)	2Pos218		1Pos141
Hengphasatporn, Kowit	2Pos179		2Pos146
Heo, Yunseok	1Pos005		3Pos110
Heo, Yunseok (許 允碩)	3Pos220		3Pos138
Hess, Henry	2Pos093		3Pos139
Hibi, Reika (日比 怜華)	2Pos152	Hirano, Taichi (平野 太一)	2Pos118
Hibino, Emi (日比野 絵美)	2Pos019	Hirano, Takashi	3SBA-1
	3Pos014	Hirano, Yasuhiro (平野 泰弘)	1Pos060
Hibino, Kayo (日比野 佳代)	1MSJ-1	Hirano, Yu (平野 優)	1MSH-6
Hibino, Masahiro (日比野 政裕)	3Pos132	Hirasawa, Rin (平澤 理音)	1SBA-1
Hidaka, Naoki (日高 直樹)	2Pos084	Hirata, Hiroaki (平田 宏聡)	1Pos216
	3Pos093		3Pos075
Hidaka, Naoki (日高 直樹)	2Pos157	Hirata, Syuzo (平田 修造)	1EB001
Hidaka, Takuya (日高 拓也)	1EB003	Hirata, Yusaku (平田 悠朔)	2Pos017
Hidaka, Yuji (日高 雄二)	1Pos025	Hiratani, Ichiro (平谷 伊智朗)	1MSJ-2
	2Pos015	Hiratsuka, Yuich (平塚 祐一)	3Pos067
Hidayati, Lisna (ヒダヤティ リスナ)	1Pos088	Hiratsuka, Yuichi (平塚 祐一)	3Pos071
Higashi, Koichi (東 光一)	2SAP-5	Hiroaki, Hidekazu	2SKA-4
	2Pos062	Hiroaki, Hidekazu (廣明 秀一)	2Pos019
	1YK0945		3Pos014
Higashi, Sayuri (東 小百合)	2SDA-4	Hirohata, Taiki (廣畠 大輝)	1GC012
Higashihara, Taisei (東原 太成)	3Pos104	Hirokane, Sora (廣兼 空)	1GG010
Higo, Junichi (肥後 順一)	1Pos173	Hirono, Moritoshi (廣野 守俊)	3Pos119
	1Pos182	Hirooka, Naoya (広岡 尚也)	2Pos168
Higuchi, Kosei (樋口 皓聖)	2Pos146	Hirosawa, Koichiro (廣澤 幸一朗)	2SDA-4
Hijikata, Atsushi (土方 敦司)	3Pos131	Hirosawa, Koichiro M (廣澤 幸一朗)	1EC003
Hijikata, Hiroko	1Pos098	Hirosawa, Koichiro M. (廣澤 幸一朗)	1GF002

Hirose, Kenzo (廣瀬 謙造)	1GG011	Horiguchi, Shuhei A. (堀口 修平)	2Pos192
Hirose, Kouta (廣瀬 功汰)	2Pos140		1YK0915
Hirose, Mika (廣瀬 未果)	1GA003	Horii, Takuto (堀井 拓登)	2SFA-2
	2Pos004	Horikawa, Akio (堀川 皓央)	3Pos009
	2Pos071	Horinouchi, Shinya (堀ノ内 慎哉)	3Pos089
	3Pos003	Horitani, Masaki (堀谷 正樹)	3Pos023
Hirose, Yuu (広瀬 侑)	1Pos006	Horiuchi, Atsushi	2SJA-4
	2Pos128	Horiuchi, Kota (堀内 滉太)	2Pos023
	1Pos060		2Pos026
Hirota, Toru (広田 亨)	1SGA-2	Horiyama, Takashi (堀山 貴史)	2Pos007
Hirota, Tsuyoshi (廣田 毅)	1Pos018	Horonushi, Dan (褓主 暖)	1Pos100
Hiruma, Takahisa (比留間 貴久)	2Pos030		1Pos102
	2Pos212		1Pos103
Hiruta, Yuki (蛭田 勇樹)	1MSG-4	Hoshida, Masayuki (星田 政行)	1Pos068
Hisabori, Toru (久堀 徹)	2SFP-4	Hoshina, Hiromichi (保科 宏道)	1Pos144
Hisada, Toshiaki (久田 俊明)	3SJA-1		2Pos058
Hisamoto, Yoko (久本 洋子)	1SEA-5	Hoshino, Masaru (星野 大)	3HL1130
Hisatomi, Osamu (久富 修)	3Pos181		2Pos014
Hisham, Dokainish	3Pos192		3Pos015
Hishida, Atsuki (菱田 温規)	1GA010		3Pos016
Hishida, Mafumi (菱田 真史)	3SBA-2		3Pos017
Hiyama, Miyabi (樋山 みやび)	3SBA-9	Hosoda, Hiroshi (細田 洋司)	3Pos119
	2Pos028	Hosoda, Kazufumi (細田 一史)	2Pos122
Hizukuri, Yohei (檜作 洋平)	2Pos164	Hosoi, Haruko (細井 晴子)	2Pos021
	2SAP-1	Hosokawa, Chie (細川 千絵)	1SCA-7
Hizume, Kohji (日詰 光治)	1GI003		3SIA-6
Hoff, Wouter D. (Hoff Wouter D.)	2SGA-3		1Pos112
Hoffmann, Christian	1EC003	Hosokawa, Yuhei (細川 雄平)	1Pos007
	3Pos055		1Pos127
Hojo, Hironobu (北條 裕信)	2SDP-1		2Pos133
Hojo, Nozomi (北條 望)	2Pos067		1YK1115
Holger, Flechsig (Holger Flechsig)	1Pos183	Hososhima, Shoko (細島 頌子)	1SGA-6
Homma, Masato (本間 大翔)	1Pos045		2SJA-3
Homma, Michio (本間 道夫)	2Pos071		1Pos142
	2SAA-5		1Pos146
Homma, Sakura (本間 さくら)	2Pos007		2Pos141
	3Pos161		3Pos142
	3Pos101	Hotta, Akitsu (堀田 秋津)	1SFA-5
Homma, Yuki (本間 優葵)	2Pos075	Hou, Yuge	1GF004
Homma, Michio (本間 道夫)	1Pos099	Hsieh, Chia-Lung (謝 佳龍)	2SJP-5
Honda, Gen (本田 玄)	1Pos068	Hsu, Wei-li	1GA007
Honda, Hajime (本多 元)	1Pos091	Huguenard, John R.	3Pos122
	1Pos093	Hukuda, Akiya (福田 諒哉)	3Pos138
	3Pos191		3Pos139
Honda, Naoki (本田 直樹)	3Pos096	Hukuda, Makoto (福田 誠)	2Pos180
Honda, Yuna (本田 裕奈)	3HL1100	Humbel, Bruno M. (Humbel Bruno M.)	2Pos138
Hondou, Kazuki (本道 主樹)	2SHP-6	Husna, Syamil MA	1GB005
Honjo, Emi (本城 恵美)	3Pos082	Huynh, Allen	1GA007
Horade, Mitsuhiro (洞出 光洋)	3Pos067	Hwang, Kwang Yeon	2SKA-1
Hori, Kensei (堀 兼誠)	2Pos066	Hyeokjin, Cho	2SKA-5
Hori, Sayaka (堀 沙耶香)	2SFA-4	Ibanez, Rosario (Ibanez Rosario)	2Pos091
Horiguchi, Shuhei (堀口 修平)		Ichida, Hikaru (市田 光)	2Pos067

Ichihashi, Norikazu (市橋 伯一)

[2SKP-5](#)

[1GJ001](#)

[1Pos150](#)

[1Pos154](#)

[1Pos158](#)

Ichikawa, Aoi (市川 葵)

[2Pos111](#)

Ichikawa, Masatoshi

[2Pos093](#)

Ichikawa, Masatoshi (市川 正敏)

[3Pos195](#)

Ichikawa, Takehiko (市川 壮彦)

[1Pos199](#)

Ichiki, Takanori (一木 隆範)

[1Pos035](#)

Ichimura, Taro (市村 垂生)

[1GG012](#)

[3Pos211](#)

Ide, Satoru (井手 聖)

[2SAP-5](#)

[2Pos062](#)

[1YK0945](#)

Ide, Toru (井出 徹)

[2Pos146](#)

[3Pos110](#)

[3Pos138](#)

[3Pos139](#)

[2Pos167](#)

Igarashi, Manabu (五十嵐 学)

[1GJ010](#)

Igarashi, Ryuji (五十嵐 龍治)

[1Pos017](#)

Igarashi, Shoma (五十嵐 将真)

[2Pos169](#)

Ihara, Masaru (井原 賢)

[1Pos027](#)

Iida, Kei (飯田 慶)

[1GF012](#)

Iida, Ririka (飯田 莉梨香)

[1Pos017](#)

Iida, Ryuki (飯田 龍暉)

[2Pos215](#)

Iijima, Kohci (飯嶋 航平)

[2Pos024](#)

Iijima, Mikuru (飯島 美来)

[2Pos039](#)

Iijima, Yoshie (飯島 良江)

[2SEP-3](#)

Iino, Ryota (飯野 亮太)

[1Pos010](#)

[1Pos073](#)

[1Pos076](#)

[1Pos153](#)

[3Pos073](#)

Iino, Yuichi (飯野 雄一)

[2SDP-2](#)

Iinuma, Kaito (飯沼 快友)

[3HL0915](#)

Iizuka, Ryo (飯塚 怜)

[3SGA-5](#)

[1GC013](#)

[2Pos218](#)

Ijuin, Ayako (伊集院 綾子)

[1GC004](#)

Ikeda, Hisako (池田 寿子)

[3Pos122](#)

Ikeda, Kazuho (池田 一穂)

[1Pos079](#)

Ikeda, Keisuke (池田 恵介)

[2SIA-1](#)

[2Pos110](#)

Ikeda, Masato (池田 将)

[2SDA-4](#)

Ikeda, Takuma (池田 拓真)

[3Pos186](#)

Ikeda, Yoshihisa (池田 善久)

[1GC012](#)

Ikegami, Akiko (池上 暁子)

[1GA003](#)

Ikeguchi, Masamichi (池口 雅道)

[3Pos024](#)

Ikeguchi, Mitsunori (池口 満徳)

[2SFP-6](#)

[2Pos162](#)

Ikenoue, Tatsuya (池之上 達哉)

[2Pos164](#)

[2SIA-2](#)

[3SEA-2](#)

Ikeuchi, Kazuna (池内 一奈)

[2Pos110](#)

Ikeuchi, Masashi (池内 真志)

[1Pos056](#)

Ikeuchi, Yoshiho

[3SJA-7](#)

[1GF004](#)

Ikeya, Teppei (池谷 鉄兵)

[3Pos008](#)

[3Pos009](#)

[3Pos025](#)

[3Pos037](#)

Iijima, Masumi (飯嶋 益巳)

[2Pos046](#)

Im, Dohyun (林 到炫)

[2SBA-2](#)

Im, Haeri (Im Haeri)

[2Pos041](#)

Imada, Katsumi (今田 勝巳)

[1GF012](#)

[1Pos080](#)

[1Pos118](#)

[2Pos071](#)

[3Pos007](#)

[3Pos077](#)

Imada, Ryota (今田 涼太)

[1Pos041](#)

Imai, Hinano (今井 日奈乃)

[3SBA-7](#)

Imai, Hiroo (今井 啓雄)

[1GI005](#)

Imai, Kazuki (今井 翔月)

[2Pos046](#)

Imai, Masayuki (今井 正幸)

[1GG001](#)

[1ED001](#)

[1Pos111](#)

Imai, Tomoya (今井 友也)

[1Pos109](#)

Imamura, Hiromi (今村 博臣)

[3Pos007](#)

Imamura, Hiroshi (今村 比呂志)

[2Pos148](#)

Imamura, Kayo (今村 香代)

[2Pos045](#)

[3Pos003](#)

Imamura, Saki (今村 咲稀)

[2Pos066](#)

Imaoka, Waren (今岡 和蓮)

[1Pos029](#)

Imasaki, Tsuyoshi (今崎 剛)

[2SHP-7](#)

Imashimizu, Masahiko (今清水 正彦)

[2Pos058](#)

[3Pos059](#)

Imayoshi, Itaru (今吉 格)

[3SHA-1](#)

Imura, Tomoki (居村 知己)

[1Pos007](#)

Inaba, Kenji (稲葉 謙次)

[2SHP-6](#)

Inada, Kazuki (稲田 一輝)

[2Pos139](#)

Inagaki, Kenji (稲垣 賢二)

[1GA004](#)

[1GA006](#)

Inagaki, Naoyuki (稲垣 直之)

[2SIP-5](#)

[1Pos193](#)

Inagaki, Shigenori (稲垣 成矩)

[2SEA-5](#)

Inagaki, Tomomi (稲垣 知美)

[2Pos134](#)

[3Pos133](#)

Inaki, Mikiko (稲木 美紀子)

[3Pos060](#)

Inokuchi, Miyu (井口 未唯)

[3Pos125](#)

Inomata, Kohsuke (猪股 晃介)

[3Pos008](#)

Inomata, Kousuke (猪股 晃介)

[3Pos009](#)

Inomata, Naoki (猪股 直生)	1SDA-1	Ishii, Yoshitaka (石井 佳誉)	3SEA-1
Inomata, Risa (猪股 璃咲)	3Pos051	Ishijima, Akihiko (石島 秋彦)	1GJ008
Inose, Tomoya (猪瀬 智也)	3Pos059		2Pos076
Inoue, Akitoshi (井上 明俊)	1GA009		2Pos084
	2Pos004		2Pos100
Inoue, Asuka (井上 飛鳥)	2Pos096		2Pos103
Inoue, Daisuke (井上 大介)	2SFA-1		3Pos092
	3Pos089	Ishikawa, Daisuke (石川 大輔)	1Pos056
Inoue, Kanta (井上 幹太)	1GA004	Ishikawa, Hiroki (石川 裕規)	1EC003
	1GA006	Ishikawa, Shion (石川 史恩)	1GB005
Inoue, Keiichi (井上 圭一)	1SGA-4	Ishikawa-Fukuda, Moe (石川 萌)	1Pos116
	1GI002	Ishikita, Hiroshi (石北 央)	2SJA-1
	1GI004		1GI004
	1GI007		3Pos122
	1GI009	Ishimori, Koichiro (石森 浩一郎)	1GF009
	1Pos125	Ishimoto, Naito (石本 直偉士)	1Pos005
	1Pos128		2Pos005
	1Pos130		1YK1030
	2Pos126	Ishino, Shuichi (石野 秀一)	3Pos216
	3Pos121	Ishitani, Tohru (石谷 太)	2SFA-6
Inoue, Masao (井上 雅郎)	2Pos164	Ishiwata, Hitoshi (石綿 整)	2SJP-6
Inoue, Masatoshi (井上 昌俊)	3Pos122	Ishiwata, Shin'ichi (石渡 信一)	1Pos216
Inoue, Masayo (井上 雅世)	2Pos122	Ishizaka, Masato (石坂 優人)	1MSG-5
Inoue, Motoki (井上 元基)	3Pos185	Ishizone, Tsuyoshi (石曾根 毅)	2SAA-5
Inoue, Rintaro	1SAA-1	Islam, Md. Din	1GA007
Inoue, Rintaro (井上 倫太郎)	1MSH-6	Iso, Naoki (磯 尚樹)	2Pos220
	1GB007	Iso, Tomomi (磯 僚海)	1GB011
	1GB009	Isobe, Noriyuki (磯部 紀之)	3SFA-3
	1Pos019	Isogai, Yasuhiro (磯貝 泰弘)	3SBA-7
	1GH002		2Pos148
Inoue, Sara (井上 紗良)	1Pos165	Isojima, Hiroshi (磯島 広)	1Pos071
Inoue, Sei (井上 静)	3Pos078	Isono, Yukiko (磯野 裕貴子)	2Pos016
Inoue, Takanari (井上 尊生)	2Pos069	Itami, Kenichiro	3Pos180
Inoue, Yusei (井上 悠聖)	1Pos139	Ito, Ai (伊藤 愛)	2Pos060
Inoue-Kashino, Natsuko (井上 (菓子野) 名津子)	3Pos054	Ito, Akiko (伊藤 明子)	1GG007
	1GI007		1Pos145
Inui, Shinnosuke (乾 慎之介)	1Pos124	Ito, An (伊藤 杏)	1SJA-4
Inukai, Shino (犬飼 紫乃)	3Pos051	Ito, Chizuru (伊藤 千鶴)	1Pos079
	1Pos121	Ito, Keisuke (伊藤 敬佑)	1GC013
Iseki, Mineo (伊関 峰生)	3Pos074	Ito, Kohji (伊藤 光二)	1Pos151
Iseki, Toshihiro (井関 敏啓)	1Pos196	Ito, Shingo (伊東 真吾)	2Pos187
Ishibashi, Kenta (石橋 健太)	1Pos059	Ito, Shinya (伊藤 進也)	2SCP-7
Ishibashi, Tomoki (石橋 朋樹)	2SFA-2	Ito, Shota (伊藤 翔太)	1GH001
Ishida, Hisashi (石田 恒)	2Pos084	Ito, Sohei (伊藤 創平)	1SJA-4
Ishida, Koki (石田 紘基)	2Pos157	Ito, Soshi	1GF004
Ishida, Tsubasa (石田 翼)	2Pos111	Ito, Sosuke (伊藤 創祐)	1ED003
	2Pos018	Ito, Takashi (伊藤 隆)	3SBA-9
Ishihara, Naotada (石原 直忠)	2Pos111	Ito, Takuya (伊藤 卓也)	2Pos011
Ishihara, Naoya (石原 尚弥)	1GD002	Ito, Yudai (伊藤 悠大)	2Pos003
Ishihara, Takaya (石原 孝也)	1GF010	Ito, Yuki (伊藤 祐希)	1Pos167
Ishii, Hiroto (石井 裕人)	1Pos205	Ito, Yuma (伊藤 侑真)	1GI004
			1GI010
Ishii, Kunihiro (石井 邦彦)			

