ISSN 0582-4052　CODEN : SEBUAL
2018 年 8 月（増刊号）

生物物理

SEIBUTSU BUTSURI

SUPPLEMENT 1-2
Vol.58

第56回年会予稿集

2018.9.15（土）～ 17（月・祝）

岡山大学 津島キャンパス

主催　一般社団法人　日本生物物理学会

The Biophysical Society of Japan
一般社団法人　日本生物物理学会　http://www.biophys.jp

第 56 回日本生物物理学会年会

The 56th Annual Meeting of the Biophysical Society of Japan

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開催概要／General Information

The 56th Annual Meeting of the Biophysical Society of Japan (BSJ2018)

第 56 回日本生物物理学会年会（2018 年度）

会期／Period

2018 年 9 月 15 日（土）– 17 日（月・祝）
September 15 (Sat.) – 17 (Mon.), 2018

会場／Venue

岡山大学 津島キャンパス
（〒 700-8530 岡山市北区津島中 1 丁目 1 番 1 号）
Tsushima Campus, Okayama University
(1-1-1 Tsushimanaka, Kita-ku, Okayama, 700-8530, Japan)

年会実行委員長／President

沈 建仁（岡山大学異分野基礎科学研究所）
Jian-Ren Shen (Okayama University)

Website　http://www2.aeplan.co.jp/bsj2018

※会期後は日本生物物理学会にデータが移行されますので，学会ホームページよりご覧ください。

抄録本文（Abstract）

※下記サイトからダウンロードいただけます。
http://www.biophys.jp/dl/pro/56th_proceedings.pdf
ID: ambsj56　Password: okayama2018

※本年会では要旨閲覧アプリは作成しておりません。

開催にあたって

第 56 回年会　実行委員長
沈　建仁
（岡山大学異分野基礎科学研究所）

一般社団法人日本生物物理学会第 56 回年会を，岡山大学津島キャンパスにて 2018 年 9 月 15 日（土）～ 17 日（月）の日程で開催いたします。岡山での開催は学会創立以来初めてのことです。まだ残暑が残る時期ですが，「晴れの国」と言われる岡山の地で最先端の生物物理学の成果や参加者同士の交流を楽しんでいただければと願っております。

岡山年会では，慣例に従いすべての発表は英語で行われます。昨年度に引き続き一般発表は口頭とポスターの 2 つの形式としました。シンポジウムについては，生物物理学の様々な分野にフォーカスしたものや，最先端の融合的研究に関する多数の応募，及び大型プロジェクトを組織している研究者による積極的な企画を採択しました。学会本部による東アジア国際シンポジウムと日中二国間交流シンポジウムとあわせて，計 35 件のシンポジウムが行われます。

一般発表の中からは，若手研究者奨励賞（第 14 回）が選考・授与されるとともに，3 回目となる若手招待講演賞と学生発表賞（優れた口頭発表に対する賞）の選考・授与も行なわれます。

さらに，男女共同参画・若手支援の観点から，それらに関するシンポジウムとキャリア支援説明会が予定され，また，総会シンポジウム（第 5 回）や BPPB 論文賞受賞講演会（第 7 回）も行われます。また，科研費説明会では，科研費に関する最近の動向や制度に関する最新の情報を提供いたします。協賛企業による展示会やランチョンセミナーにおいては，最新の計測機器や研究を支援するシステム・製品等の情報が紹介されます。さらに年会 2 日目には，一般市民向けとして天野浩先生（2014 年ノーベル物理学賞：名古屋大学）をお迎えして，「発光と吸光で開く先端基礎科学」と題した市民講演会を開催します。

本年会が，日本における生物物理学の最新の成果と，若手研究者を含めた多数の研究者の活躍を実感していただけるものとなることを期待しています。

最後に，年会の合間や参加者の交流のなかで，岡山の食，人，歴史，自然などに親しんでいただければ幸いです。

第56回日本生物物理学会年会実行委員会
Organizing Committee

実行委員長		President	
沈 建仁	（岡山大学）	Jian-Ren Shen	(Okayama University)

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山下 敦子	（岡山大学）	Atsuko Yamashita	(Okayama University)

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篠原 康雄	（徳島大学）	Yasuo Shinohara	(Tokushima University)
菅 倫寛	（岡山大学）	Michi Suga	(Okayama University)
墨 智成	（岡山大学）	Tomonari Sumi	(Okayama University)
高橋 賢	（岡山大学）	Ken Takahashi	(Okayama University)
竹居 孝二	（岡山大学）	Koji Takei	(Okayama University)
竹田 哲也	（岡山大学）	Tetsuya Takeda	(Okayama University)
楯 真一	（広島大学）	Shin-ichi Tate	(Hiroshima University)
富永 貴志	（徳島文理大学）	Takashi Tominaga	(Tokushima University)
永野 真吾	（鳥取大学）	Shingo Nagano	(Tottori University)
成瀬 恵治	（岡山大学）	Keiji Naruse	(Okayama University)
松浦 宏治	（岡山理科大学）	Koji Matsuura	(Okayama University of Science)
守屋 央朗	（岡山大学）	Hisao Moriya	(Okayama University)
安井 典久	（岡山大学）	Norihisa Yasui	(Okayama University)
山本 雅貴	（理化学研究所）	Masaki Yamamoto	(RIKEN)

※ 50 音順

交通および会場のご案内

岡山空港から

■ 岡山空港 2 番乗り場から「岡山駅運動公園口（西口）」行に乗車，「岡山大学筋」下車（所要時間約 30 分），徒歩約 7 分

※ノンストップ便は，JR 岡山駅で下車し，各種交通機関を利用

JR岡山駅から

■ **タクシー**：岡山駅運動公園口（西口）から約 7 分

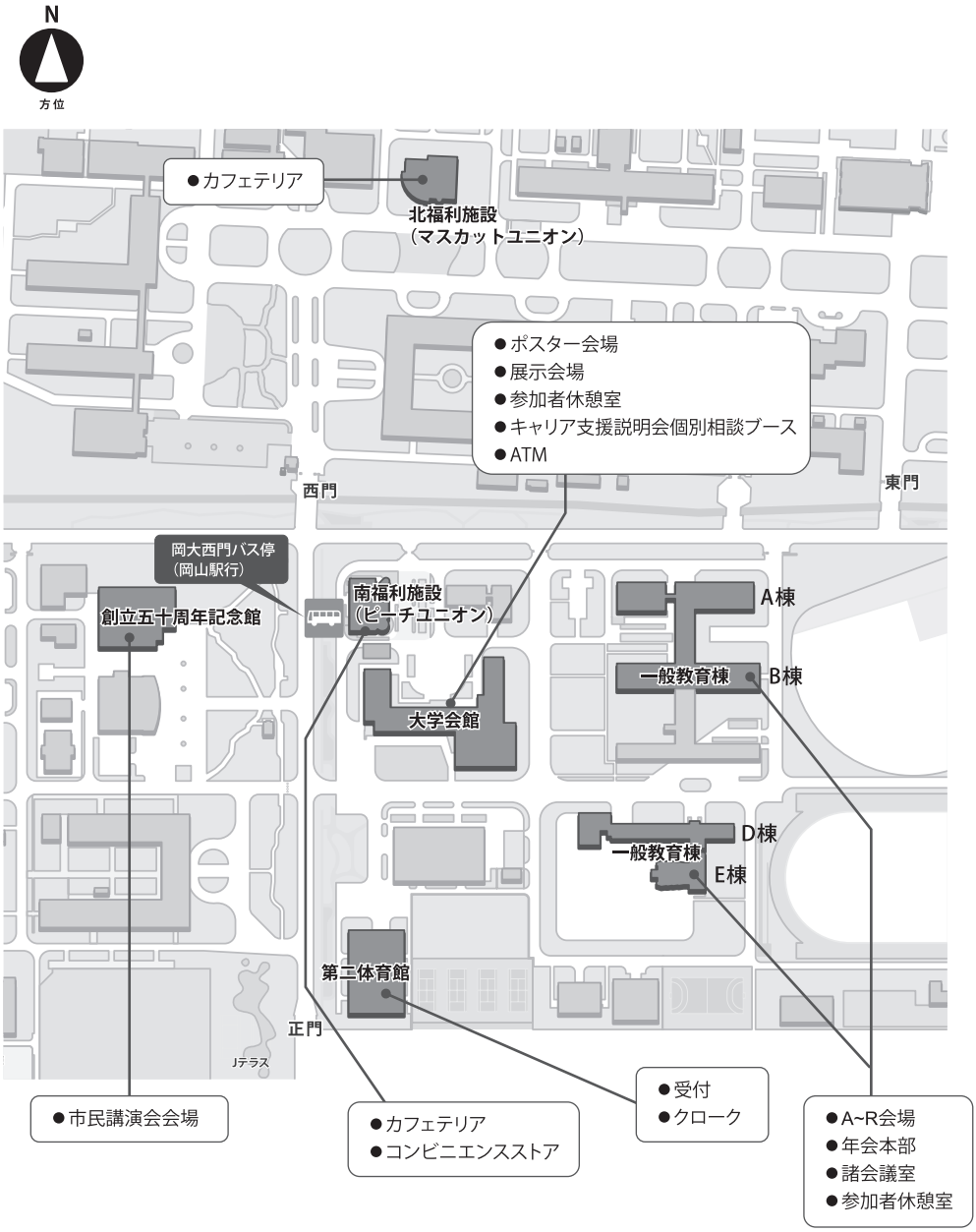
■ **JR**：津山線「法界院駅」から徒歩約 10 分

■ **バス**：岡山駅運動公園口（西口）バスターミナル 22 番乗り場から「【47】系統 岡山理科大学」行に乗車，「岡大西門」で下車（所要時間：約 7 ～ 10 分）

〈岡山駅後楽園口（東口）バスターミナル 7 番乗り場から「【16】系統 高津台団地・半田山ハイツ」行，「【26】系統 岡山医療センター国立病院」行，「【36】系統 辛香口」行，「【86】系統 運転免許センター」行に乗車，「岡山大学筋」下車（所要時間：約 10 分），徒歩約 7 分〉

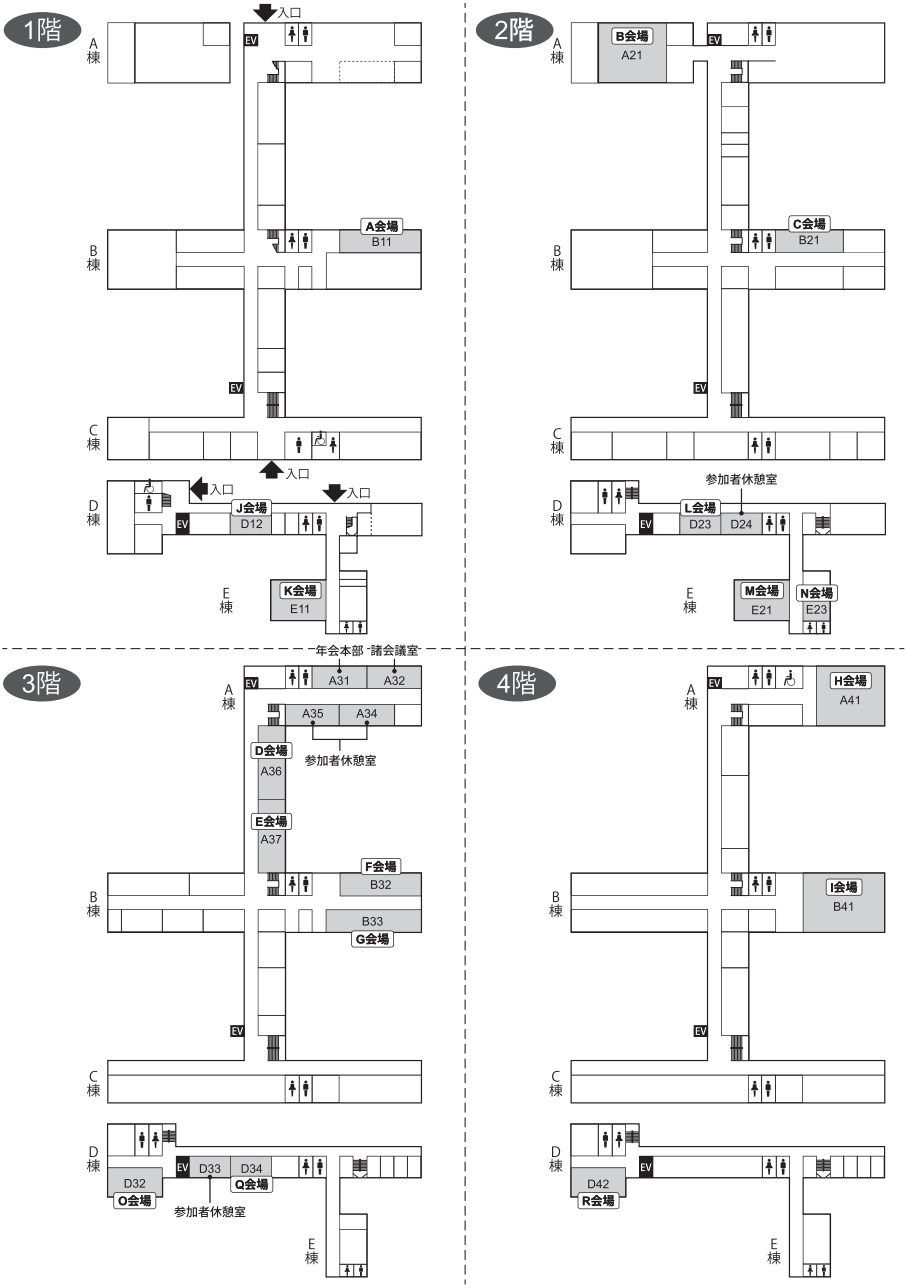
※東口からもバスは出ていますが，わかりにくいので西口からのバスをご利用ください。

岡山大学 津島キャンパス全体マップ

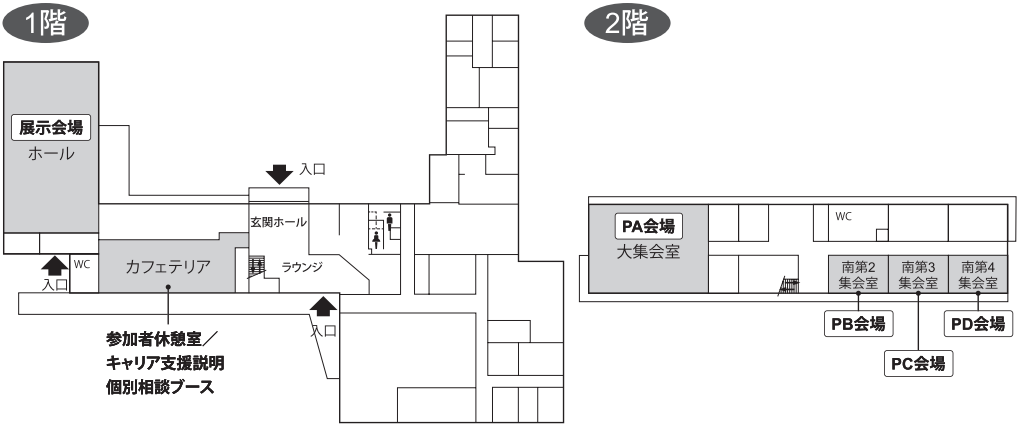


＊キャンパス内は全面禁煙が実施されており、喫煙場所はありません。

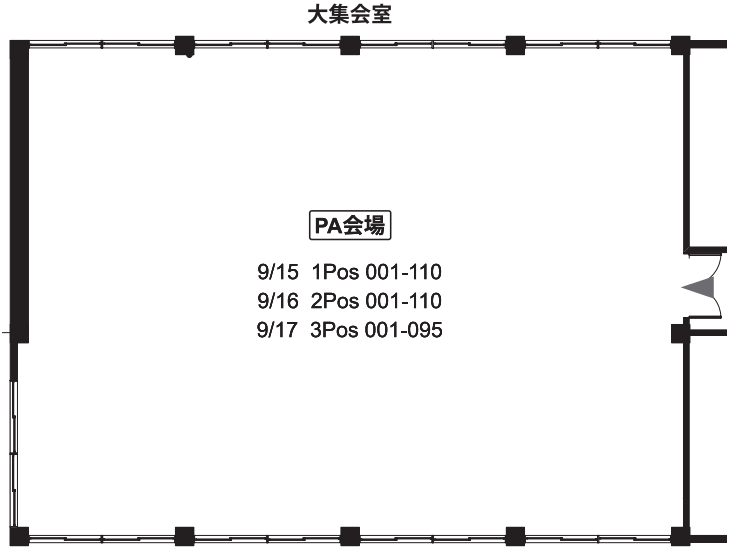
一般教育棟


1階
入口
A棟
B棟
C棟
D棟
E棟
EV
A会場
B11
入口
入口
入口
J会場
D12
K会場
E11
2階
B会場
A21
C会場
B21
参加者休憩室
L会場
D23
D24
M会場
E21
N会場
E23
3階
年会本部
諸会議室
A31
A32
A35
A34
D会場
A36
参加者休憩室
E会場
A37
F会場
B32
B33
G会場
D33
D34
Q会場
D32
O会場
参加者休憩室
4階
H会場
A41
I会場
B41
D42
R会場

大学会館


1階
展示会場
ホール
入口
玄関ホール
WC
入口
カフェテリア
ラウンジ
参加者休憩室／
キャリア支援説明
個別相談ブース
入口
2階
PA会場
大集会室
WC
南2
集会室
南3
集会室
南4
集会室
PB会場
PD会場
PC会場

ポスター会場


大集会室
PA会場
9/15 1Pos 001-110
9/16 2Pos 001-110
9/17 3Pos 001-095

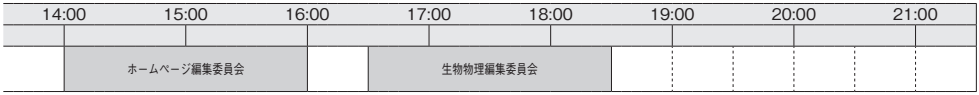

南第2集会室
PB会場
9/15 1Pos 201-228
9/16 2Pos 201-228
9/17 3Pos 201-220
南第3集会室
PC会場
9/15 1Pos 301-326
9/16 2Pos 301-326
9/17 3Pos 301-327
南第4集会室
PD会場
9/15 1Pos 401-421
9/16 2Pos 401-424
9/17 3Pos 401-421

■2018年9月14日（金）：年会前日

建物		フロア	部屋	会場	9:00	10:00	11:00	12:00	13:00
一般教育棟	A棟	3階	A32	諸会場室					

■2018年9月15日（土）：年会1日目

建物		フロア	部屋	会場	9:00	10:00	11:00	12:00	13:00
一般教育棟	A・B棟	1階	B11	A会場	1SAA　いきた形の新規生成に挑む、理論モルフォダイナミクス（澤井 哲、井上 康博）			Biophysics and Physicobiology 論文賞受賞講演 12:50-13:20	
		2階	A21	B会場	1YB　若手奨励賞招待講演シンポジウム				
			B21	C会場					
		3階	A32	諸会議室		Biophysics and Physicobiology 編集委員会9:40-10:40	出版委員会 10:40-11:40	第2回理事会 11:45-12:35	
			A36	D会場	1SDA　生体分子の機能解明に向けた3D活性サイトの構造・ダイナミクスの新規解析法（鷹野 優、関口 博史）			1LSD シグマ光機株式会社 11:45-12:35	
			A37	E会場	1SEA　分子から個体のメカノバイオ：多様な物理刺激とその応答（新井 敏、原 雄二）			1LSE 株式会社ニコンインステック 11:45-12:35	
			B32	F会場	1SFA　細胞幾何学：時空間スケールが決める秩序と機能（前多 裕介、宮崎 牧人）				
			B33	G会場	1SGA　promiscuousだが洗練されたタンパク質の分子認識（神田 大輔、塚崎 智也）			1LSG ライカマイクロシステムズ株式会社 11:45-12:35	
		4階	A41	H会場	1SHA　どこまで光は届くのか？　オプトジェネティクスの挑戦（渡邉 宙志、神取 秀樹）				
			B41	I会場	1SIA　細胞膜受容体の局在・会合とシグナル変換の制御（森垣 憲一、鈴木 健一）				
	E・D棟	1階	D12	J会場					
			E11	K会場	1SKA　1分子計測に立脚した新しいバイオ分析の潮流（渡邉 力也、小松 徹）				
		2階	D23	L会場					
			E21	M会場	1SMA　生体運動システムの自律性（上田 太郎、南野 徹）				
			E23	N会場					
		3階	D32	O会場	1SOA　タンパク質の分子内情報伝達の動的機構と機能（宮下 尚之、米澤 康滋）				
			D34	Q会場					
		4階	D42	R会場	1SRA　光合成反応中心の構築および作動原理：キノンは必須か（大岡 宏造、浅井 智広）			キャリア支援説明会 第1部 11:50-12:40（ランチョンセミナー） 第2部 12:50-13:40	
大学会館		2階	大集会室	PA会場	ポスター貼付 8:30-9:30	ポスター展示			
			南第二集会室	PB会場					
			南第三集会室	PC会場					
			南第四集会室	PD会場					
		1階	大会議室	展示会場		機器展示			
			カフェテリア						


14:00
15:00
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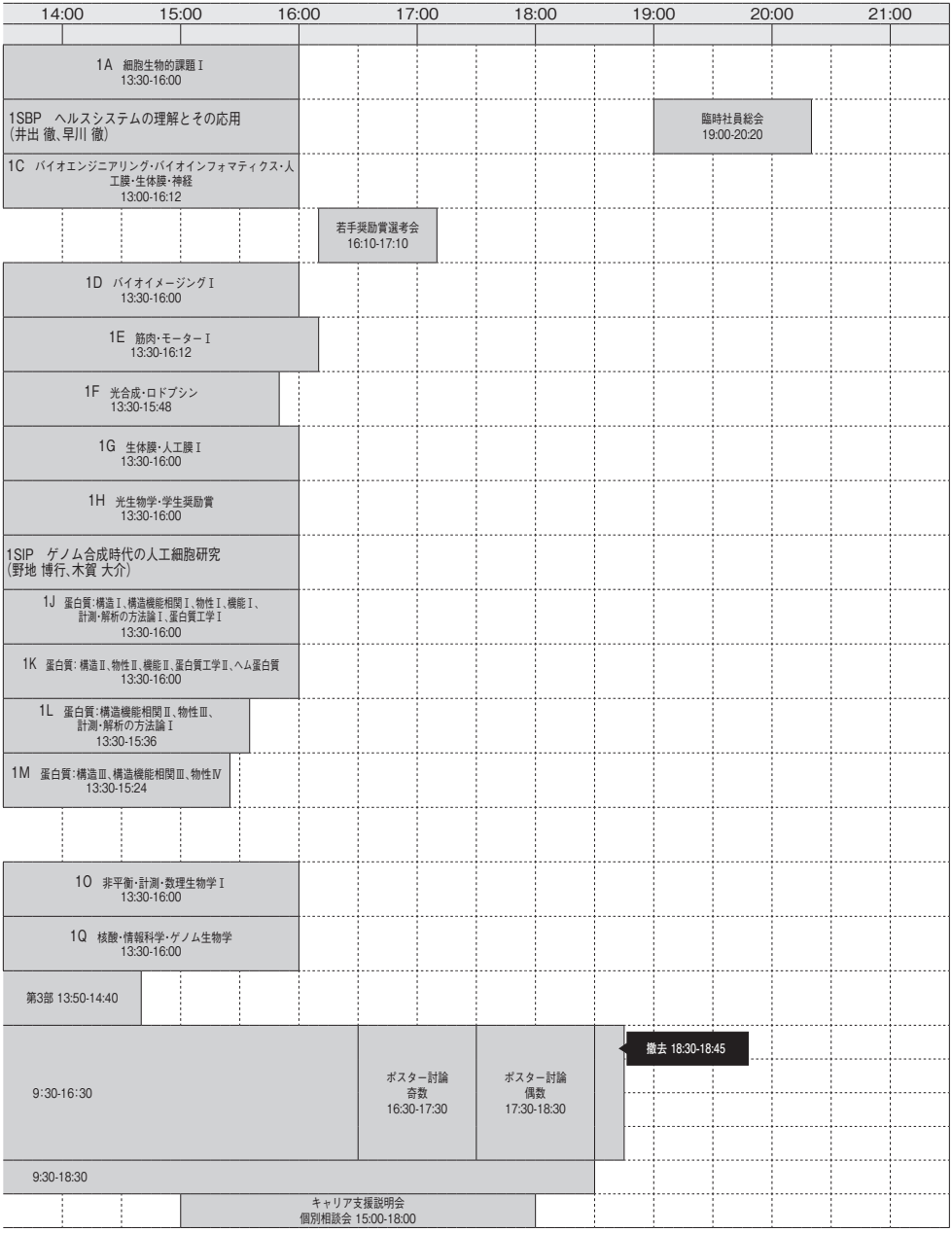
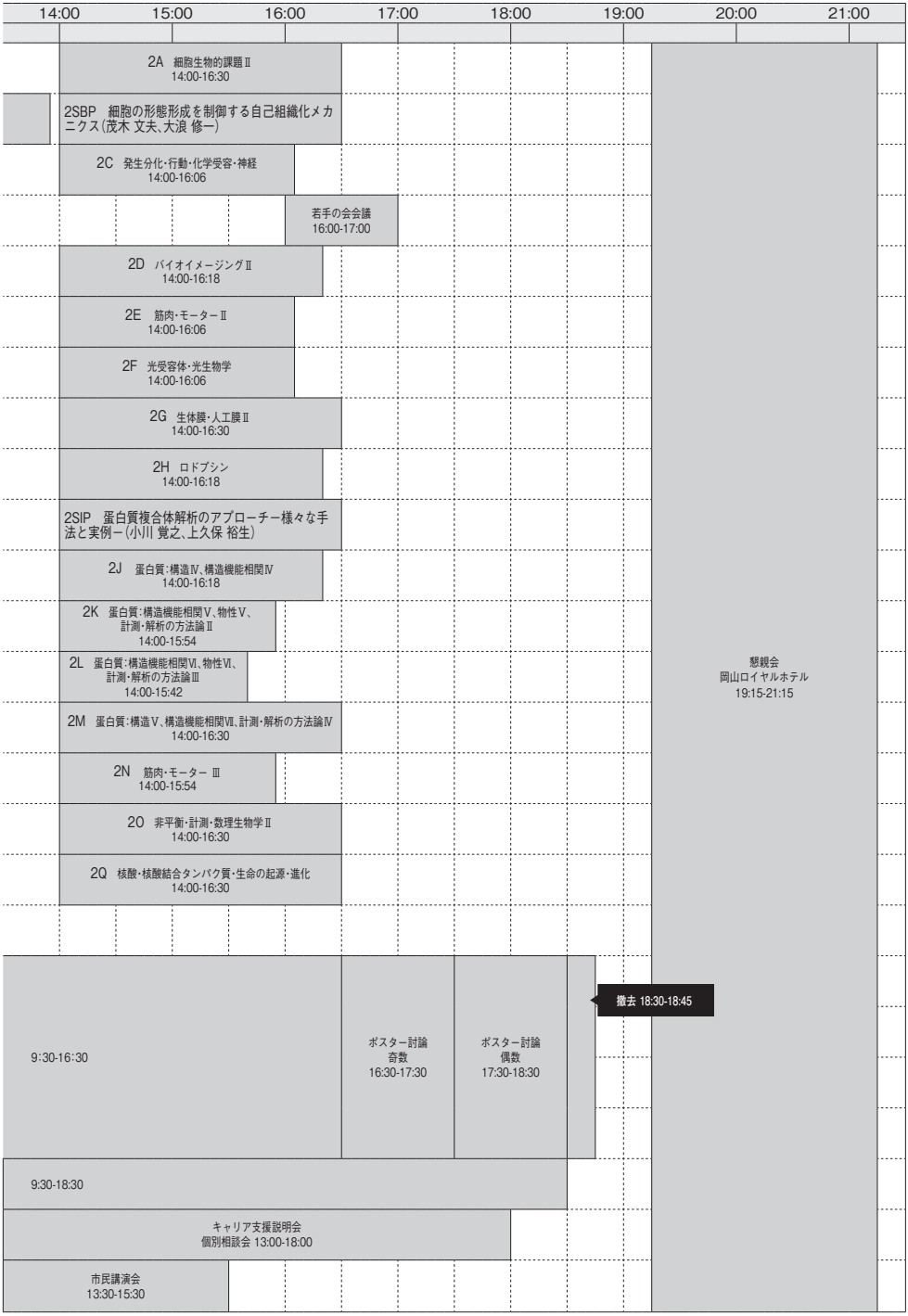
21:00
ホームページ編集委員会
生物物理編集委員会


14:00
15:00
16:00
17:00
18:00
19:00
20:00
21:00
1A 細胞生物的課題Ⅰ
13:30-16:00
1SBP ヘルスシステムの理解とその応用
(井出 徹、早川 徹)
臨時社員総会
19:00-20:20
1C バイオエンジニアリング・バイオインフォマティクス・人工膜・生体膜・神経
13:00-16:12
若手奨励賞選考会
16:10-17:10
1D バイオイメージングⅠ
13:30-16:00
1E 筋肉・モーターⅠ
13:30-16:12
1F 光合成・ロドプシン
13:30-15:48
1G 生体膜・人工膜Ⅰ
13:30-16:00
1H 光生物学・学生奨励賞
13:30-16:00
1SIP ゲノム合成時代の人工細胞研究
(野地 博行、木賀 大介)
1J 蛋白質:構造Ⅰ、構造機能相関Ⅰ、物性Ⅰ、機能Ⅰ、計測・解析の方法論Ⅰ、蛋白質工学Ⅰ
13:30-16:00
1K 蛋白質:構造Ⅱ、物性Ⅱ、機能Ⅱ、蛋白質工学Ⅱ、ヘム蛋白質
13:30-16:00
1L 蛋白質:構造機能相関Ⅱ、物性Ⅲ、計測・解析の方法論Ⅰ
13:30-15:36
1M 蛋白質:構造Ⅲ、構造機能相関Ⅲ、物性Ⅳ
13:30-15:24
1O 非平衡・計測・数理生物学Ⅰ
13:30-16:00
1Q 核酸・情報科学・ゲノム生物学
13:30-16:00
第3部 13:50-14:40
9:30-16:30
ポスター討論
奇数
16:30-17:30
ポスター討論
偶数
17:30-18:30
撤去 18:30-18:45
9:30-18:30
キャリア支援説明会
個別相談会 15:00-18:00

■2018年9月16日（日）：年会2日目

建物		フロア	部屋	会場	9:00	10:00	11:00	12:00	13:00
一般教育棟	A・B棟	1階	B11	A会場		2SAA　Taiwan-Japan biophysics symposium on molcular motors *in vivo*（Kumiko Hayashi、Chien-Jung Lo）			
		2階	A21	B会場		2SBA　クライオ電子顕微鏡（千田 俊哉、Zhenfeng Liu）		分野別専門委員会 11:45-12:35	会員総会・総会シンポジウム12:35-13:55
			B21	C会場					
		3階	A32	諸会議室			男女共同参画・若手支援委員会 10:00-11:30		
			A36	D会場		2SDA　創薬等先端技術支援基盤プラットフォーム（BINDS）（田之倉 優、由良 敬）		2LSD 日本蛋白質構造データバンク 11:45-12:35	
			A37	E会場		2SEA　機械シグナル受容応答機構解明に向けた最先端研究と未来（森松 賢順、中澤 直高）		2LSE スペクトリス株式会社マルバーン・パナリティカル事業部 11:45-12:35	
			B32	F会場		2SFA　生体機能の再構成によるセンシング技術とデバイス応用（手老 龍吾、平野 愛弓）			
			B33	G会場		2SGA　マルチスケール・フィジクスで見えてくる生体高分子のダイナミクスと機能機序（河野 秀俊、寺田 透）		2LSG 浜松ホトニクス株式会社 11:45-12:35	
		4階	A41	H会場		2SHA　ゲノム時代が切り拓く光生物の沃野（井上 圭一、山下 高廣）			
			B41	I会場					
	E・D棟	1階	D12	J会場					
			E11	K会場		2SKA　X線自由電子レーザーと融合分野が拓くタンパク質反応ダイナミクスの新しい計測（久保 稔、南後 恵理子）			
		2階	D23	L会場					
			E21	M会場		2SMA　創って知る生物物理:生命現象の再構成と理解（多田隈 尚史、古田 健也）			
			E23	N会場					
		3階	D32	O会場		2SOA　ピコバイオロジーが目指すもの（水谷 泰久、中島 聡）			
			D34	Q会場					
		4階	D42	R会場		キャリア支援説明会 第4部 9:30-10:30			
大学会館		2階	大集会室	PA会場	ポスター貼付 8:30-9:30	ポスター展示			
			南第二集会室	PB会場					
			南第三集会室	PC会場					
			南第四集会室	PD会場					
		1階	大会議室	展示会場		機器展示			
			カフェテリア						
創立五十周年記念館		1階	金光ホール	U会場					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17:00
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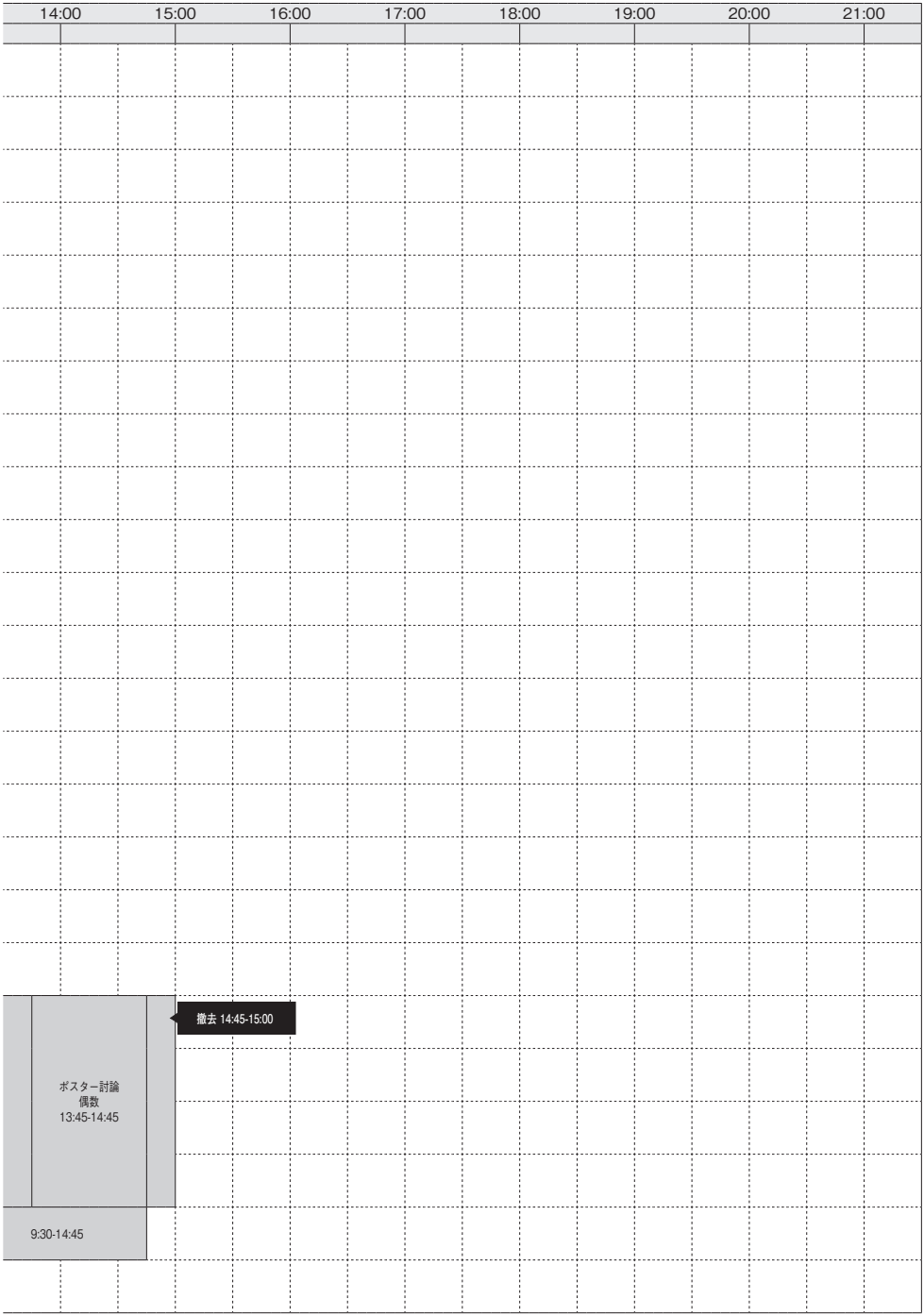
21:00
2A 細胞生物的課題Ⅱ
14:00-16:30
2SBP 細胞の形態形成を制御する自己組織化メカニクス(茂木 文夫、大浪 修一)
2C 発生分化・行動・化学受容・神経
14:00-16:06
若手の会会議
16:00-17:00
2D バイオイメージングⅡ
14:00-16:18
2E 筋肉・モーターⅡ
14:00-16:06
2F 光受容体・光生物学
14:00-16:06
2G 生体膜・人工膜Ⅱ
14:00-16:30
2H ロドプシン
14:00-16:18
2SIP 蛋白質複合体解析のアプローチー様々な手法と実例ー(小川 覚之、上久保 裕生)
2J 蛋白質:構造Ⅳ、構造機能相関Ⅳ
14:00-16:18
2K 蛋白質:構造機能相関Ⅴ、物性Ⅴ、計測・解析の方法論Ⅱ
14:00-15:54
2L 蛋白質:構造機能相関Ⅵ、物性Ⅵ、計測・解析の方法論Ⅲ
14:00-15:42
2M 蛋白質:構造Ⅴ、構造機能相関Ⅶ、計測・解析の方法論Ⅳ
14:00-16:30
2N 筋肉・モーター Ⅲ
14:00-15:54
2O 非平衡・計測・数理生物学Ⅱ
14:00-16:30
2Q 核酸・核酸結合タンパク質・生命の起源・進化
14:00-16:30
懇親会
岡山ロイヤルホテル
19:15-21:15
9:30-16:30
ポスター討論
奇数
16:30-17:30
ポスター討論
偶数
17:30-18:30
撤去 18:30-18:45
9:30-18:30
キャリア支援説明会
個別相談会 13:00-18:00
市民講演会
13:30-15:30

■2018年9月17日（月・祝）：年会3日目

建物		フロア	部屋	会場	9:00	10:00	11:00	12:00	13:00
一般教育棟	A・B棟	1階	B11	A会場		3SAA　光回復酵素／クリプトクロムスーパーファミリーの光依存的機能と多様性の最先端（山元 淳平、山田 大智）		男女参画・若手支援シンポジウム 11:45-12:35	
		2階	A21	B会場		3SBA　物理的力と生物（成瀬 恵治、東谷 篤志）		科研費説明会 11:45-12:35	
			B21	C会場					
		3階	A32	諸会議室		企業との意見交換会 9:30-11:00			
			A36	D会場		3SDA　構造生命科学の新展開（中川 敦史、清水 敏之）			
			A37	E会場		3SEA　化学感覚の新コンセプト（今井 啓雄、山下 敦子）			
			B32	F会場		3SFA　シンギュラリティ生物学（永井 健治、堀川 一樹）			
			B33	G会場		3SGA　生体分子の運動と機能理解を目指した単粒子観測実験と計算解析（宮下 治、岩崎 憲治）		3LSG サーモフィッシャーサイエンティフィック(株) 11:45-12:35	
		4階	A41	H会場		3SHA　光エネルギー変換の生物物理：光合成のメカニズムはどこまで解明されたか？（菅 倫寛、野口 巧）			
			B41	I会場		3SIA　東アジアシンポジウム：1分子生物物理学の最前線（佐甲 靖志、Ming Li、Jie Yan、Tae-Young Yoon）			
	E・D棟	1階	D12	J会場					
			E11	K会場		3SKA　細菌すごいぜ！―バクテリアを通して見る生命現象―（中根 大介、小嶋 誠司）			
		2階	D23	L会場					
			E21	M会場		3SMA　微生物における生命金属動態とその利用（古川 良明、當舎 武彦）			
			E23	N会場					
		3階	D32	O会場					
			D34	Q会場					
		4階	D42	R会場					
大学会館		2階	大集会室	PA会場	ポスター貼付 8:30-9:30	ポスター展示 9:30-12:45			ポスター討論奇数 12:45-13:45
			南第二集会室	PB会場					
			南第三集会室	PC会場					
			南第四集会室	PD会場					
		1階	大会議室	展示会場		機器展示			
			カフェテリア						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撤去 14:45-15:00
ポスター討論
偶数
13:45-14:45
9:30-14:45

参加者へのご案内

1. 年会受付と参加登録

◇年会受付

場　　所：第 2 体育館

受付時間：8:30 - 17:00（9 月 17 日（月・祝）は 14:00 まで）

◆事前登録

事前登録が完了された方は，日本生物物理学会会員・非会員共に参加証，領収証およびプログラム集冊子が事前送付されますので，会場での受付は不要です。当日は必ず参加証をお持ちください。但し，海外からの参加者は，年会受付にて参加証とプログラム集冊子をお受け取りください。

※参加証ホルダーは当日配布しますので，会場内では必ず参加証をご着用ください。
　配付場所：参加受付，建物入口付近 など

注意 1）事前登録は年会参加登録費（参加費）の振込後に完了します。振込がない場合，オンライン登録は無効となります。当日受付で当日参加費をお支払いください。

注意 2）日本生物物理学会会員は年度会費を納めていない場合，参加証が送付されません。年度会費未納者・新規入会受付デスクにて年度会費をお支払いください。

注意 3）参加費・年度会費ともに振込済みで，参加証が事前送付されていない場合は，総合受付デスクまでお越しください。

注意 4）非会員のシンポジウム招待講演者については，会員である必要はなく，また，参加登録費は免除されます。

◆当日登録

事前登録が完了していない方は当日登録をしていただきます。当日受付にお越しの上，参加費を現金でお支払いください。

◇当日年会諸費用

当日参加	会員				非会員		
	正会員	シニア会員	学生会員	学部学生	一般	大学院生	学部学生
当日参加費	¥9,000	¥5,000	¥5,000	¥0	¥12,000	¥6,000	¥0
懇親会費	¥8,000	¥5,000	¥5,000	¥3,000	¥8,000	¥5,000	¥3,000

・参加のみの学部学生は参加費無料です。当日受付で学生証を提示してください。参加証とプログラム集冊子をお渡しします。
・若手奨励賞招待講演者，Biophysics and Physicobiology 論文賞受賞講演者，Biophysics And Physicobiology Editors' Choice Award 受賞代表者は，懇親会に無料でご招待します。既に懇親会参加費を振り込まれている場合は，総合受付デスクで返金します。

◇参加証（名札）

参加証は会場内では必ずご着用ください。参加証のない方のご入場は固くお断りいたします。

◇領収書の発行

参加証とともに領収書をお渡しいたしますが，別の形式の領収書が必要な場合，お渡しした領収書と引き換えに総合受付デスクにて発行いたします。

◇プログラム集冊子/オンライン予稿集【8月17日（金）公開予定】

プログラム集冊子（前付・プログラム）は日本生物物理学会会員および事前登録が完了された非会員に事前に送付いたします（プログラム集冊子は総合受付デスクでも当日販売（3,500円/税込））を行います）。なお予稿本文はプログラム集冊子には掲載されません。予稿本文は，オンライン予稿集をダウンロードして閲覧いただくことになります。
※本年会では要旨閲覧アプリは作成しておりません。

オンライン予稿集：
http://www.biophys.jp/dl/pro/56th_proceedings.pdf
ダウンロード ID：ambsj56
パスワード：okayama2018

プログラム（タイトル，発表者，所属）と予稿集は，年会ホームページにて公開します。年会終了後は，半年ほど経て日本生物物理学会ホームページの年会の記録およびJ-STAGE にて予稿集の pdf ファイルが公開されます。

○日本生物物理学会ホームページの年会の記録（http://www.biophys.jp/ann/ann02.html）
○ J-STAGE の生物物理のページ（https://www.jstage.jst.go.jp/browse/biophys/-char/ja）

◇プログラム検索（ウェブ版）【8月9日（木）公開予定】

年会ホームページで「プログラム検索」を公開します。項目［演題タイトル（和文・英文），発表者名（共著者含む）（漢字，カナ，ローマ字），発表形式］から，演題番号，発表日，会場を検索・表示します。

◇年度会費の支払いと入会の手続き

日本生物物理学会の年度会費が未納の場合は，年会受付の年度会費未納者・新規入会受付デスクでお支払いください。また，日本生物物理学会への新規入会も受け付けます。

2. 会場内のサービス・施設

◇クローク

場　　所：第 2 体育館

利用時間：8:30 - 18:45（9 月 17 日（月・祝）のみ 15:00 まで）

※貴重品や傘，またコンピュータなどについては，破損，紛失などの責任を負いかねますので，お預かりできません。

※懇親会にご参加の際は，荷物をお引き取りください。

◇昼食

ランチョンセミナー（1 - 3 日目），キャリア支援説明会（1 日目），男女共同参画・若手支援シンポジウム（3 日目），科研費説明会（3 日目）でお弁当とお茶が無料で提供されます。当日の午前中に整理券を配布いたします。整理券のご利用方法は 20 ページ「ランチョンセミナー」をご参照ください。

なお会期中は，以下の学生食堂をご利用いただけます。

■ピーチカフェテリア

場　　所：南福利施設（ピーチユニオン）

営業時間：11:00 - 14:00

■マスカットカフェテリア

場　　所：北福利施設（マスカットユニオン）

営業時間：11:00 - 14:00

◇呼び出し

会場内での呼び出しは，緊急の場合を除いて行いません。

◇駐車場

会場には参加者用駐車場はありません。会場へは公共交通機関をご利用ください。

◇休憩室

会場内に参加者用の休憩室を設けておりますので，ご利用ください。

◇インターネット

会場全体において Wi-Fi として国際無線 LAN ローミング基盤（eduroam）がご利用いただけます。既にご自身が所属する教育・研究機関で発行した eduroam の ID をお持ちの

方は，別途申請することなく eduroam に接続することが可能です（Wi-Fi アクセス名 : eduroam）。eduroam の ID をお持ちでない方には，年会期間のみ有効の岡山大学全学無線 LAN システム利用の ID と接続パスワードを年会受付で配布します。

※一部の会場（ポスター会場など），建物の構造や電波，アクセス状況によっては接続できない場合もあります。休憩室は無線 LAN のサービスエリアとなっておりますので，お近くの休憩室をご利用ください。
※無線 LAN システム利用の ID は 1 人につき 1 つのみ発行いたします。
※講演中のインターネットご利用はご遠慮ください。

◇託児所

年会期間中は，託児所を設置いたします。詳しくは年会ホームページをご覧ください。

3. 年会行事・プログラム

◇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第 5 回会員総会を，年会 2 日目の 9 月 16 日（日）12:35 - 13:55 に B 会場（一般教育棟 A 棟 2 階 A21）で開催いたしますのでご出席ください。また，総会シンポジウムも開催します。

◇若手奨励賞招待講演

日本生物物理学会若手奨励賞及び若手招待講演賞の選考会である講演会（若手招待講演シンポジウム）を，年会 1 日目の 9 月 15 日（土）9:00 - 11:30 に B 会場（一般教育棟 A 棟 2 階 A21）で開催します。

◇学生発表賞

日本生物物理学会学生発表賞の選考会である一般口頭発表（9 月 15 日（土）13:30 - ）を開催します。

◇Biophysics and Physicobiology 論文賞受賞講演

Biophysics and Physicobiology 論文賞受賞の講演会を，年会 1 日目の 9 月 15 日（土）12:50 - 13:20 に B 会場（一般教育棟 A 棟 2 階 A21）で開催します。

◇分野別専門委員会

日　時：9 月 16 日（日）11:45 - 12:35
会　場：B 会場（一般教育棟 A 棟 2 階 A21）
対　象：分野別専門委員
昼　食：委員の皆様にはお弁当とお茶を提供します（整理券なし）。

◇懇親会

日　時：9 月 16 日（日）19:15 - 21:15

会　場：岡山ロイヤルホテル（岡山大学津島キャンパスから徒歩約 15 分）

（〒 700-0028 岡山市北区絵図町 2-4）Tel：086-255-1111

※当日参加も受け付けいたします（受付場所：総合受付デスク，または懇親会会場前）。

※当日は徒歩にて会場に向かいます（配慮が必要な方は年会受付にご相談下さい）。

◇男女共同参画･若手支援シンポジウム

日　時：9 月 17 日（月・祝）11:45 - 12:35

会　場：A 会場（一般教育棟 B 棟 1 階 B11）

昼　食：お弁当とお茶が無料で提供されます（整理券を配布いたします。「ランチョンセミナー」の項をご参照ください）。

◇キャリア支援説明会

日　時：9 月 15 日（土）第 1 部 11:50 - 12:40，第 2 部 12:50 - 13:40，第 3 部 13:50 - 14:40，
9 月 16 日（日）第 4 部 9:30 - 10:30

会　場：R 会場（一般教育棟 D 棟 4 階 D42）

対　象：就職を考えておられる学生や研究者など ※詳細は 49 ページをご参照下さい。

昼　食：第 1 部のみ，お弁当とお茶が無料で提供されます（学生・院生を優先して整理券を配布いたします。下記「ランチョンセミナー」の項を参照）。

※下記の時間帯は，大学会館 1F の相談ブースにて個別相談を行っております。

9 月 15 日（土）15:00 - 18:00 / 9 月 16 日（日）13:00 - 18:00

◇科研費説明会

日　時：9 月 17 日（月・祝）11:45 - 12:35

会　場：B 会場（一般教育棟 A 棟 2 階 A21）

昼　食：お弁当とお茶が無料で提供されます（整理券を配布いたします。「ランチョンセミナー」の項をご参照ください）。

◇ランチョンセミナー

昼食（お弁当とお茶, 無料）を摂りながらの共催企業によるセミナーにご参加ください。なお，お弁当の数に限りがあるため当日の以下の時間帯に整理券を配布いたします。セミナー開始前に，会場入り口で整理券と引き換えにお弁当を受け取り，ご入場ください（整理券の発券方法は下記参照）。

◆整理券の発券について

ランチョンセミナー整理券を下記のとおりに配布いたします。

時　間：9 月 15 日（土）- 17 日（月・祝）8:30 - 10:30
場　所：大学会館 1 階展示会場
※整理券はランチョンセミナーの共催企業，団体よりご提供いただく昼食の引換券になります。当日開催されるセミナー分のみ発券いたします。券は枚数が無くなり次第終了となります。

◆整理券の注意事項
整理券は各日，セミナー開始後，無効となります。午前のプログラム終了後，ランチョンセミナー開始時間までにご来場ください。
セミナー開始までにご来場されない場合，整理券は無効となり，お弁当は整理券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。

◆ランチョンセミナー受講時のお願い
ランチョンセミナーは企業，団体等の共催によるセミナーです。参加される場合は最後までご聴講ください。また，共催者のアンケートには，所属・氏名を記載して回答くださるよう，ご協力をお願いします。

◇機器･試薬･書籍等附設展示会
機器，試薬，ソフトウエア，書籍などの附設展示会を大学会館 1 階 ホールで行います。

◇市民講演会
テーマ：「発光と吸光で拓く先端基礎科学」詳細は 45 ページをご参照ください。
会　場：岡山大学 創立五十周年記念館 金光ホール
参加費：参加費無料・要予約

4. 禁止事項

◇撮影･録音
会場内でのカメラ, 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。一部，理事会の承認を得て，録画を行う場合があります。

◇喫煙･飲食
キャンパス内は全面禁煙となっており，喫煙場所はありません。講演会場内での飲食はランチョンセミナー，キャリア支援説明会，男女共同参画・若手支援シンポジウム，科研費説明会，各種委員会など食事が提供される場合を除いて禁止します。

◇携帯電話

講演会場内での携帯電話による通話を禁止します。会場内では電源をオフにするかマナーモードに設定し，呼び出し音が鳴らないようご注意ください。

5. 年会についての問い合わせ

◇問い合わせ先

◆年会実行委員会　E-mail：bp_nenkai56@okayama-u.ac.jp

◆参加登録・演題登録 システムサポートデスク

〒 602-8048 京都市上京区下立売通小川東入る 中西印刷株式会社内

E-mail: bsj2018sys-sprt@e-naf.jp

◆年会実行委員会サポート

〒 532-0003 大阪市淀川区宮原 2-14-14 新大阪グランドビル 6F

株式会社エー・イー企画内

Tel: 06-6350-7163　FAX: 06-6350-7164

E-mail: jbp2018@aeplan.co.jp（年会全般）

E-mail: e_jbp56@aeplan.co.jp（広告・展示関連）

◆年会本部（会期中のみ）　Tel: 080-4137-9158

オーガナイザー・座長・発表者へのご案内

◇使用言語

すべての発表の言語は原則として英語です。

◇発表方法（シンポジウム・口頭発表）

パソコンによる発表となります。必ずご自身のノートパソコンをお持ちください（会場にはパソコンを用意しておりません）。パソコンの操作は発表者ご自身で行ってください。発表データの作成や当日発表の際には以下の点にご留意ください。

注意 1）音声出力には対応しておりません。

注意 2）画像解像度は 1024 × 768 ピクセル（XGA）です。この環境下で発表データを作成してください。これより大きい画面サイズでデータを作成すると，スクリーン映写時に画面をはみ出す等の不具合が起こる可能性があります。

注意 3）会場スタッフがパソコンを会場に備え付けられた切り替え装置（セレクター）に接続いたします。

注意 4）切り替え装置に繋がるパソコンの映像出力端子は，「ミニ D-sub15 ピン端子（メス）」のみです。端子の形状が異なる場合（Macintosh 等），変換アダプターをお持ちください。
注意 5）念のため発表に使用するパワーポイントファイルが入った USB メモリーをお持ちください。
注意 4）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。
注意 5）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。

◇シンポジウムオーガナイザーへのご案内

受　　付：セッション開始の 15 分前までに各会場の「進行席」までお越しの上，係り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，講演者の講演時間を厳守し，円滑な進行にご協力ください。事前に事務局に連絡した各講演者の講演時間等に変更が生じた場合は，会場内の進行スタッフにご指示ください。

◇シンポジウム講演者の方へ

受　　付：セッション開始の 15 分前までに各会場の「PC 接続席」にお越しください。発表スライドをご確認いただいた後，会場スタッフがパソコンを PC 切り替え装置に接続いたします。
講演時間：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講演時間は，発表 10 分，討論 3 分，パソコンの交換に 2 分です。

◇一般口頭発表の座長の方へ

受　　付：担当セッション開始の 15 分前までに各会場の「進行席」までお越しの上，係りの者に来場された旨をお伝えください。
進　　行：会場には時間を計測するスタッフを配置しています。発表者の発表時間を厳守し，円滑な進行にご協力ください。

◇一般口頭発表の講演者の方へ

受　　付：セッション開始の 15 分前までに指定された会場の「PC 接続席」までお越しください。会場スタッフがパソコンを切り替え装置（セレクター）に接続いたします。
講演時間：発表 8 分，質疑応答 3 分 30 秒，交代時間 30 秒

◇ポスター発表の方へ

ポスターの貼付・展示，説明・討論，撤去：

		9 月 15 日（土）	9 月 16 日（日）	9 月 17 日（月･祝）
貼付		8:30 - 9:30	8:30 - 9:30	8:30 - 9:30
説明・討論	奇数番号	16:30 - 17:30	16:30 - 17:30	12:45 - 13:45
	偶数番号	17:30 - 18:30	17:30 - 18:30	13:45 - 14:45
撤去		18:30 - 18:45	18:30 - 18:45	14:45 - 15:00

1. ポスターは日替わりで貼り替えてください。
2. ポスターボードの大きさは，幅 90 cm，高さ 210 cm。貼付に必要な押しピンは会場に用意します。
3. 撤去時間を過ぎて残ったポスターは年会事務局にて破棄しますので，ご了承ください。

◇ポスター発表要項

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。発表代表者の氏名には左肩に小さな○印を付けてください。

※発表形式と演題番号（各予稿左上の番号）の見方

発表形式は，シンポジウム発表（Symposium Speech），若手招待講演シンポジウム（Early Career Award in Biophysics Candidate Presentation Symposium），一般口頭発表（Oral Presentation），ポスター発表（Poster Presentation），があります。

〈シンポジウム発表：（例）1SAA-03の場合〉

1（1 日目）S（シンポジウム）A（A 会場）A（AM: 午前）-03（発表順番）

〈若手招待講演シンポジウム：（例）1YK1045の場合〉

1（1 日目）Y（若手招待講演シンポジウム）K（K 会場）1045（10:45 講演開始）

〈一般口頭発表（例）2B1320の場合〉

2（2 日目）B（B 会場）1320（13:20 発表開始）

※学生発表賞に応募した発表には演題番号の右側に「*」がついております。

〈ポスター発表：（例）3Pos001の場合〉

3（3 日目）Pos（ポスター）001（ポスターパネル番号）

会員総会, 各種委員会のご案内

1. 一般社団法人日本生物物理学会第5回会員総会開催通知

一般社団法人日本生物物理学会第 5 回会員総会を開催いたします。主な議題は下記の通りです。
会員の皆様は，是非ご出席ください。

日　時：9 月 16 日（日）12:35 - 13:55
会　場：B 会場（一般教育棟 A 棟 2 階 A21）
議　長：会長 神取 秀樹
総会議題：
(1) 報告事項
・平成 29 年度決算報告ならびに監査結果報告
・平成 30 年度会計ならびに事業の中間報告と今後の計画
・次期年会について
(2) 第 5 回会員総会シンポジウム：「生物物理学の根本問題 #1: 生物の物理的境界」
※詳細は 46 ページをご覧ください。

2. 理事会, 会員総会, 各種委員会の案内

委員会等	開催日程		会場
ホームページ編集委員会	9 月 14 日（金）	14:00 - 16:00	諸会議室（一般教育棟 A 棟 3 階 A32）
生物物理編集委員会		16:30 - 18:30	
Biophysics and Physicobiology 編集委員会	9 月 15 日（土）	9:40 - 10:40	
出版委員会		10:40 - 11:40	
平成 30 年度第 2 回理事会（旧運営委員会）		11:45 - 12:35	
若手奨励賞選考委員会		16:10 - 17:10	
臨時社員総会		19:00 - 20:20	B 会場
男女共同参画・若手支援委員会	9 月 16 日（日）	10:00 - 11:30	諸会議室（一般教育棟 A 棟 3 階 A32）
分野別専門委員会		11:45 - 12:35	B 会場
会員総会・総会シンポジウム		12:35 - 13:55	B 会場
若手の会会議		16:00 - 17:00	諸会議室（一般教育棟 A 棟 3 階 A32）
企業との意見交換会	9 月 17 日（月）	9:30 - 11:00	諸会議室（一般教育棟 A 棟 3 階 A32）

( ) は法人化前の名称

謝　辞

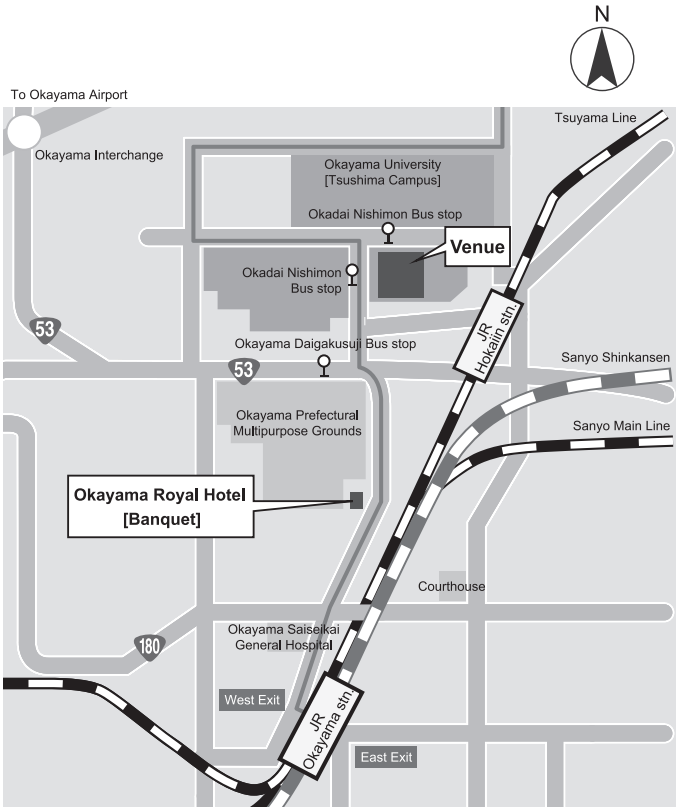
本年会の開催・運営にあたり，以下の団体よりご協力・ご援助いただきました。
関係者一同より御礼を申し上げます。

助成（敬称略）
（公社）おかやま観光コンベンション協会
（公財）岡山医学振興会

共催／協賛（敬称略）
Strategic Japan-Singapore Research Program by JST and A*STAR:New optical platform for mechanics of cellular-self-organization
日本医療研究開発機構（AMED）・創薬等ライフサイエンス研究支援基盤事業
日本医療研究開発機構　革新的先端研究開発支援事業（AMED-CREST/PRIME）
JST-CREST「超絶縁性脂質二分子膜に基づくイオン・電子ナノチャネルの創成」
JST CREST「ライフサイエンスの革新を目指した構造生命科学と先端的基盤技術」領域
CREST「二次元機能性原子・分子薄膜の創製と利用に資する基盤技術の創出」
CREST「光の特性を活用した生命機能の時空間制御技術の開発と応用」
新学術領域研究「宇宙からひも解く新たな生命制御機構の統合的理解：
　　重力変化を含む力学的ストレスに対するメカノセンシング機構」
新学術領域研究「動的構造生命科学を拓く新発想測定技術
　　―タンパク質が動作する姿を活写する―」
新学術領域研究「光合成分子機構の学理解明と時空間制御による革新的光
　　―物質変換系の創製」
新学術領域研究「新光合成：光エネルギー変換システムの再最適化」
新学術領域研究「3D 活性サイト科学」
新学術領域研究「シンギュラリティ生物学」
新学術領域研究「発動分子科学：エネルギー変換が拓く自律的機能の設計」
ポスト「京」重点課題１「生体分子システムの機能制御による革新的創薬基盤の構築」

第 56 回日本生物物理学会年会
実行委員長　沈　建仁

Access Information / Area Map



Access from Okayama Airport

■Bus:

Take a bus bound for “Okayama Station Sports Park Gate (west exit)” at No. 2 bus stop and get off at “Okayama Daigaku Suji” (approx. 30 minutes) and then 7 minutes on foot.

Access from JR Okayama Station

■Taxi: 7 minutes from Okayama Station Sports Park Gate (west exit)

■JR Tsuyama line: 10 minutes by walk from Hōkaiin Station

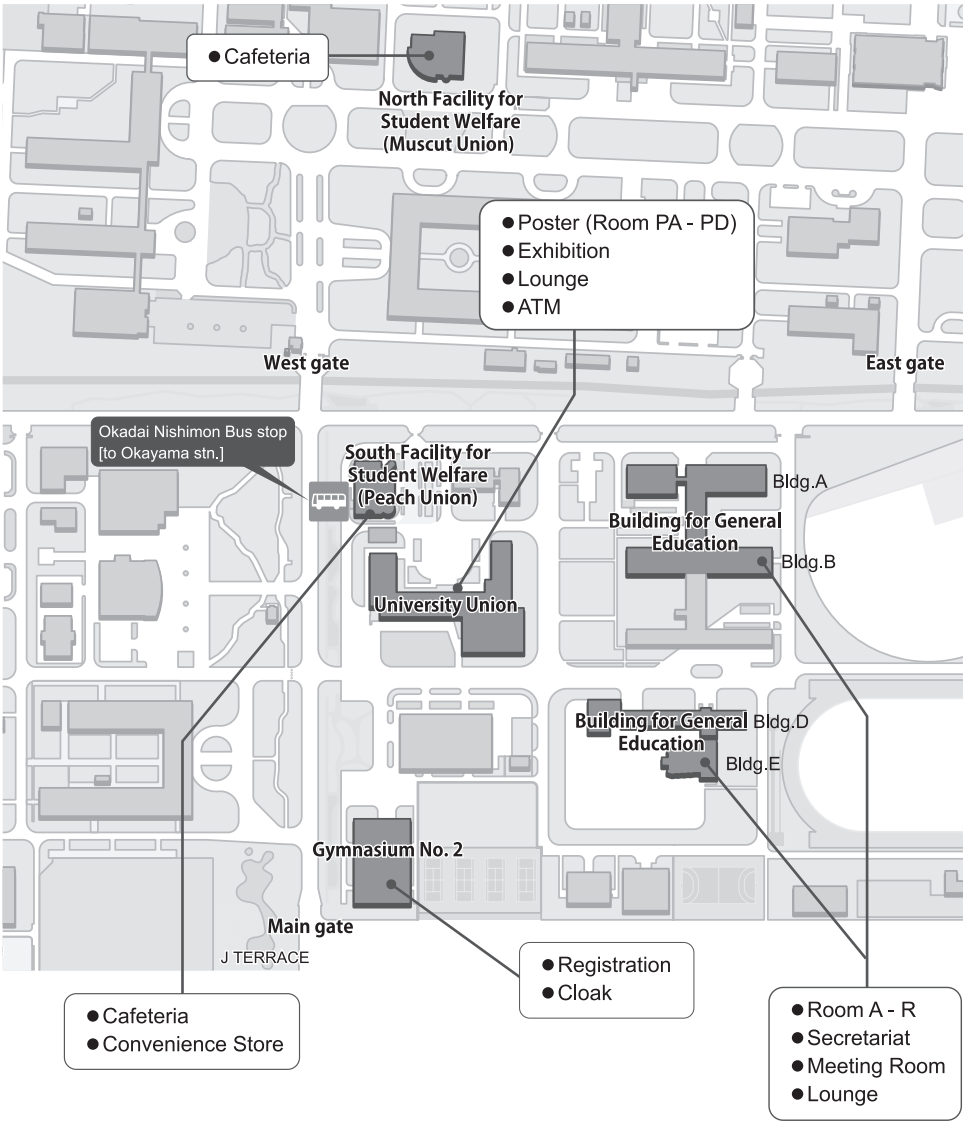
■Bus:

No. 22 bus stop, JR Okayama Station Sports Park Gate (west exit) Bus Terminal:
Take a bus route No. 47 bound for “Okayama Rika Daigaku” and get off at “Okadai Nishimon”. (approx. 7 - 10 minutes)

No. 7 bus stop, JR Okayama Station Korakuen Gate (east exit) Bus Terminal:
Take a bus route No. 16 bound for “Tsudakadai Danchi・Handayama Haitsu”, a bus route No. 26 bound for “Okayama Medical Center”, a bus route No. 36 bound for “Karakou Guchi”, or a bus route No. 86 bound for “Untenmenkyo Center” and get off at “Okayama Daigaku Suji”. (approx. 10 minutes) and then 7 minutes on foot.

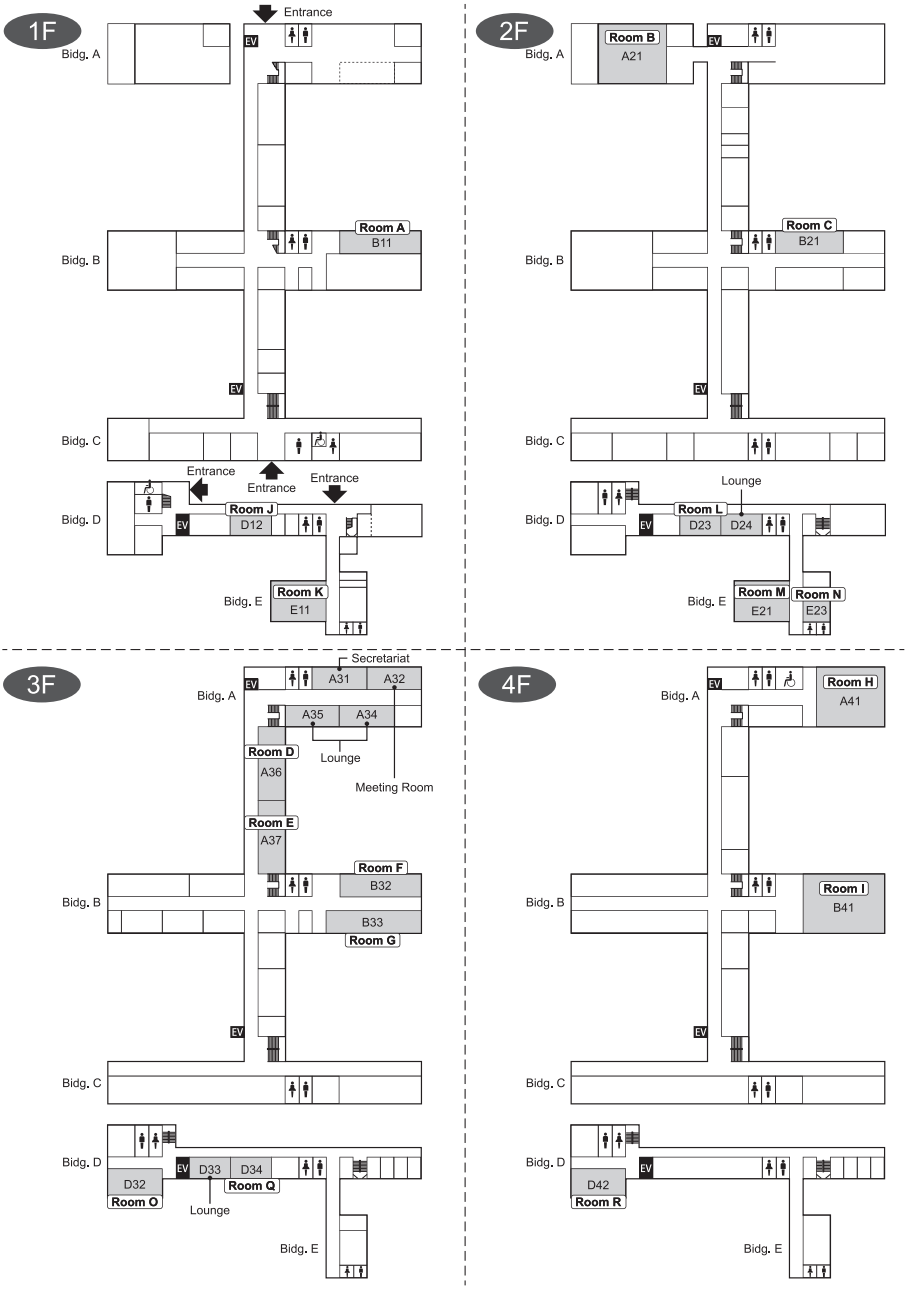
*We recommend using buses which leave from west exit because those are convenience than buses which leave from east exit.

Okayama University, Tsushima Campus

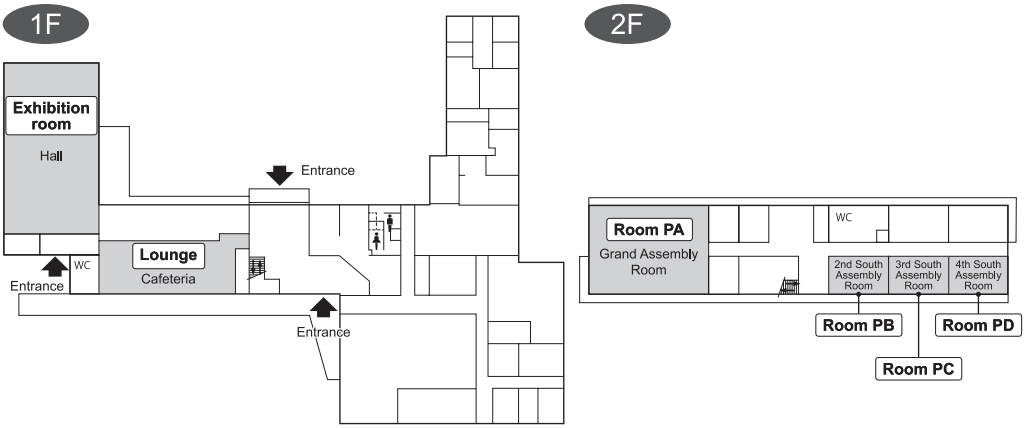


＊No smorking area in the Campus.