	1Pos145	Ji, Ruigeng (紀 瑞蔭)	2Pos169
	2Pos142	Jia, Tony Z. (ジャー トニーズィ)	1Pos147
	2Pos145	Jiang, Haiyang (Jiang Haiyang)	1Pos211
	3Pos122	Jiang, Hanting (蒋 瀚霆)	1Pos183
	3Pos140	Jinno, Masafumi (神野 雅文)	1GC012
Ito, Yutaka (伊藤 隆)	3Pos008	Jinnouchi, Ryosuke (陣内 亮典)	1SBA-7
	3Pos009	Jo, YoungJu	3Pos122
	3Pos025	Joris, Vasco (Joris Vasco)	1Pos139
	3Pos037	Julicher, Frank	3Pos218
Ito-Miwa, Kumiko (三輪 (伊藤) 久美子)	3SJA-4	Jung, Jaewoon (Jung Jaewoon)	2Pos041
Ito-miwa, Kumiko (伊藤 (三輪) 久美子)	2Pos026	Jung, Jaewoon (鄭 載運)	2SAA-6
Itoh, Ayaka (伊藤 綾香)	3Pos118	Jung, Kwang-Hwan (Jung Kwang-Hwan)	3Pos126
Itoh, Ryuhei (伊藤 龍平)	3Pos195	Kabashima, Yoshiyuki (樺島 祥介)	3Pos145
Itoh, Satoru (伊藤 暁)	2Pos178	Kabayama, Sukehiro (樺山 資大)	2Pos123
Itoh, Satoru G (伊藤 暁)	2Pos176	Kabir, Arif Md. Rashedul	1EA004
Itoh, Thoma (伊藤 冬馬)	1Pos194	Kadowaki, Reo (門脇 伶央)	3Pos166
Itoh, Toshiaki (伊藤 俊樹)	1Pos089	Kage, Azusa (鹿毛 あずさ)	2SEP-5
Itoh, Yuji (伊藤 優志)	1GB005	Kageyama, Sota (影山 颯大)	1Pos163
	1GE002	Kai, Souma (甲斐 壮馬)	1Pos180
	2Pos029	Kaizu, Kazunari (海津 一成)	2SAP-5
	2Pos031		2Pos062
Itoi, Tatsuya (糸井 達哉)	1Pos110		1YK0945
Itoke, Satomi (糸木 智美)	3Pos093	Kakizaki, Jiro (柿崎 二郎)	1Pos150
Iwadate, Yoshiaki (岩楯 好昭)	1GD003	Kakizawa, Shigeyuki (柿澤 茂行)	1Pos149
	1GD007		3Pos146
Iwai, Kazuhiro (岩井 一宏)	3Pos003		3Pos148
Iwaki, Mitsuhiro (岩城 光宏)	1GE012	Kakizuka, Taishi (垣塚 太志)	1GG012
	1EC002		3Pos211
	2Pos200	Kako, Koichiro (加香 孝一郎)	1GA003
Iwakiri, Mikage (岩切 海景)	1Pos032	Kakugo, Akira	1EA004
Iwamoto, Hiroyuki (岩本 裕之)	3Pos063		2Pos093
Iwamoto, Koji (岩本 浩司)	3Pos100	Kakugo, Akira (角五 彰)	3Pos195
Iwamoto, Masayuki (岩本 真幸)	1Pos115	Kamagata, Kiyoto (鎌形 清人)	2SIA-5
Iwano, Kazuya (岩野 和哉)	2Pos171	Kamarulzaman, Latiefia (カマルザマン ラティファ)	
Iwano, Satoshi	3SBA-1		1GC002
Iwanski, Malina	1MSF-2		1EB003
Iwao, Yuya (巖 祐哉)	1Pos017	Kamatani, Takashi (鎌谷 高志)	1EB005
Iwasa, Kantaro (岩佐 寛太郎)	3Pos018	Kambara, Taketoshi (神原 丈敏)	1SIA-3
Iwasa, Mitsusada (岩佐 充貞)	1Pos091		1MSF-3
Iwasaki, Hikaru (岩崎 光)	2Pos080		2Pos083
Iwasaki, Kanako (岩崎 奏子)	1EC002	Kameda, Tomoshi (亀田 倫史)	1GB002
Iwata, Seiya	2Pos048	Kamei, Ken-ichiro F (亀井 健一郎)	1GG004
Iwata, So (岩田 想)	1GI005	Kameo, Yoshitaka (亀尾 佳貴)	2SFA-7
Iwata, Tatsuya (岩田 達也)	1Pos068	Kamikouchi, Azusa	3Pos176
	3Pos051	Kamikubo, Hironari (上久保 裕生)	1GA003
	3Pos190		1Pos017
Iyoda, Yudai (伊與田 裕大)			1Pos023
Izuka, Takao (猪塚 昂生)	2Pos025		1Pos143
Jang, Sung-Soo	3Pos122		2Pos127
Jarin, Zack	2Pos114	Kamimoto, Kenji (神元 健児)	3SHA-3
Jeckel, Hannah (Jeckel Hannah)	2SGA-4	Kamimura, Rina (神村 理菜)	3Pos037
Jeon, Juhyeong	2SKA-3	Kaminaga, Kiich (神長 輝一)	1GJ010
Jeongmin, Yu	2SKA-5		

	1GI004	Katsumata, Ryotaro (勝又 僚汰朗)	2Pos167
	1GI005	Katsuno, Masahisa (勝野 雅央)	1GH001
	1GI007	Katsuta, Hiroki (勝田 紘基)	3Pos075
	1Pos124	Kawabata, Haruka (川端 悠)	1Pos005
	1Pos126	Kawabata, Takeshi (川端 猛)	2Pos160
	2Pos004	Kawagishi, Ikuro (川岸 郁朗)	1GF012
	3Pos121		1Pos084
	3Pos122		1Pos118
	3Pos141		2Pos119
Katayama, Koya (片山 康矢)	1ED003		3Pos093
Katayama, Naoya (片山 直哉)	1Pos220		3Pos114
Katayama, Takuya (片山 拓也)	1GB005	Kawagoe, Soichiro	3Pos219
	1GE002	Kawaguchi, Kazutomo	1GH007
Kato, Chisa (加藤 千紗)	1Pos054		3Pos168
Kato, Hideaki (加藤 英明)	1MSI-4	Kawaguchi, Kazutomo (川口 一朋)	2Pos182
	1GA008		3Pos167
	1GI005	Kawaguchi, Kyogo	2SAP-2
	2Pos006	Kawaguchi, Kyogo (川口 喬吾)	1SDA-2
Kato, Hideaki E. (加藤 加藤)	3Pos122	Kawaguchi, Shota (川口 翔大)	1Pos002
Kato, Hideaki E. (加藤 英明)	1GI004	Kawaguchi, Tomoki (川口 倫輝)	1Pos129
	3Pos121	Kawaguchi, Yoshimasa (川口 祥正)	2SDA-5
Kato, Koichi (加藤 晃一)	1GH005	Kawahara, Kazuki (河原 和樹)	3Pos020
	2Pos016	Kawai, Daiki (川井 大輝)	3SGA-5
Kato, Koichi (加藤 紘一)	3Pos170	Kawai, Haruki (川合 春輝)	3Pos030
Kato, Minoru (加藤 稔)	3Pos018	Kawai, Toui (川合 登偉)	1GF002
Kato, Riki (加藤 利樹)	2Pos045	Kawai, Tsuyoshi (川合 毅)	2Pos033
Kato, Satofumi (加藤 智史)	3Pos052	Kawakami, Haruki (川上 陽輝)	3Pos163
Kato, Seito (加藤 聖人)	3Pos009	Kawakami, Keisuke (川上 恵典)	1Pos139
Kato, Shinya (加藤 真也)	1Pos100	Kawakami, Koki (川上 耕季)	3Pos121
	1Pos102	Kawakami, Kouki (川上 耕季)	1GA008
Kato, Shotaro (加藤 笙太郎)	2Pos059	Kawamata, Ibuki	2Pos093
Kato, Shunsuke (加藤 俊介)	2SCA-2	Kawamata, Ibuki (川又 生吹)	2SEP-1
Kato, Sinya (加藤 真也)	1Pos103		1Pos056
Kato, Suguru (加藤 傑)	1SAA-3		3Pos112
Kato, Takaaki (加藤 克彬)	2SHP-7		3Pos195
Kato, Takafumi (加藤 孝郁)	1MSF-3	Kawamoto, Akihiro (川本 晃大)	2SGP-6
Kato, Takayuki (加藤 貴之)	1GA003		1GA003
	1GB001		1Pos006
	2Pos004		3Pos010
	2Pos071	Kawamoto, Jun (川本 純)	1Pos109
	3Pos003	Kawamoto, Mei (川本 芽生)	3Pos139
	3Pos087	Kawamoto, Saya (川本 紗弥)	3HL1030
Kato, Yoshitaka (加藤 善隆)	1Pos128	Kawamura, Anzu (河村 あんず)	3Pos054
Kato, Yoshitaka (加藤 義隆)	1GI002	Kawamura, Eito (河村 叡人)	2Pos103
Kato, Yuki (加藤 祐樹)	1Pos135	Kawamura, Izuru (川村 出)	3SEA-3
	1Pos138		1GA013
	1Pos141		1Pos015
Kato, Yuki S. (加藤 祐基)	1GJ006		1Pos016
Katoh, Kaoru (加藤 薫)	3Pos212		1Pos126
Katoh, Takanobu (加藤 孝信)	1SCA-8	Kawanabe, Akira (川鍋 陽)	1Pos113
Katsuma, Asako (勝間 亜沙子)	2SIP-5		1Pos123
	1Pos192	Kawano, Ryuji (川野 竜司)	1GA013

	1GC004	Kimura, Taeko (木村 妙子)	3Pos161
	1GC007	Kimura, Takahiro (木村 貴洋)	1GB005
	1GE003		1GE002
	1Pos016	Kimura, Tatsuya (木村 竜也)	1GC001
Kawano-Yamashita, Emi (川野 (山下) 絵美)	2Pos129	Kimura, Tetsunari (木村 哲也)	3Pos045
Kawasaki, Akari (川崎 愛花里)	3HL1030	Kimura, Tetsunari (木村 哲就)	3Pos042
Kawasaki, Takeshi (川崎 猛史)	1GH001		3Pos046
Kawase, Haruki (川瀬 陽輝)	3Pos074	Kimura, Yuki (木村 友字己)	1GD003
Kawashima, Shigehiro (川島 茂裕)	2SAP-4	Kimura, Yukihiko (木村 行宏)	2Pos138
Kawasumi, Takuro (川澄 琢朗)	3Pos071		2Pos139
Kawauchi, Keiko (川内 敬子)	1Pos216		2Pos140
Kawauchi, Tatsuki (河内 達輝)	1Pos063	Kinbara, Kazushi (金原 数)	1ED004
Kayamori, Fumihiko (栢森 史浩)	1GA013	Kinoshita, Keigo (木下 圭剛)	1Pos017
Kengaku, Mineko (見學 美根子)	1SIA-2	Kinoshita, Kengo (木下 賢吾)	2Pos160
Kenmotsu, Takahiro (剣持 貴弘)	1GE004	Kinoshita, Masanao (木下 祥尚)	1GF005
Kennedy, Mary B.	2SGA-3		2Pos106
Kenri, Tsuyoshi (見理 剛)	1GD006		2Pos108
Kida, Masatoshi (木田 雅俊)	2Pos134	Kinoshita, Masato (木下 政人)	1Pos188
Kidoaki, Satoru (木戸秋悟)	2SIP-6	Kinoshita, Seiichiro (木下 誠一郎)	2Pos085
	1Pos081	Kinoshita, Yoshimi (木下 慶美)	1MSJ-5
Kiga, Daisuke (木賀 大介)	3Pos035	Kinoshita, Yuna (木ノ下 佑奈)	2Pos021
Kigawa, Takanori (木川 隆則)	2Pos041	Kinosita, Yoshiaki (木下 佳昭)	2Pos097
Kiguchi, Shunsuke (木口 峻輔)	2Pos146	Kise, Ryoji (木瀬 亮次)	2Pos096
Kijima, Soichiro (木島 壮一郎)	1GA005	Kise, Yoshiaki (木瀬 孔明)	1MSF-3
Kijima, Soichiro (木島 壮一郎)	2Pos039	Kishi, Koichiro (岸 孝一郎)	2Pos006
Kikkawa, Masahide (吉川 雅英)	1Pos079	Kishi, Koichiro E. (岸 孝一郎)	1GI004
Kikkawa, Nobuaki (吉川 信明)	1SBA-7	Kishikawa, Jun-Ichi (岸川 淳一)	3Pos070
Kikuchi, Hiroto (菊地 浩人)	1Pos136	Kishikawa, Jun-ichi (岸川 淳一)	1GA004
Kikuchi, Kazuya (菊地 和也)	2Pos215		1GA006
Kikuchi, Kosuke (菊池 幸祐)	1Pos037		1Pos116
	2Pos162		2Pos071
Kikukawa, Takashi (菊川 峰志)	1Pos133	Kishikawa, Jyun-ichi (岸川 淳一)	1GA001
	3Pos123	Kita, Tomoki (北 智輝)	1GE010
	3Pos126	Kitada, Nobuo	3SBA-1
	3Pos129	Kitadume, Hana (北詰 花菜)	3Pos020
Kikukawa, Takashi (菊川 隆志)	1Pos108	Kitagawa, Daiju (北川 大樹)	1Pos090
Kikumoto, Mahito (菊本 真人)	2Pos112	Kitagawa, Moeko (北川 萌子)	1Pos018
	2Pos113	Kitaguchi, Tetsuya	3Pos085
	3Pos149	Kitahara, Ryo (北原 亮)	2SIA-4
Kim, Changsu (金 昌秀)	3SBA-9		1GB002
Kim, Hyunji (Kim Hyunji)	1Pos174		1GB004
Kim, Jin Hae	2SKA-3	Kitajima, Rei (北嶋 嶺)	3Pos175
Kim, Sooyeon (金 水縁)	1GC002	Kitajima, Tomoya (北島 智也)	1SIA-4
	1EB003	Kitajima-Ihara, Tomomi (北島 (井原) 智美)	1Pos138
Kim, Suhyang (金 穗香)	1GI004		1Pos141
	2Pos006	Kitakata, Emi (北方 恵美)	1GD012
Kim, Sulhee	3Pos121	Kitamura, Akira (北村 朗)	2SGA-1
Kim, Yoon Seok	2SKA-1		1Pos060
Kimura, Hitomi (木村 仁美)	3Pos122		3Pos030
Kimura, Masayuki (木村 将之)	2Pos053	Kitamura, Keiji (北村 奎時)	1GB002
	1SBA-7		1GB004
Kimura, Miyu (木村 妃佑)	2Pos116	Kitamura, Yoshiichiro (北村 美一郎)	2Pos123

Kitano, Ryota (北野 良太)	2SHP-7	Kobayashi, Yoshihiko (小林 芳彦)	2Pos200
Kitao, Akio	2SBA-1	Kobayashi, Yuki (小林 由紀)	2SAP-3
	1GH004	Kodera, Noriyuki (古寺 哲幸)	1SJA-1
Kitao, Akio (北尾 彰朗)	2SBA-4		2SAA-5
	2SBA-5		1EB002
	2SFP-3		2Pos051
	1GA005		2Pos067
	2Pos183		3Pos029
Kitao, Akio (北尾 彰郎)	2Pos039		3Pos040
Kitayama, Keigo (北山 慧悟)	2Pos109		3Pos048
Kitazawa, Soichiro (北沢 創一朗)	1GB002		3Pos207
Kitazume, Hana (北詰 花菜)	3Pos019	Kodera, Yoshio (小寺 義男)	2Pos002
Kito, Kentaro (鬼頭 健太郎)	1Pos101		2Pos011
	2Pos104	Koezuka, Masato (肥塚 雅人)	3SIA-7
	2Pos121	Koga, Marina (古閑 万里渚)	3Pos003
	3Pos096	Koga, Nobuyasu (古賀 信康)	1SGA-1
	3Pos097		2Pos037
Kiuchi, Tai (木内 泰)	1Pos207	Koga, Ryuichi (古賀 隆一)	1Pos149
Kiyama, Hana (木山 花)	1GD008	Koga, Taisei (古賀 大聖)	2Pos128
	1GF006	Koh, Sangho (高 相昊)	1SFA-3
	1GJ002	Kohata, Ai (木幡 愛)	1ED004
	2Pos090	Kohda, Daisuke (神田 大輔)	1SJA-4
	3Pos079	Koide, Sanetoki (小出 真諦)	1Pos119
	3Pos147	Koike, Ayumu (小池 歩)	2Pos172
	3Pos148	Koike, Ryotaro (小池 亮太郎)	1Pos176
Kiyama, Masahiro	3SBA-1		2Pos159
Kiyonaka, Shigeki (清中 茂樹)	2SDP-4	Kojima, Asato (小島 朝翔)	1GA008
Kiyooka, Ryota (清岡 亮太)	1SBA-1		1GI005
	2Pos049		3Pos121
	2Pos171	Kojima, Keiichi (小島 慧一)	2Pos132
Kiyota, Ayaka (清田 彩香)	1Pos177		3Pos125
Kiyotani, Kazuma (清谷 一馬)	1EE001	Kojima, Masaru (小嶋 勝)	3Pos082
Kluger, Ronald (Kluger Ronald)	1MSG-5	Kojima, Rei (小嶋 嶺)	1Pos080
Kobashigawa, Yuto (小橋川 雄斗)	2Pos157	Kojima, Ryo (小嶋 凌)	1Pos065
Kobayashi, Chigusa (小林 千草)	2Pos028		3Pos062
Kobayashi, Daichi (小林 大地)	1Pos213	Kojima, Ryosuke (小嶋 良輔)	1SFA-6
Kobayashi, Kazuhiro (小林 和弘)	1GA008	Kojima, Seiji (小嶋 誠司)	1Pos045
	3Pos121		2Pos071
Kobayashi, Masataka (小林 真隆)	3SBA-9		2Pos075
Kobayashi, Ryohei (小林 稜平)	1GE005	Komatsu, Aika (小松 愛華)	3SIA-7
	1GE008	Komatsu, Hideyuki (小松 英幸)	1Pos032
	1Pos038		2Pos018
Kobayashi, Ryota (小林 亮太)	1Pos009	Komatsuzaki, Tamiki	2Pos210
Kobayashi, Ryouhei (小林 亮平)	1Pos207	Komatsuzaki, Tamiki (小松崎 民樹)	3SGA-7
Kobayashi, Taiki (小林 大葵)	3Pos028	Komatsuzaki, Yoshimasa (小松崎 良将)	3Pos118
Kobayashi, Takeru (小林 丈流)	2Pos217	Komi, Yusuke (小見 悠介)	2Pos010
Kobayashi, Takuya	2Pos048	Komiya, Ken (小宮 健)	2Pos055
Kobayashi, Takuya (小林 拓也)	1GI005	Komori, Kakeru (古森 翔)	3Pos081
Kobayashi, Tatsuya (小林 達也)	2Pos028	Kondo, Akihiko (近藤 昭彦)	1MSG-7
Kobayashi, Tetsuya J. (小林 徹也)	2Pos192	Kondo, Hinase (金堂 陽生)	3Pos139
	1YK0915	Kondo, Hiroko X. (近藤 寛子)	1SBA-6
Kobayashi, Tsubasa	2Pos210	Kondo, Kanta (近藤 勘太)	3Pos041

Kondo, Kanta (近藤 貫太)	2Pos023	Kuang, Yu-Chi (匡 玉琪)	1Pos124
Kondo, Kazuki (近藤 千月)	1GB011	Kubo, Minoru	3Pos049
Kondo, Kazunori (近藤 和典)	2Pos143	Kubo, Minoru (久保 稔)	3Pos039
Kondo, Naoshi (近藤 直)	3Pos206	Kubo, Shintaro (久保 進太郎)	1SGA-3
Kondo, Takao (近藤 孝男)	3SJA-4	Kubo, Shuto (久保 柗人)	1Pos069
Kondo, Tatsuki (近藤 龍樹)	1SIA-3	Kubota, Ryusei (窪田 隆正)	3Pos009
	2Pos083	Kubota, Shigeharu (窪田 滋春)	3Pos194
Kondo, Toru (近藤 徹)	3Pos031		3Pos008
	3Pos133	Kudo, Hisashi (工藤 恒)	3Pos025
	3Pos137	Kudo, Kye (工藤 海)	1MSG-7
Kondo, Yohei (近藤 洋平)	1Pos194	Kudo, Makiko (工藤 麻希子)	3Pos117
	3Pos191	Kudo, Yusei (工藤 悠世)	1Pos199
Kong, Haonan (孔 浩南)	1Pos037	Kueda, Fuko (杭田 美子)	1Pos053
Kongchu, Natthanan	3Pos172	Kuhara, Atsushi (久原 篤)	3SIA-7
Konishi, Yuichiro (小西 雄一朗)	1GB001		1Pos120
Konno, Hiroki (紺野 宏記)	1Pos039		1Pos121
	1Pos042		1Pos123
	2Pos040		2Pos120
	3Pos028		3Pos115
Konno, Masae (今野 雅恵)	1Pos130	Kuhara, Atsushi (久原 篤)	1GD009
	2Pos126	Kukimoto-Niino, Mutsuko (柊元(新野) 睦子)	2SHP-5
Kono, Fumiaki (河野 史明)	1MSH-6	Kumagai, Momoka (熊谷 桃花)	2Pos084
Kono, Hidetoshi	3Pos056	Kumagai, Sari (熊谷 咲里)	1Pos126
Kono, Hidetoshi (河野 秀俊)	2SAP-1	Kumagai, Shunsuke	1Pos078
	1MSJ-4	Kumakura, Ryota (熊倉 綾汰)	2Pos030
	1Pos059	Kumakura, Taisei (熊倉 大誠)	1Pos118
	3Pos138	Kumanogoh, Atsushi (熊ノ郷 淳)	1GG012
	3Pos139	Kumar, Amarjeet	3Pos056
Kono, Hideya	3Pos180	Kumar, Amarjeet (Kumar Amarjeet)	2SAP-1
Kono, Yohei	1Pos095	Kumashiro, Munchiro (熊代 宗弘)	2SHP-2
Kono, Yohei (河野 洋平)	1Pos199	Kumazaki, Kaoru (熊崎 薫)	1MSF-3
Kono, Yunosuke (河野 友乃助)	3HL0900	Kumeta, Hiroyuki	3Pos219
Kosaki, Shinya (小崎 慎也)	1GI008	Kumeta, Hiroyuki (久米田 博之)	2SHP-2
	2Pos137		1MSG-1
Koshimura, Hinako (越村 日向子)	1GA003		1GF009
Koshiyama, Tomomi (越山 友美)	3SIA-4	Kunida, Katsuyuki (国田 勝行)	1Pos155
Kosono, Saori (古園 さおり)	1GB003	Kunihiro, Teiji (国広 悌二)	3SJA-5
Kosuge, Yume (小菅 友萌)	3Pos032	Kunii, Mahan (國井 真帆)	1GA002
Kosugi, Takahiro (小杉 貴洋)	1GH010		3HL1115
Kosumi, Daisuke (小澄 大輔)	1Pos139	Kuragano, Masahiro (倉賀野 正弘)	2SCP-5
	2Pos134	Kuranaga, Erina (倉永 英里奈)	2SDP-3
Kotani, Takahiro (小谷 崇博)	1GJ009	Kurata, Atsushi (倉田 淳志)	3Pos019
Koteishi, Hiroyasu (小手石 泰康)	3Pos010	Kurematsu, Kengo (興松 健吾)	1GE003
Kouno, Kazuma (神野 和磨)	2Pos218	Kuribayashi-Shigetomi, Kaori (栗林-繁富 香織)	2Pos083
Kouriki, Ryounosuke (神力 亮之介)	1Pos187		2Pos083
Kousaka, Jin (高坂 仁)	1Pos190	Kuribayashi-Shigetomi, Kaori (繁富 (栗林) 香織)	1SIA-3
Kouta, Ryohei (幸田 稜平)	3HL1100		1MSG-3
Kovalchuk, Svitlana (コヴァルチュク スヴィトラナ)	1Pos057	Kurihara, Kazuo (栗原 和男)	1MSG-6
	1Pos066	Kurihara, Tatsuo (栗原 達夫)	1Pos109
Koyama, Hiroshi (小山 宏史)	1GG007	Kurino, Shinichi (栗野 真一)	1Pos014
Koyanagi, Mitsumasa (小柳 光正)	1GI007	Kurisasi, Ikuro (栗崎 以久男)	2Pos163
		Kurusu, Genji (栗栖 源嗣)	2SGP-6