General Education Building

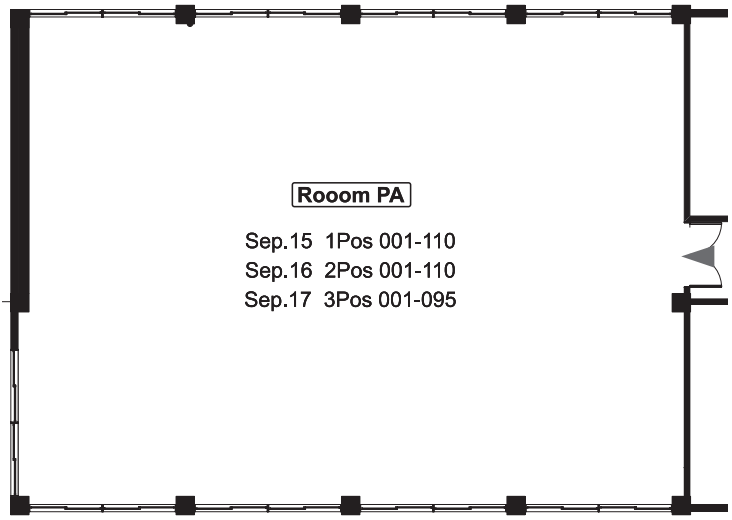


University Union



Poster Place

Grand Assembly Room



2nd South Assembly Room

Rooom PB

Sep.15 1Pos 201-228
Sep.16 2Pos 201-228
Sep.17 3Pos 201-220

3rd South Assembly Room

Rooom PC

Sep.15 1Pos 301-326
Sep.16 2Pos 301-326
Sep.17 3Pos 301-327

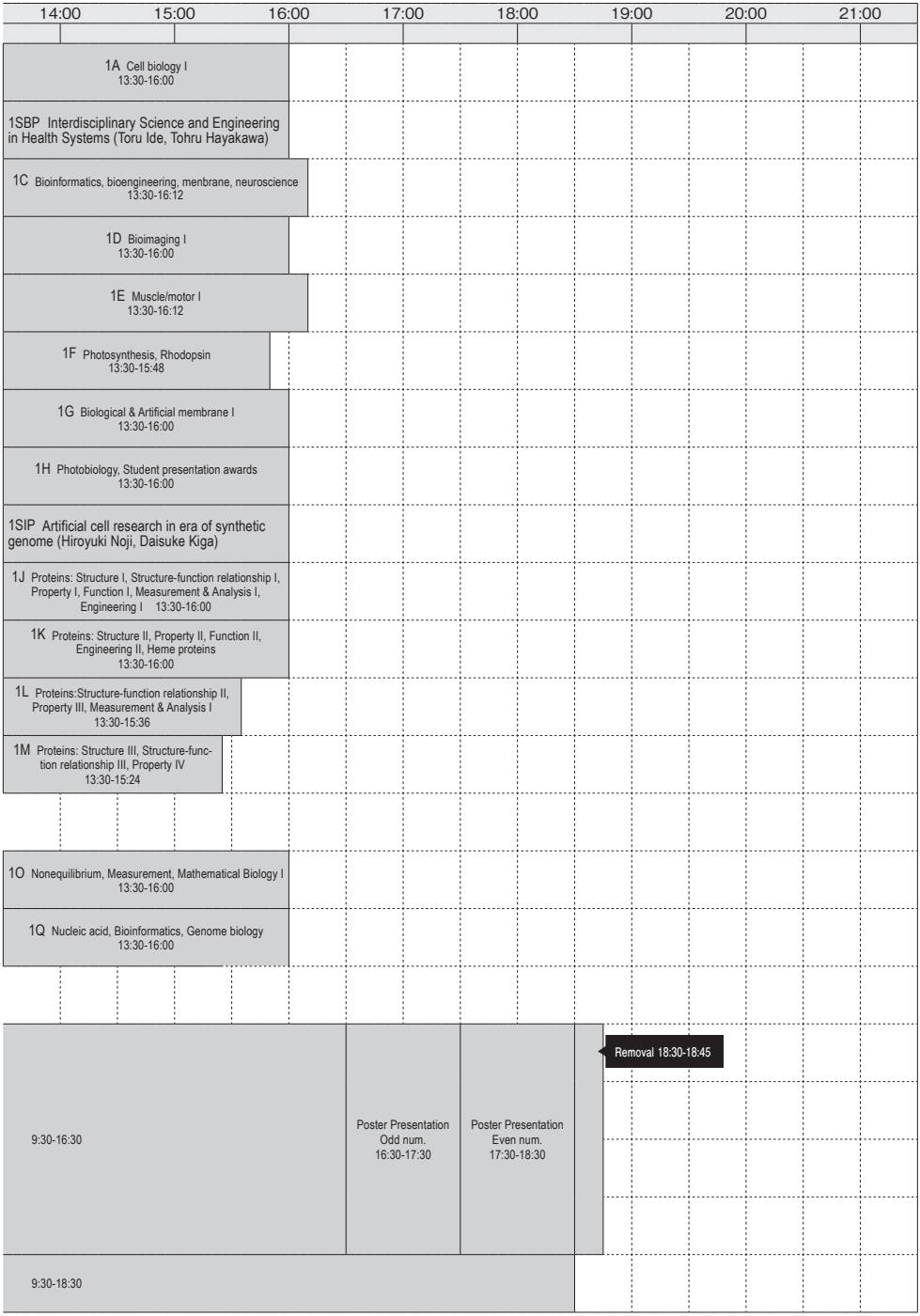
4th South Assembly Room

Rooom PD

Sep.15 1Pos 401-421
Sep.16 2Pos 401-424
Sep.17 3Pos 401-421

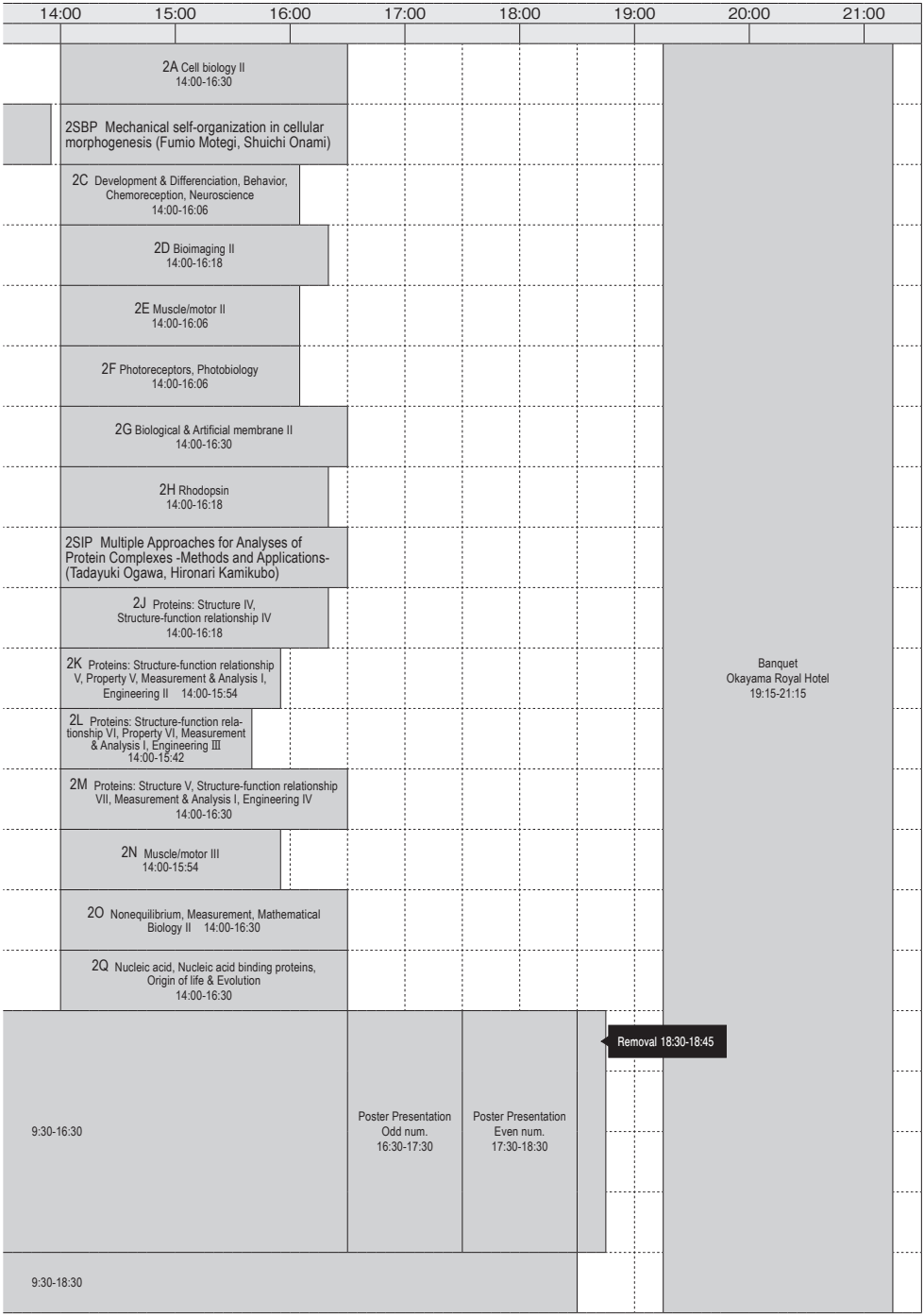
■ September 15 (Sat.) Day 1

Building		Floor	Room	Venue	9:00	10:00	11:00	12:00	13:00
General Education Building	Building A/B	1F	B11	Room A	1SAA Theoretical morphodynamics—towards understanding emerging shapes of life (Satoshi Sawai, Yasuhiro Inoue)			Award Seminar of Outstanding Biophysics and Physicobiology Paper 12:50-13:20	
		2F	A21	Room B	1YB Early Career Award in Biophysics Candidate Presentation Symposium				
			B21	Room C					
		3F	A36	Room D	1SDA Challenges and novel approaches to investigate the structures and dynamics of the 3D active sites in biomolecular systems for understanding the biochemical functions (Yu Takano, Hiroshi Sekiguchi)			1LSD SIGMAKOKI CO., LTD. 11:45-12:35	
			A37	Room E	1SEA Mechanobiology from molecules to tissues: various physical stimuli and its response system (Satoshi Arai, Yuji Hara)			1LSE NIKON INSTECH CO.,LTD. 11:45-12:35	
			B32	Room F	1SFA Geometric cell biology: Uncovering self-organization mechanisms of ordered dynamics and cellular functions by spatio-temporal perturbation (Yusuke T. Maeda, Makito Miyazaki)				
			B33	Room G	1SGA Ingenious mechanisms behind promiscuous recognition, in contrast to precise recognition, by protein molecules (Daisuke Kohda, Tomoya Tsukazaki)			1LSG Leica Microsystems K.K. 11:45-12:35	
		4F	A41	Room H	1SHA Dive into Brain Abyss by Optogenetics (Hiroshi Watanabe, Hideki Kandori)				
			B41	Room I	1SIA Regulation of the signal transduction in cell membrane via localization and clustering of receptors (Kenichi Morigaki, Kenichi Suzuki)				
	Building E/D	1F	D12	Room J					
			E11	Room K	1SKA New trends in bioanalysis based on single molecule biophysics (Rikiya Watanabe, Toru Komatsu)				
		2F	D23	Room L					
			E21	Room M	1SMA Autonomy integrated in motility systems (Taro Q.P. Uyeda, Tohru Minamino)				
			E23	Room N					
		3F	D32	Room O	1SOA The function and mechanism of intramolecular information-transmission in protein (Naoyuki Miyashita, Yasushige Yonezawa)				
			D34	Room Q					
		4F	D42	Room R	1SRA Structural and operating principles of photosynthetic reaction centers: whether quinone is essential or not (Hirozo Oh-oka, Chihiro Azai)				
University Union		2F	Grand Assembly Room	Room PA	Set Up 8:30-9:30			Poster Display	
			2nd South Assembly Room	Room PB					
			3rd South Assembly Room	Room PC					
			4th South Assembly Room	Room PD					
		1F	Large Conference Room	Exhibition				Exhibition	


14:00
15:00
16:00
17:00
18:00
19:00
20:00
21:00
1A Cell biology I
13:30-16:00
1SBP Interdisciplinary Science and Engineering in Health Systems (Toru Ide, Tohru Hayakawa)
1C Bioinformatics, bioengineering, menbrane, neuroscience
13:30-16:12
1D Bioimaging I
13:30-16:00
1E Muscle/motor I
13:30-16:12
1F Photosynthesis, Rhodopsin
13:30-15:48
1G Biological & Artificial membrane I
13:30-16:00
1H Photobiology, Student presentation awards
13:30-16:00
1SIP Artificial cell research in era of synthetic genome (Hiroyuki Noji, Daisuke Kiga)
1J Proteins: Structure I, Structure-function relationship I, Property I, Function I, Measurement & Analysis I, Engineering I 13:30-16:00
1K Proteins: Structure II, Property II, Function II, Engineering II, Heme proteins
13:30-16:00
1L Proteins:Structure-function relationship II, Property III, Measurement & Analysis I
13:30-15:36
1M Proteins: Structure III, Structure-function relationship III, Property IV
13:30-15:24
1O Nonequilibrium, Measurement, Mathematical Biology I
13:30-16:00
1Q Nucleic acid, Bioinformatics, Genome biology
13:30-16:00
9:30-16:30
Poster Presentation
Odd num.
16:30-17:30
Poster Presentation
Even num.
17:30-18:30
Removal 18:30-18:45
9:30-18:30

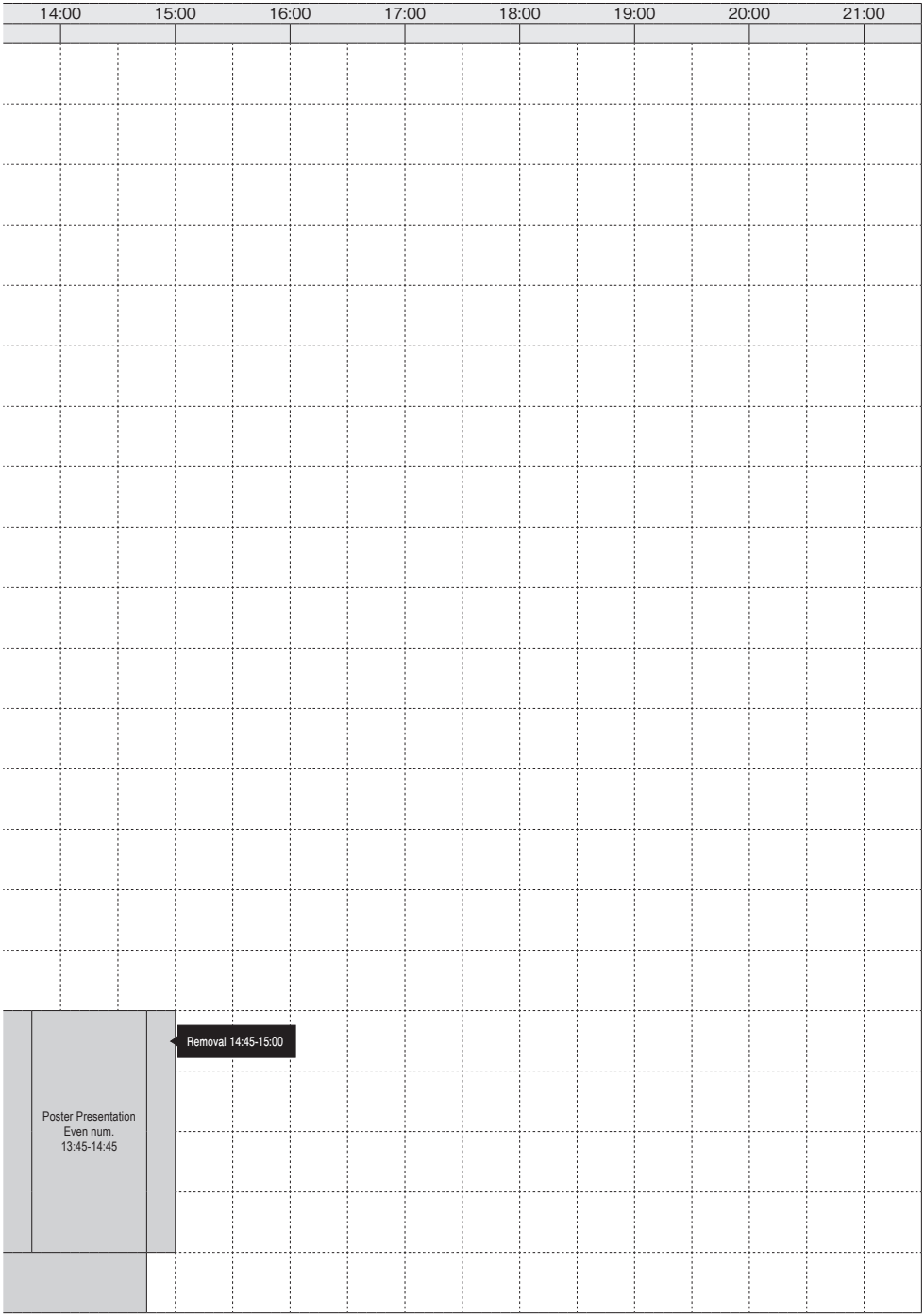
■ September 16 (Sun.) Day 2

Building		Floor	Room	Venue	9:00	10:00	11:00	12:00	13:00
General Education Building	Building A/B	1F	B11	Room A	2SAA Taiwan-Japan biophysics symposium on molcular motors *in vivo* (Kumiko Hayashi, Chien-Jung Lo)				
		2F	A21	Room B	2SBA Cryo electron microscopy (Toshiya Senda, Zhenfeng Liu)			Experts Committee 11:45-12:35	General Assembly Symposium 12:35-13:55
			B21	Room C					
		3F	A36	Room D	2SDA Basis for Supporting Innovative Drug Discovery and Life Science Research (BINDS) (Masaru Tanokura, Kei Yura)			2LSD PDBj 11:45-12:35	
			A37	Room E	2SEA Keynote of mechanosignal response for the future of mechanobiology (Masatoshi Morimatsu, Naotaka Nakazawa)			2LSE Malvern Panalytical division of Spectris Co., Ltd. 11:45-12:35	
			B32	Room F	2SFA Reconstruction of biological functions for sensing methods and device applications (Ryugo Tero, Ayumi Hirano-Iwata)				
			B33	Room G	2SGA Mechanism of Biomolecular Dynamics and Function Revealed by Multiscale Physics (Hidetoshi Kono, Tohru Terada)			2LSG HAMAMATSU PHOTONICS K.K. 11:45-12:35	
		4F	A41	Room H	2SHA The new fertile land of photobiology opened in genomic era (Keiichi Inoue, Takahiro Yamashita)				
			B41	Room I					
	Building E/D	1F	D12	Room J					
			E11	Room K	2SKA New approaches to protein reaction dynamics pioneered by X-ray free electron lasers and interdisciplinary collaborations (Minoru Kubo, Eriko Nango)				
		2F	D23	Room L					
			E21	Room M	2SMA Designing biological systems from scratch (Hisashi Tadakuma, Ken'ya Furuta)				
			E23	Room N					
		3F	D32	Room O	2SOA Developments and future of piocobiology (Yasuhisa Mizutani, Satoru Nakashima)				
			D34	Room Q					
University Union		2F	Grand Assembly Room	Room PA	Set Up 8:30-9:30			Poster Display	
			2nd South Assembly Room	Room PB					
			3rd South Assembly Room	Room PC					
			4th South Assembly Room	Room PD					
		1F	Large Conference Room	Exhibition				Exhibition	


14:00
15:00
16:00
17:00
18:00
19:00
20:00
21:00
2A Cell biology II
14:00-16:30
2SBP Mechanical self-organization in cellular morphogenesis (Fumio Motegi, Shuichi Onami)
2C Development & Differenciation, Behavior, Chemoreception, Neuroscience
14:00-16:06
2D Bioimaging II
14:00-16:18
2E Muscle/motor II
14:00-16:06
2F Photoreceptors, Photobiology
14:00-16:06
2G Biological & Artificial membrane II
14:00-16:30
2H Rhodopsin
14:00-16:18
2SIP Multiple Approaches for Analyses of Protein Complexes -Methods and Applications- (Tadayuki Ogawa, Hironari Kamikubo)
2J Proteins: Structure IV, Structure-function relationship IV
14:00-16:18
2K Proteins: Structure-function relationship V, Property V, Measurement & Analysis I, Engineering II 14:00-15:54
2L Proteins: Structure-function relationship VI, Property VI, Measurement & Analysis I, Engineering III
14:00-15:42
2M Proteins: Structure V, Structure-function relationship VII, Measurement & Analysis I, Engineering IV
14:00-16:30
2N Muscle/motor III
14:00-15:54
2O Nonequilibrium, Measurement, Mathematical Biology II 14:00-16:30
2Q Nucleic acid, Nucleic acid binding proteins, Origin of life & Evolution
14:00-16:30
Banquet
Okayama Royal Hotel
19:15-21:15
Removal 18:30-18:45
9:30-16:30
Poster Presentation
Odd num.
16:30-17:30
Poster Presentation
Even num.
17:30-18:30
9:30-18:30

■ September 17 (Mon.) Day 3

Building		Floor	Room	Venue	9:00	10:00	11:00	12:00	13:00
General Education Building	Building A/B	1F	B11	Room A	3SAA Cutting edge of diversity and light-dependent function of photolyase/cryptochrome superfamily (Junpei Yamamoto, Daichi Yamada)			Gender Equality & Young Researchers Support Symposium 11:45-12:35	
		2F	A21	Room B	3SBA Physical force in the life (Keiji Naruse, Atsushi Higashitani)			KAKENHI Guide Meeting 11:45-12:35	
			B21	Room C					
		3F	A36	Room D	3SDA New horizon of Structural Life Science (Atsushi Nakagawa, Shimizu Toshiyuki)				
			A37	Room E	3SEA Novel concepts of chemical senses (Hiroo Imai, Atsuko Yamashita)				
			B32	Room F	3SFA Singurality biology (Takeharu Nagai, Kazuki Horikawa)				
			B33	Room G	3SGA Single Particle Analysis of Biological Molecules to Study Dynamics and Functions (Osamu Miyashita, Kenji Iwasaki)			3LSG Thermo Fisher Scientific K.K. 11:45-12:35	
		4F	A41	Room H	3SHA Biophysics of light-energy conversion: To what extent has the mechanism of photosynthesis been clarified? (Takumi Noguchi, Michi Suga)				
			B41	Room I	3SIA East Asian symposium: Frontiers of single-molecule biophysics (Yasushi Sako, Ming Li, Jie Yan, Tae-Young Yoon)				
	Building E/D	1F	D12	Room J					
			E11	Room K	3SKA From the elephant to *E. coli*- is it all the same? (Daisuke Nakane, Seiji Kojima)				
		2F	D23	Room L					
			E21	Room M	3SMA "Metallodynamics" in Microorganisms and its Various Applications (Yoshiaki Furukawa, Takehiko Tosha)				
			E23	Room N					
		3F	D32	Room O					
			D34	Room Q					
University Union		2F	Grand Assembly Room	Room PA	Set Up 8:30-9:30	Poster Display 9:30-12:45			Poster Presentation Odd num. 12:45-13:45
			2nd South Assembly Room	Room PB					
			3rd South Assembly Room	Room PC					
			4th South Assembly Room	Room PD					
		1F	Large Conference Room	Exhibition		Exhibition 9:30-14:45			


14:00
15:00
16:00
17:00
18:00
19:00
20:00
21:00
Removal 14:45-15:00
Poster Presentation
Even num.
13:45-14:45

Information for Participants and Presenters

1. Registration

◇Registration desk

Location：Gymnasium No. 2

Open Hours：8:30 - 17:00 [8:30 - 14:00 on Sep. 17(Mon.)]

◆Advance registration

For participants who have completed advance registration with full payment of the registration fee by the deadline, there is no need to stop by the registration desk. A name badge, a receipt and a program booklet have already been sent to these participants.

*Participants from overseas: Receive a name badge and a program booklet at the registration desk.
*Please wear your name badge throughout the meeting. Without it, you cannot enter the meeting site. (Name badge holders will be provided at a place near the registration desk and near the building entrance.)

Note 1) Advance registration is completed only after the payment is done. In case your payment cannot be confirmed by the deadline, your registration is automatically cancelled. In this case, please register on-site at the registration desk.
Note 2) Name badges have not been sent to those who have not paid the BSJ annual membership fee. Please complete the payment at the BSJ desk of the meeting site.
Note 3) If you have already paid both registration and BSJ annual membership fees but not received a name badge, please visit the registration desk.
Note 4) For non-members who are invited to talk at a symposium, the membership is not required and your registration fee is waived.

◆On-site registration

Those who have not completed advance registration are required to register on-site at the registration desk. Only cash payment is acceptable.

◇On-site registration fees

	BSJ Member				Non-Member		
	Regular	Senior	Student	Undergraduate student	Regular	Student	Undergraduate student
Registration fee	JPY9,000	JPY5,000	JPY5,000	FREE	JPY12,000	JPY6,000	FREE
Banquet fee	JPY8,000	JPY5,000	JPY5,000	JPY3,000	JPY8,000	JPY5,000	JPY3,000

・For undergraduate students, the registration fee is waived. You are required to present your student ID at the registration desk to receive a name badge and a program booklet.
・The “Early Career Award in Biophysics” Candidate presenters, the Biophysics and Physicobiology Outstanding Paper Award presenter and the representative of Biophysics and Phys-

icobiology Editors' Choice awardee are invited for free to the banquet. If you have already paid the banquet fee, you can get a full refund at the registration desk.

◇Name badge

Please be sure to wear your name badge throughout the meeting. Entry without the badge is NOT acceptable. Remember to bring your name badge that was sent in advance.

◇Receipt

A receipt is attached to the name badge. If you need another receipt form, it will be issued in exchange for the one attached to your name badge.

◇Program booklet / Abstract online system【Release date: Aug. 17 (Fri.)】

A program booklet (a part of front matters, and program) will be sent in advance to BSJ members and non-members with advance registration. The abstracts will be released only on the online system. No printed abstract booklet will be issued. On the online system, you can browse, search and download abstracts.

Program booklets can be purchased at the meeting site: JPY3,500/booklet.

Abstract online system：
http://www.biophys.jp/dl/pro/56th_proceedings.pdf
Download ID: ambsj56
PW: okayama2018

The program (presentation title, presenter's name and affiliation) and the online abstracts will be released on the BSJ56 web site. A half year later after the meeting, the abstracts will be posted on the J-Stage web site which is linked from the BSJ web site.

BSJ web site: http://www.biophys.jp/ann/ann02.html

J-Stage web site: http://www.jstage.jst.go.jp/browse/biophys/-char/ja

◇Program search system (Web version)【Release date: Aug. 9 (Thu.)】

Program search system will be released on the BSJ56 web site.

◇BSJ membership (payment of the annual membership fee, and admission procedures)

For those who have not yet paid their annual membership fee, you can pay at the BSJ desk. For non-members, you are welcome to sign up at the BSJ desk to become a new member. For non-members who are invited to talk at a symposium or belong to institutions outside of Japan, the BSJ membership is not required.

2. Services & Facilities

◇Cloakroom

Location：Gymnasium No. 2
Open Hours：8:30 - 18:45 [8:30 - 15:00 on Sep. 17(Mon.)]

*Valuables or computers cannot be checked into the cloak since the society/meeting does not hold any responsibility for loss or damage of your items.
*Please pick your items up when you leave the meeting venue.

◇Lunch

Free lunch:
Free lunch will be provided at luncheon seminars (day 1-3), Career Support Meeting (day 1), Gender Equality & Young Researchers Support Symposium (day 3), and KAKENHI Guide Meeting (day 3). Lunch tickets will be distributed in the morning of day 1-3. Please refer to luncheon seminar page.

◆Cafeteria

A Cafeteria is available as follows:
[Peach Cafeteria]
Location: South Facility for Student Welfare (Peach Union)
Open hours: 11:00 - 14:00
[Muscut Cafeteria]
Location: North Facility for Student Welfare (Muscut Union)
Open hours: 11:00 - 14:00

◇Paging service

No paging service is available to call an individual except for an emergency.

◇Parking

Parking lot is not available for participants.

◇Lounge

Please refer to the locations on the floor map page.

◇Internet

Enduoam as Wi-Fi is available at the meeting site. You can access internet with your ID of eduroam. If you don't have an eduroam ID, please receive it at the registration desk.
*Wi-Fi can be unstable in some spots.
*Free Wi-Fi is available at the lounge.
*Please refrain from using internet during lectures.

3. Programs & Events

*Several programs and events (committee meetings, general assembly meeting and its associated

symposium, and lecture for public) are omitted here.

◇"Early Career Award in Biophysics" Candidate presentations

Date & Time: Sep. 15 (Sat.) 9:00 - 11:30
Place: Room B (A21, General Education, Bldg. A, 2F)

◇Student Presentation Award

This award will be selected from among oral presentations on Sep. 15 (Sat.) 13:30.

◇Lecture by Biophysics and Physicobiology Outstanding Paper Awardees

Date & Time: Sep. 15 (Sat.) 12:50 - 13:20
Place: Room B (A21, General Education, Bldg. A, 2F)

◇Banquet

Date & Time: Sep. 16 (Sun.) 19:15 - 21:15
Place: Okayama Royal Hotel
(a 15-minute walk from Okayama University)
Address: 2-4 Ezu-cho, Kita-ku, Okayama-city / Tel: 086-255-1111
*On-site registration is available at the registration desk or the banquet reception desk.
*There is no shuttle bus service and we'll head to the venue on foot (Those who need any assistance, please do not hesitate to consult with staff at the general information).

◇Luncheon seminar

Lunch tickets will be distributed at the luncheon seminar desk as shown below.

◆Distribution of lunch tickets

Luncheon seminar desk
Hours: Sep. 15 - 17　8:30 - 10:30
*The desk will be closed when all the tickets are distributed.
Location: Exbition room (Hall, University Union, 1F)
*Only tickets for the seminars on the day are provided on a first-come-first-served basis.
*Lunches are provided by courtesy of companies and groups co-sponsoring luncheon seminars.

◆Attention

Please note that the lunch tickets will become invalid when you do not come before the starting time of the seminars and that the resulting remaining lunches will be provided to those who are attending the seminars without lunch tickets.

◆Request

We kindly ask you to attend till the last. Also, please enter your affiliation and name in the questionnaire provided at the luncheon seminar as possible as you can.

◇Exhibition

Instruments, reagents, software, books, etc. are displayed at the exhibition hall (University Union 1F).

4. Prohibited Items

◇Photography & recording

Photography and recording with camera, video, mobile phone and any device is NOT allowed at the meeting site. Please note that some recording may be performed after obtaining the board meeting's approval.

◇Smoking, drinking & eating

Smoking is NOT allowed at the meeting site. No smorking areas in the Campus. Drinking and eating is NOT allowed inside lecture rooms except for luncheon seminars and other seminars/ meetings in which meals are served.

◇Mobile phone use

Talking on a mobile phone in the lecture/presentation rooms is NOT allowed. Please set your mobile phone on the silent mode or off, and make sure it will not make noises during lectures/ presentations.

5. Contact

◇During the meeting

Secretariat (Tel: 080-4137-9158 *phone number reachable during the meeting)

◇Before or after the meeting

◆The organizing committee of the BSJ56

bp_nenkai56@okayama-u.ac.jp

◆Registration and abstract submission support desk

Nakanishi Printing Company
Ogawa-higashiiru, Shimodachiuri-dori, Kamigyo-ku, Kyoto 602-8048
bsj2018sys-sprt@e-naf.jp

◆Support team, exhibition and advertisement secretariat

A & E planning Co., Ltd.
Shin-Osaka Grand Bldg. 6F, 2-14-14, Miyahara, Yodogawa-ku, Osaka 532-0003
Tel: 06-6350-7163 / Fax: 06-6350-7164
Support team: jbp2018@aeplan.co.jp
Exhibition and Advertisement secretariat: e_jbp56@aeplan.co.jp

Information for Organizers, Chairpersons and Presenters

◇Language

Prepare your slides in English and give your presentation in English.

◇Projector

Please bring a laptop with you for your presentation. A projector is equipped in each lecture room. A sound output is not accepted.

1) Please prepare your presentation file in Microsoft PowerPoint.
2) The output resolution should be XGA (1024 × 768). The higher resolutions would possibly lose some information.
3) Our staff will connect your laptop to a switcher.
4) The output connector of your laptop should be "miniD-sub15pin". If your connector is a different type (for example, that of Macintosh computer), please bring a conversion adaptor.
5) Bring your PowerPoint file in a USB memory.
6) Bring your AC adaptor in case that your battery would die.
7) Deactivate the screen-saver and power saving mode of your laptop.

◇For organizers of symposia

Please come to the assigned room by 15 minutes before the start of the session, and then tell our staff of your arrival. Keep the time schedule and make smooth progress in the program. As a time keeper, our staff will help you.

◇For speakers of symposia

Please come to the "Preview Desk" in the assigned room by 15 minutes before the start of the session.

Our staff will connect your computer to a switcher.

*Please note that there is no preview room.

◆Time allocation:

Symposium: Time allocation will be controlled by chairpersons.

"Early Career Award in Biophysics" Candidate Presentation: Presentation 10 min. + Discussion 3 min + Laptop change 2 min.

◇For chairpersons of oral presentation

Please come to the assigned room at least 15 min before the start of the session, and then inform our staff of your arrival. Keep the time schedule and make smooth progress of the session. As a time keeper, our staff will help you.

◇For speakers of oral presentation

Please come to the "Preview Desk" in the assigned room by 15 min before your presentation. Our staff will connect your laptop to a switcher.

* Please note that there is no preview room.

◆Time allocation: Presentation 8 min.+ Discussion 3 min. & 30 sec. + Laptop change 30 sec.

◇For poster presenters

		Day 1, Sep. 15	Day 2, Sep. 16	Day 3, Sep. 17
Setup		8:30 - 9:30	8:30 - 9:30	8:30 - 9:30
Presentation Discussion	Odd Numbers	16:30 - 17:30	16:30 - 17:30	12:45 - 13:45
	Even Numbers	17:30 - 18:30	17:30 - 18:30	13:45 - 14:45
Removal		18:30 - 18:45	18:30 - 18:45	14:45 - 15:00

*Periods of poster display: Posters will be replaced every day for the next day's poster presentations.
*Panel size: 90 cm wide × 210 cm high. Push pins are available at the site.
*Removal: Any posters remaining on panels after the removal time will be discarded by the secretariat.

◇Instructions for poster presentation

A poster must be written in English.
Put a small circle on the upper left of the presenter's name.

◇Presentation types and how to read the presentation numbers

Presentation types are Symposium Speech, "Early Career Award in Biophysics" Candidate Symposium, Oral Presentation, and Poster Presentations.

Speech at symposium: (Ex.) 1SAA-03
Presentation day (1, Sep. 15; 2, Sep. 16; 3, Sep. 17) + Symposium (S) + Session room (Room A) + AM (A) / PM (P) + Order of the talk

"Early Career Award in Biophysics" Candidate Symposium: (Ex.) 1YK1045
Presentation day (1, Sep. 15) + Young Scientists (Y) + Session room (Room K) + Starting time of the talk

Oral Presentation (Ex.) 1B1320
Presentation day (1, Sep. 15; 2, Sep. 16; 3, Sep. 17) + Session room (Room B) + Starting time of the talk
For presentations which are eligible for consideration for Student Presentation Award, "*" is attached on the right side of a presentation number.

Poster presentations: (Ex.) 1Pos001
Presentation day (1, Sep. 15; 2, Sep. 16; 3, Sep. 17) + Poster (Pos) + Panel number

第 56 回日本生物物理学会年会　市民講演会
「発光と吸光で拓く先端基礎科学」

日　時：9 月 16 日（日）13：30 ～ 15：30
会　場：岡山大学 創立五十周年記念館 金光ホール
主　催：第 56 回日本生物物理学会年会実行委員会
共　催：岡山大学
世話人：須藤 雄気（岡山大学）
　　安井 典久（岡山大学）

〈講演者〉

天野　浩　名古屋大学
未来材料・システム研究所
未来エレクトロニクス集積研究センター
センター長・教授

青色発光ダイオードの発明に貢献し
2014 年ノーベル物理学賞を受賞

沈　建仁　岡山大学
異分野基礎科学研究所
副所長・教授

光化学系 II の構造解析研究が 2011 年
サイエンス誌が選ぶ科学 10 大成果に選出

※参加費無料，講演は日本語で行われます。

第 5 回会員総会シンポジウム
生物物理学の根本問題 #1：生物の物理的境界

オーガナイザー：日本生物物理学会　理事会
日　時：9 月 16 日（日）12:35 〜 13:55（会員総会中）
会　場：B 会場（一般教育棟 A21）
司　会：林重彦

概要：今回の総会シンポジウムより，「生物物理学の根本問題」と銘打ったシンポジウムを開催することになった。本シンポジウムでは，生物物理学が中心的役割を果たす過去から未来にわたる学術的問題を俯瞰し議論することを目的とする。

第一回目は「生物の物理的境界」と題し，生物を単なるモノから分けているものは何であるかを問う。生体活動では，ミクロなモノである機能性分子が細胞空間という物質的反応場で協奏し，時々刻々と変化する多様な時空間長距離秩序が生み出されている。このような生物体の分子システムとしての物理的秩序化は，遺伝子改変に基づく合成生物学や網羅的アプローチが与える情報システムとしての生物体の観点のみからでは理解できない。そこで，本シンポジウムでは，それを相補する「生物体を生物たらしめている物理的・物質的側面」を議論し，生物の理解に対する新しい視座を見定める。

講演者・プログラム

1. 問題提起：宮田 真人（大阪市立大学）
2. 関連分野研究者による話題提供：宮﨑 牧人（京都大学），杉田 有治（理化学研究所）
3. パネルディスカッション

一般社団法人日本生物物理学会　第 7 回 Biophysics and Physicobiology 論文賞受賞講演会

The 7th 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 15 日（土）12:50 - 13:20／Sept. 15 Sat.

場　所：B 会場（一般教育棟 A21）／Room B (Building for General Education A21)

形　式：講演会／Lecture

第 7 回 Biophysics and Physicobiology 論文賞受賞者

中村由樹[1,2,3]，日比野佳代[1,4]，柳田敏雄[2]，佐甲靖志[1]

Yuki Nakamura[1,2,3], Kayo Hibino[1,4], Toshio Yanagida[2], Yasushi Sako[1]

[1]理化学研究所，[2]大阪大学，[3]現・川越南高校，[4]現・遺伝研

[1]RIKEN, [2]Osaka Univ., [3]present addresses, Kawagoe Minami H.S., [4]NIG

細胞内情報処理蛋白質 SOS の 1 分子機能解析

Single-molecule analysis of a cell signaling protein, SOS

As a guanine nucleotide exchange factor (GEF) for a small G-protein RAS, Son of sevenless (SOS) regulates cell fate decision. SOS consists of six domains, five of which possess direct or indirect membrane association activity. Because RAS is on the cytoplasmic side of the plasma membrane, controlled membrane association is essential for SOS. Actually, two of the membrane association domains of SOS are responsible for its GEF function, i.e., Cdc25 domain has GEF activity and REM domain binds with the active form of RAS to form a positive feedback loop of RAS activation. However, roles of other three membrane association domains were obscure. Even if these domains are used for SOS translocation to the plasma membrane upon cell stimulation, why so many numbers of them are required? By using single-molecule imaging of fluorescently-labelled SOS in living cells, we investigated mechanism of SOS translocation and found that at least two of the membrane association domains (PH and G domains) are cooperatively used for membrane association coupled with a structural change in SOS molecule, which seems to be important for non-linear switching of SOS activity[1]. Using the same method, we analyzed three mutants of SOS found in a genetic disease Noonan syndrome[2]. Having multiple domains is a common nature of cell signaling proteins. Our studies show that single-molecule imaging is useful for the functional analysis of multi-domain proteins in cells.

1. Nakamura et al. Biophys. Physicobiol. 13:1-11 (2016)

2. Nakamura et al. Sci. Rep. 7:14153 (2017)

男女共同参画・若手支援委員会企画シンポジウム
世代間ギャップから見えてくる今必要な若手研究者支援
(Support for young researchers visible from generation gap)

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 17 日（月・祝）11:45 - 12:35（ランチョンセミナーの時間帯）

会　場：A 会場（一般教育棟 B11）

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：問題提起プレゼンテーションとグループディスカッション

司　会：渡邉宙志（慶應大）

問題提起：高田彰二（京都大），大上雅史（東工大），光武亜代理（明治大）
（当日変更可能性あり）

概要：博士号取得から PI として独立するまでの期間は最も研究に集中できる時期ですが，近年はプロジェクトに紐付いた雇用形態が増加し，若手研究者からは自由な研究活動・チャレンジ・独立を促す制度を望む声が挙がっています。また任期付きポストが一般的となり，流動性が確保された一方で，若手研究者は多くの異動を経験するようになりました。女性の社会進出は進んでおり，共働き世帯の数は専業主婦世帯の 2 倍まで増加している中で，家庭を持つ研究者は家族との別居という選択に直面することが多くなりました。30 代〜40 代という子育て時期と，研究者としてより一層の飛躍を目指す時期が重なり，働き方が変わってきた中でどのように自身の生活と研究者としてのキャリアアップを両立していくかは大きな課題です。社会状況が急速に変化する中で，若手研究者と彼／彼女らを雇用・受け入れる側のシニア研究者との間に，働き方・キャリア形成に関する考え方のギャップが生じる可能性が高まっています。

本企画シンポジウムでは，世代間でどのようなギャップがあるかを明らかにし，今まさに必要な若手研究者への支援について考えていきたいと思います。はじめに，高田氏に統計的なデータから世代間ギャップを論じてもらいます。その後，提示されるいくつかの具体的経験談や独自のアイデアをベースに，必要な制度について世代ごとに分かれたグループで話し合ってもらいます。

学生，若手研究者の方の参加を歓迎します。生物物理という多様性のある学問分野を渡り歩いてきた，ミドル・シニア世代の方からも，厳しい世界を乗り越えられてきたご自身の貴重な経験を踏まえて，意見・助言等いただければと思います。各々の置かれている状況や意見をざっくばらんに交わすことで，今，何が必要なのか，探っていきたいと思います。

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 15 日（土）第 1 部 11:45 - 12:35，第 2 部 12:45 - 13:35，第 3 部 13:45 - 14:35，
個別相談会 14:45~
9 月 16 日（日）第 4 部 9:30 - 10:30，個別相談会 10:40~
会　場：R会場
形　式：セミナー 第 1 部のみランチョンセミナー **説明はすべて日本語で行われます。**

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）アカリクの就職支援コンサルタント 吉野宏志氏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。第 1 部のみランチョンセミナーのため参加者数に限りがありますが，第 2 部以降から参加することも可能です。また昨年度に挙がった要望を踏まえ今年度は個別相談会を実施いたします。人前では難しい個人的な相談等があれば，是非活用ください。

プログラム：　　**9 月 15 日（土）**

第 1 部 11:45 - 12:35　博士・PD の方の為の就活ガイダンス
【博士・PD 向け】 中途採用（即戦力採用）の強化，ダイバーシティ（人材の多様化）の推進などが積極的に取り組まれている現在の企業採用事情。4 ～ 5 年前と比べ，明らかにその就職事情は好転しています。しかし，その状況を活かせるかは，就職事情の理解度とその対策により変わります。そこで以下 3 点を中心に皆様が置かれた現状を紹介します。①現在の企業の採用活動 ②博士・PD の就活 ③専門性を活かせる企業の探し方

第 2 部　12:45 - 13:35　先人に学ぶ，研究職以外でどんな「活きる道」があるのか
【修士・博士・PD 向け】 第 1 部の講演内容を受けて，どのような選択肢が博士・PD にあるのかについて，先人達の就職実績に基づきながら，「生物物理」専門の方に特化した内容で講演します。生物物理と相性の良い具体的な求人も紹介します。（求人状況によって変わる可能性有）

第 3 部　13:45 - 14:45　「専門外就職」へ向けて何をすべきか
【修士・博士・PD 向け】 アカデミックの技術や知識が民間で 100% 活かせることは多くありません。そこで「専門外就職」をするにあたり何をすべきか解説します。また専門外就職では面接においてネガティブな質問を受ける場合があります。そこで書類の書き方や面接での話し方など採用のためのノウハウなど具体的な内容に踏み込んで解説します。

個別相談会 14:45 ～　私は就職できますか？
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。また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。相談予約方法は 1 ～ 3 部のセミナー中に提示します。

9 月 16 日（日）

第 4 部　09:30 - 10:35　短期集中セミナー
【修士・博士・PD 向け】 初日に参加できなかった方のために，初日情報をまとめたセミナーを実施します。

個別相談会 10:40 ～　今のあなたの市場価値は？
初日に参加できなかった方のために再度実施いたします。相談予約方法は 1 ～ 4 部のセミナー中に提示します。

「科研費」の最近の動向
Reorganization of KAKENHI: Current Activitiesof JSPS

世話人：原田慶恵（大阪大学蛋白質研究所，日本学術振興会学術研究システム研究センター専門研究員）

Organizer: Yoshie Harada (Institute for Protein Research, Osaka University; Program Officer, Research Center for Science Systems, JSPS)

日　時：9 月 17 日（月・祝）11:45 - 12:35（ランチョンセミナーの時間帯）

会　場：B 会場（一般教育棟 A21）

言　語：日本語

昼　食：お弁当とお茶が無料で提供されます。ただし，数に限りがあります。

形　式：日本語による講演会

講師：日本学術振興会　研究助成企画課長代理　坂本　真梨子

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，このシステム改革の内容を中心に，その他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 15 日（土））／Day 1（Sep. 15 Sat.）

9:00〜11:30　B 会場／Room B：A21 教室／A21
1YB　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

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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 14th year, we received 33 highly qualified applications. After the first round of competitive screening based on submitted documents, the following ten applicants were selected as the young invited speakers. In this symposium, each speaker will make 10-minute presentation followed by 3-minute discussion as the second round of screening. Up to five awardees of the Early Career Award in Biophysics will be selected and announced at the banquet held in the evening of the second day. 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 researches.

9:00　**市川　宗厳**　2M1554

1YB0900　**クライオ電子顕微鏡を用いた高分解能構造解析による軸糸ダブレット微小管の構築・安定化機構の解明**
Cryo-electron microscopy revealed a high-resolution structure of doublet microtubule and its assembly and stabilization mechanisms
○市川 宗厳 [1], Liu Dinan[1], Kastritis Panagiotis L.[2], Basu Kaustuv[3], Hsu Tzu Chin[1], Yang Shunkai[1], Bui Khanh Huy[1,4]（[1]マギル大学, [2]EMBL, [3]マギル大学, FEMR, [4]GRASP）
Muneyoshi Ichikawa[1], Dinan Liu[1], Panagiotis L. Kastritis[2], Kaustuv Basu[3], Tzu Chin Hsu[1], Shunkai Yang[1], Khanh Huy Bui[1,4] ([1]*Dept. of Anat. and Cell Biol., McGill Univ.*, [2]*Struct. and Comput. Biol. Unit, EMBL*, [3]*FEMR, McGill Univ.*, [4]*GRASP*)

9:15　**大上　雅史**　1C1448

1YB0915　**スーパーコンピューティングによる網羅的タンパク質間相互作用予測法の開発と予測結果データベースの公開**
Supercomputing-based exhaustive protein-protein interaction prediction and its open database
○大上 雅史 [1], 林 孝紀 [1], 渡辺 紘生 [1,2], 松崎 由理 [3], 内古閑 伸之 [3], 秋山 泰 [1,3]（[1]東工大 情報理工, [2]産総研, RWBC-OIL, [3]東工大 情生院）
Masahito Ohue[1], Takanori Hayashi[1], Hiroki Watanabe[1,2], Yuri Matsuzaki[3], Nobuyuki Uchikoga[3], Yutaka Akiyama[1,3] ([1]*Sch Computing, Tokyo Tech*, [2]*RWBC-OIL, AIST*, [3]*ACLS, Tokyo Tech*)

9:30　**小林　幹**　2M1618

1YB0930　Structure of a prehandover mammalian ribosomal SRP·SRP receptor targeting complex
Kan Kobayashi[1], Ahmad Jomaa[1], Jae Ho Lee[2], Sowmya Chandrasekar[2], Daniel Boehringer[1], Shu-ou Shan[2], Nenad Ban[1] ([1]*ETH Zurich*, [2]*Caltech*)

9:45　坂口　美幸　2O1606

1YB0945　一分子時間分解 FRET データの三次元解析：生体高分子の構造不均一性をモデルフリーで定量する方法の開発

Third-order correlation analysis of single-molecule time-resolved FRET data: a new method for quantification of heterogeneity

○坂口 美幸[1], 石井 邦彦[1,2], 田原 太平[1,2]（[1]理研・田原分子分光, [2]理研・光量子工学研究センター）

Miyuki Sakaguchi[1], Kunihiko Ishii[1,2], Tahei Tahara[1,2] ([1]*Molecular Spectroscopy Lab., RIKEN*, [2]*RAP, RIKEN*)

10:00　佐藤　恵太　1H1548

1YB1000　脊椎動物の光受容体 Opn5L1 は逆行性・自己再生能をもつ新しいタイプのオプシンである

Vertebrate photoreceptor, Opn5L1, is the newcomer of opsin acting as a reverse and self-regenerating photoreceptor

○佐藤 恵太[1], 山下 高廣[2], 大内 淑代[1], 竹内 敦子[3], 後藤 人志[4], 小野 勝彦[4], 水野 操[5], 水谷 泰久[5], 友成 さゆり[6], 酒井 佳寿美[2], 今元 泰[2], 和田 昭盛[7], 七田 芳則[2,8] ([1]岡大院医歯薬, [2]京大院理, [3]神薬大中央分析室, [4]京府医大生物, [5]阪大院理, [6]徳大院ソシオテクノサイエンス, [7]神薬大生命有機化, [8]立命大総科技研）

Keita Sato[1], Takahiro Yamashita[2], Hideyo Ohuchi[1], Atsuko Takeuchi[3], Hitoshi Gotoh[4], Katsuhiko Ono[4], Misao Mizuno[5], Yasuhisa Mizutani[5], Sayuri Tomonari[6], Kasumi Sakai[2], Yasushi Imamoto[2], Akimori Wada[7], Yoshinori Shichida[2,8] ([1]*Grad. Sch. of Med., Dent. and Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Sci., Kyoto Univ.*, [3]*Div. of Anal. Lab., Kobe Pharm. Univ.*, [4]*Dept. of Biol., Kyoto Pref. Univ. of Med.*, [5]*Graduate School of Science, Osaka University*, [6]*Inst. of Tech. and Sci., Tokushima Univ.*, [7]*Dept. of Org. Chem. for Life Sci., Kobe Pham. Univ.*, [8]*Res. Org. for Sci. and Tech., Ritsumeikan Univ.*)

10:15　佐藤　佑介　3Pos412

1YB1015　Environment-dependent self-assembly of DNA nanostructures on phase-separated lipid bilayer membranes

Yusuke Sato[1], Masayuki Endo[2,3], Masamune Morita[4], Masahiro Takinoue[1], Hiroshi Sugiyama[2,3], Satoshi Murata[5], Shin-ichiro M. Nomura[5], Yuki Suzuki[5,6] ([1]*Dept. Comput. Sci., Tokyo Tech*, [2]*iCeMS, Kyoto Univ.*, [3]*Grad. Sch. Sci., Kyoto Univ.*, [4]*Biomed. Res. Inst., AIST*, [5]*Grad. Sch. Eng., Tohoku Univ.*, [6]*Fronti. Res. Inst. Interdiscrip. Sci., Tohoku Univ.*)

10:30　Arno Germond　2O1400

1YB1030　Predicting gene expression of living cells from a label-free spectral imaging technique

Arno Germond[1], Vipin Kumar[1], Takaaki Horinouchi[1], Chikara Furusawa[1,2], Hideaki Fujita[1], Yuichi Taniguchi[1], Toshio Yanagida[1], Taro Ichimura[1], Tomonobu M. Watanabe[1] ([1]*RIKEN BDR*, [2]*Tokyo Univ.*)

10:45　島田　敦広　1M1448

1YB1045　チトクロム酸化酵素によるプロトンポンプは、酸素結合によって誘起されるタンパク質内構造変化によって厳密に制御されている

Structure changes induced by O_2-binding tightly regulate the proton-pumping of cytochrome c oxidase

○島田 敦広[1], 久保 稔[2], 馬場 清喜[3], 吾郷 日出夫[2], 月原 冨武[4,5], 吉川 信也[5] ([1]岐阜大・応生, [2]理研・SPring-8, [3]高輝度研, [4]阪大・蛋白研, [5]兵県大・生命理・ピコ研）

Atsuhiro Shimada[1], Minoru Kubo[2], Seiki Baba[3], Hideo Ago[2], Tomitake Tsukihara[4,5], Shinya Yoshikawa[5] ([1]*Fac. Appl. Biol. Sci., Gifu Univ.*, [2]*RIKEN, SPrng-8*, [3]*JASRI*, [4]*Inst. Protein Res., Osaka Univ.*, [5]*Picobiol. Inst., Grad. Sch. Life Sci., Univ. Hyogo*)

11:00　寺川　剛　1E1548

1YB1100　コンデンシン複合体は分子モーターである

The condensin complex is a mechanochemical molecular motor

○寺川 剛[1,2], Bisht Shveta[3], Eeftens Jorine M.[4], Dekker Cees[4], Haering Christian H.[3], Greene Eric C.[2]（[1]京大・院理, [2]コロンビア大, [3]EMBL, [4]デルフト工科大）

Tsuyoshi Terakawa[1,2], Shveta Bisht[3], Jorine M. Eeftens[4], Cees Dekker[4], Christian H. Haering[3], Eric C. Greene[2] ([1]*Kyoto Univ.*, [2]*Columbia Univ.*, [3]*EMBL*, [4]*Delft Univ. of Technology*)

11:15　中西　温子　1Pos005

1YB1115　クライオ電子顕微鏡による好熱菌 *Thermus thermophilus* 由来 V 型 ATP 合成酵素の単粒子解析

Cryo EM structure of intact rotary H^+-ATPase/synthase from *Thermus thermophilus*

○中西 温子[1], 岸川 淳一[1], 玉腰 雅忠[2], 光岡 薫[3], 横山 謙[1]（[1]京産大・総合生命科学部, [2]東京薬科大・生命科学部, [3]大阪大・超高圧電顕センター）

Atsuko Nakanishi[1], Jun-ichi Kishikawa[1], Masatada Tamakoshi[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. of Mol. Biosci., Kyoto Sangyo Univ.*, [2]*Dept. of Mol. Biol., Tokyo Univ. of Pharm. and Life Sci.*, [3]*Res. Ctr. for UHVEM, Osaka Univ.*)

9:00〜11:30　A 会場（一般教育棟 B 棟 1 階 B11）／Room A (B11, General Education Build. B, 1F)

1SAA　いきた形の新規生成に挑む、理論モルフォダイナミクス
Theoretical morphodynamics - towards understanding emerging shapes of life

オーガナイザー：澤井 哲（東京大学），井上 康博（京都大学）
Organizers: Satoshi Sawai (The University of Tokyo), Yasuhiro Inoue (Kyoto University)

Computational and theoretical approaches to understand dynamic forms of organs, tissues, cells and sub-cellular organelle have seen a rapid progress in recent years owing to accessibility to both computational power and high-dimensional imaging data. The symposium will bring together scientists to share their findings in systems as diverse as golgi, amoeba cells to animal tissues and discuss the surprisingly similar modeling methodologies and common agenda.

はじめに
Opening Remarks

1SAA-1　反応拡散とフェイズフィールドから理解する細胞変形と集団ダイナミクス
Understanding single and multicellular dynamics from reaction-diffusion and phase-field modeling
○澤井 哲[1], 井元 大輔[1], 斉藤 稔[2], 中島 昭彦[1], 藤森 大平[1]（[1]東京大学大学院総合文化研究科, [2]東京大学大学院理学系研究科）
Satoshi Sawai[1], Daisuke Imoto[1], Nen Saito[2], Akihiko Nakajima[1], Taihei Fujimori[1] ([1]*Grad Schl Arts & Sci, Univ Tokyo*, [2]*Grad Schl Sci, Grad Sch*)

1SAA-2　ゴルジ装置の自己組織化形成過程
Self-organized formation of Golgi body
○立川 正志（理化学研究所）
Masashi Tachikawa (*RIKEN*)

1SAA-3　フェーズフィールド法によるマクロピノサイトーシス動態の 3D シミュレーション
phease-field modeling for 3D morphodynamics of macropinocytosis
○斉藤 稔[1], 澤井 哲[2]（[1]東大・理, [2]東大・総合文化）
Nen Saito[1], Satoshi Sawai[2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Arts Sci., Univ. Tokyo*)

1SAA-4　ショウジョウバエ後腸の捻転現象を 3D バーテックスダイナミクスモデルから考える
A three-dimensional vertex dynamics model for understanding the rotating phenomenon of the hindgut of Drosophila embryo
○秋山 正和[1], 須志田 隆道[1], 井上 康博[3], 大久保 明野[2], 稲木 美紀子[2], Matsuno Kenji[2]（[1]北海道大学電子科学研究所, [2]大阪大学大学院 理学研究科 生物科学専攻, [3]京都大学 ウイルス・再生医科学研究所）
Masakazu Akiyama[1], Takamichi Sushida[1], Yasuhiro Inoue[3], Akino Ookubo[2], Mikiko Inaki[2], Kenji Matsuno[2] ([1]*Research Institute for Electronic Science, Hokkaido University*, [2]*Department of Biological Sciences Graduate School of Science Osaka University*, [3]*Department of Biosystems Science, Institute for Frontier Life and Medical Sciences, Kyoto University*)

1SAA-5 頭蓋骨縫合線パターン形成の数理モデル化
Modeling of skull suture pattern formation
○三浦 岳（九州大学大学院医学研究院）
Takashi Miura (*Kyushu University Graduate School of Medical Sciences*)

1SAA-6 Folding pattern formation in a confined epithelial cell sheet
Yasuhiro Inoue (*Institute for Frontier Life and Medical Sciences, Kyoto University*)

おわりに
Closing Remarks

9:00～11:30　D 会場（一般教育棟 A 棟 3 階 A36）／Room D (A36, General Education Build. A, 3F)

1SDA　文部科学省科学研究費補助金 新学術領域研究 「3D 活性サイト科学」共催
生体分子の機能解明に向けた 3D 活性サイトの構造・ダイナミクスの新規解析法
Challenges and novel approaches to investigate the structures and dynamics of the 3D active sites in biomolecular systems for understanding the biochemical functions

オーガナイザー：鷹野 優（広島市立大学），関口 博史（高輝度光科学研究センター）
Organizers: Yu Takano (Hiroshima City University), Hiroshi Sekiguchi (Japan Synchrotron Radiation Research Institute)

To effectively exert biochemical functions, biomolecules significantly change their structures at some time and slightly change them at other time. It is required to elucidate accurate 3D-structures and dynamics of the active site, where the function is exerted, to understand the mechanism of the function. In this symposium, we present insights into 3D-structures and dynamics of the active site obtained from X-ray, neutron, electron, and scanning probe, and computer simulation, and also discuss how they contribute to the elucidation of biochemical functions.

はじめに
Opening Remarks

1SDA-1 放射光 X 線と結晶プローブを用いたマルチマータンパク質・分子内運動解析
Cooperative Motion Analysis of Multimeric Proteins using Synchrotron Radiation X-ray and nanocrystal
○関口 博史（公益財団法人 高輝度光科学研究センター 利用研究促進部門）
Hiroshi Sekiguchi (*JASRI/SPring-8*)

1SDA-2 Studying ion channels in reconstituted membrane using atomic force microscopy
Ayumi Sumino[1,2], Takashi Sumikama[1], Takayuki Uchihashi[3], Shigetoshi Oiki[4] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*, [3]*Dept. Phys., Nagoya Univ.*, [4]*Facult. Med. Sci., Univ. Fukui*)

1SDA-3 Analysis of the picosecond dynamics of muscle contractile proteins and their hydration water by quasielastic neutron scattering
Tatsuhito Matsuo[1], Toshiaki Arata[2], Toshiro Oda[3], Kenji Nakajima[4], Seiko Kawamura[4], Tatsuya Kikuchi[4], Taiki Tominaga[5], Kaoru Shibata[4], Fumiaki Kono[1], Satoru Fujiwara[1] ([1]*QST*, [2]*Osaka Univ.*, [3]*Tokai-Gakuin Univ.*, [4]*J-PARC Center*, [5]*CROSS*)

1SDA-4 単結晶中ヘモグロビンの包括的構造機能解析
Comprehensive structural and functional analysis of hemoglobin in single crystals
○柴山 修哉（自治医大 生物物理）
Naoya Shibayama (*Jichi Med. Univ. Div. of Biophysics*)

1SDA-5 クライオ電子顕微鏡法による膜タンパク質複合体の構造解析
Structural Analysis of Membran Protein Complex by Cryo-EM
中西 温子[2], 岸川 淳一[2], ○光岡 薫[1], 横山 謙[2]（[1]阪大・超高圧電顕センター, [2]京産大・総合生命）
Atsuko Nakanishi[2], Jun-ichi Kishikawa[2], **Kaoru Mitsuoka**[1], Ken Yokoyama[2] ([1]*Res. Ctr. UVHEM, Univ. Osaka*, [2]*Dept. Mol. Biosci., Kyoto Sangyo Univ.*)

1SDA-6 光化学系 II 結晶における Mn4CaO5 クラスターの異常分散法を使った価数分析
Analysis of the individual valences of four Mn atoms in photosystem II crystals using anomalous diffraction technique
○梅名 泰史[1], 川上 恵典[2], 神谷 信夫[2], 沈 建仁[1]（[1]岡山大・異分野基礎研, [2]大阪市大・複合先端）
Yasufumi Umena[1], Keisuke Kawakami[2], Nobuo Kamiya[2], Shen Jian-Ren[1] ([1]*RIIS, Okayama Univ.*, [2]*The OCARINA, Osaka City Univ.*)

1SDA-7 光化学系 II 酸素発生中心における酸素分子生成および放出過程についての QM/MM 解析
QM/MM study on the O2 formation and O2 release mechanism in the oxygen-evolving complex of photosystem II
○庄司 光男[1], 磯部 寛[2], 重田 育照[1], 中嶋 隆人[3], 山口 兆[4]（[1]筑波大 CCS, [2]岡山大, [3]理研 R-CCS, [4]阪大）
Mitsuo Shoji[1], Hiroshi Isobe[2], Yasuteru Shigeta[1], Takahito Nakajima[3], Kizashi Yamaguchi[4] ([1]*CCS, Univ. Tsukuba*, [2]*Okayana Univ.*, [3]*RIKEN R-CCS*, [4]*Osaka Univ.*)

1SDA-8 Statistical and quantum-chemical analysis of the effect of heme porphyrin distortion in heme protein
Yu Takano (*Graduate School of Information Sciences, Hiroshima City University*)

おわりに
Closing Remarks

9:00～11:30　E 会場（一般教育棟 A 棟 3 階 A37）／Room E (A37, General Education Build. A, 3F)
1SEA　日本医療研究開発機構 革新的先端研究開発支援事業（AMED-CREST/PRIME）協賛
分子から個体のメカノバイオ：多様な物理刺激とその応答
Mechanobiology from molecules to tissues: various physical stimuli and its response system

オーガナイザー：新井 敏（早稲田大学），原 雄二（京都大学）
Organizers: Satoshi Arai (Waseda University), Yuji Hara (Kyoto University)

Recent years, research topics in mechanobiology have been broaden and diversified. Focusing on each stage from molecules, cells, to tissues, we further challenge to understand how it is linked with each other through the different hierarchy. This symposium includes more recent studies on mechanobiology in various types of cells and tissues sensing different physical stimuli. The development of novel methodology is also a key topic here. We also invite several speakers less familiar with biophysical meeting and enjoy fruitful discussions.

1SEA-1 Cell surface flip-flop of phosphatidylserine is critical for PIEZO1-mediated myotube formation
Yuji Hara[1,2], Masaki Tsuchiya[1], Kotaro Hirano[1], Masato Umeda[1] ([1]*Grad. Sch. Eng., Kyoto Univ.*, [2]*AMED, PRIME*)

1SEA-2 張力センサーとしてのアクチン線維：そのゆらぎ解析
Analysis of fluctuations of a single actin filament as a tension sensor
○辰巳 仁史（金沢工業大学）
Hitoshi Tatsumi (*Kanazawa Institute of Technology (KIT)*)

1SEA-3 Matrix-force dependent integrin signalling at the podosome
Cheng-han Yu (*Univ. of Hong Kong*)

1SEA-4 細胞間相互作用が制御するTリンパ球の活性化
Cell-cell interaction among immune cells regulates T lymphocyte activation
○町山 裕亮, 横須賀 忠（東京医大・免疫）
Hiroaki Machiyama, Tadashi Yokosuka (*Dept. Immunol., Tokyo Med. Univ.*)

1SEA-5 ブリルアン散乱による多細胞システムの弾性イメージング
Elasticity imaging in multicellular systems by Brillouin scattering
○市村 垂生 [1,2], 渡邉 朋信 [1]（[1]理研 BDR, [2]大阪大学 OTRI）
Taro Ichimura[1,2], Tomonobu Watanabe[1] ([1]*RIKEN BDR*, [2]*Osaka University OTRI*)

1SEA-6 Mitochondria are physiologically maintained at close to 50 °C
Malgorzata Rak (*INSERM UMR1141/CNRS*)

1SEA-7 メカノセンサーチャネル Piezo1/2 の哺乳類生体内での役割
Mechanically activated cation channel Piezo1/2 and its physiological roles in mammals
○野々村 恵子 [1,2], Lukacs Viktor[2], Cahalan Stuart[2], 蟹江 朱美 [1], 勝田 紘基 [3], 藤森 俊彦 [1], Patapoutian Ardem[2]（[1]基生研, [2]スクリプス研究所, [3]名大・院・医）
Keiko Nonomura[1,2], Viktor Lukacs[2], Stuart Cahalan[2], Akemi Kanie[1], Hiroki Katsuta[3], Toshihiko Fujimori[1], Ardem Patapoutian[2] ([1]*NIBB*, [2]*TSRI*, [3]*Med.Grad.Nagoya Univ.*)

1SEA-8 改良型振動計による内耳ナノ振動の測定と解析
Measurement and analysis of nanoscale vibrations in the inner ear by advanced vibrometries
○日比野 浩 [1,2], 太田 岳 [1,2], 崔 森悦 [2,3], 任 書晃 [1,2]（[1]新潟大・医歯学総合・分子生理, [2]AMED-CREST, AMED, [3]新潟大・工）
Hiroshi Hibino[1,2], Takeru Ota[1,2], Samuel Choi[2,3], Fumiaki Nin[1,2] ([1]*Department of Molecular Physiology, Niigata University School of Medicine*, [2]*AMED-CREST, AMED*, [3]*Department of Electrical and Electronics Engineering, Niigata University*)

9:00〜11:30　F 会場（一般教育棟 B 棟 3 階 B32）／Room F (B32, General Education Build. B, 3F)

1SFA　細胞幾何学：時空間スケールが決める秩序と機能
Geometric cell biology: Uncovering self-organization mechanisms of ordered dynamics and cellular functions by spatio-temporal perturbation

オーガナイザー：前多 裕介（九州大学），宮﨑 牧人（京都大学）
Organizers: Yusuke T. Maeda (Kyushu University), Makito Miyazaki (Kyoto University)

Cells are growing tiny capsules whose inherent size and the phase of cell cycle are regulated through self-organization mechanism. Physical self-organization such as pattern formation or oscillation gives typical length-scale or time-scale, but this fact raises a fundamental question: What physical principle underlies behind the robust cellular size, shape and time? How one can control cellular functions by spatio-temporal perturbation? In this symposium, we will show recent developments in this field, in particular, optogenetics, microfluidics, and synthetic biology approaches.

はじめに
Opening Remarks

1SFA-1 アクチン系細胞骨格の in vitro 再構成：運動と分裂の仕組みの包括的理解を目指して
In vitro reconstitution of actin cytoskeleton: Toward a unified understanding of the mechanics of cell motility and division
○宮﨑 牧人 [1,2]（[1]京大・白眉, [2]京大・院理）
Makito Miyazaki[1,2] ([1]*Hakubi Center, Kyoto Univ.*, [2]*Dept. Phys. Kyoto Univ.*)

1SFA-2 What happens in the large cytoplasm of the oocyte?
Hirohisa Kyogoku, Tomoya Kitajima (*RIKEN BDR*)

1SFA-3 細胞サイズと核内 DNA 量に依存した核のサイズの制御機構
Nuclear size scaling with cell size and DNA content in Xenopus
○原 裕貴（山口大学理学部進化細胞生物学研究室）
Yuki Hara (*Yamaguchi University, Faculty of Science, Evolutionary Cell Biology Laboratory*)

1SFA-4 遺伝子発現の振動パターンの光操作
Controlling genetic oscillators by optogenetics
○磯村 彰宏 [1,2]（[1]京大 ウイ・再生研, [2]JST さきがけ）
Akihiro Isomura[1,2] ([1]*Infront, Kyoto Univ.*, [2]*JST PRESTO*)

1SFA-5 Impact of quasi-cellular structures for evolutionary dynamics of RNA
Shigeyoshi Matsumura (*Grad. Sch. Sci. Eng., Univ. Toyama*)

1SFA-6 幾何学で紐解く細胞集団の集団運動の力学
On the geometry and mechanics in collective cell migration
○前多 裕介, 別府 航早, 福山 達也（九大・物理）
Yusuke T. Maeda, Kazusa Beppu, Tatsuya Fukuyama (*Dept. Phys., Kyushu Univ.*)

9:00～11:30　G 会場（一般教育棟 B 棟 3 階 B33）／Room G (B33, General Education Build. b, 3F)

1SGA 文部科学省科学研究費補助金 新学術領域研究 「動的構造生命科学を拓く新発想測定技術 ―タンパク質が動作する姿を活写する―」共催
promiscuous だが洗練されたタンパク質の分子認識
Ingenious mechanisms behind promiscuous recognition, in contrast to precise recognition, by protein molecules

オーガナイザー：神田 大輔（九州大学），塚崎 智也（奈良先端科学技術大学院大学）
Organizers: Daisuke Kohda (Kyushu University), Tomoya Tsukazaki (NAIST)

In this symposium, we will focus on a special type of molecular recognition by proteins. It is extremely important to understand the recognition mechanisms of interaction partners, including drugs and target proteins, by protein molecules in various biological processes. Sometimes, their recognitions are requisitely promiscuous and dynamic. The speakers will talk about their recent structural biology studies from the viewpoint of the recognitions and interactions of proteins. We expect to discuss the basic principles behind the promiscuous recognition by contrast to the precise recognition.

はじめに
Opening Remarks

1SGA-1 植物の自家不和合性における自己認識メカニズム
Mechanism of self-recognition system in plant self-incompatibility
○村瀬 浩司（東大院・農生科）
Kohji Murase (*Dept. Appl. Biol. Chem., Univ. Tokyo*)

1SGA-2 セマフォリンとプレキシンが形成する低親和性だが特異的な相互作用
Low-affinity but specific interactions between semaphorin-plexin pairs
○禾 晃和（横浜市大・院生命医）
Terukazu Nogi (*Grad. Sch. Med. Lif. Sci., Yokohama City Univ.*)

1SGA-3 pH および亜鉛を利用した ERp44 による多様な基質認識の構造基盤
Structural basis of pH- and zinc-dependent multiple client recognition by ERp44
○渡部 聡 [1], 天貝 佑太 [1], Sitia Roberto[2], 稲葉 謙次 [1]（[1]東北大 多元研, [2]San Raffaele Institute）
Satoshi Watanabe[1], Yuta Amagai[1], Roberto Sitia[2], Kenji Inaba[1] ([1]*IMRAM, Tohoku Univ.*, [2]*San Raffaele Institute*)

1SGA-4 Diverse activities of molecular chaperones through non-selective binding
Tomohide Saio[1], Charalampos G. Kalodimos[2], Koichiro Ishimori[1] ([1]*Fac. of Sci. Hokkaido Univ.*, [2]*Dept. of Struct. Biol., St. Jude Child. Res. Hosp., TN*)

1SGA-5 構造平衡により規定される多剤結合転写因子 QacR の可変的転写制御
Conformational equilibrium defines variable transcriptional repression of a multidrug binding transcriptional repressor, QacR
○竹内 恒 [1], 嶋田 一夫 [2]（[1]産総研・創薬分子, [2]東京大院・薬学系）
Koh Takeuchi[1], Ichio Shimada[2] ([1]*moleprof, AIST*, [2]*Grad. Sch. Pharm. Sci, The Univ. of Tokyo*)

1SGA-6 細菌多剤排出ポンプの機能と制御
Function and Regulation of Bacterial Multidrug Transporters
○西野 邦彦（大阪大学産業科学研究所・大阪大学大学院薬学研究科）
Kunihiko Nishino (*Institute of Scientific and Industrial Research, Graduate School of Phamaceutical Sciences, Osaka University*)

おわりに
Closing Remarks

9:00～11:30　H 会場（一般教育棟 A 棟 4 階 A41）／Room H (A41, General Education Build. A, 4F)
1SHA　CREST「光の特性を活用した生命機能の時空間制御技術の開発と応用」共催
どこまで光は届くのか？　オプトジェネティクスの挑戦
Dive into Brain Abyss by Optogenetics

オーガナイザー：渡邉 宙志（東京大学），神取 秀樹（名古屋工業大学）
Organizers: Hiroshi Watanabe (The University of Tokyo), Hideki Kandori (Nagoya Institute of Technology)

Optogenetics, opened with a light-gated cation channel channelrhodopsins, has showed the great potential of photoreceptor proteins in neuro/brain science. Today, optogenetics is shifting to the next stage seeking various targets of light control, and improving control precision. In the symposium, we introduce our contributions based on biophysical approaches to the optogenetics and cooperation with other research fields by discussing the perspectives and further possibilities of optogenetics in collaboration with CREST “Development and application of optical technology for spatiotemporal control of biological functions.”

1SHA-1 微生物型ロドプシンに基づく光遺伝学ツール開発のためのボトムアッパアプローチ
Bottom-up approach for microbial rhodopsin-based optogenetic tools
○小島 慧一, 須藤 雄気（岡山大・院・医歯薬(薬学系)）
Keiichi Kojima, Yuki Sudo (*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*)

1SHA-2 光遺伝学ツール開発につながる微生物型ロドプシン
Microbial rhodopsins leading to development of optogenetic tool
○今野 雅恵（名工大・院・工）
Masae Konno (*Grad. Sch. Eng., NIT*)

1SHA-3 Anion channelrhodopsin-2 の構造モデリングと分子シミュレーションによる機能メカニズム解析
Structural modeling and molecular simulations provide insights into the functional mechanism of anion channelrhodpsin-2
○渡邉 宙志 [1,2,3], 加藤 岬 [2], 石北 央 [1,2]（[1]東大・先端研, [2]東大・工・応化, [3]JST さきがけ）
Hiroshi Watanabe[1,2,3], Misaki Kato[2], Hiroshi Ishikita[1,2] ([1]*RCAST, Univ. Tokyo*, [2]*App. Chem., Grad. Sch. Eng., Univ. Tokyo*, [3]*JST, PRESTO*)

1SHA-4 Dark-active and light-inactivated G protein-coupled receptors based on an animal opsin, peropsin
Takashi Nagata[1], Mitsumasa Koyanagi[1,2], Robert Lucas[3], Akihisa Terakita[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*, [3]*Fac. Biol. Med. Health, Univ. Manchester*)

1SHA-5 アップコンバージョンを用いたファイバーレス光遺伝学の開発
The development of fiberless optogenetics using up conversion luminescence from lanthanide
○宮崎 杜夫 [1,2], Srikanta Chowdhury[1,2], 山下 貴之 [1,2], 八尾 寛 [3], 湯浅 英哉 [4], 山中 章弘 [1,2]（[1]名古屋大学環境医学研究所 神経系分野 2, [2]CREST 科学技術振興機構, [3]東北大学大学院 生命科学研究科 脳機能解析分野, [4]東京工業大学大学院 生命理工学研究科 分子生命科学）
Toh Miyazaki[1,2], Chowdhury Srikanta[1,2], Takayuki Yamashita[1,2], Hiromu Yawo[3], Hideya Yuasa[4], Akihiro Yamanaka[1,2] ([1]*Department of Neuroscience II Research Institute of Environmental Medicine Nagoya University*, [2]*CREST, JST*, [3]*Department of developmental biology and neuroscience, Tohoku University Graduate School of life Sciences*, [4]*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology*)

1SHA-6 光操作によるゼブラフィッシュ小脳高次機能の解析
Optogenetic manipulation of zebrafish neural circuits toward understanding higher order function of the cerebellum
○清水 貴史 [1,2], 松田 光司 [1], 日比 正彦 [1,2]（[1]名大・生物センター, [2]名大・院生命理学）
Takashi Shimizu[1,2], Koji Matsuda[1], Masahiko Hibi[1,2] ([1]*BBC, Nagoya Univ.*, [2]*Grad. Sch. Sci., Nagoya Univ.*)

9:00〜11:30　I 会場（一般教育棟 B 棟 4 階 B41）／Room I (B41, General Education Build. B, 4F)

1SIA　細胞膜受容体の局在・会合とシグナル変換の制御
Regulation of the signal transduction in cell membrane via localization and clustering of receptors

オーガナイザー：森垣 憲一（神戸大学），鈴木 健一（岐阜大学）
Organizers: Kenichi Morigaki (Kobe University), Kenichi Suzuki (Gifu University)

Localization and clustering of molecules in cell membrane play critical roles in the signal transduction. Recent studies have suggested that dynamic localization and aggregation of molecules in nano- and mesoscopic domains are regulating the signal transduction cascade. However, the regulation mechanisms remain elusive. The present symposium intends to give an overview of the current understanding by providing the most up-to-date views from recent studies on membrane receptors using cellular and model membranes as well as simulation to gain insight for the future directions.

1SIA-1 Regulation mechanisms of EGFR activity by ganglioside homodimer rafts as revealed by single-molecule imaging
Kenichi Suzuki (*Gifu Univ. G-CHAIN*)

1SIA-2 The function of the transmembrane-juxtamembrane region of EGFR
Takeshi Sato (*Kyoto Pharm Univ*)

1SIA-3 Dimerization-deficient opsin mutants: implications for disease
George Khelashvili, **Anant K. Menon** (*Weill Cornell Medical College*)

1SIA-4 Computer simulations of complex membrane models
D. Peter Tieleman (*University of Calgary*)

1SIA-5 Resolving the spatiotemporal organization of GPCRs in live cells with PIE-FCCS
Adam W. Smith (*The University of Akron*)

1SIA-6 Raftophilicity and aggregation of membrane proteins in the photo-transduction
Kenichi Morigaki[1,2], Yasushi Tanimoto[1], Hayato Yamashita[3], Akinori Awazu[4], Fumio Hayashi[5] ([1]*Kobe Univ. Biosignal*, [2]*Kobe Univ. Agrobioscience*, [3]*Osaka Univ. Eng. Sci.*, [4]*Hiroshima Univ. Sci.*, [5]*Kobe Univ. Sci.*)

9:00〜11:30　K 会場（一般教育棟 E 棟 1 階 E11）／Room K (E11, General Education Build. E, 1F)

1SKA　1 分子計測に立脚した新しいバイオ分析の潮流
New trends in bioanalysis based on single molecule biophysics

オーガナイザー：渡邉 力也（東京大学），小松 徹（東京大学）
Organizers: Rikiya Watanabe (The University of Tokyo), Toru Komatsu (The University of Tokyo)

Recent progress in single-molecule techniques enables highly sensitive and quantitative bioassays, and as well extends the versatility as analytical platforms, such as digital PCR, and next-generation DNA sequencers. In this symposium, we cover state-of-the-art single-molecule techniques, and aim to discuss about the new trends in bioanalysis based on single molecule biophysics.

1SKA-1 DNA ナノテクノロジーと 1 分子計測技術の融合が拓く分子動態・力の高解像イメージング
High-resolution imaging of molecular dynamics and force pioneered by DNA nanotechnology and single molecule detection techniques
○岩城 光宏 [1,2]（[1]理研・生命機能科学センター, [2]阪大・院生命機能）
Mitsuhiro Iwaki[1,2] ([1]*RIKEN, BDR*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*)

1SKA-2 高速 AFM による天然変性タンパク質 MeCP2 の一分子観察
Single-molecule visualization of intrinsically disordered Rett syndrome protein, MeCP2 by high-speed AFM
○古寺 哲幸 [1], Kalashnikova Anna[2], Porter-Goff Mary E.[2], 安藤 敏夫 [1], Hansen Jeffrey C.[2]（[1]金沢大・WPI-NanoLSI, [2]Dept. Biochem. & Mol. Biol., Colorado State Univ.）
Noriyuki Kodera[1], Anna Kalashnikova[2], Mary E. Porter-Goff[2], Toshio Ando[1], Jeffrey C. Hansen[2] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Dept. Biochem. & Mol. Biol., Colorado State Univ.*)

1SKA-3 マイクロチップを利用した膜タンパク質の 1 分子機能分析
Single molecule analysis of membrane proteins by using microsystems
○渡邉 力也（東京大学大学院工学系研究科応用化学専攻）
Rikiya Watanabe (*Department of Applied Chemistry, The University of Tokyo*)

1SKA-4 **酵素活性の網羅的解析（Enzymomics）法による疾患関連タンパク質の探索**
Development of enzymomics approach to search for disease-related alternation of enzymatic functions
○小松 徹[1], 小名木 淳[1], 市橋 裕樹[1], 坂本 眞伍[1], 渡邉 力也[2], 張 翼[2], 野地 博行[2,6], 長野 哲雄[4], 浦野 泰照[3,5]（[1]東京大学 大学院薬学系研究科, [2]東京大学 大学院工学系研究科, [3]東京大学 大学院医学系研究科, [4]東京大学 創薬機構, [5]AMED-CREST, [6]JST ImPACT）
Toru Komatsu[1], Jun Onagi[1], Yuki Ichihashi[1], Shingo Sakamoto[1], Rikiya Watanabe[2], Yi Zhang[2], Hiroyuki Noji[2,6], Tetsuo Nagano[4], Yasuteru Urano[3,5] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*Grad. Sch. Eng., Univ. Tokyo*, [3]*Grad. Sch. Med., Univ. Tokyo*, [4]*DDI, Univ. Tokyo*, [5]*AMED-CREST*, [6]*JST ImPACT*)

1SKA-5 **生体高分子スマートシーケンサに向けた 1 分子電気計測法の開発**
Development of Single-Molecule Electrical Identification Method For Smart Biopolymer Sequencer
○大城 敬人（大阪大学 産業科学研究所）
Takahito Ohshiro (*Osaka University, ISIR*)

1SKA-6 **細胞内全自動 1 分子解析と発展的応用**
In Cell Automated Single-molecule Analysis and Its Extensive Applications
○廣島 通夫[1,2], 安井 真人[1], 小塚 淳[1], 佐甲 靖志[2], 上田 昌宏[1]（[1]理研・BDR, [2]理研・佐甲細胞情報研究室）
Michio Hiroshima[1,2], Masato Yasui[1], Jun Kozuka[1], Yasushi Sako[2], Masahiro Ueda[1] ([1]*RIKEN BDR*, [2]*Cellular Informatics Lab., RIKEN*)

9:00〜11:30　M 会場（一般教育棟 E 棟 2 階 E21）／Room M (E21, General Education Build. E, 2F)

1SMA　生体運動システムの自律性
Autonomy integrated in motility systems

オーガナイザー：上田 太郎（早稲田大学），南野 徹（大阪大学）
Organizers: Taro Q.P. Uyeda (Waseda University), Tohru Minamino (Osaka University)

The control of the generation, directionality and transmission of force in cell motility is created by proteins that reversibly assemble into elaborate supramolecular motility machines. The dynamic assembly and disassembly of the components of these motility machines are dependent on autonomy of the proteins, rather than on chemical signals. In this symposium, we will discuss the molecular mechanisms behind such dynamic processes from the viewpoints of mechano-sensitivity, cooperativity, polymorphism and allostery, and highlight design principles that are common to apparently divergent motility systems.

1SMA-1 **生体運動システムの自律性：概観**
Autonomy integrated in motility systems : An overview
○上田 太郎（早稲田大・理工・物理）
Taro Uyeda (*Dept of Physics, Faculty of Sci and Eng, Waseda Univ*)

1SMA-2 Collective cell movements driven by actomyosin contractility in vertebrate embryos
Asako Shindo[1], Yasuhiro Inoue[2], John Wallingford[2], Makoto Kinoshita[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Inst. Front. Life Med. Sci., Kyoto Univ.*, [3]*Univ. Texas*)

1SMA-3 Mechanical design principles of the cell division apparatus
Yuta Shimamoto (*Nat'l Inst Genetics*)

1SMA-4 Coulombic interaction network and novel allostery in molecular machines
Mitsunori Takano (*Dept Pure & Appl Phys, Waseda Univ*)

1SMA-5 Directed Actin Cytoskeleton Self Organization, Contractility and Motility
Laurent Blanchoin (*Biosci. Biotechnol. Inst. Grenoble, France*)

1SMA-6 Evidence for a functional actin cytoskeleton in Asgard archaea
Bob Robinson[1,2,3], Akil Caner[2,3] ([1]*Res Inst for Interdisciplinary Sci, Okayama Univ*, [2]*Institute of Molecular and Cell Biology*, [3]*Dept. of Biochem, Sch of Medicine, Natl Univ of Singapore*)

1SMA-7 バクテリアべん毛モーターの固定子再編成における自律的制御
Autonomous stator remodeling mechanism of the bacterial flagellar motor
○南野 徹（大阪大学大学院生命機能研究科）
Tohru Minamino (*Grad. Sch. Frontier Biosci, Osaka Univ.*)

9:00〜11:30　O 会場（一般教育棟 D 棟 3 階 D32）／Room O (D32, General Education Build. D, 3F)

1SOA　タンパク質の分子内情報伝達の動的機構と機能
The function and mechanism of intramolecular information-transmission in protein

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 University), Yasushige Yonezawa (KINDAI University)

Dynamical intramolecular processes, which have been called "Intramolecular information-transmission", have been exhibited to the mechanism of the dynamics of an allosteric protein, a transporter and so on. The detail, however, has not been fully understood yet. In this symposium, we introduce six researches which are related to the Intramolecular Information-transmission from the different point of view, such as experiments, large-scale simulations, and simulation technique. Finally, we will discuss "the Intramolecular information-transmission" toward a first milestone.

はじめに
Opening Remarks

1SOA-1 多剤排出トランスポーター AcrB の薬剤排出メカニズムの解明
Elucidation of a drug efflux mechanism of multidrug efflux transporter AcrB
○山根 努（横浜市立大学大学院生命医科学研究科生命医科学専攻）
Tsutomu Yamane (*Graduate School of Medical Life Science, Yokohama City University*)

1SOA-2 多剤排出トランスポーター AcrB の機能的回転における構造変化パスウェイとエネルギー
Energetics and conformational pathways of functional rotation in the multidrug transporter AcrB
○松永 康佑[1,2]（[1]理化学研究所 計算科学研究センター, [2]JST さきがけ）
Yasuhiro Matsunaga[1,2] ([1]*RIKEN Center for Computational Science*, [2]*JST PRESTO*)

1SOA-3 分子シミュレーションで探る ABC トランスポーターの構造的・機能的ダイナミクス
Structural and Functional dynamics of ABC transporters explored by molecular simulations
○古田 忠臣（東京工業大学生命理工学院）
Tadaomi Furuta (*Sch. Life Sci. Tech., Tokyo Tech*)

1SOA-4 ヒトシスチン尿症関連トランスポーターにおける軽鎖遺伝子変異から重鎖グリコシレーションへの分子内情報伝達
Intramolecular information-transmission from light chain mutation to heavy chain glycosylation in human cystinuria-related transporter
○安西 尚彦, 坂本 信一（千葉大学大学院医学研究院）
Naohiko Anzai, Shinichi Sakamoto (*Grad. Sch. Med., Chiba Univ.*)

1SOA-5 重み付きアンサンブル法による生体分子のシミュレーション
Weighted ensemble simulation of biomolecules
○藤崎 弘士（日本医科大学 物理学教室）
Hiroshi Fujisaki (*Nippon Medical School*)

1SOA-6 Dynamic allostery in folded protein and intrinsically disordered protein (IDP)
Shin-ichi Tate (*Dept. Mathematical and Life Sciences*)

おわりに
Closing Remarks

9:00～11:30　R 会場（一般教育棟 D 棟 4 階 D42）／Room R (D42, General Education Build. D, 4F)

1SRA　文部科学省科学研究費補助金 新学術領域研究「新光合成：光エネルギー変換システムの再最適化」共催
光合成反応中心の構築および作動原理：キノンは必須か
Structural and operating principles of photosynthtetic reaction centers: whether quinone is essential or not

オーガナイザー：大岡 宏造（大阪大学），浅井 智広（立命館大学）
Organizers: Hirozo Oh-oka (Osaka University), Chihiro Azai (Ritsumeikan University)

The photosynthetic light reaction is a process by which light energy is converted into chemical energy. The primary charge separation, followed by a series of electron transfer reactions, occurs in the reaction center pigment-protein complexes (RCs). The RCs can be classified into two major types, types I and II, dependent on their terminal acceptors. However, they have almost similar reaction manners except for the functions of quinones. We will draw structural and operating principles of RCs, and discuss their evolution scenario in the aspect of versatile physicochemical properties of quinones.