	1GA003	Laurino, Paola (螺烏湮移之 端和羅)	3Pos021
	1Pos006	Lee, I-Ren (李 以仁)	3Pos049
	3Pos010	Lee, Jun-Seok	1Pos098
	3Pos177	Lee, Seohyun (イ ソ ヒ ョ ン)	1MSF-1
Kurisu, Minoru (栗栖 実)	1ED001	Lee, Young-Ho	2SKA-3
Kurisu, Yuto (栗栖 悠斗)	1EB005		1Pos005
Kuroda, Hiroshi (黒田 洋詩)	3Pos135		3Pos220
Kuroda, Kaname (黒田 要)	2Pos085	Lee, Yuan-E (Lee Yuan-E)	1Pos010
Kuroda, Shun'ichi (黒田 俊一)	1GF001		3Pos073
Kuroda, Yutaka	1GA007	Lenne, Pierre-François (Lenne Pierre-François)	1Pos086
Kurokawa, Ken (黒川 顕)	2SAP-5	Li, Chelsea	3Pos122
	2Pos062	Li, Chun-Biu	3Pos072
	1YK0945	Li, Honghan	2Pos091
Kurokawa, Yumiko (黒川 裕美子)	2Pos051	Li, Hung-Wen (李 弘文)	2SBP-2
Kuroki, Yoichi (黒木 陽一)	1GJ008	Li, Xiang	1GF004
	2Pos100	Li, Xinxuan (LI XINXUAN)	3Pos091
Kurosawa, Gen (黒澤 元)	3SJA-5	Li, Yan	1Pos005
Kuruma, Yutetsu (車 兪徹)	3SFA-3	Lilatul, Isra	3Pos143
	2Pos219	Lin, Shao-Zhen (Lin Shao-Zhen)	1Pos086
Kurumizaka, Hitoshi	3Pos056	Lin, Wei-Ting (Lin Wei-Ting)	1Pos127
Kurumizaka, Hitoshi (胡桃坂 仁志)	2SAP-3	Lin, Yuxi	1Pos005
	1Pos041		3Pos220
	3Pos057	Lintuluoro, Jua Mikael (リントウルオト ユハ ミカエ ル)	1Pos180
Kusaka, Katsuhiko	1MSH-2	Lintuluoto, Juha (リントウルオト ユハ)	2Pos168
Kusaka, Katsuhiko (日下 勝弘)	1MSH-4		2Pos181
Kusakabe, Takehiro (日下部 岳広)	2Pos129	Lintuluoto, Masami (リントウルオト 正美)	1Pos180
Kusakizako, Tsukasa (草木 迫 司)	1MSF-3		2Pos168
Kusu, Yuri (嘉数 百合)	3Pos023		2Pos181
Kusuma, Subhan Hadi	2Pos144		2SHP-7
	1YK0900	Liu, Hanjin	3Pos198
Kusumi, Akihiro	2SGA-3	Liu, Lin (劉 琳)	1GD012
	1Pos098	Liu, Yifan (劉 一帆)	1SHA-1
Kusumi, Akihiro (楠見 明弘)	1SHA-4	Liu, Ying (劉 穎)	1SHA-3
	1SHA-5	Lounis, Brahim	3Pos118
	1GF002	Lukowiak, Ken	2SBP-2
	1EC003	Luo, Shyh-Chyang (羅 世強)	2Pos204
	1Pos096	Lysenko, Artem (Lysenko Artem)	1GI009
Kuwabara, Hiromu (栗原 宙歩)	1GD001	Lyu, Zikun (呂 子琨)	3Pos176
Kuwahara, Yusuke (栗原 裕介)	2Pos127	M. Loh, YuMin	2Pos006
Kuwajima, Kunihiro (桑島 邦博)	2Pos016	Ma, Jie (馬 潔)	2Pos118
Kuwata, Takumi (桑田 巧)	3Pos024	Mabuchi, Takuya (馬渕 拓哉)	1GC011
Kuwayama, Hidekazu (桑山 秀一)	2SEP-7	Machida, Haruto (町田 温登)	2SCP-4
Kuzuhara, Miwa (葛原 美和)	1GA003	Machida, Kodai (町田 幸大)	1Pos216
Kuzuyama, Tomohiko (葛山 智久)	1Pos001	Machiyama, Hiroaki (町山 裕亮)	2Pos138
Kuzuyama, Tomohisa (葛山 智久)	1GH012	Madigan, Michael T. (Madigan Michael T.)	2Pos139
La Rocca, Romain (ラ・ラカ ローマン)	2Pos136		2Pos140
Laha, Shilpi (Laha Shilpi)	1GE002		1MSG-1
Lahore, Juliette (Lahore Juliette)	3Pos073	Maeda, Kosuke (前田 皓丞)	1GA011
Lam, Vi Toan	1GH004		1GG009
Lane, Birgitte E.	3Pos085		1Pos021
Lappalainen, Pekka	2Pos114		1ED004
Laurino, Paola	3SFA-1		

Matsuo, Takuya (松尾 拓哉)	3SJA-2	1GG002
Matsuoka, Daisuke (松岡 大佑)	3SFA-3	1Pos029
Matsuoka, Satomi (松岡 里実)	3Pos100	1Pos057
Matsusaki, Michiya (松崎 典弥)	1SCA-2	3Pos197
Matsusaki, Motonori	3Pos219	3Pos201
Matsushima, Keisuke (松島 啓介)	1GD011	3Pos215
Matsuura, Koji (松浦 宏治)	2Pos088	1Pos118
Matsuura, Tomoaki (松浦 友亮)	3Pos078	1GD009
	3Pos154	1Pos121
Matsuyama, Ayaka (松山 綾夏)	3Pos050	3Pos035
Matsuyama, Saki (松山 紗妃)	1Pos058	2Pos007
Matsuzaki, Kohei (松崎 興平)	1Pos071	2SAP-5
Matsuzaki, Miki (松崎 美紀)	1Pos025	2Pos062
Matsuzaki, Yuri (松崎 由理)	1Pos160	1YK0945
Matuski, Yoh (松木 陽)	3Pos055	1Pos012
Mayumi, Koichi (眞弓 皓一)	2Pos155	2Pos141
Maëda, Yuichiro (前田 雄一郎)	1Pos093	3SHA-2
McArthur, Steven John (マッカーサー スティーブン ジョン)	1EB002	3Pos131
McCloskey, Daniel	2SJP-1	1GJ007
McFee, Danielle (McFee Danielle)	1Pos116	2SGP-4
Md Alradzi, Islam	2Pos072	1GI008
Md Nadim, Hossain	1GJ005	2Pos137
Meghna, Sobti (Meghna Sobti)	1GE009	2Pos215
Meguro, Eiki (目黒 瑛暉)	3Pos086	1GC011
Mehta, Dalip Singh	3SAA-2	3Pos055
Meshcheryakova, Irina	2SGA-3	2SGP-7
	1Pos098	3Pos020
Meunier, Frédéric A.	3Pos117	1Pos026
Mi-ichi, Fumika (見市 文香)	1GA001	1Pos093
Michele, Lorenzo Di (Michele Lorenzo Di)	3Pos154	2Pos090
Michigami, Masataka (道上 雅孝)	2Pos038	2Pos029
Michiue, Tatsuo (道上 達男)	1GJ009	1GD001
Michiue, Yuki (道上 佑希)	1GB006	1Pos087
Mie, Yasuhiro	1Pos217	1Pos188
Mifune, Konoka (三船 心花)	2Pos199	2Pos069
	3Pos199	2Pos207
	2Pos185	2Pos009
Mikami, Bunzo (三上 文三)	1Pos217	3Pos004
Mikami, Chitose	3Pos037	3Pos005
Mikawa, Tsutomu (美川 務)	3Pos166	3Pos006
Miki, Koji (三木 康嗣)	3SAA-4	3Pos070
Mikkelporg, Marie	3Pos117	2Pos048
Millard, S. Sean	2SGA-3	3Pos212
Milovanovic, Dragomir	1EC003	3Pos153
Mimori-Kiyosue, Yuko (清末 優子)	2SCP-1	1Pos137
Mimoto, Reika (三本 麗華)	2Pos196	3Pos115
Mimura, Mone (三村 萌音)	2Pos090	1GD009
Mimura, Yutsuki (三村 唯月)	3Pos017	3Pos019
Minagawa, Jun (皆川 純)	1Pos134	3Pos020
Minagawa, Yoshihiro (皆川 慶嘉)	2SKP-4	1EA004
	1GB010	1GC008
		1GJ001
Minaki, June (皆木 珠寧)		
Minakuchi, Yohei (水口 洋平)		
Minami, Atsushi (南 篤)		
Minami, Hiroki (南 宏樹)		
Minami, Katsuhiko (南 克彦)		
Minami, Nao (南 尚)		
Minamisawa, Keito (南澤 溪翔)		
Minegishi, Misa (峯岸 美紗)		
Minei, Ryuhei (嶺井 隆平)		
Minigawa, Yoshihiro (皆川 慶嘉)		
Mino, Hiroyuki (三野 広幸)		
Minoshima, Masafumi (蓑島 維文)		
Mio, Kazuhiro (三尾 和弘)		
Mishima, Yuichi (三島 優一)		
Misima, Masaki (三島 正規)		
Mitani, Kazuki (三谷 和樹)		
Mitani, Kazuki (三谷 和輝)		
Mitani, Takahiro (三谷 隆大)		
Mitra, Shrutarshi (Mitra Shrutarshi)		
Mitsui, Toshiyuki (三井 敏之)		
Mitsuoka, Kaoru (光岡 薫)		
Mitsutake, Ayori		
Mitsuyama, Totai (光山 統泰)		
Miura, Sota (三浦 聡汰)		
Miura, Taiga (三浦 大河)		
Miura, Tohru (三浦 徹)		
Miura, Toru (三浦 徹)		
Miura, Yuto (三浦 佑斗)		
Miura, Yuuto		
Miwa, Akari (三輪 明星)		
Miyachi, Ryota (宮地 亮多)		

Miyagawa, Yasuki (宮川 靖基)	1Pos094	Mizukami, Taku (水上 卓)	1Pos141
Miyaguchi, Hide (宮口 英)	1YK1100	Mizuki, Houryou (水木 鳳了)	2Pos065
Miyakawa, Takuya (宮川 拓也)	2Pos018	Mizuno, Ayato (水野 文人)	1Pos092
Miyake, Kodai (三宅 皓大)	1Pos049	Mizuno, Daisuke	3Pos170
Miyake, Takanao (三宅 孝尚)	1GE008	Mizuno, Gaku (水野 雅玖)	1Pos206
Miyamoto, Akinori (宮本 明典)	2Pos116	Mizuno, Ikumi (水野 如海)	3SBA-7
Miyamoto, Kei (宮本 圭)	1Pos058	Mizuno, Kosuke (水野 皓介)	3Pos182
Miyamoto, Kousei (宮本 工聖)	1Pos094	Mizuno, Moea (水野 萌香)	2Pos067
Miyamoto, Shuichi (宮本 秀一)	1YK1100	Mizuno, Yosuke (水野 陽介)	1GA009
Miyasari, Yusuke (宮成 悠介)	3Pos132	Mizutani, Arisa (水谷 ありさ)	1GI001
Miyanoiri, Yohei (宮ノ入 洋平)	2Pos047	Mizutani, Azuki (水谷 淳生)	1Pos087
Miyashita, Naoyuki (宮下 尚之)	1Pos041	Mizutani, Masaki (水谷 雅希)	2Pos177
	3Pos028		2SKA-6
	3SEA-2		1GD008
	2Pos045		1Pos149
	1SBA-1		3Pos080
	2Pos049		3Pos148
	2Pos171	Mizutani, Yuki (水谷 友紀)	2Pos112
	2Pos174		2Pos113
	2Pos180	Mizutori, Ritsu (水鳥 律)	2SJA-3
	3Pos039		1MSG-2
Miyashita, Osamu	3Pos176	Mizuuchi, Ryo (水内 良)	1Pos150
Miyashita, Osamu (宮下 治)	1SJA-5		1Pos158
	2Pos190	Mochida, Keisuke (持田 啓佑)	1SJA-1
	3Pos027	Mochizuki, Atsushi (望月 敦史)	3SHA-5
Miyata, Hiroki (宮田 裕貴)	3Pos008	Mori, Hiroyuki (森 博幸)	3Pos171
	3Pos025	Mori, Joe (森 丈)	2Pos176
Miyata, Makoto (宮田 真人)	1MSG-3	Mori, Kaisei (森 凱世)	2Pos140
	1GD008	Mori, Miyu (森 美友)	1Pos065
	1GJ002		3Pos062
	2Pos090	Mori, Shinnosuke (森 新之介)	1Pos104
	3Pos055	Mori, Shoko (森 祥子)	1Pos117
	3Pos147	Mori, Takaharu (森 貴治)	2SAA-1
	3Pos148		1GH002
	3Pos209		1Pos031
Miyata, Makoto (宮田 誠)	3Pos079		1Pos186
Miyata, Tomoko (宮田 知子)	2SGP-6		3Pos158
	3Pos003		3Pos169
Miyauchi, Seiji (宮内 正二)	2Pos047		3Pos171
Miyazaki, Kana (宮崎 加菜)	3Pos123	Mori, Takahiro (森 貴裕)	1Pos169
Miyazaki, Makito	2Pos147	Mori, Toshifumi (森 俊文)	1Pos178
Miyazaki, Makito (宮崎 牧人)	1SIA-7		2Pos184
Miyazaki, Satoru (宮崎 智)	1Pos185		3Pos086
Miyazaki, Yusuke (裕介 裕介)	1GG001	Mori, Yukina (森 雪永)	1GD009
Miyazawa, Mitsuhiro (宮澤 光博)	1Pos025	Morigaki, Kenichi (森垣 憲一)	3SIA-7
	2Pos015		1Pos112
Miyazawa, Momoko (宮沢 桃子)	1Pos090		2Pos109
Miyoshi, Hideto (三芳 秀人)	1Pos116		3Pos102
Miyoshi, Kosuke (三好 晃輔)	2Pos124		3Pos104
Miyoshi, Takemasa (三好 建正)	2SFA-3		3Pos136
Miytata, Makoto (宮田 真人)	1GF006	Moriguchi, Maiko (森口 舞子)	3SBA-3
Mizue, Hatsune (水江 初音)	1Pos138	Morikawa, Syunya (森川 隼椰)	1Pos102

Morimatsu, Masatoshi (森松 賢順)	2Pos088	Mukai, Tomoya (向井 智哉)	3Pos204
Morimoto, Jumpei (森本 淳平)	3Pos175	Mukaiyama, Atsushi (向山 厚)	3SJA-3
Morimoto, Yūsuke V (森本 雄祐)	2Pos105	Munakata, Rika (宗像 里佳)	3Pos185
Morimoto, Yūsuke V. (森本 雄祐)	1GD008	Muneyuki, Eiro (宗行 英朗)	1GE011
	2Pos077	Munro, Kathryn	2SJP-1
	2Pos087	Murai, Masatoshi (村井 正俊)	1Pos116
	2Pos095	Murai, Toshiyuki (村井 稔幸)	3Pos106
	2Pos102	Murakami, Hiroshi (村上 洋)	1Pos198
	3Pos061	Murakami, Taiga (村上 大河)	2Pos182
	3Pos124	Murakami, Tatsuya (村上 達也)	2Pos214
Morino, Kohei (森野 航平)	3SFA-6		1YK1015
Morishima, Keisuke (森島 圭祐)	3Pos067	Murakoshi, Hideji (村越 秀治)	1GD010
Morishima, Ken (守島 健)	1GB007		1GD011
	1GB009	Murakoshi, Shunya (村越 峻也)	1MSF-3
	1Pos019	Muramatsu, Ryo (村松 亮)	2Pos154
Morishita, Manato (森下 愛大)	1GB004	Muramoto, Kazumasa (村本 和優)	1Pos044
Morita, Hiroto (森田 裕斗)	1Pos153	Muranaka, Tomoaki (村中 智明)	3SJA-1
Morita, Koshiro (森田 耕志郎)	2Pos146	Muraoka, Shunsuke (村岡 俊佑)	3Pos171
Morita, Rikuri (森田 陸離)	1Pos020	Murata, Kazuhoshi (村田 和義)	3Pos073
	1Pos172	Murata, Kazuyoshi	2Pos208
Morita, Shu (森田 宗)	1GA004	Murata, Kazuyoshi (村田 和義)	1Pos010
	1GA006		2Pos001
Moritsugu, Kei (森次 圭)	1Pos176	Murata, Keina (村田 景菜)	3Pos169
	2Pos185	Murata, Satoshi (村田 智)	1Pos152
	3Pos182		3Pos112
	3Pos188		3Pos113
Moriwaki, Yoshitaka (森脇 由隆)	1GH012		3Pos150
	1Pos009	Murata, Takeshi (村田 武士)	1Pos010
	1Pos183		1Pos047
Moriya, Ryohei	3SBA-1		3Pos073
Moriya, Toshio (守屋 俊夫)	1Pos010	Murata, Yutaka	3Pos047
Moriya, Wataru (森谷 亘)	2Pos063	Murayama, Keiji (村山 恵司)	1Pos158
Moriyama, Minoru (森山 実)	1Pos149	Murayama, Masanori (村山 正宜)	3SHA-4
Moriyama, Sakura (森山 さくら)	1GF001	Murayama, Yasuto (村山 泰斗)	2Pos051
Moriyama, Shunya (森山 俊哉)	3SIA-6	Murayama, Yoshihiro (村山 能宏)	1GD004
	1Pos112		1Pos058
Moriyama, Yuuta (守山 裕大)	1GD001		1Pos148
	1Pos087		3Pos054
	1Pos188	Murrell, Michael (マレル マイケル)	1SIA-6
	2Pos069	Mustakim, Mahammad	1EA004
	2Pos207	Muthahari, Yusran Abdillah (舞手八芭麗 右司 覽 亞附 弟猪拉)	3Pos021
Motegi, Fumio (茂木 文夫)	1SIA-3	Muto, Yuto (武藤 優斗)	3Pos004
	2Pos083	Mwaniki, Stephen (モワニキ ステイブン)	3Pos087
Motohashi, Masahiro (本橋 昌大)	1GE011	Nagae, Fritz (長江 文律立)	3Pos057
Motohashi, Rie (本橋 里英)	3Pos003	Nagai, Arata (長井 新)	1GD001
Motomura, Hideki (本村 英樹)	1GC012	Nagai, Shunsaku (長井 駿作)	1Pos015
Motono, Chie (本野 千恵)	3Pos034	Nagai, Takeharu (永井 健治)	1GG012
Motose, Hiroyasu (本瀬 宏康)	2Pos136		1GJ005
Mototake, Shiori (元武 葉里)	3Pos115		1Pos211
Motoyama, Yuka (本山 由佳)	3Pos099		2Pos038
Muhammad Dirgantara, Jelang (ジェラン ムハマド ディルガンタラ)	1EE001		2Pos212

	3Pos202	Nakamoto, Akane (中本 朱音)	2Pos108
	3Pos205	Nakamoto, Kaho (中本 佳歩)	3Pos040
	3Pos211		3Pos048
Nagai, Tetsuro (永井 哲郎)	1SB A-7	Nakamoto, Kodai (中元 滉大)	1Pos027
Nagai, Yuki (長井 佑樹)	3Pos109	Nakamura, Chikashi (中村 史)	2Pos046
Nagama, Misaki (永間 美咲)	1Pos037	Nakamura, Hanane (中村 花音)	3Pos019
Nagamine, Moeka (長峰 萌華)	3Pos008		3Pos020
Naganathan, Athi N (Naganathan N Athi)	1GE002	Nakamura, Hideki (中村 秀樹)	3Pos078
Naganathan, Athi N. (Naganathan Athi N.)	2Pos029	Nakamura, Humika (中村 文香)	1Pos180
Nagano, Kaito (長野 海翔)	2Pos089	Nakamura, Jun (中村 準)	3Pos164
Nagao, Hidemi	1GH007	Nakamura, Kazuha (中村 紀葉)	1Pos138
	3Pos168	Nakamura, Kazuyuki (中村 和幸)	2SAA-5
Nagao, Hidemi (長尾 秀実)	2Pos182	Nakamura, Keita (仲村 慶大)	3HL0900
	3Pos167	Nakamura, Kosuke (中村 公祐)	1Pos082
Nagao, Kaisei (長尾 海星)	3Pos033	Nakamura, Mai (中村 麻愛)	2Pos133
Nagao, Satoshi (長尾 聡)	1GF009		1YK1115
Nagaoka, Makoto (長岡 誠)	1GB003	Nakamura, Masayoshi (中村 匡良)	3Pos086
Nagashima, Kazuki (長嶋 一喜)	2Pos204	Nakamura, Naohiko (中村 直彦)	2Pos137
Nagata, Kazuhiro (永田 和宏)	2SCP-7	Nakamura, Ryuhei (中村 龍平)	3SFA-2
Nagata, Takashi (永田 崇)	1GI002	Nakamura, Seiwa (中村 星王)	2Pos006
	1GI007		3Pos121
	1Pos125		3Pos122
	1Pos130	Nakamura, Shinnosuke (中村 真乃祐)	3Pos173
	3Pos121	Nakamura, Shota (中村 祥大)	2Pos004
Nagata, Yuya (長田 祐也)	2Pos132	Nakamura, Shuichi (中村 修一)	2Pos086
Nagatomi, Isamu (永富 勇)	3Pos007	Nakamura, Takemasa (仲村 岳真)	1Pos097
Nagatsugi, Fumi (永次 史)	1GE002	Nakamura, Toshiaki (中村 敏規)	1GI006
Nagatsuka, Nanami (長塚 ななみ)	3Pos104	Nakamura, Tsukasa (中村 司)	1Pos010
Nagayama, Kuniaki (永山 國昭)	3Pos210	Nakamura-Norimoto, Aya	2SGA-3
Nagayama, Ryuna (永山 龍那)	1ED003	Nakane, Daisuke (中根 大介)	2SKA-6
Naito, Kota (内藤 航大)	1GC004		1GD004
	1GC007		1GD006
Naito, Takaharu (内藤 隆晴)	1Pos162		3Pos080
Nakabayashi, Takakazu (中林 孝和)	3Pos183		3Pos084
Nakada, Ayaka (中田 彩夏)	1GC007	Nakane, Yurina (中根 有梨奈)	1GJ010
Nakada, Shunichi (中田 俊彦)	3HL1100	Nakanishi, Atsuko (中西 温子)	2Pos009
Nakagaki, Toshiyuki (中垣 俊之)	3Pos120	Nakanishi, Jun (中西 淳)	2SDA-1
Nakagawa, Kaito (中川 開斗)	3Pos042	Nakanishi, Ren (中西 蓮)	3Pos011
Nakagawa, Yoshiko (中川 幸姫)	1Pos214	Nakano, Atsuki (中野 敦樹)	2Pos009
	1YK0930		2Pos079
Nakagawara, Ai (中川原 亜依)	1Pos108		3Pos004
Nakai, Tsubasa (中居 飛翔)	1Pos072		3Pos005
Nakajima, Daichi (中島 大地)	1Pos152		3Pos006
	3Pos078		3Pos070
Nakajima, Haruto (中嶋 悠人)	1GA013	Nakano, Haruo (中野 春男)	1Pos119
Nakajima, Kichitaro (中島 吉太郎)	2Pos042	Nakano, Haruyuki (中野 晴之)	3Pos186
	2Pos205	Nakano, Hideo (中野 秀雄)	3Pos034
	3Pos196	Nakano, Minoru (中野 実)	2Pos110
Nakajima, Yoshiki (中島 芳樹)	1GI008	Nakano, Shogo (中野 祥吾)	1MSI-2
	1Pos135	Nakano, Yoshio (中野 義雄)	1Pos185
Nakakuki, Takashi (中荃 隆)	2Pos055	Nakao, Arisa (中尾 有紗)	1Pos023
Nakamae, Hidekazu (中前 秀一)	3SBA-9	Nakao, Miku (中尾 未来)	1Pos058

	<u>1EA001</u>	<u>1GE006</u>
	<u>2Pos059</u>	<u>1GE007</u>
Nishitani, Yudai (西谷 雄大)	<u>2Pos135</u>	<u>1GE008</u>
	3Pos130	<u>1GE009</u>
Nishiyama, Akihito (西山 晃史)	<u>3Pos040</u>	<u>1GG002</u>
	<u>3Pos048</u>	<u>1GJ007</u>
Nishiyama, Ken-ichi (西山 賢一)	<u>1Pos117</u>	<u>1Pos029</u>
Nishiyama, Makoto (西山 真)	<u>1GB003</u>	<u>1Pos038</u>
Nishiyama, Masayoshi (西山 雅祥)	<u>2Pos085</u>	<u>1Pos057</u>
	2Pos088	<u>1Pos097</u>
Nishiyama, So-ichiro (西山 宗一郎)	<u>1GF012</u>	<u>2Pos079</u>
	1Pos118	<u>3Pos197</u>
Nishiyama, Tomoko (西山 朋子)	1SEA-1	<u>3Pos201</u>
	<u>1MSJ-5</u>	<u>1Pos027</u>
Nishizaka, Takayuki (西坂 崇之)	2SKA-6	<u>3SFA-3</u>
	<u>1GD008</u>	3SEA-5
	<u>3Pos080</u>	<u>1Pos117</u>
Nishizawa, Kenji (西澤 賢治)	1Pos086	<u>1Pos209</u>
Nishizawa, Ryohei (西澤 凌平)	1Pos196	<u>2Pos209</u>
Nishizawa, Tomohiro (西澤 知宏)	<u>1MSF-3</u>	<u>2SEP-2</u>
Nitta, Ryo (仁田 亮)	<u>2SHP-7</u>	<u>3Pos150</u>
Nitta, Takahiro	<u>3Pos064</u>	<u>3Pos078</u>
	<u>3Pos065</u>	<u>1EA004</u>
Nitta, Takahiro (新田 高洋)	<u>3Pos067</u>	<u>3SIA-3</u>
Niwa, Shinsuke (丹羽 伸介)	<u>1GE010</u>	<u>3Pos113</u>
Nobeyama, Tomohiro (延山 知弘)	<u>2Pos153</u>	<u>3Pos112</u>
	2Pos214	<u>1Pos152</u>
	1YK1015	<u>1Pos214</u>
	3SFA-5	<u>1YK0930</u>
Nobu, Masaru Konishi (延 優)	<u>1GF006</u>	2Pos010
Nobumoto, Kenji (信元 健智)	<u>2Pos055</u>	2Pos115
Noda, Chizuru (野田 千鶴)	2SGP-8	<u>2Pos117</u>
Noda, Nobuo N. (野田 展生)	<u>1GI005</u>	<u>1GB012</u>
Noda, Takeshi (野田 岳志)	<u>1Pos118</u>	2SGA-4
Nogami, Yuta (野上 由太)	<u>2Pos028</u>	<u>2Pos204</u>
Nogi, Terukazu (禾 晃和)	<u>2Pos164</u>	<u>3Pos057</u>
	<u>1EE001</u>	<u>2SJA-3</u>
Nogimori, Takuto (野木森 拓人)	<u>1GH009</u>	<u>1GI005</u>
Noguchi, Hiroshi (野口 博司)	1Pos188	2Pos003
Noguchi, Rikuto (野口 陸斗)	<u>2Pos207</u>	<u>1MSG-3</u>
	<u>1Pos135</u>	1Pos001
	<u>1Pos138</u>	<u>1MSF-3</u>
	<u>1Pos141</u>	<u>3Pos142</u>
Noguchi, Tomohiro (野口 智弘)	2SCA-3	<u>3SAA-2</u>
	<u>1GH012</u>	1Pos164
Noguchi, Yoshifumi (野口 良史)	3SBA-8	3SBA-5
Noh, Joseph J.	<u>3Pos122</u>	<u>3SBA-7</u>
Noji, Hiroyuki (野地 博之)	<u>2Pos215</u>	<u>1GI011</u>
Noji, Hiroyuki (野地 博行)	2SKP-4	1Pos184
	<u>1GA012</u>	<u>1Pos178</u>
	<u>1GB010</u>	<u>2Pos132</u>
	<u>1GE005</u>	<u>3Pos051</u>
	Noma, Chinatsu (野間 千夏)	<u>1Pos027</u>
	Nomaki, Hidetaka (野牧 秀隆)	<u>3SFA-3</u>
	Nomura, Kaoru (野村 薫)	3SEA-5
		<u>1Pos117</u>
	Nomura, Kayoko	<u>1Pos209</u>
	Nomura, Kayoko (野村 加代子)	<u>2Pos209</u>
	Nomura, M. Shin-ichiro (野村 M. 慎一郎)	<u>2SEP-2</u>
	Nomura, Shin-ichiro (野村 慎一郎)	<u>3Pos150</u>
	Nomura, Shin-ichiro (野村 慎一郎)	<u>3Pos078</u>
	Nomura, Shin-ichiro M.	<u>1EA004</u>
	Nomura, Shin-ichiro M. (野村 慎一郎)	3SIA-3
		<u>3Pos113</u>
	Nomura, Shinichiro (野村 慎一郎)	<u>3Pos112</u>
	Nomura, Shinichiro M. (野村 M. 慎一郎)	<u>1Pos152</u>
	Nomura, Takashi (野村 高志)	<u>1Pos214</u>
		<u>1YK0930</u>
		2Pos010
	Nomura, Takeshi (野村 健)	2Pos115
		<u>2Pos117</u>
	Norizoe, Yuki (乗添 祐樹)	<u>1GB012</u>
	Nosho, Kazuki (納庄 一樹)	2SGA-4
	Nozawa, Hikaru (野澤 光輝)	<u>2Pos204</u>
		<u>3Pos057</u>
	Nuemket, Nipawan (Nuemket Nipawan)	<u>2SJA-3</u>
		<u>1GI005</u>
	Nukui, Shiho (温井 志歩)	2Pos003
	Numoto, Nobutaka (沼本 修孝)	<u>1MSG-3</u>
	Nur Rochmah, Atika	1Pos001
	Nureki, Osamu (濡木 理)	<u>1MSF-3</u>
		<u>3Pos142</u>
	Nystadq, Mona	<u>3SAA-2</u>
	Oba, Shoya (大場 翔矢)	1Pos164
	Oba, Yuichi (大場 裕一)	3SBA-5
		<u>3SBA-7</u>
	Obana, Nozomu	<u>1GI011</u>
	Obata, Koryo (小幡 昂諒)	1Pos184
	Obayashi, Kohe (尾林 虹兵)	<u>1Pos178</u>
	Obayashi, Kohei (尾林 虹兵)	<u>2Pos132</u>
	Ochiai, Yumika (落合 優美華)	<u>3Pos051</u>

Oda, Akifumi (小田 彰史)	3Pos170	Ohnishi, Kohei (大西 康平)	3Pos120
Oda, Arisa H (小田 有沙)	3Pos177	Ohnishi, Miho (大西 美穂)	3Pos115
Oda, Masayuki (織田 昌幸)	1GG004	Ohnishi, Yusuke (大西 裕介)	3Pos110
Oda, Nanase (小田 七星)	2Pos168	Ohno, Kaisei (大野 介聖)	3Pos177
Oda, Tatsuro (小田 達郎)	3Pos148	Ohno, Kaisei (大野 介聖)	3Pos126
Oda, Toshiro (小田 俊郎)	2Pos155	Ohnuki, Jun (大貫 隼)	1Pos038
Oda, Toshiro (小田 俊郎)	1Pos091		2Pos166
Oda, Yukako (小田 裕香子)	1Pos093	Ohnuma, Kiyoshi (大沼 清)	1Pos065
Ogasawara, Hiroki (小笠原 浩輝)	2SGA-5		3Pos062
Ogasawara, Mitsuo (小笠原 光雄)	1Pos046	Ohnuma, Takayuki (大沼 貴之)	3Pos019
Ogasawara, Mitsuo (小笠原 光雄)	2SAP-3	Ohshima, Ayano (大島 彩乃)	1GB002
Ogawa, Haruto (小川 遼士)	1GE004	Ohshima, Hiromu (大島 広夢)	3HL1130
Ogawa, Kairi (小川 海吏)	1Pos025	Ohsugi, Miho (大杉 美穂)	1SIA-5
	2Pos015	Ohta, Akane (太田 茜)	1GD009
Ogawa, Shuichiro (小川 秀一郎)	1Pos207		1Pos120
Ogawa, Taiyo (小川 太陽)	3Pos029		1Pos121
Ogawa, Takuya (小川 拓哉)	1Pos109		1Pos123
Ogawa, Yuichi (小川 雄一)	3Pos206		2Pos120
Ogawa, Yuuka (小川 侑香)	1Pos063		3Pos115
Ogi, Anna (扇 杏奈)	2Pos025	Ohta, Kunihiro (太田 邦史)	1GG004
Ogi, Hirotsugu (荻 博次)	2Pos042	Ohta, Masateru (太田 雅照)	2SFP-6
	2Pos205	Ohtake, Kazumasa (大竹 和正)	3Pos035
	3Pos196	Ohtsu, Mina (大津 美奈)	2SEA-4
Ogihara, Satoshi (荻原 智)	3Pos057	Ohuchi, Hideyo (大内 淑代)	1Pos129
Ogino, Aya (荻野 綾)	1Pos042		2Pos129
	2Pos040		2Pos132
Ogino, Gaku (荻野 楽)	2Pos204		3Pos127
Ogita, Goshi (荻田 豪士)	2SFA-3	Ohzawa, Izumi (大澤 五住)	2Pos122
	1Pos196	Oide, Mao (大出 真央)	2SAA-3
Ogura, Kazuki (小椋 一輝)	1Pos135	Oikawa, Hiroyuki (小井川 浩之)	2Pos031
Ogura, Naoki (小倉 尚樹)	1GD004	Oikawa, Tsukasa (及川 司)	1Pos089
Ohashi, Gai (大橋 凱)	2Pos074	Oimoto, Rento (老本 蓮叶)	3HL0900
Ohashi, Sayaka (大橋 沙也佳)	2SJA-3	Oishi, Takumi (大石 匠美)	3Pos057
	1GI005	Oiwa, Kazuhiro (大岩 和弘)	1Pos082
Ohdaira, Takeshi (大平 猛)	1GD012	Ojima-Kato, Teruyo (加藤 晃代)	3Pos034
Ohe, Kouichi (大江 浩一)	3Pos166	Okabe, Kohki (岡部 弘基)	3SJA-6
Oheda, Hiroaki (大枝 弘明)	2Pos162		2Pos068
	2Pos164		3Pos203
Ohgita, Takashi (扇田 隆司)	1Pos012	Okabe, Manato (岡部 真翔)	3Pos051
	1Pos022	Okada, Mana (岡田 真奈)	2Pos069
Ohhara, Takashi (大原 高志)	1MSH-6	Okada, Shun (岡田 瞬)	1Pos159
	1GA002	Okada, Shunya (岡田 隼弥)	1GC009
	3HL1115	Okada, Takashi (岡田 崇)	2Pos196
Ohhashi, Yumiko (大橋 祐美子)	2SIA-3	Okada, Yasushi (岡田 康志)	1SIA-3
	1Pos042		1MSF-3
Ohkawa, Yasuyuki (大川 恭行)	2SAP-3		1GG010
Ohkubo, Tatsunari (大久保 達成)	1GC011		1EC002
Ohkubo, Tomoki (大久保 智樹)	1Pos155		1Pos069
Ohmichi, Kazuki (大道 一輝)	1Pos129		1Pos079
Ohmura, Takuto (大村 拓登)	1GH012		1Pos210
Ohmura, Takuya (大村 拓也)	1Pos201		2Pos083
	1YK1000		3Pos204