1SRA-1 紅色細菌の LH1-RC 複合体の構造：キノンゲートはどこにあるのか
Where is the quinone gate in purple photosynthetic bacterial LH1-RC complex?
○大友 征宇 [1], 木村 行宏 [2]（[1]茨城大・理, [2]神戸大・院農）
Seiu Otomo[1], Yukihiro Kimura[2] ([1]*Fac. Sci., Ibaraki Univ.*, [2]*Grad. Sch. Agri. Sci., Kobe Univ.*)

1SRA-2 光合成反応中心蛋白質の電子移動経路におけるコファクターの酸化還元電位と電子移動反応機構
Redox potentials of cofactors in electron transfer branches in photosynthetic reaction centers
○石北 央 [1,2]（[1]東大・工・応化, [2]東大・先端研）
Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Tech., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*)

1SRA-3 What can the heliobacteria teach us about the evolution of photochemical reaction centers?
Gregory S. Orf (*Center for Bioenergy & Photosynthesis, ASU*)

1SRA-4 X-ray structure of the type-I reaction center from *Heliobacterium modesticaldum* at 3.2 Å resolution
Tetsuko Nakaniwa[1], Risa Mutoh[2], Kokoro Fushimi[1,3], Aya Yasuda[1,3], Tadashi Mizoguchi[4], Hitoshi Tamiaki[4], Chihiro Azai[5], Hideaki Tanaka[1], Shigeru Itoh[6], Hirozo Oh-oka[3], Genji Kurisu[1] ([1]*IPR, Osaka Univ.*, [2]*Fac. Sci., Fukuoka Univ.*, [3]*Grad. Sch. Sci., Osaka Univ.*, [4]*Grad. Sch. Life Sci. Ritsumeikan Univ.*, [5]*Col. Life Sci., Ritsumeikan Univ.*, [6]*Grad. Sch. Sci., Nagoya Univ.*)

1SRA-5 **反応中心電子受容体として機能するキノン：原始的な光合成細菌から高等植物まで**
Quinones serve as an electron acceptor in photosynthetic reaction center of primitive bacteria to higher plants
○近藤 徹 [1,2]（[1]マサチューセッツ工科大学, [2]MIT-Harvard エキシトン工学センター）
Toru Kondo[1,2] ([1]*MIT*, [2]*MIT-Harvard Center for Excitonics*)

1SRA-6 Symmetry or asymmetry? - Site-specific structural modification of the homodimeric photosynthetic reaction center of green sulfur bacteria
Chihiro Azai (*Dept. Bioinfo., Col. Life Sci., Ritsumeikan Univ.*)

13:30〜16:00　B 会場（一般教育棟 A 棟 2 階 A21）／Room B (A21, General Education Build. A, 2F)
1SBP　**ヘルスシステムの理解とその応用**
Interdisciplinary Science and Engineering in Health Systems

オーガナイザー：井出 徹（岡山大学），早川 徹（岡山大学）
Organizers: Toru Ide (Okayama University), Tohru Hayakawa (Okayama University)

To fully understand biological systems, we need interdisciplinary personnel and tools, from single molecule physics to systems analysis. We recently established the graduate school for interdisciplinary studies and education on bio-systems. In this symposium, we will discuss proposals of interdisciplinary researches in biology based on physical, biological and medical sciences, and engineering. We will also discuss the applications of the results of such interdisciplinary cooperation to human health-systems.

1SBP-1 **PCDR 法による細胞質内 RNA 送達の原理と応用**
Mechanism and Application of photoinduced cytosolic dispersion of RNA (PCDR) method
○大槻 高史 [1,2], ソー テタット [2], 渡邉 和則 [2]（[1]岡大院統合科学, [2]岡大院自然）
Takashi Ohtsuki[1,2], Tet Htut Soe[2], Kazunori Watanabe[2] ([1]*Grad. Sch. of ISEHS, Okayama Univ.*, [2]*Grad. Sch. of Nat. Sci. & Tech, Okayama Univ.*)

1SBP-2 **濾胞樹状細胞による抗体の親和性成熟の制御機構の解明**
Immunological functions of follicular dendritic cells on affinity maturation of antibody
○曲 正樹 [1], 小川 紗也香 [2], 松岡 由希子 [2], 高田 美帆 [2], 金山 直樹 [1], 德光 浩 [1]（[1]岡山大・院ヘルスシステム統合科学, [2]岡山大・院自然科学）
Masaki Magari[1], Sayaka Ogawa[2], Yukiko Matsuoka[2], Miho Takada[2], Naoki Kanayama[1], Hiroshi Tokumitsu[1] ([1]*Grad. Sch. Interdiscip. Sci. and Eng. in Health Syst., Okayama Univ.*, [2]*Grad. Sch. of Natl. Sci. and Tech., Okayama Univ.*)

1SBP-3 Cytokine expression and immune cell function in tumor growth
Junko Masuda (*Grad. Sch. Inter. Sci. & Eng. Heal. Sys., Okayama Univ.*)

1SBP-4 **自然色、形状、奥行における脳情報処理機構に関する fMRI 研究**
A fMRI Brain Imaging Study for Visual Contextual Process of Color, Shape and Depth
○呉 瓊 [1], 李 春林 [2], 高橋 成子 [3], 孫 洪贇 [4], 郭 启勇 [4], 大谷 芳夫 [5], 江島 義道 [1], 呉 景龍 [1]（[1]岡大・ヘルスシステム統合科学研究科, [2]中国・首都医科大学, [3]京都市立芸術大学, [4]中国医科大学, [5]京都工芸繊維大）
Qiong Wu[1], Chunlin Li[2], Shigeko Takahashi[3], Hongzan Sun[4], Qiyong Guo[4], Yoshio Ohtani[5], Yoshimichi Ejima[1], Jinglong Wu[1] ([1]*Grad. Sch. of Interdiscip. Sci. & Eng. in Health Systems, Univ. Okayama*, [2]*Sch. of Bio. Eng., Capital Med. Univ.*, [3]*Kyoto City Univ. of Arts*, [4]*Shengjing HP of China Med. Univ.*, [5]*Kyoto Inst. of Tech.*)

1SBP-5　テラヘルツ工学による先端バイオセンシング
A terahertz technology for advanced bio-sensing
○紀和 利彦, 堺 健司, 塚田 啓二（岡山大学統合科学）
Toshihiko Kiwa, Kenji Sakai, Keiji Tsukada (*Okayama University*)

1SBP-6　Speech Enhancement of Glossectomy Patient's Speech using Voice Conversion Approach
Masanobu Abe, Hiroki Murakami, Seiya Ogino, Sunao Hara (*Okayama Univ.*)

13:30〜16:00　I 会場（一般教育棟 B 棟 4 階 B41）／Room I (B41, General Education Build. B, 4F)

1SIP　ゲノム合成時代の人工細胞研究
Artificial cell research in era of synthetic genome

オーガナイザー：野地 博行（東京大学），木賀 大介（早稲田大学）
Organizers: Hiroyuki Noji (The University of Tokyo), Daisuke Kiga (Waseda University)

An objective of artificial cell synthesis research is the identification of what makes an entity alive. The variety of new methods for the reconstitution of artificial cells is expanding because of recent progress in genome-scale DNA synthesis. Although such progress is led by the US and China, the traditional Japanese methodology of reconstitution has strong points in the new generation of artificial cell study as well. This symposium presents the Japanese situation of artificial cell research and genome synthesis, and discusses innovative ideas emerging from the combination of these two fields.

はじめに
Opening Remarks

1SIP-1　大腸菌複製サイクル再構成系を用いたセルフリー長鎖環状 DNA 合成
Cell-free synthesis of large circular DNA using a reconstitution system of replication cycle of Escherichia coli
○末次 正幸（立教大・理）
Masayuki Su'etsugu (*Col. of Sci., RIkkyo Univ.*)

1SIP-2　ゲノムシミュレーターを目指した人工細胞リアクタの開発
Artificial cell reactor towards genome simulator
○野地 博行（東京大学工学研究科）
Hiroyuki Noji (*Graduate School of Engineering, The University of Tokyo*)

1SIP-3　ゲノムサイズ DNA の脂質膜への自発的包埋
Spontaneous enveloping of genome-size DNA into lipid membrane
○鈴木 宏明 [1], 津金 麻実子 [1,2], 須永 史子 [1], 岡野 太治 [1]（[1]中大理工, [2]学振）
Hiroaki Suzuki[1], Mamiko Tsugane[1,2], Fumiko Sunaga[1], Taiji Okano[1] ([1]*Chuo University*, [2]*JSPS*)

1SIP-4　Synthetic Genomics for the Human Noncoding Regions
Yasunori Aizawa (*Tokyo Institute of Technology*)

1SIP-5　人工細胞内で RNA ゲノムの協力性は持続し進化するのか？
Sustainability and evolvability of cooperative RNAs in an artificial cell-like system
○市橋 伯一（大阪大学）
Norikazu Ichihashi (*Osaka University*)

1SIP-6 遺伝暗号の改変による生物学的封じ込め
Biological containment through engineering of genetic code
○木賀 大介（早稲田大学）
Daisuke Kiga (*Waseda University*)

2 日目（9 月 16 日（日））／Day 2（Sep. 16 Sun.）

9:00～11:30　A 会場（一般教育棟 B 棟 1 階 B11）／Room A (B11, General Education Build. B, 1F)
2SAA　Taiwan-Japan biophysics symposium on molcular motors *in vivo*

Organizers: Chien-Jung (National Central University, Taiwan), Kumiko Hayashi (Tohoku University)

The molecular motors have been studied intensively by single molecule experiments, however their functions in vivo have not been clarified yet. Then this symposium aims to bring together the leading international scientists of frontier biophysical researches on functions and strucutres of molecular motors. The open and international symposium offers a good opportunity for young scientists from Taiwan and Japan to exchange scientific opinions on the issue.

2SAA-1 Non-invasive force measurement reveals the number of active kinesins on a synaptic vesicle precursor regulated by ARL-8
Kumiko Hayashi[1,2], Shin Hasegawa[1], Takashi Sagawa[3], Sohei Tasaki[4,5], Shinsuke Niwa[4] ([1]*Sch. Eng., Tohoku Univ.*, [2]*PRIME, AMED*, [3]*NICT*, [4]*FRIS, Tohoku Univ.*, [5]*BDR, RIKEN*)

2SAA-2 Accommodation of mRNA on the ribosome during translation initiation
Jin-Der Wen (*Institute of Molecular and Cellular Biology, National Taiwan University*)

2SAA-3 Single-Molecule Study of Swi5-Sfr1 Stimulation on Rad51 Recombinase Filament Assembly in Mouse and Yeast
Hung-Wen Li[1], Chih-Hao Lu[1], Peter HY Chi[1], Hiroshi Iwasaki[2] ([1]*National Taiwan University*, [2]*Tokyo Institute of Technology*)

2SAA-4 Mechanics of the bacterial flagellar motor in vivo
Tsubasa Ishida[1], Taishi Kasai[2,3], Yong-Suk Che[4,5], **Yoshiyuki Sowa**[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Micro-Nano Tech, Hosei Univ.*, [3]*Dept. Life Sci., Rikkyo Univ.*, [4]*Dept. Frontier Biosci., Hosei Univ.*, [5]*Grad. Sch. Frontier Biosci., Osaka Univ.*)

2SAA-5 Measurement for the chemotaxis proteins and cellular behavior in single *E. coli* cell
Hajime Fukuoka (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

2SAA-6 Probing bacterial flagellar growth by real-time fluorescence imaging
Chien-Jung Lo (*National Central University, Taiwan*)

9:00〜11:30　B 会場（一般教育棟 A 棟 2 階 A21）／Room B (A21, General Education Build. A, 2F)
2SBA　クライオ電子顕微鏡
Cryo electron microscopy

オーガナイザー：千田 俊哉（高エネルギー加速器研究機構），Zhenfeng Liu（Chinese Academy of Science）
Organizers: Toshiya Senda (High Energy Accelerator Research Organization), Zhenfeng Liu (Chinese Academy of Science)

Due to recent developments of direct electron detection cameras, improved microscope design and advanced data-processing programs, cryo-electron microscopy (cryo-EM) is rapidly becoming a main technology for studying three-dimensional (3D) structures of proteins and their complexes at near atomic resolution. Since cryo-EM technique does not require crystallization of target proteins, it has been intensively applied in analyzing 3D structures of proteins that are difficult to crystallize, such as membrane protein complexes and supramolecular complexes. In addition, cryo-EM tomography has revealed 3D architectures of protein complexes at their native cellular localizations. Cryo-EM techniques are opening a new era in structural biology and cellular biology. In this symposium, recent results of cryo-EM studies will be presented by researchers from China and Japan.

はじめに
Opening Remarks

2SBA-1　Structural Insights into Light Harvesting and Its Regulation in Plants
Zhenfeng Liu (*Institute of Biophysics, Chinese Academy of Sciences*)

2SBA-2　**エボラウイルス・ヌクレオ蛋白質−RNA 複合体のクライオ電子顕微鏡構造**
Structure of Ebola virus nucleoprotein-RNA complex by single-particle cryo-electron microscopy
○杉田 征彦 [1,2], 松波 秀行 [1], 河岡 義裕 [3,4], 野田 岳志 [5], ウォルフ マティアス [1]（[1]沖縄科学技術大学院大学, [2]阪大蛋白研, [3]東大医科研, [4]ウィスコンシン大学マディソン校, [5]京大ウイルス・再生研）
Yukihiko Sugita[1,2], Hideyuki Matsunami[1], Yoshihiro Kawaoka[3,4], Takeshi Noda[5], Matthias Wolf[1] ([1]*OIST*, [2]*IPR, Osaka Univ.*, [3]*Inst. Med. Sci., Univ. Tokyo*, [4]*UW-Madison*, [5]*Inst. Front. Life Med. Sci., Kyoto Univ.*)

2SBA-3　Structure of Origin Recognition Complex Bound to Autonomously Replicating Sequence
Ning Gao (*School of Life Sciences, Peking University*)

2SBA-4　**クライオ電子トモグラフィーを用いたゼブラフィッシュ繊毛における PIH タンパク質の機能解析**
Cryo-electron tomography revealed zebrafish axonemal dyneins assembled by distinct PIH proteins
○山口 博史 [1], 小田 賢幸 [2], 吉川 雅英 [1], 武田 洋幸 [3]（[1]東大・院医, [2]山梨大・院医, [3]東大・院理）
Hiroshi Yamaguchi[1], Toshiyuki Oda[2], Masahide Kikkawa[1], Hiroyuki Takeda[3] ([1]*Grad. Sch. Med., Univ. Tokyo*, [2]*Grad. Sch. Med., Univ. Yamanashi*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

2SBA-5　**クライオ電子顕微鏡で明らかになったコフィリンによるアクチン線維分解機構**
Structural basis of cofilin binding and disassembling of actin filaments revealed by cryo-electron microscopy
○成田 哲博（名古屋大学理学研究科）
Akihiro Narita (*Nagoya University*)

2SBA-6　Structure of phycobilisome
Sen-Fang Sui (*School of Life Sciences, Tsinghua University*)

おわりに
Closing Remarks

9:00～11:30　D 会場（一般教育棟 A 棟 3 階 A36）／Room D (A36, General Education Build. A, 3F)
2SDA　日本医療研究開発機構（AMED）・創薬等ライフサイエンス研究支援基盤事業 共催
創薬等先端技術支援基盤プラットフォーム (BINDS)
Basis for Supporting Innovative Drug Discovery and Life Science Research (BINDS)

オーガナイザー：田之倉 優（東京大学），由良 敬（早稲田大学）
Organizers: Masaru Tanokura (The University of Tokyo), Kei Yura (Waseda University)

For application of excellent basic research outcomes in Japan to medicine and drugs, the Basis for Supporting Innovative Drug Discovery and Life Science Research (BINDS) supports drug discovery research in universities and academic research institutions by establishing platform for drug discovery and medical technology, where high technology and facilities are shared for life science research. This symposium provides a forum for developing advanced discussions on life science research including academic drug discovery by giving a lecture from BINDS program officers and researchers.

はじめに
Opening Remarks

2SDA-1　**創薬等ライフサイエンス研究のための相関構造解析プラットフォーム**
Correlative Structural Analysis Platform for Drug Discovery and Life Sciences
○山本 雅貴（理化学研究所 放射光科学研究センター）
Masaki Yamamoto (*RIKEN SPring-8 Center*)

2SDA-2　**創薬における実験化学と計算化学の融合**
Integration of experimental and computational chemistry in drug discovery
○上村 みどり（帝人ﾌｧｰﾏ(株）生物医学総合研究所）
Midori Takimoto-Kamimura (*Teijin Institute for Biomedical Research*)

2SDA-3　**蛋白質相互作用の物理化学的解析と次世代創薬**
Physicochemical Analyses of Protein Interactions for Next Generation Drug Discovery and Development
○津本 浩平, 長門石 曉（東京大学大学院工学系研究科・医科学研究所）
Kouhei Tsumoto, Satoru Nagatoishi (*School of Engineering and Institute of Medical Science, The University of Tokyo*)

2SDA-4　**BINDS バイオロジカルシーズ探索ユニットにおける支援内容のご紹介**
BINDS: supporting platform to explore biological activity of your seeds
○古関 明彦（理化学研究所・生命医科学研究センター）
Haruhiko Koseki (*RIKEN center for integrative medical sciences*)

2SDA-5　**インシリコ創薬の展望**
Perspective of in silico drug discovery
○田中 成典（神戸大学大学院システム情報学研究科）
Shigenori Tanaka (*Kobe University*)

2SDA-6　**生命科学データベースの接続をめざす VaProS から見えてくるあらたな知見**
New knowledge and ideas found through VaProS, an application for life science database integration
○由良 敬 [1,2]（[1]早大・先進理工, [2]お茶大・生命情報）
Kei Yura[1,2] ([1]*Dept. Life Sci. & Med. Bio., Waseda Univ.*, [2]*Info. Bio., Ochanomizu Univ.*)

おわりに
Closing Remarks

9:00～11:30　E 会場（一般教育棟 A 棟 3 階 A37）／Room E (A37, General Education Build. A, 3F)
2SEA　機械シグナル受容応答機構解明に向けた最先端研究と未来
Keynote of mechanosignal response for the future of mechanobiology

オーガナイザー：森松 賢順（岡山大学），中澤 直高（京都大学）
Organizers: Masatoshi Morimatsu (Okayama University), Naotaka Nakazawa (Kyoto University)

Mechanosignals on the cell- extracellular matrix and cell-cell adhesions exert profound influences on cell migration, proliferation and stem-cell differentiation. However, the fundamental mechanisms of how cells detect and respond to mechanosignals remain poorly understood.We invite the front runners of this field to this symposium to share their latest research. Furthermore, we would like to discuss the next stage of this field with the presenters and the audience at the panel session.

はじめに
Opening Remarks

2SEA-1　The molecular clutch model as a framework to understand integrin-mediated mechanotransduction
Pere Roca-Cusachs (*Institute for Bioengineering of Catalonia*)

2SEA-2　Single-molecule measurements of force transmission by integrin heterodimers in living cells
Alexander Dunn (*Stanford University*)

2SEA-3　α カテニンの張力応答性分子機構と上皮形態形成
Force-sensing device region of alpha-catenin and epithelial morphogenesis
○米村 重信 [1,2]（[1]徳島大・院医歯薬学, [2]理研・生命機能科学）
Shigenobu Yonemura[1,2] ([1]*Tokushima Univ. Grad. Sch. Med. Sci.*, [2]*Riken BDR*)

2SEA-4　細胞増殖における接触阻害のメカノバイオロジー
Mechanobiology of the contact inhibition in cell proliferation
○曽我部 正博, 平田 宏聡（名大院・医・メカノバイオロジー・ラボ）
Masahiro Sokabe, Hiroaki Hirata (*Mechanobiology Lab, Nagoya Univ., Grad., Sch., Med.*)

2SEA-5　Rigidity Sensing and Transformed cell growth
Michael Sheetz (*Mechanobiology Institute, Singapore, National University of Singapore*)

おわりに
Closing Remarks

9:00～11:30　F 会場（一般教育棟 B 棟 2 階 B32）／Room F (B32, General Education Build. B, 2F)
2SFA　JST-CREST「超絶縁性脂質二分子膜に基づくイオン・電子ナノチャネルの創成」共催
生体機能の再構成によるセンシング技術とデバイス応用
Reconstruction of biological functions for sensing methods and device applications

オーガナイザー：手老 龍吾（豊橋技術科学大学），平野 愛弓（東北大学）
Organizers: Ryugo Tero (Toyohashi University of Technology), Ayumi Hirano-Iwata (Tohoku University)

Molecular recognition properties of sugar chains and proteins are important research subjects in the fields of medicine and drug discovery, which have recently been integrated with device technology as multifunctional elements. This symposium addresses new devices that reconstitute biological functions on the levels of molecules, viruses and cells. We will introduce pioneering research achievements in which nanomaterials and microfabrication techniques were applied to integration of novel biosensing devices, and discuss current subjects and future perspectives.

はじめに
Opening Remarks

2SFA-1　細胞機能解析を目指した非標識神経伝達物質イメージセンサ
Non Label Nurotransmitter Image Sesnor for for Analysis of Cerebral Function
○澤田 和明, 李 宥奈, 岩田 達哉, 高橋 一浩（国立大学法人豊橋技術科学大学）
Kazuaki Sawada, Youna Lee, Tatsuya Iwata, Kazuhiro Takahashi (*Toyohashi University of Technology*)

2SFA-2　オンチップ・セロミクス：「履歴・記憶」と「集団効果」から見た細胞ネットワークの後天的情報の理解
On-chip Cellomics: Reconstructive Understanding of Epigenetic Information in Cellular Networks from Algebraic and Geometric Perspectives
○安田 賢二（早稲田大学 理工学術院 先進理工学部 物理学科）
Kenji Yasuda (*Department of Physics, Waseda University*)

2SFA-3　Microfabricated Silicon Devices for Ion Channel Reconstitution
Ayumi Hirano-Iwata (*Advanced Institute for Materials Research, Tohoku University*)

2SFA-4　High Sensitive Virus Sensing by Sugar Chain Modified Graphene FET
Kazuhiko Matsumoto (*Institute of Scientific & Industrial Research, Osaka University*)

9:00～11:30　G 会場（一般教育棟 B 棟 3 階 B33）／Room G (B33, General Education Build. B, 3F)
2SGA　ポスト「京」重点課題 1 「生体分子システムの機能制御による革新的創薬基盤の構築」共催
マルチスケール・フィジクスで見えてくる生体高分子のダイナミクスと機能機序
Mechanism of Biomolecular Dynamics and Function Revealed by Multiscale Physics

オーガナイザー：河野 秀俊（量子科学技術研究開発機構），寺田 透（東京大学）
Organizers: Hidetoshi Kono (QST), Tohru Terada (The University of Tokyo)

Different scales of physics have been applied to understand various phenomena in biology. Quantum mechanics, for instance, provide the mechanism of enzymes, all atom simulations can show how molecule changes the conformation less than micro-second, and coarse-grained simulations now nearly reach the time scale directly comparable with wet-experiments. Integrating the different scales of physics can deepen our understanding on biomolecules. In this symposium, approaches utilizing different spatio-temporal scales will be introduced to elucidate how biomolecules behave and function. In addition, possible simulations with post-K computer will be proposed.

はじめに
Opening Remarks

2SGA-1 ハイブリッド分子シミュレーションによる光受容体タンパク質の分子機能ダイナミクスの解明
Functional Molecular Dynamics of Photo-Receptor Proteins Revealed by a Hybrid Molecular Simulation Technique
○林 重彦（京都大学大学院理学研究科化学専攻）
Shigehiko Hayashi (*Dept. Chem., Grad. Sch. Sci., Kyoto Univ.*)

2SGA-2 全原子分子動力学シミュレーションによるヌクレオソーム内・間相互作用の自由エネルギープロファイル
Free energy profiles of the intra- and inter-nucleosomal interactions by all-atom molecular dynamics simulations
○石田 恒, 河野 秀俊（量研・量子ビーム・生体分子シミュレーション）
Hisashi Ishida, Hidetoshi Kono (*National Institutes for Quantum and Radiological Science and Technology*)

2SGA-3 大規模計算によるマルチコピーマルチスケールシミュレーションとその応用研究
Multicopy/multiscale simulations and their applications using massive computing
○森次 圭 [1], 寺田 透 [2], 石田 竜次 [1], 木寺 詔紀 [1]（[1]横浜市立院・生命医, [2]東大・情報学環）
Kei Moritsugu[1], Tohru Terada[2], Ryuji Ishida[1], Akinori Kidera[1] ([1]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [2]*III, Univ. Tokyo*)

2SGA-4 マルコフ状態モデルによるタンパク質の立体構造変化のダイナミクス解析
Analysis of the dynamics of protein conformational change using Markov state model
○寺田 透 [1,2], 根上 樹 [2]（[1]東大・情報学環, [2]東大・院農）
Tohru Terada[1,2], Tatsuki Negami[2] ([1]*III, Univ. Tokyo*, [2]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*)

2SGA-5 Quantitative Coarse-Grained Molecular Modeling of Biomembranes
Wataru Shinoda (*Nagoya Univ.*)

2SGA-6 Investigating Genome Organization and Regulation with Coarse-Grained Molecular Simulations
Cheng Tan, Shoji Takada (*Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.*)

2SGA-7 タンパク質の構造揺らぎを考慮したリガンド結合部位解析と創薬支援
Ligand binding site analysis with protein flexibility for drug design
○広川 貴次（産業技術総合研究所・創薬プロ研）
Takatsugu Hirokawa (*molprof, AIST*)

おわりに
Closing Remarks

9:00〜11:30　H 会場（一般教育棟 A 棟 4 階 A41）／Room H (A41, General Education Build. A, 4F)
2SHA　ゲノム時代が切り拓く光生物の沃野
The new fertile land of photobiology opened in genomic era

オーガナイザー：井上 圭一（東京大学），山下 高廣（京都大学）
Organizers: Keiichi Inoue (The University of Tokyo), Takahiro Yamashita (Kyoto University)

Photoreceptor proteins can be instantaneously triggered by light. This unique property has been a big advantage for providing important information about the structure and function relationships of proteins. Recently, rapid accumulation of genomic data has unveiled novel photoreceptor proteins that have unexpected functions. In this symposium, we would like to introduce frontier studies of photoreceptor proteins in the genomic era and discuss about a variety of connections between light and life and future applications to optogenetics.

はじめに
Opening Remarks

2SHA-1　ゲノム科学により拡がる新奇微生物型ロドプシンの多様性と光化学
New diversity of microbial rhodopsins revealed by genome science
○井上 圭一 [1,2]（[1]東大物性研, [2]JST・さきがけ）
Keiichi Inoue[1,2] ([1]*Univ. Tokyo, Inst. Solid State Phys.*, [2]*JST PRESTO*)

2SHA-2　PYP タンパク質における多様な分光学的性質と相互作用
Divergent spectroscopic features and interactions of PYP proteins
○山崎 洋一（奈良先端科学技術大学院大学先端科学技術研究科物質創成科学領域）
Yoichi Yamazaki (*Division of Materials Science, Graduate School of Science and Technology, NAIST*)

2SHA-3　Flavin 結合タンパク質の光反応の多様性
Diversity of photochemical reactions of Flavin-based photoreceptors
○中曽根 祐介（京大院理）
Yusuke Nakasone (*Graduate school of Science, Kyoto University*)

2SHA-4　Cyanobacteriochromes covering UV-to-FR region: Newcomers to the photoreceptor field potentially useful for bio-imaging and optogenetics
Rei Narikawa (*Dept. Biol. Sci., Shizuoka Univ.*)

2SHA-5　オプトジェネティクス応用へ向けた酵素型ロドプシンの分子機構理解
Enzyme rhodopsins -molecular properties of potential optogenetics tools-
○角田 聡 [1,2]（[1]JST さきがけ, [2]名古屋工業大学 大学院工学研究科 生命応用化学専攻）
Satoshi Tsunoda[1,2] ([1]*JST PRESTO*, [2]*Nagoya Institute of Technology*)

2SHA-6　脊椎動物の暗所視獲得プロセスを再考する
Revisit of the acquisition process of vertebrate scotopic vision
○山下 高廣（京大・院理・生物物理）
Takahiro Yamashita (*Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.*)

おわりに
Closing Remarks

9:00〜11:30　K 会場（一般教育棟 E 棟 1 階 E11）／Room K (E11, General Education Build. E, 1F)

2SKA　X 線自由電子レーザーと融合分野が拓くタンパク質反応ダイナミクスの新しい計測
New approaches to protein reaction dynamics pioneered by X-ray free electron lasers and interdisciplinary collaborations

オーガナイザー：久保 稔（兵庫県立大学），南後 恵理子（理化学研究所）
Organizers: Minoru Kubo (University of Hyogo), Eriko Nango (RIKEN)

Time-resolved crystallography using X-ray free electron lasers (XFELs) is being established and increasingly applied to proteins for visualizing their structural dynamics as "molecular movies". Interdisciplinary collaborations of this XFEL technique with other advanced techniques will take us to the next stage of structural biophysics. In this symposium, researchers at the forefront of various fields, such as spectroscopy, solution scattering, chemical biology, computation, as well as XFEL crystallography, will present their techniques and latest applications. We will also discuss the possible interplay of different techniques and future prospects of protein dynamics science.

はじめに
Opening Remarks

2SKA-1　XFEL analysis of light-mediated pyrimidine dimer repair by DNA photolyase
Yoshitaka Bessho[1,2] ([1]*Academia Sinica, IBC*, [2]*RIKEN SPring-8 Center*)

2SKA-2　細胞内結晶工学を利用したタンパク質結晶の機能設計
Functional design of protein crystals by in vivo crystal engineering
○安部 聡, 上野 隆史（東工大 生命理工）
Satoshi Abe, Takafumi Ueno (*Sch. Life Sci. Technol. Tokyo Tech.*)

2SKA-3　X 線自由電子レーザーによる生体高分子 X 線溶液散乱
BioSAXS with X-ray Free Electron Lasers
○清水 伸隆（高エネ機構・物構研・放射光）
Nobutaka Shimizu (*PF, IMSS, KEK*)

2SKA-4　QM/MM 法による金属酵素の構造活性相関の研究
QM/MM studies on structure-function relationships of metalloenzymes
○重田 育照（筑波大学計算科学研究センター）
Yasuteru Shigeta (*Center for Computational Sciences, University of Tsukuba*)

2SKA-5　X 線自由電子レーザーによるタンパク質中で起こる化学反応の三次元動画
Three-dimensional movie of chemical reactions in proteins captured by X-ray free electron lasers
○岩田 想（京都大学医学部）
So Iwata (*Kyoto Univ. Grad.Sch.Med.*)

2SKA-6　フェムト秒ラマン分光による光受容タンパク質の超高速構造ダイナミクスの観測
Ultrafast structural dynamics of photoreceptor proteins revealed by femtosecond Raman spectroscopy
○田原 太平 [1,2]（[1]理化学研究所 田原分子分光研究室, [2]理化学研究所 光量子工学領域）
Tahei Tahara[1,2] ([1]*Molecular Spectroscopy Laboratory, RIKEN*, [2]*RIKEN Center for Advanced Photonics (RAP)*)

9:00〜11:30　M 会場（一般教育棟 E 棟 2 階 E21）／Room M (E21, General Education Build. E, 2F)

2SMA　文部科学省科学研究費補助金 新学術領域研究「発動分子科学：エネルギー変換が拓く自律的機能の設計」共催
創って知る生物物理：生命現象の再構成と理解
Designing biological systems from scratch

オーガナイザー：多田隈 尚史（大阪大学），古田 健也（情報通信総研究機構）
Organizers: Hisashi Tadakuma (Osaka University), Ken'ya Furuta (NICT)

Biological systems are driven by intra- and inter-molecular orchestration of diverse molecules. Recent advances of biophysical techniques allow us to design the molecules and the systems from scratch. In this symposium, we will discuss the bottom up molecular design approach to understand the mechanisms of various life phenomena, ranging from the molecules to cells.

はじめに
Opening Remarks

2SMA-1　ATP 結合部位の合理設計: 分子モーターを理解する試み
Rational Design of ATP Binding Site: An Attempt to Understand Molecular Motor
○小杉 貴洋 [1,2,3]（[1]分子研・CIMoS, [2]総研大, [3]生命創成探究センター）
Takahiro Kosugi[1,2,3] ([1]*CIMoS, IMS*, [2]*SOKENDAI*, [3]*ExCELLS*)

2SMA-2　生物分子モーターの再デザイン
Re-design of biomolecular motors
指宿 良太 [1], 古田 茜 [2], 大岩 和弘 [1,2], 小嶋 寛明 [2], ○古田 健也 [2]（[1]兵庫県立大学, [2]国立研究開発法人情報通信研究機構）
Ryota Ibusuki[1], Akane Furuta[2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[2], **Ken'ya Furuta**[2] ([1]*University of Hyogo*, [2]*National Institute of Information and Communications Technology*)

2SMA-3　Design and evolution of synthetic nucleocapsids
Marc Lajoie (*Univ Washington, Molecular Engineering and Sciences*)

2SMA-4　集積型遺伝子チップの構築
Construction of integrated gene chip
○多田隈 尚史（大阪大学 蛋白質研究所）
Hisashi Tadakuma (*IPR Osaka University*)

2SMA-5　Structural DNA Nanotechnology: Complex Self-Assembly and Applications
Yonggang Ke (*Emory University*)

2SMA-6　RNA synthetic biology and nanotechnology to program cells
Hirohide Saito (*Kyoto University, CiRA*)

9:00〜11:30　O 会場（一般教育棟 D 棟 3 階 D32）／Room O (D32, General Education Build. D, 3F)
2SOA　ピコバイオロジーが目指すもの
Developments and future of piocobiology

オーガナイザー：水谷 泰久（大阪大学），中島 聡（奈良先端科学技術大学院大学）
Organizers: Yasuhisa Mizutani (Osaka University), Satoru Nakashima (NAIST)

All physiological processes are comprised of chemical reactions, each driven by proteins. The field of picobiology is defined as an aim to understand the mechanism of physiological processes by performing the picometer-level structural analyses to characterize the location and states of individual atoms of the functional centers that drive the physiological processes. The symposium focuses on developments and future of piocobiology based on studies using crystallography, vibrational spectroscopy, and synthetic chemistry on active sites.

はじめに
Opening Remarks

2SOA-1　脱窒菌の一酸化窒素還元酵素：反応機構と分子進化
Bacterial Nitric Oxide Reductases: Reaction Mechanism and Molecular Evolution
○城 宜嗣（兵庫県立大学大学院生命理学研究科）
Yoshitsugu Shiro (*U. Hyogo*)

2SOA-2　Development of Raman spectroscopic measurement system for analyzing the enzymatic reaction with gaseous substrate
Koji Nishikawa, Yuka Nakagawa, Yoshiki Higuchi, Takashi Ogura (*Grad. Sch. Sci., Univ. Hyogo*)

2SOA-3　Picobiology of metalloproteins: Vibrational spectroscopic studies of cytochrome *c* and hydrogenase
Shun Hirota[1], Hulin Tai[1], Yoshiki Higuchi[2], Sachiko Yanagisawa[2], Takashi Ogura[2] ([1]*Grad. Sch. Sci. Tech., Nara Inst. Sci. Tech.*, [2]*Grad. Sch. Sci., Univ. Hyogo*)

2SOA-4　時間分解振動分光法によるチトクローム酸化酵素のプロトンポンプ機構
Proton pumping mechanism of cytochrome *c* oxidase by time-resolved vibrational spectroscopy
○中島 聡（奈良先端科学技術大学院大学）
Satoru Nakashima (*Nara Institute for Science and Technology*)

2SOA-5　Oxygen Activation Mechanism by Copper Monooxygenases and Models
Shinobu Itoh (*Osaka University*)

2SOA-6　イオン液体中における小分子活性化の分光学的アプローチ
Spectroscopic study on the activation of CO_2 and N_2 in an ionic liquid
○増田 秀樹（名古屋工業大学）
Hideki Masuda (*Nagoya Institute of Technology*)

2SOA-7　シトクロム *c* 酸化酵素における触媒反応のピコバイオロジー
Pico-biology in Catalytic Reactions of Cyotchrome *c* Oxidase
○北川 禎三（兵県大・院生命理学）
Teizo Kitagawa (*Grad.Sch.Sci.Univ.Hyogo*)

14:00〜16:30　B 会場（一般教育棟 A 棟 2 階 A21）／Room B (A21, General Education Build. A, 2F)

2SBP　Strategic Japan-Singapore Research Program by JST and A*STAR:
New optical platform for mechanics of cellular-self-organization　共催
細胞の形態形成を制御する自己組織化メカニクス
Mechanical self-organization in cellular morphogenesis

オーガナイザー：茂木 文夫（Temasek Lifesciences Laboratory），大浪 修一（理化学研究所）
Organizers: Fumio Motegi (Temasek Lifesciences Laboratory), Shuichi Onami (RIKEN)

Physical force has been emerged as new discipline in cell physiology. Mechanical strains play a crucial role in biological self-organization, by which cellular components become ordered in space and time, leading to emergence of functional biological patterns. This symposium will feature 1) innovative techniques to visualize interplay between molecular components and mechanical forces applied on cellular architectures, and 2) the unifying principle in cellular self-organizing mechanics, which underlies development and function of many cell types, including embryos, neurons, hepatocyte cells, and ES-derived tissues.

はじめに
Opening Remarks

2SBP-1　Deconstruction and reconstruction of cell polarity networks
Fumio Motegi[1,2,3] ([1]*Temasek Lifesciences Lab.*, [2]*Mechanobiology Institute*, [3]*National Univ. of Singapore*)

2SBP-2　微小管の構造変化による細胞内物質輸送の極性制御
Conformational switching of microtubule as the basis for the polarized intracellular transport
○岡田 康志 [1,2]（[1]理研　生命機能科学研究センター, [2]東大・理・物理，生物普遍性研究機構）
Yasushi Okada[1,2] ([1]*Center for Biosystems Dynamics Research (BDR), RIKEN*, [2]*Dept Phys & Univ Biol Inst (UBI), Univ Tokyo*)

2SBP-3　The cytoskeleton as a smart composite material: A unified pathway linking microtubules, myosin-II filaments and integrin adhesions
Rafiq Nisha Bte Mohd[1], Yukako Nishimura[1], Sergey V. Plotnikov[2], Visalatchi Thiagarajan[1], Zhen Zhang[1], Meenubharathi Natarajan[1], Shidong Shi[1], Viasnoff Virgile[1,3,4], Gareth E. Jones[5], Pakorn Kanchanawong[1,6], **Alexander D. Bershadsky**[7] ([1]*Mechanobiology Institute, National University of Singapore*, [2]*Department of Cell and Systems Biology, University of Toronto*, [3]*CNRS UMI*, [4]*Department of Biological Sciences, National university of Singapore*, [5]*Randall Centre for Cell & Molecular Biophysics, King's College London*, [6]*Deparment of Biomedical Engineering, National University of Singapore*, [7]*Department of Molecular Cell Biology, Weizmann Institute of Science*)

2SBP-4　3D micro-environmental control around single hepatocytes to induce apico basal polarization and lumenogenesis
Virgile Viasnoff[1] ([1]*National University of Singapore*, [2]*CNRS France*)

2SBP-5　Collective cell movement driven by cellular torque generation
Takaki Yamamoto[1], Tetsuya Hiraiwa[2], **Tatsuo Shibata**[1] ([1]*RIKEN BDR*, [2]*The university of Tokyo*)

2SBP-6　多細胞の自己組織化と発生制御による in vitro での機能的な神経組織形成
Functional three-dimensional tissue formation by in vitro manipulation and multicellular autonomy
○永樂 元次（京都大学　ウイルス・再生医科学研究所）
Mototsugu Eiraku (*Institute for Frontier Life and Medical Sciences, Kyoto University*)

2SBP-7 Quantitative analysis of cellular dynamics in C. elegans embryo
Shuichi Onami (*RIKEN Center for Biosystems Dynamics Research*)

おわりに
Closing Remarks

14:00〜16:30　I 会場（一般教育棟 B 棟 4 階 B41）／Room I (B41, General Education Build. B, 4F)
2SIP　蛋白質複合体解析のアプローチ　−様々な手法と実例−
Multiple Approaches for Analyses of Protein Complexes -Methods and Applications-

オーガナイザー：小川 覚之（東京大学），上久保 裕生（奈良先端科学技術大学院大学）
Organizers: Tadayuki Ogawa (The University of Tokyo), Hironari Kamikubo (NAIST)

Dramatic improvements have recently occurred in the field of protein analyses; theory, methods, measurement equipment, and computers for calculation. This symposium focuses on the analyses of protein complexes and dynamics, and introduces the multiple approaches such as MALS, AUC, MS, cryo-EM, SAXS, NMR and AFM. The combination and integration of multiple methods will permit our deeper understanding of protein complexes and dynamics.

2SIP-1 Mechanism of Protein Dynamics Revealed by the Combination of Multiple Protein Analyses in Solution
Tadayuki Ogawa, Nobutaka Hirokawa (*Grad. Sch. Med., Univ. Tokyo*)

2SIP-2 Modern analytical ultracentrifugation for quantitative studies on intermolecular interactions
Susumu Uchiyama[1,2,3] ([1]*Grad. Sch. Eng. Osaka Univ.*, [2]*ExCELLS, NINS*, [3]*IPBS, Guangdong Univ. Tech.*)

2SIP-3 高速原子間力顕微鏡で観る機能中のタンパク質動態
Watching single proteins in action using high-speed AFM
○柴田 幹大 [1,2]（[1]金沢大・WPI-NanoLSI, [2]金沢大・新学術創成）
Mikihiro Shibata[1,2] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*)

2SIP-4 Structural characterization of antibody interactions in situ
Saeko Yanaka[1,2,3], Hiroki Watanabe[4], Rina Yogo[1,3], Hirokazu Yagi[3], Takayuki Uchihashi[4], Koichi Kato[1,2,3] ([1]*Inst. for Mol. Sci.*, [2]*ExCELLS*, [3]*Nagoya City Univ.*, [4]*Nagoya Univ.*)

2SIP-5 クライオ電子顕微鏡によるタンパク質複合体の構造解析
Structural Analysis of Protein Complexes by Cryo-Electron Microscopy
○包 明久, 吉川 雅英（東京大学　大学院医学系研究科）
Akihisa Tsutsumi, Masahide Kikkawa (*Graduate School of Medicine, The University of Tokyo*)

2SIP-6 連続滴定 SAXS 測定を利用した多成分混合溶液中のタンパク質の構造解析
Structural analysis of multiple-component systems using continuous titration SAXS
○上久保 裕生（奈良先端大 物資創成）
Hironari Kamikubo (*MS, NAIST*)

2SIP-7 人工タンパク質ナノブロックによる自己集合超分子複合体ナノ構造の創製と解析
Construction and analyses of self-assembling supramolecular complex nanostructures constructed from de novo protein nanobuilding blocks
○新井 亮一 [1,2]（[1]信州大・繊維・応用生物, [2]菌類微生物セ）
Ryoichi Arai[1,2] ([1]*Appl. Biol., FTST, Shinshu Univ.*, [2]*CFMD, Shinshu Univ.*)

おわりに
Closing Remarks

3 日目（9 月 17 日（月・祝））／Day 3（Sep. 17 Mon. Pub holiday）

9:00～11:30　A 会場（一般教育棟 B 棟 1 階 B11）／Room A (B11, General Education Build. B, 1F)
3SAA　光回復酵素／クリプトクロムスーパーファミリーの光依存的機能と多様性の最先端
Cutting edge of diversity and light-dependent function of photolyase/cryptochrome superfamily

オーガナイザー：山元 淳平（大阪大学），山田 大智（名古屋工業大学）
Organizers: Junpei Yamamoto (Osaka University), Daichi Yamada (Nagoya Institute of Technology)

Photolyase/cryptochrome superfamily (PCSf) functions as regulatory proteins in maintenance of genome stability, signal transduction, and circadian clock. Although their biological functions are diverse, they share common protein fold with high similarity in amino acid sequence and light-harnessing center, flavin adenine dinucleotide (FAD). How does PCSf acquire distinct functions with the same structure? In this symposium, we will focus on the diversity and light-dependent function of respective proteins in PCSf, and will try to look for the molecular origin of diversity of PCSf.

はじめに
Opening Remarks

3SAA-1　DNA binding and light-dependent DNA repair abilities of photolyases
Junpei Yamamoto (*Grad. Sch. Eng. Sci., Osaka Univ.*)

3SAA-2　Differences and similarities in (6-4) photolyase DNA repair pathways
Hisham Dokainish[1], Daichi Yamada[2], Hideki Kandori[2], Akio Kitao[3] ([1]*Theoretical Molecular Science Laboratory, Riken*, [2]*Nagoya Institute of Technology*, [3]*Tokyo Institute of Technology*)

3SAA-3　The undistorted photolyase: photoreduction stages revealed via serial femtosecond crystallography
Manuel Maestre-Reyna (*Inst. Biol. Chem., Academia Sinica*)

3SAA-4　Light-induced electron (and proton) transfer underlying the activation of cryptochromes and photolyases
Pavel Müller (*CNRS/I2BC*)

3SAA-5　光回復酵素/クリプトクロムスーパーファミリーの機能転換研究
Functional conversion of photolyases/cryptochrome superfamily (PCSf): Toward finding the ancestor of PCSf
○山田 大智（名工大・院工）
Daichi Yamada (*Nagoya Inst. Tech.*)

おわりに
Closing Remarks

9:00〜11:30　B 会場（一般教育棟 A 棟 2 階 A21）／Room B (A21, General Education Build. A, 2F)

3SBA　文部科学省科学研究費補助金 新学術領域研究「宇宙からひも解く新たな生命制御機構の統合的理解：重力変化を含む力学的ストレスに対するメカノセンシング機構」共催

物理的力と生物

Physical force in the life

オーガナイザー：成瀬 恵治（岡山大学），東谷 篤志（東北大学）

Organizers: Keiji Naruse (Okayama University), Atsushi Higashitani (Tohoku University)

Maintenance and destruction of homeostasis play key roles in biological adaptation to extreme environments such as space. Integrated understanding of the adaptation mechanism at a molecular, cellular, and human level opens the new bioscience field. We invite the front runners of this field to this symposium and discuss the future of this field.

はじめに
Opening Remarks

3SBA-1　高圧力で誘起される細胞運動
Pressure-induced activation of the cell motility
○西山 雅祥（近畿大）
Masayoshi Nishiyama (*Kindai Univ.*)

3SBA-2　心筋細胞伸展感受性のマクロ・ミクロ連関
Macro-micro linkages in cardiac response to stretch
○入部 玄太郎（岡山大学医歯薬学総合研究科）
Gentaro Iribe (*Grad. Sch. Med. Dent. Pharm., Univ. Okayama*)

3SBA-3　Combined effects of microgravity and UVB radiation on plant
Jun Hidema[1], Akihisa Takahashi[2] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*Gunma Univ., Heavy Ion Med. Center*)

3SBA-4　線虫の物理的力に対する応答
Response to physical force in *C. elegans*
○東谷 篤志（東北大・院・生命科学）
Atsushi Higashitani (*Grad Schl Life Sci. Tohoku Univ.*)

3SBA-5　骨格筋維持における重力の役割―ゼブラフィッシュの宇宙滞在から学ぶこと
Roles of the gravity in the maintenance of skeletal muscle—what we can learn from space stay of zebrafish
○瀬原 淳子（京都大学）
Atsuko Sehara (*Institute for Frontier Life and Medical Sciences, Kyoto University, Japan*)

おわりに
Closing Remarks

9:00～11:30　D 会場（一般教育棟 A 棟 3 階 A36）／Room D (A36, General Education Build. A, 3F)

3SDA　JST CREST「ライフサイエンスの革新を目指した構造生命科学と先端的基盤技術」領域 共催
構造生命科学の新展開
New horizon of Structural Life Science

オーガナイザー：中川 敦史（大阪大学），清水 敏之（東京大学）
Organizers: Atsushi Nakagawa (Osaka University), Shimizu Toshiyuki (The University of Tokyo)

"Structural life science" aims to integrate cutting-edge life science areas with structural biology for innovation in life science. In this symposium, young top scientists who are opening up this field will be invited to present their recent results and novel techniques to facilitate thier researches. This symposium is prgrammed to initiate the discussion on the future development of structural life sciences.

3SDA-1　筋小胞体カルシウム ATP アーゼ SERCA2b の膜貫通ヘリックス相互作用による制御機構の構造基盤
Structural basis of Sarco/Endoplasmic reticulum Ca2+-ATPase 2b regulation via transmembrane helix interplay

○井上 道雄[1], 作田 菜奈美[1], 渡部 聡[1], 田中 良樹[2], 潮田 亮[3], 加藤 幸成[4], 高木 淳一[5], 塚崎 智也[2], 永田 和宏[3], 稲葉 謙次[1]（[1]東北大・多元研, [2]奈良先端大・バイオ, [3]京産大・総合生命, [4]東北大・医, [5]阪大・蛋白研）

Michio Inoue[1], Nanami Sakuta[1], Satoshi Watanabe[1], Yoshiki Tanaka[2], Ryo Ushioda[3], Yukinari Kato[4], Junichi Takagi[5], Tomoya Tsukazaki[2], Kazuhiro Nagata[3], Kenji Inaba[1] ([1]*IMRAM, Tohoku Univ*, [2]*Grad. Sch. Biol. Sci., NAIST*, [3]*Fac. of Life Sci., KSU*, [4]*Med., Tohoku Univ.*, [5]*IPR, Osaka Univ.*)

3SDA-2　循環型電子伝達に関わる NDH-1 複合体の構造および相互作用解析
Structure and interaction studies on the cyanobacterial NDH-1 complex involved in the photosynthetic cyclic electron flow

○田中 秀明[1], 梅野 恵太[1], 三角 裕子[1], 金 宙妍[1], レグナー マティアス[2], 池上 貴久[3], ノヴァチク マーク[2], 栗栖 源嗣[1]（[1]阪大蛋白研, [2]Ruhr University Bochum, [3]横市大・生命医科学）

Hideaki Tanaka[1], Keita Umeno[1], Yuko Misumi[1], Ju Yaen Kim[1], Matthias Rögner[2], Takahisa Ikegami[3], Marc Nowaczyk[2], Genji Kurisu[1] ([1]*IPR, Osaka Univ.*, [2]*Ruhr University Bochum*, [3]*Grad. Sch. of Medical Life Science, Yokohama City Univ.*)

3SDA-3　てんかん関連リガンド-受容体複合体 LGI1-ADAM22 の構造基盤
Structural basis of epilepsy-related ligand-receptor complex LGI1-ADAM22

○山形 敦史[1], 宮崎 裕理[2], 重松 秀樹[3], 白水 美香子[3], 深田 優子[2], 深田 正紀[2], 深井 周也[1]（[1]東京大学・定量生命科学研究所・蛋白質複合体解析研究分野, [2]自然科学研究機構・生理学研究所・生体膜研究部門, [3]理研・生命機能科学研究センター）

Atsushi Yamagata[1], Yuri Miyazaki[2], Hideki Shigematsu[3], Mikako Shirouzu[3], Yuko Fukata[2], Masaki Fukata[2], Shuya Fukai[1] ([1]*Institute for Quantitative Biosciences, Univ. of Tokyo*, [2]*Div. of Membrane Physiology, NIPS*, [3]*RIKEN Center for Biosystems Dynamics Research*)

3SDA-4　電位依存性ホスファターゼ VSP の構造生物学的研究
Structural analysis of voltage-sensing phosphatase (VSP) on the electrochemical coupling

○成田 宏隆[1], 松田 真[2], 岡村 康司[3], 中川 敦史[2]（[1]名工大, [2]阪大・蛋白研, [3]阪大・院医）

Hirotaka Narita[1], Makoto Matsuda[2], Yasushi Okamura[3], Atsushi Nakagawa[2] ([1]*Nagoya Inst. Tech.*, [2]*Inst. Protein Res., Osaka Univ.*, [3]*Gra. Sch. of Med., Osaka Univ.*)

3SDA-5 [NiFe]ヒドロゲナーゼがもつ鉄硫黄クラスターの新規機能
Novel functions of the Fe-S clusters in the [NiFe]-hydrogenases
○庄村 康人（茨城大・院理工）
Yasuhito Shomura (*Grad. Sch. Sci. and Eng., Ibaraki Univ.*)

3SDA-6 Toll 様受容体の構造生物学
Structural biology of Toll-like receptors
○大戸 梅治, 清水 敏之（東京大学大学院薬学系研究科）
Umeharu Ohto, Toshiyuki Shimizu (*Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

9:00～11:30　E 会場（一般教育棟 A 棟 3 階 A37）／Room E (A37, General Education Build. A, 3F)
3SEA　化学感覚の新コンセプト
Novel concepts of chemical senses

オーガナイザー：今井 啓雄（京都大学），山下 敦子（岡山大学）
Organizers: Hiroo Imai (Kyoto University), Atsuko Yamashita (Okayama University)

Recent elucidation of molecular mechanisms of chemical senses allows us to integrate the biophysical points of views: structure, function, evolution, and neural network for taste and olfaction. In this symposium, we will introduce the examples of integrative studies on chemical senses for various environmental signals. These studies would give novel concepts of chemical signals and stimulate further studies and discussions for the biophysical understanding of chemical senses.

3SEA-1 Taste perception approached by biophysics and structural biology
Atsuko Yamashita (*Grad. Sch. Med. Dent. & Pharm. Sci., Okayama University*)

3SEA-2 甘味受容体のアゴニスト/アンタゴニスト特性
Agonistic/antagonist properties of sweet taste receptor
○實松 敬介 [1,2], 重村 憲徳 [1,2], 二ノ宮 裕三 [1,2,3]（[1]九大院 歯 口腔機能, [2]九大 味嗅覚センサ 感覚生理, [3]モネル研）
Keisuke Sanematsu[1,2], Noriatsu Shigemura[1,2], Yuzo Ninomiya[1,2,3] ([1]*Sect. Oral Neurosci., Grad.Sch. of Dent. Sci., Kyushu Univ.*, [2]*Div. Sensory Physiol. R & D TAOS, Kyushu Univ.*, [3]*Monell Chem. Senses Ctr.*)

3SEA-3 霊長類味覚受容体の機能多様性
Functional diversities of primate taste receptors
○今井 啓雄（京都大・霊長研）
Hiroo Imai (*Primate Research Institute, Kyoto University*)

3SEA-4 Taste cells lacking synapses open a wide pore channel for rapid neurotransmission of tastes
Akiyuki Taruno (*Dept. Mol. Cell Physiol., Kyoto Pref. Univ. Med.*)

3SEA-5 光遺伝子操作による単一の糸球体の活性により誘因される恐怖行動の探索
Immobility responses are induced by photoactivation of single glomerular species responsive to fox odour TMT
○斎藤 治美 [1,2,3], 西住 裕文 [2,3], 鈴木 悟 [3], 松本 英之 [4], 家城 直 [4], 阿部 拓哉 [5], 清成 寛 [5,6], 横田 秀夫 [7], 森田 正彦 [7], 平山 望 [8], 菊水 健史 [8], 森 憲作 [4], 坂野 仁 [2,3]（[1]玉川大学脳科学研究所, [2]福井大学医学部高次機能領域, [3]東京大学理学研究科生化学専攻, [4]東京大学医学研究科細胞分子生理学教室, [5]理研ライブサイエンス技術基盤研究センター, [6]理研生命機能科学研究センター生体モデル開発ユニット, [7]理化学研究所 光量子工学研究センター 画像情報処理研究チーム, [8]麻布大学 獣医学部伴侶動物学教室）
Harumi Saito[1,2,3], Hirofumi Nishizumi[2,3], Satoshi Suzuki[3], Hideyuki Matsumoto[4], Nao Ieki[4], Takaya Abe[5], Hiroshi Kiyonari[5,6], Masahiko Morita[7], Masahiko Morita[7], Nozomi Hirayama[8], Takefumi Kikusui[8], Kensaku Mori[4], Hitoshi Sakano[2,3] ([1]*Brain Science Institute, Tamagawa University*, [2]*Department of Brain Function, Faculty of Medical Sciences, University of Fukui*, [3]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, [4]*Department of Physiology, Cellular and Molecular Physiology, Graduate School of Medicine, The University of Tokyo*, [5]*Genetic Engineering Team, RIKEN, Center for Life Science, Technologies*, [6]*Animal Resource Development Unit, RIKEN, Center for Life Science Technologies*, [7]*Image Processing Research Team, RIKEN,*, [8]*Department of Animal Science and Biotechnology, School of Veterinary, Medicine, Azabu University*)

3SEA-6 Male glandular odorants evoke female attractive behavior among ring-tailed lemurs (*Lemur catta*): A putative pheromone in primates
Mika Shirasu[1,2] ([1]*Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences,*, [2]*ERATO Touhara Chemosensory Signal Project*)

9:00〜11:30　F 会場（一般教育棟 B 棟 3 階 B32）／Room F (B32, General Education Build. B, 3F)

3SFA　文部科学省科学研究費補助金 新学術領域研究「シンギュラリティ生物学」共催 シンギュラリティ生物学
Singularity biology

オーガナイザー：永井 健治（大阪大学），堀川 一樹（徳島大学）
Organizers: Takeharu Nagai (Osaka University), Kazuki Horikawa (Tokushima University)

If we carefully observe the cell population that at first glance looks uniform and homogeneous, we may find small number of heterogeneous cells with a different nature. Moreover, this minor element in cellular population would sometimes work as a key for causing singularity, at which living system is significantly and drastically changed to different status. In this symposium, we would like to discuss analytical methods for sensitive detection or visualization as well as the theories regarding principle or mechanism how such minor elements give rize to the singularity-associated phenomena.

はじめに
Opening Remarks

3SFA-1 シンギュラリティ生物学による神経変性疾患へのアプローチ
Approach to neurodegenerative disease by singularity biology
○坂内 博子 [1,2], 金谷 美沙 [3], 前田 純宏 [4], 廣瀬 松美 [2], 高島 明彦 [3], 御子柴 克彦 [2]（[1]JST・さきがけ, [2]理研・脳センター, [3]学習院大・理, [4]慶應大・医）
Hiroko Bannai[1,2], Misa Kanatani[3], Sumihiro Maeda[4], Matsumi Hirose[2], Akihiko Takashima[3], Katsuhiko Mikoshiba[2] ([1]*JST PRESTO*, [2]*RIKEN CBS*, [3]*Gakushuin Univ, Faculty. Sci.*, [4]*Keio Univ. Sch. Med.*)

3SFA-2　シンギュラリティ生物学を定量する情報理論的アプローチ
Information theoretic approach to quantify singularity in biology
○小松崎 民樹 [1,2]（[1]北海道大学 電子科学研究所, [2]リヨン高等師範学校）
Tamiki Komatsuzaki[1,2] ([1]*Hokkaido Univ. RIES MSC*, [2]*ENS de Lyon*)

3SFA-3　シンギュラリティ細胞を探索する技術：散乱光を使った非染色細胞状態計測
A Challenges to use scattering lights for singularity biology
○渡邉 朋信（理化学研究所・生命機能）
Tomonobu M. Watanabe (*RIKEN, BDR*)

3SFA-4　シンギュラリティ生物学へ向けて：１細胞の観察・分取とそのシークエンシング解析
An automated system of single cell picking and sequencing for singularity biology
○城口 克之 [1,2,3]（[1]理研・生命機能セ, [2]理研・生命医セ, [3]JST さきがけ）
Katsuyuki Shiroguchi[1,2,3] ([1]*RIKEN BDR*, [2]*RIKEN IMS*, [3]*JST PRESTO*)

3SFA-5　高速・高拡張性全脳イメージングシステム FAST：アンバイアスで仮説フリーに脳内のシンギュラリティを検出する手法へ
High-speed and scalable whole-brain imaging system FAST: unbiased and hypothesis-free approach to detect singularity in the brain
○橋本 均 [1,2,3,4], 笠井 淳司 [1], 勢力 薫 [1,5], 中澤 敬信 [1,6]（[1]大阪大学大学院薬学研究科神経薬理学分野, [2]連合小児発達学研究科附属子どものこころの発達研究センター, [3]データビリティフロンティア機構バイオサイエンス部門, [4]先導的学際研究機構超次元ライフイメージング研究部門, [5]大阪大学未来戦略機構, [6]大阪大学大学院歯学研究科薬理学教室）
Hitoshi Hashimoto[1,2,3,4], Atsushi Kasai[1], Kaoru Seiriki[1,5], Takanobu Nakazawa[1,6] ([1]*Lab. of Mol. Neuropharmacol., Grad. Sch. of Pharmaceutical Sci., Osaka Univ.*, [2]*Center for Child Mental Dev., United Grad. Sch. of Child Dev.*, [3]*Div. of Biosci., Inst. for Datability Sci.*, [4]*Dep. of Transdimensional Life Imaging, Open and Transdisciplinary Res. Initiatives*, [5]*Inst. for Academic Initiatives, Osaka Univ.*, [6]*Dep. of Pharmacology, Grad. Sch. of Dentistry, Osaka Univ.*)

3SFA-6　シンギュラリティ生物学による自己免疫疾患制御機構の解明
Singularity cell research in autoimmunity
○岡崎 拓（徳島大学先端酵素学研究所免疫制御学分野）
Taku Okazaki (*Div. Immun. Reg., Inst. Adv. Med. Sci., Tokushima U.*)

おわりに
Closing Remarks

9:00～11:30　G 会場（一般教育棟 B 棟 3 階 B33）／Room G (B33, General Education Build. B, 3F)
3SGA　生体分子の運動と機能理解を目指した単粒子観測実験と計算解析
Single Particle Analysis of Biological Molecules to Study Dynamics and Functions

オーガナイザー：宮下 治（理化学研究所），岩崎 憲治（大阪大学）
Organizers: Osamu Miyashita (RIKEN), Kenji Iwasaki (Osaka University)

Biological molecules perform their functions through dynamical transitions and molecular interactions, and thus, we need to study not only their static structures but also their conformational transitions. For this purpose, information from biomolecular “single particles”, i.e., non-averaged information of molecular conformations, is critically important. In this symposium, various experimental techniques to obtain such information – spectroscopy, cryo-EM, AFM, XFEL – as well as theoretical and computational studies to take advantage of such experimental data for obtaining further information will be discussed.

3SGA-1 Single molecule fluorescence tracking at 10-μs resolution: Application to protein folding and functional dynamics
Satoshi Takahashi, Hiroyuki Oikawa (*IMRAM, Tohoku Univ.*)

3SGA-2 蛋白質の複雑なコンフォメーション変化の解明を目指して-ハイブリッドアプローチ
Toward the elucidation of complicated conformational change in proteins by using a hybrid approach
○岩崎 憲治 [1], 松本 淳 [2], 川口 敦史 [3]（[1]阪大・蛋白研, [2]量子科学技術研究開発機構, [3]筑波大・人間総合科学）
Kenji Iwasaki[1], Atsushi Matsumoto[2], Atsushi Kawaguchi[3] ([1]*IPR, Osaka Univ.*, [2]*QST*, [3]*Grad. Sch. Comprehensive Human Sciences, Univ. of Tsukuba*)

3SGA-3 一分子ダイナミクス理解のための高速 AFM データの画像処理と定量解析
Image Processing and Quantitative Analysis of High-Speed AFM data for studying single-molecule dynamic
○内橋 貴之（名古屋大学大学院理学研究科）
Takayuki Uchihashi (*Department of Physics, Nagoya University*)

3SGA-4 Controlled Environment Nano-Imaging Free From Radiation Damage by X-ray Laser Diffraction
Yoshinori Nishino[1], Takashi Kimura[1], Akihiro Suzuki[1], Yasumasa Joti[2], Yoshitaka Bessho[3] ([1]*RIES, Hokkaido Univ.*, [2]*JASRI*, [3]*Inst. Bio. Chem., Academia Sinica*)

3SGA-5 Temporal hierarchy in the energy landscape of adenylate kinase folding/unfolding
J. Nicholas Taylor (*Research Institute for Electronic Science, Hokkaido University*)

3SGA-6 Hybrid modeling approaches to study structures and dynamics of biological systems
Florence Tama[1,2] ([1]*Nagoya University*, [2]*RIKEN*)

9:00～11:30　H 会場（一般教育棟 A 棟 4 階 A41）／Room H (A41, General Education Build. A, 4F)

3SHA　文部科学省科学研究費補助金 新学術領域研究「光合成分子機構の学理解明と時空間制御による革新的光ー物質変換系の創製」共催
光エネルギー変換の生物物理：光合成のメカニズムはどこまで解明されたか？
Biophysics of light-energy conversion: To what extent has the mechanism of photosynthesis been clarified?

オーガナイザー：菅 倫寛（岡山大学），野口 巧（名古屋大学）
Organizers: Michi Suga (Okayama University), Takumi Noguchi (Nagoya University)

Photosynthesis is an elaborate biological system for light-energy conversion. It not only provides an energy source for biological activities but also sustains life on earth by O_2 evolution. Although recent high-resolution structures of photosynthetic proteins have significantly advanced the photosynthesis researches, many unsolved problems still remain in the mechanism of light-energy conversion. In this symposium, we will introduce state-of-art researches with theoretical and experimental biophysical approaches to unravel the photosynthetic mechanism and discuss the future perspectives in this field.

はじめに
Opening Remarks

3SHA-1 Intramolecular vibrations complement robustness of the primary charge separation in Photosystem II reaction center
Akihito Ishizaki (*Institute for Molecular Science*)

3SHA-2 極低温顕微分光による光化学系複合体の単一分子分光
Single Molecule Spectroscopy of Photosystem Complex by Cryomicroscopy
○柴田 穣（東北大院理・化学）
Yutaka Shibata (*Tohoku Univ. Chemistry*)

3SHA-3 Crystal structure of PSII in the intermediate states and possible mechanism for the O=O bond formation
Michi Suga, Jian-Ren Shen (*Research Institute for Interdisciplinary Science*)

3SHA-4 光合成初期反応の電子スピン画像解析
Electron Spin Polarization Imaging Analyses of Primary Charge Separations in Photosynthesis
○小堀 康博 [1,2], 長嶋 宏樹 [1], 見延 玲奈 [2], 長谷川 将司 [2], 三野 広幸 [3], Norris James[4]（[1]神戸大分子フォト, [2]神戸大院理, [3]名大院理, [4]シカゴ大化）
Yasuhiro Kobori[1,2], Hiroki Nagashima[1], Reina Minobe[2], Masashi Hasegawa[2], Hiroyuki Mino[3], James Norris[4] ([1]*Molecular Photoscience Research Center, Kobe Univ.*, [2]*Graduate School of Science, Kobe Univ.*, [3]*Graduate School of Science, Nagoya Univ.*, [4]*Dep. Chem. Univ. of Chicago*)

3SHA-5 光化学系 II における水分解酸素発生反応の分子機構
Molecular mechanism of the water-splitting and oxygen-evolving reaction in photosystem II
○斉藤 圭亮（東京大学 先端科学技術研究センター）
Keisuke Saito (*RCAST, Univ. Tokyo*)

3SHA-6 光合成光エネルギー変換におけるプロトン共役電子移動の赤外分光解析
Infrared analyses of proton-coupled electron transfer in photosynthetic light-energy conversion
○野口 巧（名大・理）
Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

おわりに
Closing Remarks

9:00〜11:30　I 会場（一般教育棟 B 棟 4 階 B41）／Room I (B41, General Education Build. B, 4F)
3SIA　東アジアシンポジウム：１分子生物物理学の最前線
East Asian symposium: Frontiers of single-molecule biophysics

オーガナイザー：佐甲 靖志（理化学研究所），Ming Li（Chinese Academy of Sciences），Jie Yan（National University of Singapore），Tae-Young Yoon（Seoul University）
Organizers: Yasushi Sako (RIKEN), Ming Li (Chinese Academy of Sciences), Jie Yan (National University of Singapore), Tae-Young Yoon (Seoul University)

Single molecule imaging and manipulation has been a powerful toolkit for elucidating many biological phenomena. These include the biological function, mechanics, intermolecular interactions, and dynamics of proteins and nucleic acids. Recently, the field of single molecule biophysics heralds spectacular technical breakthroughs, such as improvement of spatial and temporal resolution and development of optics for investigating complicated biological processes in living cells. This symposium provides a forum for the world-leading East Asian scientists to share recent advances in field of single molecule biophysics, and discuss future applications in both academic and medical settings.

はじめに
Opening Remarks

3SIA-1 Watching single proteins dancing at biological membranes
Ming Li (*The Institute of Physics, Chinese Academy of Sciences*)

3SIA-2 1 分子イメージングを用いた GPCR の薬理学に向けて
Toward single-molecule imaging-based pharmacology of G protein-coupled receptors
○柳川 正隆（理研・細胞情報）
Masataka Yanagawa (*Cell. Info. Lab., Riken*)

3SIA-3 Biophysics of intercellular nanotube
Minhyeok Chang[1], Jaeho Oh[1], **Jong-Bong Lee**[1,2] ([1]*Department of Physics, POSTECH*, [2]*Department of Interdisciplinary Bioscience & Bioengineering, POSTECH*)

3SIA-4 Resolving nano-architectural dynamics of molecular assembly in living cells with emission dipole orientation imaging
Tomomi Tani (*Marine Biological Laboratory, Woods Hole*)

3SIA-5 Single-Molecule fluorescence studies on cotranscriptional folding and intrinsic termination Dynamics
Sungchul Hohng (*Department of Physics and Astronomy, Institute of Applied Physics, and National Center of Creative Research Initiatives, Seoul National University*)

3SIA-6 Single-molecule mechanical (un)folding of RNA: Unravelling mRNA structure's role in translational regulation
Gang Chen (*Division of Chemistry and Biological Chemistry, School of Physical and Mathematical Sciences, Nanyang Technological University*)

3SIA-7 Studies on the dynamics and regulation of 30-nm chromatin fiber by single molecule force spectroscopy
Wei Li[1], Ping Chen[2], Ming Li[1], Guohong Li[2] ([1]*National Laboratory for Condensed Matter Physics and Key Laboratory of Soft Matter Physics, Institute of Physics, Chinese Academy of Sciences*, [2]*National Laboratory of Biomacromolecules, CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences*)

3SIA-8 Mechanical lifetime of biomolecules under physiological forces
Shiwen Guo[1], Qingnan Tang[2], **Jie Yan**[1,2] ([1]*Mechanobiology Institute, National University of Singapore*, [2]*Department of Physics, Faculty of Science, National University of Singapore*)

9:00～11:30　K 会場（一般教育棟 E 棟 1 階 E11）／Room K (E11, General Education Build. E, 1F)

3SKA　細菌すごいぜ！―バクテリアを通して見る生命現象―
From the elephant to *E. coli*- is it all the same?

オーガナイザー：中根 大介（学習院大学），小嶋 誠司（名古屋大学）
Organizers: Daisuke Nakane (Gakushuin University), Seiji Kojima (Nagoya University)

"Anything found to be true of *E. coli* must also be true of elephants." It is a slogan of the early days of molecular biology. On the aspect of cell biology, bacterial life systems are partially common but something 'eccentric' from the higher organisms. In this symposium, we will focus on the energy and information through the bacterial cell surface, and introduce you the latest findings on the life at the small size.

はじめに
Opening Remarks

3SKA-1 小さなスパイダーマン： 糸をひっぱるバクテリア
Tiny Spider-Man: Bacteria pulling fibers
○中根 大介, 西坂 崇之（学習院大・物理）
Daisuke Nakane, Takayuki Nishizaka (*Dept. Phys., Gakushuin Univ.*)

3SKA-2 生命の根幹の理解に向けた ミニマムゲノム細菌における CRISPRi の開発
Toward understanding of the Fundamentals of Life: minimal bacterium and inducible CRISPRi
○柿澤 茂行 [1,2]（[1]ベンター研・合成生物学, [2]産総研・生物プロセス）
Shigeyuki Kakizawa[1,2] ([1]*JCVI, Synthetic Biology&Bioenergy*, [2]*AIST, Bioprocess*)

3SKA-3 To use light or to avoid it? Light-adaptation strategies in marine bacteria
Susumu Yoshizawa[1,2] ([1]*AORI, UTokyo*, [2]*Grad. Sch. Front. Sci., UTokyo*)

3SKA-4 Investigating the Unique Swimming Style of *Campylobacter jejuni*
Eli J. Cohen, Morgan Beeby (*Department of Life Sciences, Imperial College London*)

3SKA-5 The second messenger signaling drives chromosome replication in the asymmetrically dividing bacterium *Caulobacter crescentus*
Shogo Ozaki[1,2], Christian Lori[1], Urs Jenal[1] ([1]*Biozentrum, University of Basel*, [2]*Kyushu University*)

3SKA-6 Bacterial surface motility and biofilm formation in motile and non-motile bacteria
Andrew Utada (*U of Tsukuba*)

おわりに
Closing Remarks

9:00〜11:30　M 会場（一般教育棟 E 棟 2 階 E21）／Room M (E21, General Education Build. E, 2F)

3SMA　微生物における生命金属動態とその利用
"Metallodynamics" in Microorganisms and its Various Applications

オーガナイザー：古川 良明（慶應義塾大学），當舎 武彦（理化学研究所）
Organizers: Yoshiaki Furukawa (Keio University), Takehiko Tosha (RIKEN)

In order to survive under various conditions, microorganisms have developed biological systems utilizing metal ions. Besides, microorganisms are often equipped with unprecedented metalloproteins that can perform very specific reactions. In this symposium, we will review recent advances in our understandings on the metal-related processes in microorganisms such as the metal acquisition and the functions of metalloproteins. Together with the application of those metal-related processes to engineering use, furthermore, dynamics of metal ions (or “metallodynamics”) in microorganisms will be discussed.