Okada, Yuki (岡田 由紀)	1SEA-4	Onozato, Kota (小野里 幸太)	1Pos091
Okahata, Misaki (岡畑 美咲)	1GD009	Ooka, Hideshi (大岡 英史)	3SFA-2
Okajima, Takaharu (岡嶋 孝治)	1GJ009	Ooka, Koji (大岡 紘治)	2Pos017
Okamoto, Kenji (岡本 憲二)	1Pos003	Ooka, Mako (大岡 真子)	3Pos140
Okano, Keiko (岡野 恵子)	2Pos025	Oosawa, Chikoo (大澤 智興)	2Pos105
Okano, Toshiyuki (岡野 俊行)	2Pos025	Orii, Ryota (折井 良太)	1SIA-3
Okawa, Atsushi (大川 敦司)	1GA004		2Pos092
	1GA006	Orita, Takuya (織田 拓也)	1GH10
Okazaki, Kei-ichi (岡崎 圭一)	1GE005	Oroguchi, Tomotaka (荳口 友隆)	1SAA-2
	1Pos038	Osaka, Hirona (大坂 紘奈)	1Pos212
	1Pos116	Osaka, Jiro (小坂 二郎)	2SBP-6
	2Pos166	Osawa, Tsukihō (大澤 月穂)	1Pos117
Okazaki, Shigetoshi (岡崎 茂俊)	1Pos013	Oshima, Atsunori (大嶋 篤典)	1Pos002
Okazaki, Susumu (岡崎 進)	1SBA-7	Oshima, Hiraku (尾嶋 拓)	2Pos186
Oki, Hiroya (沖 大也)	3Pos020		2Pos187
Okimura, Chika (沖村 千夏)	3SAA-1	Oshiro, Takumi (大城 拓末)	2Pos002
	1GD003		2Pos011
	1GD007	Ota, Motonori (太田 元規)	1Pos176
Okuda, Mitsuhiro (奥田 充宏)	3Pos214		2Pos159
Okuda, Momoka (奥田 桃加)	3HL1030	Ota, Tomoki (太田 朝貴)	2Pos042
Okuda, Satoru	3Pos187	Otomo, Akihiro (大友 章裕)	1Pos010
Okuda, Satoru (奥田 覚)	2SFA-4		1Pos073
	2Pos191		1Pos076
	3Pos060		3Pos073
	3Pos075	Otomo, Kohei (大友 康平)	2SEA-6
Okuda, Sota (奥田 宗太)	3Pos035	Otosu, Takuhiro (乙須 拓洋)	1Pos051
Okumura, Hisashi (奥村 久士)	2SGA-2		1Pos205
	2Pos176	Otsuka, Takuya	2Pos210
	2Pos178	Ottevaere, Heidi (Ottevaere Heidi)	1Pos013
Okuno, Takashi (奥野 貴士)	3Pos107	Otuska, Mizuho	1GF004
Okuno, Yasushi (奥野 恭史)	2SFP-1	Ou, Rui kinshinn (王 銳瑾萱)	3HL1000
	2SFP-6	Owada, Azusa (大和田 梓)	1Pos140
Okuyama, Kohei (奥山 紘平)	3Pos195	Oya, Momoko (大矢 桃子)	2Pos038
Okuzumi, Ayami (奥住 文美)	1SJA-3	Oya, Tatsuya (大矢 辰哉)	1GE005
Oliveira, Leonardo (Oliveira Leonardo)	2SJA-3	Ozaki-Noma, Ryohei (尾崎-野間 涼平)	2Pos038
Olivucci, Massimo (Olivucci Massimo)	2SJA-3	Ozaki-Noma, Ryohei (尾崎-野間 涼平)	3Pos205
	1GI005		1Pos211
Oma, Yukako (尾間 由佳子)	2Pos213	Ozeki, Yasuyuki (小関 泰之)	1EB005
Omatsu, Takashige (尾松 孝茂)	1SCA-1	P. Su, Matthew	3Pos176
Omori, Fuga (大森 楓河)	1GF012	P.M., Sayeesh	3Pos009
	1Pos118	Paczia, Nicole (Paczia Nicole)	2SGA-4
	3Pos114	Paggi, Joseph M.	3Pos122
Omori, Satoshi (大森 聡)	3Pos131	Paitio, Jose (バイティオ ジョゼ)	3SBA-7
Omoto, Kenta (尾本 健太)	3Pos189	Palombo, Riccardo (Palombo Riccardo)	2SJA-3
Onaka, Yoshimitsu (尾中 良充)	1GI003	Paramio, Olivia (Paramio Olivia)	2Pos005
Onda, Maki (恩田 真紀)	2Pos185		1YK1030
Onizuka, Kazumitsu (鬼塚 和光)	1GE002	Park, Ingyo	2SKA-1
Onoe, Hiroaki (尾上 弘晃)	3Pos052	Park, Jae-Hyun	1Pos005
	3Pos071	Park, Sam-Yong	1Pos005
Onoue, Yasuhiro (尾上 靖宏)	3SJA-4	Park, Seonha	2SKA-1
	1Pos024	Patron, Kishandra A.	3Pos122
	2Pos023	Pavlovich, Martin	3Pos176

Peng, Zugui (彭 祖癸)	1GA013	Rupprecht, Jean-François (Rupprecht Jean-François)	1Pos086
Penka, Elke (Penka Elke)	1MSG-5	Rutkowski, David (David Rutkowski)	1SHA-1
Perez, Alberto (Perez Alberto)	2Pos177	Sadakane, Koichiro (貞包 浩一朗)	2Pos059
Pestana Nobles, Roberto Carlos	3Pos176		2Pos155
Peterson, Walker	2Pos210		3Pos153
Pham, Quynh (Quynh Pham)	1Pos041		3Pos155
Phan, Tri Minh	2Pos035	Saga, Yoshitaka (佐賀 佳央)	1Pos137
Postrado, Michael (ポストラド マイケル)	1Pos107	Sagawa, Naoya (佐川 直也)	1Pos017
Prabhat, Verma (プラブハット バルマ)	1Pos200	Sagawa, Takahiro (沙川 貴大)	3Pos072
Pradipta Bandyopadhyay, Pooja	1EE003	Saha, Dibya (Saha Dibya)	2SGA-4
Prete, Gabriela	3Pos214	Sahashi, Kentaro (佐橋 健太郎)	1GH001
Priyambada, Kamila Putridifa (Priyambada Putridifa		Saini, Mohit. K. (Saini Mohit. K.)	2Pos138
Kamila)	1GE002	Saio, Tomohide	3Pos219
Prosser, Robert Scott	2SBA-1	Saio, Tomohide (齋尾 智英)	2SHP-2
Purba, Endang R. (Purba Endang R.)	2Pos138		3SEA-4
Putera, Fachruddin Hari Anggara	3Pos168	Saito, Ami (齋藤 碧海)	2Pos107
Pyo, Ki Eun	3Pos122	Saito, Atsushi (齋藤 敦)	1EC001
Quang Vu, Cong	1Pos208	Saito, Hikaru (齋藤 光)	1Pos127
Quirin, Sean	3Pos122	Saito, Hiroyuki (齋藤 博幸)	1Pos012
Rabe von Pappenheim, Fabian (Rabe von Pappenheim			1Pos022
Fabian)	1MSG-5	Saito, Katsuya (齋藤 克哉)	3Pos164
Rafidah, Izzati (ラフィダー イッサティ)	1GG012	Saito, Keisuke (齋藤 圭亮)	2SJA-1
Rafiq, Nisha Mohd (ニーシャ モハド ラフィク)	1EC001	Saito, Keiya (齋藤 啓哉)	1Pos016
Rajendran, Divya (Rajendran Divya)	2Pos029	Saito, Kohei (齋藤 康平)	1Pos203
Ramakrishnan, Charu	3Pos122		1Pos204
Rashid, Rubaya	1EA004	Saito, Makoto (齋藤 諒)	1SDA-5
Rattanasombat, Petlada	3Pos039	Saito, Minoru (齋藤 稔)	3Pos118
Raul, Emilio Macias Estrada (RAUL Emilio Macias		Saito, Nen (斉藤 稔)	2SFA-5
Estrada)	1Pos065		1Pos194
Razavi, Shiva	3Pos078		1Pos195
Razib, Datta	2SFA-4		2Pos124
Re, Suyong (李 秀榮)	1EE001	Saito, Ren (齋藤 蓮)	3Pos197
Reja, Shahi Imam (レジャ シャヒ イمام)	2Pos215	Saito, Takumi (齋藤 匠)	2SIP-2
Ren, Weitong (任 衛同)	3SAA-3		3Pos076
	2Pos008	Saito, Yasuhisa (齋藤 保久)	2Pos196
Rerganan, Pattarisa (ルークアナン パッタリサー)	3Pos016	Saito, Yutaka (齋藤 裕)	2SCA-3
			1MSI-1
Rhee, Hyun-woo	1Pos040		1GE008
Ries, Jonas	1MSF-2	Saitoh, Akiyoshi (齋藤 顕宜)	1Pos185
Rimbara, Emiko (林原 絵美子)	1GD006	Saitoh, Tsuyoshi (斉藤 毅)	1GA008
Rindfleisch, Sören (Rindfleisch Sören)	1MSG-5	Saitou, Shinnosuke (齋藤 真之介)	1GE002
Robinson, Robert	2Pos147	Saitou, Suzuka (齋藤 涼華)	1Pos182
Robinson, Robert (ロビンソン ボブ)	1Pos092	Sakae, Mao (栄 真央)	3Pos162
Robinson, Robert C. (Robert C. Robinson)	1MSG-3	Sakae, Yoshitake (榮 慶丈)	1GH001
Robinson, Robert Charles	2SCP-2	Sakaguchi, Ayuri (坂口 歩理)	1Pos101
Romain, Amyot (Romain Amyot)	2Pos067	Sakaguchi, Miyuki (坂口 美幸)	1Pos051
Royant, Antoine	2Pos133		1Pos205
	1YK1115	Sakaguchi, Wataru (坂口 航)	3Pos004
Rozenberg, Andrey	1GI002	Sakaguchi, Yuya (阪口 裕哉)	3HL1045
Rozenberg, Andrey (Rozenberg Andrey)	1Pos125	Sakai, Gaku (坂井 岳)	3Pos026
Ruan, Xiaomi (阮 曉米)	3HL1015	Sakai, Hayata (酒井 颯太)	3Pos136

Sakai, Kazumi	2SJA-4	Sano, Yutaka (佐野 豊)	2Pos029
Sakai, Kazumi (酒井 佳寿美)	2Pos131	Saper, Gadiel	2Pos093
Sakai, Keisuke (坂井 恵輔)	2Pos087	Sasaki, Daiki (佐々木 大樹)	1EC003
Sakai, Makoto (酒井 誠)	2Pos199	Sasaki, Daisuke (佐々木 大輔)	1GC011
	3Pos199		3Pos058
Sakai, Yusuke (酒井 祐輔)	1Pos124	Sasaki, Kodai (佐々木 洸大)	1GG011
Sakai, Yusuke (酒井 雄介)	1Pos034	Sasaki, Mirai (佐々木 弥来)	1GG002
Sakakibara, Haruki (榊原 晴希)	3Pos024	Sasaki, Naoya (佐々木 直哉)	2Pos201
Sakakura, Terutoshi	1MSH-2	Sasaki, Risa (佐々木 里瑳)	3SFA-2
Sakamoto, Ayu (坂本 亜優)	3Pos053	Sasaki, Takanori (佐々木 貴規)	1Pos162
Sakamoto, Kantaro (坂本 貫太郎)	3Pos023		1Pos163
Sakamoto, Ritsuki (坂本 璃月)	1Pos019		1Pos164
Sakamoto, Ryota (坂本 遼太)	1SIA-6	Sasaki, Yuji. C (佐々木 裕次)	1GC011
Sakamoto, Tatsuya (坂本 達哉)	2Pos145	Sasamori, Kansuke (笹森 貴佑)	2Pos194
Sakamoto, Yuta (阪本 悠太)	1Pos219	Sato, Chikara (佐藤 主税)	3Pos164
Sakane, Reibun (坂根 礼文)	3Pos107	Sato, Daisuke (佐藤 大輔)	1GA013
Sakanoue, Rin (坂上 凜)	1Pos094		1Pos016
	1YK1100	Sato, Hajime (佐藤 玄)	1Pos183
Sakashita, Nanase (坂下 七瀬)	2Pos185	Sato, Hikari (佐藤 光利)	3Pos008
Sakata, Ayaka	3SGA-3	Sato, Hisako (佐藤 久子)	1Pos015
Sakata, Eri (坂田 絵理)	1MSG-5	Sato, Imari (佐藤 いまり)	1Pos211
Sakata, Nana (阪田 奈菜)	2Pos015	Sato, Katsuhiko (佐藤 勝彦)	3Pos120
Sakata, Nana (阪田 菜奈)	1Pos025	Sato, Katsuki (佐藤 克樹)	1Pos031
Sakaue, Takahiro (坂上 貴洋)	1GB012	Sato, Kazuhisa (佐藤 和久)	2Pos206
	1Pos219	Sato, Kazunobu (佐藤 和信)	3Pos055
	1Pos220	Sato, Keisuke (佐藤 慶典)	1Pos114
	2Pos060	Sato, Keita (佐藤 恵太)	2SJA-5
	2Pos220		1Pos129
Sako, Yasushi (佐甲 靖志)	1Pos003		2Pos129
	2Pos099		2Pos132
	1GC003		3Pos127
Sakuma, Koya (佐久間 航也)	2Pos054	Sato, Riho (佐藤 璃歩)	3Pos001
Sakuma, Tatsumi (佐久間 達海)	1Pos111	Sato, Ryu (佐藤 龍)	1GG007
Sakuma, Yuka (佐久間 由香)	2SIP-5	Sato, Shoko	3Pos056
Sakumura, Yuichi (作村 諭一)	1GG006	Sato, Shoko (佐藤 祥子)	1Pos041
	1Pos088	Sato, Shumpei (佐藤 駿平)	3Pos146
	1Pos155	Sato, Shun (佐藤 駿)	2Pos081
	1Pos192	Sato, Suguru (佐藤 優)	1Pos151
	1Pos193	Sato, Taiyo (佐藤 大洋)	3Pos067
Sakuraba, Syun (桜庭 俊)	3Pos138	Sato, Yuki (佐藤 優輝)	1Pos203
	3Pos139	Sato, Yuki (佐藤 夕希)	1Pos123
Sakurai, Akari (櫻井 あかり)	2Pos150		3Pos115
Sakurai, Kazumasa (櫻井 一正)	3Pos013	Sato, Yusei (佐藤 優成)	1GF010
Sakurai, Tatsunari (櫻井 建成)	1GD003		1Pos151
Sakuta, Hiroki (作田 浩輝)	2Pos155	Sato, Yusuke (佐藤 佑介)	1GJ004
	3Pos149		2Pos118
Salvatore, Corrado	1GI011		3Pos217
Samatsu, Yuki (佐松 優希)	1Pos126	Satou, Hazime (佐藤 玄)	2Pos161
Sampson, Josephina (サンブソン ジョセフィナ)	2Pos098	Satouh, Yuhkoh (佐藤 裕公)	2Pos080
	3Pos175	Sawa, Masato (澤 征都)	1Pos210
Sando, Shinsuke (山東 信介)	2Pos073	Sawada, Yasuyuki (澤田 康之)	2Pos115
Sano, Taisei (佐野 太星)			2Pos117

Sawai, Satoshi (澤井 哲)	1Pos099				3Pos070
Sawazaki, Yoshihito (澤崎 義仁)	3Pos191			Shigeta, Yasuteru (重田 育照)	1GH003
Schmidt, Roman	1MSF-2				1Pos020
Schmitt, Cassidy	2Pos031				1Pos172
Schwitter, Ariane (スクウイター アリアナ)	1GF008				1Pos184
Seddon, Chloe (Seddon Chloe)	2Pos005				2Pos179
	1YK1030			Shih, Hsuan-Yu (Shih Hsuan-Yu)	1Pos007
Sega, Jumpei (瀬賀 純平)	3Pos080			Shihoya, Wataru (志甫 谷 渉)	3Pos142
Seito, Daito (清藤 大翔)	1Pos148			Shima, Tomohiro (島 知弘)	2Pos102
Seki, Soichiro (関 莊一郎)	2SGP-6			Shimada, Akari (島田 明星)	3HL1115
	1Pos006			Shimada, Atsuhiro (島田 敦広)	1GF009
Seki, Takehito (関 健仁)	1Pos116			Shimada, Kazuki (島田 和樹)	1GH006
Sekiyama, Naotaka (関山 直孝)	2Pos040			Shimada, Yoshiki (島田 佳季)	1GD006
Semwal, Vivek	2Pos094			Shimada, Yuichiro (嶋田 友一郎)	1Pos141
Sengoku, Sakura (仙石 桜)	2Pos120			Shimakawa, Ginga (嶋川 銀河)	3Pos010
Senju, Yosuke (千住 洋介)	2Pos114			Shimamoto, Kana (島本 花菜)	3Pos087
Sergeev, Nikolay	1MSF-2			Shimamoto, Keiko (島本 啓子)	1Pos117
Seto, Mayumi (瀬戸 繭美)	3SFA-2			Shimamoto, Shigeru (島本 茂)	1Pos025
Shen, Jian-Ren (沈 建仁)	1MSG-3				1Pos026
	1GI008				1Pos027
	1Pos135				2Pos015
	2Pos136				3Pos019
Shen, Simiao (潘 思淼)	3Pos126				3Pos020
Shenoy, Thanh-Nga C.	3Pos122			Shimamoto, Yuta (島本 勇太)	1SIA-1
Shi, Jenny	3Pos122				1Pos094
Shiba, Tomoo (志波 智生)	1GA001				1YK1100
	1GA004			Shimamura, Hisashi (嶋村 悠)	1GB012
	1GA006			Shimamura, Ryotaro (嶋村 亮太郎)	1Pos142
Shibagaki, Mitsuki (柴垣 光希)	1MSG-1			Shimamura, Saya (島村 冴矢)	3HL1045
Shibai, Atsushi (芝井 厚)	3Pos146			Shimamura, Yuiki (島村 惟葵)	3Pos135
Shibasaki, Ryota (芝崎 亮汰)	2Pos180			Shimane, Yasuhiro (嶋根 康弘)	3SFA-3
Shibata, Kei (柴田 圭)	1Pos102			Shimazaki, Yukihiko (嶋崎 幸穂)	2Pos068
Shibata, Keisei (柴田 桂成)	3SBA-9			Shimbo, Ayaka (新保 綾花)	1Pos186
Shibata, Keitaro (柴田 桂太郎)	2SFA-2			Shimi, Takeshi	1Pos095
	3Pos083			Shimi, Takeshi (志見 剛)	1Pos199
Shibata, Mikihiro (柴田 幹大)	1GD010			Shimizu, Hirofumi (清水 啓史)	3Pos044
	1GD011			Shimizu, Kazuma (清水 和真)	1GD007
	1Pos041			Shimizu, Kotaro (清水 浩太郎)	1GF005
	1Pos114			Shimizu, Masahiro (清水 将裕)	2Pos032
	3Pos028			Shimizu, Miho (清水 美穂)	3Pos089
Shibata, Tatsuo	2Pos094			Shimizu, Rei	2Pos202
Shibata, Tatsuo (柴田 達夫)	2SFA-3			Shimizu, Rumi (清水 瑠美)	1MSH-6
	2SEP-7			Shimizu, Sasa (清水 早沙)	3Pos098
	1Pos196			Shimizu, Yoshihiro (清水 義宏)	2SHA-2
Shibata, Yutaka (柴田 穰)	1Pos134				1GJ001
	3Pos134			Shimizu, Yosuke (清水 洋祐)	2Pos028
	3Pos135			Shimizume, Kota (清水目 孝太)	2Pos096
	3Pos136			Shimoaka, Takafumi (下赤 卓史)	1Pos108
Shibayama, Naoya (柴山 修哉)	1Pos043				1Pos133
Shiga, Yasuhiro (志賀 靖弘)	2Pos131			Shimogochi, Shota (下河内 翔太)	1SBA-1
Shigematsu, Hideki (重松 秀樹)	2SHP-7				2Pos171
	2Pos190			Shimogoochi, Shota (下河内 翔太)	2Pos049

Shimomae, Koki (下前 弘稀)	3Pos139	Shirouzu, Mikako (白水 美香子)	2Pos010
Shimono, Kazumi (下野 和美)	2Pos047	Shirranc, Sally (Shirranc Sally)	2Pos005
Shimoyama, Hiromitsu (下山 紘充)	2Pos022		1YK1030
Shimura, Naoki (志村 直輝)	3Pos107	Shoji, Hiroto (庄司 紘都)	1GD005
Shin, Byeongmin	2SKA-1	Shoji, Kan (庄司 観)	1EB004
Shin, Fujishiro (藤城 新)	2Pos061		1Pos159
Shinkai, Arisa (新開 有紗)	1GA008		2Pos118
Shinkai, Soya (新海 創也)	1SEA-3	Shoji, Kentaro (庄司 健太郎)	1Pos154
Shinkai, Yasuhiro (新開 泰弘)	1Pos119	Shoji, Tomoya (庄司 智哉)	2Pos084
Shinobu, Ai	1Pos170	Shono, Mayu (庄野 真由)	1Pos157
Shinobu, Ai (信夫 愛)	2SFP-2		2Pos057
	2Pos050	Shota, Tsuji (辻 章太)	1Pos065
Shinoda, Wataru (篠田 渉)	1GF007	Simpson, David	2SJP-1
	1GG001	Singh, Manish (Singh Manish)	1GI006
	3Pos105	Singha, Nanki (Singha Nanki)	2Pos005
	3Pos166		1YK1030
Shinohara, Akira (篠原 彰)	3Pos087	Skinner, Dominic (Skinner Dominic)	2SGA-4
Shinozaki, Ryuto (Shinozaki Ryuto)	1SHA-4	Skinner, Dominic J.	1Pos201
Shintaku, Hirofumi (新宅 博文)	3SHA-2		1YK1000
Shintani, Seine A. (新谷 正嶺)	1EC004	Sljoka, Adnan	2SBA-1
Shinya, Kumagai (熊谷 慎也)	2Pos217		2SBA-6
Shinzawa-Ito, Kyoko (新澤 伊藤 恭子)	1Pos139	So, Masatomo (宗 正智)	2SBP-4
Shinzawa-Itoh, Kyoko (伊藤・新澤 恭子)	1Pos044	Sobaih, Mohamed Marzouk (ソベ モハメド マルゾー	2Pos050
Shioda, Norifumi (塩田 倫史)	2Pos052	ク)	1GE007
Shioi, Akihisa (塩井 章久)	1Pos157	Sobti, Meghna (Sobti Meghna)	2Pos115
Shioi, Takuro (塩井 琢郎)	2SAP-3	Sokabe, Masahiro (曽我部 正博)	2Pos117
Shiomi, Akifumi (塩見 晃史)	3SHA-2		1SFA-4
Shiomi, Gaku (塩見 岳)	3HL0915	Sonani, Ravi (Sonanic Ravi)	2Pos005
Shiomi, Shunsuke (汐見 駿佑)	2Pos156		1YK1030
	3Pos152	Sono, Hidekazu (園 英和)	1Pos082
Shionyu, Masafumi (塩生 真史)	3Pos160	Sonobe, Seiji (園部 誠司)	2Pos210
Shiota, Yuma (塩田 優真)	1SBA-1	Sonoshita, Masahiro	1Pos108
	2Pos171	Sonoyama, Masashi (園山 正史)	1Pos133
Shiraga, Keiichiro (白神 慧一郎)	3Pos206	Soshino, Ibuki (曾篠 一蒔)	2Pos029
Shirahama, Ranmaru (白浜 蘭丸)	1Pos143	Sotoma, Shingo (外間 進悟)	1GJ006
Shirai, Tsuyoshi (白井 剛)	3SBA-7	Sowa, Yoshiyuki (曾和 義幸)	2Pos084
	2Pos148		2Pos157
	3Pos131		3Pos093
Shiraishi, Taro (白石 太郎)	1GH012	Stenhammar, Joakim	2SEP-6
Shiraiwa, Hiromasa (白岩 弘将)	2Pos156	Stewart, Alastair G. (Stewart Alastair G.)	1GE007
	3Pos152	Stokes, David L.	1EE002
Shiraki, Kentaro (白木 賢太郎)	2Pos153	Sudo, Yuki (須藤 雄気)	2Pos132
	2Pos214		3Pos125
	1YK1015		3Pos126
Shiramasa, Yutaro (白砂 雄太郎)	1GB004	Suenaga, Naoki (末永 尚基)	1Pos139
Shirasaki, Yoshitaka (白崎 善隆)	1EB005	Suetaka, Shunji (季高 駿士)	1GC009
Shiro, Yoshitsugu (城 宜嗣)	3Pos042		1GC010
	3Pos046		3Pos033
Shiroguchi, Katsuyuki	1GJ011	Suetake, Isao (末武 勲)	3Pos055
Shiroguchi, Katsuyuki (城口 克之)	2SDP-1	Suetsugu, Shiro (末次 志郎)	1SFA-1
Shiroshita, Honori (城下 穂乃里)	1Pos022		
Shirota, Hideaki (城田 秀明)	1GA010		

Sugai, Hiroka (菅井 祥加)	2SDA-3	Sumikama, Takashi (炭竈 享司)	2SAA-4
Sugao, Kanon (菅尾 果音)	3Pos019		1GD010
	3Pos020		1GD011
Sugasawa, Haruka (菅澤 はるか)	3Pos008	Sumino, Ayumi (角野 歩)	1Pos215
	3Pos025	Sumitomo, Kakeru (住友 翔)	1Pos084
	3Pos037	Sumiyoshi, Rieko (住吉 里英子)	1Pos077
Sugase, Kenji (菅瀬 謙治)	2SBP-4		1YK1045
Sugata, Daiki (菅田 大輝)	1Pos061		1Pos151
Sugawara, Ren (菅原 蓮)	3Pos023		2Pos073
Sugawara, Takeshi (菅原 武志)	3Pos193	Sunaga, Junko (須長 純子)	2SFA-7
Sugi, Takuma (杉 拓磨)	2SJP-2	Sunami, Tomoko	3Pos056
	1GJ010	Sunami, Tomoko (角南 智子)	2SAP-1
Sugie, Atsushi (杉江 淳)	2SBP-6		1MSH-4
Sugihara, Kaori	1GF004	Suno, Chiyo (寿野 千代)	1GA009
	1ED002	Suno, Ryoji	2Pos048
	2Pos198	Suno, Ryoji (寿野 良二)	1GA009
Sugihara, Kaori (杉原 加織)	1GF003		1GI005
	1GF008		2Pos004
	1GF011	Suno-Ikeda, Chiyo	2Pos048
	2Pos034	Suwa, Makiko (諏訪 牧子)	3Pos156
Sugijo, Yovin (洲砥恕 葉浮音)	3Pos021		3Pos164
Sugimoto, Hiroshi (杉本 宏)	3Pos041	Suwa, Manami (諏訪 麻菜美)	2Pos014
	3Pos042	Suzuki, Aussie (Suzuki Aussie)	1Pos094
	3Pos046		1YK1100
Sugimoto, Hisroshi (杉本 宏)	3Pos045	Suzuki, Daiki (鈴木 大樹)	2Pos168
Sugimoto, Teppei (杉本 哲平)	3Pos140	Suzuki, Hinako X. (鈴木 日奈子)	2Pos178
Sugimoto, Yukihiro (杉本 幸裕)	1Pos183	Suzuki, Kano (鈴木 花野)	1Pos010
Sugishiata, Tomoaki (杉下 友晃)	3Pos055		3Pos073
Sugita, Masatake (杉田 昌岳)	2Pos175	Suzuki, Kenichi (鈴木 健一)	2SDA-4
Sugita, Yuji	1Pos179	Suzuki, Kenichi G. N. (鈴木 健一)	1SFA-2
Sugita, Yuji (杉田 有治)	1SBA-2		1GF002
	2SAA-3	Suzuki, Kenichi G.N. (鈴木 健一)	3Pos104
	2SAA-6	Suzuki, Kenichi GN (鈴木 健一)	1EC003
	2SHP-3	Suzuki, Kenta T. (鈴木 健大)	1GG006
	1GE011	Suzuki, Madoka	3Pos085
	1Pos028	Suzuki, Madoka (鈴木 団)	1Pos216
	2Pos041		2Pos098
	2Pos177	Suzuki, Makoto (鈴木 誠)	1Pos070
	2Pos187	Suzuki, Masato (鈴木 允人)	2Pos151
	3Pos165	Suzuki, Michio (鈴木 道生)	1GB009
Sugita, Yukihiro (杉田 征彦)	1GI005	Suzuki, Naoya (鈴木 直哉)	1Pos122
Sugiura, Kazunori (杉浦 一徳)	2Pos038	Suzuki, Nobuhiro (鈴木 喜大)	3HL1130
	3Pos205		2Pos014
Sugiura, Masahiro (杉浦 雅大)	1GI004		3Pos016
	3Pos122	Suzuki, Nobutake (鈴木 信勇)	1EB005
Sugiura, Yuya (杉浦 勇也)	1GA009	Suzuki, Ryunosuke (鈴木 龍之介)	1GG005
Sugiyama, Haruki	1MSH-2	Suzuki, Shino (鈴木 志野)	2SKP-1
Sugiyama, Hironori (杉山 博紀)	3SHA-5	Suzuki, Shota (鈴木 翔大)	2SBA-4
	3Pos197		1Pos002
Sugiyama, Masaaki (杉山 正明)	1GB007	Suzuki, Souta (鈴木 爽太)	1Pos100
	1GB009	Suzuki, Taisei (鈴木 大晴)	1GD010
	1Pos019	Suzuki, Takao (鈴木 誉保)	2Pos149

Suzuki, Takehiro (鈴木 健裕)	1Pos138	1Pos069
	1Pos141	2Pos170
Suzuki, Tateki (鈴木 干城)	2Pos031	3Pos057
Suzuki, Tetsuhito (鈴木 哲仁)	3Pos206	1Pos121
Suzuki, Tsutomu (鈴木 勉)	2Pos204	1Pos055
Suzuki, Yuki (鈴木 勇輝)	3Pos053	3Pos072
Suzuki, Yukihito (鈴木 文丈)	1GG006	3Pos110
Tabata, Kazuhito (田端 和仁)	1Pos097	3Pos136
Tabata, Koji	2Pos210	3HL1015
Tabata, Yota (田端 陽多)	3Pos144	1Pos108
Tabe, Jinichiro (多部 仁一朗)	1Pos146	1GH011
Tachi, Tomohiro (館 知宏)	2Pos007	3Pos179
Tachikawa, Masashi (立川 正志)	2Pos189	3HL0915
	3Pos108	1MSG-3
Tadokoro, Yoshitaka (田所 良崇)	2Pos174	2Pos047
Tagami, Daiki (田上 大輝)	3HL1130	3Pos051
Tagami, Shunsuke	1GC006	2Pos199
Tagami, Shunsuke (田上 俊輔)	2SEA-1	3Pos199
Tagawa, Haruna (田川 晴奈)	2SIP-5	1Pos107
Tagawa, Hauna (田川 晴奈)	1Pos192	1Pos108
Tagawa, Shotaro (田川 翔大朗)	3SFA-6	3Pos101
Tagishi, Ryouma (田岸 亮馬)	3Pos009	1Pos125
Taguchi, Hideki (田口 英樹)	2SIA-3	1GI002
	1Pos042	3Pos022
Taguchi, Kazuma (田口 主馬)	3HL0900	3Pos112
Taguchi, Mai (田口 真衣)	1GE008	2SAP-5
Taguchi, Masahiko (田口 真彦)	3Pos050	2Pos062
	3Pos138	1YK0945
	3Pos139	2Pos132
Taguchi, Seiichi (田口 精一)	1SFA-3	1GJ010
Tahara, Shinya (田原 進也)	3Pos183	1GC001
Tahara, Tahei (田原 太平)	1Pos205	3SJA-1
Tahara, Yuhei (田原 悠平)	3Pos209	2Pos164
Tahara, Yuhei O (田原 悠平)	3Pos148	1GB005
Taji, Teruaki (太治 輝明)	2Pos120	1GE002
Tajima, Hirotaka (田島 寛隆)	2Pos119	2Pos029
	3Pos114	2Pos031
Tajima, Kenya (田島 研也)	1Pos034	1Pos119
Tajima, Seiya (但馬 聖也)	1GI004	1Pos133
	2Pos006	1Pos182
	3Pos122	1Pos168
Tajima, Shuma (田島 秀真)	2Pos004	1Pos171
Tajitsu, Motoharu (田實 元陽)	3Pos161	1Pos174
Takabatake, Haru (高島 晴)	2SIA-3	1Pos175
Takada, Sakura (高田 咲良)	2Pos155	3Pos173
Takada, Sakura (高田 咲良)	2SKP-3	3Pos145
Takada, Shoji	3Pos047	3Pos181
Takada, Shoji (高田 彰二)	1SAA-3	3Pos135
	2SBP-1	1Pos119
	1MSG-6	1MSF-3
	1GC003	1GE012
	1Pos061	
Takagaki, Natsune (高垣 菜式)		
Takagi, Kanta (高木 幹太)		
Takagi, Ken (高木 堅)		
Takagi, Kohta (高木 鴻太)		
Takagi, Koki (高木 洸希)		
Takagi, Kosuke (高木 宏輔)		
Takagi, Toshiyuki (高木 俊之)		
Takagi, Yusuke (高木 悠丞)		
Takahara, Yuma (高原 佑真)		
Takahashi, Daichi (高橋 大地)		
Takahashi, Daisuke (高橋 大輔)		
Takahashi, Fumio (高橋 文雄)		
Takahashi, Hirona (高橋 広奈)		
Takahashi, Hiroshi (高橋 浩)		
Takahashi, Hiroto (高橋 大翔)		
Takahashi, Hiroto (高橋 大翔)		
Takahashi, Kaoru (高橋 郁)		
Takahashi, Kazumo (高橋 風雲)		
Takahashi, Koichi (高橋 恒一)		
Takahashi, Kuto (高橋 空翔)		
Takahashi, Manami (高橋 真奈美)		
Takahashi, Nao (高橋 尚央)		
Takahashi, Nozomu (高橋 望)		
Takahashi, Remii (高橋 怜見衣)		
Takahashi, Satoshi (高橋 聡)		
Takahashi, Shigeru (高橋 滋)		
Takahashi, Shota (高橋 渉太)		
Takahashi, Takuya (高橋 卓也)		
Takahashi, Takuya (高橋 卓也)		
Takahashi, Tomoei (高橋 智栄)		
Takahashi, Yoshimasa		
Takahashi, Yuichiro (高橋 裕一郎)		
Takahashi, Yuji (高橋 勇二)		
Takai, Akira (高井 啓)		
Takamatsu, Nobumichi (高松 宣道)		

Takano, Kazunori (高野 和儀)	1Pos089	Takemura, Masaharu (武村 政春)	2SKP-2
Takano, Kento (高野 健人)	2Pos125	Takenaka, Shinji (竹中 慎治)	2Pos138
Takano, Mistunori (高野 光則)	2Pos184		2Pos140
Takano, Mitsunori (高野 光則)	1Pos072	Takeno, Yuka E. (竹野 有香)	1GI004
	2Pos024	Takeshima, Gento (竹島 源斗)	3Pos076
	2Pos063	Takeuchi, Chihiro (竹内 千尋)	1Pos065
	2Pos078		3Pos062
Takano, Yu (鷹野 優)	3Pos177	Takeuchi, Dai (竹内 大)	3Pos128
Takao, Daisuke (高尾 大輔)	1Pos079	Takeuchi, Koh (竹内 恒)	2Pos058
Takarada, Masaharu (寶田 雅治)	3Pos203	Takeuchi, Nahoko (武内 菜穂子)	3HL0900
Takaramoto, Shunki (宝本 俊輝)	1GI009	Takeuchi, Noriko (竹内 法子)	1Pos068
	1Pos125	Takiguchi, Kingo (瀧口 金吾)	2Pos090
Takaramoto, Shunki (寶本 俊輝)	1GI002		2Pos112
	1GI004		2Pos113
Takasawa, Taichi (高澤 太一)	2Pos002	Takinoue, Masahiro	3Pos149
Takase, Ryoya (高清 稜也)	2Pos103	Takinoue, Masahiro (瀧ノ上 正浩)	1EA003
Takase, Yurina (高瀬 祐理菜)	3HL0945		2SKP-6
Takase, Yuzuki (高瀬 悠月)	3Pos175		1Pos053
Takashima, Yui (高島 柚衣)	3HL1000		1Pos054
Takaso, Nanato (高相 虹翔)	3Pos215		1Pos055
Takasu, Atsushi (鷹巣 篤志)	1Pos094		2Pos054
	1YK1100		2Pos056
Takata, Koji (高田 耕児)	2Pos214		2Pos057
	1YK1015		3Pos052
Takatsuka, Hiroto (高塚 大知)	1SDA-4	Takizawa, Yoshimasa (滝沢 由政)	2SAP-3
Takayama, Yuki (高山 裕貴)	1GG008	Takizuka, Hiroto (瀧塚 寛音)	1Pos145
	2Pos213	Takui, Takeji (工位 武治)	3Pos055
Takayama, Yuto (高山 優翔)	1Pos204	Takuwa, Hiroyuki (田桑 弘之)	1GJ010
Takazaki, Hiroko (高崎 寛子)	3Pos044	Tama, Florence	2SAA-7
Takazaki, Hiroko (高崎 寛子)	3Pos087		3Pos039
Takazawa, Momoka (高沢 桃花)	2Pos036		3Pos176
Takebe, Gen (建部 厳)	1Pos013		3Pos178
Takebe, Masumi (建部 益美)	3Pos138		3Pos180
	3Pos139	Tama, Florence (Tama Florence)	2Pos190
Takeda, Seiji (武田 晴治)	1Pos018		3Pos027
	2Pos030	Tamada, Taro (玉田 太郎)	1MSH-6
Takeda, Shuichi (武田 修一)	1Pos091	Tamai, Shingo (玉井 真悟)	1Pos214
	1Pos092		1YK0930
	1Pos093	Tamaki, Kenta (玉木 健太)	1Pos153
Takeda, Youtaro (武田 陽太郎)	3Pos179	Tamano, Tomoaki (玉野 智章)	2Pos022
Takeguchi, Miki (竹口 未来)	3Pos129	Tambo, Mai (端保 舞)	1Pos215
Takei, Kohji (竹居 孝二)	1Pos212	Tame, Jeremy R.H.	1Pos005
Takei, Riku (武井 陸)	2Pos119	Tamogami, Jun (田母神 淳)	2Pos130
Takei, Toshiaki (武居 俊樹)	3Pos055		3Pos129
Takekawa, Norihiro (竹川 宜宏)	1GF012	Tamura, Hideki (田村 英紀)	1Pos180
	1Pos045		2Pos181
	1Pos080	Tamura, Hiroki (田村 洋樹)	3Pos206
	2Pos071	Tamura, Itaru (田村 格良)	1MSH-6
	2Pos075	Tamura, Ryota (田村 遼太)	1GE009
	3Pos007	Tamura, Sachiko (田村 佐知子)	2SAP-5
	3Pos077		2Pos062
Takemori, Kenta (竹森 健太)	2Pos077		1YK0945

Terui, Yudai (照井 雄大)	3Pos038	Toshimori, Kiyotaka (年森 清隆)	1Pos079
Teshima, Taku (手嶋 琢)	3Pos128	Toshino, Kenta (歳納 健太)	1Pos075
Teshirogi, Yosuke (手代木 陽介)	2Pos184	Toshioka, Fumi (利岡 文美)	1Pos035
Tetsunari, Kimura (木村 哲就)	1GA004	Tostani, Fofou Yonta	1Pos078
Tezuka, Ataru (手塚 陽琉)	1GH008	Toyabe, Shoichi (鳥谷部 祥一)	1Pos074
Thi Ngoc Nguyen, Loan	3Pos041		3Pos072
Thiel, Vera (Thiel Vera)	3HL0930	Toyama, Rene (外山 玲音)	1Pos051
Thiticharoentam, Chayanit	1Pos208	Toyoda, Atsushi (豊田 敦)	2SAP-5
Thiyagarajan, Dhivya B.	2Pos138		1GD009
Timonen, Jaakko V. I.	3Pos187		1Pos121
Tinguely, Jean-Claude	3SAA-4		2Pos062
Tittmann, Kai (Tittmann Kai)	2SEP-6		1YK0945
Tochio, Hidehito (柊尾 豪人)	3SAA-2	Toyoda, Yusei (豊田 裕生)	3Pos046
	1MSG-5	Toyonaga, Takuma (豊永 拓真)	3Pos066
	2Pos003	Toyooka, Ryuya (豊岡 龍弥)	2Pos007
	2Pos040	Toyoshima, Fumiko (豊島 文子)	2Pos200
	2Pos045	Toyoshima, Yu (豊島 有)	2SDP-2
	2Pos052	Toyota, Taro (豊田 太郎)	2Pos158
	3Pos003	Traiphothon, Darunee	2Pos188
Tochio, Naoya (柊尾 尚哉)	2Pos041	Tran, Duy (チャンズイ)	2SFP-3
Toda, Hirofumi (戸田 浩史)	1SDA-6	Tran, Duy Phuoc	2SBA-4
Toda, Satoshi (戸田 聡)	2SEA-3		1GH004
	2Pos067		2Pos183
Todaka, Reiko (戸高 玲子)	2Pos001	Tran, Duy Phuoc Tran	2SBA-1
Togashi, Yuichi (富桵 祐一)	1Pos177	Tran, Linh	2Pos147
	1Pos189	Tran, PhuocDuy	2Pos039
	1Pos190	Trebbia, Jean-Baptiste	1SHA-3
Togo, Azusa (都甲 梓)	2Pos153	Tsai, Chieh-Yu (蔡 傑宇)	2SBP-2
Tohru, Terada (寺田 遼)	2Pos161	Tsai, Feng-Ching	2Pos114
Toji, Takumi (田路 卓巳)	1Pos068	Tsai, Ming-Daw	2Pos133
Tojo, Yoshihiro (東條 義大)	3Pos133		1YK1115
Tokita, Kei (時田 恵一郎)	3Pos145	Tsai, Pi-Cheng (蔡 弼丞)	2Pos136
Tokonami, Shunro (床次 俊郎)	2Pos027	Tseng, Ching-yu	1GA007
Tokuhisa, Atsushi (徳久 淳師)	1SAA-4	Tsubaki, Motonari (鐸木 基成)	3Pos045
Tokunaga, Etsuko (徳永 恵津子)	1Pos030	Tsuboi, Hazuki (坪井 葉月)	1Pos065
Tokunaga, Yuji (徳永 裕二)	2Pos058	Tsuchida, Arata (土田 新)	3SHA-2
Tokuraku, Kiyotaka (徳樂 清孝)	2SCP-5	Tsuchida, Misaki (土田 美咲)	1GC002
Tokutsu, Ryutaro (得津 隆太郎)	1Pos134	Tsuchihashi, Shuhei (土橋 周平)	3Pos124
Tokuyasu, Ayama (徳安 礼磨)	3Pos090	Tsuchiya, Wataru (土屋 渉)	3Pos198
Toma, Sachiko (藤間 祥子)	1Pos017	Tsuchiya, Yuko (土屋 裕子)	1SBA-3
Toma-Fukai, Sachiko (藤間 祥子)	1GA003		3Pos131
	2Pos127	Tsuda, Sakae (津田 栄)	1GA011
Tominaga, Daichi (富永 大智)	3Pos217		1GG009
Tominaga, Kanan (富永 果楠)	3Pos095		1Pos021
Tominaga, Yuri (富永 侑利)	1Pos124	Tsudome, Mikiko (津留 美紀子)	2Pos219
Tomioka, Yosuke (富岡 洋介)	2Pos213	Tsudzuki, Taiku (都築 大空)	1Pos109
Tomishige, Michio (富重 道雄)	1Pos071	Tsuji, Akihiro (辻 明宏)	1SEA-5
Tomita, Taisuke (富田 泰輔)	3Pos161		1Pos049
Tomoda, Yugo (巴田 侑吾)	2Pos100	Tsuji, Miho (辻 美帆)	2Pos217
Tomohara, Kanji (友原 貫志)	1GJ007	Tsuji, Shosei (辻 翔成)	3HL1015
Torii, Kotaro (鳥井 孝太郎)	3SHA-2	Tsuji, Yoshinori (辻 敬典)	3Pos010
Tosaka, Toshiyuki (登坂 俊行)	1GJ003	Tsujikawa, Koyo (辻河 高陽)	1GH001