はじめに
Opening Remarks

3SMA-1 *Corynebacterium glutamicum* によるヘム取り込み反応の構造基盤
Structural Basis for Heme Uptake Reaction in *Corynebacterium glutamicum*
○青野 重利 [1,2]（[1]自然機構・生命創成センター, [2]自然機構・分子研）
Shigetoshi Aono[1,2] ([1]*NINS, ExCELLS*, [2]*NINS, IMS*)

3SMA-2 anammox 反応を担う金属タンパク質
Metalloproteins responsible for anammox reaction
○平 大輔（崇城大・生物生命）
Daisuke Hira (*Fac. of Biotech. and Life Sci., Sojo Univ.*)

3SMA-3 脱窒にみられる金属タンパク質複合体による効率的な連続化学反応
Effective consecutive chemical reactions catalyzed by metalloprotein complex in denitrification
○當舎 武彦（理研・播磨）
Takehiko Tosha (*RIKEN SPring-8*)

3SMA-4 スーパーオキシドディスムターゼを通じたバクテリアにおける銅イオン動態の理解
A mechanism on copper acquisition of bacterial Cu/Zn-superoxide dismutase
○古川 良明（慶應大・理工）
Yoshiaki Furukawa (*Dept. of Chem., Keio Univ.*)

3SMA-5 硫酸性環境に生息する単細胞性紅藻を利用した貴金属回収
Study on the effective and selective recovery of precious metal ions using a sulfo-thermophilic red alga, Galdieria sulphuraria
○蓑田 歩（筑波大学 生命環境系 環境バイオマス共生学専攻）
Ayumi Minoda (*Fac. of Life and Environ. Sci., Univ. of Tsukuba*)

3SMA-6 微生物による金属腐食
Metal corrosion by microorganisms
○若井 暁（神戸大院・科技イノベ）
Satoshi Wakai (*Grad. Sch. Sci. Tech. Innov., Kobe Univ.*)

口頭発表　Oral Presentation

1 日目（9 月 15 日（土））／Day 1（Sep. 15 Sat.）

13:30〜16:00　A 会場（B11）／Room A (B11)
1A 細胞生物的課題／Cell biology

1A1330* *Spiroplasma eriocheiris* 遊泳運動に関係する 5 つの MreB の機能及び構造解析
Structural and functional analyses of five MreB proteins involved in swimming motility of *Spiroplasma eriocheiris*
○高橋 大地 [1], 児玉 彩 [1], 今田 勝巳 [2], 宮田 真人 [1,3]（[1]大阪市大・院理, [2]大阪大・院理, [3]大阪市大・複合先端研）
Daichi Takahashi[1], Aya Kodama[1], Katsumi Imada[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Univ. Osaka City*, [2]*Grad. Sch. Sci., Univ. Osaka*, [3]*OCARINA, Univ. Osaka City*)

1A1342* マイコプラズマ・ガリセプティカム滑走運動の詳細測定
Detailed measurements of gliding behavior in *Mycoplasma gallisepticum*
○水谷 雅希 [1], 宮田 真人 [1,2]（[1]大阪市大・院理, [2]大阪市大・複合先端）
Masaki Mizutani[1], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*)

1A1354* 細胞内温度動態における微小管の寄与の検討
Investigating the contribution of microtubule on intracellular temperature dynamics
○柳 昂志 [1], 岡部 弘基 [1,2], 船津 高志 [1]（[1]東大院薬, [2]JST さきがけ）
Takashi Yanagi[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ of Tokyo*, [2]*JST, PRESTO*)

1A1406* A mechanical effect of oriented actin fibers on the nuclear morphology during osteogenic differentiation of mesenchymal stem cell
Masashi Yamazaki[1], Shota Iwakura[2], Manabu Numao[1], Hiromichi Fujie[1,2], Hiromi Miyoshi[1,2] ([1]*Grad. Sch. Syst., Tokyo Metro. Univ.*, [2]*Faculty Syst., Tokyo Metro. Univ.*)

1A1418* Helicity formed by actin homologs in swimming bacterium, Spiroplasma
Yuya Sasajima[1], Isil Tulum[1,2], Makoto Miyata[1,2] ([1]*Graduate School of Science, Osaka City University, Japan*, [2]*The OCU Advanced Research Institute for Natural Science and Technology (OCARINA), Osaka City University, Japan.*)

1A1430 Focal adhesions of cells to the matrix are mediators and targets of cooperative activity of microtubules and actomyosin cytoskeleton
Yukako Nishimura[1], Nisha Bte Mohd Rafiq[1,5], Sergey V. Plotnikov[2], Visalatchi Thiagarajan[1], Zhen Zhang[1], Meenubharathi Natarajan[1], Shidong Shi[1], Virgile Viasnoff[1,3,4], Gareth E. Jones[5], Pakorn Kanchanawong[1,6], Alexander D. Bershadsky[1,7] ([1]*MBI, NUS*, [2]*Dept. of Cell and Syst. Biol., Univ. Toronto*, [3]*CNRS UMI*, [4]*Dept. of Biol. Sci., NUS*, [5]*Randall Center for Cell and Mol.Biophys., KCL*, [6]*Dept. of Biomed. Eng., NUS*, [7]*Dept. of Mol. Cell Biol., WIS*)

休憩（Coffee Break）　14:42–14:48

1A1448 Mechanical stress modulates the homeostasis of periodontal ligament
Ayano Fujita[1], Masatoshi Morimatsu[1], Masayoshi Nishiyama[2], Shogo Takashiba[1], Keiji Naruse[1] ([1]*Grad Sch of Med, Dent and Pharma Sci, Okayama Univ*, [2]*Department of Physics, Kindai Univ*)

1A1500* 肝線維症における肝星細胞活性化とメカノセンシング
Hepatic Stellate Cell Activation and Mechanosensing in Liver Fibrosis
○有本 睦子 [1], 住吉 孝明 [2]（[1]京都工繊大, [2]関西大学）
Mutsuko Arimoto[1], Takaaki Sumiyoshi[2] ([1]*KIT*, [2]*Kansai Univ.*)

1A1512* **デスミン中間径フィラメントを包含する細胞サイズ液滴の変形と突出**
Deformation and protrusion of cell-sized droplets containing intermediate filaments of desmin
○宮坂 禎也, 伊藤 光司, 羽鳥 晋由（山形大・院理工）
Yoshiya Miyasaka, Koji Ito, Kuniyuki Hatori (*Grad. Sch. Sci. Eng., Yamagata Univ.*)

1A1524* **アクチン束化タンパク質 fascin の成長円錐ラメリポディアの弾性率に対する寄与**
Contribution of actin bundling protein fascin to the elasticity of lamellipodial region in the growth cone
○田中 みなみ [1], 藤井 裕紀 [2], 石川 良樹 [3], 平野 和己 [4], 岡嶋 孝治 [2], 加藤 薫 [4]（[1]*筑波大大学院 生命環境科学, [2]北海道大学 大学院情報科学人間情報科学専攻, [3]群馬県立県民健康科学大, [4]産総研 バイオメディカル）
Minami Tanaka[1], Yuki Fujii[2], Ryoki Ishikawa[3], Kazumi Hirano[4], Takaharu Okajima[2], Kaoru Katoh[4] ([1]*Grad. Sch. Life & Env. Sci., Univ. Tsukuba*, [2]*Grad. Schl. Inform. Sci & Tech. Univ., Hokkaido*, [3]*Gunma Pref. Coll. Health Sci*, [4]*Bio Mes Res. Inst., AIST*)

1A1536* **クシクラゲの巨大複合繊毛を構成する新規タンパク質 CTENO64 の同定と櫛板繊毛の協調的運動における役割**
Identification of a novel protein CTENO64 in giant compound cilia in the ctenophore and its role in the coordinated ciliary movement
○城倉 圭 [1], 柴田 大輔 [1], 山口 勝司 [2], 重信 秀治 [2], 柴 小菊 [1], 稲葉 一男 [1]（[1]筑波大・下田臨海, [2]基生研・機能解析セ）
Kei Jokura[1], Daisuke Shibata[1], Katsushi Yamaguchi[2], Shuji Shigenobu[2], Kogiku Shiba[1], Kazuo Inaba[1] ([1]*Shimoda Marine Res. Ctr., Tsukuba Univ.*, [2]*Functional Genomics Facility, NIBB.*)

1A1548 **細胞外環境のダイナミックリモデリングが支配する細胞集団行動解析**
Spatio-temporal remodeling of microenvironment regulates the directionality of collective cell migration
○萩原 将也 [1], 丸本 萌 [1,2], 丸山 央峰 [3], 森 英樹 [2], 新井 史人 [3]（[1]大阪府立大学 NanoSquare 拠点研究所, [2]大阪府立大学大学院理学系研究科生物科学専攻, [3]名古屋大学大学院工学研究科マイクロ・ナノ機械理工専攻）
Masaya Hagiwara[1], Moegi Marumoto[1,2], Hisataka Maruyama[3], Hideki Mori[2], Fumihito Arai[3] ([1]*NanoSquare Research Institute, Osaka Prefecture University*, [2]*Department of Biological Science, Osaka Prefecture University*, [3]*Department of Micro-Nano Systems Engineering, Nagoya University*)

13:30〜16:12　C 会場（B21）／Room C (B21)
1C バイオインフォマティクス・バイオエンジニアリング・膜・神経／
Bioinformatics, bioengineering, menbrane, neuroscience

1C1330 **マスク付きガウス関数による電顕３次元密度マップ内の α ヘリックスを認識する手法の開発**
Detection of alpha-helices from the 3D EM density map using masked single Gaussian functions
○川端 猛, 中村 春木, 栗栖 源嗣（大阪大 蛋白研）
Takeshi Kawabata, Haruki Nakamura, Genji Kurisu (*Inst. Prot. Res., Osaka Univ.*)

1C1342 Multiscale Modeling of Bacterial Lipid Recognition in Mammalian Immune Receptor Pathways, and Regulation by Novel Host Defense Peptides
Peter J. Bond (*BII A*STAR Singapore*)

1C1354 **p53C 末端ドメインのエクストラ・ディスオーダー状態**
Extra-Disordered State of p53 C-terminal Domain
○飯田 慎仁 [1], 中村 春木 [2], 肥後 順一 [3]（[1]大阪大学蛋白質研究所, [2]遺伝研 DDBJ センター, [3]兵県大院・シミュレーション）
Shinji Iida[1], Haruki Nakamura[2], Junichi Higo[3] ([1]*IPR, Osak Univ.*, [2]*DDBJ center, NIG, ROIS*, [3]*Grd. Sch. Sim., Univ. Hyogo*)

1C1406 **相互作用パターンと機械学習を用いたタンパク質-低分子化合物ドッキング手法の改良**
A new method to improve the accuracy for protein-small molecule docking by using interaction pattern fingerprint and machine learning
○佐藤 史彬 [1], 笠原 浩太 [2], 高橋 卓也 [2]（[1]立命館大・院・生命, [2]立命館大・生命）
Fumiaki Sato[1], Kota Kasahara[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

1C1418 **剛体ドッキングで得られた相互作用部位のアミノ酸配列情報の解析**
Analysis of amino acid sequences of protein interaction surfaces by rigid-body docking for known and unknown protein complex pairs
○内古閑 伸之 [1], 松崎 由理 [2]（[1]カタリスト, [2]東工大 リーダーシップ教育院）
Nobuyuki Uchikoga[1], Yuri Matsuzaki[2] ([1]*Catalyst, Inc.*, [2]*ToTAL*)

1C1430 **分子動力学法を用いたタンパク質球状ドメイン外の相互作用メカニズムの解明**
Elucidation of the mechanism of protein-protein interaction between regions out of globular domains with molecular dynamics simulations
○島戸 拓也 [1], 笠原 浩太 [2], 肥後 順一 [3], 高橋 卓也 [2]（[1]立命館大学・院・生命, [2]立命館大・生命, [3]兵庫県立大・院・シミュレーション）
Takuya Shimato[1], Kota Kasahara[2], Junichi Higo[3], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Sim. Studies, Univ. Hyogo*)

休憩（Coffee Break） 14:42–14:48

1C1448 **スーパーコンピューティングによる網羅的タンパク質間相互作用予測法の開発と予測結果データベースの公開**
Supercomputing-based exhaustive protein-protein interaction prediction and its open database
○大上 雅史 [1], 林 孝紀 [1], 渡辺 紘生 [1,2], 松崎 由理 [3], 内古閑 伸之 [3], 秋山 泰 [1,3]（[1]東工大 情報理工, [2]産総研, RWBC-OIL, [3]東工大 情生院）
Masahito Ohue[1], Takanori Hayashi[1], Hiroki Watanabe[1,2], Yuri Matsuzaki[3], Nobuyuki Uchikoga[3], Yutaka Akiyama[1,3] ([1]*Sch Computing, Tokyo Tech*, [2]*RWBC-OIL, AIST*, [3]*ACLS, Tokyo Tech*)

1C1500 **室温で凍るソフトマテリアル中の水**
Water freezing in soft materials at room temperature
○村上 洋 [1], 金原 裕子 [2]（[1]量研・関西光, [2]奈良女大・生活環境）
Hiroshi Murakami[1], Yuko Kanahara[2] ([1]*QST, KPSI*, [2]*Nara Women's Univ.*)

1C1512 **細菌とリポソームの融合によるゲノム封入とリポソーム内ゲノムの精製法の開発**
Investigation of encapsulation and purification of genome by fusion between liposome and bacteria
○辻 岳志 [1,2], 角南 武志 [1], 市橋 伯一 [2,3]（[1]阪大・未来戦略, [2]阪大・情報科学, [3]阪大・生命機能）
Gakushi Tsuji[1,2], Takeshi Sunami[1], Norikazu Ichihashi[2,3] ([1]*IAI, Osaka Univ.*, [2]*IST, Osaka Univ.*, [3]*FBS, Osaka Univ.*)

1C1524* **微小液滴内における 1 分子からの DNA 複製**
DNA amplification from single molecule in micro-sized droplet
○澤田 浩樹 [1], 曽我 直樹 [1], 佐久間 守仁 [1], 末次 正幸 [2], 田端 和仁 [1], 野地 博行 [1]（[1]東大・院工・応化, [2]立教大・理・生命理学）
Hiroki Sawada[1], Naoki Soga[1], Morito Sakuma[1], Masayuki Su'estugu[2], Kazuhito Tabata[1], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem. Grad. Eng. Univ. Tokyo*, [2]*Dept. Life Sci. Coll. Sci. Univ. Rikkyo*)

1C1536* **三次元培養プラットフォームによる気管支分岐パターンの定量解析**
Quantitative measurement of developed brunch pattern formation by using in vitro 3D culture platform
○野畑 李奈 [1,2], 萩原 将也 [1]（[1]大阪府大 NanoSquare 拠点研究所, [2]大阪府立大院理生物）
Rina Nobata[1,2], Masaya Hagiwara[1] ([1]*N2RI, Osaka Pref. Univ.*, [2]*Dept. of Biol. Sci., Osaka Pref. Univ.*)

1C1548* **集光フェムト秒レーザー刺激による神経活動の時空間ダイナミクス**
Spatio-Temporal Dynamics of Neuronal Spikes Induced by a Focused Femtosecond Laser
○藤岡 祐次[1,2], 工藤 卓[2], 田口 隆久[3], 細川 千絵[1,2,4]（[1]産総研 バイオメディカル, [2]関西学院大 理工, [3]情通機構 脳情報, [4]産総研-阪大 フォトバイオ OIL）
Yuji Fujioka[1,2], Suguru N. Kudoh[2], Takahisa Taguchi[3], Chie Hosokawa[1,2,4] ([1]*Biomed. Res. Inst., AIST*, [2]*Grad. Sci. & Tech., Kwansei Gakuin Univ.*, [3]*CiNet, NICT*, [4]*PhotoBIO-OIL, AIST-Osaka-Univ.*)

1C1600* **幅に依存したライン状心筋細胞ネットワークの伝導速度解析**
Analysis of Conduction Velocity Depending Width of Line-Networked Cardiomyocytes
○吉田 鉄郎, 藤井 洸希, 金子 智行（法政大院生命機能学）
Tetsuro Yoshida, Koki Fujii, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

13:30〜16:00　D 会場（A36）／Room D (A36)
1D バイオイメージング I ／Bioimaging I

1D1330 Toward Automated Identification and Analysis of Cell Differentiation Stages using Bright Field Microscope Image by Artificial Intelligence
Archana Bajpai, Toutai Mitsuyama (*Artificial Intelligence Research Center, National Institute of Advanced Industrial Science and Technology (AIST)*)

1D1342* Three-dimensional vesicle motion in complex cytoskeletal network revealed by numerical analysis method
Seohyun Lee, Hideo Higuchi (*Dept. of Physics, Graduate School of Science, The University of Tokyo*)

1D1354* **演題取り消し**

1D1406* mRNA の一分子観察を用いたストレス顆粒形成初期のメカニズム解明
Investigating initiation mechanism of stress granule formation in cells by observing single mRNA molecules
○今関 眞倫[1], 菅原 皓[2], 岡部 弘基[2,3], 船津 高志[2]（[1]東大薬, [2]東大院薬, [3]JST, PRESTO.）
Masamichi Imaseki[1], Ko Sugawara[2], Kohki Okabe[2,3], Takashi Funatsu[2] ([1]*Pharm. Sci., Univ. Tokyo*, [2]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [3]*JST, PRESTO.*)

1D1418* **転写装置 RNA ポリメラーゼ II によるクロマチンの安定化**
Chromatin stabilization regulated by transcription machinery
○永島 崚甫[1,2], 日比野 佳代[1,2], 前島 一博[1,2]（[1]国立遺伝学研究所 構造遺伝学研究センター 生体高分子研究室, [2]総合研究大学院大学 生命科学研究科遺伝学専攻）
Ryosuke Nagashima[1,2], Kayo Hibino[1,2], Kazuhiro Maeshima[1,2] ([1]*Biological Macromolecules Laboratory, Structural Biology Center, National Institute of Genetics.*, [2]*Department of Genetics, School of Life Science, SOKENDAI (Graduate University for Advanced Studies)*)

1D1430 **高速 AFM による天然変性タンパク質 CAMP の構造動態観察**
Structural dynamics of the intrinsically disordered protein CAMP revealed by high-speed AFM
○成田 知恕[1], 池田 真教[2], 清水 将裕[3], 田中 耕三[2], 古寺 哲幸[3]（[1]金沢大・院数物, [2]東北大・加齢研・分子腫瘍, [3]金沢大・WPI-NanoLSI）
Tomoyuki Narita[1], Masanori Ikeda[2], Masahiro Shimizu[3], Kozo Tanaka[2], Noriyuki Kodera[3] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Dept. Mol. Oncol., Inst. Dev. Aging Cancer, Tohoku Univ.*, [3]*WPI-NanoLSI, Kanazawa Univ.*)

休憩（Coffee Break）　14:42–14:48

1D1448 曲率を持った膜上のタンパク質の集合-解離現象の高速 AFM 観察
High-speed AFM imaging of protein assembly-disassembly on curved membranes
○石黒 大輝 [1], 後藤 朱音 [1], 豊田 貴大 [1], 角野 歩 [2,3], 柴田 幹大 [2,3], 古寺 哲幸 [2]（[1]金沢大・院数物, [2]金沢大・WPI-NanoLSI, [3]金沢大・新学術創成）
Daiki Ishikuro[1], Akane Goto[1], Takahiro Toyoda[1], Ayumi Sumino[2,3], Mikihiro Shibata[2,3], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ*, [3]*InFiniti, Kanazawa Univ*)

1D1500 L_p 正則化最尤推定による超解像画像再構成計算を用いた高生体適合性 SPoD-ExPAN 超解像イメージング
Highly-biocompatible superresolution imaging by SPoD-ExPAN with L_p-regularized image reconstruction
○和沢 鉄一, 新井 由之, 河原 吉伸, 鷲尾 隆, 永井 健治（大阪大学 産業科学研究所）
Tetsuichi Wazawa, Yoshiyuki Arai, Yoshinobu Kawahara, Takashi Washio, Takeharu Nagai (*ISIR, Osaka Univ*)

1D1512* マニピュレーター付き高速 AFM スキャナーの開発
Development of high-speed AFM scanner with manipulator
○高野 純 [1], 渡辺 信嗣 [2], 安藤 敏夫 [2], 古寺 哲幸 [2]（[1]金沢大・院数物, [2]金沢大・WPI-NanoLSI）
Jun Takano[1], Shinji Watanabe[2], Toshio Ando[2], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

1D1524 高速 AFM 観察結果を解析するための粗視化分子動力学計算手法の開発
Development of a method for analyzing high-speed AFM observations by coarse-grained molecular dynamics simulation
○清水 将裕 [1], 成田 知恕 [2], 古寺 哲幸 [1]（[1]金沢大・WPI-NanoLSI, [2]金沢大・院数物）
Masahiro Shimizu[1], Tomoyuki Narita[2], Noriyuki Kodera[1] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Grad. Sch. Math. & Phys., Kanazawa Univ.*)

1D1536 Automatic single-neuron reconstruction from fluorescent images
Chi-Tin Shih (*Tunghai University*)

1D1548* Machine Learning Approaches to Raman Micro-spectroscopic Images
Khalifa Mohammad Helal[1], Harsono Cahyadi[4], J. Nicholas Taylor[2,3], Akira Okajima[5], Yasuaki Kumamoto[5], Hideo Tanaka[5], Yoshinori Harada[3,5], Tamiki Komatsuzaki[1,2,3] ([1]*Grad. Sch. Life Sci. Hokkaido Univ.*, [2]*Research Institute for Electronic Science, Hokkaido Univ.*, [3]*JST/CREST*, [4]*Dept. of Methodologies for Medical Research, Kyoto Prefectural Univ. of Medicine*, [5]*Dept. of Pathology and Cell Regulation, Kyoto Prefectural Univ. of Medicine*)

13:30〜16:12　E 会場（A37）／Room E (A37)
1E 筋肉・モーター／Muscle/motor

1E1330* 垂直力成分を決定する in vitro 滑り運動系による肥大型心筋症特異的なトロポミオシン変異体 (V95A および D175N)の収縮機能異常の計測
Effect of HCM mutants of tropomyosin on actomyosin interaction by in vitro motility assay determining both horizontal and vertical forces
○石井 秀弥 [1], 石渡 信一 [2], 河合 正隆 [3], 鈴木 団 [4,5]（[1]早大・理工学術院・先進理工, [2]早大・理工学術院, [3]アイオワ大・医学部, [4]阪大・蛋白研, [5]JST さきがけ）
Shuya Ishii[1], Shin'ichi Ishiwata[2], Masataka Kawai[3], Madoka Suzuki[4,5] ([1]*Sch. Adv. Sci. Engn., Fac. Sci. Engn., Waseda Univ.*, [2]*Fac. Sci. Engn., Waseda Univ.*, [3]*Coll. Med., Univ. Iowa*, [4]*IPR, Osaka Univ.*, [5]*PRESTO, JST*)

1E1342* 心機能に適した心筋ミオシンの集団的性質
Collective behaviors of cardiac myosins for effective cardiac function
○黄 勇太, 樋口 秀男, 茅 元司（東京大学）
Yongtae Hwang, Hideo Higuchi, Motoshi Kaya (*Univ. of Tokyo Dep. science*)

1E1354* F_O 回転モーターの回転角と保存残基のプロトン化状態の連関
Coupling of protonation state of conserved residues and rotation angle in F_O rotary motor
○山越 大希, パーキン 暖, 手塚 晃太, 高野 光則（早大・物理応物）
Daiki Yamakoshi, Dan Parkin, Kota Tezuka, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1E1406* ハイブリッド F_1-ATPase の 1 分子回転観察
Rotation of hybrid F_1-ATPases between bacterial and mammalian ones
○渡邉 亮, 上野 博史, 鈴木 俊治, 小林 稜平, 野地 博行（東大・院工・応化）
Ryo Watanabe, Hiroshi Ueno, Toshiharu Suzuki, Ryohei Kobayashi, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

1E1418* シアノバクテリア ATP 合成酵素 ε サブユニットの N 末端側領域の機能
Function of the N-terminal region of the ε subunit of cyanobacterial ATP synthase
○稲辺 宏輔, 若林 憲一, 久堀 徹（東京工業大学 化学生命科学研究所）
Kosuke Inabe, Ken-ichi Wakabayashi, Toru Hisabori (*CLS., Tokyo tech.*)

1E1430* 電位駆動型モータープレスチン以外の SLC26 イオン輸送体も電位感受能を持つ。
Prestin, a membrane-based voltage-driven motor, is not the sole member of the SLC26 family that can sense voltage
○桑原 誠 [1], 和佐野 浩一郎 [2], 高橋 里枝 [2], Bodner Justin[3], 小森 智貴 [1], 上村 想太郎 [1], Zheng Jing[2], 島 知弘 [1], 本間 和明 [2]（[1]東大・院理・生物科学, [2]ノースウェスタン大・医, [3]デポール大）
Makoto Kuwabara[1], Koichiro Wasano[2], Satoe Takahashi[2], Justin Bodner[3], Tomotaka Komori[1], Sotaro Uemura[1], Jing Zheng[2], Tomohiro Shima[1], Kazuaki Homma[2] ([1]*Dep. of Biol. Sci., Grad Sch. of Sci., The Univ. of Tokyo*, [2]*Feinberg Sch. of Med., Northwestern Univ.*, [3]*DePaul Univ.*)

休憩（Coffee Break） 14:42–14:48

1E1448* 高速 AFM を用いたマイコプラズマモービレ滑走装置の可視化
Gliding machinery of *Mycoplasma mobile* visualized by high-speed AFM
○小林 昂平 [1], 古寺 哲幸 [2], 田原 悠平 [1,3], 豊永 拓真 [1], 笠井 大司 [1], 安藤 敏夫 [2], 宮田 真人 [1,3]（[1]大阪市大・院理, [2]金沢大・バイオ AFM, [3]大阪市大・オカリナ）
Kohei Kobayashi[1], Noriyuki Kodera[2], Yuhei Tahara[1,3], Takuma Toyonaga[1], Taishi Kasai[1], Toshio Ando[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Bio-AFM FRC, Kanazawa Univ.*, [3]*OCARINA, Osaka City Univ.*)

1E1500* 細菌べん毛モーターの回転速度と構成ユニット数の関係
The dependence of the speed of the bacterial flagellar motor on the number of stator units
○石田 翼 [1], 吉多 美祐 [2], 南野 徹 [3], 曽和 義幸 [1,2,4]（[1]法政大・院理工, [2]法政大・生命機能, [3]大阪大・院生命機能, [4]法政大・マイクロナノ）
Tsubasa Ishida[1], Myu Yoshida[2], Tohru Minamino[3], Yoshiyuki Sowa[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [4]*Micro-nano Tech., Hosei Univ.*)

1E1512* アーキアべん毛モーターが発生するトルクの精密測定
Measurement of the torque generated by the archaellar rotary motor in microscopic detail
○岩田 誠司, 木下 佳昭, 中根 大介, 西坂 崇之（学習院大学 理 物理）
Seiji Iwata, Yoshiaki Kinosita, Daisuke Nakane, Takayuki Nishizaka (*Department of Physics, Gakushuin Univ*)

1E1524* 広い負荷領域の測定から明らかになったキネシン 1 分子のステップ運動
Kinesin's stepping motion clarified from wide range load measurement
○近藤 雄一 [1], 佐々木 一夫 [2], 樋口 秀男 [1]（[1]東京大学, [2]東北大学）
Yuichi Kondo[1], Kazuo Sasaki[2], Hideo Higuchi[1] ([1]*Grad. Sch. Sci., Univ. of Tokyo*, [2]*Grad. Sch. Eng., Tohoku Univ.*)

1E1536 金ナノピラーへの選択的固定を用いた kinesin-1 および Ncd の協働性の計測
Investigating coordination of kinesin-1 and Ncd using their selective immobilization on gold nano-pillars
○金子 泰洸ポール [1], 大庭 将太郎 [1], 古田 健也 [2], 大岩 和弘 [2], 新宅 博文 [3], 小寺 秀俊 [3], 横川 隆司 [1]（[1]京大・工・マイクロ, [2]NICT, [3]理研）
Taikopaul Kaneko[1], Shotaro Ohba[1], Ken'ya Furuta[2], Kazuhiro Oiwa[2], Hirofumi Shintaku[3], Hidetoshi Kotera[3], Ryuji Yokokawa[1] ([1]*Micro Eng., Kyoto Univ.*, [2]*NICT*, [3]*Riken*)

1E1548 コンデンシン複合体は分子モーターである
The condensin complex is a mechanochemical molecular motor
○寺川 剛 [1,2], Bisht Shveta[3], Eeftens Jorine M.[4], Dekker Cees[4], Haering Christian H.[3], Greene Eric C.[2]（[1]京大・院理, [2]コロンビア大, [3]EMBL, [4]デルフト工科大）
Tsuyoshi Terakawa[1,2], Shveta Bisht[3], Jorine M. Eeftens[4], Cees Dekker[4], Christian H. Haering[3], Eric C. Greene[2] ([1]*Kyoto Univ.*, [2]*Columbia Univ.*, [3]*EMBL*, [4]*Delft Univ. of Technology*)

1E1600 滑走するフラボバクテリアの集団運動は予期せぬ渦格子と回転を伴う動的プレートを形成する
Collective motion of gliding Flavobacteria exhibits unforeseen vortex lattice and dynamic plate with rotation
○中根 大介, 小高 祥子, 鈴木 香菜, 西坂 崇之（学習院大・物理）
Daisuke Nakane, Shouko Odaka, Kana Suzuki, Takayuki Nishizaka (*Dept. Phys., Gakushuin Univ.*)

13:30〜15:48　F 会場（B32）／Room F (B32)
1F 光合成・ロドプシン／Photosynthesis, Rhodopsin

1F1330 Cryo-EM structure of a supercomplex containing photosystem II and fucoxanthin chlorophyll binding proteins from a diatom
Fusamichi Akita[1,2], Ryo Nagao[1], Koji Kato[1], Naoyuki Miyazaki[3], Jian-Ren Shen[1] ([1]*RIIS, Okayama University*, [2]*PRESTO, JST*, [3]*IPR, Osaka University*)

1F1342 FTIR study on the S-state cycle of water oxidation in the microcrystals of photosystem II
Yuki Kato[1], Fusamichi Akita[2,3], Yoshiki Nakajima[2], Michihiro Suga[2], Yasufumi Umena[2], Jian-Ren Shen[2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya University*, [2]*Res. Inst. Interdiscip. Sci., Okayama Univ.*, [3]*JST-PRESTO*)

1F1354 Ca^{2+}除去した光化学系 II の高酸化状態でのスピン構造
High spin state in Ca^{2+}-depleted photosystem II
酒井 貴弘, ○三野 広幸（名古屋大学大学院理学研究科）
Takahiro Sakai, **Hiroyuki Mino** (*Grad. School of Sci., Nagoya Univ.*)

1F1406 Proton transfer or H_3O^+ stabilization
Hiroshi Ishikita[1,2], Keisuke Saito[1,2] ([1]*Grad. Sch. Tech., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*)

1F1418 単一分子蛍光寿命相関解析：光合成光反応を制御する複数のタンパク質ダイナミクス
Multiple protein dynamics regulating photosynthetic photoreaction revealed by single-molecule fluorescence lifetime correlation analysis
○近藤 徹 [1,2], Gordon Jesse B.[1,2], Pinnola Alberta[3], Dall'Osto Luca[3], Bassi Roberto[3], Schlau-Cohen Gabriela S.[1,2]（[1]マサチューセッツ工科大学, [2]MIT-Harvard エキシトン工学センター, [3]ヴェローナ大学）
Toru Kondo[1,2], Jesse B. Gordon[1,2], Alberta Pinnola[3], Luca Dall'Osto[3], Roberto Bassi[3], Gabriela S. Schlau-Cohen[1,2] ([1]*MIT*, [2]*MIT-Harvard Center for Excitonics*, [3]*Univ. Verona*)

1F1430 人工色素を付加した光収穫系複合体の再構成膜系での超高速エネルギー移動
Ultrafast Energy Transfer of Light-Harvesting Complex 2 Covalently Attached Artificial Chromophores in Reconstituted Lipid Bilayer
○出羽 毅久[1], 米田 勇祐[2], 後東 あかり[1], 近藤 政晴[1], 宮坂 博[2], 長澤 裕[3] ([1]名工大院工, [2]阪大院基礎工, [3]立命館大)
Takehisa Dewa[1], Yusuke Yoneda[2], Akari Goto[1], Masaharu Kondo[1], Hiroshi Miyasaka[2], Yutaka Nagasawa[3] ([1]*Nagoya Inst. Tech.*, [2]*Osaka Univ.*, [3]*Ritsumeikan Univ.*)

休憩（Coffee Break） 14:42–14:48

1F1448 Reconstitution and functional analysis of thylakoid membrane on a glass substrate
Takuro Yoneda[1], Yasushi Tanimoto[1], Daisuke Takagi[2], Kenichi Morigaki[1,3] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Grad. Sch. Agr., Univ. Tohoku*, [3]*Biosignal., Univ. Kobe*)

1F1500 フコキサンチン会合体のアセトン-水混合溶媒中での分光特性
Optical property of aggregated fucoxanthin in acetone-water mixture
○山野 奈美, 藤井 律子（大阪市立大学大学院）
Nami Yamano, Ritsuko Fujii (*Grad. Sch. Sci., Osaka City Univ.*)

1F1512 Mutation study of heliorhodopsin 48C12
Manish Singh[1], Keiichi Inoue[1,2,3], Alina Pushkarev[4], Oded Beja[4], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Univ. Tokyo*, [3]*JST. CREST*, [4]*Israel Inst. Tech.*)

1F1524 リン酸イオン結合による光駆動型硫酸イオン輸送体 SyHR の分光特性の調節
Phosphate ion binding modulates photochemical properties of a light-driven SO_4^{2-} transporter, SyHR
○小島 慧一[1], 仲間 政樹[2], 栗原 眞理恵[1], 吉澤 晋[3], 須藤 雄気[1,2] ([1]岡山大・院・医歯薬(薬), [2]岡山大・薬, [3]東大・大気海洋研)
Keiichi Kojima[1], Masaki Nakama[2], Marie Kurihara[1], Susumu Yoshizawa[3], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*AORI, UTokyo*)

1F1536 膜電位モニタリングのための高蛍光性微生物型ロドプシンの実装に向けて
Towards implementation of highly fluorescent microbial rhodopsins for monitoring membrane potential
○栗原 里佳[1], 小島 慧一[1], 坂本 雅行[2], 尾藤 晴彦[2], 須藤 雄気[1] ([1]岡大・院・医歯薬（薬）, [2]東大・院・医)
Rika Kurihara[1], Keiichi Kojima[1], Masayuki Skamoto[2], Haruhiko Bito[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Med., The Univ. of Tokyo*)

13:30〜16:00 G 会場（B33）／Room G (B33)
1G 生体膜・人工膜／Biological & Artificial membrane

1G1330 Single molecule observation of membrane proteins in a model biological membrane integrated with a nanometric gap structure
Ryota Komatsu[1], Yasushi Tanimoto[2], Fumio Hayashi[3], Kenichi Morigaki[1,2] ([1]*Grad. Sch. Agr., Kobe Univ.*, [2]*biosignal, Kobe Univ.*, [3]*Grad. Sch. sci., Kobe Univ.*)

1G1342 高速 AFM 解析により明らかになったグラム陰性菌及びグラム陽性菌の産生するメンブランベシクルの物性多様性
High-speed AFM imaging revealed the physical diversity of membrane vesicles produced from Gram-negative and Gram-positive bacteria
○菊池 洋輔 [1], 尾花 望 [2], 豊福 雅典 [2], 野村 暢彦 [2], 古寺 哲幸 [3], 安藤 敏夫 [3], 福森 義宏 [4], 田岡 東 [1,3] ([1]金沢大・理工, [2]筑波大・生命, [3]金沢大・新学術・ナノ生命科学, [4]金沢大・理事（副学長）)
Yousuke Kikuchi[1], Nozomu Obana[2], Masanori Toyofuku[2], Nobuhiko Nomura[2], Noriyuki Kodera[3], Toshio Ando[3], Yoshihiro Fukumori[4], Azuma Taoka[1,3] ([1]*Col. of Sci. and Eng., Kanazawa Univ.*, [2]*Life and Env. Sci., Tsukuba Univ.*, [3]*NanoLSI, InFiniti, Kanazawa Univ.*, [4]*Vice President, Kanazawa Univ.*)

1G1354* リポソームの 1 粒子膜融合解析
Single particle analysis for membrane fusion of liposomes
○山田 雅人, 曽我 直樹, 野地 博行, 渡邉 力也（東大・応化）
Masato Yamada, Naoki Soga, Hiroyuki Noji, Rikiya Watanabe (*Dept. Appl. Chem., Univ. Tokyo.*)

1G1406* DNA ナノポアプローブを用いたナノ空間内溶液物性の評価
NANOPORE PROBE WITH DNA: ANALYSIS OF SOLUTION BEHAVIOR IN NANOSPACE
○松下 雅季, 川野 竜司（東京農工大学 工学府 生命工学専攻）
Masaki Matsushita, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

1G1418* 抗菌ペプチド・マガイニン２が誘起するポア形成の初期過程のメカニズム
Mechanism of Initial Stage of Pore Formation Induced by Antimicrobial Peptide Magainin 2 (mag)
○ハーサン モイヌル [1], カラール モハマド アブ サエム [1], レバツニー ビクター [1,2], 山崎 昌一 [1,3,4] ([1]静大・創造院, [2]ロシア科学アカデミー, [3]静大・電研, [4]静大・院理)
Moynul Hasan[1], Mohammad Abu Sayem Karal[1], Victor Levadny[1,2], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ*, [2]*Rus. Acad. Sci.*, [3]*Res. Inst. Ele., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

1G1430* The effects of different alkali metal ions on KR2 structure revealed by multidimensional solid-state NMR
Rina Kaneko[1], Arisu Shigeta[2], Toshio Nagashima[3], Toshio Yamazaki[3], Keiichi Inoue[4,5,6], Hideki Kandori[5], Izuru Kawamura[1,2] ([1]*Grad. Sch. Eng. Sci., Yokohama National Univ.*, [2]*Grad. Sch. Eng., Yokohama National Univ.*, [3]*RIKEN*, [4]*Tokyo Univ.*, [5]*Nagoya Inst. Tech.*, [6]*JST PRESTO*)

休憩（Coffee Break） 14:42–14:48

1G1448* 糖脂質 S-TGA-1 との特異的相互作用を通したバクテリオロドプシンの構造化および機能発現
Crucial Role of Specific Interactions with Archeal Glycolipid S-TGA-1 in Structuralization and Functionalization of Bacteriorhodopsin
○稲田 壮峰, 木下 祥尚, 松森 信明（九大・院理）
Masataka Inada, Masanao Kinoshita, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ*)

1G1500* 脂質膜環境によるリン脂質輸送タンパク質 Sec14 の機能制御メカニズムの解明
Regulation of Sec14-mediated lipid transfer by lipid-membrane environment
○杉浦 太一, 吉田 右京, 中尾 裕之, 池田 恵介, 中野 実（富山大院医薬）
Taichi Sugiura, Ukyo Yoshida, Hiroyuki Nakao, Keisuke Ikeda, Minoru Nakano (*Grad. Sch. Med. Pharm. Sci., Univ. Toyama*)

1G1512* 細菌の排出システムにおける多剤認識の構造に基づく解析
Structure-based Analysis for Multidrug Recognition in Bacterial Efflux System
○中尾 香 [1], 櫻井 啓介 [2], 山崎 聖司 [1], 西野 邦彦 [1], 山口 明人 [1], 中島 良介 [1] ([1]阪大産研, [2]東北大院情報）
Kaori Nakao[1], Keisuke Sakurai[2], Seiji Yamasaki[1], Kunihiko Nishino[1], Akihito Yamaguchi[1], Ryousuke Nakashima[1] ([1]*ISIR*, [2]*GSIS, Tohoku Univ.*)

1G1524 Interrogation of a bacterial sugar transporter for novel biomedicines and biotechnologies
Lingbing Kong[1,2] ([1]*International Institute of Rare Sugar Research and Education, Kagawa University*, [2]*Visiting Academic in University of Oxford*)

1G1536* ミトコンドリアの電子伝達系の働きとクリステ構造の安定性について
Stability of cristae structures of mitochondria and the electron transfer chain activities
○米田 真由, 柴田 貴弘, 太田 善浩（農工大院 太田研）
Mayu Yoneda, Takahiro Shibata, Yoshihiro Ohta (*Ohta. lab., Grad. Univ. Noko*)

1G1548 A unique respiratory adaptation in Drosophila independent of supercomplex formation
Satoru Shimada[1,2], Marika Oosaki[1], Ryoko Takahashi[1], Shigefumi Uene[1], Sachiko Yanagisawa[1], Tomitake Tsukihara[1], **Kyoko Shinzawa-Itoh**[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*KNC Lab Co., Ltd.*)

13:30〜16:00　H 会場（A41）／Room H (A41)
1H 光生物／Photobiology

1H1330* レチニリデンシッフ塩基の対イオンの高い pK_a は Na^+ポンプロドプシン の効率的なイオン輸送に必須である
An elevated pK_a of the retinylidene Schiff base counterion is prerequisite for efficient ion transport in Na^+ pumping rhodopsins
○栗原 眞理恵 [1], 橋本 美沙 [2], 吉澤 晋 [3], 小島 慧一 [1,2], 塚本 卓 [1,2], 菊川 峰志 [4,5], 須藤 雄気 [1,2]（[1]岡大・院医歯薬 (薬), [2]岡大・薬 (薬), [3]東大・大気海洋研, [4]北大・院・先端生命, [5]北大・国際連携研究教育局）
Marie Kurihara[1], Misa Hashimoto[2], Susumu Yoshizawa[3], Keiichi Kojima[1,2], Takashi Tsukamoto[1,2], Takashi Kikukawa[4,5], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*AORI, UTokyo.*, [4]*Fac. Adv. Life Sci., Hokkaido Univ.*, [5]*GSS, GI-CoRE, Hokkaido Univ.*)

1H1342* KR2 の水素結合ネットワークとナトリウム輸送メカニズムに関する構造解析
Structural analysis on the hydrogen bonding network in KR2 and its sodium pump mechanism
○富田 紗穂子 [1], 伊藤 奨太 [1], 井上 圭一 [1,2,3], 神取 秀樹 [1]（[1]名工大院工, [2]PRESTO, JST, [3]東京大学）
Sahoko Tomida[1], Shota Ito[1], Keiichi Inoue[1,2,3], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*PRESTO, JST*, [3]*Tokyo Univ.*)

1H1354* 微生物型ロドプシンで広く保存される波長制御に重要な２残基のアミノ酸変異による制御メカニズムの解明と光遺伝学への応用
Elucidation of wavelength regulation mechanism by widely-preserved amino-acid mutation in rhodopsins and its application to optogenetics
○中島 悠太 [1], 井上 圭一 [1,2,3], 神取 秀樹 [1]（[1]名工大・院工, [2]東大・物性研, [3]JST さきがけ）
Yuta Nakajima[1], Keiichi Inoue[1,2,3], Hideki Kandori[1] ([1]*Grad. Sch. Eng, NIT.*, [2]*ISSP, Univ. Tokyo.*, [3]*PRESTO, JST*)

1H1406* 霊長類緑感受性視物質の 100 K 以上での赤外分光解析
FTIR study of primate green-sensitive cone visual pigment at >100 K
○佐々木 拓磨 [1], 片山 耕大 [1], 吉住 玲 [1], 今井 啓雄 [2], 神取 秀樹 [1]（[1]名工大・院工, [2]京大・霊長研）
Takuma Sasaki[1], Kota Katayama[1], Rei Abe-Yoshizumi[1], Hiroo Imai[2], Hideki Kandori[1] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Primate Res. Inst., Kyoto Univ.*)

1H1418* 紅色細菌 strain 970 が最も大きいエネルギー勾配を遡って光合成を行うことができるのはなぜか
Origin of the anomalous uphill energy gap in the light-harvesting reaction center from purple photosynthetic bacterium strain 970
○今西 三千絵 [1], 小林 正幸 [2], 竹中 慎治 [1], Madigan M. T.[3], 大友 征宇 [4], 木村 行宏 [1]（[1]神戸大・院農学, [2]有明高専, [3]Dept. of Microbio., Southern Illinois Univ., [4]茨城大・理学）
Michie Imanishi[1], Masayuki Kobayashi[2], Shinji Takenaka[1], M.T. Madigan[3], Zheng-Yu Wang-Otomo[4], Yukihiro Kimura[1] ([1]*Grad. Sch. Agri., Kobe Univ.*, [2]*Tech., Ariake National College.*, [3]*Dept. of Microbio., Southern Illinois Univ.*, [4]*Fac. Sci., Ibaraki Univ.*)

1H1430* **多孔質ガラス板内部における光化学系 I から白金ナノ粒子への光誘起電子移動反応**
The light induced electron transfer reaction from photosystem I to Pt nanoparticles inside a nanoporous glass plate
○平野 誠人 [1], 野地 智康 [2], 川上 恵典 [2], 神 哲郎 [3], 近藤 政晴 [4], 大岡 宏造 [5], 神谷 信夫 [1,2] ([1]大阪市大・院・理, [2]大阪市大・複合先端, [3]産総研・機能調和材料, [4]名工大・院・工, [5]阪大・院・理)
Makoto Hirano[1], Tomoyasu Noji[2], Keisuke Kawakami[2], Teturo Jin[3], Masaharu Kondo[4], Hirozo Oh-oka[5], Nobuo Kamiya[1,2] ([1]*Grad. Sch. Sci., Univ. Osaka City*, [2]*OCARINA, Univ. Osaka City*, [3]*AIST*, [4]*Grad. Sch. Engi., Univ. Nagoya Institute of Technology*, [5]*Grad. Sch. Sci., Univ. Osaka University*)

休憩（Coffee Break） 14:42–14:48

1H1448* **過渡回折格子法と活性測定を用いた BlrP1 の光強度センサー機能**
Non-linear light intensity sensing of BlrP1 studied by TG spectroscopy and enzymatic assay
○柴田 耕生, 中曽根 祐介, 寺嶋 正秀（京大・院理学）
Kosei Shibata, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

1H1500* LOV ドメインに保存されるグルタミン残基の役割
The role of Gln residue conserved among the LOV domains
○小林 樹, 久冨 修（阪大・院理）
Itsuki Kobayashi, Osamu Hisatomi (*Grad. Sch. Sci., Univ. Osaka*)

1H1512 Crystallization of squid metarhodopsin
Midori Murakami (*Dept. Physics, Nagoya Univ.*)

1H1524 **ハロロドプシンのイオン輸送におけるレチナール異性化反応**
Retinal isomerization during the anion pumping cycle of halorhodopsin
○神山 勉（名古屋大学）
Tsutomu Kouyama (*Nagoya University*)

1H1536 **光照射固体ＮＭＲとＤＦＴ計算によるファラオニスホボロドプシン中間体のレチナールの配座の解析**
Retinal configuration of pharaonis phoborhodopsin intermediates revealed by photo-irradiation solid-state NMR and DFT calculation
槇野 義輝 [1], 川村 出 [1], 沖津 貴志 [2], 和田 昭盛 [2], 加茂 直樹 [3], 須藤 雄気 [4], 上田 一義 [1], ○内藤 晶 [1] ([1]横浜国立大学 院工, [2]神戸薬大 生命有機化学, [3]北大 先端生命科学院, [4]岡山大 医歯薬学総合研究科)
Yoshiteru Makino[1], Izuru Kawamura[1], Takashi Okitsu[2], Akimori Wada[2], Naoki Kamo[3], Yuki Sudo[4], Kazuyoshi Ueda[1], **Akira Naito**[1] ([1]*Grad. Sch. Eng. Yokohama National University*, [2]*Laboratory of Organic Chemistry for Life Science Kobe Pharmaceutical University*, [3]*Faculty of Advanced Life Science, Hokkaido University*, [4]*Grad. Sch. Medicine, Dentistry and Pharmaceutical Science, Okayama University*)

1H1548 **脊椎動物の光受容体 Opn5L1 は逆行性・自己再生能をもつ新しいタイプのオプシンである**
Vertebrate photoreceptor, Opn5L1, is the newcomer of opsin acting as a reverse and self-regenerating photoreceptor
○佐藤 恵太 [1], 山下 高廣 [2], 大内 淑代 [1], 竹内 敦子 [3], 後藤 人志 [4], 小野 勝彦 [4], 水野 操 [5], 水谷 泰久 [5], 友成 さゆり [6], 酒井 佳寿美 [2], 今元 泰 [2], 和田 昭盛 [7], 七田 芳則 [2,8] ([1]岡大院医歯薬, [2]京大院理, [3]神薬大中央分析室, [4]京府医大生物, [5]阪大院理, [6]徳大院ソシオテクノサイエンス, [7]神薬大生命有機化, [8]立命大総科技研)
Keita Sato[1], Takahiro Yamashita[2], Hideyo Ohuchi[1], Atsuko Takeuchi[3], Hitoshi Gotoh[4], Katsuhiko Ono[4], Misao Mizuno[5], Yasuhisa Mizutani[5], Sayuri Tomonari[6], Kasumi Sakai[2], Yasushi Imamoto[2], Akimori Wada[7], Yoshinori Shichida[2,8] ([1]*Grad. Sch. of Med., Dent. and Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Sci., Kyoto Univ.*, [3]*Div. of Anal. Lab., Kobe Pharm. Univ.*, [4]*Dept. of Biol., Kyoto Pref. Univ. of Med.*, [5]*Graduate School of Science, Osaka University*, [6]*Inst. of Tech. and Sci., Tokushima Univ.*, [7]*Dept. of Org. Chem. for Life Sci., Kobe Pham. Univ.*, [8]*Res. Org. for Sci. and Tech., Ritsumeikan Univ.*)

13:30〜16:00　J 会場（D12）／Room J (D12)

1J 蛋白質：構造Ⅰ、構造機能相関Ⅰ、物性Ⅰ、機能Ⅰ、計測・解析の方法論Ⅰ、蛋白質工学Ⅰ／Proteins: Structure I, Structure-function relationship I, Property I, Function I, Measurement & Analysis I, Engineering I

1J1330 Structure-based analysis of ILEI/FAM3C activity to inhibit Aβ generation

Emi Hibino[1], Masatake Sugita[2], Yachiyo Mitsuishi[1], Naoki Watanabe[1], Masaki Nakano[1], Takuma Sugi[1], Masaki Nishimura[1] ([1]*Mol. Neurosci. Res. Ctr., Shiga Univ. of Med. Sci.*, [2]*Col. Life Sci., Ritsumeikan Univ.*)

1J1342 Domain motion of Fv-fragment in anti-dansyl immunoglobulin G controls conformation of its flexible antigen-binding region

Tomotaka Oroguchi[1,2], Masayoshi Nakasako[1,2] ([1]*Faclt. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 Center*)

1J1406 B 型肝炎ウイルスの薬剤の吸収に関する自由エネルギー計算

Free energy evaluation of drug absorption on Hepatitis B virus capsid

○浦野 諒, 吉井 範行, 篠田 渉, 岡崎 進（名古屋大学工学研究科）

Ryo Urano, Noriyuki Yoshii, Wataru Shinoda, Susumu Okazaki (*Grad. Sch. Engnr., Univ. Nagoya*)

1J1418 3D-RISM 理論と新しい溶媒和自由エネルギー表式を用いた蛋白質の構造安定性

Structural stability of proteins using 3D-RISM with new solvation free energy functional

○丸山 豊 [1], 光武 亜代理 [2]（[1]理研 R-CCS, [2]明治大学・物理）

Yutaka Maruyama[1], Ayori Mitsutake[2] ([1]*RIKEN R-CCS*, [2]*Dept. Phys, Meiji Univ.*)

1J1430 生体高分子立体構造生成およびタンパク質間相互作用解析の高速処理について

Fast Processing of Biopolymer Structure Generation and Protein-Protein Interaction Analysis

○杉原 崇憲 [1,5], 笠原 浩太 [2], 肥後 順一 [3,5], 嶋田 一夫 [4,5] ([1]バイオ産業情報化コンソーシアム, [2]立命館大学, [3]兵庫県立大学, [4]東京大学, [5]次世代天然物化学技術研究組合）

Takanori Sugihara[1,5], Kota Kasahara[2], Junichi Higo[3,5], Ichio Shimada[4,5] ([1]*JBIC*, [2]*Ritsumeikan Univ.*, [3]*Univ. Hyogo*, [4]*Univ. Tokyo*, [5]*N2PC*)

休憩（Coffee Break）　14:42–14:48

1J1448 Accurate temperature evaluation in molecular dynamics for long time simulations of biological systems with large time step

Jaewoon Jung[1,2], Chigusa Kobayashi[1], Yuji Sugita[1,2,3] ([1]*R-CCS*, [2]*RIKEN*, [3]*RIKEN BDR*)

1J1500 Computational design of symmetric protein scaffold and assembly with inorganics into hybrid materials

Hiroki Noguchi[1], Staf Wouters[1], Bram Mylemans[1], Jeremy Tame[2], Arnout Voet[1] ([1]*Dept. Chem., KU LEUVEN*, [2]*Drug Design Lab., Yokohama City Univ.*)

1J1512 量子化学計算を用いた催涙因子合成酵素の反応機構の解明

Elucidation of catalytic reaction mechanism of lachrymatory factor synthase using quantum chemical calculation

○山田 真行 [1], 森脇 由隆 [2], 寺田 透 [2,3], 佐藤 優太 [2], 荒川 孝俊 [2], 伏信 進矢 [2], 清水 謙多郎 [1,2]（[1]東大・院情報理工, [2]東大・院農学生命科学, [3]東大・情報学環）

Masayuki Yamada[1], Yoshitaka Moriwaki[2], Tohru Terada[2,3], Yuta Sato[2], Takatoshi Arakawa[2], Shinya Fushinobu[2], Kentaro Shimizu[1,2] ([1]*Grad. Sch. Info. Sci. Tech., Univ. Tokyo*, [2]*Grad. Sch. Agri. Life Sci., Univ. Tokyo*, [3]*Interfaculty Initiative in Info. Studies, Univ. Tokyo*)

1J1524 酸化や酵素処理が LDL の硬さ変化を起こすメカニズムについて

Putative mechanism of the elastic modulus change of low density-lipoprotein by oxidation or enzyme treatment

○武田 晴治 [1], 櫻井 俊宏 [1], 惠 淑萍 [1], 布田 博俊 [1], 千葉 仁志 [2]（[1]北海道大学大学院保健科学研究院, [2]札幌保健医療大学）

Seiji Takeda[1], Toshihiro Sakurai[1], Shu-Ping Hui[1], Hirotoshi Fuda[1], Hitoshi Chiba[2] ([1]*Hokkaido University*, [2]*Sapporo University of Health Sciences*)

1J1536 **高速原子間力顕微鏡 1 分子計測データの粒子フィルタを用いたデータ同化によるヌクレオソームの動的構造解析**
Dynamic structure analysis of nucleosome using particle filter data assimilation of single molecule measurement data by HS-AFM
○渕上 壮太郎 [1,2], 新稲 亮 [1], 高田 彰二 [1,2]（[1]京大院・理, [2]JST・CREST）
Sotaro Fuchigami[1,2], Toru Niina[1], Shoji Takada[1,2] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*CREST, JST*)

1J1548 **口腔細菌グルカンスクラーゼのドメイン間屈曲運動**
A hinge-bending domain motion in oral bacterial glucansucrase
○村田 雄大, 楠本 朋一郎, 平 順一, 坂本 寛, 小松 英幸（九工大・生命情報工）
Yudai Murata, Tomoichirou Kusumoto, Junichi Taira, Hiroshi Sakamoto, Hideyuki Komatsu (*Dept. Biosci. Bioinf., Kyushu Inst. Tech.*)

13:30〜16:00　K 会場（E11）／Room K (E11)
1K 蛋白質：構造Ⅱ、物性Ⅱ、機能Ⅱ、蛋白質工学Ⅱ、ヘム蛋白質／
Proteins: Structure II, Property II, Function II, Engineering II, Heme proteins

1K1330* **TnaC の翻訳停止に依存したフレームシフトの解析**
Analysis of the frameshift depending on TnaC-mediated ribosome stalling
○篠沢 智伎, 飯塚 怜, 船津 高志（東大・院薬）
Tomoki Shinozawa, Ryo Iizuka, Takashi Funatsu (*Grad. Sch. Pharm. Sci., Univ. Tokyo*)

1K1342* **演題取り消し**

1K1354* **ラン藻由来アルデヒド脱ホルミル化オキシゲナーゼによる炭化水素合成の向上に重要なアミノ酸残基の同定**
Identification of amino acid residues essential for high production of hydrocarbons in aldehyde deformylating oxygenase from cyanobacteria
○工藤 恒 [1], 林 勇樹 [1], 新井 宗仁 [1,2]（[1]東大・総合文化・生命環境, [2]東大・理・物理）
Hisashi Kudo[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1K1406* **ジョロウグモ牽引糸の配列に基づく合成ペプチドの β 構造の繊維形成性の評価**
Potential Fiber-Forming Regions in the Dragline Silk of Nephila clavata Possess a β-Structure
○山脇 裕貴, 橋本 慎二, 佐伯 政俊（市立山口東理大院）
Yuki Yamawaki, Shinji Hashimoto, Masatoshi Saiki (*Department of Applied Chemistry, Faculty of Engineering, Sanyo-onoda City University*)

1K1418* **転写因子 c-Myb と転写コアクチベーター CBP の KIX ドメインとの相互作用を阻害するペプチドの合理的設計**
Rational design of peptides that inhibit interaction of the transcription factor c-Myb with the KIX domain of CBP
○季高 駿士 [1], 岡 芳樹 [1], 梶原 朋子 [1], 林 勇樹 [1], 新井 宗仁 [1,2]（[1]東大・総合文化・生命環境, [2]東大・理・物理）
Shunji Suetaka[1], Yoshiki Oka[1], Tomoko Kunihara[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1K1430* **ショウジョウバエ Argonaute2 の N 末端はアミロイド繊維形成能を持つ**
N-terminal residues of Drosophila Argonaute2 possess the ability to form amyloid fibrils
○成田 晴香, 桑原 誠, 小森 智貴, 村上 僚, 島 知弘, 塩見 美喜子, 上村 想太郎（東大院・理・生科）
Haruka Narita, Makoto Kuwabara, Tomotka Komori, Ryo Murakami, Tomohiro Shima, Mikiko Siomi, Sotaro Uemura (*Grad. Sch. Sci., Univ. of Tokyo*)

休憩（Coffee Break）　14:42–14:48

1K1448* **天然変性タンパク質 c-Jun の構造解析と転写コアクチベータ CBP の KIX ドメインとの相互作用**
Structural analysis of the intrinsically disordered c-Jun and its interaction with the KIX domain of the transcriptional coactivator CBP
○吉崎 慧 [1], 末松 佑麿 [1], 季高 駿士 [1], 梱原 朋子 [1], 林 勇樹 [1], 新井 宗仁 [1,2]（[1]東大院・総合文化・生命環境, [2]東大・理・物理）
Satoru Yoshizaki[1], Yuma Suematsu[1], Shunji Suetaka[1], Tomoko Kunihara[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1K1500* **システイン残基の酸化修飾が制御する SOD1 の分解メカニズム**
Roles of cysteine oxidation as a signal for degradation of SOD1
○安齋 樹 [1], 向山 厚 [2,3], 秋山 修志 [2,3], 古川 良明 [1]（[1]慶應・理工・化学, [2]分子研協奏分子システム, [3]総研大）
Itsuki Anzai[1], Atsushi Mukaiyama[2,3], Shuji Akiyama[2,3], Yoshiaki Furukawa[1] ([1]*Dept. of Chem., Keio Univ.*, [2]*CIMoS, IMS*, [3]*SOKENDAI*)

1K1512* ***Mycoplasma mobile* の滑走に必須な Gli123 タンパク質の構造変化**
Structural change of Gli123 protein, essential for *Mycoplasma mobile* gliding
○松生 大輝 [1], 田原 悠平 [1,2], 濵口 祐 [1,2,4], 新井 宗仁 [3], 宮田 真人 [1,2]（[1]大阪市立大学 院理, [2]大阪市立大学 複合先端研究機構, [3]東京大学 大学院総合文化研究科, [4]理研 SPring-8）
Daiki Matsuike[1], Yuhei Tahara[1,2], Tasuku Hamaguchi[1,2,4], Munehito Arai[3], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*, [3]*Grad. Sch. Arts and Sci., The Univ. of Tokyo*, [4]*SPring-8 center, RIKEN*)

1K1524* **糖はタンパク質の溶媒和と構造安定性にどのように影響するのか？ ：WAXS 及び SANS によるタンパク質の化学変性及び熱変性の研究**
How do sugars affect protein solvation and structure stability? : WAXS and SANS studies of chemical and thermal denaturation of proteins
○味戸 聡志, 平井 光博（群馬大・院理工学）
Satoshi Ajito, Mitsuhiro Hirai (*Grad. Sch. Sci. and Tec., Univ. Gunma*)

1K1536* **マイクロフロー・フラッシュ赤外分光法を用いた膜内在性 NO 還元酵素の触媒反応の直接観測**
Direct observation of the enzymatic reaction catalyzed by an integral membrane NO reductase using microflow-flash IR spectroscopy
○武田 英恵 [1,2], 木村 哲就 [3], 野村 高志 [1], 石井 頌子 [1], 松林 亜希子 [1], 横田 あずさ [1], 當舎 武彦 [1,2], 城 宜嗣 [1], 久保 稔 [1,2]（[1]兵県大・院生命理, [2]理研・播磨, [3]神戸大・院理）
Hanae Takeda[1,2], Tetsunari Kimura[3], Takashi Nomura[1], Shoko Ishii[1], Akiko Matsubayashi[1], Azusa Yokota[1], Takehiko Tosha[1,2], Yoshitsugu Shiro[1], Minoru Kubo[1,2] ([1]*Grad. Sch. Lif Sci., Univ. Hyogo*, [2]*SPring-8 Center, RIKEN*, [3]*Grad. Sch. Sci., Kobe Univ.*)

1K1548* **all-α タンパク質のデザイン**
Design of all-α proteins
○佐久間 航也 [1,2], 小林 直宏 [3], 鈴木 花野 [4], 杉木 俊彦 [3], 小林 直也 [2], 小杉 貴洋 [1,2,5], 村田 武士 [4], 藤原 敏道 [3], 古賀 理恵 [2], 古賀 信康 [1,2,5]（[1]総研大, [2]生命創成探究, [3]阪大・蛋白研, [4]千葉大・理学研究院, [5]分子研）
Koya Sakuma[1,2], Naohiro Kobayashi[3], Kano Suzuki[4], Toshihiko Sugiki[3], Naoya Kobayashi[2], Takahiro Kosugi[1,2,5], Takeshi Murata[4], Toshimichi Fujiwara[3], Rie Koga[2], Nobuyasu Koga[1,2,5] ([1]*SOKENDAI*, [2]*NINS ExCELLS*, [3]*Institute for Protein Research, Osaka Univ.*, [4]*Dept. Sci. Chiba Univ.*, [5]*NINS IMS*)

13:30〜15:36　L 会場（D23）／Room L (D23)
1L 蛋白質：構造機能相関Ⅱ、物性Ⅲ、計測・解析の方法論Ⅰ／
Proteins: Structure-function relationship II, Property III, Measurement & Analysis I

1L1330* Theoretical Study on the Contribution of Spin Structure to Redox Potential of [2Fe-2S] Core Cluster from Iron-Sulfur Proteins
Isman Kurniawan[1,2], Kazutomo Kawaguchi[1], Mitsuo Shoji[3], Toru Matsui[4], Yasuteru Shigeta[3], Hidemi Nagao[1] ([1]*Div Mathematical and Physical Science, Kanazawa University*, [2]*School of Computing, Telkom University, Indonesia*, [3]*Center of Computational Science, University of Tsukuba*, [4]*College of Chemistry, University of Tsukuba*)

1L1342* 分子動力学計算を用いた 4 つの蛋白質ファミリーによるリン酸化認識機構の解明
How proteins recognize a phosphoserine residue: diversity and heterogeneity in different protonation states revealed by MD simulations
○河出 来時 [1], 黒田 大祐 [1], 津本 浩平 [1,2]（[1]東大院・工, [2]東大・医科研）
Raiji Kawade[1], Daisuke Kuroda[1], Kouhei Tsumoto[1,2] ([1]*Grad. Sch. Eng,. Univ. Tokyo*, [2]*Med. Sci. Inst., Univ. Tokyo*)

1L1354* 誘電アロステリーによるシトクロム P450 還元酵素の酸化還元状態と構造状態のカップリング
Coupling of redox and structural states in cytochrome P450 reductase via dielectric allostery
○飯島 美来, 佐藤 昂人, 大貫 隼, 高野 光則（早大・物理応物）
Mikuru Iijima, Takato Sato, Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1L1406* Crystal Molecular Dynamics Simulations to study the dynamics of presequence peptide in Crystal Contact-Free Space
Arpita Srivastava[1], Florence Tama[1,2,3], Daisuke Kohda[4], Osamu Miyashita[2] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Cent. for Comp. Sci., RIKEN*, [3]*Inst. of Trans. Bio-molecules, Univ. Nagoya*, [4]*Med. Inst. of Bioregulation, Univ. Kyushu*)

1L1418* Molecular dynamics coupled with virtual system for effective conformational sampling
Tomonori Hayami[1,2], Takuya Shimato[3], Haruki Nakamura[4], Kota Kasahara[5], Junichi Higo[6] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Fro. Bio., Osaka Univ.*, [3]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [4]*NIG, ROIS*, [5]*Coll. Life Sci., Ritsumeikan Univ.*, [6]*Grad. Sch. Sim. Studies, Univ. Hyogo*)

1L1430* 翻訳伸長因子 EF-1α 及び EFL のインシリコモデル構造解析
In silico structural analysis of Elongation factor-1 alpha and Elongation factor-like
○坂本 航太郎 [1], 栢沼 愛 [2], 重田 育照 [2]（[1]筑波大・院・ＨＢＰ, [2]筑波大 CCS）
Kotaro Sakamoto[1], Megumi Kayanuma[2], Yasuteru Shigeta[2] ([1]*HBP, Univ. of Tsukuba*, [2]*CCS, Univ. of Tsukuba*)

休憩（Coffee Break）　14:42–14:48

1L1448* 統計力学モデルの拡張によるマルチドメインタンパク質のフォールディング機構の予測
Prediction of folding mechanisms of multi-domain proteins by an extended statistical mechanical model
○大岡 紘治 [1], 新井 宗仁 [1,2]（[1]東大・理・物理, [2]東大・総合文化・生命環境）
Koji Ooka[1], Munehito Arai[1,2] ([1]*Dept. Phys., Univ. Tokyo*, [2]*Dept. Life Sci., Univ. Tokyo*)

1L1500* NMR study of N-terminal SH2 domain of phosphatidylinositol 3-kinase and its interaction with CD28
Yuhi Hosoe[1], Satomi Inaba[1,2], Yohei Miyanoiri[3], Hisayuki Morii[4], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*JASRI/SPring-8*, [3]*IPR, Osaka Univ.*, [4]*College Liberal Arts Sci., Tokyo Med. Dent. Univ.*)

1L1512* caged-GTP を用いた時間依存的な NMR 信号変化のモニタリングによるガン遺伝子産物 Ras の GTP 加水分解過程における構造変化の解明

Conformational changes on GTP hydrolysis of oncogene product Ras revealed by monitoring of time-dependent NMR signal using caged-GTP

○萩原 睦[1], 槇野 義輝[1], 松本 篤幸[2], 河村 高志[3], 南後 恵理子[4], 森 一郎[1], 片岡 徹[2], 熊坂 崇[3], 島 扶美[1]（[1]神戸大学 院科学技術イノベーション, [2]神戸大学 院医, [3]高輝度光科学研究センター, [4]理研 放射光科学研究センター.）

Chika Hagihara[1], Yoshiteru Makino[1], Shigeyuki Matsumoto[2], Takashi Kawamura[3], Eriko Nango[4], Ichiro Mori[1], Tohru Kataoka[2], Takashi Kumasaka[3], Fumi Shima[1] ([1]*Grad. Sch. Sci. Tec. Innov., Kobe Univ.*, [2]*Grad. Sch. Med., Kobe Univ.*, [3]*SPring-8, JASRI*, [4]*RSC., RIKEN*)

1L1524* An Initial Interaction Difference between Bombinin H2 and H4 on Leishmania mimetic membrane

Batsaikhan Mijiddorj[1,2], Shiho Kaneda[1], Hisako Sato[3], Yuki Kitahashi[1], Namsrai Javkhlantugs[2], Akira Naito[1], Kazuyoshi Ueda[1], Izuru Kawamura[1] ([1]*Graduate School of Engineering, Yokohama National University, Yokohama, Japan*, [2]*School of Engineering and Applied Sciences, National University of Mongolia, Ulaanbaatar, Mongolia*, [3]*Graduate School of Science and Engineering, Ehime University, Matsuyama, Japan*)

13:30〜15:24　M 会場（E21）／Room M (E21)
1M 蛋白質：構造Ⅲ、構造機能相関Ⅲ、物性Ⅳ／
Proteins: Structure III, Structure-function relationship III, Property IV

1M1330 真空紫外円二色性分光による α1 酸性糖蛋白質の生体膜相互作用機構の研究

Interaction Mechanism between α_1-Acid Glycoprotein and Membrane Characterized by Vacuum-Ultraviolet Circular-Dichroism Spectroscopy

○松尾 光一, 生天目 博文, 谷口 雅樹, 月向 邦彦（広大・放射光）

Koichi Matsuo, Hirofumi Namatame, Masaki Taniguchi, Kunihiko Gekko (*HiSOR, Hiroshima Univ.*)

1M1342 時計タンパク質 KaiC の C1 リングの構造変化が KaiB との結合のタイミングを計る

Conformational rearrangements of the C1 ring in KaiC measure the timing of assembly with KaiB via a conformational selection mechanism

○向山 厚[1,2], 古池 美彦[1,2], 山下 栄樹[3], 近藤 孝男[4], 秋山 修志[1,2]（[1]自然科学研究機構分子科学研究所, [2]総研大, [3]阪大・蛋白研, [4]名大院・理）

Atsushi Mukaiyama[1,2], Yoshihiko Furuike[1,2], Eiki Yamashita[3], Takao Kondo[4], Shuji Akiyama[1,2] ([1]*Inst. for Mol. Sci.*, [2]*The Grad. Univ. for Adv. Studies*, [3]*Inst. for Protein Res.*, [4]*Div. of Biol. Sci., Grad. Sch. of Sci., Nagoya Univ.*)

1M1354 RXRα リガンド結合ドメイン四量体と新規合成パーシャルアゴニストとの複合体結晶構造

Crystal structure of the tetrameric ligand binding domain of RXRα complexed with a novel synthetic partial agonist

宮下 由里奈[1,2], ○沼本 修孝[3], ラジャ サンダラム[1], 中野 祥吾[4], 松尾 直也[1], 清水 奏[1], 芝原 理[5], 藤原 美智子[5], 加来田 博貴[5], 伊藤 創平[4], 伊倉 貞吉[3], 伊藤 暢聡[3], 常盤 広明[1,2,6]（[1]立教大, [2]AMED-CREST, [3]医科歯科大・難研, [4]静岡県大・食品栄養科学, [5]岡山大・院医歯薬, [6]立教大・未来分子研究センター）

Yurina Miyashita[1,2], **Nobutaka Numoto**[3], Sundaram Arulmozhiraja[1], Shogo Nakano[4], Naoya Matsuo[1], Kanade Shimizu[1], Osamu Shibahara[5], Michiko Fujihara[5], Hiroki Kakuta[5], Sohei Ito[4], Teikichi Ikura[3], Nobutoshi Ito[3], Hiroaki Tokiwa[1,2,6] ([1]*Rikkyo Univ.*, [2]*AMED-CREST*, [3]*Medical Research Inst., Tokyo Medical and Dental Univ.*, [4]*Sch. of Food and Nutritional Sci., Univ. of Shizuoka*, [5]*Grad. Sch. of Med. Dent. and Pharm. Sci., Okayama Univ.*, [6]*Research Center for Smart Molecules, Rikkyo Univ.*)

1M1406 **植物硝酸輸送体 NRT2-NAR2 複合体の結晶構造**
Crystal structure of plant high affinity nitrate transporter NRT2 in complex with the accessory protein NAR2
○福田 昌弘[1,2], 石谷 隆一郎[1], 横川 真梨子[2], 大澤 匡範[2], 濡木 理[1]（[1]東京大・院理, [2]慶應大・薬）
Masahiro Fukuda[1,2], Ryuichiro Ishitani[1], Mariko Yokogawa[2], Masanori Osawa[2], Osamu Nureki[1] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Fac. Pharm., Keio Univ.*)

1M1418 **動的核偏極タンパク質中性子結晶解析に向けた高圧凍結最適化と新たなラジカルドーピング**
Optimization of high-pressure freezing and new radical doping for neutron protein crystallography by dynamic nuclear polarization
青木 晃次[1], 新井 隆介[1], 加藤 康平[1], 杉山 玲[1], ○田中 伊知朗[1,2]（[1]茨城大院理工, [2]茨城大フロンティア）
Kouji Aoki[1], Ryusuke Arai[1], Kohei Kato[1], Rei Sugiyama[1], **Ichiro Tanaka**[1,2] ([1]*Grad. Sch. Sci. and Eng., Ibaraki Univ.*, [2]*Frontier Ctr, Ibaraki Univ.*)

1M1430 **中性子準弾性散乱及び動的光散乱による蛋白質のマルチスケールダイナミクス測定**
The multiscale dynamics of proteins measured by quasielastic neutron scattering and dynamic light scattering
○藤原 悟[1], 松尾 龍人[1], 河野 史明[1], 柴田 薫[2]（[1]量子科学技術研究開発機構, [2]J-PARC センター）
Satoru Fujiwara[1], Tatsuhito Matsuo[1], Fumiaki Kono[1], Kaoru Shibata[2] ([1]*QuBS, QST*, [2]*J-PARC Center*)

休憩（Coffee Break） 14:42–14:48

1M1448 **チトクロム酸化酵素によるプロトンポンプは、酸素結合によって誘起されるタンパク質内構造変化によって厳密に制御されている**
Structure changes induced by O_2-binding tightly regulate the proton-pumping of cytochrome c oxidase
○島田 敦広[1], 久保 稔[2], 馬場 清喜[3], 吾郷 日出夫[2], 月原 冨武[4,5], 吉川 信也[5]（[1]岐阜大・応生, [2]理研・SPring-8, [3]高輝度研, [4]阪大・蛋白研, [5]兵県大・生命理・ピコ研）
Atsuhiro Shimada[1], Minoru Kubo[2], Seiki Baba[3], Hideo Ago[2], Tomitake Tsukihara[4,5], Shinya Yoshikawa[5] ([1]*Fac. Appl. Biol. Sci., Gifu Univ.*, [2]*RIKEN, SPrng-8*, [3]*JASRI*, [4]*Inst. Protein Res., Osaka Univ.*, [5]*Picobiol. Inst., Grad. Sch. Life Sci., Univ. Hyogo*)

1M1500 Finding potential 3D biological shapes for a small number of XFEL diffraction patterns
Sandhya Premnath Tiwari[1], Osamu Miyashita[1], Florence Tama[1,2,3] ([1]*Riken Center for Computational Science*, [2]*Department of Physics, University of Nagoya*, [3]*Institute of Transformative Bio-molecules, University of Nagoya*)

1M1512 **単粒子解析における X 線自由電子レーザー回折像の定量的評価**
Quantitative evaluation of the diffraction images for single particle analysis by X-ray free electron laser experiment
○中野 美紀[1], 宮下 治[1], ジョニック スラビカ[2], タマ フロハンス[1,3,4]（[1]理研 計算科学研究センター, [2]IMPMC, Sorbonne Univ. CNRS, UPMC Univ Paris 6, MNHN, IRD, [3]名古屋大院理学研究科, [4]名古屋大トランス フォーマティブ生命分子研究所）
Miki Nakano[1], Osamu Miyashita[1], Slavica Jonic[2], Florence Tama[1,3,4] ([1]*R-CCS*, [2]*IMPMC, Sorbonne Univ. CNRS, UPMC Univ Paris 6, MNHN, IRD*, [3]*Grad. Sch. Science, Nagoya Univ.*, [4]*ITbM, Nagoya Univ.*)

13:30〜16:00 O 会場（D32）／Room O (D32)
1O 非平衡・計測・数理生物学／Nonequilibrium, Measurement, Mathematical Biology

1O1330* **微小管の滑り運動における進行方向の長時間シミュレーション**
Long-time simulation for the traveling direction of a microtubule in motility assays
○品川 遼太, 佐々木 一夫（東北大・院工学）
Ryota Shinagawa, Kazuo Sasaki (*Grad. Sch. Eng., Tohoku Univ.*)

1O1342* キネシン駆動微小管の集団運動における立体障害相互作用の役割
The role of steric interaction in collective motion of microtubules driven by kinesins
○谷田 桜子 [1], 古田 健也 [2], 西川 香里 [1], 平岩 徹也 [1], 小嶋 寛明 [2], 大岩 弘和 [2] ([1]東大・理, [2]情報通信研究機構)
Sakurako Tanida[1], Ken'ya Furuta[2], Kaori Nishikawa[1], Tetsuya Hiraiwa[1], Hiroaki Kojima[2], Kazuhiro Oiwa[2] ([1]*Grad. Sch. Sci, The Univ. of Tokyo*, [2]*NICT*)

1O1354 境界に拘束されたアクトミオシンゲルの周期的な収縮現象と位置対称性の破れ
Periodic contraction of actomyosin gel and nucleus-like cluster positioning in a confined geometry
○坂本 遼太 [1], 平岩 徹也 [2], 田邉 優敏 [3], 石渡 信一 [3], 前多 裕介 [1], 宮﨑 牧人 [4,5] ([1]九大院理, [2]東大理, [3]早大理工, [4]京大白眉, [5]京大理)
Ryota Sakamoto[1], Tetsuya Hiraiwa[2], Masatoshi Tanabe[3], Shin'ichi Ishiwata[3], Yusuke Maeda[1], Makito Miyazaki[4,5] ([1]*Dept. Phys., Kyushu Univ.*, [2]*Dept. Phys., Tokyo Univ.*, [3]*Dept. Phys., Waseda Univ.*, [4]*Hakubi Cent. Kyoto Univ.*, [5]*Dept. Phys., Kyoto Univ.*)

1O1406 生化学反応における情報幾何と熱力学的な不確定性関係
Information geometry and thermodynamic uncertainty for biochemical process
○伊藤 創祐（北海道大学 電子科学研究所）
Sosuke Ito (*Hokkaido Univ. RIES*)

1O1418 Chemical potential formalism for polymer entropic forces
Hong-Qing Xie, **Cheng-Hung Chang** (*Institute of Physics, National Chiao Tung University, Taiwan*)

1O1430* A new measure of the interrelation of cellular phenotypes in cellular reproductive systems
Shunpei Yamauchi, Yuichi Wakamoto (*Graduate School of Arts and Sciences, University of Tokyo*)

休憩（Coffee Break） 14:42–14:48

1O1448 A robotic system for combining single-cell RNA-seq with live cell imaging
Taisaku Ogawa[1], Tomokatsu Ikawa[2,3], Katsuyuki Shiroguchi[1,3,4] ([1]*RIKEN BDR*, [2]*RIBS, Tokyo Univ of Sci*, [3]*RIKEN IMS*, [4]*JST PRESTO*)

1O1500* 糖摂取後のヒト血中分子濃度の時間変動解析
Time-series analysis of metabolic responsiveness to the oral glucose intake
○藤田 卓 [1], 住友 洋平 [1], 唐沢 康暉 [2], 藤井 雅史 [1], 宇田 新介 [3], 大橋 郁 [1], 平山 明由 [4], 曽我 朋義 [4], 黒田 真也 [1] ([1]東京・院理, [2]東大病院・リハビリ, [3]九州大・生体防御医学研, [4]慶應大・先端生命科学研)
Suguru Fujita[1], Yohei Sumitomo[1], Yasuaki Karasawa[2], Masashi Fujii[1], Shinsuke Uda[3], Kaoru Ohashi[1], Akiyoshi Hirayama[4], Tomoyoshi Soga[4], Shinya Kuroda[1] ([1]*Grad. Sch. of Sci., Univ. of Tokyo.*, [2]*Rehab. Med., Univ. of Tokyo. Hosp.*, [3]*Med. Inst. of Bioreg., Kyushu Univ.*, [4]*Inst. for Adv. Biosci., Keio Univ.*)

1O1512* 線虫の Lifespan 解析に向けたマイクロ流体デバイスの構築
A two-story structured microfluidic device (WormFlo) toward recording of C. elegans motion during lifespan at the video-rate
○池田 優作 [1], 荒田 幸信 [2], 佐甲 靖志 [2], 木村 啓志 [3,4] ([1]東海大・院工, [2]理研・和光, [3]東海大・工・機械, [4]東海大・MNTC)
Yusaku Ikeda[1], Yukinobu Arata[2], Yasushi Sako[2], Hiroshi Kimura[3,4] ([1]*Grad. Sch. Eng., Univ. Tokai*, [2]*Wako Inst., Riken*, [3]*Dept. of. Mec. Eng., Univ. Tokai*, [4]*MNTC., Univ. Tokai*)

1O1524* 細胞内微小環境における高分子と熱ダイナミクスの関係の解明
Study on the relationship between macromolecules and thermodynamics in intracellular microenvironment
○寶田 雅治 [1], 岡部 弘基 [1,2], 船津 高志 [1] ([1]東京大学大学院薬学系研究科, [2]科学技術振興機構 さきがけ)
Masaharu Takarada[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Graduate School of Pharmaceutical Science, The University of Tokyo.*, [2]*PRESTO, JST*)

1O1536* **単一細胞におけるミトコンドリアの４つのプロトンポンプ活性の連続計測**
Sequential imaging of four proton pump activities of mitochondria in a single cell
○柏木 広子, 太田 善浩（農工大院 太田研）
Hiroko Kashiwagi, Yoshihiro Ohta (*Ohta. lab., Grad. Sch., Univ. Noko*)

1O1548* **一粒子軌跡解析による洗浄工程を必要としないタンパク質のデジタル検出技術**
Wash-free digital protein detection method by single particle tracking analysis
○赤間 健司 [1,2], 野地 博行 [1]（[1]東大・院応化, [2]シスメックス(株)）
Kenji Akama[1,2], Hiroyuki Noji[1] ([1]*Grad. Sch. Appl. Chem., Univ. Tokyo*, [2]*Sysmex.corp.*)

13:30〜16:00　Q 会場（D34）／Room Q (D34)
1Q 核酸・情報科学・ゲノム生物学／Nucleic acid, Bioinformatics, Genome biology

1Q1330* **DNA 整列固定技術を用いた構造的 DNA 結合タンパク質のスライディング運動の単分子観察**
Single-molecule investigation of the sliding dynamics of architectural DNA-binding proteins along crowded DNA using DNA garden technique
○大内 華奈 [1,2], Johnson Reid C.[3], 高橋 聡 [1], 鎌形 清人 [1]（[1]東北大学多元物質科学研究所, [2]東北大学大学院生命科学研究科, [3]カリフォルニア大学ロサンゼルス校）
Kana Ouchi[1,2], Reid C. Johnson[3], Satoshi Takahashi[1], Kiyoto Kamagata[1] ([1]*IMRAM, Tohoku University*, [2]*Grad. Sch. Life Science, Tohoku University*, [3]*UCLA*)

1Q1342* **人工細胞デバイス内に封入した長鎖 DNA １分子からの遺伝子発現**
Gene expression from a single large DNA encapsulated in artificial cell device
○落合 悠人 [1], 上野 博史 [1], 末次 正幸 [2], 野地 博行 [1]（[1]東大・院工・応化, [2]立教大・理・生命理）
Yuto Ochiai[1], Hiroshi Ueno[1], Masayuki Su'etsugu[2], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Dept. Life Sci., Col. Sci., Rikkyo Univ.*)

1Q1354* **シスプラチンとトランスプラチンによる DNA への異なる作用：DNA 高次構造と遺伝子発現**
Different effect between cisplatin and transplatin on the higher order structure of DNA and gene expression
○岸本 幹史 [1], 吉川 祐子 [1], 米田 誠治 [2], 吉川 研一 [1]（[1]同志社生命医科学研究科, [2]鈴鹿医療科学大学薬学部）
Toshifumi Kishimoto[1], Yuko Yoshikawa[1], Seiji Komeda[2], Kenichi Yoshikawa[1] ([1]*Grad. Sch. Life Med. Sci., Univ. Doshisha*, [2]*Fac. Pharm., Univ. Suzuka. Med. Sci*)

1Q1406* Elucidating transcriptional mechanisms of NF-kB target gene expression based on various sequence data
Minami Ando, Shigeyuki Magi, Kazunari Iwamoto, Mariko Okada (*Institute for Protein Research, Osaka University*)

1Q1418 **海洋性細菌 *Vibrio alginolyticus* ４株 (138-2, VIO5, YM4, YM19)のゲノム構造比較解析**
Comparative analysis of whole genome structure of marine bacteria *Vibrio alginolyticus* spp. strains 138-2, VIO5, YM4 and YM19
○井原 邦夫 [1], 稲葉 啓太 [1], 上坂 一馬 [1], 中郁 真之 [1], 西岡 典子 [2], 小嶋 誠司 [2], 本間 道夫 [2]（[1]名古屋大学 遺伝子実験施設, [2]名古屋大学大学院 理学研究科）
Kunio Ihara[1], Keita Inaba[1], Kazuma Uesaka[1], Masayuki Nakamura[1], Noriko Nishioka[2], Seiji Kojima[2], Michio Homma[2] ([1]*Nagoya University Center for Gene Research*, [2]*Nagoya University Graduate School of Science*)

1Q1430 Discovering novel functional genome structures in Dengue and Zika viruses through experiment and multi-scale modeling
Roland G. Huber[1], Yue Wan[2], Peter J. Bond[1] ([1]*Bioinformatics Institute (BII), Agency for Science, Technology and Research (A*STAR)*, [2]*Genome Institute of Singapore (GIS), Agency for Science, Technology and Research (A*STAR)*)

休憩（Coffee Break）　14:42–14:48

1Q1448* **モデルペプチドを用いた MD シミュレーションによる膜タンパク質複合体形成にコレステロールが及ぼす影響の検討**
Influence of cholesterol on membrane protein complex formation by molecular dynamics simulations with model peptides
○板谷 颯人 [1], 笠原 浩太 [1], 松崎 勝巳 [2], 矢野 義明 [2], 高橋 卓也 [1]（[1]立命館大・生命科学, [2]京大院・薬）
Hayato Itaya[1], Kota Kasahara[1], Katumi Matsuzaki[2], Yoshiaki Yano[2], Takuya Takahashi[1] ([1]*Coll. Life Sci., Ritsumeikan Univ*, [2]*Grad. Sch. Pharm.Sci., Kyoto Univ*)

1Q1500 Chiral selectivity mechanism on aminoacylation of an RNA minihelix examined by molecular dynamics simulations
Tadashi Ando[1], Koji Tamura[2] ([1]*Dept. Appl. Elec., Tokyo Univ. of Sci.*, [2]*Dept. Biol. Sci. & Tech. Tokyo Univ. of Sci.*)

1Q1512* **タンパク質 FUS の液滴・凝集形成に関する分子動力学シミュレーション**
Molecular dynamics simulations of liquid droplet and aggregation formations of protein FUS
○寺澤 裕樹, 笠原 浩太, 高橋 卓也（立命館大・生命）
Hiroki Terazawa, Kota Kasahara, Takuya Takahashi (*Coll. Life Sci., Ritsumeikan Univ*)

1Q1524 **深層学習を用いたゲノムシークエンスのクラスター解析**
Graphical Classification of DNA Sequences of using Deep Learning
○三宅 淳 [1], 馬場 俊輔 [1], 島林 真人 [2], 山本 修也 [2], 田川 聖一 [3], 新岡 宏彦 [4]（[1]大阪大学国際医工情報センター, [2]大阪大学・基礎工学研究科, [3]大阪大学・先導的学際研究機構, [4]大阪大学・データビリティーフロンティア機構）
Jun Miyake[1], Shunsuke Baba[1], Masato Shimabayashi[2], Shuya Yamamoto[2], Seiichi Tagawa[3], Hirohiko Niioka[4] ([1]*Global Center for Medical Engineering and Informatics, Osaka U.*, [2]*School of Engineering Science, Osaka U.*, [3]*Open and Transdisciplinary Research Initiatives, Osaka U.*, [4]*Institute for Datability Science, Osaka U.*)

1Q1536* **ニューラルネットワークを用いたタンパク質 N-gram 配列間相互作用の予測**
Predicting interactions between N-gram sequences in proteins by using Neural Network
○近藤 遼平 [1], 笠原 浩太 [2], 高橋 卓也 [2]（[1]立命館大・院・生命, [2]立命館大・生命）
Ryohei Kondo[1], Kota Kasahara[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

1Q1548 **蛋白質立体構造と機能に影響しうるゲノムバリアントの選択と解析**
Extraction and analysis of missense variants with possible impact on protein structure and function
○城田 松之 [1,2,3]（[1]東北大・院医, [2]東北大・東メガ, [3]東北大・院情報）
Matsuyuki Shirota[1,2,3] ([1]*Grad. Sch. Med., Tohoku Univ.*, [2]*ToMMo, Tohoku Univ.*, [3]*Grad. Sch. Inform. Sci., Tohoku Univ.*)

2 日目（9 月 16 日（日））／Day 2（Sep. 16 Sun.）

14:00〜16:30　A 会場（B11）／Room A (B11)
2A 細胞生物的課題／Cell biology

2A1400 Cell-size dependent polarity dynamics revealed by high-throughput imaging and machine learning analysis
Akihiko Nakajima[1], Motohiko Ishida[2], Taihei Fujimori[2], Ayaka Matsumoto[3], Satoshi Sawai[1,2] ([1]*Comp. Sys. Biol. Cent., Univ. Tokyo*, [2]*Grad. Sch. Arts. Sci., Univ. Tokyo*, [3]*Dept. Biol., Univ. Tokyo*)