Tsujimoto, Taiki (辻本 泰輝)	1Pos213	Udono, Hirotake (鵜殿 寛岳)	1Pos021
Tsujimura, Masaki (辻村 真樹)	2SJA-1	Ueda, Fuka (上田 楓華)	2SEP-2
	1GI004	Ueda, Kensuke (植田 健介)	2Pos009
	3Pos122	Ueda, Masahiro (上田 昌宏)	1Pos158
Tsujita, Kazuya (辻田 和也)	1Pos089	Ueda, Motoki (上田 一樹)	3Pos100
Tsujiuchi, Yutaka (辻内 裕)	1Pos203	Ueda, Toshiaki (上田 稔淳)	3SIA-2
	1Pos204	Ueda, Yuika (上田 唯花)	3Pos012
Tsukamoto, Hisao (塚本 寿夫)	1Pos129	Uegaki, Koichi (上垣 浩一)	2SIP-7
	1Pos178		1Pos026
	2Pos125		3Pos019
	2Pos132	Uehara, Shuta (上原 秀太)	2Pos011
Tsukamoto, Takashi (塚本 卓)	3Pos126	Ueki, Misuzu (植木 美鈴)	1Pos115
Tsukazaki, Tomoya (塚崎 智也)	1Pos031	Ueki, Shoko (植木 尚子)	3Pos084
Tsukui, Itta (津久井 一太)	1GB002	Uemura, Naoki (上村 直輝)	1GD006
Tsumoto, Kanta (湊元 幹太)	3Pos149		3Pos084
Tsuneshige, Antonio (常重 アントニオ)	2Pos044	Uemura, Sotaro (上村 想太郎)	3SGA-5
	2Pos148		1GC013
Tsunoda, Satoshi (角田 聡)	2SJA-3		2Pos204
	1Pos142		2Pos218
	1Pos146		3Pos057
	2Pos141	Ueno, Hiroshi (上野 博史)	1GA012
	3Pos142		1GE005
Tsunoda, Tatsuhiko (角田 達彦)	3SGA-5		1GE006
	2Pos204		1GE007
	2SGA-3		1GE008
Tsunoyama, Taka A.	1SHA-4		1GE009
Tsunoyama, Taka A. (角山 貴昭)	1Pos098		1Pos029
Tsunoyama, Taka-Aki	1Pos096		2Pos079
Tsunoyama, Taka-Aki (角山 貴昭)	1EC003	Ueno, Riki (上野 力樹)	2Pos184
Tsunoyama, Taka-aki (角山 貴昭)	1GA007	Ueno, Shingo (上野 真吾)	1Pos035
Tu, Le Ngoc Thao	3Pos062	Ueno, Taiji (上野 大慈)	1GB010
Tuboi, Hazuki (坪井 葉月)	2Pos191	Ueno, Takafumi (上野 隆史)	1Pos037
Tyukosova, Valentina	1Pos193		2Pos162
Uchida, Akane (内田 朱音)	1GF009	Ugarte La Torre, Diego Renato (ウガルテ ラ トレ)	
Uchida, Takeshi (内田 毅)	1Pos064	ディエゴ レナト)	1SBA-2
Uchida, Tsutomu (内田 努)	1GJ008	Ukai, Kotaro (鵜飼 幸太郎)	2Pos165
Uchida, Yumiko (内田 裕美子)	2Pos076	Ukawa, Mai (鵜川 真衣)	1Pos171
	2Pos084	Umakoshi, Takayuki (馬越 貴之)	1SCA-4
	2Pos100		1Pos200
	2Pos103		1SJA-1
	3Pos092	Umeda, Kenichi (梅田 健一)	1EB002
	3Pos213		2Pos051
Uchihashi, Takayuki	1SGA-7		3Pos029
Uchihashi, Takayuki (内橋 貴之)	1Pos031		3Pos040
	1Pos047		3Pos048
	1Pos153		3Pos207
	1Pos200	Umemura, Maiko (梅村 舞子)	2SCA-4
	1Pos212	Umemura, Mariko (梅村 真理子)	1Pos119
Uchikoga, Nobuyuki (内古閑 伸之)	1Pos160	Umena, Yasufumi (梅名 泰史)	1Pos030
Uchiyama, Tomo (内山 友)	1GE007	Umezawa, Haruka (梅澤 遥佳)	1Pos005
Uchizawa, Kaho (内澤 風穂)	1GA011		1Pos008
	1GG009	Umezawa, Koji (梅澤 公二)	3Pos012

Unabara, Daisuke (海原 大輔)	3Pos175	Warisaya, Kanata (割鞘 奏太)	2Pos007
Unno, Masashi (海野 雅司)	3Pos066	Washio, Takashi (鷺尾 隆)	3SGA-1
	1GI003	Washio, Takumi (鷺尾 巧)	2SFP-4
	2Pos128	Watanabe, Atsuya (渡辺 敦也)	1GC010
	2Pos130	Watanabe, Chiho (渡邊 千穂)	1Pos105
	2Pos201	Watanabe, Daisuke (渡邊 大介)	3Pos200
	3Pos123	Watanabe, Go (渡辺 豪)	2Pos002
Urano, Ryo (浦野 諒)	3Pos105	Watanabe, Hiroshi (渡邊 宙志)	3Pos186
Urui, Taito (潤井 泰斗)	2SJA-2	Watanabe, Kaito (渡邊 開斗)	3Pos116
Ushioda, Ryo (潮田 亮)	2SCP-7	Watanabe, Kento (渡邊 健人)	2Pos004
Ushioda, Suguru (潮田 優)	2Pos189	Watanabe, Kyosuke (渡辺 喬介)	3Pos134
Usuda, Hatsuho (臼田 初穂)	2Pos153	Watanabe, Maho (渡辺 真歩)	3Pos037
Usui, Kenji (臼井 健二)	1GA013	Watanabe, Mai (渡辺 麻衣)	3Pos137
Usuki, Shin (臼杵 深)	1GJ010	Watanabe, Masaya (渡部 誠也)	1GI004
Utada, Andrew	1GI011	Watanabe, Naoki (渡邊 直樹)	1SHA-1
	1GI012		1Pos207
Utada, Andrew S.	2Pos202	Watanabe, Naoko (渡邊 直子)	1Pos094
Uyeda, Taro (上田 太郎)	3Pos026		1YK1100
Uyeda, Taro Q.P. (上田 太郎)	1Pos075	Watanabe, Rikiya (渡邊 力也)	2Pos097
	3Pos022	Watanabe, Ryo (渡邊 亮)	1GE009
Vanderpoorten, Oliver	3SAA-6	Watanabe, Satoshi (渡部 聡)	2SHP-6
Vattulainen, Ilpo	2Pos114	Watanabe, Tomonobu (渡邊 朋信)	1Pos040
Vavylonis, Dimitrios	1Pos207	Watanabe, Tomonobu M (渡邊 朋信)	3SGA-6
Vavylonis, Dimitrios (Dimitrios Vavylonis)	1SHA-1	Watanabe, Toshiyuki (渡邊 敏行)	3Pos089
Voth, Gregory	2Pos114	Watanabe-Nakayama, Takahiro (中山 隆宏)	1SJA-2
Vu, Cong Quang (ブー コンクアン)	2Pos209		1GC001
Vu, Quang Cong	3Pos036	Wazawa, Tetsuichi (和沢 鉄一)	1GG012
Wada, Hitomi (和田 眸)	2Pos080		1Pos211
Wadati, Hiroki (和達 大樹)	2Pos206		2Pos038
Waizumi, Tatsuyuki (和泉 達幸)	3Pos149		2Pos212
Wakabayashi, Ken-ichi (若林 憲一)	1MSG-4		3Pos205
Wakabayashi, Takatoshi (若林 孝俊)	1Pos183	Wei, Fan-Yan (魏 范研)	3Pos198
Wakamoto, Yuchi (若本 祐一)	1GG004	Wei, Fangqian (衛 方千)	2Pos063
Wakita, Nodoka (脇田 和佳)	1GG007	Wen, Jin-Der (溫 進德)	1Pos052
Walkup IV, Ward G.	2SGA-3	Weng, Wei Chun	2Pos034
Wan, Biao (万 彪)	1EE005	Wenting, Huo	3Pos166
Wan, Yumeng (万 育萌)	1Pos089	Widada, Alike Andjani (Widada Alike Andjani)	1Pos150
Wang, Feng-Yu (王 鳳宇)	2SBP-2	Woei-Chyn, Chu	1Pos004
Wang, Jun (王 駿)	3SAA-3	Wolfson, Deanna Lynn	3SAA-4
	2Pos008	Wong, Joshua (Wong Joshua)	2Pos005
Wang, Maoji	1Pos098		1YK1030
Wang, Maoji (王 茂基)	1SHA-4	Wu, Kingsley	2SHP-4
	1Pos096	Wu, Ti (呉 題)	1GJ005
Wang, Peter Y.	3Pos122	Wu, Yichao	1Pos170
Wang, Po-Hsun	2Pos133	Xie, Bingxin (シー ビンシン)	3Pos159
	1YK1115	Xuesi, Zhou	1SHA-3
Wang, Tingting (WANG Tingting)	2Pos190	Yabuki, Yasushi (矢吹 遒)	2Pos052
Wang, Yuzhu (王 雨竹)	3Pos142	Yabuuchi, Sho (薮内 翔)	1Pos121
Wang-Otomo, Zheng-Yu (Wang-Otomo Zheng-Yu)	2Pos139	Yadav, Ajeet Kumar	3Pos178
	2Pos138	Yagasaki, Rei (矢ヶ崎 怜)	2SFA-4
Wang-Otomo, Zheng-Yu (大友 征宇)	2Pos140	Yagi, Hirokazu (矢木 宏和)	1GH005
		Yagi, Maho (矢木 真穂)	2Pos016

Yagi, Sota	1GC006	Yamamoto, Eiji (山本 詠士)	3Pos130
Yagi, Toshiki (八木 俊樹)	2Pos088		1GH011
	3Pos081		3Pos179
Yagi-Utsumi, Maho (矢木 真穂)	2SBP-5	Yamamoto, Johtaro (山本 条太郎)	2Pos203
Yaguchi, Junko	2SJA-4		3Pos059
Yaguchi, Shunsuke	2SJA-4	Yamamoto, Junpei (山元 淳平)	1Pos007
Yajima, Junichiro (矢島 潤一郎)	1GD002		1Pos127
Yajima, Junichiro (矢島 潤一郎)	1GF010		2Pos133
	1Pos077		1YK1115
	1YK1045	Yamamoto, Kentaro (山本 健太郎)	2Pos119
	1Pos151	Yamamoto, Kodai (山本 高大)	2Pos002
	2Pos073	Yamamoto, Masahiro (山本 将大)	2Pos145
	3Pos068	Yamamoto, Masaki (山本 雅貴)	2Pos190
Yamada, Daisuke (山田 大輔)	1Pos185	Yamamoto, Miki (山本 実季)	1GJ009
Yamada, Hiroshi (山田 浩司)	1Pos212	Yamamoto, Naoki (山本 直樹)	1GB007
Yamada, Issaku (山田 一作)	2Pos022	Yamamoto, Norifumi (山本 典史)	3SBA-6
Yamada, Koyo (山田 航洋)	1Pos132		2Pos167
Yamada, Mayu (山田 麻友)	2Pos101		2Pos172
Yamada, Risa (山田 莉彩)	2SBP-1		3Pos183
Yamada, Soma (山田 壮真)	3HL1000	Yamamoto, Shohei (山本 昌平)	1Pos090
Yamada, Teppei (山田 哲平)	1GF007		3Pos089
Yamada, Yoichi (山田 洋一)	2Pos214		1Pos039
	1YK1015	Yamamoto, Soma (山本 颯馬)	
Yamada, Yuhei (山田 雄平)	1ED004	Yamamoto, Takashi	2SJA-4
Yamagata, Atsushi (山形 敦史)	2Pos010	Yamamoto, Takayoshi (山元 孝佳)	1GJ009
Yamagishi, Ayana (山岸 彩奈)	2Pos046	Yamamoto, Takuya (山本 拓也)	1EE001
Yamagishi, Jumpei (山岸 純平)	3SFA-4	Yamamoto, Tatsuya	2Pos202
Yamagishi, Mai (山岸 舞)	1EB005	Yamamoto, Tetsuya (山本 哲也)	1MSJ-6
Yamagishi, Masahiko (山岸 雅彦)	1GD002		1GH009
	1GF010	Yamamoto, Yuka (山本 優果)	3HL0900
	1Pos077	Yamanaka, Masanori (山中 雅則)	1Pos062
	1YK1045		1Pos166
	1Pos151	Yamane, Koki (山根 晃輝)	2Pos106
	2Pos073	Yamane, Tsutomu (山根 努)	2SFP-6
	3Pos068		2Pos162
Yamaguchi, Keiichi (山口 圭一)	2Pos042		2Pos164
Yamaguchi, Manami (山口 真稔)	3Pos014	Yamano, Nami (山野 奈美)	2Pos135
Yamaguchi, Satoshi (山口 哲志)	3SGA-4	Yamano, Yuuhei (山野 雄平)	1GE002
Yamaguchi, Shin (山口 真)	1GD002	Yamaoka, Yoshiyuki (山岡 祥之)	3Pos175
Yamaguchi, Shoichi (山口 祥一)	1Pos051	Yamase, Keidai (山瀬 桂大)	3Pos184
	1Pos205	Yamashiro, Sawako	1Pos098
Yamaguchi, Takehiro (山口 雄大)	1MSF-4	Yamashiro, Sawako (山城 佐和子)	1SHA-1
Yamaguchi, Takumi (山口 拓実)	1GH005	Yamashita, Aimi (山下 愛海)	1Pos188
Yamaguchi, Takumi (山口 拓海)	2Pos121		2Pos207
	3Pos116	Yamashita, Hayato (山下 隼人)	1SEA-5
Yamaguchi, Tomoyuki (山口 智之)	2Pos193		1Pos049
Yamakawa, Minori (山川 実莉)	2Pos199	Yamashita, Ibuki (山下 息吹)	1GB008
	3Pos199	Yamashita, Takahiro	2SJA-4
Yamamori, Yu (山守 優)	1Pos020	Yamashita, Takahiro (山下 高廣)	2Pos129
Yamamoto, Aika (山本 愛華)	3Pos109		2Pos131
Yamamoto, Daisuke (山本 大輔)	1Pos140		2Pos132
	2Pos135	Yamashita, Takefumi (山下 雄史)	3Pos185
		Yamashita, Yo (山下 陽)	1GI004

Yamauchi, Masataka (山内 仁喬)	1MSG-6	Yasui, Masato (安井 正人)	1Pos064
Yamauchi, Tsugumi (山内 つぐみ)	1Pos185	Yasui, Reito (保井 伶斗)	3Pos138
Yamauchi, Yuhei (山内 悠平)	3SHA-5	Yasunaga, Takuo (安永 卓生)	2Pos070
Yamazaki, Hirohito (山崎 洋人)	3Pos198		2Pos080
Yamazaki, Ryuichiro (山崎 隆一郎)	2Pos207		2Pos095
Yamazaki, Shunsuke (山崎 隼佑)	2Pos220		2Pos105
Yamazaki, Takeru	1Pos209		3Pos001
Yamazaki, Takeru (山崎 健)	1EB001		3Pos044
	2Pos209	Yasutake, Yoshiaki	1Pos217
Yamazaki, Tomohiro (山崎 智弘)	2SEA-2	Ye, Shen (叶 深)	1Pos134
Yamazaki, Toshio	1GA007		3Pos134
Yamazaki, Yoichi (山崎 洋一)	1Pos017		3Pos135
	1Pos023		3Pos136
	1Pos143	Yi, Ruiqin (蟻 瑞欽)	1Pos147
Yamazaki, Youichi (山崎 洋一)	2Pos127	Yoda, Takao (依田 隆夫)	2Pos041
Yamazawa, Toshiko (山澤 徳志子)	1EB001	Yohei, Hayashi (洋平 林)	1Pos065
Yan, Xi (晏 晞)	1GE001	Yokohama, Sarara (横濱 さらら)	1GD006
Yanagawa, Masataka (柳川 正隆)	2Pos096	Yokoi, Shun	2Pos048
	2Pos099	Yokono, Masaya (横野 雅也)	1Pos202
Yanagisawa, Keisuke (柳澤 溪甫)	2Pos175	Yokota, Hiroaki (横田 浩章)	1Pos050
Yanagisawa, Miho (柳澤 実穂)	1Pos099	Yokota, Tatsuya (横田 達也)	3SGA-5
	2Pos155	Yokota, Yasunari (横田 康成)	1GF002
Yanagisawa, Naoya (柳沢 直也)	2Pos155	Yokoyama, Daiki (横山 大輝)	1GA004
Yanagisawa, Sachiko	3Pos039	Yokoyama, Kazuki (横山 和輝)	1Pos045
Yanai, Takeshi	3Pos180		2Pos075
Yanaka, Saeko (谷中 冴子)	2Pos016	Yokoyama, Ken (横山 謙)	2Pos009
Yanase, Tomoki (梁瀬 智輝)	1GJ012		3Pos004
Yanase, Yuta (柳瀬 雄太)	3Pos026		3Pos005
Yang, Kai-Chun (Yang Kai-Chun)	1Pos007		3Pos006
	1Pos127		3Pos070
Yang, Keishi (楊 惠詩)	1Pos200	Yokoyama, Takeshi (横山 武司)	1Pos156
Yang, Wonjin	2SKA-3		2Pos074
Yang, Xiaoxiong (楊 曉雄)	2SDP-2		2Pos154
Yang, Xuchun (Yang Xuchun)	1GI005	Yokoyama, Yuka (横山 優花)	2SFA-7
Yang, Ya-Ching (楊 雅晴)	2SBP-2	Yonekura, Koji (米倉 功治)	1MSH-3
Yang, Zhuohao (楊 倬皓)	1EB005		1Pos139
Yanick Besong, Ateke	1Pos218		3Pos066
Yano, Daichi (矢野 大地)	3SBA-7	Yonekura, Naoto (米倉 直努)	2Pos195
Yano, Kotaku (矢野 甲拓)	3Pos044	Yonemura, Shigenobu (米村 重信)	2SFA-2
Yasuda, Haruto (安田 悠人)	3HL0930		3Pos083
Yasuda, Kenji (安田 賢二)	1Pos100	Yonetani, Yoshiteru (米谷 佳晃)	2Pos064
	1Pos102	Yonezawa, Kento (米澤 健人)	1Pos017
	1Pos103		1Pos023
Yasuda, Koki (安田 光希)	3Pos069		1Pos143
Yasuda, Kyota (安田 恭大)	1GB011		2Pos127
	1Pos040	Yonezawa, Yasushige (米澤 康滋)	1SBA-5
	2Pos053	Yoon, Ina	2SKA-1
Yasuda, Takashi	1GF004	Yoshida, Haruna (吉田 春菜)	2Pos019
Yasuda, Takunori (保田 拓範)	1Pos172	Yoshida, Koki (吉田 光輝)	3Pos071
Yasufumi, Umena (梅名 泰史)	3Pos058	Yoshida, Naoki (吉田 直樹)	2Pos057
Yasuhara, Kazuma (安原 主馬)	3SIA-1	Yoshida, Norio (吉田 紀生)	2SDA-4
	3Pos106		2SBP-3