2A1412 Elucidating pathogenesis of congenital muscular and neuronal diseases caused by defective membrane remodeling of dynamin GTPase
Tetsuya Takeda, Kenshiro Fujise, Yuta Nobunaga, Hiroshi Yamada, Kohji Takei (*Grad Sch Med Dent Pharm Sci, Okayama Univ*)

2A1424 **イノシトールリン脂質代謝系の細胞内自己組織化現象の超解像イメージングによる解析**
Super-resolution imaging analysis of self-organization mechanism in phosphoinositide signaling system on the cell membrane
○松岡 里実[1,2], 高木 拓明[1,3], 福島 誠也[2], 宮永 之寛[1,2], 上田 昌宏[1,2]（[1]理研・生命機能科学研究センター, [2]阪大・院生命機能, [3]奈良医大・医）
Satomi Matsuoka[1,2], Hiroaki Takagi[1,3], Seiya Fukushima[2], Yukihiro Miyanaga[1,2], Masahiro Ueda[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. Frontier Biosciences, Osaka Univ.*, [3]*Sch. Med., Nara Med. Univ.*)

2A1436 **Ras 依存的に作られる PIP3 局在パターン形成の観察とモデル化**
Observation and modeling of Ras dependent PIP3 localization pattern formation
○福島 誠也[1], 松岡 里実[2], 上田 昌宏[2,3]（[1]阪大・理学, [2]理研 BDR, [3]阪大・生命）
Seiya Fukushima[1], Satomi Matsuoka[2], Masahiro Ueda[2,3] ([1]*Grad. Sch. of Sci., The Univ. of Osaka*, [2]*Riken BDR*, [3]*Grad. Sch. of Frontier Bio-Sci., The Univ. of Osaka*)

2A1448 **走化性 G タンパク質共役受容体は濃度依存的に三量体 G タンパク質の制御機構を切り替えて走化性レンジを拡張する**
Chemoattractant receptor-mediated activation, membrane recruitment and capture of G proteins enable wide range chemotaxis
○宮永 之寛[1], 上村 陽一郎[2], 桑山 秀一[3], 上田 昌宏[1,2]([1]大阪大学大学院 生命機能研究科, [2]理化学研究所 生命機能科学研究センター, [3]筑波大学 生命環境系）
Yukihiro Miyanaga[1], Yoichiro Kamimura[2], Hidekazu Kuwayama[3], Masahiro Ueda[1,2] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*RIKEN Center for Biosystems Dynamics Research*, [3]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

2A1500 **CLIP-170 は細胞接着表面でタンパク質をプラス端へ運ぶことにより免疫 T 細胞活性化における中心体の細胞表面への移動を制御している**
CLIP-170 is essential for MTOC repositioning during T cell activation by recruiting proteins to the plus-end tracking on the cell surface
林 偉銘[1], 伊藤 由馬[1], 十川 久美子[1,2], ○徳永 万喜洋[1]（[1]東工大・生命理工学院, [2]東北大・院農学）
Wei Ming Lim[1], Yuma Ito[1], Kumiko Sakata-Sogawa[1,2], **Makio Tokunaga**[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Grad. Sch. Agr. Sci., Tohoku Univ.*)

休憩（Coffee Break） 15:12–15:18

2A1518 **大腸菌走化性応答適応過程の CW bias タイムトレースを記述するパラメータは、培養停止時の OD600 値に相関する**
Parameters describing CW bias time traces of adaptation of chemotaxis of cells of E. coli correlate to OD 600 value at cell culture stop
○田中 裕人[1], 數田 恭章[1], 坪本 梨沙[1,2], 大岩 和弘[1,2], 小嶋 寛明[1]（[1]情報通信研究機構 神戸研究所 未来 ICT 研究所, [2]兵庫県立大学）
Hiroto Tanaka[1], Yasuaki Kazuta[1], Risa Tsubomoto[1,2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[1] ([1]*KARC, NICT*, [2]*University of Hyogo*)

2A1530 **ヒト精子運動性に影響を与える静水圧負荷の閾値**
Hydrostatic pressure threshold for the reduction of human sperm motility
田中 登己[1,2], 仁科 咲織[1], 藤田 彩乃[2], 森松 賢順[2], 浅野 友香[1], ○松浦 宏治[1], 成瀬 恵治[2]([1]岡山理科大学工学部生命医療工学科, [2]岡山大学大学院医歯薬学総合研究科）
Noriki Tanaka[1,2], Saori Nishina[1], Ayano Fujita[2], Masatoshi Morimatsu[2], Yuka Asano[1], **Koji Matsuura**[1], Keiji Naruse[2] ([1]*Department of Biomedical Engineering, Faculty of Engineering, Okayama University of Science*, [2]*Cardiovascular Physiology, Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University*)

2A1542 **カルシウムイオンを介した精子鞭毛波形制御における cAMP の調整効果**
cAMP modulates Ca^{2+}-mediated regulation of sperm flagellar waveform
○柴 小菊[1], 坂野 太一[2], 古田 寿昭[2], 藤原 英史[3], 馬場 昭次[4], 稲葉 一男[1]（[1]筑波大・下田臨海, [2]東邦大・理, [3]ドキュメンタリーチャネル, [4]お茶大・理）
Kogiku Shiba[1], Taichi Sakano[2], Toshiaki Furuta[2], Eiji Fujiwara[3], Shoji A. Baba[4], Kazuo Inaba[1] ([1]*Tsukuba Univ., Shimoda Marine Res. Ctr.*, [2]*Toho Univ., Fac. Sci.*, [3]*Documentary Ch. Co. Ltd.*, [4]*Ochanomizu Univ., Fac. Sci.*)

2A1554 **緑藻クラミドモナスの走光性における鞭毛運動調節**
Regulation of flagellar motion for phototactic turning in *Chlamydomonas*
中島 昌子[1], 井手 隆広[2], 植木 紀子[3], 久堀 徹[1], ○若林 憲一[1]（[1]東工大・化生研, [2]理研 BDR, [3]ニューヨーク市立大学ブルックリン校）
Masako Nakajima[1], Takahiro Ide[2], Noriko Ueki[3], Toru Hisabori[1], **Ken-ichi Wakabayashi**[1] ([1]*CLS, Tokyo Tech*, [2]*RIKEN BDR*, [3]*Brooklyn College, CUNY*)

2A1606 **細菌べん毛繊維の成長端の構造**
Structure of the growing end of the bacterial flagellar filament
木田 葵[1], 牧野 文信[2], 木下 実紀[2], 宮田 知子[2], 加藤 貴之[2], 南野 徹[2], 難波 啓一[2], ○今田 勝巳[1]（[1]阪大・院理, [2]阪大・院生命機能）
Mamoru Kida[1], Fumiaki Makino[2], Miki Kinoshita[2], Tomoko Miyata[2], Takayuki Kato[2], Tohru Minamino[2], Keiichi Namba[2], **Katsumi Imada**[1] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*Grad. Sch. of Front. Biosci., Osaka Univ.*)

2A1618 **FliF 構造から見出された細菌べん毛と III 型ニードル複合体の構造類似性**
Similarity between the bacterial flagellum and the type III injectisome revealed by the X-ray crystal structure of FliF fragment
○竹川 宜宏[1], 佐久間 麻由子[2,3], 小嶋 誠司[2], 本間 道夫[2], 今田 勝巳[1]（[1]阪大・院理・高分子科学, [2]名大・院理・生命理学, [3]名大・RI センター）
Norihiro Takekawa[1], Mayuko Sakuma[2,3], Seiji Kojima[2], Michio Homma[2], Katsumi Imada[1] ([1]*Dept. of Macromol. Sci., Grad. Sch. of Sci., Osaka Univ.*, [2]*Div. of Biol. Sci., Grad. Sch. of Sci., Nagoya Univ.*, [3]*Radioisotope Res. Cent., Nagoya Univ.*)

14:00〜16:06　C 会場（B21）／Room C (B21)
2C 発生分化・行動・化学受容・神経／
Development & Differenciation, Behavior, Chemoreception, Neuroscience

2C1400 **細胞分化への現象論的アプローチ：エピジェティクスによる安定細胞タイプの形成**
Phenomenological approach to cell differentiation: generation of stable cell type by epigenetics
○松下 優貴, 金子 邦彦（東京大学大学院総合文化研究科 広域科学専攻 相関基礎科学系）
Yuki Matsushita, Kunihiko Kaneko (*The University of Tokyo Department of Basic Science*)

2C1412 **ヒト iPS 細胞由来の原腸形成期の中胚葉と内胚葉はランダムに動く**
Random Migration of Induced Pluripotent Stem Cell-Derived Human Gastrulation-Stage Mesoderm and endoderm
山本 悠太[1], 宮崎 翔太[1], 丸山 兼四朗[1], レ ミン[1], 加納 歩[1], 近藤 晶子[2], 藤井 修治[3], ○大沼 清[1]（[1]長岡技科大, [2]藤田保健衛生大, [3]北大）
Yuta Yamamoto[1], Shota Miyazaki[1], Kenshiro Maruyama[1], Minh Le[1], Ayumu Kano[1], Akiko Kondow[2], Shuji Fujii[3], **Kiyoshi Ohnuma**[1] ([1]*Nagaoka Univ Tech*, [2]*Fujita Health Univ*, [3]*Hokkaido Univ*)

2C1424 **肺上皮シートの分岐形態形成における ERK 活性を介したメカノ応答**
ERK activity-mediated mechanoresponse in branching morphogenesis of lung epithelial sheet
○平島 剛志[1], 吉田 琢哉[2], 松田 道行[1,2]（[1]京大・医, [2]京大・生命科学）
Tsuyoshi Hirashima[1], Takuya Yoshida[2], Michiyuki Matsuda[1,2] ([1]*Grad. Sch. Med., Kyoto Univ.*, [2]*Grad. Sch. Biostudies, Kyoto Univ.*)

2C1436 流体力学における「クラミドモナスのモデル種」の重力走性
Gravitaxis of "*Chlamydomonas* model species" in hydrodynamics
○鹿毛 あずさ（豊橋技科大・機械工学系）
Azusa Kage (*Dept. Mech. Eng., Toyohashi Univ. Of Technology*)

2C1448 走化性受容体クラスター形成に対するヒスチジンキナーゼとアダプターの影響
Effects of the histidine kinase and the adaptor protein on chemoreceptor clustering in the bacterial cytoplasmic membrane
山崎 友也[1], 伊藤 那奈[1], 西川 正俊[1], 曽和 義幸[1,2], ○川岸 郁朗[1,2]（[1]法政大・生命, [2]法政大・ナノテクセ）
Tomoya Yamazaki[1], Nana Ito[1], Masatoshi Nishikawa[1], Yoshiyuki Sowa[1,2], **Ikuro Kawagishi**[1,2] ([1]*Dept. Frontier Biosci., Hosei Univ.*, [2]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

2C1500 コレラ菌新規アミノ酸走性応答系の同定
The novel chemotactic transducer Mlp3 of *Vibrio cholerae* mediates serine chemotaxis via a putative periplasmic binding protein
○田島 寛隆[1,2], 川口 徹也[3], 山元 季実子[3,4], 曽和 義幸[1,2,3], 西山 宗一郎[1,2,5], 川岸 郁朗[1,2,3]（[1]法政大・生命, [2]法政大・ナノテクセ, [3]法政大・院工, [4]農環研, [5]新潟薬科大・応用生命）
Hirotaka Tajima[1,2], Tetsuya Kawaguchi[3], Kimiko Yamamoto[3,4], Yoshiyuki Sowa[1,2,3], Soichiro Nishiyama[1,2,5], Ikuro Kawagishi[1,2,3] ([1]*Dept. Front. Biosci., Hosei Univ.*, [2]*Res. Cent. Micro-Nano Tech., Hosei Univ.*, [3]*Grad. Sch. Eng., Hosei Univ.*, [4]*Natl. Inst. Agro-Environ. Sci*, [5]*Fac. Appl. Life Sci., NUPALS*)

休憩（Coffee Break） 15:12–15:18

2C1518 マウス脳スライスの温度イメージング法の開発と虚血性脳浮腫のメカニズムの解明
Imaging temperature of mouse brain slice reveals the mechanism of ischemic brain edema
○岡部 弘基[1], 星 雄高[1], 柴崎 貢志[2], 船津 高志[1], 池谷 裕二[1], 小山 隆太[1]（[1]東大院薬, [2]群大院医）
Kohki Okabe[1], Yutaka Hoshi[1], Koji Shibasaki[2], Takashi Funatsu[1], Yuji Ikegaya[1], Ryuta Koyama[1] ([1]*Dept Pharmac, Univ Tokyo*, [2]*Dept Med, Gumma Univ*)

2C1530 生体神経回路網における連続入力刺激に対する応答パターンの再現性と階層性
The hierarchical feature and reproducibility of electrical response patterns induced by sequential inputs in a living neuronal circuit
○久内 晴加[2], 工藤 卓[1]（[1]関西学院大学 理工学部, [2]関西学院大学 大学院 理工学研究科）
Haruka Hisauchi[2], Suguru N. Kudoh[1] ([1]*Sch. of Sci. & Tech., Kwansei Gakuin Univ.*, [2]*Grad. Sch. of Sci. & Tech., Kwansei Gakuin Univ.*)

2C1542 Voltage-sensitive dye imaging of the interhemispheric neural activity across the anterior cingulate cortex (ACC) via corpus callosum
Pooja Gusain, Makiko Taketoshi, Yoko Tominaga, Takashi Tominaga (*Tokushima Bunri University*)

2C1554 海馬 CA1 でペアドバースト促通（PBF)はフィードバックとフィードフォワードの異なる GABA 作動性制御を使う
The paired burst facilitation (PBF) of the hippocampus employ the distinct feedforward- and feedback- GABAergic controls in the circuit
○冨永 貴志, 冨永 洋子（徳島文理大・神経研）
Takashi Tominaga, Yoko Tominaga (*Inst. Neurosci., Tokushima Bunri Univ.*)

14:00〜16:18 D 会場（A36）／Room D (A36)
2D バイオイメージング II／Bioimaging II

2D1400 Multimodal persistence of antibiotic-stressed Escherichia coli
Miho Fujisawa[1], Miki Umetani[1], Yuichi Wakamoto[1,2,3] ([1]*Graduate School of Arts and Sciences, University of Tokyo*, [2]*Research Center for Complex Systems Biology, University of Tokyo*, [3]*Universal Biology Institute, University of Tokyo*)

2D1412 β1, 3 インテグリンの接着班形成・分解における機能：超長時間蛍光 1 分子追跡法による解明
β1 and 3 integrin function in focal adhesion formation and disintegration: unraveling by super-long single-fluorescent molecule tracking
○角山 貴昭 [1], 笠井 倫士 [2], 鈴木 健一 [3], 藤原 敬宏 [4], 楠見 明弘 [1,4]（[1]沖縄科学技術大学院大学, [2]京都大 ウイルス・再生研, [3]岐阜大 生命の鎖統合研究センター, [4]京都大・物質-細胞統合システム拠点）
Taka A. Tsunoyama[1], Rinshi S. Kasai[2], Kenichi G.N. Suzuki[3], Takahiro K. Fujiwara[4], Akihiro Kusumi[1,4] ([1]*OIST*, [2]*Inst. Frontier Life and Medical Sciences, Kyoto Univ.*, [3]*G-CHAIN, Gifu Univ.*, [4]*Inst. Integrated Cell-Material Sciences (WPI-iCeMS), Kyoto Univ.*)

2D1424 生理的 RNA 顆粒形成過程の細胞内温度測定
Intracellular temperature measurement during RNA granule formation for thermal biology
○時 ベイニ [1], 岡部 弘基 [1,2], 船津 高志 [1]（[1]東大院・薬, [2]さきがけ）
Beini Shi[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*JST, PRESTO*)

2D1436 Genetically encoded photoswitchable indicators towards super-resolution calcium imaging
Kai Lu, Tomoki Matsuda, Tetsuichi Wazawa, Satsuki Fujiwara, Takeharu Nagai (*ISIR, Osaka Univ.*)

2D1448 遺伝子コード可能な HyperCEST MRI 造影剤の開発
Multiplexed HyperCEST detection of genetically-reconstituted gas vesicle nanoparticles in human cancer cells in vitro
○水島 良太 [1,2,3], 井上 加奈子 [4], 永井 里奈 [2], 岩根 敦子 [2], 渡邊 朋信 [2], 木村 敦臣 [3]（[1]東京医科大学ナノ粒子先端医学応用講座, [2]理研 BDR, [3]阪大・院医学系, [4]阪大超高圧電顕センター）
Ryota Mizushima[1,2,3], Kanako Inoue[4], Rina Nagai[2], Atsuko Iwane[2], Tomonobu Watanabe[2], Atsuomi Kimura[3] ([1]*Dept. nanoparticle translational research, Tokyo Medical Univ.*, [2]*BDR, RIKEN*, [3]*Grad. Sch. Med. , Osaka Univ.*, [4]*UHVEM, Osaka Univ.*)

2D1500 回折限界内に位置するミオシン複数分子の動態計測
Measuring dynamics of individual skeletal myosin molecules located within diffraction limit space
○茅 元司, 蘆田 祐人, 上田 正仁, 樋口 秀男（東京大学 大学院理学系研究科 物理学専攻）
Motoshi Kaya, Yuto Ashida, Masahito Ueda, Hideo Higuchi (*Graduate School of Science, The University of Tokyo*)

休憩（Coffee Break） 15:12–15:18

2D1518 Microtubule defects, self-healing, and tubulin bond energies with high-speed AFM
Christian Ganser, Takayuki Uchihashi (*Nagoya University, Department of Physics*)

2D1530 光ピンセット・探針走査型高速 AFM 複合装置を用いた外力印加中の一分子ライブイメージング
Live Imaging of Single-Molecules under External Force using Tip-Scan High-Speed AFM Combined with Optical Tweezers
○今村 元紀 [1], 梅田 健一 [1], 山中 信之介 [2], 古寺 哲幸 [1], 安藤 敏夫 [1]（[1]金沢大・WPI-NanoLSI, [2]金沢大・院数物）
Motonori Imamura[1], Kenichi Umeda[1], Shin'nosuke Yamanaka[2], Noriyuki Kodera[1], Toshio Ando[1] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Grad. Sch. Math. & Phys., Kanazawa Univ.*)

2D1542 高速イオン電導顕微鏡を用いた脂質膜の表面電荷密度のナノ解像マッピング手法の開発
Development of nanoscale mapping of surface charge density of lipid membranes by high-speed ion conductance microscopy
○開発 秀星 [1], 執行 航希 [2], 安藤 敏夫 [2], 渡辺 信嗣 [2]（[1]金沢大・院数物, [2]金沢大・WPI-NanoLSI）
Shusei Kaihatsu[1], Kazuki Shigyo[2], Toshio Ando[2], Shinji Watanabe[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

2D1554 高速イオン伝導顕微鏡による生細胞表面の観察
Observation of Morphological Changes in Nanostructures on Live Cell Surfaces by High Speed Ion Conductance Microscopy
○北澤 怜子 [1], 芳坂 綾子 [2], 中山 隆宏 [2], 紺野 宏記 [2], 渡辺 信嗣 [2]（[1]金沢大・院数物, [2]金沢大・WPI-NanoLSI）
Satoko Kitazawa[1], Ayako Housaka[2], Takahiro Watanabe-Nakayama[2], Hiroki Konno[2], Shinji Watanabe[2] ([1]*Grad.Sch.Math.& Phys.,Kanazawa Univ.*, [2]*WPI-NanoLSI,Kanazawa Univ.*)

2D1606 平行光走査型 4 次元顕微鏡法
Parallel Light Scanning 4-Dimensional Microscopy
○永山 國昭（リスコ、 永山顕微鏡研）
Kuniaki Nagayama (*Nagayama Microsc. Lab., LisCo*)

14:00〜16:06　E 会場（A37）／Room E (A37)
2E 筋肉・モーター／Muscle/motor

2E1400 1 分子偏光 FRET 法により検出した F_1-ATPase α-β 間の遂次的な構造変化
Single-molecule polarized FRET measurements revealed sequential conformational changes between α and β of F_1-ATPase
○横田 龍一 [1], 須河 光弘 [2], 矢島 潤一郎 [2], 政池 知子 [1,3]（[1]東京理科大院・応用生物科学専攻, [2]東京大・総合文化研究科, [3]東京理科大・イメージングフロンティアセンター）
Ryuichi Yokota[1], Mitsuhiro Sugawa[2], Junichiro Yajima[2], Tomoko Masaike[1,3] ([1]*Dept. Appl. Biol. Sci., Tokyo Univ. Sci.*, [2]*Grad. Sch. Arts and Sci.*, [3]*Imaging Frontier Center, Tokyo Univ. of Sci.*)

2E1412 X 線結晶構造解析により明らかになった回転分子モーター F_1-ATPase の力発生の仕組み
Physical power generation mechanism of rotary molecular motor F_1-ATPase by X-ray Crystallographic Study
○鈴木 俊治 [1,2,3], 山下 栄樹 [4], 馬場 清喜 [5], 平田 邦生 [6], 飯田 直也 [7], 遠藤 斗志也 [3], 熊坂 崇 [5], 久堀 徹 [2], 吉田 賢右 [3], 野地 博行 [1]（[1]東大院・工・応化, [2]東工大・化学生命研, [3]京産大・総合生命, [4]阪大・蛋白研, [5]高輝度光科学研究センター(JASRI), [6]理研・SPring8 センター, [7]早大・物理）
Toshiharu Suzuki[1,2,3], Eiki Yamashita[4], Seiki Baba[5], Kunio Hirata[6], Naoya Iida[7], Toshiya Endo[3], Takashi Kumasaka[5], Toru Hisabori[2], Masasuke Yoshida[3], Hiroyuki Noji[1] ([1]*Dept of Applied Chem, Graduate School of Eng, The Univ of Tokyo*, [2]*CLS, Inst of Innovative Res, Tokyo Tech*, [3]*Dept of Mol Bioscience, Kyoto-Sangyo Univ*, [4]*Inst of Protein Res, Osaka Univ*, [5]*Japan Synchrotron Radiation Research Inst (JASRI)*, [6]*SPring8-center, Riken*, [7]*Dept of Physics, Waseda Univ*)

2E1424 結晶構造との対応付けを目指したミトコンドリア F_1-ATPase の回転解析
Single-molecule analysis of bovine mitochondrial F_1-ATPase for direct assignment of crystal structures and rotational pausing states
○小林 稜平, 上野 博史, 鈴木 俊治, 原 舞雪, 野地 博行（東大・院工・応化）
Ryohei Kobayashi, Hiroshi Ueno, Toshiharu Suzuki, Mayu Hara, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

2E1436 Thermodynamic Efficiency of F_1-ATPase at High Temperature
Tomoaki Okaniwa, Yohei Nakayama, Eiro Muneyuki (*Dept. Phys., Faculty of Science and Engineering, Chuo Univ.*)

2E1448 Chemomechanical Coupling of the Paracoccus denitrificans F1-ATPase
Mariel Zarco - Zavala[1], Duncan G.G McMillan[2], Suzuki Toshiharu[1], Hiroshi Ueno[1], Rikiya Watanabe[1], Francisco Mendoza - Hoffmann[3], Jose J. Garcia-Trejo[3], Hiroyuki Noji[1] ([1]*Noji Laboratory, Department of Applied Chemistry, School of Engineering, The University of Tokyo*, [2]*Department of Biotechnology, Delft University of Technology, Delft 2629 HZ, The Netherlands*, [3]*Department of Biology, Chemistry Faculty, National Autonomous University of Mexico, Mexico city 04510, Mexico*)

2E1500 Na+駆動型べん毛モーター PomA/PomB の Thr 残基のイオン透過における役割: MD シミュレーション結果
Role of Threonine residues in ion permeation for the Na+ driven flagellar motor PomA/PomB: insights from MD simulations
尾上 靖宏 [1], 岩城 雅代 [2], ○信夫 愛 [3], 西原 泰孝 [4], 岩月 哲人 [1], 寺島 浩行 [1], 北尾 彰朗 [3], 神取 秀樹 [2], 本間 道夫 [1]（[1]名大, [2]名工大, [3]東工大, [4]東大）
Yasushiro Onoue[1], Masayo Iwaki[2], **Ai Shinobu**[3], Yasutaka Nishihara[4], Hiroto Iwatsuki[1], Hiroyuki Terashima[1], Akio Kitao[3], Hideki Kandori[2], Michio Homma[1] ([1]*Nagoya Univ.*, [2]*Nitech*, [3]*Tokyo Tech*, [4]*UTokyo*)

休憩（Coffee Break） 15:12–15:18

2E1518 光ピンセットを用いた細菌べん毛モーター回転計測系の確立
Measuring the bacterial flagellar rotation with optical trap nanometry
○飯島 悠太 [1], 笠井 大司 [2,3], 長谷川 爽 [1], 曽和 義幸 [1,2]（[1]法政大・院理工・生命機能, [2]法政大・ナノテク, [3]立教大・理）
Yuta Iijima[1], Taishi Kasai[2,3], So Hasegawa[1], Yoshiyuki Sowa[1,2] ([1]*Dept. Frontier Bio-Sci., Hosei Univ.*, [2]*Research Center for Micro-Nano Tech. Hosei Univ.*, [3]*Rikkyo Univ.*)

2E1530 Visualization of the motor switching and subcellular localization of chemotaxis proteins in a halophilic archaeon, *Haloferax volcanii*
Yoshiaki Kinosita, Nagisa Mikami, Zhengqun Li, Tessa Quax, Sonja-Verena Albers (*Freiburg University*)

2E1542 トラジェクトリから多エネルギー面を乗り移る拡散モデルの推定：生体分子モーターへの応用
Estimating a diffusion model hopping on multiple energy surfaces from trajectories: Toward application to biomolecular motors
○岡崎 圭一, 中村 彰彦, 飯野 亮太（分子科学研究所）
Kei-ichi Okazaki, Akihiko Nakamura, Ryota Iino (*Inst. for Mol. Sci.*)

2E1554 Characterization and engineering of chitin-hydrolyzing Brownian linear motor from marine bacteria
Akihiko Nakamura[1,2], Veda Boorla[1], Hiroki Watanabe[3], Takayuki Uchihashi[3], Ryota Iino[1,2] ([1]*IMS*, [2]*SOKENDAI*, [3]*Nagoya Univ.*)

14:00〜16:06 F 会場（B32）／Room F (B32)
2F 光受容体・光生物／Photoreceptors, Photobiology

2F1400 Molecular simulation on light-activation mechanism of LOV photoreceptor protein
Masahiko Taguchi, Cheng Cheng, Chika Higashimura, Shigehiko Hayashi (*Kyoto Univ.*)

2F1412 光遺伝学ツールとして用いられる植物クリプトクロム２の分光研究
Spectroscopic analysis of AtCRY2 used in optogenetics
○縣 和哉, 山田 大智, 神取 秀樹（名工大院工）
Kazuya Agata, Daichi Yamada, Hideki Kandori (*Nagoya Inst. Tech., Dept. Life Sci. Appl. Chem.*)

2F1424 プロトンによって調節されるシアノバクテリオクロム型光受容体の光感知機構
Proton-mediated spectral tuning in a cyanobacteriochrome photoreceptor family
○広瀬 侑, 佐藤 哲平, 米川 千夏, 浴 俊彦（豊橋技術科学大学 大学院工学研究科 環境・生命工学系）
Yuu Hirose, Teppei Sato, Chinatsu Yonekawa, Toshihiko Eki (*Toyohashi Univ. of Tech, Dep. Env. and Life Sci.*)

2F1436 QCM による bZIP 型転写因子の basic 領域に存在する Asn 残基の解析
The role of Asn residue conserved among the basic region of bZIP transcription factors studied by QCM
館山 佐夢, 小林 樹, ○久冨 修（阪大・院理）
Samu Tateyama, Itsuki Kobayashi, **Osamu Hisatomi** (*Grad. Sch. f Sci., Osaka Univ.*)

2F1448 光回復酵素/クリプトクロムスーパーファミリーにおける FAD 酸化還元状態の FTIR 研究
FTIR study of FAD redox state in photolyase/cryptochrome superfamily
○酒井 結衣 [1], 山田 大智 [1], 岩田 達也 [2], 神取 秀樹 [1]（[1]名工大, [2]東邦大）
Yui Sakai[1], Daichi Yamada[1], Tatsuya Iwata[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Toho Univ.*)

2F1500 Class II CPD 光回復酵素の電子移動反応の理論研究
Theoretical Study on Electron Transfer Reactions in Class II CPD Photolyases
○鬼頭（西岡） 宏任 [1,2], 原田 隆平 [2], 佐藤 竜馬 [3], 重田 育照 [2]（[1]JST さきがけ, [2]筑波大計算セ, [3]理研 BDR）
Hirotaka Kitoh-Nishioka[1,2], Ryuhei Harada[2], Ryuma Sato[3], Yasuteru Shigeta[2] ([1]*JST-PRESTO*, [2]*CCS, Univ. of Tsukuba*, [3]*RIKEN BDR*)

休憩（Coffee Break） 15:12–15:18

2F1518 二光子顕微鏡によるマウス単離網膜での一細胞キナーゼ活性測定
Single-cell kinase activity measurements of the mouse retina by two-photon ex vivo imaging
○佐藤 慎哉 [1], 松田 道行 [1,2]（[1]京都大・院生命科学, [2]京都大・医学研究科）
Shinya Sato[1], Michiyuki Matsuda[1,2] ([1]*Grad. Sch. Biostudies, Kyoto Univ.*, [2]*Grad. Sch. Med., Kyoto Univ.*)

2F1530 イエロープロテインの 115 ループの構造揺らぎと光反応サイクル
Conformational Fluctuation of 115 Loop during the Photocycle of Photoactive Yellow Protein
○今元 泰 [1], 沈 宜中 [1], 古谷 祐詞 [2]（[1]京大・院理・生物物理, [2]分子研・錯体生命）
Yasushi Imamoto[1], Yi-Chung Shen[1], Yuji Furutani[2] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Inst. Mol. Sci.*)

2F1542 アゾベンゼン架橋タンパク質の光異性化反応による変性温度変化
Photoisomerization of azobenzene-crosslinked protein switches its denaturation temperature
○長島 敏雄, 植田 啓介, 山崎 俊夫（理研 RSC）
Tosho Nagashima, Keisuke Ueda, Toshio Yamazaki (*RIKEN RSC*)

2F1554 脂肪細胞のトリアシルグリセロールにおけるレーザーエネルギーの選択的吸収
Selective delivery of laser energy to ester bonds of triacylglycerol in 3T3-L1 adipocyte
○正木 紀隆, 岡崎 茂俊（浜松医科大学 医学分光応用寄附研究室）
Noritaka Masaki, Shigetoshi Okazaki (*Department of Medical Spectroscopy*)

14:00〜16:30 G 会場（B33）／Room G (B33)
2G 生体膜・人工膜／Biological & Artificial membrane

2G1400 細胞透過ペプチド・トランスポータン 10 のベシクル内腔への侵入の連続的な検出法の開発
Continuous Detection of Entry of Cell-Penetrating Peptide (CPP) Transportan 10 (TP10) into Single Vesicle Lumens
○モゴール エムディ ミザヌル [1], イスラム エムディ ザヒドゥル [1], シャーミン サブリナ [1], レバツニー ビクター [1,2], モニルザマン エムディー [1], 山崎 昌一 [1,3,4]（[1]静大・創造院, [2]ロシア科学アカデミー, [3]静大・電研, [4]静大・院理）
Md. Mizanur Moghal[1], Md. Zahidul Islam[1], Sabrina Sharmin[1], Victor Levadnyy[1,2], Md. Moniruzzaman[1], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Rus. Acad. Sci.*, [3]*Res. Inst. Elec., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

2G1412 両親媒性ポリマーによる脂質膜パッキングの認識
Recognition of lipid packing in membrane by amphiphilic polymers
○安原 主馬, 山中 諒, 菊池 純一（国立大学法人 奈良先端科学技術大学院大学 物質創成科学領域）
Kazuma Yasuhara, Ryo Yamanaka, Jun-ichi Kikuchi (*Division of Materials Science, Nara Institute of Science and Tecnology*)

2G1424 バナナ状たんぱく質の集合による膜チューブ形成：キラリティの効果
Membrane tubulation induced by assembly of chiral banana-shaped protein rods
○野口 博司（東大物性研）
Hiroshi Noguchi (*ISSP, Univ. Tokyo*)

2G1436 Surface Enhanced IR study of insertion and folding process of membrane protein on the solid supported lipid bilayer

Kenichi Ataka[1], Joachim Heberle[1], Ramona Schlesinger[1], Nicola Harris[2], Eamonn Reading[2], Paula Booth[2] ([1]*Freie Universitaet Berlin, Fachbereich Physik*, [2]*King's College London, Department of Chemistry*)

2G1448 Molecular dynamics simulations of domain formation in mixed lipid bilayers

Sangjae Seo, Wataru Shinoda (*Grad. Sch. Eng., Nagoya Univ.*)

2G1500 **全原子分子動力学シミュレーションによる静止膜電位に関する理論的研究**

Theoretical study on a resting membrane potential by using all-atom molecular dynamics simulations

○川口 一朋, 長尾 秀実（金沢大・理工）

Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

休憩（Coffee Break） 15:12–15:18

2G1518 **脂質膜環境の変化は細菌機械受容チャネル MscL のゲーティングにどのような影響を与えるか？**

How can the change in membrane environment affect Mechano-Gating of the Bacterial Mechanosensitive Channel MscL?

○澤田 康之 [1], 橋本 賢一 [2], 川崎 寿 [2], 曽我部 正博 [3]（[1]名経大・管理栄養, [2]東京電機大・工, [3]名大院・医・メカノバイオロジーラボ）

Yasuyuki Sawada[1], Ken'ichi Hashimoto[2], Hisashi Kawasaki[2], Masahiro Sokabe[3] ([1]*Dept. Nutrition Nagoya Univ. Economics Fac. Human Life Sci.*, [2]*Tokyo Denki Univ. Fac. Eng.*, [3]*Mechanobiology Lab. Nagoya Univ. Grad. Sch. Med.*)

2G1530 “Force-From-Lipids” (FFL) gating of mechanosensitive channels of Corynebacterium glutamicum

Yoshitaka Nakayama[1], Kosuke Komazawa[2], Navid Bavi[1,3], Ken-ichi Hashimoto[2], Hisashi Kawasaki[2], Boris Martinac[1,3] ([1]*Victor Chang Cardiac Research Institute*, [2]*Tokyo Denki University*, [3]*University of New South Wales*)

2G1542 **四量体型ナトリウムチャネルにみられる透過イオンや阻害剤との非対称な相互作用**

Asymmetric interaction of permeating cation and local anesthetic with homo-tetrameric sodium channel

○入江 克雅 [1,2], 芳賀 ゆかり [2], 中村 駿 [1], 藤吉 好則 [1,3]（[1]名大 CeSPI, [2]名大 院創薬, [3]（株）CeSPIA）

Katsumasa Irie[1,2], Yukari Haga[2], Shun Nakamura[1], Yoshinori Fujiyoshi[1,3] ([1]*CeSPI, Nagoya univ*, [2]*Grad. Pharm. Med. Sci., Nagoya univ.*, [3]*CeSPIA Co., Ltd*)

2G1554 **Na^+イオンは KcsA K^+チャネルを遅いが透過する**

Na^+ ions permeate through the KcsA K^+c channel slowly

○炭竈 享司 [1], 三田 建一郎 [2], 老木 成稔 [2]（[1]金沢大学新学術創成研究機構ナノ生命科学研究所, [2]福井大学医学部）

Takashi Sumikama[1], Kenichiro Mita[2], Shigetoshi Oiki[2] ([1]*Kanazawa University, WPI Nano Life Science Institute*, [2]*University of Fukui, Faculty of Medical Sciences*)

2G1606 Functional roles of Mg^{2+} binding sites in ion-dependent gating of a Mg^{2+} channel, MgtE, revealed by solution NMR

Tatsuro Maruyama[1], Shunsuke Imai[1], Tsukasa Kusakizako[2], Motoyuki Hattori[3], Ryuichiro Ishitani[2], Osamu Nureki[2], Koichi Ito[4], Andres D. Maturana[5], Ichio Shimada[1], **Masanori Osawa**[1,6] ([1]*Grad. Sch. Pharm. Sci., The Univ. of Tokyo*, [2]*Grad. Sch. Sci., The Univ. of Tokyo*, [3]*Sch. of Life Sci., Fudan Univ.*, [4]*Grad. Sch. Frontier Sci., The Univ. of Tokyo*, [5]*Grad. Sch. Bioagricultural Sci.,Navoya Univ.*, [6]*Keio Univ. Fac. of Pharmacy*.)

2G1618 膜ータンパク間の協同性による上皮成長因子受容体の膜近傍ドメイン二量体形成機構
Membrane-protein interplay in the dimerization of juxtamembrane domains of epidermal growth factor receptor
○前田 亮[1], 佐藤 毅[2], 佐甲 靖志[1]（[1]理研・佐甲細胞情報, [2]京都薬科大学）
Ryo Maeda[1], Takeshi Sato[2], Yasushi Sako[1] ([1]*Cellular Informatics Lab., RIKEN*, [2]*Kyoto Pharmaceutical Univ.*)

14:00〜16:18　H 会場（A41）／Room H (A41)
2H ロドプシン／Rhodopsin

2H1400 Distinctively small distortion of retinal chromophore in K intermediate of proteorhodopsin observed by low-temperature Raman spectroscopy
Tomtotsumi Fujisawa[1], Jun Tamogami[2], Takashi Kikukawa[3], Masashi Unno[1] ([1]*Fac. Sci. Eng., Saga Univ.*, [2]*College Pharm. Sci., Matsuyama Univ.*, [3]*Fac. Adv. Life Sci., Hokkaido Univ.*)

2H1412 Structural changes in retinal-binding site of the *Krokinobacter* rhodopsin 2 mutant H30A
Izuru Kawamura[1], Arisu Shigeta[1], Shota Ito[2], Rina Kaneko[1], Sahoko Tomida[2], Keiichi Inoue[2,3,4], Hideki Kandori[2] ([1]*Yokohama Natl. Univ.*, [2]*Nagoya Inst. Tech.*, [3]*Univ. Tokyo*, [4]*JST PRESTO*)

2H1424 赤外分光法を用いた酵素型ロドプシン Rh-PDE の反応機構解析
Reaction mechanism of enzymatic rhodopsin Rh-PDE analyzed by infrared spectroscopy
○渡 雅仁[1], 生田 達也[2], 山田 大智[1], 志甫谷 渉[2], 吉田 一帆[1], 角田 聡[1,3], 濡木 理[2], 神取 秀樹[1]（[1]名工大・院工, [2]東大・院理・生物化学, [3]JST さきがけ）
Masahito Watari[1], Tatsuya Ikuta[2], Daichi Yamada[1], Wataru Shihoya[2], Kazuho Yoshida[1], Satoshi Tsunoda[1,3], Osamu Nureki[2], Hideki Kandori[1] ([1]*Life Sci. Appl. Chem., Nagoya Inst. Tech.*, [2]*Grad. Sch. Sci., Univ. Tokyo.*, [3]*PREST, JST*)

2H1436 新たに発見された TAT モチーフを持つ微生物型ロドプシンの分光研究
Spectroscopic study of newly discovered microbial rhodopsin with TAT motif
○片岡 千尋[1], 井上 圭一[1,2,3], 片山 耕大[1], Beja Oded[4], 神取 秀樹[1]（[1]名工大院工, [2]東大物性研, [3]JST さきがけ, [4]イスラエル工科大学）
Chihiro Kataoka[1], Keiichi Inoue[1,2,3], Kouta Katayama[1], Oded Beja[4], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Tokyo Univ.*, [3]*JST PRESTO*, [4]*Technion - Israel Inst. Tech.*)

2H1448 クリプト藻由来カチオンチャネルロドプシン Gt_CCR4 のパッチクランプ法によるイオン輸送特性評価
Electrophysiological characterization of cation channelrhodopsin Gt_CCR4 from cryptophyte algae
○重村 竣太[1], 細島 頌子[1], 角田 聡[1,2], 神取 秀樹[1]（[1]名工大 院工, [2]JST さきがけ）
Shunta Shigemura[1], Shouko Hososhima[1], Satoshi Tsunoda[1,2], Hideki Kandori[1] ([1]*Grad. Sch. Eng., NIT*, [2]*JST PRESTO*)

2H1500 Substrate anion concentration significantly affects the fast channel function of *Proteomonas sulcata* anion channelrhodopsin-1
Takashi Tsukamoto[1,2,3,4], Chihiro Kikuchi[3,4], Hiromu Suzuki[3], Tomoyasu Aizawa[1,2,3,4], Takashi Kikukawa[1,2,3,4], Makoto Demura[1,2,3,4] ([1]*Fac. Adv. Life Sci., Hokkaido Univ.*, [2]*GSS, GI-CoRE, Hokkaido Univ.*, [3]*Sch. Sci., Hokkaido Univ.*, [4]*Grad. Sch. Life Sci., Hokkaido Univ.*)

休憩（Coffee Break）　15:12–15:18

2H1518 アニオンチャネルロドプシン 2(ACR2)の機能及び分光特性に与える R129 の影響
Impact of R129 on the functional and spectroscopic properties of anion channelrhodopsin-2 (ACR2)
○三好 菜月 [1], 土井 聡子 [1], 小島 慧一 [1], 渡邊 宙志 [2], 石北 央 [2], 須藤 雄気 [1] ([1]岡大・院・医歯薬（薬）, [2]東大・院・工学)
Natsuki Miyoshi[1], Satoko Doi[1], Keiichi Kojima[1], Hiroshi Watanabe[2], Hiroshi Ishikita[2], Yuki Sudo[1] ([1]*Grad. Sch. Of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. Of Eng., The Univ. Of Tokyo*)

2H1530 アニオンチャネルロドプシンによる線虫の超高感度光神経抑制
The hypersensitive optical neural silencing by anion channelrhodopsins (ACRs) in the nematode *C. elegans*
○山梨 太郎 [1], 真木 美紗代 [1], 小島 慧一 [1], 渋川 敦史 [1], 高木 新 [2], 須藤 雄気 [1] ([1]岡山大・院・医歯薬(薬), [2]名大・院・理)
Taro Yamanashi[1], Misayo Maki[1], Keiichi Kojima[1], Atsushi Shibukawa[1], Shin Takagi[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Sci., Nagoya Univ.*)

2H1542 ナトリウムポンプロドプシンの初期中間体における発色団の構造変化に対して極低温ラマン分光法を用いた研究
Chromophore structural change in the primary photointermediate of sodium-pump rhodopsin studied by low-temperature Raman spectroscopy
○中溝 祐志 [1], 菊川 峰志 [2], 藤澤 知績 [1], 海野 雅司 [1] ([1]佐大 理工, [2]北大・先端生命科学研究院)
Yushi Nakamizo[1], Takashi Kikukawa[2], Tomotsumi Fujisawa[1], Masashi Unno[1] ([1]*Fac. Sci. Eng., Saga Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

2H1554 Photochemical analysis of sodium ion-pumping rhodopsin from Indibacter alkaliphilus
Tomoya Kato[1], Keisuke Murabe[1], Takashi Kikukawa[1,2], Takashi Tsukamoto[1,2], Tomoyasu Aizawa[1,2], Makoto Demura[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*GI-CoRE, Hokkaido Univ.*)

2H1606 ビニレン基挿入レチナール誘導体による光開閉型プロトンチャネルの創成
Production of a Light-gated Proton Channel by Replacing the Retinal Chromophore with Its Synthetic Vinylene Derivative
○金子 明正 [1], 高山 理穂 [1], 沖津 貴志 [2], 角田 聡 [3,4], 下野 和実 [5,6], 水野 操 [7], 小島 慧一 [1], 塚本 卓 [1], 神取 秀樹 [3], 水谷 泰久 [7], 和田 昭盛 [2], 須藤 雄気 [1] ([1]岡山大学, [2]神戸薬科大学, [3]名古屋工業大学, [4]JST さきがけ, [5]東邦大学, [6]崇城大学, [7]大阪大学)
Akimasa Kaneko[1], Riho Takayama[1], Takashi Okitsu[2], Satoshi P. Tsunoda[3,4], Kazumi Shimono[5,6], Misao Mizuno[7], Keiichi Kojima[1], Takashi Tsukamoto[1], Hideki Kandori[3], Yasuhisa Mizutani[7], Akimori Wada[2], Yuki Sudo[1] ([1]*Okayama Univ.*, [2]*Kobe Pharm. Univ.*, [3]*Nagoya Inst. Tech.*, [4]*JST PRESTO*, [5]*Toho Univ.*, [6]*Sojo Univ.*, [7]*Osaka Univ.*)

14:00〜16:18　J 会場（D12）／Room J (D12)
2J 蛋白質：構造Ⅳ、構造機能相関Ⅳ／Proteins: Structure IV, Structure-function relationship IV

2J1400 Structural and dynamical insights into functional differences in mammalian cryptochromes
Ashutosh Srivastava[1], Christin Rakers[2], Tsuyoshi Hirota[1], Florence Tama[1,3,4] ([1]*Inst. of Trans. Bio-Mol., Nagoya Univ.*, [2]*Grad. Sch. Pharm. Sci., Kyoto Univ.*, [3]*Dept. of Phys., Sch. of Sci., Nagoya Univ.*, [4]*Riken Center for Comp. Sci.*)

2J1412 酸素センサータンパク質の情報伝達機構のコンピューターによる研究
Computational study on the signal transduction mechanism of oxygen sensor protein
太田 匡隆 [1], ○倭 剛久 [1,2] ([1]名大院理, [2]ストラスブール大, IGBMC)
Kunitaka Ota[1], **Takahisa Yamato**[1,2] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*IGBMC, Univ. Strasbourg*)

2J1424 **アミロイドペプチド高次複合体形成に関する高次元自由エネルギー地形の分子動力学的解析**
Molecular dynamics study on high-dimensional free-energy landscape of amyloid peptide higher-order complexes
○笠原 浩太 [1], 肥後 順一 [2], 速水 智教 [3,4], 髙橋 卓也 [1]（[1]立命館大・生命, [2]兵庫県立大・院・シミュレーション, [3]阪大・蛋白研, [4]阪大・院・生命機能）
Kota Kasahara[1], Junichi Higo[2], Tomonori Hayami[3,4], Takuya Takahashi[1] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Sim. Studies, Univ. Hyogo*, [3]*IPR, Osaka Univ.*, [4]*Grad. Sch. Fro. Bio., Osaka Univ.*)

2J1436 **分子動力学シミュレーションを用いたモジュール型 CRISPR/CAS システムの核酸切断ダイナミクス**
Dynamics of the cleavage of DNA/RNA in module type CRISPR/CAS system by using molecular dynamics
○宮下 尚之, 大橋 燎, 竹内 レイワ, 竹友 唯（近畿大学 生物理工学部）
Naoyuki Miyashita, Ryo Ohashi, Reiwat Takeuchi, Yui Taketomo (*BOST KINDAI Univ.*)

2J1448 ColDock: Concentrated ligand Docking method for an efficient protein-ligand complex structure prediction using all-atom MD
Kazuhiro Takemura, Akio Kitao (*Sch. Life Sci. Tech., Tokyo Tech.*)

2J1500 Extensive molecular dynamics sampling characterizes ligand binding pathway to Src kinase
Suyong Re[1], Hiraku Oshima[1], Motoshi Kamiya[2], Yuji Sugita[1] ([1]*RIKEN BDR*, [2]*RIKEN R-CCS*)

休憩（Coffee Break） 15:12–15:18

2J1518 **自由エネルギー計算による hERG イオンチャネルと薬剤分子の結合親和性予測**
Prediction of hERG-drug binding affinities by free energy calculation
○根上 樹 [1], 寺田 透 [1,2]（[1]東大・院農, [2]東大・院情報学環）
Tatsuki Negami[1], Tohru Terada[1,2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

2J1530 **分子動力学シミュレーションによる単一ドメイン抗体に対する安定性の評価**
Estimation of Single Domain Antibody Stability by MD Simulations
○ベッカー ゲルトヤン [1], マ ベンソン [2], 神谷 成敏 [3]（[1]阪大・蛋白研, [2]ジョージア工科大学, [3]兵県大・シミュレーション）
Gert-Jan Bekker[1], Benson Ma[2], Narutoshi Kamiya[3] ([1]*IPR, Osaka Univ.*, [2]*Georgia Tech.*, [3]*Grad. Sch. Sim., Univ. Hyogo*)

2J1542 **Go モデルを用いた GA・GB ドメイン関連タンパク質のフォールディングシミュレーション**
Folding simulations of GA / GB domain related proteins based on coarse-grained go-model
○浜上 翔矢, 菊地 武司（立命館大学 生命科学部 生命情報学科）
Shoya Hamaue, Takeshi Kikuchi (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

2J1554 **蛋白質のフォールディングシミュレーションに関する緩和モード解析**
Analysis of a protein folding simulation by using relaxation mode analysis
○光武 亜代理 [1], 高野 宏 [2]（[1]明治大学理工学部物理学科, [2]慶應義塾大学理工学部物理学科）
Ayori Mitsutake[1], Hiroshi Takano[2] ([1]*Dept. of Physics, Meiji Univ.*, [2]*Dept. of Physics, Keio Univ.*)

2J1606 **中サイズの酵素の立体構造上で４つのイントロン位置が形成する平面**
The planes formed with the 4-intron-positions in an enzyme of medium size
○野坂 通子, ボンサクシッド ポーンサイ, 力武 柾人（佐世保工業高等専門学校物質工学科）
Michiko Nosaka, Vongsaksid Phonexay, Masato Rikitake (*National Institute of Technology, Sasebo College*)

14:00〜15:54　K 会場（E11）／Room K (E11)
2K 蛋白質：構造機能相関Ⅴ、物性Ⅴ、計測・解析の方法論Ⅱ／
Proteins: Structure-function relationship V, Property V, Measurement & Analysis I, Engineering II

2K1400 Destabilizing effects of residues in the hydrophobic core of three helix-bundle peptide
Ikuko Iizumi[1], Takahiro Maruno[2], Toshiki Tanaka[3], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*Grad. Sch. Eng., Osaka Univ.*, [3]*Nagoya Inst. Technol.*)

2K1412 Structure elements are building blocks of protein tertiary structure responsible for protein stability
Yasumichi Takase, Yugo Hayashi, Yoichi Yamazaki, Hironari Kamikubo (*Div. Mat. Sci., NAIST*)

2K1424 The reaction mechanism of RSC-mediated nucleosome remodeling
Hsiu-Fang Fan, Kuan-Wei Hsu, Sih-Yao Chow, Bo-Yu Su (*National Yang-Ming University*)

2K1448 ファージ宿主認識蛋白質の構造と機能
Structure and function of phage receptor binding protein
○金丸 周司（東工大・生命）
Shuji Kanamaru (*Dep. of Life Science & Tech., Tokyo Inst. of Tech.*)

2K1500 SecM 翻訳アレスト安定化機構の解析
Analysis of the stabilization mechanism of SecM-mediated translation arrest
○牟田 幹悠, 飯塚 怜, 船津 高志（東京大学大学院薬学系研究科 生体分析化学教室）
Mikihisa Muta, Ryo Iizuka, Takashi Funatsu (*Laboratory of Bio-Analytical Chemistry Graduate School of Pharmaceutical Sciences The University of Tokyo*)

休憩（Coffee Break）　15:12–15:18

2K1518 鶏卵白リゾチームに対する一本鎖抗体の作製と抗原認識機構の解明
Generation of single-chain Fv antibody against hen egg lysozyme and analysis of its antigen recognition mechanism
○山岡 敬典 [1], 鎌足 雄司 [2], 東 隆親 [3], 織田 昌幸 [1]（[1]京府大・院生命環境科学, [2]岐阜大・生命科学総合研究支援センター, [3]抗体工学研究センター）
Takanori Yamaoka[1], Yuji Kamatari O[2], Takachika Azuma[3], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*Life Sci. Res. Center, Gifu University.*, [3]*Antibody Eng. Res. Center.*)

2K1530 不凍タンパク質は低温環境下における線虫の細胞を保護し、生存率を上昇させる
The ice-binding proteins protect the cells and contribute to increase the survival rate in Caenorhabditis elegans under cold environments
○倉持 昌弘 [1,2,3], 高梨 千晶 [1,3], 山内 彩加林 [4], 津田 栄 [4], 戸井 基道 [2], 三尾 和弘 [3], 佐々木 裕次 [1,3]（[1]東京大・院新領域, [2]産総研・バイオメディカル, [3]産総研・東大オペランド OIL, [4]産総研・生物プロセス）
Masahiro Kuramochi[1,2,3], Chiaki Takanashi[1,3], Akari Yamauchi[4], Sakae Tsuda[4], Motomichi Doi[2], Kazuhiro Mio[3], Yuji Sasaki[1,3] ([1]*Grad. Sch. Fron. Sci., Univ. of Tokyo*, [2]*Biomedical R.I., AIST*, [3]*AIST-UTokyo OPERANDO OIL*, [4]*Bioproduction R.I., AIST*)

2K1542 哺乳類概日時計における温度補償されたリン酸化反応の再構成
Reconstitution of Temperature-compensated Phosphorylation in the Circadian Clock
○篠原 雄太 [1], 小山 洋平 [1], 上田 泰己 [1,2]（[1]理化学研究所 生命機能科学研究センター 合成生物学研究チーム, [2]東京大学 医学系研究科）
Yuta Shinohara[1], Yohei Koyama[1], Hiroki Ueda[1,2] ([1]*Center for Biosystems Dynamics Research, RIKEN*, [2]*Graduate School of Medicine, University of Tokyo*)

2L1400 溶液条件の違いから EGFR C-tail 天然変性ドメインの構造情報を得る
Structural information of intrinsically disordered C-terminal domain of the EGFR revealed by changing solution condition
岡本 憲二, ○佐甲 靖志（理研）
Kenji Okamoto, **Yasushi Sako** (*RIKEN*)

2L1412 インスリン B 鎖における多段階的なアミロイド核形成および阻害の解析
Investigation of multi-step nucleation of insulin B chain amyloid fibrils and its inhibition
山本 直樹 [1], 赤井 大気 [1], 津原 祥子 [1], 井上 倫太郎 [2], 杉山 正明 [2], 田村 厚夫 [1], ○茶谷 絵理 [1]（[1]神戸大学大学院理学研究科, [2]京都大学複合原子力科学研究所）
Naoki Yamamoto[1], Taiki Akai[1], Shoko Tsuhara[1], Rintaro Inoue[2], Masaaki Sugiyama[2], Atsuo Tamura[1], **Eri Chatani**[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Institute for Integrated Radiation and Nuclear Science, Kyoto Univ.*)

2L1424 An RNA aptamer disrupts the interaction of prion protein with Amyloid β
Mamiko Iida[1,2], **Tsukasa Mashima**[1,2], Yudai Yamaoki[1], Masatomo So[3], Takashi Nagata[1,2], Masato Katahira[1,2] ([1]*Institute of Advanced Energy, Kyoto University*, [2]*Graduate School of Energy Science, Kyoto University*, [3]*Institute for Protein Research, Osaka University*)

2L1436 ナノスペースビデオイメージングによる食品関連因子アミロイド凝集抑制作用機序の解明
Nano-space video imaging reveals structural dynamics of amyloidogenic protein aggregation inhibition by food components
○中山 隆宏 [1], 小野 賢二郎 [2], 山田 正仁 [3]（[1]金沢大・WPI-NanoLSI, [2]昭和大・医・神経内科, [3]金沢大・院医・神経内科）
Takahiro Watanabe-Nakayama[1], Kenjiro Ono[2], Masahito Yamada[3] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Dept. Neuro., Showa Univ. Sch. Med.*, [3]*Dept. Neuro. & Neurobiol of Aging, Kanazawa Univ. Grad. Sch.*)

2L1448 Protein Structures Define Misfolding and Prion-like Propagation of Alzheimer's Amyloid-β: Solid-state NMR Studies
Yoshitaka Ishii[1,2], Yiling Xiao[2], Brian Yoo[2], Isamu Matsuda[1], Dan McElheny[2] ([1]*Ti Tech*, [2]*Univ. Illinois at Chicago*)

2L1500 EPR 法による Shewanella 由来無機ピロフォスファターゼにおける複核 Mn サイトの構造解析
Structural analysis on di-Mn ion site for Shewanella inorganic pyrophosphatase by EPR
○堀谷 正樹, 榊原 由季, 渡邉 啓一（佐賀大・農学部）
Masaki Horitani, Yuki Sakakibara, Keiichi Watanabe (*Saga Univ., Fac. Agr.*)

休憩（Coffee Break）　15:12–15:18

2L1518 Kinetics of reversible NADP$^+$/H reduction/oxidation reaction catalyzed by a ferredoxin-NADP$^+$ oxidoreductase from *Rhodopseudomonas palustris*
Daisuke Seo (*Div. Mat. Sci., Grad. Sch. Nat. Sci. Tec., Kanazawa Univ.*)

2L1530 シトクロム c-シトクロム c 酸化酵素間電子伝達反応における特異的脱水和の機能的役割
Functional role of specific dehydration from cytochrome c in electron transfer to cytochrome c oxidase
○佐藤 航 [1,2], 内田 毅 [1], 斎尾 智英 [1], 石森 浩一郎 [1]（[1]北大 院理, [2]ストックホルム大 院理）
Wataru Sato[1,2], Takeshi Uchida[1], Tomohide Saio[1], Koichiro Ishimori[1] ([1]*Fac. of Sci. Hokkaido Univ.*, [2]*Sci. Acad. Area Stockholm Univ.*)

14:00〜16:30　M 会場（E21）／Room M (E21)
2M 蛋白質：構造Ⅴ、構造機能相関Ⅶ、計測・解析の方法論Ⅳ／
Proteins: Structure V, Structure-function relationship VII, Measurement & Analysis I, Engineering IV

2M1400 **高圧力 NMR 法による蛋白質水和に関する研究**
High-pressure NMR reveals water-protein interactions coupled with protein conformational transition
北沢 創一郎[1], 青島 佑[2], 若本 拓朗[2], ○北原 亮[1]（[1]立命館大学薬学部, [2]立命館大学生命科学研究科）
Soichiro Kitazawa[1], Yu Aoshima[2], Takuro Wakamoto[2], **Ryo Kitahara**[1] ([1]*Pharmaceutical Sciences, Ritsumeikan University*, [2]*Graduate School of Life Sciences, Ritsumeikan University*)

2M1412 **PDZ ドメインと低分子リガンドの分子認識機構の NMR 法による解析**
Molecular recognition of PDZ domains and their non-peptidic ligands revealed by NMR
天野 剛志[1,2], 安河内 章太郎[1], 久田 美咲[1], ○廣明 秀一[1,2]（[1]名古屋大学大学院創薬科学研究科, [2]合同会社 BeCellBar）
Takeshi Tenno[1,2], Shotaro Yasukochi[1], Misaki Hisada[1], **Hidekazu Hiroaki**[1,2] ([1]*Graduate School of Pharmaceutical Sciences*, [2]*BeCellBar LLC.*)

2M1424 NMR characterization of conformational dynamics of cyclic and linear Lys48-linked ubiquitin chains
Methanee Hiranyakorn[1,2,3], Saeko Yanaka[1,2,3], Maho Yagi-Utsumi[1,2,3], Koichi Kato[1,2,3] ([1]*Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences*, [2]*Institute for Molecular Science, National Institutes of Natural Sciences*, [3]*SOKENDAI*)

2M1436 **NMR による天然変性アルファーシヌクレイン蛋白質の残存構造解析**
Residual structure of alpha-synuclein mutants elucidated by NMR
○西村 千秋（帝京平成大学薬学部）
Chiaki Nishimura (*Teikyo Heisei University*)

2M1448 **解鎖タンパク質の全アミノ酸残基の構造分布情報を化学シフトから得る方法の開発**
Method for deriving information of the structural distribution of amino acid residues of unfolded proteins from their chemical shifts
○関 安孝（高知大学 医学部 生体分子構造学講座）
Yasutaka Seki (*Molec. Biophys., Kochi Med. Sch., Kochi Univ.*)

2M1500 **クライオ電子顕微鏡で解き明かす細菌べん毛モーターのトルク伝達に重要な回転対称構造**
Rotational symmetry structure of the bacterial flagellar motor for torque transmission revealed by electron cryomicroscopy
○川本 晃大[1,2], 宮田 知子[2], 木下 実紀[2], 南野 徹[2], 今田 勝巳[3], 加藤 貴之[2], 難波 啓一[2,4]（[1]阪大・蛋白研, [2]阪大・生命機能, [3]阪大・院理学, [4]理研・生命機能センター）
Akihiro Kawamoto[1,2], Tomoko Miyata[2], Miki Kinoshita[2], Tohru Minamino[2], Katsumi Imada[3], Takayuki Kato[2], Keiichi Namba[2,4] ([1]*IPR, Osaka Univ*, [2]*Grad. Sch. Frontier Biosci, Osaka Univ*, [3]*Grad. Sch. Sci, Osaka Univ*, [4]*BDR, RIKEN*)

休憩（Coffee Break）　15:12–15:18

2M1518 Gwatch: **クライオ電顕におけるハイスループット評価システムの構築と評価**
Gwatch: the pipeline program for quick evaluation of sample quality in CryoEM
○牧野 文信[1], 加藤 貴之[1], 深川 竜郎[1], 難波 啓一[1,2]（[1]大阪大学大学院生命機能研究科, [2]理化学研究所 生命機能科学研究センター）
Fumiaki Makino[1], Takayuki Kato[1], Tatsuo Fukagawa[1], Keiichi Namba[1,2] ([1]*Graduate School of Frontier Bioscience, Osaka University*, [2]*BDR and SPring-8, RIKEN*)

2M1530 The near-atomic resolution cryo-EM structure of the infectious Staphylococcus bacteriophage S13'
Naoyuki Miyazaki[1], Jumpei Uchiyama[2], Shigenobu Matsuzaki[3], Kazuyoshi Murata[4], Kenji Iwasaki[1] ([1]*IPR*, [2]*Azabu Univ.*, [3]*Kochi Univ.*, [4]*NIPS*)

2M1542 Structural analysis of Type V pilus by Cryo-electron microscopy
Satoshi Shibata[1], Mikio Shoji[2], Kodai Okada[3], Katsumi Imada[3], Koji Nakayama[2], Matthias Wolf[1] ([1]*OIST Molecular Cryo-Electron Microscopy Unit*, [2]*Grad. Sch. BioMedical Sci., Nagasaki Univ.*, [3]*Dept. MacroMol Sci., Osaka Univ.*)

2M1554 クライオ電子顕微鏡を用いた高分解能構造解析による軸糸ダブレット微小管の構築・安定化機構の解明
Cryo-electron microscopy revealed a high-resolution structure of doublet microtubule and its assembly and stabilization mechanisms
○市川 宗厳 [1], Liu Dinan[1], Kastritis Panagiotis L.[2], Basu Kaustuv[3], Hsu Tzu Chin[1], Yang Shunkai[1], Bui Khanh Huy[1,4]（[1]マギル大学, [2]EMBL, [3]マギル大学, FEMR, [4]GRASP）
Muneyoshi Ichikawa[1], Dinan Liu[1], Panagiotis L. Kastritis[2], Kaustuv Basu[3], Tzu Chin Hsu[1], Shunkai Yang[1], Khanh Huy Bui[1,4] ([1]*Dept. of Anat. and Cell Biol., McGill Univ.*, [2]*Struct. and Comput. Biol. Unit, EMBL*, [3]*FEMR, McGill Univ.*, [4]*GRASP*)

2M1606 クライオ電子顕微鏡における高分解能構造解析のためのスクリーニング法の検討
Screening method for samples for high resolution structural analysis by cryoEM
○加藤 貴之 [1], 寺原 直矢 [1], 宮田 知子 [1], 難波 啓一 [1,2]（[1]阪大・生命, [2]理研・生命センター）
Takayuki Kato[1], Naoya Terahara[1], Tomoko Miyata[1], Keiichi Namba[1,2] ([1]*Grad. Sch. Front. Bio., Osaka univ.*, [2]*BDR & SPring-8, RIKEN*)

2M1618 Structure of a prehandover mammalian ribosomal SRP·SRP receptor targeting complex
Kan Kobayashi[1], Ahmad Jomaa[1], Jae Ho Lee[2], Sowmya Chandrasekar[2], Daniel Boehringer[1], Shu-ou Shan[2], Nenad Ban[1] ([1]*ETH Zurich*, [2]*Caltech*)

14:00〜15:54　N 会場（E23）／Room N (E23)
2N 筋肉・モーター／Muscle/motor

2N1400 アクチン繊維の極性揃えた配向はミオシンとの相互作用により引き起こされる
Self-organization of actin filaments of the same polarity by myosin
吉村 孝平 [1], 鯉江 信慶 [1], 原口 武士 [1], 富永 基樹 [2,3], 平塚 祐一 [4], ○伊藤 光二 [1]（[1]千葉大・院・理学生物, [2]早稲田大・教育, [3]早稲田大・院・先進理工, [4]北陸先端大・院・マテリアルサイエンス）
Kohei Yoshimura[1], Nobuyoshi Koie[1], Takeshi Haraguchi[1], Motoki Tominaga[2,3], Yuichi Hiratsuka[4], **Kohji Ito**[1] ([1]*Dept. Biol. Grad. Sch. Sci., Chiba Univ.*, [2]*Fac. Edu. and Int. Arts and Sci., Waseda Univ.*, [3]*Grad. Sch. Adv. Sci. and Eng., Waseda Univ.*, [4]*Sch. Mat. Sci., JAIST*)

2N1412 心筋・骨格筋のサルコメア集団が生み出すメカニカルな波動特性
Mechanical wave characteristics generated by sarcomere group of cardiac / skeletal muscle
○新谷 正嶺（中部大・生健・生命医科学科）
Seine Shintani (*Dep. Biomed. Sci., Col. Life and Health Sci.*)

2N1424 *In vivo* マウス心筋における単一サルコメア動態のナノイメージング
Nano-imaging of individual sarcomere dynamics in the beating mouse heart *in vivo*
○小北類巻 生 [1], 下澤 東吾 [2], 大山 廣太郎 [3,4], 石渡 信一 [5], 福田 紀男 [1]（[1]慈恵医大細胞生理学, [2]東大理学部技術部, [3]量研, [4]JST さきがけ, [5]早大理工学術院）
Fuyu Kobirumaki-Shimozawa[1], Togo Shimozawa[2], Kotaro Oyama[3,4], Shin'ich Isiwata[5], Norio Fukuda[1] ([1]*Dept Cell Physiol, The Jikei Univ Sch of Med*, [2]*Tech Div, Sch of Sci, The Univ of Tokyo*, [3]*QST*, [4]*PRESTO, JST*, [5]*Waseda Univ*)

2N1448 クシクラゲの櫛板はほぼ完全な動く巨大蛋白単結晶である
The comb plate of ctenophore is a nearly perfect giant single protein crystal that moves
○岩本 裕之 [1], 城倉 圭 [2], 稲葉 一男 [2]（[1]SPring-8・JASRI, [2]筑波大・下田臨海）
Hiroyuki Iwamoto[1], Kei Jokura[2], Kazuo Inaba[2] ([1]*SPring-8, JASRI*, [2]*Shimoda Marine Research Center, Univ. Tsukuba*)

2N1500 ダイニン・微小管・DNA 折り紙複合体の運動および構造の解析
Motility and structure of the dynein-microtubule complex crosslinked with DNA-origami
Abdellatef Shimaa A.[1], 多田隈 尚史[2], 近藤 雄一[3], 厳 康敏[1], 樋口 秀男[3], ○広瀬 恵子[1]（[1]産総研・バイオメディカル, [2]大阪大・蛋白研, [3]東京大・院理）
Shimaa A. Abdellatef[1], Hisashi Tadakuma[2], Yuichi Kondo[3], Kangmin Yan[1], Hideo Higuchi[3], **Keiko Hirose**[1] ([1]*Biomed. Res. Inst., AIST*, [2]*Inst. Protein Res., Univ. Osaka*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

休憩（Coffee Break） 15:12–15:18

2N1518 細胞質ダイニンの不活性化状態から活性状態への新規遷移構造
Novel intermediate structures of cytoplasmic dynein between shutdown and active states
塩井 拓真, ○福永 晃, 下 理恵子, 山本 遼介, 今井 洋, 昆 隆英（阪大・院理）
Takuma Shioi, **Akira Fukunaga**, Rieko Shimo, Ryousuke Yamamoto, Hiroshi Imai, Takahide Kon (*Dep. Biol. Sci., Grad. Sch. of Sci., Osaka Univ*)

2N1530 Cell-like movement of self-organized microtubule aster
Takayuki Torisawa[1,2], Shuji Ishihara[3], Kazuhiro Oiwa[2] ([1]*Cell Arch Lab., NIG*, [2]*Adv. ICT Res. Inst., NICT*, [3]*Grad. Sch. Arts and Sciences, Univ. Tokyo*)

2N1542 ダイニン c 尾部先端の糸状構造
The String-Like Structure on the Tip of Dynein-c Tail
○榊原 斉, 小嶋 寛明（情報通信研究機構未来 ICT 研究所）
Hitoshi Sakakibara, Hiroaki Kojima (*Adv. ICT Res. Inst., NICT*)

14:00〜16:30 O 会場（D32）／Room O (D32)
2O 非平衡・計測・数理生物学／Nonequilibrium, Measurement, Mathematical Biology

2O1400 Predicting gene expression of living cells from a label-free spectral imaging technique
Arno Germond[1], Vipin Kumar[1], Takaaki Horinouchi[1], Chikara Furusawa[1,2], Hideaki Fujita[1], Yuichi Taniguchi[1], Toshio Yanagida[1], Taro Ichimura[1], Tomonobu M. Watanabe[1] ([1]*RIKEN BDR*, [2]*Tokyo Univ.*)

2O1412 Quantifying heterogeneity of stochastic gene expression
Keita Iida[1], Nobuaki Obata[2], Yoshitaka Kimura[1] ([1]*Grad. Sch. Med., Univ. Tohoku*, [2]*Grad. Sch. Sci., Univ. Tohoku*)

2O1424 対称性の自発的破れにより生起する分子生物学のセントラルドグマ
The origin of the central dogma of molecular biology through spontaneous symmetry breaking
○竹内 信人, 金子 邦彦（東大総合文化）
Nobuto Takeuchi, Kunihiko Kaneko (*Grad. Sch. Arts and Sci. UTokyo*)

2O1436 変異生成と増殖阻害のトレードオフとしての最適変異率モデル
An optimal mutation rate model as a trade-off between mutation generation and growth inhibition
○芝井 厚[1], 井筒 弥那子[2], 古澤 力[1]（[1]理研 BDR, [2]ミシガン州立大）
Atsushi Shibai[1], Minako Izutsu[2], Chikara Furusawa[1] ([1]*RIKEN BDR*, [2]*Michigan State University*)

2O1448 Mathematical Analysis of Copper Efflux System in Escherichia coli
Jun-ichi Ishihara[1], Tomohiro Mekubo[2], Chikako Kusaka[2], Suguru Kondou[2], Naotake Ogasawara[2], Taku Oshima[3], Hiroki Takahashi[1,4] ([1]*Medical Mycology Research Center, Univ. Chiba*, [2]*Grad. Sch. Bio. Sci., NAIST*, [3]*Grad. Sch. Eng., Univ. Toyama Pref.*, [4]*Molecular Chirality Research Center, Univ. Chiba*)

2O1500 Model-based prediction of ErbB signaling activities on cell cycle entry
Hiroaki Imoto, Kazunari Iwamoto, Shigeyuki Magi, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

休憩（Coffee Break） 15:12–15:18

2O1518 **孤立した遊走細胞の集団での挙動の理論**
Theory on collective behavior of migrating eukaryotic cells
○平岩 徹也（東京大・院理）
Tetsuya Hiraiwa (*Grad. Sch. Sci., Univ. Tokyo*)

2O1530 **C. elegans の遊泳運動は、フラクタルノイズを介した状態遷移による**
C. elegans swimming motion is a fractal process
○荒田 幸信 [1], 池田 優作 [1,2], 木村 啓志 [2], 新土 優樹 [1], ユリツァ ペテル [1], スツルジグ ズビグニェフ [3,4], 高木 拓明 [5], 佐甲 靖志 [1]（[1]理研・佐甲細胞, [2]東海大・工, [3]東京大学・大学院教育学研究科, [4]理研・情報基盤, [5]奈良医科大・物理学教室）
Yukinobu Arata[1], Yusaku Ikeda[1,2], Hiroshi Kimura[2], Yuki Shindo[1], Peter Jurica[1], Zbigniew Struzik[3,4], Hiroaki Takagi[5], Yasushi Sako[1] ([1]*Cell Info, Riken*, [2]*Biomed. Microfluidic System Lab., Tokai Univ.*, [3]*Grad. Sch. of Ed., Univ. of Tokyo*, [4]*ACCC, RIKEN*, [5]*Dept. of Phys., Nara Medical Univ.*)

2O1542 **境界形状が誘起するバクテリア集団運動と転移現象**
Geometry-driven collective ordering of bacterial vortices
別府 航早, イズリ ジャン, ○前多 裕介（九大・物理）
Kazusa Beppu, Ziane Izri, **Yusuke T. Maeda** (*Dept. Phys., Kyushu Univ.*)

2O1554 **変形菌 Physarum polycephalum の微小変形体にみられる間欠的細胞運動**
Emergence of intermittent break in cell motion for tiny plasmodium of Myxomycete Physarum polycephalum
○垣内 康孝, 西山 宣昭（金沢大学国際基幹教育院）
Yasutaka Kakiuchi, Nobuaki Nishiyama (*Kanazawa Univ.*)

2O1606 **一分子時間分解 FRET データの三次元解析：生体高分子の構造不均一性をモデルフリーで定量する方法の開発**
Third-order correlation analysis of single-molecule time-resolved FRET data: a new method for quantification of heterogeneity
○坂口 美幸 [1], 石井 邦彦 [1,2], 田原 太平 [1,2]（[1]理研・田原分子分光, [2]理研・光量子工学研究センター）
Miyuki Sakaguchi[1], Kunihiko Ishii[1,2], Tahei Tahara[1,2] ([1]*Molecular Spectroscopy Lab., RIKEN*, [2]*RAP, RIKEN*)

2O1618 **分子数絶対定量に向けた認証標準物質による蛍光相関分光装置の校正**
System calibration of fluorescence correlation spectroscopy for absolute quantification of molecular number
○佐々木 章 [1], 山本 条太郎 [1,2], 金城 政孝 [2], 野田 尚宏 [1]（[1]産総研・バイオメディカル研究部門, [2]北大・先端生命）
Akira Sasaki[1], Johtaro Yamamoto[1,2], Masataka Kinjo[2], Naohiro Noda[1] ([1]*BMRI, AIST*, [2]*Faculty Adv. Life Sci., Hokkaido Univ.*)

14:00〜16:30　Q 会場（D34）／Room Q (D34)
2Q 核酸・核酸結合タンパク質・生命の起源・進化／
Nucleic acid, Nucleic acid binding proteins, Origin of life & Evolution

2Q1400 Chromatin remodelers couple inchworm motion with twist-defect formation to slide nucleosomal DNA
Giovanni Brandani, Shoji Takada (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

2Q1412 **単一ヌクレオソームイメージングによる生細胞中の分裂期染色体の局所ゆらぎ計測**
Local nucleosome dynamics in mitotic chromosomes in living cells
○日比野 佳代 [1,2], 前島 一博 [1,2]（[1]遺伝研, [2]総研大）
Kayo Hibino[1,2], Kazuhiro Maeshima[1,2] ([1]*NIG*, [2]*SOKENDAI*)

2Q1424 **リンカー DNA によって大きく決まるポリヌクレオソームの局所構造**
Local structures of poly-nucleosome largely restricted by linker DNA
○検崎 博生 [1], 高田 彰二 [2]（[1]理化学研究所情報システム部, [2]京都大学理学研究科生物物理学教室）
Hiroo Kenzaki[1], Shoji Takada[2] ([1]*Info. Sys. Div., RIKEN*, [2]*Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.*)

2Q1436 Investigating the influence of Argine Dimethylation on Nucleosome Dynamics using All-atom Simulation and Kinetic Analysis
Zhenhai Li, Hidetoshi Kono (*QST*)

2Q1448 大腸菌非六量体型 DNA ヘリカーゼ UvrD 変異体の 1 分子イメージング
Single-molecule imaging of mutants of the non-hexameric *Escherichia coli* helicase UvrD
○横田 浩章（光産創大・光バイオ）
Hiroaki Yokota (*Biooptics Lab, Grad. Sch. Creation Photon. Indust.*)

2Q1500 in vitro と in vivo での DNA 結合タンパク質の単分子蛍光測定
Single-molecule fluorescence imaging of architectural DNA-binding proteins in vitro and in vivo
○鎌形 清人 [1], 間野 絵梨子 [1], Mandali Sridhar[2], 伊藤 優志 [1], Johnson Reid[2]（[1]東北大多元所, [2]カリフォルニア大学ロサンゼルス校）
Kiyoto Kamagata[1], Eriko Mano[1], Sridhar Mandali[2], Yuji Itoh[1], Reid Johnson[2] ([1]*IMRAM, Tohoku Univ.*, [2]*UCLA*)

休憩（Coffee Break） 15:12–15:18

2Q1518 クライオ電顕フィッティングによる RNA ポリメラーゼ-DNA 複合体の構造精密化
Cryo-EM structure refinement of RNA polymerase by molecular dynamics simulations
○森 貴治 [1], 江原 晴彦 [2], 関根 俊一 [2], 杉田 有治 [1,2,3]（[1]理研 杉田理論分子科学, [2]理研 BDR, [3]理研 R-CCS）
Takaharu Mori[1], Haruhiko Ehara[2], Shun-ichi Sekine[2], Yuji Sugita[1,2,3] ([1]*RIKEN Theor. Mol. Sci. Lab*, [2]*RIKEN BDR*, [3]*RIKEN R-CCS*)

2Q1530 種々のポリアミンによる遺伝子発現活性制御
Effect of polyamines on in vitro gene expression
○田中 寛子 [1], 吉川 祐子 [1], 梅澤 直樹 [2], 剣持 貴弘 [1], 吉川 研一 [1]（[1]同志社,生命医科,生命物理科学研究室, [2]名古屋市立,薬学）
Hiroko Tanaka[1], Yuko Yoshikawa[1], Naoki Umezawa[2], Takahiro Kenmotsu[1], Kenichi Yoshikawa[1] ([1]*Lab. Life Phys., Grad. Sch. Life Med. Sci., Doshisha Univ.*, [2]*Grad. Sch. Phar. Sci., Nagoya City Univ.*)

2Q1542 選択的な DNA ライゲーションと情報成長の分子的起源：「富むものはより富む」モデル
Molecular origin of selective DNA ligation and information growth: The rich-get-richer model
○白木 天晴 [1], 亀井 謙一郎 [2], 前多 裕介 [1]（[1]九州大学理学府, [2]京都大学 iCeMS）
Takaharu Shiraki[1], Ken-ichiro Kamei[2], Yusuke T. Maeda[1] ([1]*Dept. Phys. Kyushu Univ.*, [2]*WPI-iCeMS, Kyoto Univ.*)

2Q1554 転写因子 NF-κB がつくる核内クラスターと転写応答の解析
Analysis of NF-κB clusters and transcriptional initiations
○稲葉 岳彦 [1], 岩本 一成 [2], 岡田 眞里子 [2], 佐甲 靖志 [1]（[1]独立行政法人 理化学研究所 佐甲細胞情報研究室, [2]大阪大学 蛋白研 細胞システム研）
Takehiko Inaba[1], Kazunari Iwamoto[2], Mariko Okada[2], Yasushi Sako[1] ([1]*RIKEN Cellular informatics*, [2]*Laboratory of Cell Systems, Institute for Protein Research, Osaka U.*)

2Q1606 Biopolymer self-assembly and combinatorial evolution at the origin of life
Tony Z Jia[1], Charalampos G Pappas[2], Ankit Jain[2], Daniela Kroiss[2], Nadeesha K Wijerathne[2], James M Aramini[2], Ayan Pal[3], Jack W. Szostak[3], Rein V Ulijn[2], Kuhan Chandru[1], Rehana Afrin[1], Yayoi Hongo[1], Henderson J Cleaves[1] ([1]*Earth-Life Science Institute, Tokyo Institute of Technology*, [2]*Advanced Science Research Center, City University of New York*, [3]*Massachusetts General Hospital, Harvard Medical School*)

2Q1618 アクチン線維封入巨大リポソームからの光応答性の膜チューブの伸張短縮は自身の移動を引き起こす
Photoresponsive elongation and retraction of membrane tubes from F-actin-encapsulating giant liposome can move its cell body
○林 真人 [1], 田中 駿介 [2], 瀧口 金吾 [2]（[1]理研・脳神経科学研究センター, [2]名古屋大学 院理）
Masahito Hayashi[1], Shunsuke Tanaka[2], Kingo Takiguchi[2] ([1]*RIKEN CBS*, [2]*Grad Sch of Sci, Nagoya Univ*)