Yoshida, Shuya (吉田 終哉)	1Pos119	Zhang, Zecheng	2Pos012
Yoshida, Yuko (吉田 悠紘)	1Pos054	Zhang, Zecheng (张 泽成)	2Pos008
	1Pos055	Zhang, Zecheng (張 澤成)	3SAA-3
Yoshidome, Takashi (吉留 崇)	1Pos167	Zhang, Zhejing (張 喆菁)	1SIA-2
Yoshikawa, Eri (吉川 英里)	3HL1045	Zhang, Ziyun (張 梓芸)	2Pos216
Yoshikawa, Kenichi (吉川 研一)	1GE004	Zhao, Fan (趙 凡)	1GH012
	1Pos157	Zhao, Shufeng	1GI011
	2Pos057		1GI012
	2Pos059		2Pos202
	3Pos149	Zhao, Wenyang (趙 文洋)	3Pos027
Yoshikawa, Taichi (吉川 太智)	3Pos196	Zhao, Yimeng (Zhao Yimeng)	1Pos114
Yoshikawa, Yuko (吉川 祐子)	1GE004	Zheng, Yinqiang (Zheng Yinqiang)	1Pos211
	2Pos059	Zheng, Yuxiang	2Pos012
Yoshiki, Niino (吉木 新雪)	2Pos168	Zhong, Chongxia (仲 崇霞)	2Pos098
Yoshimi, Akira (吉見 啓)	1GC001	Zhou, Qianfan (周 千帆)	2Pos126
Yoshimi, Tsubura	3Pos039	Zhu, Zhangliang (朱 張亮)	1Pos049
Yoshimura, Haruka (吉村 悠)	3Pos045	Zhuang, Haotong (庄 皓桐)	2SAP-3
Yoshimura, Kenjiro (吉村 建二郎)	2Pos116	Zimmermann, Timo	1MSF-2
Yoshimura, Shige H. (吉村 成弘)	1GB012	Ziyun, Zhang (張 梓芸)	2Pos143
Yoshimura, Yu (吉村 優)	3Pos104	Zou, Ruisi (鄒 瑞思)	1Pos178
Yoshimura, Yukihide (吉村 至偉)	2Pos161	Zugui, Peng (彭 祖癸)	1Pos016
Yoshinaga, Takuro (吉永 琢朗)	1GJ004		
Yoshinari, Kaho (吉成 佳穂)	3Pos092		
Yoshioka, Aoba (吉岡 青葉)	1GD004		
Yoshizawa, Kazumi (吉澤 一巳)	1Pos185		
Yoshizawa, Ryuta (吉澤 龍汰)	3Pos081		
Young, David	2SBA-1		
Yu, Isseki (優 乙石)	3Pos165		
Yu, Jin (喻 进)	1EE005		
Yu, Sangya (俞 翔也)	3Pos037		
Yu, Wookyung	2SKA-3		
Yuan, Hanna S. (袁 小琿)	1Pos004		
Yuasa, Hina (湯淺 日菜)	1GA001		
Yuki, Atsunori (由岐 淳憲)	3Pos174		
Yuki, Haruka (結城 遥香)	1Pos100		
	1Pos102		
	1Pos103		
Yumita, Momoko (弓田 桃子)	1Pos007		
Yurtsever, Ayhan	2SHP-7		
Yuzu, Keisuke (柚 佳祐)	1SCA-5		
	1GB006		
	1GB007		
Zhan, Feng-Yueh (詹 豐嶽)	1Pos200		
Zhang, Bicheng (張 畢澄)	1GJ007		
Zhang, Boyang (張 博洋)	3Pos119		
Zhang, Han	2Pos169		
Zhang, Hongtao	1GI012		
Zhang, Jing (張 景)	1GF004		
Zhang, Wancheng (Zhang Wancheng)	3Pos154		
Zhang, Xianjun (張 先駿)	1Pos134		
Zhang, Yangyang	1Pos179		
Zhang, Yue (張 悦)	1GH005		

第63回 日本生物物理学会年会

浜松ホトニクス株式会社 BP セミナー

日時：2025年 9月 24日（水） 11:50-12:40

会場：奈良県コンベンションセンター F会場（202）

演題 1 コンピュータショナル4Dイメージングによる 脳の情報処理機構の解明

演者 杉 拓磨 先生

広島大学 大学院統合生命科学研究科
超階層システム数理行動学研究室 准教授

セミナー内容

光工学と情報科学が融合したコンピュータショナルイメージングの1つのライトフィールドイメージングでは、空間スキャン無しにシングルショットで3D撮影できる。我々はこの技術の汎用化を妨げる低解像度の問題を解決し、ユーザーの顕微鏡にアドオンするだけで誰でも共焦点顕微鏡の100倍以上の速度で3D動態を計測可能な4Dイメージング技術を開発した。本発表ではこの4D技術と線虫やマウスの神経回路における情報処理機構の研究を紹介する。

演題2 浜松ホトニクスの最新イメージング技術

演者 豊田 浩

浜松ホトニクス株式会社 画像計測機器営業推進部

浜松ホトニクス株式会社
www.hamamatsu.com

□ 画像計測機器営業推進部 〒431-3196 静岡県浜松市中央区常光町812
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島津製作所 バイオフィジックスセミナー2

日時 9月24日(水) 11:50~12:40

会場 I会場〈205〉

生体のナノ領域での組織構造や物理特性を解き明かす！
走査電子顕微鏡SUPERSCANシリーズの特長とSPM/AFMを用いた測定事例をご紹介します

セミナー内容

SUPERSCANシリーズは、操作性や観察能力、拡張性に優れた最新の走査電子顕微鏡です。
生体組織の構造や働きを解明するのに役立つ、各種の拡張システムにも幅広く対応します。
これらの特長について、動画や図説などを交えて詳しくご説明します。
また、SPM/AFMは、ナノ領域での形態観察に留まらず、様々な物理的特性を測ることもできます。
様々な生体試料についてSPM/AFMを用いてナノ領域での力学特性を測定した例をご紹介します。
幅広い倍率レンジでのイメージングが可能であるという、両者の特長を活かした複合的な
解析方法についても考察します。

演者 坂前 浩 (株式会社 島津製作所)

司会 北村 孝平 (株式会社 島津製作所)

お問合せ (株)島津製作所 分析計測事業部 営業企画部
〒604-8511 京都市中京区西ノ京桑原町1 メールアドレス: an_seminar@group.shimadzu.co.jp

第63回 日本生物物理学会年会 ランチョンセミナー BPセミナー3

日時 2025年
9月24日 (水) 11:50-12:40

会場 J会場 (206)
奈良コンベンションセンター

**FRET、バイオセンサーから超解像顕微鏡までできる
蛍光寿命イメージング**



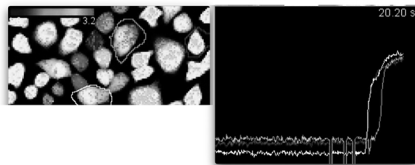
蛍光寿命は、励起スペクトルや蛍光のスペクトルと同様に、蛍光物質がもつ固有の物理特性の一つであり、輝度とは異なる情報を持っています。共焦点顕微鏡STELLARISを用いた蛍光寿命イメージング (Fluorescence Lifetime Imaging Microscopy, FLIM) により、これまでの輝度イメージングと全く異なる情報が得られ、より定量的なFRET効率の測定、カルシウムイオン濃度測定などバイオセンサーとしての利用、蛍光物質同士や蛍光物質と自家蛍光の分離、そして超解像顕微鏡STEDの分解能の向上などが可能となりました。本セミナーでは、新井 敏 先生（金沢大学ナノ生命科学研究所）をお招きし、絶え間無く起こる細胞内での複雑な現象をとらえるバイオセンサー研究の最先端について、実例とともにご発表いただきます。またLeicaからは、STELLARISを用いた蛍光寿命イメージングの有用性について紹介します。

演者1 **新井 敏 先生**
金沢大学 ナノ生命科学研究所

演者2 **長利 卓**
ライカマイクロシステムズ株式会社



▲高速蛍光寿命イメージング顕微鏡 STELLARIS FALCON



▲イオノマイシンを添加したHeLa細胞のカルシウムレベルの変動。

共催：第63回 日本生物物理学会年会 / ライカマイクロシステムズ株式会社

隠れた生命現象を可視化する 蛍光偏光イメージング

講演者

東京科学大学 教授 寺田 純雄 先生

セミナー番号 BP セミナー 4

日時 9月25日(木) 11:45-12:35

会場 E 会場 (201)

● 関連製品



共焦点スキャナユニット CSU

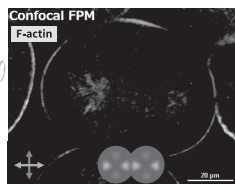
隠れた生命現象を可視化する蛍光偏光イメージング

蛍光偏光は利用の進んでいない蛍光の性質であるが、その観測により蛍光分子の向きを知ることができる。生体分子を蛍光分子により相互の分子の位置関係を固定した状態で標識すれば、蛍光偏光観測により標識された分子の位置と向きの同時観測が可能となる。進化分子工学的スクリーニング法を利用した組換えバインダを足場とした蛍光標識法 POLARis 法の開発により、任意の生体分子につき蛍光偏光観測可能な標識が実現する (PNAS 118, e2019071118, 2021; BBRC 565:50-56, 2021)。超解像法を含め従来の蛍光イメージングはいわば蛍光輝点の位置情報の精密計測による「点描画」であり、1分子イメージングは蛍光輝点の並進運動の観測が大勢であった。しかし、POLARis 法による蛍光偏光観測では分子の位置と向きの変化が同時かつ経時的に可視化される。ニポウディスク方式の共焦点スキャナユニットは褪色を抑えつつ高速なライブイメージングを可能とするが、蛍光偏光特性への攪乱が少ない点で、蛍光偏光イメージングにおいても優れた性能を発揮する。

本セミナーでは POLARis 法開発とその発展の経緯、ニポウディスク方式の共焦点スキャナユニット利用による蛍光偏光イメージングを中心とする実験例を提示し、新しい手法により隠れた生命現象が可視化される様子を共有したい。



Crystal structure of POLARis[®]



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〒180-8750 東京都武蔵野市中町 2-9-32

E-mail : CSU@CSV.yokogawa.co.jp

URL : <https://www.yokogawa.co.jp/solutions/products-and-services/life-science/spinning-disk-confocal/>



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[Ed:01/d]

第63回 日本生物物理学会年会 ZEISS BPセミナーのご案内

「マルチモーダル共焦点レーザー顕微鏡 LSM 990 のご紹介」



Seeing beyond

森と木を見ることを可能にした革新的共焦点レーザー顕微鏡

新たに 1 分子レベルの拡散や濃度計測を可能とした様々な蛍光相関分光機能と
共にイメージング機器の新たな時代の幕を開く

開催日時 9月25日(木) 11:45-12:35

開催会場 F会場(部屋番号 202)

Carl Zeiss 株式会社 プロダクト&アプリケーションセールス

座長 滝口 正人 光学顕微鏡スペシャリスト

演者 佐藤 康彦 光学顕微鏡エキスパート



ZEISSは新しい共焦点レーザー顕微鏡 LSM 990を2025年3月に発表した。これまでの技術に更に磨きをかけた高度な共焦点技術として13色を超える多色イメージングを1スキャンで達成できるスペクトルマルチプレキシング技術を基軸に、高速広範囲マッピング画像の作成から共焦点超解像撮影までを誰もが手軽に操作できるように仕上げています。上位機種では最大分解能をXY軸80nm、Z軸200nmまで飛躍させ、超解像顕微鏡専用機とも言える分解能にまで進化をさせた。

そして革新的とも言える 1 volume / 1 Snap を実現する Lightfield 顕微鏡技術を加えることで3次元顕微鏡の新たな時代の幕を開いた。Lightfield 4D と名付けたこの技術は Widefield ベースの蛍光顕微鏡技術を応用。共焦点レーザー顕微鏡が苦手とする森をタイムラグなしに一気に見るような Volume イメージングをカバーできるようになった。

さらに木を見る、というより、木の間を縫って飛び虫を見るかのような分子レベルの拡散挙動計測を2つも備えている。一つは分子の拡散情報や濃度だけではなく、液-液相分離にも見られる膜を持たない構造境界面での拡散非対称性や分子フローを解析できる技術。二つ目は、画像全体の分子の拡散挙動や近接蛍光によるクロストークの影響を除外した相互相関解析をヒートマップ化して客観的に捉える技術である。ZEISSは古くから分子蛍光相関解析を共焦点レーザー顕微鏡に取り入れてきたが、新たな2手法により、従来のFRAPなどの拡散計測手法と合わせて強力な細胞内分子挙動解析を後押しすることとなる。

本セミナーでは新たに加わったLightfield 4Dと合わせてユーザの期待する実験を包括的にサポートすることができる革新的なマルチモーダル共焦点レーザー顕微鏡LSM 990をご紹介します。

皆様のご来場をお待ち申し上げます。

Carl Zeiss 株式会社
ZEISS Research Microscopy Solutions



SSBD: バイオイメージングデータのグローバルな共有



理化学研究所生命機能科学研究センター

大浪 修一・SSBD チーム



SSBDは、NBDC統合化推進プログラムの支援を受けて2013年より構築・運用を開始した、**バイオイメージングデータを共有・再利用するための公共リポジトリおよびデータベース**です。論文に基づいた多様な画像データを受け入れる**SSBD:repository**と、再利用性の高いキュレート済みデータを提供する**SSBD:database**の二階層で構成され、国際的なバイオイメージングデータ共有ネットワーク（GIDE）とも連携し、世界規模でのデータ公開・利活用を推進しています。

さらに、2025年度の科研費公募分からは、**論文発表時に根拠データの即時公開が義務化される**こととなっており、これまで以上にデータ公開と、信頼できる公開先の選定が求められています。**SSBD**は、こうした要請に応えることができる国内のデータ公開基盤のひとつとして活用されています。

本セミナーでは、バイオイメージングデータ共有に関する国際的な動向、**SSBD:repository**へのデータ登録方法、データ公開時に求められるメタデータやフォーマットの実際について、具体的な事例とともに紹介します。

論文データの公開対応に悩む方、これからバイオイメージングデータの共有を検討している方は、ぜひご参加ください。研究データ公開の第一歩をこの機会にサポートします。

プログラム番号 BPセミナー7 (E会場: 201)
開催日時 2025年9月26日 (金) 12:00 – 12:50

演題1：招待講演

タンパク質プロトタイピング技術に対する展望もしくは妄想

東京大学大学院 工学系研究科 応用化学専攻 教授

野地 博行 先生

近年、計算的なタンパク質モデリング技術や配列設計手法の進展により、in silico でタンパク質構造を合理的に設計することが可能となってきた。一方で、機能を持つタンパク質分子や分子システムの合理的設計は依然として大きな課題であり、実験的な検証を必要とする。こうした背景のもと、多数の候補タンパク質を迅速かつ低コストで合成・評価するためのプロトタイピング技術の刷新が求められている。特に、oligonucleotide library mix から目的配列を選択的に取得し、高効率にDNAを構築する分子操作技術の開発が重要である。一方、各種一分子計測技術の確立により、プロトタイピングに必要なDNAやタンパク質は微量で済むケースも増えている。本講演では、現行の設計・評価技術を俯瞰した上で、1分子スケールでの分子操作・分子評価を前提とした、将来的な超高効率プロトタイピング技術の可能性について展望（妄想）する。

演題2：企業講演

Writing the Future: あなたの最高の研究アイデアを実現するTwist人工遺伝子ツール

Twist Bioscienceシニアビジネスディベロップメントマネージャー
金城 一貴

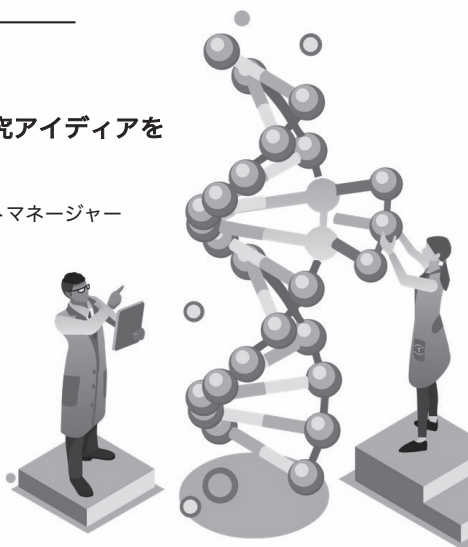
【お問い合わせ先】

Twist Bioscience

Email: jsalescustomer@twistbioscience.com

Phone: 045-345-5840

または、こちらのフォームから→



第 63 回日本生物物理学会 BPセミナー

2025 年 9 月 26 日 (金)

BPセミナー8 I会場 (205) 12:00-12:50

1. PDBj の最近の活動と wwPDB の今後の活動方針について Activity report of PDBj and activity plan of wwPDB

栗栖源嗣 (大阪大学蛋白質研究所)

Genji Kurisu, Institute for Protein Research

The University of Osaka

PDBj (<https://pdbj.org>) は, worldwide PDB (<https://wwpdb.org>) の設立メンバーとしてアジア・中東地区で決定された蛋白質等の生体高分子の構造を wwPDB が管理するコアアーカイブ (PDB, BMRB, EMDB) に登録処理し, 国際的に協調して座標と実験データを全世界へ無償で公開しています。今回のセミナーでは, wwPDB が管理するコアアーカイブの今後の運営体制とデータ検証の方向性について説明いたします。さらに2024年PDBjが主催し日本で行ったwwPDB運営諮問委員会で議論されたPDB周辺の最近の状況を紹介いたします。PDBjの最近の活動として昨年10月に新しくスタートしたUniProtポータル機能を中心に複数の新サービスについて解説します。

2. 計算によって得られたデータと結晶回折像のPDBjへの登録 Deposition of computationally derived data and crystal diffraction images to PDBj

Gert-Jan Bekker (大阪大学蛋白質研究所)

Institute for Protein Research

The University of Osaka

PDBj has developed two novel archives for deposition of data beyond structures to the PDB. The Biological Structure Model Archive (BSMA or BSM-Arc, <https://bsma.pdbj.org/>) enables researchers to submit data derived from computational methods, such as molecular dynamics simulations. On the other hand, the Xtal Raw Data Archive (XRDa, <https://xrda.pdbj.org/>) enables researchers to submit raw crystal diffraction images to PDBj. For both archives, depositors login using their ORCID ID to submit or modify an entry. Data can either be uploaded via a web form, or via RSYNC/SFTP, and upon publication, the data becomes publicly available and can be downloaded via HTTPS or RSYNC. Each entry is also assigned a unique DOI for linking from publications. We invite researchers to submit their raw data to BSM-Arc and XRDa to publicly share the data in a similar manner as structural data is being shared via the PDB.

Protein Data Bank Japan
<https://pdbj.org>

日本蛋白質構造データバンク (PDBj) 事務局
〒565-0871 大阪府吹田市山田丘 3-2
大阪大学蛋白質研究所 蛋白質構造データバンク構築研究室
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本学会の連絡先は下記の通りです。

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6. 日本生物物理学会のウェブサイト

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日本生物物理学会

SEIBUTSU BUTSURI

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