口頭発表座長一覧

会場	部屋	9月15日（土） 13:30-16:00	9月16日（日） 14:00-16:30
A会場	B11	1A　細胞生物的課題Ⅰ	2A　細胞生物的課題Ⅱ
		宮田 真人（大阪市大）、成瀬 恵治（岡山大）	松浦 宏冶（岡山理科大）、竹居 孝二（岡山大）
C会場	B21	1C　バイオエンジニアリング・バイオインフォマティクス・人工膜・生体膜・神経	2C　発生分化・行動・化学受容・神経
		大上 雅史（東工大）、長尾 秀実（金沢大）	冨永 貴志（徳島文理大）、平島 剛志（京都大）
D会場	A36	1D　バイオイメージングⅠ	2D　バイオイメージングⅡ
		古寺 哲幸（金沢大）、日比野 佳代（理研）	内橋 貴之（名古屋大）、船津 高志（東大）
E会場	A37	1E　筋肉・モーターⅠ	2E　筋肉・モーターⅡ
		樋口 秀男（東大）、政池 知子（東京理科大）	飯野 良太（分子研）、南野 徹（大阪大）
F会場	B32	1F　光合成・ロドプシン	2F　光受容体・光生物学
		菅 倫寛（岡山大）、石北 央（東大）	岩田 達也（東邦大）、久冨 修（大阪大）
G会場	B33	1G　生体膜・人工膜Ⅰ	2G　生体膜・人工膜Ⅱ
		渡邉 力也（東大）、川村 出（横浜国大）	山崎 昌一（静岡大）、安宅 憲一（ベルリン自由大）
H会場	A41	1H　光生物学	2H　ロドプシン
		井上 圭一（東大）、村上 緑（名古屋大）	菊川 峰志（北海道大）、寺北 明久（大阪市大）
J会場	D12	1J　蛋白質：構造Ⅰ、構造機能相関Ⅰ、物性Ⅰ、機能Ⅰ、計測・解析の方法論Ⅰ、蛋白質工学Ⅰ	2J　蛋白質：構造Ⅳ、構造機能相関Ⅳ
		光武 亜代理（明治大）、粟津 暁紀（広島大）	倭 剛久（名古屋大）、北尾 彰朗（東大）
K会場	E11	1K　蛋白質:構造Ⅱ、物性Ⅱ、機能Ⅱ、蛋白質工学Ⅱ、ヘム蛋白質	2K　蛋白質：構造機能相関Ⅴ、物性Ⅴ、計測・解析の方法論Ⅱ
		上村 想太郎（東大）、新井 宗仁（東大）	織田 昌幸（京都府立大）、永野 真吾（鳥取大）
L会場	D23	1L　蛋白質：構造機能相関Ⅱ、物性Ⅲ、計測・解析の方法論Ⅰ	2L　蛋白質：構造機能相関Ⅵ、物性Ⅵ、計測・解析の方法論Ⅲ
		高野 光則（早稲田大）、高橋 聡（東北大）	茶谷 絵理（神戸大）、楯 真一（広島大）
M会場	E21	1M　蛋白質：構造Ⅲ、構造機能相関Ⅲ、物性Ⅳ	2M　蛋白質：構造Ⅴ、構造機能相関Ⅶ、計測・解析の方法論Ⅳ
		秋山 修志（分子研）、田中 伊知朗（茨城大学）	廣明 秀一（名古屋大）、難波 啓一（大阪大）
N会場	E23	－	2N　筋肉・モーター Ⅲ
		－	昆 隆英（大阪大）、福田 紀男（慈恵医大）
O会場	D32	1O　非平衡・計測・数理生物学Ⅰ	2O　非平衡・計測・数理生物学Ⅱ
		若本 祐一（東大）、城口 克之（理研）	古澤 力（理研）、佐甲 靖志（理研）
Q会場	D34	1Q　核酸・情報科学・ゲノム生物学	2Q　核酸・核酸結合タンパク質・生命の起源・進化
		岡田 眞里子（大阪大）、井原 邦夫（名古屋大）	吉川 研一（同志社大）、河野 秀俊（量子科学）

ポスター　Poster

1 日目（9 月 15 日（土））／Day 1（Sep. 15 Sat.）
PA 会場（大集会室），PB 会場（南第二集会室），PC 会場（南第三集会室），PD 会場（南第四集会室）／
Room PA (Large Assembly Room), Room PB (2nd South Assembly Room),
Room PC (3rd South Assembly Room), Room PD (4th South Assembly Room)

蛋白質：構造／Protein: Structure

1Pos001 分子動力学法を用いた Hras-GTP/GDP 複合体の各部の構造変化と各部の水素結合との動的関連性の研究
Molecular dynamics study of dynamical relationship between structures and the hydrogen bonds of some parts in the Hras-GTP/GDP complexes
Takeshi Miyakawa[1], Ryota Morikawa[1], Masako Takasu[1], Kimikazu Sugimori[2], Kazutomo Kawaguchi[3], Hidemi Nagao[3] ([1]*Sch. of Life Sci, Tokyo Univ. of Pharm. and Life Sci.*, [2]*Inst. of Liberal Arts. and Sci., Kanazawa Univ.*, [3]*Coll. of Sci. and Eng., Kanazawa Univ.*)

1Pos002 分子シミュレーションを用いた複数ドッキングポーズからの正しい結合ポーズの特定―自動デザインに向けて
Identifying correct ligand binding pose out of multiple docking poses by MD simulations toward AutoDesign
Hironori Kokubo (*Axcelead, Inc.*)

1Pos003 α シヌクレインフラグメントの 2 量体形成過程の解明に向けた定温定圧レプリカ置換分子動力学シミュレーション
Isothermal-isobaric replica-permutation molecular dynamics simulation to reveal dimerization process of α-synuclein fragments
Masataka Yamauchi[1,2,3], Hisashi Okumura[1,2,3] ([1]*SOKENDAI*, [2]*IMS*, [3]*ExCELLS*)

1Pos004 Cryo-tomography and sub-tomogram averaging of dimeric F type ATP synthase at bovine sub-mitochondrial particle
Jun-chi Kishikawa[1], Atsuko Nakanishi[1], Masatoshi Murai[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. Mol. BioSci., Kyoto Sangyo Univ.*, [2]*Div. Appl. Life Sci., Grad. Sch. Agrci., Kyoto Univ.*, [3]*Res. Ctr. UHVEM, Osaka Univ.*)

1Pos005 クライオ電子顕微鏡による好熱菌 *Thermus thermophilus* 由来 V 型 ATP 合成酵素の単粒子解析
Cryo EM structure of intact rotary H^+-ATPase/synthase from *Thermus thermophilus*
Atsuko Nakanishi[1], Jun-ichi Kishikawa[1], Masatada Tamakoshi[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. of Mol. Biosci., Kyoto Sangyo Univ.*, [2]*Dept. of Mol. Biol., Tokyo Univ. of Pharm. and Life Sci.*, [3]*Res. Ctr. for UHVEM, Osaka Univ.*)

1Pos006 Startup of Laboratory-scale SEC-SAXS (La-SSS) system
Rintaro Inoue, Ken Morishima, Nobuhiro Sato, Masaaki Sugiyama (*Institute for Integrated Radiation and Nuclear Science, Kyoto UniversityInstitute for Integrated Radiation and Nuclear Science, Kyoto University*)

1Pos007 Determination and Comparsion of the Structural Ensemble of Molten Globule State of Proteins by Computer Simulations
Masahiro Shimizu, Yuko Okamoto (*Grad. Sch. Sci., Univ. Nagoya*)

1Pos008 GPI アタッチメントシグナルの二次構造解析
Secondary structural analysis of GPI attachment signal
Keiya Inoue[1], Daiki Takahashi[1], Tatsuki Kikegawa[1], Kenji Etchuya[2], Yuri Mukai[1] ([1]*Dept. Electronics, Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Biomed. Res. Inst., AIST*)

1Pos009 位相差クライオ電子顕微鏡単粒子解析法を用いた腸球菌 V-ATPase の構造解析
Single Particle Analysis of *Eh*V-ATPase by Phase-Plate electron cryo-microscopy
Jun Tsunoda[1,2], Chihong Song[2], Fabiana Lica Yakushiji[3], Takeshi Murata[3], Hiroshi Ueno[4], Naoyuki Miyazaki[5], Kenji Iwasaki[5], Junichi Takagi[5], Ryota Iino[1,6], Kazuyoshi Murata[1,2] ([1]*SOKENDAI*, [2]*NIPS*, [3]*Dept.Chem., Chiba Univ.*, [4]*Dept. Appl. Chem., Sch. Eng., Univ. Tokyo*, [5]*IPR, Osaka Univ.*, [6]*IMS*)

1Pos010 マルチスケールシミュレーションと構造比較を用いた、シグナル蛋白質カルモジュリンの研究
Multiscale simulation and Structural comparison of Calmodulin
Hiromitsu Shimoyama (*Kitasato University*)

1Pos011 Investigation of the common sequence-structural patterns in different protein folds using cross-profile analysis and simulation
Yu Yamamori, Kentaro Tomii (*AIST*)

1Pos012 Modeling three-dimensional (3D) volume of protein from Atomic-Force Microscopy (AFM) images
Bhaskar Dasgupta[1], Osamu Miyashita[2], Florence Tama[1,2,3] ([1]*Department of Physics, Graduate School of Science, Nagoya University*, [2]*Center for Computational Science, RIKEN, Kobe.*, [3]*Institute of Transformative Bio-Molecules (WPI-ITbM), Nagoya University*)

1Pos013 結合ヌクレオチド依存的なチューブリン C 末端テイルの構造分布に関する分子動力学計算解析
The bound-nucleotide (GDP or GTP) effects on C-terminal tails of tubulins investigated by molecular dynamics simulation
Takuma Todoroki[1], Yukinobu Mizuhara[2], Jun Ohnuki[2], Mitsunori Takano[2], Koji Umezawa[1,3] ([1]*Grad. Sch. of Sci. & Tech., Shinshu Univ.*, [2]*Grad. Scl. of Adv. Sci. & Eng., Waseda Univ.*, [3]*IBS, Shinshu Univ.*)

1Pos014 クライオ電子顕微鏡によるグルタミン酸脱水素酵素ドメイン運動の可視化
Visualizing the domain motion of Glutamate Dehydrogenase by using cryo-electron microscopy
Mao Oide[1,2], Takayuki Kato[3], Tomotaka Oroguchi[1,2], Keiichi Namba[3,4], Masayoshi Nakasako[1,2] ([1]*Grad. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 center*, [3]*Grad. Sch. of Front. Biosci., Osaka Univ.*, [4]*RIKEN, QBiC*)

1Pos015 クライオ電子顕微鏡単粒子解析法を用いた KcsA の構造解析
Structural Analysis of KcsA by Cryo-EM Single Particle Analysis
Hiroko Takazaki[1], Hirofumi Shimizu[2], Kaoru Mitsuoka[3], Takuo Yasunaga[1] ([1]*Grad. Sch. Comp. Sci. Syst. Eng., KIT*, [2]*Fac. Med. Sci., Univ. Fukui*, [3]*Research Center for UHVEM, Univ. Osaka*)

1Pos016 *Porphyromonas gingivitis* の線毛蛋白質 FimA の構造
Structure of FimA, a major component protein of fimbriae of *Porphyromonas gingivitis*
Kodai Okada[1], Koji Nakayama[2], Mikio Shoji[2], Satoshi Shibata[3], Katsumi Imada[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Biomedical Sci., Nagasaki Univ.*, [3]*OIST*)

1Pos017 好熱菌 V1-ATPase の単粒子解析
Single particle analysis of V1-ATPase from Thermus thermophilus
Aya Furuta[1] ([1]*Division of Life Sciences, Kyoto Sangyo University, Kyoto (Japan)*, [2]*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University, Osaka (Japan)*)

1Pos018 マベガイ由来 PPL3 の構造解析
Structure analysis of PPL3 regulating pearl shell biomineralization
Setsu Nakae[1], Masafumi Shionyu[1], Tomohisa Ogawa[2], Tsuyoshi Shirai[1] ([1]*Fac. Bio-Sci., Nagahama Inst. Bio-Sci. Tech.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*)

1Pos019 Application of the solution technique to identify a binding site and mode of a ligand in a protein
Masataka Hamano, Masatake Sugita, Takeshi Kikuchi, Fumio Hirata (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

1Pos020 MM/3D ー RISM 法を用いた水・エタノール混合溶液中における小分子間における結合エネルギー予測
Cosolvent effect on the binding affinity between small molecules in a water-ethanol mixture : MM/3D-RISM study
Kazuma Kondo[1], Masatake Sugita[1], Takeshi Kikuchi[1], Fumio Hirata[2] ([1]*Dept. of Bioinf., Col. Life Sci., Ritsumeikan Univ.*,, [2]*Toyota Phys. & Chem. Res. Inst.*)

1Pos021 MD シミュレーションを用いた BAF の野生型と変異体の揺らぎの解析
Analyses of fluctuations of wild type and mutant of BAF using MD simulation
Chiaki Yamaguchi[1], Siyao Li[2], Masatake Sugita[1], Toshiya Hayano[2], Takeshi Kikuchi[1] ([1]*Dept. of Bioinf., Col. Life Sci., Ritsumeikan Univ.*, [2]*Dept. of Biomed., Col. Life Sci., Ritsumeikan Univ.*)

1Pos022 Bio-SAXS を活用したタンパク質相関構造解析
Hybrid Approach of the Protein Structure Analysis utilizing Biological Small-Angle X-ray Scattering
Kento Yonezawa, Keiko Yatabe, Masatsuyo Takahashi, Yasuko Nagatani, Nobutaka Shimizu (*Photon Factory, IMSS, KEK*)

1Pos023 Chk1 阻害剤系の分類と自由エネルギー変分原理に基づく相対的結合自由エネルギー予測
Classification of Chk1 inhibitor system and Prediction of relative binding free energy based on a free energy variational principal
Daichi Kondo, Takeshi Ashida, Takeshi Kikuchi (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

1Pos024 Sensitivity to radiation dose of buried waters in Green Fluorescent Protein
Hoang Anh Dao, Kiyofumi Takaba, Yang Tai, Nagayuki Hasegawa, Kazuki Takeda (*Kyoto University Graduate School of Science*)

1Pos025 ジスルフィド結合は β-ストランドを逆平行に会合することに関与している？
Do disulfide bonds involve in β-strand assembly in anti-parallel manner ?
Hiromi Suzuki (*Sch. Agri., Meiji Univ.*)

1Pos026 単粒子コヒーレント回折パターンを用いた粗視化分子モデリングのためのテンプレートマッチング法
A template matching method for coarse-grained molecular modelling using a noisy single particle coherent diffraction pattern
Atsushi Tokuhisa[1,5], Ryo Kanada[1], Shuntaro Chiba[2], Yuta Isaka[3], Biao Ma[3], Shigeyuki Matsumoto[2], Kei Terayama[4,6], Narutoshi Kamiya[7], Yasushi Okuno[1,2,3,4] ([1]*RIKEN. RCSTI. RCH*, [2]*RIKEN. RCSTI. MIH*, [3]*FBRI. CCD*, [4]*Grad. Sch. Med., Univ. Kyoto*, [5]*RIKEN. R-CCS*, [6]*RIKEN. AIP*, [7]*Grad. Sch. Sim., Univ. Hyogo*)

1Pos027 テンプレートの MD シミュレーションを利用したタンパク質モデリングツールの開発
Development of Template-based Protein Structure Modeling Software using Molecular Dynamics Simulations of Template proteins
Masaya Furue, Naoyuki Miyashita, Mitsutaka Nemoto (*BOST, KINDAI Univ.*)

1Pos028 Hsp90 をターゲットとするペプチドアプタマーの構造と、シミュレーションのための力場作成支援プログラムの開発
Dynamics of peptide aptamer which targeting Hsp90 and the development of supporting program for modification of force field parameters
Lisa Matsukura[1], Kazuto Mochizuki[2], Masumi Taki[2], Naoyuki Miyashita[1], Shinichi Watanabe[2] ([1]*BOST, KINDAI Univ.*, [2]*GSIE, UEC.*)

1Pos029 A skewed distribution of psi-loop motifs in the protein structure database
Koki Fukuda, George Chikenji (*Dept. Appl. Phys. ,Grad. Sch. Eng. , Nagoya Univ.*)

1Pos030 The protein structure database analysis of the greek key motif and its similar structures
Ryuichiro Ueda, George Chikenji (*Dept. Appl. Phys. , Grad. Sch. Eng. , Nagoya Univ.*)

1Pos031 Observation of the dynamics associated with ubiquitination of HECT E3 ubiquitin ligase using High speed AFM
Ikumi Muro[1], Huminori Kobayashi[1], Takahiro Nakayama[2], Noriyuki Kodera[2], Toshio Ando[2], Hiroki Konno[2] ([1]*Graduate School of Natural Science & Technology, Kanazawa University*, [2]*Nano life science institute, Kanazawa University*)

1Pos032 転写制御因子 LmrR および QacR における多剤認識メカニズムに関する分子シミュレーション研究
Molecular simulation study of the underlying mechanism of multidrug recognition in transcriptional regulators LmrR and QacR
Kazuho Cryershinozuka, **Tadaomi Furuta**, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

1Pos033 Attempts at CA-type formal analysis of fibrous assembly of particles
Takashi Konno (*Mol. Physiol. Med. Univ. Fukui*)

1Pos034 ファーマコフォア解析を用いたビタミン D 受容体のアゴニスト/アンタゴニスト活性調節機構の研究
Regulation mechanism of agonistic / antagonistic activities of vitamin D receptor studied by pharmacophore analysis
Takafumi Kudo, Toru Ekimoto, Mitsunori Ikeguchi (*Grad. Sch. Medical Life Sci., Yokohama City Univ.*)

1Pos035 基準振動のネットワーク解析による TCR-pMHC 複合体の動的構造
Dynamic structures of TCR-pMHC complexes studied by a network analysis of normal modes
Hiroshi Wako[1], Yuko Tsuchiya[2], Shigeru Endo[3] ([1]*Sch. of Soc. Sci., Waseda Univ.*, [2]*AIRC, AIST*, [3]*Sch. of Sci., Kitasato Univ.*)

蛋白質：構造機能相関／Protein: Structure & Function

1Pos036 サルモネラ菌べん毛タンパク質 FliC と FljB で構成された繊維構造の比較と機能の違い
Structural comparison between Salmonella flagellar filaments consisting of FliC and FljB and the implication for their functions
Tomoko Yamaguchi[1], Takayuki Kato[1], Naoya Terahara[1], Shoko Toma[1], Keiichi Namba[1,2] ([1]*Osaka University FBS*, [2]*BDR & SPRING-8, RIKEN*)

1Pos037 溶液 NMR 法を用いた MAPK p38α によるストレスシグナル伝達最適化の構造機構の解明
Structural Basis for the Optimum Stress Signal Transduction via MAPK p38α under the ATP-depleted, Low pH Condition Elucidated by NMR
Yuji Tokunaga[1,2], Koh Takeuchi[1], Hideo Takahashi[3], Ichio Shimada[1,4] ([1]*molprof, AIST*, [2]*JBIC*, [3]*Grad Sch Med Life Sci, YCU*, [4]*Grad Sch Pharm Sci, UTokyo*)

1Pos038 自由エネルギー地形による T686A 変異 AMPA 受容体の部分作動メカニズムの解明
Free-energy landscapes reveal partial agonism at T686A mutation of AMPA receptor
Hiraku Oshima[1], Suyong Re[1], Masayoshi Sakakura[2], Hideo Takahashi[2], Yuji Sugita[1] ([1]*RIKEN BDR*, [2]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

1Pos039 糖転移酵素の基質特異性メカニズムの解明
Clarify of the substrate specificity mechanism of glycosyltransferase
Go Miyasaka[1], Kenji Etchuya[2], Yuri Mukai[1] ([1]*Dept. Electronics, Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Biomed. Res. Inst., AIST*)

1Pos040 Pin1 由来のタンパク質分解酵素の触媒部位の変異解析
Mutational analysis on the catalytic site of a protease derived from Pin1
Teikichi Ikura, Nobutoshi Ito (*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

1Pos041 酵素 PHBH の 2 つの没食子酸産生変異体の違いについての理論的考察
Theoretical insight into differences in two PHBH mutants that can produce gallic acid
Yoshitaka Moriwaki[1], Mirai Yato[1], Tohru Terada[2], Takatoshi Arakawa[1], Shinya Fushinobu[1], Kentaro Shimizu[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci.*, [2]*Interfaculty Initiative in Information Studies*)

1Pos042 LysW・LysY・LysZ 三者複合体仮説のモデリング
Modeling of a hypothetical ternary complex of LysW, LysY, and LysZ
Ryo Shimura[1], Yoshitaka Moriwaki[1], Tohru Terada[1,2], Takeo Tomita[1], Makoto Nishiyama[1], Kentaro Shimizu[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, [2]*Interfaculty Initiative in Information Studies*)

1Pos043 How Toll-like receptor 4 dimerization is activated in lipid raft studied by molecular simulations
Manami Ikeda, Shyouzi Takada (*Dept. of Biophys., Div. of Bio. Sci., Grad. Sch. of Sci., Univ. of Kyoto*)

1Pos044 全反射赤外分光法による電位依存性タンパク質の構造研究
The chemistry-induced structural changes in voltage-sensing proteins studied by ATR-FTIR
Masayo Iwaki[1], Hirotaka Narita[1,2], Kohei Takeshita[2], Yasushi Okamura[3], Atsushi Nakagawa[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Inst. Protein Res., Osaka Univ.*, [3]*Grad. Sch. Med., Osaka Univ.*)

1Pos045 タンパク質の局所構造のサンプリングと構造コンプライアンス特性の解析
Sampling of Localized Structures of Proteins and Analysis of their Structural Compliance Properties
Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

1Pos046 実験と計算で明らかにした β-1,2-グルコオリゴ糖結合タンパク質の構造機能相関
Structure-function relationships of β-1,2-glucooligosaccharide-binding protein revealed by experimental and computational methods
Koichi Abe[1], Naoki Sunagawa[1], Tohru Terada[2], Takatoshi Arakawa[1], Kiyohiko Igarashi[1], Masahiro Samejima[1], Hiroyuki Nakai[3], Hayao Taguchi[4], Masahiro Nakajima[4], Shinya Fushinobu[1] ([1]*Grad. Sch. Agric. Life Sci., Univ. Tokyo*, [2]*GSII, Univ. Tokyo*, [3]*Grad. Sch. Sci. Technol., Niigata Univ.*, [4]*Dept. Appl. Bio. Sci., TUS*)

1Pos047 Wide-angle x-ray scattering study on cyanobacterial circadian clock system
Shuji Akiyama[1,2,3], Yoshihiko Furuike[1,2,3], Atsushi Mukaiyama[1,2,3], Takaaki Hikima[3] ([1]*CIMoS, IMS, NINS*, [2]*SOKENDAI*, [3]*RIKEN SPring-8 Center*)

1Pos048 Minimum free energy path of the conformational change in multidrug ABC transporter
Ryuji Ishida[1], Kei Moritsugu[1], Hiroaki Kato[2], **Akinori Kidera**[1] ([1]*Department of Medical Life Science, Yokohama City University*, [2]*Graduate School of Pharmaceutical Sciences, Kyoto University*)

1Pos049 シクロスポリン A の CHARMM 力場の開発
Development of the CHARMM force field for Cyclosporine A
Tsutomu Yamane, Yuta Watanabe, Toru Ekimoto, Mitsunori Ikeguchi (*Graduate School of Medical Life Science, Yokohama City University*)

1Pos050 Evaluation of tau's effects on flexural rigidity and growth rate of microtubule under nanometer-level precision
Hang Zhou[1], Naoto Isozaki[1], Taviare L. Hawkins[2], Jennifer L. Ross[3], Ryuji Yokokawa[1] ([1]*Kyoto University*, [2]*University of Wisconsin La Crosse*, [3]*University of Massachusetts Amherst*)

1Pos051 4-ヒドロキシイソロイシン脱水素酵素（ＨＩＬＤＨ）変異体における特異的反応に関する計算化学的研究
Computational investigation of the selective reaction in the 4-hydroxyisoleucine dehydrogenase (HILDH) mutant
Takaaki Sato[1], Yoshitaka Moriwaki[1], Tohru Terada[1,2], Kentaro Shimizu[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, [2]*Interfaculty Initiative in Information Studies, Univ. of Tokyo*)

1Pos052 重水素化支援中性子小角散乱と超遠心分析を協奏的に用いた αB-クリスタリンの構造と動態
Structure and kinetics of αB-crystallin by complementary use of deuteration-assisted SANS and AUC
Ken Morishima, Yusuke Sakamaki, Rintaro Inoue, Nobuhiro Sato, Masaaki Sugiyama (*Institute for Integrated Radiation and Nuclear Science*)

1Pos053 タンパク質ダイナミクスに対する多様体学習の適用
Applications of a manifold learning technique to protein dynamics
Hiroto Kikuchi, Hiroshi Fujisaki (*Dept. of Phys. Nippon Med. Sch.*)

1Pos054 培養細胞に一過性発現されたヒトヘアケラチン K85 と K35 の中間径フィラメント形成
Intermediate filament assembly of transiently expressed human hair keratins K85 and K35 in cultured cells
Yasuko Sakamoto[1], Masaki Yamamoto[1], Yuko Honda[2], Kenzo Koike[3], Toshihiko Matsumoto[1], Shoji Ando[1] ([1]*Sojo Univ. Fac. Biotech. Life Sci.*, [2]*Saga Univ. Fac. Med.*, [3]*Kao Corp.*)

1Pos055 ヤナギマツタケ（Agrocybe cylindracea）の子実体特異的蛋白質 PRI4 の免疫組織化学と分子物性
Immunohistochemistry and molecular property of a fruiting body-specific protein, PRI4, of the basidiomycete Agrocybe cylindracea
Mitsuki Hashimoto[1], **Chika Abematsu**[1], Masayuki Ikeda[1], Masashi Shin[1], Makoto Iwata[2], Toshihiko Matsumoto[1], Shoji Ando[1] ([1]*Sojo Univ. Fac. Biotech. Life Sci.*, [2]*IMB*)

1Pos056 Crystal structure of human oxidative nucleotide hydrolase in complex with a newly found substrate

Kana Fujimiya[1], **Teruya Nakamura**[1,2,3], Yuta Suzuki[1], Shaimaa Waz[2], Keisuke Hirata[2], Mami Chirifu[2], Shinji Ikemizu[1,2], Yuriko Yamagata[1,2] ([1]*Sch. of Pharmacy, Kumamoto Univ.*, [2]*Grad. Sch. of Pharmaceut. Sci., Kumamoto Univ.*, [3]*Priority Organization for Innovation and Excellence, Kumamoto Univ.*)

1Pos057 細菌 9 型分泌装置蛋白質 PorM の構造

Structure of PorM, a core component of bacterial type IX secretion system

Keiko Sato[1], Kodai Okada[2], Daisuke Nakane[3], Koji Nakayama[1], Katsumi Imada[2] ([1]*Grad. Sch. Biomedical Sci., Nagasaki Univ.*, [2]*Grad. Sch. Sci. Osaka Univ.*, [3]*Dept. Phy. Gakushuin Univ.*)

1Pos058 高速 AFM による IV 型線毛 ATPase-PilB の観察

Observation of the type IV pilus assembly ATPase PilB by using High-Speed AFM

Shogo Sugiyama[1], Zhaomin Yang[2], Takayuki Uchihashi[3] ([1]*Dept. of Phys., Kanazawa Univ.*, [2]*Dept. of Biol. Sci., Virginia tech.*, [3]*Dept. of Phys., Nagoya Univ.*)

1Pos059 3D−RISM 理論を応用した溶液中における Met−enkephalin の構造揺らぎの解析

Analysis of structural fluctuations of Met-encephalin in the solution phase by means of 3D-RISM theory

Masatake Sugita[1], Fumio Hirata[2] ([1]*Dept. of Bioinfo., Col. of Life Sci., Ritsumeikan Univ.*, [2]*Toyota Phys. & Chem. Res. Inst.*)

1Pos060 Design of peptides to hasten actin depolymerization

Clement P. M. Scipion[1,2], Robert C. Robinson[1,2,3] ([1]*INSTITUTE OF MOLECULAR AND CELL BIOLOGY*, [2]*NATIONAL UNIVERSITY OF SINGAPORE*, [3]*Research Institute for Interdisciplinary Science, Okayama University*)

1Pos061 残基間コンタクトプロファイルに基づく MD 計算トラジェクトリの比較手法：PDZ3 ドメインと CypA タンパク質への応用

Comparing two MD simulation trajectories in terms of residue-residue contact: detection of allostery in PDZ3 domain and CypA protein

Chie Motono[1], Takatsugu Hirokawa[1,2] ([1]*molprof, AIST*, [2]*Fac Med., Univ. Tsukuba*)

1Pos062 細胞骨格タンパク質であるビメンチンの細胞膜上への出現機構の解明

Elucidation of recruitment mechanism of vimentin to cell surface

Beomju Hwang[1], Hirohiko Ise[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

1Pos063 酵素の触媒塩基におけるプロトンの配座転移に関するアンブレラ・サンプリング

Umbrella sampling on proton shift in catalytic base of enzyme

Kyosuke Sato (*Dept. Mol. Phys., Fac. Life Sci., Kumamoto Univ.*)

1Pos064 滴定 X 線溶液散乱を用いた GGA の構造と相互作用の解析

Structure and interaction analysis of GGA by using titration SAXS measurement

Yugo Hayashi[1], Natsumi Endo[1], Yoichi Yamazaki[1], Kazuhisa Nakayama[2], Soichi Wakatsuki[3], Hironari Kamikubo[1] ([1]*Div. Mat. Sci., NAIST*, [2]*Grad. Sch. Pharm., Kyoto Univ.*, [3]*Stanford Univ.*)

1Pos065 Ragulator-Rag GTPases 複合体構造における p18 の重要性

Crucial role of p18 component in assembly of Ragulator-Rag GTPases complex

Ryo Yonehara[1], Shigeyuki Nada[2], Tomokazu Nakai[2], Masahiro Nakai[2], Ayaka Kitamura[2], Akira Ogawa[2], Hirokazu Nakatsumi[3], Keiichi I. Nakayama[3], Songling Li[2], Daron M. Standley[2], Eiki Yamashita[1], Atsushi Nakagawa[1], Masato Okada[2] ([1]*Inst. for Protein Res., Osaka Univ.*, [2]*RIMD, Osaka Univ.*, [3]*Med. Inst. of Bioregulation, Kyushu Univ.*)

1Pos066 植物ホルモン「ブラシノステロイド」の生合成の鍵酵素 CYP90B1 の結晶構造解析

Structural insights into a key step of brassinosteroid biosynthesis

Keisuke Fujiyama[1], Tomoya Hino[1], Bunta Watanabe[2], Hyoung Jae Lee[3], Masaharu Mizutani[3], **Shingo Nagano**[1] ([1]*Grad. Sch. Eng., Tottori Univ.*, [2]*Inst. Chem. Res., Kyoto Univ.*, [3]*Grad. Sch. Agr., Kobe Univ.*)

1Pos067 分子動力学シミュレーションを用いた抗 HIV 中和抗体 PG9 と PG16 の CDR-H3 についての構造揺らぎの比較
Molecular dynamics study of structural Fluctuations in CDR-H3 of anti-HIV antibodies PG9 and PG16
Naoki Tanabe[1], Ryo Kiribayashi[1], Hiroko X Kondo[1], Daisuke Kuroda[2], Toru Saito[1], Jiro Kohda[1], Akimitsu Kugimiya[1], Yasuhisa Nakano[1], Kouhei Tsumoto[3], Yu Takano[1] ([1]*Sch. Info. Sci., Hiroshima City Univ.*, [2]*Grad. Sch. Eng., Univ. Tokyo*, [3]*Inst. Med., Univ. Tokyo*)

1Pos068 Crystal analysis investigates signaling molecule for general response protein RsbQ in Bacillus subtilis
Nipawan Nuemket[1], Kazuki Omichi[2], Takashi Kumasaka[1] ([1]*JASRI/SPring-8*, [2]*Kwansei Kaguin University*)

1Pos069 部位特異的スピンラベル EPR 分光法による ABC トランスポーター; BhuUV の構造変化の実時間測定
Real-time measurements of the conformational changes in ABC transporter; BhuUV, revealed by site-directed spin-labeling EPR spectroscopy
Kizashi Onishi, Motonari Tsubaki, Yasuhiro Kobori, Tetsunari Kimura (*Grad. Sch. Sci., Kobe Univ.*)

1Pos070 SR-Ca^{2+}-ATPase におけるリガンド解離の分子動力学法シミュレーション
Molecular dynamics simulations for dissociation of ligands in SR-Ca^{2+}-ATPase
Chigusa Kobayashi[1], Yasuhiro Matsunaga[1,2], Jaewoon Jung[1,3], Yuji Sugita[1,3,4] ([1]*RIKEN R-CCS*, [2]*JST PRESTO*, [3]*RIKEN TMS*, [4]*RIKEN BDR*)

1Pos071 Molecular simulation of protein conformational transition using a two-structure based model
Mashiho Ito, Ryota Mori, Tomoki P. Terada, Masaki Sasai (*Nagoya Univ.*)

1Pos072 網羅的構造解析によって示された基質結合蛋白質の天然変性領域の動的役割
Dynamic roles of intrinsically disordered regions of ligand binding proteins suggested by the comprehensive structural search
Satoshi Omori, Hafumi Nishi, Kengo Kinoshita (*Grad. Sch. of Info. Sci., Tohoku Univ.*)

1Pos073 時計タンパク質 KaiC に組み込まれたアロステリック制御
Allosteric Regulation Designed in Clock Protein KaiC
Yoshihiko Furuike[1,2], Atsushi Mukaiyama[1,2], Eiki Yamashita[3], Takao Kondo[4], Shuji Akiyama[1,2] ([1]*Research Center of Integrative Molecular Systems (CIMoS), Institute for Molecular Science (IMS)*, [2]*Department of Functional Molecular Science, SOKENDAI (The Graduate University for Advanced Studies)*, [3]*Institute for Protein Research, Osaka University*, [4]*Graduate School of Science, Nagoya University*)

1Pos074 全原子および粗視化シミュレーションによるバクテリアフリッパーゼ Pg1K の動作機構研究
Flipping mechanisms of bacterial flippase Pg1K studied by all-atom and coarse grained simulations
Yutaka Murata, Toru Niina, Shoji Takada (*Biophys. Sci. Kyoto Univ*)

1Pos075 タンパク質の折れ畳みの協同性が語るトポロジーの選択性
Cooperativity of protein folding tells us about topology selectivity in genome
Nobu C. Shirai[1], Shintaro Minami[2] ([1]*Center for Info. Tech. and Networks, Mie Univ.*, [2]*NINS, ExCELLS*)

放射線生物：活性酸素／Radiobiology: Active oxygen

1Pos076 銅イオン結合したプリオンペプチドのレドックスポテンシャル
Redox potential of copper-binding prion peptide
Shuhei Murakami, Yukihaya Watanabe, Wakako Hiraoka (*Grad.Sch.of Sci.& Tech.,Meiji Univ*)

1Pos077 酸化ストレスによるミトコンドリア電子伝達系機能異常の ESR 分析
ESR analysis of ROS-induced dysfunction of electron transport chain of mitochondria
Yukihaya Watanabe, Syuhei Murakami, Wakako Hiraoka (*Grad. Sch. of Sci. & Tech., Meiji Univ*)

1Pos078 NHEJ pathway mainly repairs lethal damage caused by the direct action of X-irradiation
Ryoichi Hirayama, Akiko Uzawa, Motofumi Suzuki, Sumitaka Hasegawa (*QST NIRS*)

生命の起源・進化／Origin of life & Evolution

1Pos079 Evaluation of correlation between fluctuation of enzyme activity and evolvability by single enzyme activity measurement
Morito Sakuma[1], Hiroshi Ueno[1], Kentaro Miyazaki[2], Kazuhito Tabata[1], Hiroyuki Noji[1,3] ([1]*Graduate School of Engineering, The University of Tokyo*, [2]*National Institute of Advanced Industrial Science and Technology (AIST)*, [3]*Impulsing Paradigm Change through Disruptive Technologies Program (ImPACT, JST)*)

1Pos080 High-throughput Laboratory Evolution of E. coli to Unveil Phenotypic Plasticity and Constraint
Chikara Furusawa[1,2], Takaaki Horinouchi[1], Tomoya Maeda[1] ([1]*BDR, RIKEN*, [2]*UBI, Univ. Tokyo*)

1Pos081 Natural Peptide-Oligomerization under Aqueous Condition
Muneyuki Matsuo[1,2], Kensuke Kurihara[2,3] ([1]*The Univ. of Tokyo*, [2]*Institute for Molecular Science*, [3]*Exploratory Research Center on Life and Living Systems*)

1Pos082 鋳型ライゲーションにおいて頻度依存的な選択がエラーカタストロフィーを抑制する
Suppression of error catastrophe by frequency-dependent information selection in template-directed ligation
Yasuhiro Magi, Shoichi Toyabe (*Appl. Phys., Tohoku Univ.*)

1Pos083 Experimental demonstration of information retention against diffusional mixing in templated ligation
Kazuki Hata, Shoichi Toyabe, Yasuhiro Magi (*Tohoku University*)

生体膜・人工膜／Biological & Artificial membrane: Structure & Property

1Pos084 せん断変形と狭窄変形における細胞粘弾性の負荷時間依存性
Loading-time dependence of cellular viscoelasticity under shear and squeezing deformation
Hiroaki Ito[1], Atsushi Kirimoto[1], Naoki Takeishi[2], Makoto Kaneko[1] ([1]*School of Engineering, Osaka University*, [2]*School of Engineering Science, Osaka University*)

1Pos085 Effect of lateral phase separation on mechanical stability of lipid membrane
Mika Terada, Yukihiro Tamba (*Natl. Inst. of Tech., Suzuka Coll.*)

1Pos086 抗菌ペプチド・PGLa と単一 GUV との相互作用とそれが誘起するポア形成
Interaction of Antimicrobial Peptide PGLa with Single Giant Unilamellar Vesicles and its Induced Pore Formation
Farliza Parvez[1], Md Jahangir Alam[3], Hideo Dohra[2], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Green Sci. Tech., Shizuoka University*, [3]*Res. Inst. Ele., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

1Pos087 脂質分子のフリップ・フロップに対する膜張力の効果
Effect of Membrane Tension on Transbilayer Movement of Lipids
Moynul Hasan[1], Samiron Kumar Saha[1], **Masahito Yamazaki**[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

1Pos088 リン脂質フリッパーゼ発現による細胞膜の粘度への影響
Effect of flippases expression on viscosity of plasma membranes
Haruna Hayashi[1], Naoto Takada[2], Akira Takakado[1], Hye-Won Shin[2], Koichi Iwata[1] ([1]*Fac. of Sci., Gakushuin Univ.*, [2]*Grad. of Pharm. Sci., Kyoto Univ.*)

1Pos089 バクテリアの推進力によるリポソーム膜の形態変化
Morphological changes of liposomes by bacterial propulsion force
Mai Hayakawa[1], Terajima Hazuki[1], Masamune Morita[2], Tomoyuki Kaneko[1] ([1]*LaRC, FB, Hosei Univ.*, [2]*Biomed. Res. Inst. AIST*)

1Pos090 抗菌ペプチド・マガイニン２が誘起するポア形成に対する膜界面疎水性の効果
Role of Interfacial Hydrophobicity in Antimicrobial Peptide Magainin 2 (mag)-Induced Pore Formation
Moynul Hasan[1], **Md. Mamun Or Rashid**[1], Hideo Dohra[2], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Green Sci. Tech., Shizuoka University*, [3]*Res. Inst. Ele., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

1Pos091 モデル膜を用いたコレステロール依存性細胞溶解毒素の膜結合活性評価
Evaluation of binding activity of cholesterol-dependent cytolytic toxin using model membranes
Nobutake Tamai[1], Tohru Morimitsu[2], Masaki Goto[1], Hideaki Nagamune[1], Hitoshi Matsuki[1] ([1]*Grad. Sch. Tech. Indus. Soc. Sci., Tokushima Univ.*, [2]*Grad. Sch. Adv. Tech. Sci., Tokushima Univ.*)

1Pos092 コレステロールによる薬剤クロルゾキサゾン脂質膜結合抑制効果のリン脂質種依存性
Phospholipid species dependence of cholesterol inhibition effect on the bind of chlorzoxazone to lipid membrane
Hiroshi Takahashi, Shosei Kano (*Biophys. Lab. Gunma Univ.*)

1Pos093 気液界面における脂質単分子膜へのコレステロールと人工肺サーファクタントタンパク質 B の影響
Effect of cholesterol and synthetic lung surfactant protein B on a lipid monolayer at the air-water interface
Hideyuki Nagatsuka, **Masahiro Hibino** (*Div. Sustain. Environ. Eng., Muroran Inst. Tech.*)

1Pos094 粗視化モデルによる二成分脂質膜の構造安定性に関する理論的研究
Theoretical study on the conformational stability of binary lipid membrane by a coarse-grained model
Tetsu Matsuura, Tomoya Maeda, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Nat. Sci. Tech. Kanazawa Univ.*)

1Pos095 抗菌ペプチド・ラクトフェリシン B と単一大腸菌や大腸菌由来の脂質の GUV との相互作用
Interaction of antimicrobial peptide lactoferricin B (Lfcin B) with single *E. coli* cells and single vesicles of extract lipids
Farzana Hossain[1], Md. Moniruzzaman[1], Md. Mizanur Moghal[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

1Pos096 膜透過ペプチド・オリゴアルギニンの抗菌活性と単一大腸菌との相互作用
Antimicrobial activity of cell-penetrating peptide oligoarginine and its interaction with single cells of *Escherichia coli*
Sabrina Sharmin[1], Hideo Dohra[2], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Green Sci. Tech., Shizuoka University*, [3]*Res. Inst. Ele., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

1Pos097 脂質二重膜の組成が EGFR JM 領域の二量体構造に与える影響
Investigation of the correlation between lipid composition and the dimer structure of EGFR JM region
Daisuke Matsuoka[1], Yasuhiro Matsunaga[2], Yuji Sugita[1,2,3] ([1]*RIKEN, Theoreitcal Molecular Science*, [2]*RIKEN R-CCS*, [3]*RIKEN BDR*)

1Pos098 Substrate-supported model biological membrane with controlled two-dimensional and three-dimensional structures
Sawako Kobayashi[1], Ryota Komatsu[1], Kennichi Morigaki[2] ([1]*Graduate School of Agricultural Science, Kobe University*, [2]*Biosignal Research Center, Kobe University*)

1Pos099 非対称膜組成の小胞封入ベシクルの作製
Formation of giant vesicle containing small vesicles with asymmetric lipid membranes
Koki Kamiya[1], Toshihisa Osaki[1,2], Shoji Takeuchi[1,2] ([1]*Kanagawa Institute of Industrial Science and Technology*, [2]*IIS, university of Tokyo*)

1Pos100 逆相遠心法による巨大リポソームの迅速形成・精製とその特性
Giant vesicles rapidly prepared and purified using a reverse-phase/centrifugation method
Kanta Tsumoto, Kohei Nakano, Yuki Hayashi, Masahiro Tomita (*Grad. Sch. Eng., Mie Univ.*)

1Pos101 Development of a polarized coarse grained water model and its application in lipid membrane systems
Yuusuke Miyazaki, Susumu Okazaki, Wataru Shinoda (*Grad. Sch. Eng., Nagoya Univ.*)

ゲノム生物学／Genome biology: Genome analysis

1Pos102 ニック DNA のナノポアへのつまりと特異的挙動
Clogging and returning of nicked DNA at nanopores
Kento Lloyd, Seiya Minato, Tomoya Kubota, Toshiyuki Mitsui (*Grad. Sch. of Sci. & Eng., Aoyama Gakuin Univ.*)

1Pos103 A datamining approach for genotype-phenotype correlation of *SCN1A*-related epilepsies based on physico-chemical properties changes
Shuichi Yoshida, Takuhiro Nishio (*Dept. of Physics, Hamamatsu Univ. Sch. Med.*)

1Pos104 数理モデルとライブイメージングデータを用いた分裂酵母間期核内構造の解析
Analysis of fission yeast interphase intranuclear structure by mathematical model and live imaging data
Yuki Takayama[1], Hiroaki Ito[2], Hisamichi Senda[2], Hiraku Nishimori[1], Masaru Ueno[2], Akinori Awazu[1] ([1]*Grad. Sch. Sci., Univ. Hiroshima*, [2]*Grad. Sch. Advanced Sciences of Matter, Univ. Hiroshima*)

1Pos105 ヌクレオチド組成空間におけるハビタブルゾーンの生物的意味
Biological meaning of “habitable zone” in nucleotide composition space
Shigeki Mitaku[1], Ryusuke Sawada[2] ([1]*Emeritus Prof. Nagoya Univ.*, [2]*Med. Inst. Bioregulation, Kyushu Univ.*)

1Pos106 Dynamic changes in the interchromosomal interaction of early histone gene loci during development of sea urchin
Masaya Matsushita, Hiroshi Ochiai, Ken-ichi Suzuki, Sayaka Hayashi, Ayaka Sugiyama, Takashi Yamamoto, **Akinori Awazu**, Naoaki Sakamoto (*Dept. of Math and Life Sci. Hiroshima Univ.*)

1Pos107 大腸菌における走化性関連タンパク質のコドン使用傾向
Pattern of codon usage for chemotaxis related protein genes in E.coli
Serika Taga[1], Nobuyuki Uchikoga[2], Takanori Sasaki[3] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ*, [2]*Catalyst*, [3]*Grad. Sch. Adv. Math. Sci., Meiji Univ*)

1Pos108 遅発性アルツハイマー病に関連する新規ゲノム領域の網羅的探索
Comprehensive Search of Novel Genome Regions Related to Late-Onset Alzheimer’s Disease
Yudai Hirose, Hiraku Nishimori, Akinori Awazu (*Department of Mathematical and Life Sciences, Hiroshima University*)

1Pos109 核膜変形と核内流体を考慮した分裂酵母染色体動態の物理モデル
Physical model of fission yeast chromosome dynamics considering nuclear envelope deformation and intranuclear hydrodynamics
Kazutaka Takao, Hiraku Nishimori, Akinori Awazu (*Dept. Math and Life Sci., Hiroshima Univ.*)

1Pos110 Dynamics and organization of slow nucleosomes in live mammalian cells
Ashwin Selvarajan S[1], Tadasu Nozaki[2], Kazuhiro Maeshima[2], Masaki Sasai[1] ([1]*Department of Applied Physics, Nagoya University, Nagoya, Japan*, [2]*Structural Biology Center, National Institute of Genetics, Mishima, Japan*)

筋肉／Muscle

1Pos201 心筋の調節タンパク質トロポニンは構造多型をカルシウムとリン酸化により部分的にシフトさせる：二量子遷移(DQC)ESR 距離測定による研究
Calcium and phosphorylation partially shifts multiple conformations of cardiac troponin: Distance study by double quantum coherence ESR
Toshiaki Arata[1,2], Jun Abe[3], Shoji Ueki[4], Yasunori Ohba[3] ([1]*Dept. Biol., Grad. Sch. Sci., Osaka City Univ.*, [2]*Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.*, [3]*Inst. Multidisciplinary Res. Adv. Materials, Tohoku Univ.*, [4]*Kagawa Sch. Pharmaceutical Sci., Tokushima Bunri Univ.*)

1Pos202 FRET で捉えたアクチン繊維末端付近の構造ゆらぎ
B- or P-ends of actin filament can be determined by measuring the fluctuation of FRET efficiencies
Ryota Mashiko[1], Hirotaka Ito[1], Ryusei G Ebata[1], Kenji Kamimura[2], Hajime Honda[1] ([1]*Dep. Bioeng., Nagaoka Univ.*, [2]*Tech, Dep. Elect. Contr. Eng., NIT, Nagaoka College*)

1Pos203 細胞クラスター構成法を用いた心筋細胞の拍動同期化における集団効果の解明
Community effect of cardiomyocytes in synchronous behavior of beating by constructing cell cluster (1): Experimental approach
Naoki Takahashi[1], Akihiro Yamashita[2], Kazuhumi Sakamoto[3], Masao Odaka[4,5], Akihiro Hattori[4,5], Kenji Matsuura[4,5], Kenji Yasuda[1,3,4,5] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Adv. Sci. & Eng., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [4]*Org. Univ. Res. Initiatives, Waseda Univ.*, [5]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos204 アクチン分子の構造多様性について
Polymorphism of actin molecules
Toshiro Oda[1], Shuichi Takeda[2], Akihiro Narita[2], Yuichiro Maeda[2,3] ([1]*Fac. Health and Welfare, Tokaigakuin Univ.*, [2]*Struct. Biol. Res. Center, Grad. Sch. Sci., Nagoya Univ.*, [3]*TOYOTA RIKEN*)

1Pos205 表面プラズモン共鳴を用いた β-アドレナリン刺激に関わる心筋トロポニン分子内相互作用の研究
Surface plasmon resonance studies of the intramolecular interaction in cardiac troponin concerned with β-adrenergic stimulation
Yurie Inamoto[1], Toshiaki Arata[2], Shoji Ueki[1] ([1]*Kagawa Sch. of Pharm.Sci.,Tokushima Bunri Univ.*, [2]*Grad.Sch.Sci.,Osaka City Univ.*)

1Pos206 高静水圧下におけるマウス心筋細胞への影響
High hydrostatic pressure induces cardiomyocyte contraction
Yohhei Yamaguchi[1], **Masayoshi Nishiyama**[2], Hiroaki Kai[3], Gentaro Iribe[3], Keiji Naruse[3], Masatoshi Morimatsu[3] ([1]*Asahikawa Med. Univ.*, [2]*Kindai Univ.*, [3]*Okayama Univ.*)

分子モーター／Molecular motor

1Pos207 *Bacillus* PS3 F_oF_1-ATP 合成酵素の H^+輸送活性の顕微鏡 1 リポソーム解析
Microscopic single liposome analysis of H^+-translocating activity of *Bacillus* PS3 F_oF_1-ATP synthase
Naoya Iida[1], Yuzo Kasuya[1], Naoki Soga[2], Taro Uyeda[1], Masasuke Yoshida[3], Kazuhiko Kinosita[1], Toshiharu Suzuki[2,3,4] ([1]*Dept. Physics, Waseda Univ.*, [2]*Dept. Eng, Univ. of Tokyo*, [3]*Dept. Mol Biochem, Kyoto Sangyo Univ*, [4]*CLS, Tokyo Inst of Tech*)

1Pos208 Rotation of the engineered F_1-ATPase with non-catalytic α-type P-loops
Hiroshi Ueno[1], Rie Koga[2], Tomoko Masaike[3], Nobuyasu Koga[2], Hiroyuki Noji[1] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*ExCELLS, NINS*, [3]*Grad. Sch. Sci. Tech., Tokyo Univ. of Sci.*)

1Pos209 ヒンジ領域を非触媒型に置換した触媒サブユニットをもつ F_1-ATPase の回転トルクと反応速度
Rotational torque and kinetics of F_1-ATPase containing the catalytic subunit with a non-catalytic hinge
Tomoyasu Sato[1], Hiroshi Ueno[2], Kumiko Hayashi[3], Rie Koga[4], Nobuyasu Koga[4], Hiroyuki Noji[2], Tomoko Masaike[1] ([1]*Dept. Appl. Biol. Sci., Grad. Sch. Sci. Tech., Tokyo Univ. of Sci.*, [2]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [3]*Dept. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*, [4]*ExCELLS, NINS*)

1Pos210 好熱菌 F1 による ATP 加水分解におけるリン酸解離のタイミング
On the timing of phosphate release in the ATPase reaction by TF1
Eiro Muneyuki[1], Yohei Nakayama[1], Shoichi Toyabe[2], Hiroshi Ueno[3] ([1]*Department of Physics, Faculty of Science and Engineering, Chuo University*, [2]*Department of Applied Physics, Graduate School of Engineering, Tohoku University*, [3]*Department of Applied Chemistry, Graduate School of Engineering, The University of Tokyo*)

1Pos211 F1-ATPase の構造変化に α と β の P-loop 配列の違いが及ぼす影響
Impact of the sequence difference of P-loop on the conformational changes of F1-ATPase
Rie Koga[1], Hiroshi Ueno[2], Tomoko Masaike[3], Hiroyuki Noji[2,4], Nobuyasu Koga[1] ([1]*ExCELLS, NINS*, [2]*Dept. Appl. Chem., The Univ. Tokyo*, [3]*Dept. Appl. Biol. Sci., Tokyo Univ. of Sci.*, [4]*ImPACT, JST*)

1Pos212 Assignment of subunit components in motor evolved from F-ATPase for *Mycoplasma mobile* gliding
Takuma Toyonaga[1], Takayuki Kato[2], Akihiro Kawamoto[3], Noriyuki Kodera[4], Toshio Ando[4], Keiichi Namba[2,5], Makoto Miyata[1,6] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*IPR, Osaka Univ.*, [4]*Bio-AFM FRC, Kanazawa Univ.*, [5]*BDR & SPring-8, Riken*, [6]*OCARINA, Osaka City Univ.*)

1Pos213 Half channels and unidirectional rotation in the F_O sector of *E. coli* ATP synthase observed by molecular dynamics simulation
Dan Parkin, Daiki yamakoshi, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1Pos214 細菌べん毛モーターの回転方向変換制御機構の解明
Elucidation of the directional switching mechanism of the bacterial flagellar motor by electron cryomicroscopy
Tomoko Miyata[1], Takayuki Kato[1], Akihiro Kawamoto[2], Fumiaki Makino[1], Namba Keiichi[1,3] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*IPR, Osaka Univ.*, [3]*BDR & SPring-8, RIKEN*)

1Pos215 Effect of pH on rotation of the proton-driven bacterial flagellar motor under near zero load
Yuta Hanaizumi[1], Shuichi Nakamura[1,2], Yusuke V. Morimoto[2,3], Tohru Minamino[2], Keiichi Namba[2,4] ([1]*Grad.Sch.Eng.,Tohoku Univ.*, [2]*Grad.Sch.Frontier Biosci.,Osaka Univ.*, [3]*Dept. of Biosci. Bioinfo., Kyushu Inst. Tech.*, [4]*QBiC,RIKEN*)

1Pos216 Feedback regulation of the ion channel activity of the flagellar motor stator complex
Naoya Terahara[1], Keiichi Namba[1,2], Tohru Minamino[1] ([1]*Grad. Sch. Frontier BioSci., Univ. Osaka*, [2]*BDR and Spring8 RIKEN*)

1Pos217 海洋性ビブリオ菌べん毛モーター固定子 PomA タンパク質の Cys 変異導入を用いた細胞質領域荷電残基の構造解析
Analysis of charged residues by Cys mutagenesis in cytoplasmic loop of flagellar motor protein PomA of marine *Vibrio*
Taira Mino, Tatsuro Nishikino, Hiroto Iwatsuki, Seiji Kojima, **Michio Homma** (*Nagoya Univ, Sch Science, Biological Sci*)

1Pos218 Stator-units distribution and dynamics of E. coli sodium-driven chimera flagella motor
Tsai-Shun Lin[1], Michio Homma[2], Seiji Kojima[2], Chien-Jung Lo[1] ([1]*National Central Univ.,Taiwan*, [2]*Grad. sch. of Sci., Nagoya Univ.*)

1Pos219 *Paenibacillus* sp. TCA20 がもつ二価カチオン駆動型べん毛モーター固定子 MotA1MotB1 の機能解析
Characterization of ion specificity of MotA1/MotB1 in *Paenibacillus* sp. TCA20
Sakura Onoe[1], Myu Yoshida[2], Masahiro Ito[3], Yoshiyuki Sowa[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Grad. Sch. Life Sci. Toyo Univ.*, [4]*RC. Micro-nano Tech., Hosei Univ.*)

1Pos220 Investigating the Growth Mechanism of Bacterial Flagella by Real-time Fluorescencet Imaging
Xiang-Yu Zhuang, Chien-Jung Lo (*Department of physics, National Central University*)

1Pos221 線毛を使って運動する桿菌とその走化性に関するシミュレーション
Simulation study of bacillus moving with pili and its chemotaxis
Ryota Morikawa, Masatada Tamakoshi, Takeshi Miyakawa, Masako Takasu (*School of Life Sciences, Tokyo University of Pharmacy and Life Sciences*)

1Pos222 Rng2 のアクチン結合部位は、HMM で駆動されるアクチン運動を強くかつ協同的に阻害する
Potent and highly cooperative inhibition of actin movement on HMM by actin binding domain of Rng2
Yuuki Hayakawa[1], Kien X Ngo[2], Noriyuki Kodera[2], Taro Uyeda[1] ([1]*Grad. Sch. Faculty of Sci. and Eng., Waseda Univ.*, [2]*WPI NanoLSI., Kanazawa Univ.*)

1Pos223 Molecular Structures of Actin Filaments Bound with α-Actinin, Tropomyosin-Troponin and Myosin II Analyzed by High Speed AFM
Kien Xuan Ngo[1], Noriyuki Kodera[1], Taro Q.P. Uyeda[2] ([1]*Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*, [2]*Department of Physics, Faculty of Advanced Science and Engineering, Waseda University*)

1Pos224 Myosin minifilament-driven fragmentation of actin filaments triggers contraction of a disordered actin network
Kyohei Matsuda[1], Takuya Kobayashi[2], Mitsuhiro Sugawa[1], Yurika Koiso[1], Yoko Y. Toyoshima[1], Junichiro Yajima[1] ([1]*Grad school of arts and sciences, Univ. of Tokyo*, [2]*Juntendo Univ. Grad School of Medicine*)

1Pos225 歩行運動中のミオシン VI の前足のブラウン運動の自由エネルギーランドスケープ
Free energy landscape for the Brownian motion of the leading head of myosin VI during the stepping motion
Tomoki P. Terada[1], Qing-Miao Nie[2], Masaki Sasai[1] ([1]*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*, [2]*Dept. Appl. Phys., Zhejiang Univ. Tech.*)

1Pos226 DNA オリガミ-ミオシン II モーター混合システムの 1 分子解析
Single molecule analysis of DNA origami-myosin II motor hybrid system
Hiroki Fukunaga[1], Masashi Ohmachi[2], Keisuke Fujita[2], Keigo Ikezaki[3], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*FBS, Univ. Osaka*, [2]*BDR, Riken*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

1Pos227 アクチンフィラメントに対するヘビーメロミオシンの協同的結合の方向性の解析
Analysis of the direction of cooperative binding of heavy meromyosin to actin filaments
Naoyuki Muratsubaki[1], Rika Hirakawa[1], Taro Q.P. Uyeda[2], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Sustain, Environ. Eng., Muroran Inst. Technol.*, [2]*Waseda Univ.*)

1Pos228 高速原子間力顕微鏡による人工ミオシンフィラメントでのミオシン II モーターの可視化
Direct visualization of individual myosin II motors in artificial myosin filaments by high-speed AFM
Masashi Ohmachi[1], Keigo Ikezaki[3], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*BDR, Riken*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

神経・感覚／Neuroscience & Sensory systems

1Pos301 アミロイド β（1-40）ペプチドと人工 GM1 糖鎖クラスターの複合体形成シミュレーション p
Binding Simulations of an Amyloid-β (1-40) peptide to an Artificial GM1 Glycan Cluster
Yuhei Tachi[1,2], Yuko Okamoto[1], Hisashi Okumura[2,3,4] ([1]*Graduate school of Science, Nagoya University*, [2]*Institute for Molecular Science*, [3]*The Graduate University for Advanced Studies*, [4]*Exploratory Research Center on Life and Living Systems*)

1Pos302 アミロイドβの凝集はアクチンに富む細胞辺縁部で凝集が促進される
Aggregation of amyloid β was induced at the actin-rich cell periphery
Yusaku Chikai[1], Ryota Yamashita[2], Masahiro Kuragano[3], Masayuki Takahashi[4], Kiyotaka Tokuraku[5] ([1]*Dep. App. Sci., Muroran Inst. Technol.*, [2]*Grad. Sch. Sustain., Environ. Eng., Muroran Inst. Technol.*, [3]*Grad. Sch. Chem. Sci. Eng., Univ. Hokkaido.*, [4]*Grad. Sch. Chem. Sci. Eng., Univ. Hokkaido.*, [5]*Grad. Sch. Sustain., Environ. Eng., Muroran Inst. Technol.*)

1Pos303 シナプス後肥厚部タンパク質群の自己集積のメソスケール分子シミュレーション研究
Mesoscopic Molecular Simulation for Self-assembly of the Postsynaptic Density Proteins
Hana Slevin Ohama, Diego Ugarte, Shoji Takada (*Dept. Biophysics, Div. Biology, Graduate School of Science, Kyoto University*)

1Pos304 AFM 細胞間接着力測定技術を用いた腫瘍内細胞間接着力の in vitro 解析
Measurements of intercellular adhesions of tumor microenvironment cells in vitro by using AFM
Kenta Ishibashi[1], Tomoko Okada[2], Chikashi Nakamura[1,2], Hyonchol Kim[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Biomed. Res. Inst., AIST*)

1Pos305 全身麻酔薬プロポフォールによる蛙坐骨神経の複合活動電位抑制とその化学構造
Inhibition by general anesthetic propofol of frog sciatic nerve compound action potential and its chemical structure
Nobuya Magori, Tsugumi Fujita, Kotaro Mizuta, **Eiichi Kumamoto** (*Department of Physiology, Faculty of Medicine, Saga University*)

1Pos306 Chemosensing-neuron regulates cold tolerance via Ca2+-dependent endoribonuclease with apoptotic signaling in C. elegans
Atsushi Kuhara[1,5], Tomoyo Ujisawa[1], Atsushi Toyoda[3], Katsushi Arisaka[4], Miki Ii[2], Akane Ohta[1] ([1]*Institute for Integrative Neurobiology, Konan University*, [2]*University of Alaska Anchorage*, [3]*National Institute of Genetics*, [4]*UCLA*, [5]*PRIME, AMED*)

1Pos307 ミミズ繰り返し体壁刺激による慣れの神経機構
Mechanism of habituation by repeated tactile stimulus in earthworm
Yoshiichiro Kitamura, Haruya Fujita, Yoshiki Funahashi (*Department of Mathematical Sciences and Physics College of Science and Engineering, Kanto Gakuin University*)

1Pos308 エピカテキンはヨーロッパモノアラガイの味覚嫌悪学習による長期記憶形成を増強する
Epicatechin enhances the long-term memory formation for taste-aversive conditioning in the pond snail
Yoshimasa Komatsuzaki[1], Tetsuya Iwahori[1], Shogo Nakada[2], Ayaka Itoh[2], Sho Tozawa[1], Ken Lukowiak[3], Minoru Saito[2] ([1]*Dept. Phys., Coll. Sci. Tech., Nihon Univ.*, [2]*Dept. Biosci., Coll. Hum. Sci., Nihon Univ.*, [3]*Hotchkiss Brain Inst., Fac. Med., Univ. Calgary*)

神経回路・脳の情報処理／Neuronal circuit & Information processing

1Pos309 インビボでの周波数依存性シナプス可塑性の数学的解析
Mathematical analysis of the frequency-dependent synaptic plasticity in vivo
Katsuhiko Hata[1,2,3,4,5], Osamu Araki[6], Osamu Yokoi[2,4], Toshiaki Kaminaka[2,4], Tatsuya Saka[2,4], Izumi Kuboyama[1], Susumu Ito[3], Tetsuro Nikuni[5] ([1]*Sch. Emerg. Med. Sys. Kokushikan Univ.*, [2]*DPEMS, Kokushikan Univ*, [3]*High-Tech Res. Cent., Kokushikan Univ*, [4]*Res Cent for Math Med*, [5]*Dept of Phys TUS*, [6]*Dept of Ap Phys TUS*)

1Pos310 Reinforcement learning using Deep Deterministic Policy Gradient (DDPG) with image input
Keisuke Hara[1], Naoto Kobayashi[1], Hideo Mukai[2] ([1]*Graduate School of Science and Technology, Meiji University*, [2]*School of Science and Technology, Meiji University*)

1Pos311 光ファイバー集束光加熱光学系を用いた高精度・非侵襲オンチップアガロースパターン構築技術の開発
A 1064/1480-nm photo-thermal etching system with fiber optics for an accurate and non-invasive micropatterning of an agarose thin layer
Takahito Kikuchi[1], Shota Aoki[1], Yuhei Tanaka[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

1Pos312 プラズモニックチップ上の増強蛍光による培養神経細胞の自発活動計測
Spontaneous activity in cultured neurons measured with the enhanced fluorescence on the plasmonic chip
Wataru Minoshima[1], Chie Hosokawa[2], Suguru Kudoh[1], Keiko Tawa[1] ([1]*Kwnasei Gakuin University*, [2]*National Institute of Advanced Industrial Science and Technology*)

1Pos313 神経突起伸長速度に対する細胞集団サイズとチャネル幅の効果
Effect of cell cluster size and channel width to neurite elongation rate
Hayato Toriumi, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ*)

1Pos314 外部からの磁気刺激に対する神経細胞の応答 - 刺激強度依存性
Response of nerve cells to external magnetic stimulation - Stimulation intensity dependence
Toshiaki Kaminaka[1,2], Osamu Yokoi[1,2,3], Tatsuya Saka[1,2,3], Susumu Ito[4], Izumi Kuboyama[5], Katsuhiko Hata[1,2,3,4,5] ([1]*Res Cent for Math Med*, [2]*DPEMS Kokushikan Univ*, [3]*TUS*, [4]*HRC,Kokushikan Univ*, [5]*Sch. Emerg. Med. Sys, Kokushikan Univ*)

1Pos315 オンチップ多電極システムによる孤立神経 1 細胞自発発火の電位変化の解析
Extracellular field potential change analysis of spontaneous firing of an isolated neuron by an on-chip multi-electrode array system
Shota Aoki[1], Takahito Kikuchi[1], Yuhei Tanaka[2], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

1Pos316 神経活動電位系列の生成解読様式とその情報伝送容量について
Encoding and decoding of neural pulse code system and its channel capacity
Susumu Ito[1], Toshiaki Kaminaka[2], Katsuhiko Hata[1,2,3], Izumi Kuboyama[3] ([1]*HRC,Kokushikan Univ*, [2]*Res.Cent.Math.Med*, [3]*Sch.Emerg.Med.Sys, Kokushikan Univ*)

1Pos317 線虫のシナプス結合経路と全中枢神経細胞活動データから推定したシグナル経路の頑健性
Robustness of synaptic pathway and signaling pathway estimated from the whole-brain activity data in C. elegans
Yuishi Iwasaki[1], Hirofumi Sato[2], Suzu Oe[3], Sayuri Kuge[3], Takayuki Teramoto[3], Terumasa Tokunaga[4], Osamu Hirose[5], Stephen Wu[6], Yu Toyoshima[2], Moon Sun Jang[2], Ryo Yoshida[6], Yuichi Iino[2], Takeshi Ishihara[3] ([1]*Fac. Eng., Ibaraki Univ.*, [2]*Grad. Sch. Sci., Univ. Tokyo*, [3]*Grad. Sch. Sci., Kyushu Univ.*, [4]*Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Institute Tech.*, [5]*Institute. Sci. and Eng., Kanazawa Univ.*, [6]*Institute Stat. Math.*)

1Pos318 海馬で合成される男性・女性ホルモンやストレスホルモンによる記憶シナプスの non-genomic な制御
Non-genomic modulation of synapses by hippocampus-synthesized androgen, estrogen and stress steroid
Suguru Kawato[1,2], Mika Soma[1], Mari Ogiue-Ikeda[1] ([1]*Dep. Cognitive Neuroscience, Pharma-Science, Teikyo Univ.*, [2]*Dep. Urology, Grad Sch Medicine, Juntendo Univ.*)

1Pos319 アガロース微細構造を用いた二つの海馬細胞から伸長する２つの神経突起の反発相互作用の解析
Repulsive interactions of two neurites elongated from two isolated hippocampal cells in agarose width-length-controlled microchannels
Yuhei Tanaka[1], Takahito Kikuchi[2], Shota Aoki[2], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos320 小脳核ペリニューロナルネットによる GABA シナプス伝達修飾と運動学習制御
Perineuronal nets in the deep cerebellar nuclei modulate GABAergic transmission and regulate motor learning
Moritoshi Hirono[1], Satoshi Watanabe[2], Fuyuki Karube[1], Fumino Fujiyama[1], Shigenori Kawahara[3], Soichi Nagao[4,5], Yuchio Yanagawa[6], Hiroaki Misonou[1] ([1]*Grad. Sch. Brain Sci., Doshisha Univ.*, [2]*Natl Inst Neurosci, NCNP*, [3]*Grad. Sch. Sci. Eng., Univ. Toyama*, [4]*Lab. Motor Learning Control, RIKEN BSI*, [5]*Lab. Integrative Brain Functions, Nozomi Hospital*, [6]*Dep. Genetic and Behav. Neurosci., Gunma Univ. Grad. Sch. Med.*)

発生・分化／Development & Differentiation

1Pos321 どのように神経突起は軸索および樹状突起へと個性化するのか？ ～微小管配向動態の観点から～
How neurites acquire identity of axon and dendrites through microtubule orientation dynamics?
Naoki Honda (*Grad. Sch. Biostudies., Kyoto Univ.*)

1Pos322 細胞性粘菌の細胞分化に伴う細胞質 pH 変化
Changes in cytoplasmic pH following the cell differentiation in *Dictyostelium*
Yusuke V. Morimoto[1,2], Masahiro Ueda[2,3] ([1]*Dept. of Biosci. Bioinfo., Kyushu Inst. Tech.*, [2]*RIKEN, BDR*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*)

1Pos323 ヒト誘導多能性幹細胞由来の内胚葉および中胚葉による原腸形成期の移動
Migration of Endoderm and Mesoderm Derived from Human Induced Pluripotent Stem Cells during Human Gastrulation Stage
Kenshiro Maruyama[1], Ryo Kobayashi[2], **Kiyoshi Ohnuma**[1] ([1]*Grad. Sch. Eng., Univ. Nagaoka Tech.*, [2]*Dept. BioEng., Univ. Nagaoka Tech.*)

1Pos324 細胞分裂、分化、発生過程を細胞内小器官の 3D 構造モデルから読み解くための試み
Attempt to understand cell division, differentiated, developmental process from 3D structural model of intracellular organelle
Takako M. Ichinose[1], Takeshi Itabashi[1,2,3], Hikari Mori[1], Junpei Kuroda[4], Shigeru Kondo[4], **Atsuko H. Iwane**[1,2,3] ([1]*Cell Field Struc., BDR, Riken*, [2]*Spec. Res. Promot. Group, Grad. Sch. Fronti., Biosci., Osaka Univ.*, [3]*Grad. Sci., Hiroshima Univ.*, [4]*Pattern formation, Grad. Sch. Fronti., Biosci., Osaka Univ.*)

1Pos325 線虫 *C. elegans* 胚発生における細胞形状ダイナミクスの定量解析
Quantitative analysis of cell shape dynamics in *C. elegans* embryogenesis
Yusuke Azuma, Shuichi Onami (*RIKEN BDR*)

1Pos326 初期胚発生における力学モデルの解析
Analyzing and modeling of early embryo development
Takaaki Matsui[1], Tetsuya Kobayashi[2] ([1]*Grad. Sch. Eng. EEIS, Univ.Tokyo*, [2]*IIS, Univ.Tokyo*)

1Pos401 紫外可視光変換システムとゲル固体電気化学素子のセンサーへの応用と水素化アモルファスシリコン薄膜の効果
Ultra violet visible light conversion system and gel electrochemical element for sensor and the effect of hydrogenated amorphous silicon
Koki Shimanaka[1], Makoto Horigane[1], Shotaro Minato[1], Miku Kaneta[1], Norimi Takahashi[1], Shota Murakami[1], Hiroshi Masumoto[2], Takashi Goto[3], **Yutaka Tsujiuchi**[1] ([1]*Material Science and Engineering, Akita University*, [2]*Frontier Research Institute for Interdisciplinary, Tohoku University*, [3]*Institute for Materials Research, Tohoku University*)

1Pos402 マイクロ流路を用いた連続滴定用オートサンプリングシステムの改良
Improvement of the micro-fluidics based auto sampling system designed for continuous titration experiments
Shinji Amano, Yugo Hayashi, Yoichi Yamazaki, Hionari Kamikubo (*Div. Mat. Sci., NAIST*)

1Pos403 HPD による広視野多色蛍光 1 分子検出
Wide-field single-molecule multicolor fluorescence detection by hybrid photo-detectors (HPDs)
Atsuhito Fukasawa[1], Gaku Nakano[1], Hiroaki Yokota[2], Minako Hirano[2], Toru Ide[3] ([1]*Hamamatsu Photonics K.K.*, [2]*Grad. Sch. Creation Photon Indust.*, [3]*Grad. Sch. Nat. Sci. Technol., Okayama Univ.*)

1Pos404 水溶液中における蛍光タンパク質発色団の赤外スペクトル−過渡蛍光を利用した新規手法の開発−
IR spectrum of fluorescent protein chromospheres in water -Development of a transient fluorescence-detected resonance IR spectroscopy-
Hirona Takahashi, Tomoya Miyake, Tatsuya Oue, Makoto Sakai (*Okayama University of Science*)

1Pos405 偏光蛍光相関分光法(Pol-FCS)による回転拡散成分振幅の配向依存性の研究
Study of the orientation dependency of fraction of rotational diffusion in Polarization-dependent Fluorescence Correlation Spectroscopy
Satoru Momosaki[1], Johtaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Faculty of Advanced Life Science, Hokkaido University*, [3]*Biomedical Research Institute, AIST*)

1Pos406 赤外超解像顕微鏡による羽毛内ケラチンタンパク質の分布・配向観察
Orientation-sensitive molecular imaging of feather keratin proteins by an IR super-resolution micro-spectroscopy
Hirona Takahashi, Masanobu Miyoshi, Takeshi Fujimoto, **Makoto Sakai** (*Faculty of Science, Okayama University of Science*)

1Pos407 マイクロデバイス中の単一酵素活性検出による病態診断法の開発
Development of Novel Disease Diagnosis Platform based on Enzyme Activity Detection at Single Protein Level
Shingo Sakamoto[1], Toru Komatsu[1,5], Rikiya Watanabe[4,5], Zhang Yi[4], Hiroyuki Noji[4], Yasuteru Urano[1,2,3] ([1]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [2]*Grad. Sch. Med., The Univ. Tokyo*, [3]*AMED CREST*, [4]*Grad. Sch. Eng., The Univ. Tokyo*, [5]*JST PRESTO*)

1Pos408 Highly sensitive detections of protein-nucleic acid interactions and redox enzyme reactions using nanostructured electrode
Yasuhiro Mie, Yasuo Komatsu, Yoshiaki Yasutake, Tomohiro Tamura (*Bioproduction Res. Inst., AIST*)

1Pos409 フォトクロミック分子を利用した蛋白質の高時間分解拡散観測手法
Protein diffusion probed by the transient grating method with a photochromic molecule
Shunki Takaramoto, Yusuke Nakasone, Masahide Terazima (*Dep. Chem., Sch. Sci, Kyoto Univ.*)

1Pos410 リン酸結合タンパクを封入した水滴チャンバーアレイによるリン酸検出系の高度化
Advanced phosphate detection method by phosphate binding protein encapsulated in droplet chamber arrays
Akane Kumayama[1], Taisuke Inage[1], Masayuki Higuchi[1], Hiroshi Ueno[2], Kazuhito Tabata[2,3], Hiroyuki Noji[2], Tomoko Masaike[1,4] ([1]*Dept. Appl. Biol. Sci., Grad. Sch. Sci. Tech., Tokyo Univ. of Sci.*, [2]*Dept. Appl. Chem., Sch. Eng., Univ. of Tokyo*, [3]*PRESTO, JST*, [4]*PRESTO, JSTRes. Inst. for Sci and Tech., Tokyo Univ. of Sci.*)

1Pos411 細胞内高分子クラウディング状態モデル検証と細胞周期研究への応用
Verification of macromolecule species in intracellular macromolecular crowding condition application to cell cycle study
Akito Matsui[1], Johtaro Yamamoto[3], Masataka Kinjo[2] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Faculty of Advanced Life Science, Hokkaido University*, [3]*AIST*)

1Pos412 マクロファージにおける貪食効率の評価のための抗原 free-flow 法の開発
Development of free-flow assay for precise evaluation of phagocytosis efficiency of macrophages
Yuya Furumoto[1], Yoshiki Nakata[1], Toshiki Azuma[2], Amane Yoshida[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos413 オンチップ１細胞計測におけるマクロファージの同一点連続貪食の履歴効果評価
Hysteresis of single point sequential phagocytoses in macrophages using on-chip single cell measurement assay
Toshki Azuma[1], Yoshiki Nakata[2], Yuya Furumoto[2], Amane Yoshida[1], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos414 オンチップ１細胞計測系によるマクロファージの貪食限界の測定
Identifying the maximum size of phagocytosis in macrophages using on-chip single cell measurement assay
Amane Yoshida[1], Yoshiki Nakata[2], Yuya Furumoto[2], Toshiki Azuma[1], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos415 血管内皮細胞のダイナミクス解明に向けた集束光によるゼラチン三次元微細加工技術の評価
Evaluation of photo-thermal three-dimensional gelatin-gel microfabrication technology for clarification of endothelial cells' dynamics
Hiromichi Hashimoto[1], Kento Iida[2], Yuki Yamanaka[2], Ryuji Takano[1], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos416 アガロースマイクロチャンバーを用いた多電極アレイによる心筋細胞小細胞群における細胞外電位の測定
Measurement of extracellular potential in small cluster of cardiomyocytes by multi electrode array with agarose microchamber
Naoki Tadokoro, Tomoyuki Kaneko (*LaRc, FB, Hosei Univ.*)

1Pos417 細胞のマクロな特徴量とラマンスペクトルの間に対応はあるか
Is There A Correspondence between Cellular Macroscopic Quantities and Raman Spectra?
Ken-ichiro F. Kamei[1], Koseki J. Kobayashi-Kirschvink[1], Yuichi Wakamoto[1,2,3] ([1]*Graduate School of Arts and Sciences, The University of Tokyo*, [2]*Research Center for Complex Systems Biology, The University of Tokyo*, [3]*Universal Biology Institute, The University of Tokyo*)

1Pos418 オンチップ１点連続貪食計測系によるマクロファージの貪食飽和停止現象の解析
Analysis of neglecting phase in phagocytosis of macrophages using on-chip sequential single-point phagocytoses measurement assay
Yoshiki Nakata[1], Yuya Furumoto[1], Toshiki Azuma[2], Amane Yoshida[2], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos419 集束光によるゼラチンの 3 次元微細加工技術を用いた毛細血管形成のダイナミクス計測
Direct observation of blood vein formation dynamics exploiting flexible three-dimensional gelatin-gel microfabrication technology
Kento Iida[1], Yuki Yamanaka[1], Hiromichi Hashimoto[2], Ryuji Takano[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

1Pos420 Model comparison for inverse tissue mechanics of epithelial spreading
Yohei Kondo[1], Kazuhiro Aoki[1], Shin Ishii[2] ([1]*ExCELLS*, [2]*GSI, Kyoto Univ.*)

1Pos421 High precision single-molecule techniques for molecular biophysics
Ying Lu, Chun-Hua Xu, Shu-Xin Hu, Ming Li (*Institute of Physics, Chinese Academy of Sciences*)

2 日目（9 月 16 日（日））／Day 2（Sep. 16 Sun.）

PA 会場（大集会室），PB 会場（南第二集会室），PC 会場（南第三集会室），PD 会場（南第四集会室）／
Room PA (Large Assembly Room), Room PB (2nd South Assembly Room),
Room PC (3rd South Assembly Room), Room PD (4th South Assembly Room)

蛋白質：物性・構造／Protein: Property & Structure

2Pos001 Substrate analogue-induced folding of staphylococcal nuclease analyzed by statistical mechanical model
Shunta Furuzawa, Kosuke Maki (*Grad. Schl. Sci., Nagoya Univ.*)

2Pos002 Analysis of pH, salt and mutation effects on folding of the N-terminal domain of ribosomal protein L9 using statistical mechanical model
Takuya Mizukami[1,2], **Kosuke Maki**[1] ([1]*Schl. Sci., Nagoya Univ.*, [2]*Fox Chase Cancer Ctr.*)

2Pos003 Theoretical study on the structural stability of alanine dipeptide in supercritical carbon dioxide
Satoshi Nakagawa[1], Tatsuki Kataoka[1], Tomoya Maeda[1], Kazutomo Kawaguchi[1], Francesca Ingrosso[2], Marilia Martines-Costa[2], Manuel F Ruiz-Lopez[2], Hidemi Nagao[1] ([1]*Grad. Sch. Nat. Sci. Tech., Kanazawa Univ.*, [2]*Laboratoire de Physique et Chimie Theoriques, UMR CNRS 7019, Universite de Lorraine, 54506 Vandoeuvre-les-Nancy, France*)

2Pos004 Ribosome-assisted co-translational folding of a CFTR domain and its deletion mutant studied by molecular simulations
Suguru Kato, Kazushi Mochizuki, Shoji Takada (*Kyoto University*)

2Pos005 回転拡散より見積もられるリゾチーム間相互作用に対するホフマイスター効果
Hofmeister effects on lysozyme-lysozyme interaction estimated by rotational diffusion analysis
Akane Kato[1], Yudai Katsuki[1], Etsuko Nishimoto[2] ([1]*Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ.*, [2]*Fac. Agr., Kyushu Univ.*)

2Pos006 改良カメレオンモデルによるアデニル酸キナーゼの構造転移の解析
A study on conformational transition of adenylate kinase with an improved chameleon model
Ryota Mori, Mashiho Ito, Tomoki P. Terada, Masaki Sasai (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

2Pos007 A thermodynamic model of amyloid-β protein oligomerization on negatively charged lipid bilayers
Keisuke Ikeda, Yuuki Sugiura, Minoru Nakano (*Graduate School of Medicine and Pharmaceutical Sciences, University of Toyama*)

2Pos008 タンパク質フォールディングにおける自由エネルギー面の理論的解析
Theoretical analysis of free energy profile for folding of chignolin
Tomonari Sumi, Kenichiro Koga (*Res. Inst. Interdisciplinary Sci., Okayama Univ.*)

2Pos009 天然変性ペプチド pKID は高圧力下でフォールドするか
Do an intrinsically disordered peptide, pKID fold under high pressure?
Minoru Kato, Soichiro Kubota, Tubasa Yamamoto (*Dept. Applied Chem., Ritsumeikan Univ.*)

2Pos010 Ultra-fast dynamics of simple polyalanine peptides by using nanosecond region fluorescence correlation spectroscopy
Supawich Kamonprasertsuk[1,2], Hiroyuki Oikawa[1,2], Satoshi Takahashi[1,2] ([1]*IMRAM, Univ. Tohoku*, [2]*Chem, Grad. Sch. Sci., Univ. Tohoku*)

2Pos011 蛋白質-蛋白質相互作用面の二次構造に着目した分類手法の開発
Development of classification method of protein-protein interfaces based on their secondary structures
Takashi Fujii, Kazuo Fujiwara, Masamichi Ikeguchi (*Grad. Sch. of Eng., Soka Univ*)

2Pos012 水溶性および膜貫通 β-バレル構造における β-ストランドのねじれ/曲がり
β-strand twisting/bending in soluble and transmembrane β-barrel structures
Nobuaki Kikuchi, **Kazuo Fujiwara**, Masamichi Ikeguchi (*Dept. Bioinfo., Grad. Sch. Eng., Soka Univ.*)

2Pos013 アクチンフィラメントの圧電・誘電アロステリーがコフィリンの選択的結合に与える影響
Piezoelectric and dielectric allostery of an actin filament and its effect on binding preference of cofilin
Jun Ohnuki, Akira Yodogawa, Takato Sato, Taro Q.P. Uyeda, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

2Pos014 The effect of a soft/discontinuity driveshaft on the rotation of F_1-ATPase
Shou Furuike[1], Naoki Soga[2], Yasushi Maki[1], Hideji Yoshida[1] ([1]*Osaka Med. Col.*, [2]*Sch. Eng., Univ. Tokyo*)

2Pos015 Investigation on the structural properties of proteins included in non-membraneous granule droplets
Saya Nakano[1,2], Hiroyuki Oikawa[1], Satoshi Takahashi[1] ([1]*IMRAM*, [2]*Grad. school of Life Science, Tohoku Univ.*)

2Pos016 フェリチン変異体の帯電限界
Charge limit of ferritin mutants
Takumi Kuwata[1], Daisuke Sato[2], Atushi Kurobe[1], Satuki Takebe[1], Kazuo Fujiwara[1,2], Masamichi Ikeguchi[1,2] ([1]*Grad. Sch. of Eng., Soka Univ.*, [2]*Fac. of Sci. and Eng., Soka Univ*)

2Pos017 蛍光寿命計測によるアシル CoA 結合タンパク質のフォールディング機構の研究
Folding dynamics of acyl-CoA binding protein revealed by fluorescence lifetime measurements
Koichi Fujii, Motonari Tsubaki, Tetsunari Kimura (*Grad. Sch. Sci., Kobe Univ*)

2Pos018 Influence of ligand binding on the glass transition temperature
Alexander Krah[1], Peter John Bond[2,3] ([1]*School of Computational Sciences, Korea Institute for Advanced Study (KIAS)*, [2]*Bioinformatics Institute, A*STAR*, [3]*Department of Biological Sciences, National University of Singapore*)

2Pos019 回転対称軸周辺における相互作用の摂動による球殻状超分子のアセンブリ・メカニズムへの影響
Change in the assembly mechanism by disrupting of local interactions around symmetry axes of a spherical shell-shaped supermolecule
Daisuke Sato[1], Takumi Kuwata[2], Eriko Aoki[1], Kazuo Fujiwara[1,2], Masamichi Ikeguchi[1,2] ([1]*Fac. of Sci. and Eng., Soka Univ.*, [2]*Grad. Sch. of Eng., Soka Univ.*)

2Pos020 ポリミアン優先取込システムに関与する好熱菌由来 PotA の結晶構造解析
Crystal structure of PotA, a membrane-associated ATPase of the spermidine-preferential uptake system in Thermotoga maritima
Mihoka Amano[1], Taichi Naruse[1], Keiko Kashiwagi[2], Kazuei Igarashi[3], Shigeru Sugiyama[4] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*Fac. Pharm., Chiba Ins. Sci.*, [3]*Amine Pharma Res. Ins.*, [4]*Fac. Sci. & Tec., Kochi Univ.*)

2Pos021 ヨツヒメゾウリムシ由来アルギニンキナーゼの構造学的研究
Structural studies of arginine kinase from Paramecium tetraurelia
Yumeto Otsuka[1], Junko Tanaka[1], Daichi Yano[2], Koji Uda[2], Tomohiko Suzuki[2], Shigeru Sugiyama[2] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*Fac. Sci. & Tec., Kochi Univ.*)

2Pos022 FABP3 の低分子薬剤に対する分子認識機構の解明
Elucidation of the molecular recognition mechanism of FABP3 in complex with low-molecular medicines
Junko Tanaka[1], Yumeto Otsuka[1], Daisuke Matsuoka[2], Osamu Hiraoka[3], Shigeru Matsuoka[4], Masashi Sonoyama[5], Michio Murata[2], Shigeru Sugiyama[6] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*Grad. Sch. Sci., Osaka Univ. & JST ERATO*, [3]*Sch. Pharm., Shujitsu Univ.*, [4]*Fac. Med., Oita Univ*, [5]*Sch. Sci. & Tec., Gumma Univ.*, [6]*Fac.Sci & Tec.,Kochi Univ*)

2Pos023 Conformational fluctuations and diffusive dynamics of small proteins
Eiji Yamamoto[1], Takuma Akimoto[2] ([1]*Dept. System Design Engineering, Keio Univ.*, [2]*Dept. Phys., Tokyo Univ. Sci.*)

2Pos024 カロテノイド結合とアミノ酸変異による微生物型ロドプシン TR の熱安定化
Thermostabilization of the microbial rhodopsin TR by carotenoid binding and amino-acid mutation
Tomoki Akiyama[1], Keigo Nishikawa[3], Sayaka Nemoto[4], Satoshi Yasuda[2,4,5], Daisuke Umeno[6], Masahiro Kinoshita[2], Yuki Sudo[3], Takeshi Murata[4,7] ([1]*Graduate School of Science and Engineering, Chiba University*, [2]*Institute of Advanced Energy, Kyoto University*, [3]*Graduate School of Medicine, Dentistry, and Pharmaceutical Sciences, Okayama University*, [4]*Graduate School of Science, Chiba University*, [5]*Molecular Chirality Research Center, Chiba University*, [6]*Graduate School of Engineering, Chiba University*, [7]*PRESTO*)

2Pos025 多糖モノオキシゲナーゼ，CBP21 の熱安定性に対する金属イオンの効果
Effects of metal ions on the thermal unfolding of lytic polysaccharide monooxygenase, CBP21
Hayuki Sugimoto, Ayaka Motoyama, Erina Katagiri, Takeshi Watanabe, Kazushi Suzuki (*Fac. Agri., Niigata Univ.*)

2Pos026 水棲哺乳類ミオグロビンの分子進化：二つの適応戦略
Tracing evolution of aquatic mammal myoglobins: the two adaptation mechanisms
Yasuhiro Isogai[1], Hiroshi Imamura[2], Setsu Nakae[3], Tomonari Sumi[4], Ken-ichi Takahashi[3], Taro Nakagawa[3], Antonio Tsuneshige[5], Tsuyoshi Shirai[3] ([1]*Dept. Pharm. Eng., Toyama Pref. Univ.*, [2]*Life Sci., Ritsumeikan Univ.*, [3]*Dept. Comp. Bio-Sci., Nagahama Inst. Bio-Sci. Tech.*, [4]*Dept. Chem., Okayama Univ.*, [5]*Dept. Frontier Biosci., Hosei Univ.*)

核酸結合蛋白質／Nucleic acid binding proteins

2Pos027 スピンラベル ESR によるヘテロクロマチンタンパク質 HP1 の動的構造の研究
Structural dynamics of heterochromatin protein HP1 studied by site-directed spin labeling ESR spectroscopy
Toshiaki Arata[3,4], Yuichi Mishima[4], Shigeaki Nakazawa[5], Kazunobu Sato[5], Takeji Takui[5], Toshimichi Fujiwara[4], Makoto Miyata[3], **Isao Suetake**[1,2,4] ([1]*Koshien Univ.*, [2]*Twin Research Center, Osaka Univ.*, [3]*Dept. Biol., Grad. Sch. Sci., Osaka City Univ.*, [4]*IPR, Osaka Univ.*, [5]*Dept. Chem., Grad. Sch. Sci., Osaka City Univ.*)

2Pos028 TALE 蛋白質の新規構築法と応用
A simple and accurate construction of TALEs and its applications
Kazuho Ikeda, Yoko Terahara, Yasushi Okada (*RIKEN, BDR*)

2Pos029 標的 RNA の切断前後の CRISPR-CMR の動力学
The dynamics of CRISPR-CMR before/after the cleavage of targeted RNA
Tomohiro Yamaguchi, Ryo Ohashi, Naoyuki Miyashita (*BOST, KINDAI Univ.*)

2Pos030 Distinct binding of nuclear proteins to non B-type DNA studied by molecular simulations
Mami Saito, Shoji Takada (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

2Pos031 Theoretical Studies on Stability of RA-VII for Anti-Cancer Agent by Docking and Molecular Dynamics Simulations
Muhammad Arwansyah Saleh[1], Yoh Noguchi[2], Takeshi Miyakawa[2], Kazutomo Kawaguchi[1], Yukio Hitotsuyanagi[3], Satoshi Yokojima[3], Ryota Morikawa[2], Masako Takasu[2], Hidemi Nagao[1] ([1]*Division of Mathematical and Physical Sciences, Kanazawa University*, [2]*School of Life Sciences, Tokyo University of Pharmacy and Life Sciences*, [3]*School of Pharmacy, Tokyo University of Pharmacy and Life Sciences*)

2Pos032 Combinatorial DNA Binding of Sox/Oct Transcription Factors Studied with Molecular Dynamics Simulations
Cheng Tan, Shoji Takada (*Department of Biophysics, Kyoto University*)

2Pos033 蛍光相互相関分光法による単量体/二量体グルココルチコイド受容体の DNA 結合様式解明に向けた研究
Single-oligonucleotide mutated GRE impacts on glucocorticoid receptor binding studied by FCCS
Daisuke Yamashita[1], Sho Oasa[2], Jhotaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Grad. Shc. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [3]*Biomed. Res. Inst. AIST*)

2Pos034 Comparing Nucleoprotein Filament Assembly of Yeast Dmc1 and Rad51 Recombinases at the Single-Molecule Level
Wei-Hsuan Lan[1], Sheng-Yao Lin[1], Wen-Hsuan Chang[1], Chih-Yuan Kao[2], Peter Chi[2,3], Hung-Wen Li[1] ([1]*Dept. of Chemistry, NTU*, [2]*Inst. of Biochemical Sciences,NTU*, [3]*Inst. of Biological Chemistry, Academia Sinica*)

2Pos035 がん抑制タンパク質ｐ５３の標的探索ダイナミクスの一分子観察
Single-molecule observation of the target search dynamics of a tumor suppressor p53
Yuji Itoh, Agato Murata, Satoshi Takahashi, Kiyoto Kamagata (*IMRAM*)

2Pos036 Using Single-Molecule Optical Microscopy to Study How PriA Helicase Restarts replication
Han Lin Yang[1], Hung-Wen Li[1], Min Guan Lin[2], Chwan-Deng (David) Hsiao[2] ([1]*Dept. Chem, NTU*, [2]*IMB, Academia Sinica*)

核酸／Nucleic acid

2Pos037 二面角系疎視化モデルによる巨大核酸分子の立体構造ゆらぎ―Ｘ線構造の温度因子との比較
Structure fluctuations of large nucleic acids with a corse-grained model in torsional angle space–A comparison with temperature factors
Shigeru Endo[1], Hiroshi Wako[2] ([1]*Dept. Phys., Sch. Sci., Kitasato Univ.*, [2]*Sch. Socical Sci., Waseda Univ.*)

2Pos038 SAXS および SANS プロファイルに基づくオーバーラッピングダイヌクレオソームのモデル構築
Model building of overlapping dinucleosome based on SAXS and SANS profiles
Atsushi Matsumoto[1], Hidetoshi Kono[1], Rintaro Inoue[2], Masaaki Sugiyama[2], Yasuhiro Arimura[3], Hitoshi Kurumizaka[3] ([1]*QST*, [2]*Kyoto U.*, [3]*U. Tokyo*)

2Pos039 分子輪投げによる環状 DNA1 分子のトラップ
Trapping of Single Circular DNA Molecules by Molecular Ringtoss
Ken Hirano[1], Taiki Dohi[1,2], Kyohei Terao[2] ([1]*Health Res. Inst., AIST*, [2]*Dep. Eng., Kagawa Univ.*)

2Pos040 siRNA を安定化するカチオン性分子と二本鎖 RNA の NMR による相互作用解析
NMR analysis of interactions between dsRNA and cationic oligomers that stabilize small interfering RNA
Taiichi Sakamoto[1], Rintaro Hara[2], Yusuke Maeda[2], Takeshi Wada[2] ([1]*Fac. Adv. Eng., Chiba Inst. Tech.*, [2]*Fac. Pharm., Tokyo Univ. Sci.*)

2Pos041 DNA の構造の揺らぎへの溶媒粘性の影響
Effect of solvent viscosity on configuration fluctuations of DNA
Masato Tanigawa, Takafumi Iwaki (*Biophysics, Faculty of Medicine, Oita University*)

2Pos042 Structural effect of spermine analogues on inducing DNA compaction
Tomoki Kitagawa, Tkashi Nishio, Yuuko Yoshikawa, Takahiro Kenmotsu, Kenichi Yoshikawa (*Faculty of Biological and Medical Sciences, Doshisha University Laboratory of Life Physics*)

2Pos043 1-propanol causes reentrant transition on DNA whereas 2-propanol does not: Experimental verification through single molecular observation
Yue Ma, Yuko Yoshikawa, Koichiro Sadakane, Kenichi Yoshikawa (*Grad. Sch. Life Med. Sci, Doshisha Univ.*)

2Pos044 Direct Observation of the Protein-DNA Interaction Using Passive Force-Clamp Optical tweezers
Yen Chan Chang, Hung Wen Li (*Department of Chemistry, National Taiwan University, Taipei, Taiwan*)

2Pos045 X 線小角散乱法による RecA タンパク質ーDNA 複合体フィラメントの構造解析とシミュレーションモデルとの比較
Structural changes of RecA protein/DNA complex filament promoted by Mg ions analyzed using SAXS and compared with its models
Satomi Inaba[1], Chantal Prevost[2], Tsutomu Mikawa[3], Hiroshi Sekiguchi[1], Masayuki Takahashi[4] ([1]*JASRI/SPring-8*, [2]*CNRS*, [3]*RIKEN BDC*, [4]*Tokyo Inst. Technol.*)

2Pos046 DNA インターカレーションと光応答
DNA intercalation and optical response
Satoshi Yokojima (*Tokyo University of Pharmacy and Life Sciences*)

2Pos047 転写開始複合体における DNA 開裂の粗視化分子シミュレーション研究
DNA Opening in Transcription Initiation Complex Studied by Coarse-grained Molecular Simulation
Genki Shino, Masahiro Shimizu, Shintaroh Kubo, Toru Niina, Shoji Takada (*Dept. of Biophys., Div. of Bio. Sci., Grad. Sch. of Sci., Univ. of Kyoto*)

2Pos048 光照射で構築した DNA マイクロ構造体の熱力学的特性の解析
Analysis of the thermodynamic property of DNA microstructures formed by photo-irradiation
Yu Kasahara, Masahiro Takinoue (*Tokyo Institute of Technology/School of Computing/Computer Science.*)

2Pos049 細胞核様 DNA ゲルカプセルの形成のシミュレーション
Numerical simulation of phase separation-based formation of cell nucleus-like DNA gel capsule
Tetsuro Sakamoto, Masamune Morita, Masahiro Takinoue (*Department of Computer Science, Tokyo Institute of Technology*)

2Pos050 Heterogeneous chromatin accessibility establishes human nuclear organization
Shin Fujishiro[1,2], **Masaki Sasai**[1,2] ([1]*Dept. Comp. Sci. & Eng., Nagoya Univ.*, [2]*Dept. Appl. Phys., Nagoya Univ.*)

2Pos051 ヌクレオソーム排他的領域のインスレーター機能の解析
Analysis of insulator function of nucleosome exclusive genome regions
Yuki Matsushima, Hiraku Nishimori, Naoaki Sakamoto, Akinori Awazu (*Dept. of Math and Life Science, Hiroshima Univ.*)

2Pos052 過渡的に生じる中間体ヌクレオソームにおけるヒストンテール動態
Histone Tail Dynamics in Transient Intermediate Single Nucleosomes
Takeru Kameda, Yuichi Togashi, Akinori Awazu (*Department of Mathematical and Life Sciences, Hiroshima University*)

電子状態／Electronic state

2Pos053 アミロイド β 凝集の初期過程に対する QM/MM 法を用いた解析
QM/MM analysis of the initial aggregation of amyloid-β peptides
Hiroaki Nishizawa[1,2], Hisashi Okumura[1,2,3] ([1]*ExCELLS*, [2]*IMS*, [3]*Sokendai*)

2Pos054 Relative stability between hydroxide models and oxo models of S1 state of the OEC of PSII by DFT and beyond DFT methods
Koichi Miyagawa[2], Takashi Kawakami[1], Hiroshi Isobe[3], Mitsuo Shoji[4], Shusuke Yamanaka[1], Kazuhiko Nakatani[2], Mitsutaka Okumura[1], Kizashi Yamaguchi[2,5] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*ISIR, Osaka Univ.*, [3]*Grad. Sch. Nat. Sci. and Tech., Okayama Univ.*, [4]*CCS, Tsukuba Univ.*, [5]*Inst. Nanosci. Design, Osaka Univ.*)

2Pos055 DASH 型クリプトクロムにおける電子移動反応に関する理論的解析
Theoretical Analysis of Electron Transfer Reaction for Cryptochrome-DASH
Ryuma Sato, Makoto Taiji (*RIKEN*)

2Pos056 光電子放出を用いた TR の電子構造の観測 2：RxR との比較
Electronic structure of a film with TR observed by technique using photoelectron emission 2: Comparison with RxR
Daisuke Sano[1], Yuki Takeda[1], Tomoki Akiyama[1], Kanae Kanahara[2], Takeshi Murata[1,3], Yuki Sudo[2], Hisao Ishi[1,3,4] ([1]*GSSE Chiba Univ.*, [2]*GSMP Okayama Univ.*, [3]*MCRC Chiba Univ.*, [4]*CFS Chiba Univ.*)

2Pos057 高感度紫外光電子分光を用いたリゾチーム薄膜のギャップ内準位の観測
Gap state of lysozyme thin film observed by high-sensitivity UV photoelectron spectroscopy
Ichiro Ide[1], Daisuke Sano[1], Shintaro Maruyama[1], Yuya Tanaka[3], Takeshi Murata[2], Hisao Ishii[4] ([1]*Grad. Sch. Sci. Eng., Univ. Chiba*, [2]*Grad. Sch. Sci. Eng, Chi. Res. Cen., Univ. Chiba*, [3]*Grad. Sch. Sci. Eng., Cen. Fro. Sci., Univ. Chiba*, [4]*Grad. Sch. Sci. Eng., Fro. Sci. Cen., Chi. Res. Cen., Univ. Chiba*)

水・水和／電解質／Water & Hydration & Electrolyte

2Pos058 各種溶質周囲の水分子ダイナミクスの分子動力学計算と解析
MD simulations and analysis of hydration dynamics around several types of solute molecules
Takuya Takahashi, Kota Kasahara, Ryoi Ashida, Nobuya Hasegawa, Daigo Itsuji, Tomomi Kura (*College of Life Science, Ritsumeikan University*)

2Pos059 細胞混雑中の蛋白質間相互作用に及ぼす代謝物とイオンの影響:分子動力学法による理論的研究
Influence of metabolites and ions on the protein-protein interactions in cellular crowding: Theoretical study with MD simulations
Isseki Yu[1,2], Michael Feig[3], Yuji Sugita[2] ([1]*Maebashi Institute of Technology*, [2]*RIKEN Theoretical Molecular Science Lab.*, [3]*Michigan State University*)

2Pos060 機械学習アプローチによる物理化学量の予測
Classification and prediction of physicochemical properties by machine-learning approach: molecular dynamic study of hydration water
Taku Mizukami[1], Viet Cuong Nguyen[3], Tien Lam Pham[2], Heui Chi Dam[2] ([1]*JAIST, Materials*, [2]*JAIST, Knowledge*, [3]*HPC.Inc*)

2Pos061 MDM2-p53NTD と MDM2-MIP の結合自由エネルギーに見られる大きな差の物理起源
Physical origin of the large difference between MDM2-p53NTD and -MIP complexes in binding free energy
Tatsuya Yamada[1], Tomohiko Hayashi[1], Naohiro Kobayashi[2], Hiroshi Yanagawa[3], Masato Katahira[1], Takashi Nagata[1], Masahiro Kinoshita[1] ([1]*Inst. of Adv. Energy, Kyoto Univ.*, [2]*Inst. for Protein Res., Osaka Univ.*, [3]*IDAC Theranostics, Inc.*)

2Pos062 溶媒の種類が蛋白質の安定構造に及ぼす効果
Effects of solvent species on the stabilized structure of a protein
Tomohiko Hayashi[1], **Masao Inoue**[1], Satoshi Yasuda[1,2,3], Emanuele Petretto[4], Tatjana Skrbic[4], Achille Giacometti[4], Masahiro Kinoshita[1] ([1]*Inst. Adv. Energ., Kyoto Univ.*, [2]*Grad. Sch. Sci., Chiba Univ.*, [3]*MCRC, Chiba Univ.*, [4]*Dept. of Molecular Sciences and Nanosystems, Venezia Univ.*)

2Pos063 セロビオースとマルトースの水への溶解度の大きな差に関する統計熱力学
Statistical thermodynamics on the large difference between maltose and cellobiose in terms of solubility in water
Simon Hikiri[1,2], Tomohiko Hayashi[2], Mitsunori Ikeguchi[3,4], Masahiro Kinoshita[2] ([1]*Grad. Sch. of Sci., Chiba Univ.*, [2]*Inst. of Adv. Energy, Kyoto Univ.*, [3]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*, [4]*RIKEN, MIH*)

分子遺伝・遺伝情報制御／Molecular genetics & Gene expression

2Pos064 The analysis of Housekeeping Gene Expression Variations During iPS Reprogramming Process
Yulia Panina, Arno Germond, Tomonobu Watanabe (*RIKEN BDR*)

2Pos065 エピジェネティックな状態変化と遺伝子相互作用が細胞のがん化に及ぼす影響のランドスケープ理論による解析
Landscape analyses of coupled dynamics of epigenetic state change and gene interaction in carcerization
Yutaro Kameyama, Masaki Sasai (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

生体膜・人工膜／Biological & Artificial membrane: Structure & Property

2Pos066 細胞膜アンカーを目指したαヘリックス型ペプトイドの合成
Synthesis of an α-helix peptoid for cell-membrane anchoring
George Mogami, Wato Oba, Masaya Yamamoto (*Grad. Sch. Eng., Tohoku Univ.*)

2Pos067 Implicit Solvent Coarse-Grained Lipid Model for Molecular Simulations of Multicomponent Membrane Systems
Diego Ugarte, Shoji Takada (*Dept. Biophysics, Div. Biology, Graduate School of Science, Kyoto University*)

2Pos068 細胞模倣系における蛍光相関分光法による分子拡散測定
Molecular diffusion in cell-mimicking system measured by fluorescence correlation spectroscopy
Chiho Watanabe, Yuta Kobori, Miho Yanagisawa (*Tokyo Univ. Agri. Technol.*)

2Pos069 Single molecule analysis of transport protein using small liposome with size uniformity
Naoki Soga[1], Rikiya Watanabe[1,2], Hiroyuki Noji[1] ([1]*Dept. of Appl. Chem., The Univ. of Tokyo*, [2]*AMED-PRIME, JST*)

2Pos070 高速 AFM を用いた光受容体ロドプシンクラスターとトランスデューシンとの相互作用観察
Observing the interaction between rhodopsin cluster and transducin by high-speed AFM
Yasushi Tanimoto[1], Hayato Yamashita[2,3], Kento Nomura[2], Masayuki Abe[2], Fumio Hayashi[4], Kenichi Morigaki[1,5] ([1]*Biosignal research Center, Univ Kobe*, [2]*Grad. Sch. Eng. Sci., Univ Osaka*, [3]*PRESTO, JST*, [4]*Grad. Sch. Scie, Univ. Kobe*, [5]*Grad. Sch. Agr., Univ. Kobe*)

2Pos071 全反射赤外分光法によるGタンパク質共役受容体-リガンド間相互作用の解析
Investigation of ligand-protein interaction in a G protein-coupled receptor via ATR-FTIR spectroscopy
Hisao Tsukamoto[1,2], Yuji Furutani[1] ([1]*Institute for Molecular Science*, [2]*PRESTO, JST*)

2Pos072 細胞骨格封入巨大リポソームの繰返し屈伸運動
Repetitive stretching of cytoskeleton-encapsulating giant liposomes
Masahito Hayashi[2], Shunsuke Tanaka[1], Masayoshi Nishiyama[3], Taro Toyota[4], **Kingo Takiguchi**[1] ([1]*Grad Sch of Sci, Nagoya Univ*, [2]*CBS, RIKEN*, [3]*Dept of Phys, Kindai Univ*, [4]*Graduate School of Arts and Sciences, The University of Tokyo*)

2Pos073 アガロースマイクロチャンバー内でのマクロファージの運動の観察
Observation of Macrophage Migration in Agarose Microchamber
Nami Morizono, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ*)

2Pos074 *In vitro* reconstitution system for traveling waves of PIP3
Hitomi Matsubara[1,2], Satomi Matsuoka[1,2], Masahiro Ueda[1,2] ([1]*Grad. Sch. FBS., Univ. Osaka*, [2]*RIKEN*)

2Pos075 クラミドモナスの機械反応における TRP11 の役割
Roles of TRP11 in Mechanoresponces in Chlamydomonas
Kosuke Anzai[1], Akiko Yoshida[1], Megumi Yoshida[1], Ken-ichi Wakabayashi[2], Kenjiro Yoshimura[1] ([1]*Dept. Machinery & Control Systems., Shibaura Inst. Technol.*, [2]*Inst. Innovative Res., Tokyo Inst. Technol.*)

2Pos076 ナノポアによる一分子 AND ゲートの構築とリポソームへの搭載
Single molecule AND gate with a biological nanopore integrated into a liposome
Ping Liu, Keisuke Shimizu, Masayuki Ohara, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

2Pos077 A simple method for single ion channel recordings
Kota Kaneko[1], Huimin Ma[1], Minako Hirano[2], Toru Ide[1] ([1]*Okayama University*, [2]*The Graduate School for the Creation of New Photonics Industries*)

2Pos078 イオンチャネルの特性の改変
Modifications of K^+ channel property
Tomoya Ishido[1], Toru Ide[1], Minako Hirano[2] ([1]*Okayama University*, [2]*GPI*)

2Pos079 ステロールによる膜張力を介した KcsA カリウムチャネル活性の制御
Regulation of the activity of the KcsA potassium channel via bilayer tension-mediated sterol action
Masayuki Iwamoto, Shigetoshi Oiki (*Dept. Mol. Physiol. Biophys., Univ. Fukui Facul. Med. Sci.*)

2Pos080 ATP 合成阻害時の細胞内ミトコンドリアの膜電位モニタリング
Monitoring of mitochondrial membrane potential upon addition of oligomycin
Emika Shida, Yshihiro Ohta (*Tokyo University of Agriculture and Technology*)

2Pos081 多剤輸送担体 EmrE の多剤認識における熱力学
Thermodynamics of multidrug recognition in multidrug transporter, EmrE
Kazumi Shimono[1,2], Keisuke Matsuda[2], Shoko Suzuki[2], Kaho Yajima[2], Sakiyo Yamamoto[2], Seiji Miyauchi[2] ([1]*Fac. Pharm. Sci., Sojo Univ.*, [2]*Fac. Pharm. Sci., Toho Univ.*)

2Pos082 移動性細胞における $PI(3,4,5)P_3$ の非対称分布を安定化する PTEN-$PI(4,5)P_2$ ポジティブフィードバック機構
PTEN-$PI(4,5)P_2$ positive feedback mechanism for stabilizing asymmetric $PI(3,4,5)P_3$ localization in migrating cell
Daisuke Yoshioka[1,3], Hiroyasu Koteishi[3], Daichi Okuno[3], Satomi Matsuoka[3], Toru Ide[4], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*Grad. Sch. of Front. Biosci., Osaka Univ.*, [3]*RIKEN*, [4]*Grad. Sch. of Nat. Sci. and Tech., Okayama Univ.*)

2Pos083 Simulation of Shape Transformation of Vesicle Including Particles
Hibiki Itoga[1], Ryota Morikawa[1], Tsuyoshi Ueta[2], Takeshi Miyakawa[1], Yuno Natsume[3], Masako Takasu[1] ([1]*Tokyo Univ. Pharm. Life Sci.*, [2]*Jikei Univ.*, [3]*J. Women's Univ.*)

行動／Behavior

2Pos084 機械刺激がゾウリムシの逃走反応を誘導するしくみ
Molecular mechanism of escape response induced by mechanical stimulation in Paramecium
Mutsumi Kawano[1], Ayaka Seto[1], Takashi Tominaga[2], Masaki Ishida[3], **Manabu Hori**[1] ([1]*Fac. Sci, Yamaguchi Univ.*, [2]*Inst Neurosci, Tokushima BUNRI Univ.*, [3]*Sch. Sci. Edu., Nara Univ. Edu.*)

2Pos085 三次元空間における真正粘菌変形体の管ネットワーク形成
Tubular network formation in three dimensional space by the true slime mold
Seiji Takagi (*Future University Hakodate*)

光生物学：視覚・光受容／Photobiology: Vision & Photoreception

2Pos086 珪藻および渦鞭毛藻由来の真核生物型 H^+ポンプロドプシンの機能・光化学的解析
Characterization of eukaryotic H^+ pumping rhodopsins from the diatom *Pseudo-nitzschia granii* and dinoflagellate *Oxyrrhis marina*
Masuzu Kikuchi[1], Susumu Yoshizawa[2], Akimasa Kaneko[1], Keiichi Kojima[1,3], Yuki Sudo[1,3] ([1]*Fac. of Pharm. Sci., Okayama Univ.*, [2]*AORI, UTokyo.*, [3]*Grad. Sch. of Med. Dent Pharm. Sci., Okayama Univ.*)

2Pos087 スチレンマレイン酸 (SMA) コポリマーを用いた微生物型ロドプシンの可溶化とその分光学的解析
Solubilization and spectroscopic analysis of microbial rhodopsins in styrene-maleic acid (SMA) copolymers
Tetsuya Ueta[1], Kanae Kanehara[1], Keiichi Kojima[1,2], Tomoya Hino[3], Shingo Nagano[3], Yuki Sudo[1,2] ([1]*Fac. of Pharm. Sci. Okayama Univ.*, [2]*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*, [3]*Grad. Sch. of Eng., Tottori Univ.*)

2Pos088 光駆動ナトリウムポンプ KR2 における Ser70 の役割
Role of Ser70 for transport activity of a light-driven sodium ion pump
Rei Abe-Yoshizumi[1], Aki Nemoto[1], Keiichi Inoue[1,2,3], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*ISSP Univ. of Tokyo*, [3]*JST PRESTO*)

2Pos089 光駆動 SO_4^{2-}輸送体（SyHR）のアニオン輸送と選択性への塩基性アミノ酸残基の役割
Role of basic amino acid residues on the anion transport and its selectivity in a light-driven SO_4^{2-} transporter SyHR
Masaki Nakama[1], Keiichi Kojima[1,2], Marie Kurihara[2], Susumu Yoshizawa[3], Yuki Sudo[1,2] ([1]*Fac. of Pharm. Sci. Okayama Univ*, [2]*Grad. Sch. of Med. Dent. & Pharm. Sci. Okayama Univ*, [3]*AORI, UTokyo*)

2Pos090 出芽酵母を用いたアニオンチャネルロドプシンの発現と分光学的解析
Expression and spectroscopic analysis of anion channelrhodopsins using a eukaryotic yeast, *Saccaromyces cerevisiae*
Ryota Ono[1], Taro Yamanashi[2], Keiichi Kojima[1,2], Hisao Moriya[3], Yuki Sudo[1,2] ([1]*Div. of Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Med., Dent. & Pharm. Sci., Okayama Univ.*, [3]*Res. Core for Interdiscip. Sci., Okayama Univ.*)

2Pos091 海洋性真核藻類 *Guillardia theta* における 44 種類の微生物型ロドプシン様タンパク質の遺伝子発現解析
Gene expression analysis of 44 microbial rhodopsin-like proteins from marine algae *Guillardia theta*
Yumeka Yamauchi[1], Masae Konno[1,2], Keiichi Inoue[1,3,4], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*PRESTO, JST*)

2Pos092 円石藻ウイルス由来のヘリオロドプシンの分子物性解析
Molecular characterization of heliorhodopsin from Emiliania huxleyi virus
Ritsu Mizutori[1], Masae Konno[1,2], Keiichi Inoue[1,2,3,4], Oded Beja[5], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*PRESTO, JST*, [5]*Technion-Israel Inst. Tech.*)

2Pos093 Mutational analysis of amino acid residues surrounding the electron-transferring terminal Trp of plant (6-4) photolyase
Yuhei Hosokawa[1], Ryuma Sato[2], Shigenori Iwai[1], Junpei Yamamoto[1] ([1]*Grad. Sch. Eng. Sci., Univ. Osaka*, [2]*Riken*)

2Pos094 Analysis of binding of light-harvesting secondary chromophore to animal and plant (6-4) photolyase
Ayaka Morimoto, Kumar Rajiv, Yuhei Hosokawa, Yuma Terai, Shigenori Iwai, Junpei Yamamoto (*Grad. Sch. Eng., Univ. Osaka*)

2Pos095 過渡回折格子法を用いた orange carotenoid protein の光反応ダイナミクスの研究
Study on photoreaction dynamics of orange carotenoid protein using transient grating method
Takatoshi Ohata, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

2Pos096 ビリベルジン結合型シアノバクテリオクロムの遠赤／橙色光変換過程での構造変化の検出
Detection of structural change during far-red/orange reversible photoconversion of biliverdin-binding cyanobacteriaochrome
Yuka Takeda, Keiji Fushimi, Rei Narikawa (*Grad. Sch. Integrated Science and Technology, Univ. Shizuoka*)

2Pos097 Application of electron spin polarization imaging method to obtain geometries of photoinduced charge-separated states in cryptochrome
Hiroki Nagashima[1], Misato Hamada[2], Takashi Tachikawa[1,2], Tatsuya Iwata[3], Hideki Kandori[4], Till Biskup[5], Stefan Weber[5], Yasuhiro Kobori[1,2] ([1]*Mol. PhotoSci., Kobe Univ.*, [2]*Grad. Sch. Sci., Kobe Univ.,*, [3]*Facul. Pharmaceutical Sci., Toho Univ.*, [4]*Grad. Sch. Eng., Nagoya Inst. Tech.,*, [5]*Inst. Phys. Chem., Albert-Ludwigs-Univ. Freiburg*)

2Pos098 Rc-PYP(K72Q)を用いた複合体形成過程の解析
Elucidation of the complex formation process using Rc-PYP mutant K72Q
Natsuki Oka, Yoichi Yamazaki, Yugo Hayashi, Hironari Kamikubo (*Nara Institute of Science and Technology*)

2Pos099 膜脂質環境が G タンパク質トランスデューシンの活性化効率に及ぼす影響
The effect of lipid environment of outer segment membranes on the activation of photoreceptor specific G protein, Transducin
Kyoko Kadomatsu[1], Keiji Seno[2], Yuki Ito[1], Satoru Kawamura[1], Shuji Tachibanaki[1] ([1]*Grad. Sch. of Frontier Biosci., Osaka Univ.*, [2]*Department of Biology, Faculty of Medicine, Hamamatsu University School of Medicine*)

2Pos100 色覚視物質の結晶構造解析に向けたユニークな戦略
Unique approaches towards cone opsin crystallization
Kota Katayama, Hideki Kandori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

2Pos101 フーリエ変換赤外分光法によるロドプシンと錐体視物質の発色団／蛋白質相互作用の比較
Comparison of chromophore/protein interaction between rhodopsin and cone pigment using Fourier transform infrared spectroscopy
Naoto Noguchi[1], Takahiro Yamashita[1], Yoshinori Shichida[2], Yasushi Imamoto[1] ([1]*Kyoto University*, [2]*Ritsumeikan University*)

2Pos102 網膜桿体細胞内円盤膜上の脂質-光受容タンパク質の秩序形成の数理モデル
A mathematical model of pattern formation of lipid-photoreceptor proteins on disk membranes of retinal cells
Yukito Kaneshige[1], Akinori Awazu[1], Hiraku Nishimori[1], Humio Hayashi[3], Kenichi Morigaki[2], Taishi Tanimoto[2] ([1]*Grad. Sci. Univ. Hiroshima*, [2]*Grad. Agri. Univ. Kobe*, [3]*Grad. Sci. Univ. Kobe*)

2Pos103 バクテリオロドプシンにおける 1 段階目のプロトン移動を対象とした大規模量子分子動力学シミュレーション
Large-scale quantum-mechanical molecular dynamics simulations for the primary proton transfer in bacteriorhodopsin
Junichi Ono[1], Minori Imai[2], Yoshifumi Nishimura[1], Hiromi Nakai[1,2,3] ([1]*RISE, Waseda Univ.*, [2]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [3]*ESICB, Kyoto Univ.*)

2Pos104 大規模励起状態計算手法の開発と光活性イエロータンパク質に対する応用研究
Development of large-scale excited-state calculation method and applied research on photoactive yellow protein
Nana Komoto[1], Takeshi Yoshikawa[1], Junichi Ono[2], Hiromi Nakai[1,2,3] ([1]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [2]*RISE, Waseda Univ.*, [3]*ESICB, Kyoto Univ.*)

その他／Miscellaneous topics

2Pos105 ポリリジン残基の付加は、DNA オリガミへの SNAPf 融合蛋白質の結合速度を向上させる
Poly-lysine tag increase the binding rate of SNAPf-fused protein to DNA origami
Kodai Fukumoto[1], Yuya Miyazono[2], Hisashi Tadakuma[1], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

2Pos106 希少糖生産に関わる単糖間異性化反応の熱力学的研究
Thermodynamic investigation on the isomerization of monosaccharides for rare sugar production
Akihide Yoshihara, Mitsuki Murakami, Ryoko Iwata, Taro Kozakai, Kimi Fujiwara, **Kazuhiro Fukada** (*Fac. Agric., Kagawa Univ.*)

2Pos107 試料環境による eGFP の電子誘起変換の依存性
The environmental dependence of the "electron-induced" conversion of eGFP
Koki Matsui, Keiichirou Akiba, Hiroki Minoda (*TUAT*)

2Pos108 A model for analyzing phenomena in multicellular organisms with multivariable polynomials: Polynomial-life model
Hiroshi Yoshida (*Grad. Schools of Math. & Systems Life Sci. Kyushu Univ.*)

2Pos109 The ancient gods of the modern cytoskeleton
Caner Akil[1,2], Robert C. Robinson[1,2,3] ([1]*Institute of Molecular and Cell Biology, A*STAR (Agency for Science, Technology and Research)*, [2]*Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore*, [3]*Research Institute for Interdisciplinary Science, Okayama University*)

2Pos110 Structural characterization of ALP37, a potential chromosome segregating ParM
Samson Ali[1,2], N Akihiro[3], D Popp[1], Robert C. Robinson[1,2,4] ([1]*Institute of Molecular and Cell Biology*, [2]*National University of Singapore, NUS, Yong Loo Lin School of Medicine*, [3]*Nagoya University Graduate School of Science, Structural Biology Research Center and Division of Biological Sciences*, [4]*Research Institute for Interdisciplinary Science (RIIS), Okayama University*)

分子モーター／Molecular motor

2Pos201 アクトミオシンの運動を利用した抗原抗体反応の促進
Acceleration of antigen-antibody reaction by actomyosin motility
Shohta Takamori[1], Kaito Kobayashi[1], Takashi Ishiguro[2], Hajime Honda[1] ([1]*Nagaoka Univ. Tech.*, [2]*Taiyo Yuden Co., Ltd.*)

2Pos202 水晶振動子微量天秤によるアクチン繊維とミオシンの見かけの質量変化
QCM revealed the changes of apparent mass of actin filaments and myosin molecules
Kaho Yokomuro[1], Shota Takamori[1], Kazuya Soda[1], Takashi Ishiguro[2], Hajime Honda[1] ([1]*Nagaoka Univ. Tech.*, [2]*Taiyo Yuden Co., Ltd.*)

2Pos203 Single-molecule fluorescence imaging analysis of Serratia marcescens ChitinaseA (SmChiA) Trp-active mutant
Akasit Visootsat[1,2], Paul Vignon[3], Akihiko Nakamura[1,2], Ryota Iino[1,2] ([1]*SOKENDAI*, [2]*Institute for Molecular Science*, [3]*ParisTECH*)

2Pos204 DNA ナノチューブに沿って移動する生体分子モーターの設計
Engineering motor proteins to move along DNA nanotubes
Ryota Ibusuki[1], Akane Furuta[2], Tatsuya Morishita[1], Kazuhiro Oiwa[1,2], Hiroaki Kojima[2], Ken'ya Furuta[2] ([1]*Graduate School of Biological Science, University of Hyogo*, [2]*Adv. ICR. Res. Ins., NICT. Kobe*)

2Pos205 高速 AFM を用いた DNA terminase の構造と動態の研究
Study of structure and dynamics of DNA terminase using high-speed AFM
Hirotaka Ariyama, Toshio Ando (*WPI-NanoLSI, Kanazawa Univ.*)

2Pos206 プロセッシブダイニンモータードメインのマイクロ秒時間分解能、ナノメーター位置決定精度 1 粒子トラッキング
Single-particle tracking of motor domain of a processive dynein at microsecond time resolution and nanometer localization precision
Jun Ando[1,2], Tomohiro Shima[3], Akihiko Nakamura[1,2], Akasit Visootsat[1,2], Mayuko Yamamoto[1], Takahide Kon[4], Ryota Iino[1,2] ([1]*IMS, NINS*, [2]*SOKENDAI*, [3]*Univ. Tokyo*, [4]*Osaka Univ.*)

2Pos207 中間鎖点変異による外腕ダイニンモーター活性の低下
A point mutation in intermediate chain gene reduces motor activity of outer-arm dynein
Yusuke Kondo[1], Tomoka Ogawa[1], Emiri Kanno[2], Masafumi Hirono[3], Takako Minoura[2], Ritsu Kamiya[2], Toshiki Yagi[1] ([1]*Dept. Biol. Sci., Pref. Univ. Hiroshima*, [2]*Dept. Biol. Sci., Chuo Univ*, [3]*Dept. of Front. Life Sci., Hosei Univ*)

2Pos208 単一軸糸ダイニンを欠失した新規クラミドモナス変異株９種の単離と解析
Identification of nine kinds of Chlamydomonas mutants missing single axonemal dynein heavy chains
Tomohiro Komatsu, Yusuke Kondo, Natsuki Tanaka, Kohei Fujimoto, Kazuhiro Takeshima (*Dept. Life Sci., Pref. Univ. of Hiroshima*)

2Pos209 X 線繊維回折法で明らかにするクラミドモナス鞭毛軸糸構成要素の Ca2+濃度依存的らせん対称性の変化
Ca^{2+} dependent changes in helical symmetry of axonemal components of *Chlamydomonas* flagella studied by X-ray fiber diffraction
Kazuhiro Oiwa[1], Hiroyuki Iwamoto[2] ([1]*Natl. Inst. Info.Commun.Technol.*, [2]*Japan Sync. Rad. Res. Inst., SPring-8*)

2Pos210 Behavior of polymerized microtubules interacted with dyneins still attached on a doublet microtubule detected by laser tweezers
Takashi Fujiwara[1], Chikako Shingyoji[1], Hideo Higuchi[2] ([1]*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*, [2]*Dept. Phys., Grad. Sch. Sci., The Univ. Tokyo*)

2Pos211 細胞質ダイニンの二足歩行メカニズムに関するマルコフ状態モデリング
Bi-pedal motions of cytoplasmic dynein via Markov state modeling
Shintaroh Kubo, Shoji Takada (*Takada Lab., Grad. Sch. of Sci., Kyoto Univ.*)

2Pos212 高速原子間力顕微鏡により観察されたクラミドモナス軸糸ダイニンの調整機構
High-speed atomic force microscopic observations on demembranated Chlamydomonas axonemes and dynein arms
Kenta Ishibashi[1,2], Kazuhiro Oiwa[2,3] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ*, [2]*Advanced ICT Inst., NICT*, [3]*Grad. Sch. Sci., Univ. Hyogo*)

2Pos213 Step sizes and rate constants of single-headed cytoplasmic dynein
Yoshimi Kinoshita[1], Taketoshi Kambara[1,2], Kaori Nishikawa[1], Motoshi Kaya[1], Hideo Higuchi[1] ([1]*Dept. Phys., Univ of Tokyo*, [2]*RIKEN QBiC*)

2Pos214 DNA-templated assembly of axonemal outer arm dynein complexes in vitro
Yuka Matsuda[1], Akane Furuta[2], Hiroaki Kojima[2], Kazuhiro Oiwa[1,2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ Hyogo*, [2]*Adv ICT Res Ins, NICT*)

2Pos215 クライオ電子顕微鏡画像解析により明らかになった細胞質ダイニンの新たな歩行パターン
Cryo-EM observation of stepping patterns of cytoplasmic dynein on microtubules with new freezing conditions
Riko Kanazawa[1], Hiroshi Imai[1], Takuma Shioi[1], Rieko Shimo[1], Ryousuke Yamamoto[1], Kaoru Mitsuoka[2], Takahide Kon[1] ([1]*Dep. Boil. Grad. Sch. of Sci. Osaka Univ*, [2]*Res. Ctr. UVHEM, Univ. Osaka*)

2Pos216 細胞質ダイニンが運動活性を示す蛍光 ATP の合成
Synthesis of fluorescent ATP to elucidate coordination of multiple ATPase sites in cytoplasmic dynein
Karibu Sakai, Tomotaka Komori, Tomohiro Shima, Sotaro Uemura (*Dep. of Bio. Sci., Grad. Sch. of Sci., The Univ. of Tokyo*)

2Pos217 粘弾性溶液中におけるキネシンによる微小管の運動についての研究
Investigation of motility of microtubules driven by kinesins in viscoelastic media
Masayuki Furukawa[1], Taikopaul Kaneko[1], Farhana Tammana[1], Hirohumi Shintaku[2], Hidetoshi Kotera[2], Ryuji Yokokawa[1] ([1]*Kyoto Univ. Micro Eng.*, [2]*Riken*)

2Pos218 糸状菌キネシンへの１残基置換が低温適性をもたらす代わりに熱安定性を損なう
Single amino acid substitution for the fungal kinesin offers possible cold-adaptation but impairs thermal stability
Youske Shimizu, Toru Togawa, Shigeru Chaen (*Dept. Biosciences, Nihon Univ.*)

2Pos219 細胞分裂に関わるキネシン 5 の高速一分子観察
High-speed single molecule observations of the stepping motion of mitotic kinesin-5
Taiga Yamada, Kohei Matsuzaki, Michio Tomishige, Yoko Sakai (*Aoyamagakuinuniversity Tomishige lab.*)

2Pos220 遺伝性痙性対麻痺を引き起こす変異型ヒト KIF1A の神経細胞内 Run-time 分布
Run-time distributions of human KIF1A mutants in hippocampal neurons in relation to hereditary spastic paraplegia
Shiori Matsumoto[1], Shinsuke Niwa[2], Kumiko Hayashi[1,3] ([1]*Dep. Appl. Phys., Grad. Sch. of Eng., Tohoku Univ.*, [2]*FRIS, Tohoku Univ.*, [3]*PRIME, AMED*)

2Pos221 キネシン 1 二量体の前頭部における微小管からの解離抑制の直接観察
Direct observation of the suppression of the leading head of kinesin-1 dimer from detachment from microtubule
Kohei Matsuzaki, Michio Tomishige (*Dept. Math. Phys., Col. Sci. Eng., Aoyama Univ.*)

2Pos222 Selective nano-patterning of kinesin motor-proteins and its effect on collective motion of microtubules
Tamanna Ishrat Farhana, Taikopaul Kaneko, Ryuji Yokokawa (*Dep. of microengineering, Kyoto university*)

2Pos223 Does giraffe kinesin move faster than mouse?
Taketoshi Kambara[1], Yasushi Okada[1,2] ([1]*RIKEN BDR*, [2]*Univ of Tokyo, Grad. Sci.*)

2Pos224 Photoregulation of kinesin Eg5 using photochromic compound composed of azobenzene and spiropyran which forms three isomerization states
Md Alrazi Islam, Kei Sadakane, Shinsaku Maruta (*Soka University*)

2Pos225 2 つのアゾベンゼンを持つ新規フォトクロミック阻害剤を介したキネシン Eg5 の光制御
Photo-regulation of mitotic kinesin Eg5 using a novel photochromic inhibitor composed of two azobenzene
Kei Sadakane, Kenichi Taii, Alrazi M.D. Islam, Shinsaku Maruta (*Dept. Bioinfo., Soka Univ.*)

2Pos226 Photo-control of Ras GDP-GTP exchange using the peptide modified with spiropyran derivative
Kenichi Taii, Nobuyuki Nishibe, Shinsaku Maruta (*Dept. of Bioinfo, Grad. Sch. of Engin, Soka Univ.*)

2Pos227 鞭毛軸糸再構築系における微小管の繰り返し座屈運動の観察
Repetitive buckling of microtubules driven by axonemal dynein arrays reconstituted on a microtubule
Misaki Sagawa[1], Misaki Shiraga[2], Hitoshi Sakakibara[3], Kazuhiro Oiwa[3] ([1]*Sch. Sci, Univ. Hyogo*, [2]*Grad. Sch. Sci, Univ. Hyogo*, [3]*Adv. ICT Res. Inst., NICT*)

2Pos228 Identifying actin regulators from complex cellular lysates through profilin pull down
Dennis Mweti Mwangangi[1,2], R. Robinson[1,2,3], S. Widyawillis[1] ([1]*Institute of Molecular and Cell Biology, A*STAR*, [2]*Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore*, [3]*Research Institute for Interdisciplinary Science (RIIS), Okayama University*)

細胞生物的課題／Cell biology

2Pos301 Cellular localization of SAS6-L, a paralog of a flagellar basal body protein that self-assembles into a 9-fold symmetrical structure
Yuki Nakazawa[1], Masahito Nagao[1], Akira Noga[2], Manuel Hilbert[3], Michel O. Steinmetz[3], Masafumi Hirono[1] ([1]*Dept. of Frontier Biosci., Hosei Univ.*, [2]*Dept. of Biosci., Grad. Sch. Sci, Univ. Tokyo*, [3]*PSI*)

2Pos302 ビブリオ菌の極べん毛本数制御における FlhG の ATPase モチーフおよび ATPase 活性の役割
The role of ATPase motif and ATPase activity of FlhG in flagellar number regulation at cell pole of Vibrio alginolyticus
Yoshino Imura, Seiji Kojima, Michio Homma (*Grad. Sch. Sci., Univ. Nagoya*)

2Pos303 ビブリオ菌細胞の極に局在するタンパク質 FlhF による極べん毛形成促進機構の解析
Role of FlhF localized at cell pole on initiating the polar flagellar formation of Vibrio alginolyticus
Yuna Inoue, Seiji Kojima, Michio Homma (*Division of Biological Science, Graduate School of Science, Nagoya University*)

2Pos304 ナトリウムイオン透過における、べん毛モーター固定子タンパク質 PomA のペリプラズムループ領域の構造機能解析
Structural and functional characterization of periplasmic loop regions of PomA, a stator protein of flagellar motor, in sodium ion flux
Hiroto Iwatsuki[1], Masayo Iwaki[2], Hiroyuki Terashima[1], Seiji Kojima[1], Hideki Kandori[2], Michio Homma[1] ([1]*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, [2]*Grad. Sch. Eng., Nagoya Inst. Tech*)

2Pos305 細菌べん毛モーター形成の中心となる超分子膜構造体 MS リングの形成メカニズムの解明
Assembly mechanism of supramolecular membrane structure of bacterial flagellar MS-ring composed of FliF
Keiichi Hirano, Hiroyuki Terashima, Michio Homma (*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ*)

2Pos306 細菌べん毛 III 型分泌装置のある構成因子は翻訳後多段階プロセシングを受ける
A component of the bacterial flagellar type III secretion apparatus receives multistep post-translational processing
Yohei Hizukuri[1], Takehiro Suzuki[2], Kosuke Terushima[1], Naoshi Dohmae[2], Yoshinori Akiyama[1] ([1]*Inst. Front. Life Med. Sci., Kyoto Univ.*, [2]*Center Sust. Res. Sci., RIKEN*)

2Pos307 バクテリアべん毛輸送ゲート複合体の構造機能解析
Structural and functional analyses of the bacterial flagellar type III export gate complex
Miki Kinoshita[1], Tomoko Miyata[1], Akihiro Kawamoto[2], Takayuki Kato[1], Keiichi Namba[1,3], Tohru Minamino[1] ([1]*Grad. Sch. Frontier Biosci, Osaka Univ.*, [2]*IPR, Osaka Univ.*, [3]*RIKEN Quantitative Biology Center*)

2Pos308 海洋性ビブリオ菌の極べん毛本数制御機構における FlhG の N 末端領域の解析
Role of N-terminal region of FlhG in polar flagellar number regulation in Vibrio alginolyticus
Seiji Kojima, Akira Mizuno, Michio Homma (*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

2Pos309 Quantitative observation of CheY-GFP binding to a flagellar motor in the presence of external load by electrorotation
Kenta Morishima, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front Biosciences, Osaka Univ*)

2Pos310 Difference on chemotaxis response of E.coli derived from the dependency of flagellar motor
Akinori Nagataki, Yong-Suk Che, Akihiko Ishijima, Hajime Hukuoka (*Grad. Sch Front Biosciences, Osaka Univ.*)

2Pos311 モーターの回転方向の同調的制御における CheR, CheB の役割
The role of CheR and CheB in coordinated switching of flagellar motor in *Escherichia coli*
Tatsuki Hamamoto, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

2Pos312 Quantitative analysis for the ratio of WT and mutant receptors that collapses receptor cooperativity in chemotaxis in *Escherichia coli*
Shin Koguchi, Hajime Fukuoka, Akihiko Ishijima, Yong-Suk Che (*Grad.Sch. Frontier Biosci., Osaka Univ*)

2Pos313 Probing cell-wall synthesis dynamic using bacterial membrane protein-complex
Yi-Jen Sun, Chien-Jung Lo (*Department of Physics and Graduate Institute of Biophysics, National Central University, Zhongli, Taiwan 32001*)

2Pos314 らせん形細菌スピロヘータの推進力測定
Force measurement of the spirochete *Leptospira* swimming
Keigo Abe[1], Kyosuke Takabe[2], Shuichi Nakamura[1] ([1]*Grad.Sch.Eng., Tohoku Univ.*, [2]*Life and Env.Sci., Tsukuba Univ.*)

2Pos315 細胞性粘菌や好中球の基質の硬さ感知
Rigidity sensing of fast-moving cell types
Chika Okimura[1], Yuichi Sakumura[2,3], Katsuya Shimabukuro[4], Yoshiaki Iwadate[1] ([1]*Fac. Sci., Yamaguchi Univ.*, [2]*Sch. Inf. Sci. Tech., Aichi Pref. Univ.*, [3]*Grad. Sch. Sci. Tech., NIST*, [4]*Nat. Ins. Tech. Ube Col.*)

2Pos316 アクチンフィラメントに結合した MAPs の微小管重合促進活性の評価
Microtubule assembly-promoting activity of MAPs bound to actin filaments
Chihiro Doki[1], Miyuki Siga[1], Syoma Saitou[1], Susumu Kotani[2], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Sustain, Environ. Eng., Muroran Inst. Technol.*, [2]*Fac. Sci., Kanagawa Univ.*)

2Pos317 アクチン繊維の集団運動により形成されるベルト状パターン
The shape of belt-like patterns with millimeter size emerged from actomyosin motility
Kentaro Ozawa[1], Hirotaka Taomori[1], Itsuki Kunita[2], Shigeru Sakurazawa[3], Hajime Honda[1] ([1]*Dept. Bioeng., Nagaoka Univ. Tech.*, [2]*Univ. Ryukyus*, [3]*Future Univ. Hakodate*)

2Pos318 重力下での形態形成に対する YAP 依存のアクトミオシンネットワークの寄与
Theoretical study of contribution of YAP-dependent actomyosin network to morphogenesis under gravity
Kazunori Takamiya, Seirin Ri, Hiraku Nishimori, Akinori Awazu (*Grad. Sch. Sci., Univ. Hiroshima Dept. Math and Life Sci*)

2Pos319 中心体アクチンネットワークによる微小管の形成制御
Regulation of microtubule growth by centrosomal actin network
Daisuke Inoue[1], Dorian Obino[2,3,4], Francesca Farina[5], Jeremie Gaillard[5], Christophe Guerin[5], Laurent Blanchoin[1,5,6,7,8,9], Ana-Maria Lennon-Dumenil[2,3,4], Manuel Thery[1,5,6,7,8,9] ([1]*CEA, BIG*, [2]*PSL Research Univ.*, [3]*INSERM*, [4]*Institute Curie*, [5]*CNRS*, [6]*INRA*, [7]*Grenoble-Alpes Univ.*, [8]*Paris 7 Univ., Univ. Inst. Hematology*, [9]*Saint Louis Hospital*)

2Pos320 FilGAP PH ドメインの構造と機能の解析
Structural and functional analysis of FilGAP PH domain
Koji Tsutsumi[1], Yurina Suzuki[1], Shunsuke Sato[2], Go Watanabe[2], Yasutaka Ohta[1] ([1]*Div. of Cell Biol., Sch. of Sci., Kitasato Univ.*, [2]*Div. of Biophysics., Sch. of Sci., Kitasato Univ.*)

2Pos321 微小管結合蛋白質が微小管の強度と曲がりやすさに与える影響
Influence of microtubule-associated protein on strength and flexibility of microtubules
Miki Tamura[1], Kazuhumi Matsui[1], Kabir Arif Md. Rashedul[2], Akira Kakugo[2], Susumu Kotani[3], Kiyotaka Tokuraku[1] ([1]*Div. Sust. Env. Eng. Muroran Inst. Tech*, [2]*Fac. Sci. Hokkaido Univ*, [3]*Fac. Sci, Kanagawa Univ.*)

2Pos322 アメーバ運動中の ABP 局在形成機構の解明のためのアクチンと ABP からなる in vitro 系の構築
A new, actin and ABP-based in vitro system for elucidating the mechanism of intracellular ABP localization during amoeboid movement
Yosuke Yamazaki, Taro Q.P. Uyeda (*Dept. Physics, Waseda Univ.*)

2Pos323 Examining force regulation of anaphase cell
Takeshi Itabashi[1,2], Shin'ichi Ishiwata[2] ([1]*RIKEN BDR*, [2]*Fac. Sci. Eng., Waseda Univ.*)

2Pos324 C 型インフルエンザウイルスの直進的運動
Directional motility of influenza C virus
Tatsuya Sakai[1], Hiroaki Takagi[2], Yasushi Muraki[3], Mineki Saito[1] ([1]*Department of Microbiology, Kawasaki Medical School*, [2]*Department of Physics, School of Medicine, Nara Medical University*, [3]*Department of Microbiology, School of Medicine, Iwate Medical University*)

2Pos325 紡錘状細胞集団の示す配向秩序と牽引力
Traction Force and Dynamics in Orientation Order of Spindle-shaped Cells
Masahito Uwamichi[1], Kyogo Kawaguchi[2], Masaki Sano[1] ([1]*Dept. of Phys, Univ. of Tokyo*, [2]*Dept. of System Biol, Harvard Med. Sch.*)

2Pos326 ARF1 activation initiates a regulation circuit for ARF1 and RAC1 activities in GPCR-mediated neutrophil chemotaxis
Yuichi Mazaki[1], Yasuhito Onodera[2], Tsunehito Higashi[1], Takahiro Horinouchi[1], Tsukasa Oikawa[2], Hisataka Sabe[2] ([1]*Dept. Cell. Pharm., Grad. Sch. Med., Hokkaido Univ.*, [2]*Dept. Mol. Biol., Grad. Sch. Med., Hokkaido Univ.*)

バイオイメージング／Bioimaging

2Pos401 Investigation of binding mechanism of E-cadherin by high-speed atomic force microscopy (HS-AFM)
Hiroki Watanabe[1], Sivasankar Sanjeevi[2], Takayuki Uchihashi[3] ([1]*RIBM Co., Ltd.*, [2]*Dept. of Phys. and Astron., Iowa State Univ.*, [3]*Dept. of Phys., Nagoya Univ.*)

2Pos402 ホウレンソウ由来ストロマラメラに内在する F0 c-リングの原子間力顕微鏡による観察
Observation of the c subunit ring of F0 in stroma lamellae membrane from spinach by atomic force microscopy
Daisuke Yamamoto, Risa Mutoh (*Fac. Sci. Fukuoka Univ.*)

2Pos403 Simultaneous observation of a living COS7 cell using high-speed atomic force microscopy and fluorescence microscopy
Hiroki Furuhashi[1], Mikihiro Shibata[2,3] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Infiniti, Kanazawa Univ.*, [3]*WPI-NanoLSI, Kanazawa Univ.*)

2Pos404 マウスノロウイルス MNV-S7 のクライオ電顕単粒子構造解析
Capsid Structure of Murine Norovirus S7 revealed by cryo-electron microscopy
Chihong Song[1], Reiko Todaka[2], Kei Haga[2], Akira Fujimoto[2], Masaru Yokoyama[3], Naoyuki Miyazaki[4], Kenji Iwasaki[4], Kazuhiko Katayama[2], Kazuyoshi Murata[1] ([1]*National Institute for Physiological Sciences*, [2]*Kitasato University*, [3]*National Institute of Infectious Diseases*, [4]*Institute for Protein Research, Osaka University*)

2Pos405 銀、金、銀金合金ナノ粒子を用いたマルチカラー１分子イメージング
Multi-color single-molecule imaging with silver, gold, and silver/gold-alloy nanoparticles
Jun Ando[1,2], Akihiko Nakamura[1,2], Mayuko Yamamoto[1], **Ryota Iino**[1,2] ([1]*IMS, NINS*, [2]*SOKENDAI*)

2Pos406 細胞内自発的発熱の検出と生理的意義の解明
Investigating the detection and the significance of spontaneous intracellular thermogenesis
Cuiyuan Cai[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*PRESTO, JST*)

2Pos407 Fluorescence correlation spectroscopy analysis of RNA degradation in cells
Naotaka Shimada[1], Kazunori Watanabe[1], Takashi Ohtsuki[1,2] ([1]*Grad. Sch. Nat., Univ. okayama*, [2]*Grad. Sch. Int., Univ. okayama*)

2Pos408 The fast reporter system for quantification of the transcription by using BRET and the split luciferase complementation
Taishi Kakizuka[1,2], Akira Takai[2], Keiko Yoshizawa[2], Yasushi Okada[2], Tomonobu Watanabe[1,2] ([1]*FBS, Univ. Osaka*, [2]*BDR, Riken*)

2Pos409 高次粒子数輝度解析法を用いたタンパク質オリゴマー分布解析：多成分系への応用に向けて
Protein Oligomer Distribution Analysis by High Order Number and Brightness Analysis: towards the Application to Multiple Components
Ryosuke Fukushima[1], Johtaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [3]*Biomed. Res. Inst., AIST*)

2Pos410 Single fluorophore imaging using a DIY microscope with high extensibility
Takashi Sagawa, Wataru Nakashima, Kazuki Nakajima, Shin Yamaguchi, Tomohiro Masuda, Yuichi Inoue (*SIGMAKOKI Co.,LTD.*)

2Pos411 A multi-emitter fitting algorithm for potential live cell super-resolution imaging over a wide range of molecular densities
Tomochika Takeshima[1], Teruo Takahashi[1], Jiro Yamashita[1], Yasushi Okada[2], **Shigeo Watanabe**[1] ([1]*Hamamatsu Photonics K.K., System division*, [2]*RIKEN Center for Biosystems Dynamics Research*)

2Pos412 単一細胞 ATP イメージングにより明らかになった不均一な代謝状況下での頑健なエネルギー量調節
Single-cell ATP imaging reveals robust energy level control despite unequal metabolic contexts
Hideyuki Yaginuma, Yasushi Okada (*BDR, RIKEN*)

2Pos413 Development of programmable RNA-binding protein and its application for live-cell imaging and manipulation of authentic RNAs
Akira Takai[1], Yasushi Okada[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. of Sci., Univ. of Tokyo*)

2Pos414 共焦点画像解析による新規 FCS/FCCS 法の開発とその応用
A new FCS/FCCS method based on the image processing of a confocal laser scanning microscope and applications for it
Kazunari Mouri[1], Yasushi Okada[1,2] ([1]*BDR, RIKEN*, [2]*Univ. Tokyo, Grad. Sch. Sci., Dept. Phys.*)

2Pos415 Single-molecule detection of combinatorial histone modifications for key genes in Epithelial-Mesenchymal-Transition
Jen-Chien Chang[1], Ye Liu[1], Kazuhide Watanabe[1], Prashanti Jeyamohan[1], Haruka Yabukami[1], Yuko Sato[2], Hiroshi Kimura[2], Akiko Minoda[1] ([1]*RIKEN IMS*, [2]*Tokyo Tech, Dept. Life Sci. Tech.*)

2Pos416 X 線自由電子レーザーを用いた低温 X 線回折イメージングによる異なる細胞周期にある酵母細胞核の構造解析
Structural analyses of yeast nuclei in different cell phases by X-ray diffraction imaging at cryogenic temperature using XFEL
Takahiro Yamamoto[1,2], Amane Kobayashi[2], Mao Oide[1,2], Koji Okajima[1,2], Tomotaka Oroguchi[1], Masaki Yamamoto[2], Masayoshi Nakasako[1,2] ([1]*Grad. Sci. Tech. Keio Univ.*, [2]*RSC, RIKEN*)

2Pos417 High-speed imaging of muscle myosin and super-resolution imaging of epidermal growth factor receptor with DNA origami technique
Keisuke Fujita[1,2], Michio Hiroshima[1], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. of Front. Bioscience., Osaka Univ.*)

2Pos418 ゆらぎを利用した非侵襲力測定の軸索輸送動画解析への応用
Fluctuation-based non-invasive force measurement for dynamic image analysis of axonal transport
Yasuhiro Hieda[1], Takashi Sagawa[2], Kyoko Chiba[3,4], Kumiko Hayashi[1,5] ([1]*Dep. Appl. Phys., Grad. Sch. of Eng., Tohoku Univ.*, [2]*NICT*, [3]*Lab. Neuroscience, Grad. Sch. Pharm. Sci., Hokkaido Univ.*, [4]*Col. Biol. Sci., UC DAVIS*, [5]*PRIME, AMED*)

2Pos419 生細胞核内における転写因子 MafG の２量体化に依存した１分子動態
Dimerization dependent single-molecule dynamics of MafG transcription factor in living cell
Yuma Ito[1], Takahiro Maeda[1], Kumiko Sakata-Sogawa[3], Masaaki Shiina[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [3]*Grad. Sch. Agr. Sci., Tohoku Univ.*)

2Pos420 遺伝子コード型抗体プローブを用いた翻訳後修飾の１分子イメージング
Single-molecule imaging of post-translational modification using genetically encoded antibody probe
Shuntaro Sato[1], Yuma Ito[1], Yuko Sato[2], Hiroshi Kimura[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*IIR, Tokyo Inst. Tech.*)

2Pos421 ヘテロクロマチンタンパク HP1α 動態の生細胞１分子イメージング
Dynamics of Heterochromatin protein 1α in living cells using single-molecule imaging
Takahiro Maeda[1], Yuma Ito[1], Shin-Ya Isobe[2], Chikashi Obuse[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Biosci. Grad Sch Sci., Osaka Univ*)

2Pos422 悪性高熱症関連変異を有する骨格筋型リアノジン受容体の構造と機能変化
Structure and function change of skeletal muscle-type ryanodine receptor
Toshiko Yamazawa[1], Maki Yamaguchi[1], Haruo Ogawa[2], Takashi Murayama[3], Hideto Oyamada[4], Nagomi Kurebayashi[3], Junji Suzuki[5], Kazunori Kanemaru[5,6], Takashi Sakurai[3], Masamitsu Iino[5,6] ([1]*Dept Mol. Physiol., Jikei Univ. Sch. Med.*, [2]*Institute Quantitative Biosci., The Univ.Tokyo*, [3]*Dept. Pharmacol., Juntendo Univ. Sch. Med.*, [4]*Dept. Pharmacol., Sch. Med., Showa Univ.*, [5]*Dept. Pharmacol., Grad. Sch. Med., The Univ.Tokyo*, [6]*Dept. Cell. Mol. Pharmacol., Nihon Univ. Sch. Med.*)

2Pos423 ゼロモード導波路(ZMW)を用いた生体分子複合体の定量分析
Quantitative analysis of biomolecular complexes using Zero-Mode Waveguides (ZMW)
Kimiko Nakao[1], Hisashi Tadakuma[1], Yong-Woon Han[2], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*IMS., RIKEN*)

2Pos424 線形ゼロモード導波路を用いたアクチン重合の 1 分子解析
Single-molecule analysis of actin polymerization using linear zero-mode waveguides
Soichiro Fujii[1], Ryo Iizuka[1], Masamichi Yamamoto[1], Makoto Tsunoda[1], Takashi Tanii[2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*Fac. Sci. Eng., Waseda Univ.*)

3 日目（9 月 17 日（月））／Day 3（Sep. 17 Mon.）
PA 会場（大集会室），PB 会場（南第二集会室），PC 会場（南第三集会室），PD 会場（南第四集会室）／
Room PA (Large Assembly Room), Room PB (2nd South Assembly Room),
Room PC (3rd South Assembly Room), Room PD (4th South Assembly Room)

ヘム蛋白質／Heme proteins

3Pos001 ヒト成人ヘモグロビンの四量体構造の安定性に対する β サブユニットの Fe-His 結合の寄与
Contribution of the Fe-His Bond of the β Subunit to Stability of Tetramer of α2β2 in Human Adult Hemoglobin
Shigenori Nagatomo[1], Masako Nagai[2], Teizo Kitagawa[3] ([1]*Dept. Chem., Univ. Tsukuba*, [2]*Res. Center Micro-Nano Tech., Hosei Univ.*, [3]*Grad. Sch. Life Sci., Univ. Hyogo*)

3Pos002 ヘムタンパク質におけるヘム周囲のタンパク質環境の網羅解析
Global analysis of the protein environment around heme in hemeproteins
Hiroko X. Kondo[1], Masanori Fujii[1], Yusuke Kanematsu[2], Yasuhiro Imada[3], Yu Takano[2] ([1]*Fac. Eng., Kitami Inst. Tech.*, [2]*Grad. Sch. Info. Sci., Hiroshima City Univ.*, [3]*IPR, Osaka Univ.*)

3Pos003 鉄還元酵素ヒト Steap3 の分子機能解明
Analyses on the molecular function of human Steap3 as a ferric reductase
Akito Nakata[1], Mika Fujimura[1], Fusako Takeuchi[2], Motonari Tsubaki[1] ([1]*Dept. of Chem., Grad. Sch. Sci., Kobe Univ.*, [2]*IPHE, Kobe Univ.*)

3Pos004 呼吸鎖 A タイプ酸素還元酵素のカルシウムイオン結合構造
Calcium ion-binding structure of respiratory A-type oxygen reductase
Kazumasa Muramoto, Kyoko Shinzawa-Itoh (*Grad. Sch. Life Sci., Univ. Hyogo*)

3Pos005 金属タンパク質の酸化還元電位の第一原理計算
Ab initio evaluation of redox potential of metalloprotein
Cheng Cheng, Shigehiko Hayashi (*Kyoto Univ*)

3Pos006 レーザーフラッシュフォトリシスによるリン脂質二分子膜へ再構成した proteorhodopsin の光サイクルに関する研究
A study on photocycle of proteorhodopsin reconstituted in phospholipid bilayer by laser flash photolysis
Airi Yamamoto[1], Fumio Hayashi[2], Toshinori Motegi[1], Takashi Kikukawa[3,4], Masashi Sonoyama[1] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Ctr. Inst. Anl., Gunma Univ.*, [3]*Fac. Adv. Life Sci., Hokkaido Univ.*, [4]*GI-CoRE, Hokkaido Univ.*)

3Pos007 カロテノイド末端基のアシル化が及ぼすハロロドプシン-バクテリオルベリン複合体形成への影響
Effect of acylation of carotenoid terminal group on halorhodopsin-bacterioruberin complex formation
Fumiya Hattori, Takanori Sasaki (*Grad.Sch.Adv.Math.Sci.,Meiji Univ*)

3Pos008 古細菌膜上におけるハロロドプシンのレチナール再結合能力
Retinal rebinding ability of halorhodopsin on archaeal membrane
Shun Yano, Takanori Sasaki (*Graduate School of Advanced Mathematical Sciences, Meiji University*)

3Pos009 古細菌 *N.Pharaonis* 由来の膜タンパク質ハロロドプシンの複素環式化合物存在下における安定化
Thermal stability of halorhodopsin from *N.Pharaonis* in the presence of heterocyclic compound
Shinichiro Hayashi, Takanori Sasaki (*Grad. Sch. Adv. Math. Sci., Meiji Univ.*)

3Pos010 RxR の極めて高い熱安定性に対する統計熱力学
Statistical thermodynamics for the extremely high thermostability of a microbial rhodopsin from the eubacterium *Rubrobacter* (RxR)
Tomohiko Hayashi[1], Satoshi Yasuda[1,2,3], Kano Suzuki[2], Tomoki Akiyama[2], Kanae Kanehara[4], Yuki Sudo[4], Takeshi Murata[2,3,5], Masahiro Kinoshita[1] ([1]*Inst. Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Sci., Chiba Univ.*, [3]*MCRC, Chiba Univ.*, [4]*Fal. Pharm. Sci., Okayama Univ.*, [5]*PREST, JST*)

3Pos011 サーモフィリックロドプシンの非常に高い熱安定性の物理起源
Physical origin of exceptionally high thermostability of thermophilic rhodopsin
Satoshi Yasuda[1,2,3], Tomohiko Hayashi[3], Yuta Kajiwara[4], Takeshi Murata[1,2,5], Masahiro Kinoshita[3] ([1]*Chiba Univ., Grad. Sch. Sci.*, [2]*Chiba Univ., MCRC*, [3]*Kyoto Univ., IAE*, [4]*Kyoto Univ., Grad. Sch. Ene. Sci.*, [5]*PRESTO*)

3Pos012 アルカリ条件下におけるバクテリオルベリンと古細菌脂質の結合に伴うハロロドプシンの熱安定化
Thermal stabilization of halorhodopsin by binding of bacterioruberin and archaeal lipids under alkaline condition
Kenichi Takeda[1], Takashi Kikukawa[2], Makoto Demura[2], Takanori Sasaki[1] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

3Pos013 脂質二重膜中の AMPA 受容体の高速 AFM 観察
High-speed atomic force microscopy imaging of AMPA receptors in lipids
Kento Ikeda[1], Wenlong Gao[2], Yao Wang[2], Motoyuki Hattori[2], Mikihiro Shibata[3,4] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Sch. Life Sci., Fudan Univ.*, [3]*InFiniti, Kanazawa Univ.*, [4]*WPI-NanoLSI, Kanazawa Univ.*)

3Pos014 High-speed AFM imaging of membrane protein embedded in Nanodisc
Takamitsu Haruyama[1], Yasunori Sugano[1], Noriyuki Kodera[2], Takayuki Uchihashi[3], Toshio Ando[2], Yoshiki Tanaka[1], Hiroki Konno[2], **Tomoya Tsukazaki**[1] ([1]*Nara Inst. of Sci. and Tech.*, [2]*WPI-NanoLSI, Kanazawa Univ.*, [3]*Dept. of Physics, Nagoya Univ.*)

3Pos015 構造生物学的解析に向けた TRPV3 のナノディスク化について
Reconstitution of TRPV3 into Nanodiscs for structural study
Tomoki Maeda[1], Kaname Ojima[1], Shingo Nagano[2], **Tomoya Hino**[2] ([1]*Grad. Sch. Sus. Sci., Tottori Univ.*, [2]*Grad. Sch. Eng., Tottori Univ.*)

3Pos016 X 線 1 分子追跡法による TRPV1 チャネルの 3 次元運動
3D motion of TRPV1 cation channel depicted by diffracted X-ray tracking method
Shoko Fujimura[1], Kazuhiro Mio[1], Masahiro Kuramochi[2], Hiroshi Sekiguchi[3], Muneyo Mio[1], Tai Kubo[1], Yuji C. Sasaki[1,2,3] ([1]*OPERANDO-OIL, AIST*, [2]*Grad. Sch. Frontier Sci., Univ. Tokyo*, [3]*JASRI/Spring-8*)

3Pos017 分子シミュレーションによるヘムインポーターの化学-力学共役機構の解明
Deciphering chemomechanical coupling mechanism of a heme importer with molecular simulations
Koichi Tamura[1], Hiroshi Sugimoto[2,3], Yoshitsugu Shiro[2], Yuji Sugita[1,4,5] ([1]*RIKEN R-CCS*, [2]*Grad. Sch. Life Sci., Univ. Hyogo*, [3]*RIKEN SPring-8*, [4]*RIKEN TMS*, [5]*RIKEN BDR*)

3Pos018 Nanodisc を用いたリン脂質二重膜環境中におけるヒトセロトニン受容体の機能解析
Functional analyses of human serotonin receptor in phospholipid membrane environments using Nanodisc
Kouhei Yoshida[1], Daisuke Kuroda[1,2,3], Satoru Nagatosihi[1,3,4], Kouhei Tsumoto[1,3,4] ([1]*Dept. of Bioeng., Sch. of Eng,. Univ. of Tokyo*, [2]*RS Med. Dev. Dev. Reg. Res. Center, Sch. of Eng., Univ. of Tokyo*, [3]*Dept. of Chem. Biotech., Sch. of Eng., Univ. of Tokyo*, [4]*Inst. of Med. Sci., Univ. of Tokyo*)

3Pos019 ATR-FTIR を用いた細菌べん毛固定子のイオン透過経路の解析
Analysis of Na+-conducting pathway in the stator complex of the bacterial flagellar motor by ATR-FTIR spectroscopy
Hiroyuki Terashima[1], Masayo Iwaki[2], Hideki Kandori[2], Michio Homma[1] ([1]*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, [2]*Dept. Life Sci. Appl. Chem., Nagoya Inst. Tech.*)

3Pos020 マグネシウムイオンチャネル MgtE のイオン―タンパク質間相互作用の振動解析
Vibrational analysis for studying ion-protein interactions of a magnesium ion channel, MgtE
Tetsunari Kimura[1,2,7], Victor Lorenz-Fonfria[3,4], Shintaro Doki[5], Hideyoshi Motoki[6], Ryuichiro Ishitani[5], Osamu Nureki[5], Masahiro Higashi[6], **Yuji Furutani**[1,2] ([1]*Inst. Mol. Sci.*, [2]*SOKENDAI*, [3]*ICMol, Univ. Valencia*, [4]*Dep. Biochem. Mol. Biol., Univ. Valencia*, [5]*Grad. Sch. Sci., Univ. Tokyo*, [6]*Grad. Sch. Eng. Sci., Univ. Ryukyus*, [7]*Grad. Sch. Sci., Kobe Univ.*)

3Pos021 A Multiscale Model for Flavivirus Dynamics & Host Interactions
Jan K. Marzinek, Roland G. Huber, Daniel A. Holdbrook, Peter J. Bond (*Bioinformatics Institute (A*STAR), #07-01, Matrix, 138671 Singapore*)

3Pos022 Direct reconstitution of membrane proteins from cell membrane blebs into a model biological membrane
Rurika Nagai[1], Yasushi Tanimoto[2], Rinshi Kasai[3], Kenichi Suzuki[4,7], Fumio Hayashi[5], Kenichi Morigaki[6] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Biosignal research Center., Univ. Kobe*, [3]*Institute for Frontier Life and Medical Sciences., Univ. Kyoto*, [4]*G-chain., Univ. Gifu*, [5]*Grad. Sch. Scie., Univ. Kobe*, [6]*Grad. Sch. Agr., Univ. Kobe*, [7]*Grad of Nat. Scie and Tech., Univ. Gifu*)

3Pos023 1 分子イメージングによる PDGF 受容体-Akt シグナル伝達の研究
Single molecule imaging study on PDGF receptor and Akt signal transduction
Hideaki Yoshimura, Takeaki Ozawa (*Department of Chemistry, School of Science, The University of Tokyo*)

3Pos024 Solubilization and purification of the Rieske/cytochrome *b* complex in green sulfur bacteria
Hiraku Kishimoto[1], Chihiro Azai[2], Risa Mutoh[3], Hideaki Tanaka[4], Genji Kurisu[4], Hirozo Oh-oka[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Lif. Sci., Ritsumeikan Univ.*, [3]*Fac. Sci., Fukuoka Univ.*, [4]*Inst. Protein Res., Osaka Univ.*)

3Pos025 線虫 Cytochromeb_{561} ホモログ Cecytb-2 のアスコルビン酸特異的電子伝達反応解析
Analyses on the ascorbate-specific electron transfer function of Cecytb-2, a cytochrome b_{561} homolog in *Caenorhabditis elegans*
Misaki Fukuzawa, Mika Fujimura, Masahiro Miura, Tetsunari Kimura, Motonari Tsubaki (*Dept. of Chem., Grad. Sch. Sci., Kobe Univ.*)

3Pos026 三量体オートトランスポーターの構造形成における荷電残基の役割
Roles of charged residues on assembly of the trimeric autotransporter transmembrane domain
Eriko Aoki, Daisuke Sato, Kazuo Fujiwara, Masamichi Ikeguchi (*Fac. of Sci. and Eng., Soka Univ.*)

3Pos027 Ubiquitination of MHCII changes tendency of antigen presentation due to structral conversion of MHCII
Takashi Kawamoto[1], Yuko Kozono[1], Jae-won Chang[2], Masahiro Kuramochi[2], Yuji Sasaki[2], Haruo Kozono[1] ([1]*Grad. Sch. bio, TUS*, [2]*Grad. Sch. fro, Univ. Tokyo*)

光生物／Photobiology: Photosynthesis

3Pos028 Light-induced FTIR spectroscopic studies on quinone exchange mechanism of the LH1-RC complexes from native and chimeric purple bacteria
Rikako Kishi[1], Michie Imanishi[1], Kanako Hashimoto[1], Kenji Nagashima[2], Masayuki Kobayashi[3], Shinji Takenaka[1], Zheng-yu Wang-Otomo[4], Yukihiro Kimura[1] ([1]*Grad. Agri., Univ. Kobe*, [2]*Photobio Inst., Univ. Kanagawa*, [3]*Ariake Kosen*, [4]*Sci., Univ. Ibaraki*)

3Pos029 光化学系 II の水の酸化反応における D1/V185 の役割
The role of D1/V185 in the water oxidation mechanism in Photosystem II
Itsuki Takachi[1], Yuya Hara[1], Alain Boussac[2], Miwa Sugiura[3] ([1]*Grad. Sch. Sci and Eng, Ehime Univ*, [2]*CEA Saclay*, [3]*PROS, Ehime Univ*)

3Pos030 Thermodynamic Dissociation Kinetics assay to determine the binding strengths within a membrane protein complex
Eunchul Kim, Ryutaro Tokutsu, Akimasa Watanabe, Jun Minagawa (*National Institute for Basic Biology*)

3Pos031 Biosynthesis of Gold Nanoparticles by photosynthetic apparatus
Hiroki Matsumura[1], Rie Nagayoshi[1], Mariko Miyachi[2], Daiki Nishiori[2], Yoshinori Yamanoi[2], Hiroshi Nishihara[2], **Tatsuya Tomo**[1] ([1]*Faculty of Science, Tokyo University of Science*, [2]*School of Science, The University of Tokyo*)

3Pos032 クロロフィル d を主要色素とするシアノバクテリア光化学系 II における分光特性
Absorption and fluorescence properties of Photosystem II complex in a chlorophyll d-dominated cyanobacterium
Reona Toyofuku[1], Seiji Akimoto[2], Toshiyuki Shinoda[1], Tatsuya Tomo[1] ([1]*Grad. Sch. Sci., Tokyo Univ. Sci.*, [2]*Grad. Sch. Sci., Univ. Kobe.*)

3Pos033 The orientation of menaquinone in the heliobacterial reaction center analyzed with the EPR spectroscopy
Toru Kondo[1], Chihiro Azai[2], Shigeru Itoh[3], **Hirozo Oh-oka**[4] ([1]*Dept. Chem., MIT*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Sci., Nagoya Univ.*, [4]*Grad. Sch. Sci., Osaka Univ.*)

3Pos034 Role of D1-Ser169 near O4 of the Mn4CaO5 cluster in photosynthetic water oxidation
Yuichio Shimada[1], Tomomi Kitajima-Ihara[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*RIIS, Okayama Univ.*)

3Pos035 光合成水分解反応の S2→S3 遷移におけるプロトン共役電子移動の時間分解赤外分光解析
Mechanism of proton-coupled electron transfer in the S2-S3 transition of photosynthetic water oxidation revealed by TRIR analysis
Hiroshi Takemoto, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

3Pos036 Effect of replacement of Cl- with NO3- on photosynthetic water oxidation as studied by time-resolved infrared spectroscopy
Yasutada Okamoto, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

3Pos037 FTIR-spectroelectrochemical study on the pH dependence of the redox potential of the non-heme iron in photosystem II
Hiroki Watanabe, Takumi Noguchi, Yuki Kato (*Grad. Sch. Sci., Nagoya Univ.*)

3Pos038 QM/MM analysis of the DOD vibrations of water molecules around the Mn4CaO5 cluster in photosystem II
Masao Yamamoto, Shin Nakamura, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

3Pos039 光合成における電子伝達体拡散のルーメン環境依存性に関する理論的研究
Theoretical studies on dependence of diffusion of electron carriers in photosynthesis on environment in lumen side
Hidemi Nagao, Isman Kurniawan, Arwansyah Saleh, Koichi Kodama, Satoshi Nakagawa, Kazutomo Kawaguchi (*Kanazawa University*)

3Pos040 LOV を導入したファシンによるアクチン束化の制御
Regulation of actin bundles by using LOV-fused fascin
Ikuko Fujiwara[1], Miki Iwatani[1], Yumeka Yamauchi[2], Tatsuya Iwata[3], Shuichi Takeda[4], Toshiro Oda[5], Tomoharu Matsumoto[4], Akihiro Narita[4], Satoshi Tsunoda[2,6], Hideki Kandori[2] ([1]*NITech*, [2]*Grad Sch Eng, Nagoya Inst Tech*, [3]*Toho University*, [4]*Grad. Sch. Sci., Univ. Nagoya*, [5]*Univ. Tokaigakuin*, [6]*JST*)

3Pos041 Aureo 1 における C 末端 Jα ヘリックスの役割
The role of the C-terminal Jα helix in Aureochrome-1
Hiroto Nakjima, Osamu Hisatomi, Itsuki Kobayashi (*grad.sch.sci.,Univ.Osaka*)

3Pos042 Calcium concentration modulation in HeLa cells induced by mid-infrared laser irradiation
Yoshiyuki Shimizu, Toyohiko Yamauchi, Tatsuo Dougakiuchi, Gen Takebe (*Hamamatsu Photonics K.K.*)

3Pos043 光駆動プロトンポンプ型ロドプシンのシロイヌナズナへの異種発現の試み
An attempt of heterologous expression of light-driven proton pump rhodopsins in the higher plant *Arabidopsis thaliana*
Saki Inoue[1], Yurie Nagase[2], Kyohei Harada[3], Keiichi Kojima[1,2], Shintaro Munemasa[4], Susumu Yoshizawa[5], Yoshiyuki Murata[4], Shinji Masuda[6], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*Grad. Sch. Biosci. Biotechnol., Tokyo Inst. Technol.*, [4]*Grad. Sch. Environ. Life Sci., Okayama Univ.*, [5]*AORI, UTokyo*, [6]*Cent. Biolog. Resources & Informatics, Tokyo Inst. Technol.*)

3Pos044 緑藻クラミドモナスの葉緑体へのプロトンポンプ型ロドプシンの異所発現と葉緑体プロトン濃度勾配制御の試み
Expression of proton pump rhodopsins in the chloroplast of the alga *Chlamydomonas reinhardtii* for optical control of proton gradient
Yurie Nagase[1], Saki Inoue[2], Hiroshi Kuroda[3], Keiichi Kojima[1,2], Susumu Yoshizawa[4], Yuichiro Takahashi[3], Yuki Sudo[1,2] ([1]*Fac. of Pharm. Sci. Okayama Univ.*, [2]*Grad. Sch. of Med. Dent. Pharm. Sci. Okayama Univ.*, [3]*RIIS. Okayama Univ.*, [4]*AORI, UTokyo.*)

3Pos045 Development of Red-Shifted Channelrhodopsin Variants Using Long-Conjugated Retinal Analogues
Yi-Chung Shen[1], Toshikazu Sasaki[1], Takesi Matsuyama Hoyos[1], Takahiro Yamashita[1], Yoshinori Shichida[1,2], Takashi Okitsu[3], Yumiko Yamano[3], Akimori Wada[3], Toru Ishizuka[4], Hiromu Yawo[4], Yasushi Imamoto[1] ([1]*Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.*, [2]*Res. Org. for Sci. & Tech., Ritsumeikan Univ.*, [3]*Lab. of Organ. Chem. for Life Sci., Kobe Pharm. Univ.*, [4]*Dept. of Dev. Bio. & Neurosci., Grad. Sch. of Life Sci., Tohoku Univ.*)

3Pos046 Theoretical study on molecular mechanism of a light-driven ion transport of Halorhodopsin
Ryo Oyama, Taisuke Hasegawa, Shigehiko Hayashi (*Grad. Sch. Sci., Univ. Kyoto*)

化学受容／Chemoreception

3Pos047 シグナル伝達分子の細胞膜上空間分布解析
Spatial distribution analysis of signaling proteins on the cell membrane
Hiroaki Takagi[1], Yukihiro Miyanaga[2], Satomi Matsuoka[3], Masahiro Ueda[2,3] ([1]*Sch. Med., Nara Med. Univ.*, [2]*Grad. Sch. Front. Bio. Sci., Osaka Univ.*, [3]*BDR, Riken*)

3Pos048 大腸菌走化性応答における CheY 極局在の役割
Role of polar localization of chemotaxis protein CheY for the intracellular signaling under non-stimulated conditions in *Escherichia coli*
Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Dept. Frontier Biosci., Osaka Univ*)

3Pos049 コレラ菌タウリン走性受容体 Mlp37 の温度依存的遺伝子発現
Temperature-dependent gene expression of the taurine sensor Mlp37 of *Vibrio cholerae*
So-ichiro Nishiyama[3], Shiori Onogi[1], Yoshiyuki Sowa[1,2], Hiroshi Urakami[3], Ikuro Kawagishi[1,2] ([1]*Dept. Frontier Biosci., Hosei Univ.*, [2]*Res. Cen. Micro-Nano Tech., Hosei Univ.*, [3]*Fac. App. Life Sci., Niigata Univ. Pharm. App. Life Sci.*)

結晶成長・結晶化技術／Crystal growth & Crystallization technique

3Pos050 ファインバブル水を利用したタンパク質結晶化の新しいアプローチ
Novel approach for protein crystallization with ultrafine bubble water
Taichi Naruse[1], Mihoka Amano[1], Hiroaki Adachi[2], Shigeo Maeda[3], Toshihiro Fujita[3], Yusuke Mori[4], Shigeru Sugiyama[5] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*SOSHO Inc.*, [3]*IDEC Corp.*, [4]*Grad. Sch. Eng., Osaka Univ.*, [5]*Fac. Sci. & Tec., Kochi Univ.*)

蛋白質：機能／Protein: Function

3Pos051 国産無償創薬ソフトウェア myPresto の進展：ΔG 推算を中心に
Progress of free drug development software suite myPresto: focusing on ΔG estimation
Tadaaki Mashimo[1,2], Yoshifumi Fukunishi[3] ([1]*N2PC*, [2]*IMSBIO Co., Ltd.*, [3]*AIST(molprof)*)

3Pos052 The binding mechanism of Hepatitis B virus X protein to Smc5/6 complex
Katsumi Omagari, Yasuhito Tanaka (*Nagoya City Univ.*)

3Pos053 タンパク質–タンパク質結合の粗視化 MD シミュレーション: barnase と barstar を例として
Coarse grained molecular dynamics simulation of barnase-barstar binding
Yu Sugimoto[1,3], Yoshitaka Moriwaki[1], Tohru Terada[1,2], Kentaro Shimizu[1] ([1]*Grad. Sch. Agri. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*, [3]*JSPS*)

3Pos054 アルケミカル自由エネルギー計算における遅い緩和
Slow relaxation on alchemical free energy calculations
Yoshiaki Tanida, Azuma Matsuura (*Fujitsu Laboratories Ltd.*)

3Pos055 Rationalization of sampling space for searching fragment-binding poses
Hiroyuki Sato, Yoshiaki Tanida, Azuma Matsuura (*Fujitsu Lab. Ltd.*)

3Pos056 QM/MM metadynamics シミュレーションによる trehalose-6-phosphate phosphatase の触媒機構に関する研究
QM/MM metadynamics study of the catalytic mechanism of trehalose-6-phosphate phosphatase
Toshihiro Hayashi, Tadaomi Furuta, **Minoru Sakurai** (*Tokyo Tech*)

3Pos057 QM/MM metadynamics 計算による Chitinase A の加水分解機構の解析
Theoretical analysis of the hydrolysis mechanism in Chitinase A using QM/MM metadynamics simulation
Tsubasa Iino, Tadaomi Furuta, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

3Pos058 Spectroscopic analysis of an electron-bifurcating [FeFe] hydrogenase
Krzysztof Pawlak[1], Nipa Chongdar[1], Olaf Rudiger[1], Edward Reijerse[1], Wolfgang Lubitz[1], James Birrell[1], **Hideaki Ogata**[1,2] ([1]*MPI CEC*, [2]*ILTS Hokkaido Univ.*)

3Pos059 鉄硫黄クラスターを利用した tRNA 硫黄修飾酵素 TtuA の反応機構の解明
Elucidation of the tRNA thiolation mechanism of TtuA involved in Fe-S cluster
Masato Ishizaka[1], Minghao Chen[1], Syun Narai[1], Masaki Horitani[2], Seiko Oka[3], Yoshikazu Tanaka[4], Min Yao[1,5] ([1]*Grad. Sch. Life Sci., Univ. Hokkaido*, [2]*Fac. Agric., Univ. Saga*, [3]*G.F.C., Univ. Hokkaido*, [4]*Grad. Sch. Life Sci., Univ. Tohoku*, [5]*Grad. Sch. Adv. Life Sci., Univ. Hokkaido*)

3Pos060 無機ポリリン酸存在下でのアクチンとミオシン間の相互作用
Interactions between actin and myosin in the presence of inorganic polyphosphates
Koji Ito, Yoshiya Miyasaka, Kuniyuki Hatori (*Grad. Sch. Sci. Eng., Yamagata Univ.*)

3Pos061 テトラヒメナ外腕ダイニンにおける致死性 P ループ変異の機能解析
Functional characterization of lethal P-loop mutations in Tetrahymena outer arm dynein (Dyh3p)
Masaki Edamatsu (*Department of Life Sciences, The University of Tokyo*)

3Pos062 ヒトジヒドロリポアミドデヒドロゲナーゼの酵素反応の制御機構における定常状態と時間分割蛍光についての研究
Steady-state and Time-resolved Fluorescence Studies on the Enzymatic Reaction Mechanism of Human Dihydrolipoamide Dehydrogenase
Yayoi Hara[1], Etsuko Nishimoto[2] ([1]*Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ.*, [2]*Fac. Agr., Kyushu Univ.*)

3Pos063 Optimizing the protocol for accelerating the analysis of the ATPase activity of circadian clock protein KaiC
Dongyan Ouyang[1], Atsushi Mukaiyama[1,2], Yoshihiko Furuike[1,2], Shuji Akiyama[1,2] ([1]*IMS*, [2]*SOKENDAI*)

3Pos064 多分子のキネシンによる協調運動の高速一分子観察
High-speed nanometer-precision tracking of the cargo transport by multiple kinesin-1 motor proteins
Tsukasa Enomoto (*Grad. Life science., Univ. Aoyama*)

蛋白質：計測・解析／Protein: Measurement & Analysis

3Pos065 質量分析によるヌクレオソームにおけるヒストンアセチル化の解析
Characterization of histone acetylation in nucleosome core particle using mass spectrometry
Haruna Hidaka[1], Shunsuke Izumi[1], Satoko Akashi[2], Kazumi Saikusa[1,2] ([1]*Hiroshima university*, [2]*Yokohama city university*)

3Pos066 異なる pH で形成したインスリン B 鎖アミロイド核形成中間体の構造比較
Structural comparison of amyloid nucleation intermediates of insulin B chain formed at different pH values
Yuhki Yoshikawa, Naoki Yamamoto, Atsuo Tamura, Eri Chatani (*Grad.Sch.Sci.,Kobe Univ.*)

3Pos067 固体 NMR 常磁性緩和促進法による大腸菌細胞内生体分子の局在化解析
Localization of biomolecules in E. coli cells as studied by solid-state NMR under paramagnetic relaxation enhancement
Zhongliang Zhang, Hajime Tamaki, Kazuya Yamada, Toshimichi Fujiwara (*Institute for Protein Research, Osaka Univ.*)

3Pos068 High-speed single molecule tracking of allosteric transitions in hemoglobin using Diffracted X-ray Tracking (DXT)
Yuu Okamura[1], Masahiro Kuramochi[1,2], Toshiki Hiraki[3], Naoki Yamamoto[3], Naoya Shibayama[3], Hiroshi Sekiguchi[4], Yuji Sasaki[1,2,4] ([1]*The Univ. of Tokyo Grad Sch FS*, [2]*AIST-UTokyo OPELAND-OIL*, [3]*Jichi Med Univ*, [4]*SPring8/JASRI*)

3Pos069 Protein Motion Analyzed by Diffracted X-ray Blinking
Hiroshi Sekiguchi[1], Masahiro Kuramochi[2], Noboru Ohta[1], Yuji Sasaki[1,2] ([1]*JASRI/SPring-8*, [2]*Frontier Sci., Univ. Tokyo*)

3Pos070 Nanopore probe with protein: Electrical observation of small protein motility in the nanospace
Misa Yamaji, Masaki Matsushita, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

3Pos071 インスリンアミロイドに結合したチオフラビン T の蛍光寿命特性に対する pH の影響
Effect of pH on fluorescence lifetime behavior of Thioflavin T binding to insulin amyloid
Akinori Oda, Hiroshi Satozono, Tomoo Inubushi (*Hamamatsu Photonics K.K.*)

3Pos072 高速 AFM 画像データに対する生体分子立体構造のフレキシブルフィッティング
Flexible fitting of biomolecular structures to high-speed AFM image data
Toru Niina, Sotaro Fuchigami, Shoji Takada (*Kyoto Univ. Grad. Sch. Sci.*)

3Pos073 高転移性マウス乳癌細胞の細胞弾性におけるネスチンテールドメインの機能解析
Functional analysis of nestin tail domain in elastic modulus of highly metastatic mouse breast cancer cells
Moe Susaki[1], Mei Mizusawa[1], Ayana Yamagishi[2], Chikashi Nakamura[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Biomed. Res. Inst., AIST*)

3Pos074 タンパク質の水和／溶媒和層の定量的な評価
Quantitatively characterization of the hydration and/or solvation shell of protein
M. Hirai[1], S. Ajito[1], H. Iwase[2], S. Arai[3] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Comp. Res. Org. Sci. Soc.*, [3]*Nat. Inst. Quan. Rad. Sci. Tech.*)

3Pos075 物理系と温度系の合成：カップルされた能勢ーフーバー方程式
A coupling of physical system and a temperature system: Coupled Nose-Hoover equations
Ikuo Fukuda[1], Kei Moritsugu[2] ([1]*Grad. Sch. Sim., Univ. Hyogo*, [2]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

3Pos076 周期境界条件下の分子動力学シミュレーションを使った結合自由エネルギー計算で生じる有限サイズ効果を抑えるアルケミカル摂動法の開発
An effective alchemical perturbation method eliminating finite-size effect on binding free energies
Toru Ekimoto, Tsutomu Yamane, Mitsunori Ikeguchi (*Yokohama City Univ.*)

蛋白質工学／Protein: Engineering

3Pos077 アレルギー性喘息を引き起こすインターロイキン 33 の阻害タンパク質の開発
Development of a protein that inhibits interleukin-33 responsible for allergic asthma
Mio Sano[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

3Pos078 細胞内ヌクレオチド定量センサーの合理的設計
Rational design of nucleotide sensors for intracellular quantitative imaging
Yoshiki Oka[1], Shunji Suetaka[1], Hinako Ago[2], Yuna Miyachi[2], Yuuki Hayashi[1,2], Munehito Arai[1,2,3] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*College Arts Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

3Pos079 抗体の親和性向上におけるフレームワーク領域へのアルギニンクラスター導入の効果
Role of Arg cluster (R5) introduced into framework region (FR3) in affinity improvement
Shingo Maeta[1], Makoto Nakakido[1,2,3], Kouhei Tsumoto[1,2,3] ([1]*Dept. of Bioeng., Univ. of Tokyo*, [2]*Dept. of Chem and Biotech., Univ. of Tokyo*, [3]*Med Proteom., Inst. of Med Sci., Univ. of Tokyo*)

3Pos080 Characterization of the “scrap-and-build” process in the proteasome α ring formation
Taichiro Sekiguchi[1,2,4], Tadashi Satoh[3], Kentaro Ishii[1,4], Hirokazu Yagi[3], Koichi Kato[1,2,3,4] ([1]*ExCELLS*, [2]*SOKENDAI*, [3]*Nagoya City Univ*, [4]*Inst. for Mol. Sci.*)

3Pos081 状態選択的に安定化された G タンパク質共役受容体の合理デザイン
Rational Design of G-Protein Coupled Receptors Stabilized in Aimed State
Masaya Mitsumoto[1,2], Ryosuke Nakano[3], Takeshi Murata[3,4], Nobuyasu Koga[1,2] ([1]*ExCELLS, NINS*, [2]*SOKENDAI*, [3]*Fac. of Sci., Chiba Univ.*, [4]*PRESTO, JST*)

3Pos082 ファージディスプレイ法への応用を目指した蛍光検出ファージソーターの改良
Improvement of the fluorescent detected phage sorter for the application to phage display
Hitomi Urabe[1,2], Saya Nakano[1,3], Yuki Shimizu[1,2], Naoki Mikosiba[1,3], Hiroyuki Oikawa[1,2,3], Satoshi Takahashi[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Sci., Tohoku Univ.*, [3]*Grad. Sch. Life Sci., Tohoku Univ.*)

3Pos083 Design of multi-domain protein structures for small molecule binding
Hiroko Yamada[1], Nobuyasu Koga[2] ([1]*SOKENDAI*, [2]*NINS ExCELLS*)

3Pos084 Designing an artificial transcription factor with a small molecular weight based on engrailed homeodomain
Tomoko Sunami, Yu Hirano, Taro Tamada, Hidetoshi Kono (*QST*)

3Pos085 立体構造に基づく配列プロファイルを利用した熱安定化 β-グルコシダーゼの設計に向けて
Toward design of thermostable β-glucosidase with structure-based sequence profile
Naoya Kobayashi[1], Shintaro Minami[1], Taku Uchiyama[2], Naoki Sunagawa[2], Kiyohiko Igarashi[2], Hiroyuki Noji[3,4], Nobuyasu Koga[1] ([1]*ExCELLS, NINS*, [2]*Dept. Biomater. Sci., Grad. Sch. Agri. Life Sci., Univ. Tokyo*, [3]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [4]*ImPACT, JST*)

3Pos086 平行ベータシート蛋白質の設計図におけるデザイナビリティの評価基準
Criteria for evaluating designability of pure parallel beta sheet structures
Hayao Imakawa[1], Nobuyasu Koga[2], George Chikenji[1] ([1]*Dept. of App. Phys., Nagoya Univ.*, [2]*CIMoS, IMS*)

3Pos087 タンパク質-タンパク質結合部位の予測とエピトープマッピング
Prediction of Protein-Protein Binding Sites and Epitope Mapping
John Gunn[2], Elizabeth Sourial[2], **Kinya Toda**[1], Paul Labute[2] ([1]*MOLSIS Inc.*, [2]*Chemical Computing Group ULC*)

3Pos088 理論的変異解析によるジヒドロ葉酸還元酵素の高活性化
Enhancing activity of dihydrofolate reductase by theoretical mutational analysis
Kazuhisa Ohara[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

非平衡・発生リズム／Nonequilibrium state & Biological rhythm

3Pos089 Mathematical Modeling for Morphallactic Segment Formation Using a Size-Dependent Multi-Loop Negative Feedback System
Yusuke Shibasaki[1], Chikako Yoshida-Noro[2], Minoru Saito[1] ([1]*Graduate School of Integrated Basic Sciences, Nihon University*, [2]*College of Industrial Technology, Nihon University*)

3Pos090 Maximizing Local Information Transfer in Boolean Networks
Taichi Haruna[1], Kohei Nakajima[2,3] ([1]*Tokyo Woman's Christian University*, [2]*The University of Tokyo*, [3]*PRESTO, JST*)

3Pos091 局所情報流最大化に駆動される時空間ダイナミクス
Spatiotemporal dynamics driven by maximization of local information transfer
Kohei Nakajima[1,3], Taichi Haruna[2] ([1]*The University of Tokyo*, [2]*Tokyo Woman's Christian University*, [3]*JST PRESTO*)

3Pos092 Spatial Cooperation between DNA and Actin in Micro-Confinement Generated through Spontaneous Phase Segregation
Hiroki Sakuta[1], Naoki Nakatani[1], Masahito Hayashi[2], Kingo Takiguchi[3], Kanta Tsumoto[4], Kenichi Yoshikawa[1] ([1]*Grad. Sch. Life Med. Sci., Doshisha Univ.*, [2]*Center of Brain Sci., RIKEN*, [3]*Grad. Sch. Sci., Nagoya Univ.*, [4]*Grad. Sch. Eng., Mie Univ.*)

3Pos093 Theoretical model of dynamics of epithelial tissue with cellular chirality
Takaki Yamamoto[1], Tetsuya Hiraiwa[2], Tatsuo Shibata[1] ([1]*Riken, Lab. Phys. Biol.*, [2]*Univ. Tokyo, Sci. Phys.*)

3Pos094 Analysis of soliton-like collective migration of non-chemotactic *dictyostelium* cells
Masayuki Hayakawa[1], Hidekazu Kuwayama[2], Yuko Wada[1], Tatsuo Shibata[1] ([1]*BDR, Riken*, [2]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

3Pos095 多電極システムによる心筋細胞ネットワークにおける拍動伝導の計測技術の開発
Development of a method to track conductions in cardiomyocyte network with a multi-electrode system
Kazufumi Sakamoto[1], Natsuki Seki[1], Shota Aoki[2], Naoki Takahashi[2], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

生命情報科学／Bioinformatics

3Pos201 タンパク質複合体構造モデリングの評価のためのベンチマークデータセット
A large decoy dataset for protein-protein docking model quality assessment
Takanori Hayashi[1], Masahito Ohue[1], Juliette Martin[2], Guillaume Launay[2], Yuri Matsuzaki[3], Nobuyuki Uchikoga[3], Yutaka Akiyama[1,3] ([1]*Sch Computing, Tokyo Tech*, [2]*MMSB, CNRS, Univ Lyon*, [3]*ACLS, Tokyo Tech*)

3Pos202 Sequence profile for protein design based on database analysis of backbone environment
Shintaro Minami, Rie Koga, Nobuyasu Koga (*NINS, ExCELLS*)

3Pos203 Development of a method for predicting pathogenicity of missense variants incorporating supramolecular structural information
Atsushi Hijikata, Masafumi Shionyu, Tsuyoshi Shirai (*Nagahama Inst. Bio-Sci. Tech.*)

3Pos204 Performance improvement of the method for large-scale structural comparison of protein pockets
Tsukasa Nakamura[1,2], Kentaro Tomii[1,2] ([1]*CBMS, GSFS, Univ. Tokyo*, [2]*AIRC, AIST*)

3Pos205 ヒト機能未知スプライシングアイソフォームの特徴解析
Analysis of characteristics of function-unknown splicing isoforms in human
Masafumi Shionyu, Atsushi Hijikata (*Fac. Biosci., Nagahama Inst. Bio-Sci. Tech.*)

3Pos206 Characterizing SLC transporters by sequence and functional networks
Hafumi Nishi[1], Yuya Hanazono[1], Hitoshi Yamagata[2], Kengo Kinoshita[1] ([1]*Grad. Sch. Info. Sci., Tohoku Univ.*, [2]*Adv. Res. Lab., Canon Medical Systems Corp.*)

3Pos207 肺癌細胞の発現変動遺伝子を対象としたクラスタセントロイド間の相関ネットワーク
Correlated network by cluster centroids for differentially expressed genes in lung cancer cell
Kohei Misu[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, [2]*RDCMIT, Tokyo Med. Univ.*)

3Pos208 機能に関する選択シミュレーションにおける P-loop 蛋白質構造の多様化
Diversification of P-loop protein structure simulated by imposing the functional requirement as a selection pressure
Kohei Inukai, Masaki Sasai, George Chikenji (*Department of Engineering, Nagoya University*)

数理生物学／Mathematical biology

3Pos209 脳の階差成長による皺形成シミュレーション
Winkling simulation of differential growth of brain
Katsuyoshi Matsushita[1], Kazuya Horibe[1], Naoya Kamamoto[1], Ken-ichi Hironaka[2], Koichi Fujimoto[1] ([1]*Depertment of Biological Science, Graduate School of Science, Osaka University*, [2]*Department of Biological Sciences, Graduate School of Science, University of Tokyo*)

3Pos210 機械学習を利用した集団内細胞行動解析
System analysis of cellular behavior with machine learning during collective cell migration
Moegi Marumoto[1,2], Masaya Hagiwara[1] ([1]*N2RI, Osaka Pref. Univ.*, [2]*Dept. of Biol. Sci., Osaka Pref. Univ.*)

3Pos211 多細胞の協調的な運動時における細胞の複雑な変形のフェーズフィールドモデル
Phase-field modeling of complex cell deformation and multi-cellular motion
Daisuke Imoto[1], Nen Saito[4], Satoshi Sawai[1,2,3] ([1]*Dept Basic Sci, Grad School of Arts and Sci, Univ of Tokyo*, [2]*Research Ctr for Complex Systems Biology, Univ of Tokyo*, [3]*JST PRESTO, School of Science, The University of Tokyo,*, [4]*Universal Biology Institute, The University of Tokyo*)

3Pos212 不正確な素子から正確な情報伝達をおこなうためのネットワーク構造と協同性
Cooperative reliable response from sloppy gene expression dynamics
Masayo Inoue[1], Kunihiko Kaneko[2] ([1]*IMS, Meiji Univ.*, [2]*Univ. of Tokyo*)

3Pos213 A data-driven model for collective cell motion in Dictyostelium discoideum
Keizaburo Nishikino[1], Ryo Yokota[2], Tetsuya J. Kobayashi[1,2,3] ([1]*EEIS, Univ Tokyo*, [2]*IIS, Univ Tokyo*, [3]*IST, Univ Tokyo*)

3Pos214 ATPase activity of individual KaiC molecules decisively influences the ensemble-level oscillation of cyanobacterial KaiABC clock
Sumita Das[1,2], Tomoki P. Terada[1,2], Masaki Sasai[1,2] ([1]*Deparment of Computational Science and Engineering, Nagoya University, Nagoya*, [2]*Department of Applied Physics, Nagoya University, Nagoya*)

3Pos215 Effects of the binding domain of Pin1 interacting with proteins of variable conformations
Romain Amyot, **Yuichi Togashi** (*Grad. Sch. Sci., Univ. Hiroshima*)

3Pos216 Experimental Validation of a Mathematical Model of ErbB Receptor Signaling to Cell Cycle
Kyoichi Ebata, Hiroaki Imoto, Kazunari Iwamoto, Shigeyuki Magi, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

3Pos217 蟻の死骸の山の形成プロセスにおける一考察
Ant Cemeteries Grow via the Ambiguous Local Environment
Tomoko Sakiyama (*Grad. Sch. Nat. Sci. Tech., Univ. Okayama*)

3Pos218 Reduction of a Markov operator representing the dynamics of stochastic neuronal model by sparse discrete cosine transform
Takanobu Yamanobe (*Hokkaido University School of Medicine*)

3Pos219 アルツハイマー病とシロスタゾール ー傾向スコアを用いた医療費の検討ー
Alzheimer's disease and cilostazol -medical cost through propensity score-
Izumi Kuboyama, Susumu Ito, Toshiaki Kaminaka, Katsuhiko Hata (*Kokushikan University*)

3Pos220 Coupled epigenetic and genetic network gives rise to a probability landscape with eddy currents
Bhaswati Bhattacharyya, Masaki Sasai (*Department of Computational Science and Engineering, Nagoya University*)

細胞生物学／Cell Biology

3Pos301 SPI-2 感染装置先端蛋白質 SseB の集合体形成
Assembly characteristics of SseB, a putative tip protein of the SPI-2 injectisome
Takumi Tsujimoto[1], Yuki Yamanaka[2], Linda J Kenny[2], Katsumi Imada[1] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*MBI., NUS.*)

3Pos302 GPCR ダイマーを構成する一部の分子は、リガンド刺激前に自発的に活性化している
Spontaneous activation in a transient GPCR dimer before ligation as revealed by dual-channel single fluorescent molecule imaging
Rinshi Kasai (*Inst. Front. Life. Med. Sci., Kyoto Univ.*)

3Pos303 MCF 細胞内における p52Shc の Grb2 シグナル伝達制御
Regulation of Grb2 signaling dynamics by p52Shc scaffold protein in MCF7 cells
Ryo Yoshizawa[1,2], Nobuhisa Umeki[2], Masataka Yanagawa[2], Masayuki Murata[1], Yasushi Sako[2] ([1]*Grad.sch.arts and ahi., the univ. Tokyo*, [2]*Wako Inst., Riken*)

3Pos304 RhoA activation inhibits proliferation of skin cancer cells
Oleg Dobrokhotov[1,2], Atsushi Enomoto[3], Masaki Sunagawa[3], Masahide Takahashi[3], Mikhail Samsonov[4], Masahiro Sokabe[2], Hiroaki Hirata[1,2] ([1]*R-Pharm Japan*, [2]*Mechanobiology Lab., Grad. Sch. Med., Nagoya Univ.*, [3]*Dept. Pathology, Grad. Sch. Med., Nagoya Univ.*, [4]*R-Pharm*)

3Pos305 Size-dependent beating rate changes of cardiomyocyte clusters by environmental thermal changes
Wei Wang, Tomoyuki Kaneko (*LaRC, FB, Grad.Sch., Hosei Univ.*)

3Pos306 心筋細胞メカニクスに NADPH オキシダーゼ 4 が及ぼす影響
Single cell mechanics effects of NADPH oxidase (NOX) 4 in mouse ventricular cardiomyocytes
Keiko Kaihara, Gentaro Iribe, Hiroaki Kai, Keiji Naruse (*Dept Cardio Physiol, Grad Sch med, Okayama Univ*)

3Pos307 1細胞レベルの電気信号伝導速度計測に向けた心筋細胞ネットワーク再構築
Reconstruction of cardiomyocyte network for measuring the signal conduction velocity at single cell level
Koki Fujii, Tomoyuki Kaneko (*LaRC, FB, Hosei univ*)

3Pos308 間葉系幹細胞の温度依存形態振動に伴うメカノシグナル転写因子の核ー細胞質シャトリング
Nucleocytoplasmic shuttling of the mechanotransducing proteins in temperature-dependent shape-oscillating mesenchymal stem cells
Sayaka Masaike[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

3Pos309 iPS 細胞は最適弾性率を持つハイドロゲル表面に移動し増殖する
iPS cells move toward and efficiently proliferate on the hydrogel surface with optimal elasticity
Mengfan Wang[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

3Pos310 ハイドロゲル上でのマスト細胞の刺激応答
Inhibition of degranulation in mast cells cultured on hydrogel
Atsushi Shiki, Yoshikazu Inoh, Satoru Yokawa, Tadahide Furuno (*Sch. Pharm., Univ. Aichi Gakuin*)

3Pos311 三次元細胞構造体の構築：高分子混雑環境下におけるレーザーピンセットの活用
Constructing 3D Cellular Assembly: Laser Tweezering under Depletion Effect on Albumin Solution
Ritsuki Ito, Kakehiro Yamazaki, Satoshi Kishimoto, Takahiro Kenmotsu, Koichiro Sadakane, Kenichi Yoshikawa (*Faculty of Biological and Medical Sciences, Doshisha University*)

3Pos312 Investigation for the crosstalk mechanism of two damping oscillators, p38 MAP kinase and NF-κB
Hiroki Michida, Minami Ando, Shigeyuki Magi, Kazunari Iwamoto, Mariko Okada (*IPR Osaka Univ.*)

3Pos313 多繊毛上皮細胞の基底小体の配列・配向秩序化の数理モデル
Mathematical model for alignment and orientation order of basal bodies in a multi-ciliated cell
Toshinori Namba[1], Shuji Ishihara[1,2] ([1]*Graduate School of Arts and Sciences, The University of Tokyo*, [2]*Universal Biology Institute, The University of Tokyo*)

3Pos314 隣接させた心臓組織片の同期化プロセスの解明
Synchronization processes of cardiac tissue fragment pair and the regional differences in the heart
Shin Arai[1], Tomoyuki Kaneko[2], Toshiyuki Mitsui[1] ([1]*Grad. Sch. of Sci. & Eng., Aoyama Gakuin Univ.*, [2]*LaRC, Grad. Sci. Eng., Hosei Univ.*)

3Pos315 長期的機械刺激による心筋細胞集合体への影響
Long-term influence of external mechanical stimulus on cardiomyocyte aggregations
Takashi Miyazawa, Shin Arai, Takahiro Uehara, Shogo Yahagi, Toshiyuki Mitsui (*Grad. Sch. of Sci. & Eng., Aoyama Gakuin Univ.*)

3Pos316 Exploring the basic law that determines the shape of fast moving cells
Gen Honda[1], Satoshi Sawai[1,2] ([1]*Department of Basic Science, Graduate School of Arts and Sciences, University of Tokyo*, [2]*Research Center for Complex Systems Biology, Graduate School of Arts and Sciences, University of Tokyo*)

3Pos317 AFM を用いた腫瘍微小環境を構成する細胞間の接着剥離力と細胞接触時間の関係評価
Relationship between detachment force and contact time for cells making up tumor microenvironments measured by AFM
Kenta Ishibashi[1], Tomoko Okada[2], Chikashi Nakamura[1,2], **Hyonchol Kim**[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Biomed. Res. Inst., AIST*)

3Pos318 生物発光イメージング法を用いた ECM と接着したマスト細胞の脱顆粒の可視化解析
Video-Rate Bioluminescence Imaging of Degranulation of Mast Cells Attached to the Extracellular Matrix
Satoru Yokawa[1], Takahiro Suzuki[2], Ayumi Hayashi[1], Satoshi Inouye[3], Yoshikazu Inoh[1], Tadahide Furuno[1] ([1]*Sch. Pharm., Aichi Gakuin Univ.*, [2]*Sch. Dent., Aichi Gakuin Univ.*, [3]*JNC Co., Yokohama.*)

3Pos319 FERT 法による走化性受容体クラスター活性とべん毛モーター回転の 1 細胞同時計測
Simultaneous measurement of chemoreceptor array's activity and the flagellar motor rotation utilizing single cell FRET
Hajime Fukuoka, Tatsuya Yamakoshi, Sarina Nishimura, Yong-Suk Che, Akihiko Ishijima (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

3Pos320 大腸菌におけるべん毛の回転方向と CheY の細胞内動態の同時計測
Simultaneous measurement of flagellar motor rotation and dynamics of CheY in a single *E.coli* cell
Tatsuya Yamakoshi, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad.Sch.Frontier.Osaka Univ.*)

3Pos321 T 細胞シグナルの超解像イメージング法の開発
Development of the superresolutional imaging in T cell signaling
Hiroaki Machiyama, Ei Wakamatsu, Tadashi Yokosuka (*Dept. Immunol., Tokyo Med. Univ.*)

3Pos322 磁性細菌の走磁性運動におけるべん毛回転運動の生細胞イメージング
Live-cell imaging of flagellar rotation in magnetotactic bacterial cell during magneto-aerotaxis
Yuta Takaoka[1], Azuma Taoka[1], Yoshihiro Fukumori[2] ([1]*Grad. Sch. of Nat. Sci. and Tech., Kanazawa Univ.*, [2]*Vice President, Kanazawa Univ.*)

3Pos323 高速 AFM による細胞表面の分子イメージング
Molecular imaging of dynamic process on bacterial cell surface by high speed AFM
Hayato Yamashita[1,2], Azuma Taoka[3,4], Masayuki Abe[1] ([1]*Grad. Sch. of Eng. Sci., Osaka Univ.*, [2]*PRESTO, JST*, [3]*Grad. Sch. of Nat. Sci. & Tech., Kanazawa Univ.*, [4]*Bio-AFM Frontier Research Center, Kanazawa Univ.*)

3Pos324 魚類ケラトサイトの遊走メカニズムに微小管は必要ない
Microtubules are not required for crawling migration of keratocytes
Hitomi Nakashima, Chika Okimura, **Yoshiaki Iwadate** (*Fac. Sci., Yamaguchi Univ.*)

3Pos325 神経突起との接着による膵島 α 細胞の細胞内顆粒動態とグルカゴン分泌の抑制
Decreased intracellular granule movement and glucagon secretion in pancreatic α cells attached to superior cervical ganglion neurites
Tadahide Furuno[1], Satoru Yokawa[1], Kiyoto Watabe[1], Yoshikazu Inoh[1], Takahiro Suzuki[2] ([1]*Sch. Pharm., Aichi Gakuin Univ.*, [2]*Sch. Dent., Aichi Gakuin Univ.*)

3Pos326 赤外線レーザー照射刺激による心筋細胞拍動変化の物理的要因
Physical effect on beating rate change of cardiomyocytes induced by infrared laser irradiation
Yukino Motohashi, Kento Nozawa, Maki Ishii, Tomoyuki Kaneko (*LaRC, FB, Hosei univ.*)

3Pos327 100 分子ほどの膜貫通足場タンパク LAT がマスト細胞の免疫反応を担っている
Only ~100 copies of a transmembrane scaffolding protein LAT are responsible in the immune response in mast cells
Koichiro M. Hirosawa[1], Nao Hiramoto-Yamaki[2], Shohei Nozaki[3], Taka A. Tsunoyama[4], Bo Tang[5], Kenichi G.N. Suzuki[1,2], Kazuhisa Nakayama[3], Takahiro K. Fujiwara[2], Akihiro Kusumi[4] ([1]*G-CHAIN, Gifu Univ.*, [2]*iCeMS, Kyoto Univ.*, [3]*Grad. Sch. Pharma., Kyoto Univ.*, [4]*OIST*, [5]*Wuhan University*)

バイオエンジニアリング／Bioengineering

3Pos401 Stiffness measurement of cell by using micro-hand systems with plate shape end effector
Masaru Kojima[1], Taisei Tanaka[1], Yasushi Mae[1], Toshihiko Ogura[2], Tatsuo Arai[3,4] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*IDAC, Tohoku Univ.*, [3]*Glob. Alliance Lab., The Univ. of Electro-Communications*, [4]*Beijing Inst. of Tech.*)

3Pos402 油中水滴界面を利用した DNA ハイドロゲルマイクロカプセルの構築
Construction of DNA hydrogel microcapsules using water-in-oil droplet interface
Yuji Nakashima, Yusuke Sato, Yu Kasahara, Masahiro Takinoue (*Dept. of com. sci., TITech*)

3Pos403 DNA でつくるシグナル伝達機構の実現に向けた DNA 生成反応回路の構築
Construction of a DNA Generation Circuit toward Engineering of DNA-based Signal Transduction Systems
Ken Komiya, Chizuru Noda, Masayuki Yamamura (*Sch. Comp., Tokyo Tech.*)

3Pos404 iPS 細胞の心筋分化誘導における血管内皮細胞の影響
Effect of vascular endothelial cells on cardiac differentiation of iPS cells
Chika Tada, Ken Takahashi, Masatoshi Morimatsu, Keiji Naruse (*Grad. Sch Med Dent Pharm Sci., Okayama Univ.*)

3Pos405 Evaluation of membrane shape deformation of giant vesicles prepared by droplet transfer method
Masamune Morita, Naohiro Noda (*Biomed. Res. Inst., AIST*)

3Pos406 細胞外電位測定による心筋細胞集団と心臓組織片の拍動同期過程の解析
Analysis of signal synchronization process between dispersed cardiomyocyte and cardiac tissue piece by measuring extracellular potential
Toru Nakamura, Chiho Nihei, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell biology, Department of Frontier Bioscience, Hosei University*)

3Pos407 新規心毒性検査技術を目指した心臓組織片の細胞外電位計測
Measurement of Extracellular Potential on Heart Tissue for Novel Cardiotoxicity Test
Ryohei Kobayashi, Koji Emura, Tomoyuki Kaneko (*LaRC,FB,Hosei Univ.*)

3Pos408 細胞外電位計測による心臓組織片の拍動同期解析
Analysis of beating synchronization of cardiac tissue pieces by field potential measurement
Yousuke Kamei[1], Toshiyuki Mitsui[2], **Tomoyuki Kaneko**[1] ([1]*LaRC, FB, Hosei Univ.*, [2]*Dept. Math. Phys., Col. Sci. Eng., Aoyama Univ.*)

3Pos409 血中循環腫瘍細胞をサイズ分画するための流路チップデザインの加工工程における形状の転写の加工精度の定量的評価
Quantitative evaluation of preciseness in design copy in microfabrication procedures of circulating tumor cell cluster size-filtration
Ayako Kawai[1], Moe Iwamura[2], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

3Pos410 血中循環腫瘍細胞を選択回収するサイズ分画機能を備えた画像認識型セルソーターの開発
Development of size filtration-imaging cell sorter for real time selective collection of circulating tumor cells (CTCs) in blood
Moe Iwamura[1], Kenji Matsuura[3,4], Ayako Kawai[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

3Pos411 単一細胞分析のための Ba2 + / Ca2 +アルギン酸微小滴からの選択的な細胞回収方法の検討
Selective digestion of Ba2+/Ca2+ alginate microdroplets for single-cell-analysis
Masao Odaka[1,2], Moe Iwamura[3], Ayako Kawai[4], Akihiro Hattori[1,2], Kenji Matsuura[1,2], Kenji Yasuda[1,2,3,4] ([1]*Org. Univ. Res. Initiatives, Waseda Univ.*, [2]*WASEDA Biosci. Res. Ins. in Singapore*, [3]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [4]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos412 Environment-dependent self-assembly of DNA nanostructures on phase-separated lipid bilayer membranes
Yusuke Sato[1], Masayuki Endo[2,3], Masamune Morita[4], Masahiro Takinoue[1], Hiroshi Sugiyama[2,3], Satoshi Murata[5], Shin-ichiro M. Nomura[5], Yuki Suzuki[5,6] ([1]*Dept. Comput. Sci., Tokyo Tech*, [2]*iCeMS, Kyoto Univ.*, [3]*Grad. Sch. Sci., Kyoto Univ.*, [4]*Biomed. Res. Inst., AIST*, [5]*Grad. Sch. Eng., Tohoku Univ.*, [6]*Fronti. Res. Inst. Interdiscrip. Sci., Tohoku Univ.*)

3Pos413 血管新生の遺伝子発現解析のためのマトリゲル構造を用いた発芽的血管内皮細胞の回収方法の開発
Development of sprouting vascular endothelial cell collection method using flexible design of Matrigel for expression analysis
Yuki Yamanaka[1], Kento Iida[1], Ryuji Takano[2], Hiromichi Hashimoto[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

3Pos414 交流磁場によるフェリチン内合成マグネタイトナノ粒子の加熱
Heating effect of magnetite nanoparticles synthesized in the ferritin cavity by alternating magnetic field
Daisuke Katayama[1], Hideyuki Yoshimura[2] ([1]*Grad. Sch. Sci Eng. Phys, Univ. Meiji*, [2]*Sci Eng. Phys, Univ. Meiji*)

3Pos415 Insertion of cancer cell specific binding peptide into ferritin
Naoki Takashima[1], Hideyuki Yhoshimura[2], Tomoko Kanamaru[2] ([1]*Grad. Sch. Sci/Eng Phy. Univ. Meiji*, [2]*Sci/Eng Phy. Univ. Meiji*)

3Pos416 蛍光・発光タンパク質に基づくマイクロディスプレイ
Micro-display devices based on fluorescence and bioluminescence proteins
Kosuke Hama[1], Trisha.D Farha[1], Mieko Imayasu[1], Ken-ichi Shinohara[1], Yuichi Hiratsuka[1], Atsushi Miyawaki[2], Hidekazu Tsutsui[1,2] ([1]*JAIST, material Sci*, [2]*Wako Inst., Riken*)

3Pos417 Photo-regulation of Small GTPase Ras using Photochromic SOS-Peptide
Masahiro Kuboyama[1], Nobuyuki Nishibe[1], Kenichi Taii[1], Kazunori Kondo[2], Shinsaku Maruta[1] ([1]*Dept. of Bioinformatics, Graduate School of Engineering, Soka University*, [2]*Department of Science and Engineering, Faculty of Science and Engineering, Soka University*)

3Pos418 High-throughput in vitro selection method for obtaining peptide agonists of G protein-coupled receptors
Anna Matsueda[1], Takashi Sakurai[1], Ryo Iizuka[1], Yasuyuki Nakamura[2], Jun Ishii[3], Akihiko Kondo[2], Ayaka Iguchi[4], Dong Hyun Yoon[5], Tetsushi Sekiguchi[5], Shuichi Shoji[4], Yuu Fujimura[6], Jin Akagi[6], Masayuki Ishige[6], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*, [2]*Grad. Sch. of Eng., Kobe Univ.*, [3]*Org. of Adv. Sci. and Technol., Kobe Univ.*, [4]*Dept. of Nanosci. and Nanoeng., Waseda Univ.*, [5]*Res. Org. for Nano & Life Innov., Waseda Univ.*, [6]*On-chip Biotechnol. Co., Ltd.*)

3Pos419 Droplet-based microfluidic screening for obtaining microbes producing macromolecule-degrading enzymes
Ryo Iizuka[1], Kai Saito[1], Eiji Shigihara[1], Wataru Kawakubo[2], Daiki Tanaka[3], Dong Hyun Yoon[3], Tetsushi Sekiguchi[3], Shuichi Shoji[2], Mei Ito[4], Yuji Hatada[4], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*, [2]*Dept. of Nanosci. and Nanoeng., Waseda Univ.*, [3]*Res. Org. for Nano & Life Innov., Waseda Univ.*, [4]*Dept. of Life Sci. and Green Chem., Saitama Inst. of Technol.*)

3Pos420 統合情報理論に基づく意識を持つ DNA ネットワークの設計と解析
Design and analysis of DNA network with consciousness based on integrated information theory
Hiroki Watanabe[1], Ryuji Kawano[2], Masahiro Takinoue[1] ([1]*Dept. Compt. Sci., Tokyo Tech*, [2]*Dept. Bio. Life Sci., Tokyo Univ. Agri. Tech.*)

3Pos421 The way to the perfect observation!! ~Research of drone that mimics the birds~
Ayumu Kuroda (*Tokyo Metropolitan high sch .,F-pro*)

1SAA-1 反応拡散とフェイズフィールドから理解する細胞変形と集団ダイナミクス
Understanding single and multicellular dynamics from reaction-diffusion and phase-field modeling

Satoshi Sawai[1], Daisuke Imoto[1], Nen Saito[2], Akihiko Nakajima[1], Taihei Fujimori[1] ([1]*Grad Schl Arts & Sci, Univ Tokyo*, [2]*Grad Schl Sci, Grad Sch*)

Cell shape deformation is complex and highly dynamic especially in fast moving cells such as *Dictyostelium* amoeba and immune cells. In this talk, I will introduce a mathematical model describing a deformable system coupled with two to three reaction modules that drive cell protrusions. We show that depending on the parameters that determine the strength of the cell polarity, excitability and membrane rigidity, the model exhibits three distinct modes of cell shape characterized by the number and the size of the protrusions. We compare the results with experimental data based on sparse analysis and discuss the implications on the governing dynamics.

1SAA-2 ゴルジ装置の自己組織化形成過程
Self-organized formation of Golgi body

Masashi Tachikawa (*RIKEN*)

Golgi body is a membrane-bounded organelle with the characteristic morphology; several flattened membrane sacs stacking to each other. Although the morphology is thought to be important for its function, the mechanisms to generate and maintain it remain unrevealed. To understand the mechanism, we constructed a physical model and demonstrated the Golgi formation by coarse-grained membrane simulations. We focused on the Golgi reassembly process in mammalian cells, where vesicles assemble into the shape at the end of mitosis. We found that the characteristic Golgi shape was spontaneously organized from the assembly of vesicles. We also demonstrated that the Golgi shape forms via a balance in three reaction speeds: vesicle aggregation, membrane fusion, and shape relaxation.

1SAA-3 フェーズフィールド法によるマクロピノサイトーシス動態の 3D シミュレーション
phease-field modeling for 3D morphodynamics of macropinocytosis

Nen Saito[1], Satoshi Sawai[2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Arts Sci., Univ. Tokyo*)

Macropinocytosis is clathrin-independent endocytosis and allows internalization of large volume of extracellular fluid. D. discoideum and tumor cells show constitutive macropinocytosis for uptake of nutrients from extracellular fluid. The mechanism of it remains still unclear. We introduce a mathematical model based on 3D phase-field method, which enables reaction-diffusion process on the membrane and large membrane deformation simultaneously. Simulation results indicate that simple chemical reactions lead to drastic membrane deformation, which results in an engulfment of extracellular fluid. This study provides a new insight for macropinocytosis as a self-organization phenomenon via feedback between drastic deformation of membrane and reaction-diffusion on it.

1SAA-4 ショウジョウバエ後腸の捻転現象を 3D バーテックスダイナミクスモデルから考える
A three-dimensional vertex dynamics model for understanding the rotating phenomenon of the hindgut of Drosophila embryo

Masakazu Akiyama[1], Takamichi Sushida[1], Yasuhiro Inoue[3], Akino Ookubo[2], Mikiko Inaki[2], Kenji Matsuno[2] ([1]*Research Institute for Electronic Science, Hokkaido University*, [2]*Department of Biological Sciences Graduate School of Science Osaka University*, [3]*Department of Biosystems Science, Institute for Frontier Life and Medical Sciences, Kyoto University*)

Epithelial tissue morphogenesis requires morphologic changes such as migration or deformation of individual epithelial cells constituting the tissue. To reveal 3D morphologic changes of the cells contributing to the tissue deformation, we constructed a 3D vertex dynamics model in which the hindgut epithelial cells were represented by hexagonal cylinders. Numerical simulations suggested that twisting of individual cells along apico-basal axes can induce the directional tube rotation. To see whether the cell twisting predicted by the simulation occurs in vivo, we quantified the cell shape change using time-lapse imaging of the hindgut rotation. As a result, the hindgut epithelial cells directionally twist before and during the rotation.

1SAA-5 頭蓋骨縫合線パターン形成の数理モデル化
Modeling of skull suture pattern formation

Takashi Miura (*Kyushu University Graduate School of Medical Sciences*)

Our skull bone consists of several bones, and thin mesenchyme tissue between the bones are called suture tissue. Suture tissues are wide and straight at birth, and then become thinner and start winding, resulting in interdigitated structure. In some individuals the suture is reported to form fractal structure. How the pattern is formed is still remain to be elucidated. At first we reduced known molecular interactions to simple model interface equation and kernel to make the system easier to analyze mathematically. Then we made further simplified model, which represents the linear dynamics of band solution. Then we introduce noise term to the model to understand the fractality of skull suture in weakly-bend case.

1SAA-6 Folding pattern formation in a confined epithelial cell sheet

Yasuhiro Inoue (*Institute for Frontier Life and Medical Sciences, Kyoto University*)

Folding patterns are widely observed in biological soft tissue such as villi of intestinal epithelium, mouse oviduct and drosophila imaginal discs. These folding patterns should emerge not only from chemical patterning but also from mechanical instabilities in epithelium, while the latter is not fully understood in biology. We introduce a possible mechanism on folding pattern formation induced by mechanical instability in a confined epithelial cell sheet using multicellular dynamics simulation. Growing cell sheet in a confined space results in compression of the sheet itself, causing a sheet buckling. Depending on cell division orientation, we show an emergence of spontaneous pattern formation of multiple folds of the cell sheet by the buckling.

1SDA-1 放射光 X 線と結晶プローブを用いたマルチマータンパク質・分子内運動解析
Cooperative Motion Analysis of Multimeric Proteins using Synchrotron Radiation X-ray and nanocrystal

Hiroshi Sekiguchi (*JASRI/SPring-8*)

Diffracted X-ray Tracking (DXT) is one of single molecule techniques for investigating intra-molecule dynamics of functional proteins. In DXT, a gold nanocrystal is immobilized on a target protein, is used as motion probe, and the trajectory of its diffracted spot is investigated as the motion of the protein. The size of gold nanocrystal used for our measurements is ranged from 20 to 80 nm in diameter, and cooperative motions of multimeric protein could be tracked by immobilizing the probe on multi-sites on the protein. In this presentation, we review cooperative active motions of multimeric proteins, group II chaperonin (PLoS ONE 2013, JMB 2014, FEBS Open 2016, PLoS ONE 2017) or hemoglobin.

1SDA-2 Studying ion channels in reconstituted membrane using atomic force microscopy

Ayumi Sumino[1,2], Takashi Sumikama[1], Takayuki Uchihashi[3], Shigetoshi Oiki[4] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*, [3]*Dept. Phys., Nagoya Univ.*, [4]*Facult. Med. Sci., Univ. Fukui*)

High-speed AFM (HS-AFM) is a useful technique for observing membrane proteins dynamics at nanometer resolution. Here, we will introduce a simple method for oriented reconstitution of K+ channel KcsA on the AFM substrate, and its application for the single-molecule observation of scorpion toxin binding on the channel. The solubilized channels with His-tags on its cytoplasmic end were attached on Ni2+-coated mica surface with its extracellular surface upward, then reconstituted into the lipid bilayer by using DDM-destabilized liposomes. On the extracellular surface of the channel, scorpion toxin AgTx2 was bound with the elevated height by about 0.5 nm. We analyzed binding dynamics and found that the channel took at least two states with high- and low-affinity to AgTx2.

1SDA-3 Analysis of the picosecond dynamics of muscle contractile proteins and their hydration water by quasielastic neutron scattering

Tatsuhito Matsuo[1], Toshiaki Arata[2], Toshiro Oda[3], Kenji Nakajima[4], Seiko Kawamura[4], Tatsuya Kikuchi[4], Taiki Tominaga[5], Kaoru Shibata[4], Fumiaki Kono[1], Satoru Fujiwara[1] ([1]*QST*, [2]*Osaka Univ.*, [3]*Tokai-Gakuin Univ.*, [4]*J-PARC Center*, [5]*CROSS*)

Quasielastic neutron scattering (QENS) is a powerful tool to study the picosecond dynamics of proteins and their hydration water. Picosecond motions of proteins are known to facilitate structural changes required for biological functions, and are affected by the dynamics of their hydration water. Characterization of these motions is thus crucial for elucidating the mechanism of protein functions. In this talk, we will describe our recent QENS studies on muscle contractile proteins and their hydration water. We found that each protein shows distinct protein dynamics and hydration water mobility, and that a disease-causing mutation modulates protein dynamics. Based on these findings, how the picosecond dynamics is correlated with muscle contraction will be discussed.

1SDA-4 単結晶中ヘモグロビンの包括的構造機能解析
Comprehensive structural and functional analysis of hemoglobin in single crystals

Naoya Shibayama (*Jichi Med. Univ. Div. of Biophysics*)

Hemoglobin is one of the most thoroughly characterized allosteric proteins using X-ray crystallography and solution oxygen binding curves. It is anomalous therefore that its structure-function relationship remains elusive, apparently due to the plasticity of the protein brought about by a dynamic equilibrium between multiple, not just two, conformations. We present a new crystal form in which the protein is free to adopt any allosteric structure, depending on the conditions, and at the same time allows oxygen binding to be monitored directly in the crystal. Our work has identified a wide range of structures including a novel form, intermediate between the oxy and deoxy forms, and appears to resolve the conflict concerning hemoglobin allostery over a period of decades.

1SDA-5 クライオ電子顕微鏡法による膜タンパク質複合体の構造解析
Structural Analysis of Membran Protein Complex by Cryo-EM

Atsuko Nakanishi[2], Jun-ichi Kishikawa[2], **Kaoru Mitsuoka**[1], Ken Yokoyama[2] ([1]*Res. Ctr. UVHEM, Univ. Osaka*, [2]*Dept. Mol. Biosci., Kyoto Sangyo Univ.*)

To understand the function of protein complex fully, several structures of the functional states are usually necessary, though it is difficult to get several high-resolution structures of protein complex. This situation is changing recently because of the recent improvement of structural analysis by cryo-electron microscopy (cryo-EM). Single particle cryo-EM analysis can give several different structures from one data set by classifying them in the EM images. Here we show our result visualizing three different structures of V/A type H^+-rotary ATPase from the bacterium *Thermus thermophilus*. These reconstructions provide a detailed molecular basis of their functional states by visualizing their substrates.

1SDA-6 光化学系 II 結晶における Mn4CaO5 クラスターの異常分散法を使った価数分析
Analysis of the individual valences of four Mn atoms in photosystem II crystals using anomalous diffraction technique

Yasufumi Umena[1], Keisuke Kawakami[2], Nobuo Kamiya[2], Shen Jian-Ren[1] ([1]*RIIS, Okayama Univ.*, [2]*The OCARINA, Osaka City Univ.*)

Photosystem II (PSII) catalyzes light-induced water oxidation in photosynthesis, and the catalytic center is composed of mixed valent Mn4CaO5-cluster. However, the valence of each of the four Mn atoms are still under debates. In this study, we estimated the individual valence of these four Mn atoms in the PSII crystals by unique crystallographic analysis using anomalous difference Fourier map collected at Mn absorption K-edge wavelength, where the anomalous scattering factor of Mn changes depending on the oxidation state. These maps obtained showed different intensities of the maps corresponding to the Mn atoms. We will discuss the valence of the four Mn atoms using this unique technique.

1SDA-7 光化学系 II 酸素発生中心における酸素分子生成および放出過程についての QM/MM 解析
QM/MM study on the O2 formation and O2 release mechanism in the oxygen-evolving complex of photosystem II

Mitsuo Shoji[1], Hiroshi Isobe[2], Yasuteru Shigeta[1], Takahito Nakajima[3], Kizashi Yamaguchi[4] ([1]*CCS, Univ. Tsukuba*, [2]*Okayana Univ.*, [3]*RIKEN R-CCS*, [4]*Osaka Univ.*)

The O2 formation and release mechanisms in the oxygen-evolving complex of photosystem II (PSII-OEC) are critical to inform the highly efficient reaction of the water decomposition. Despite their importance, the detailed reaction pathways are not fully discussed or investigated. In the present study, we discuss the most candidate scenario for the O2 formation and O2 release process revealed by using the quantum mechanics/molecular mechanics (QM/MM) calculations. The present mechanisms can explain the efficient formation and removal of O2 in PSII-OEC. Roles of surrounding amino acids near the active site are also discussed.

1SDA-8 Statistical and quantum-chemical analysis of the effect of heme porphyrin distortion in heme protein

Yu Takano (*Graduate School of Information Sciences, Hiroshima City University*)

Proteins function at a local region called the active site. Heme proteins have heme at the active site, which are involved in various biochemical functions such as electron transfer. Elucidation of the structure-function relationships means that we can design new functional molecules. We report a combined study of Fisher linear discriminant analysis (LDA) and density functional theory (DFT) on heme distortions in oxidoreductases and oxygen carrier proteins in the Protein Data Bank. LDA provided a characteristic heme distortion separating the structural distributions reasonably. We evaluated redox potentials and oxygen affinities of hemes with the characteristic distortion with DFT. This implies the distortion provided by LDA is related to them.

1SEA-1 Cell surface flip-flop of phosphatidylserine is critical for PIEZO1-mediated myotube formation

Yuji Hara[1,2], Masaki Tsuchiya[1], Kotaro Hirano[1], Masato Umeda[1] ([1]*Grad. Sch. Eng., Kyoto Univ.*, [2]*AMED, PRIME*)

Mammalian skeletal muscles are formed by the fusion of myogenic precursor cells (myoblasts) into unusually elongated multinucleated cells called myotubes. Here we identified PIEZO1, a mechanosensitive ion channel, as a key regulator of myoblast fusion and myotube morphology. Our results show that the cell surface-exposed PS strongly inhibits PIEZO1 activity, and that the inward translocation (flip) of cell surface-exposed phosphatidylserine (PS), which is driven by the phospholipid flippase complex of ATP11A and CDC50A, is a prerequisite for PIEZO1 to induce subsequent actomyosin assemblies at the lateral cortex of myotubes. Thus, PS-flipping at the plasma membrane acts as a molecular switch for PIEZO1 activation that governs proper morphogenesis in myotube formation.

1SEA-2 張力センサーとしてのアクチン線維：そのゆらぎ解析
Analysis of fluctuations of a single actin filament as a tension sensor

Hitoshi Tatsumi (*Kanazawa Institute of Technology (KIT)*)

The cells are continually exposed to various mechanical stimuli, and mechanical forces are sensed by mechanosensors that presumably undergo change in their enzymatic activity or interaction with signaling molecules in response to forces. However, the molecular entities and the underlying biophysical mechanisms of mechanosensing molecules are largely unknown. A recent in vitro study (Hayakawa et al., 2011, JBC) revealed that the actin filament itself functions as a mechanosensor. We have constructed a newly designed microscope to conduct the 3D analysis of torsional fluctuations of actin filaments, which presumably play a significant role in mechano sensing.

1SEA-3 Matrix-force dependent integrin signalling at the podosome

Cheng-han Yu (*Univ. of Hong Kong*)

Cells utilize integrin to assemble focal adhesions. However, when the cell-matrix interface becomes viscous, cells can develop podosomes as primary adhesion structure. Previously, we revealed that integrin activation recruits endocytic proteins Dab2 and clathrin on viscous RGD membranes. However, the functional link between podosome and integrin endocytosis remains unclear. Here, we find that the levels of internalized RGD are positively correlated with the podosome assembly on RGD membranes. Our observations suggest that protrusive F-actin polymerization and BIN1-dynamin2 interaction facilitate integrin-beta3 endocytosis at the podosome. The functional role of podosomes in integrin endocytosis will provide more insight in cell motility and cancer invasive migration.

1SEA-4 細胞間相互作用が制御するＴリンパ球の活性化
Cell-cell interaction among immune cells regulates T lymphocyte activation

Hiroaki Machiyama, Tadashi Yokosuka (*Dept. Immunol., Tokyo Med. Univ.*)

Adaptive immunity is involved in the specific-antigen recognition between T lymphocytes (T cells) and antigen presenting cells (APCs). Using single cell manipulation system, we showed poor antigen-specific-reaction between individual T cells and APCs. We also showed that interaction of activated T cells or regulatory T cells with APC altered the reactivity of newly coming T cells. The alteration of T cell reactivity can be induced by cell membrane morphology due by cell-cell interaction. We now try to visualizing the cell membrane morphology using superresolution microscopy. Membrane morphology may be able to regulate T cell responses through the alteration of the mechanical micro-environment.

1SEA-5 ブリルアン散乱による多細胞システムの弾性イメージング
Elasticity imaging in multicellular systems by Brillouin scattering

Taro Ichimura[1,2], Tomonobu Watanabe[1] ([1]*RIKEN BDR*, [2]*Osaka University OTRI*)

Brillouin scattering is an inelastic optical scattering process involving a small spectral shift in the GHz frequency region, which is a result of Doppler shift in the interaction between propagating photon and intrinsic acoustic phonon. From measurement of Brillouin shift, viscoelastic property of a medium can be deduced. We designed and built a Brillouin microscope for bioimaging, and successfully realized elasticity imaging in single cell and multicellular system. This microscope is the only technique that achieves 3-dimensional mapping of elasticity with sub-cell spatial resolution, and thus, we believe, it has a great potential in mechanobiological researches. The presentation will introduce our Brillouin microscopy study for various biological targets.

1SEA-6 Mitochondria are physiologically maintained at close to 50 °C

Malgorzata Rak (*INSERM UMR1141/CNRS*)

To ensure a stable internal temperature, endothermic species make use of heat released during the last steps of food burning by the mitochondria present in all cells of the body. Indeed only a fraction of the energy released by the oxidation of respiratory substrates is used to generate ATP, while a substantial proportion is released as heat. Using a temperature-sensitive fluorescent probe targeted to mitochondria, we measured the temperature of active mitochondria in cultured intact human cells. Mitochondria were found to be more than 10 °C warmer when the respiratory chain was functional. The activity of various RC enzymes was maximal near 50 °C. In view of their potential consequences, the observations must be explored further and validated by independent methods.

1SEA-7 メカノセンサーチャネル Piezo1/2 の哺乳類生体内での役割
Mechanically activated cation channel Piezo1/2 and its physiological roles in mammals

Keiko Nonomura[1,2], Viktor Lukacs[2], Stuart Cahalan[2], Akemi Kanie[1], Hiroki Katsuta[3], Toshihiko Fujimori[1], Ardem Patapoutian[2] ([1]*NIBB*, [2]*TSRI*, [3]*Med.Grad.Nagoya Univ.*)

Our group recently identified Piezo1 and 2 as mechanoactivated cation channel functioning in mammalian cells. Piezo1/2 has up to 38 transmembrane domains, mainly locates on cell membrane, and is activated by mechanical stimuli, such as suction stretch, mechanical indentation of cell membrane or shear stress. Piezo2 is highly expressed in sensory neurons and functions as the key mechanotransducer for cutaneous touch sensation, proprioception and lung volume control during breathing, while Piezo1 is highly expressed in red blood cells and blood/lymphatic endothelial cells. In my talk, I'll introduce molecular features of Piezo1/2 and lines evidence showing that Piezo1/2 is a versatile mechanosensor regulating various physiological events in mammals.

1SEA-8 改良型振動計による内耳ナノ振動の測定と解析
Measurement and analysis of nanoscale vibrations in the inner ear by advanced vibrometries

Hiroshi Hibino[1,2], Takeru Ota[1,2], Samuel Choi[2,3], Fumiaki Nin[1,2] ([1]*Department of Molecular Physiology, Niigata University School of Medicine*, [2]*AMED-CREST, AMED*, [3]*Department of Electrical and Electronics Engineering, Niigata University*)

Animals minutely analyze diverse sounds in the environment to obtain information necessary for their survival. Humans, whose audition ranges from 20 to 20,000 Hz, can distinguish frequencies that are only 0.2% apart, whereas they perceive millionfold differences in sound pressure level. These marked performances stem from sound-induced nanoscale vibrations of mechanoelectrical sensory epithelium inside the inner ear. The characteristics of this epithelial motion and its underlying mechanisms remain uncertain. Recently we have developed two different vibrometries. These advanced instruments detected parameters of the epithelial vibrations, which are inaccessible to conventional methods. Theoretical approach further suggested significance of the identified motions.

1SFA-1 アクチン系細胞骨格の in vitro 再構成：運動と分裂の仕組みの包括的理解を目指して
In vitro reconstitution of actin cytoskeleton: Toward a unified understanding of the mechanics of cell motility and division

Makito Miyazaki[1,2] ([1]*Hakubi Center, Kyoto Univ.*, [2]*Dept. Phys. Kyoto Univ.*)

The actin cytoskeleton is a key regulator of cell motility and division. Over several decades, the molecular components and the regulatory proteins have been identified step by step. However, it is little known how the cytoskeleton is assembled and how it regulates biological functions. We have employed an artificial cell system prepared by encapsulating a mixture of purified proteins or cytoplasmic extracts into vesicles. Using this system, we systematically investigate the effects of molecular components and boundary conditions on the architecture of self-organized cytoskeletal network and its function. I will present our resent results about reconstitution of actin cortex and cytokinetic rings, and discuss how cells regulate motility and division.

1SFA-2 What happens in the large cytoplasm of the oocyte?

Hirohisa Kyogoku, Tomoya Kitajima (*RIKEN BDR*)

It is known that the frequency of chromosome segregation errors is high during meiosis in oocytes. However, why chromosome segregation is error-prone in oocytes remains poorly understood. Our studies show that cytoplasmic size, which is extremely large in oocytes, affects the fidelity of chromosome segregation. We generated the mouse oocytes carrying doubled and halved cytoplasmic sizes by micromanipulation. Live imaging analysis demonstrated that spindle size scaled with cytoplasmic size. Larger spindles forming in larger oocytes exhibited less-focused spindle poles and facilitated chromosome misalignment. These results suggest that large cytoplasmic size weakens the robustness of the spindle architecture, which explains the inherent error-prone nature of oocytes.

1SFA-3 細胞サイズと核内 DNA 量に依存した核のサイズの制御機構
Nuclear size scaling with cell size and DNA content in Xenopus

Yuki Hara (*Yamaguchi University, Faculty of Science, Evolutionary Cell Biology Laboratory*)

The size of a nucleus varies greatly with cellular geometries and intracellular properties such as “outside” cytoplasmic volume and a DNA content “inside” the nucleus. Although proper nuclear size control appears to be significant in vivo, the underlying mechanisms had largely remained unclear. To gain insights into them, here we systematically manipulated either a local cytoplasmic volume surrounding the nucleus or the DNA content using a cell–free nuclear reconstruction system from Xenopus egg extracts. Our data shows that the dynamics of nuclear expansion can scale separately with the size of microtubule—occupied space surrounding the nucleus and the DNA content inside the nucleus. Taken together, we propose a mechanistic overview of nuclear size scaling in Xenopus.

1SFA-4 遺伝子発現の振動パターンの光操作
Controlling genetic oscillators by optogenetics

Akihiro Isomura[1,2] ([1]*Infront, Kyoto Univ.*, [2]*JST PRESTO*)

Cells communicate with each other to coordinate their gene activities at the population level. In embryonic development, many genes represent oscillatory expression patterns that could encode various types of information. However, whether or how such oscillatory information is transmitted from cell to cell remains unknown. Here, we developed an integrated approach that combines optogenetics and live-cell imaging to visualize and reconstitute synchronized oscillatory gene expression in signal-sending and signal-receiving processes. In this talk, we show our applications to understanding how genetic oscillators transmit and decode dynamic information between adjacent cells through Notch signaling pathway for synchronizing the population of oscillators.

1SFA-5 Impact of quasi-cellular structures for evolutionary dynamics of RNA

Shigeyoshi Matsumura (*Grad. Sch. Sci. Eng., Univ. Toyama*)

The minimal unit of all life forms is a cell. This raises a question: why cellularity must be a fundamental feature for life? A recent advanced technology “droplet microfluidics” handling precisely tiny emulsion droplets enables us to approach the question above by building a mimic of cellular structures. To explore how does the cellular structure make impacts on the evolution of molecules inside, we have carried out experimental evolution of a catalytic RNA (ribozyme) compartmentalized in the droplets. It reveals that the compartmentalization changes evolutionary dynamics of RNA, allowing symbiosis of different molecules. This situation lead accumulation of molecular diversity of RNA, which would be source of further evolution.

1SFA-6 幾何学で紐解く細胞集団の集団運動の力学
On the geometry and mechanics in collective cell migration

Yusuke T. Maeda, Kazusa Beppu, Tatsuya Fukuyama (*Dept. Phys., Kyushu Univ.*)

As expressed by W. Pauli “God made the bulk, surfaces were invented by the devil.”, the surface brings remarkable properties due to its anisotropic nature, especially in microscopic systems. In this talk, we show how geometry organizes collective dynamics in the group of cells from bacteria to eukaryotic cells. When the group of cells is confined under microwells with designed geometry, ordered phases of active vortices arise from the guiding interaction. The rich patterns of ordered vortices can be explained by theoretical model of self-propelled elements. The transition point where active vortices change its configuration is given by one geometric quantity, suggesting fundamental rule between geometry and mechanics in collective migration.

1SGA-1 植物の自家不和合性における自己認識メカニズム
Mechanism of self-recognition system in plant self-incompatibility

Kohji Murase (*Dept. Appl. Biol. Chem., Univ. Tokyo*)

Self-incompatibility is a system for promoting out-breeding by rejecting self-pollen. In Brassicaceae, Self-incompatibility is regulated by the haplotype specific interaction between pistil receptor kinase SRK and pollen ligand SP11. Although the specific recognition is thought to be arising from the amino acid differences in SRK and SP11, the mechanism of self/non-self-discrimination is still largely unknown. We determined crystal structure of the SRK-SP11 complex, uncovering the mode of self-specific recognition in Brassicaceae self-incompatibility.

1SGA-2 セマフォリンとプレキシンが形成する低親和性だが特異的な相互作用
Low-affinity but specific interactions between semaphorin-plexin pairs

Terukazu Nogi (*Grad. Sch. Med. Lif. Sci., Yokohama City Univ.*)

Semaphorin is an extracellular signaling molecule that has been discovered as an axon guidance cue. Semaphorin binds with and signals through a cell-surface receptor plexin. In vertebrates, 21 different semaphorins are identified and devided into five classes (classes 3 to 7) based on the domain organization while a plexin family contains 9 members belonging to four types (types A to D). Despite high sequence homologies, each semaphorin binds with specific plexin(s). In particular, it is known that specific binding between class 6 semaphorins and type A plexins is regulated by low-affinity interactions. We performed structural and biophysical analyses to examine the molecular recognition mechanism of the semaphorin-plexin pairs.

1SGA-3 pH および亜鉛を利用した ERp44 による多様な基質認識の構造基盤
Structural basis of pH- and zinc-dependent multiple client recognition by ERp44

Satoshi Watanabe[1], Yuta Amagai[1], Roberto Sitia[2], Kenji Inaba[1] ([1]*IMRAM, Tohoku Univ.*, [2]*San Raffaele Institute*)

ERp44 transports immature multiple secretory proteins and some ER-resident proteins from the Golgi to the ER in pH and zinc-dependent manners. However, the molecular details remain unclear. Our new crystal structures of ERp44 at neutral and weakly acidic pH reveal its pH-dependent domain movements and local helix unwinding, which results in significant changes in charge distribution on the molecular surface and the C-terminal tail dynamics. Furthermore, the crystal structure of zinc-bound ERp44 reveals that zinc binding to the conserved histidines induces large displacements of the C-terminal tail, leading to full exposure of the positively charged client-binding site. These results provide a novel framework for the pH/zinc dependent client recognition by ERp44.

1SGA-4 Diverse activities of molecular chaperones through non-selective binding

Tomohide Saio[1], Charalampos G. Kalodimos[2], Koichiro Ishimori[1] ([1]*Fac. of Sci. Hokkaido Univ.*, [2]*Dept. of Struct. Biol., St. Jude Child. Res. Hosp., TN*)

Molecular chaperones exert their distinct activities through seemingly non-selective, promiscuous interaction with unfolded client proteins. The chaperones often share the recognition motifs and bind to common hydrophobic stretches in the unfolded client proteins, but the outcome, i.e. the effect to the folding of the client proteins, varies among the chaperones. Here we show the structure of a 100 kDa dimeric chaperone Trigger Factor in the absence and presence of the client protein and demonstrate how the chaperone achieves broad substrate recognition. We also show the results of the kinetic studies exploiting NMR and stopped-flow and discuss about the mechanism by which the chaperones having similar binding specificity exhibit distinct activities.

1SGA-5 構造平衡により規定される多剤結合転写因子 QacR の可変的転写制御
Conformational equilibrium defines variable transcriptional repression of a multidrug binding transcriptional repressor, QacR

Koh Takeuchi[1], Ichio Shimada[2] ([1]*moleprof, AIST*, [2]*Grad. Sch. Pharm. Sci, The Univ. of Tokyo*)

QacR is a multidrug-binding transcriptional repressor in pathogenic bacteria S. aureus. QacR releases the transcriptional repression allowing the inducted expression of a multidrug transporter gene, qacA, to various extents depending on the compounds. However, since the X-ray structures of QacR bound to compounds are identical, the structural basis that defines the various extents of induction remains unknown. Here, we found that the population of resting and induced QacR conformations in an equilibrium defines the induction level of the protein. The changes of the conformational equilibrium is not correlated with the affinity of the compounds to QacR, but their volume. Thus, the size of the compound allosterically define the variable transcriptional activity of QacR.

1SGA-6 細菌多剤排出ポンプの機能と制御
Function and Regulation of Bacterial Multidrug Transporters

Kunihiko Nishino (*Institute of Scientific and Industrial Research, Graduate School of Phamaceutical Sciences, Osaka University*)

Multidrug efflux is an obstacle to the successful treatment of infectious diseases, and it is mediated by multidrug transporters that recognize and export a broad spectrum of chemically dissimilar toxic compounds. Many bacterial genome sequences have been determined, allowing us to identify drug efflux genes encoded in the bacterial genome. Here, I present an approach to identifying bacterial drug efflux genes and their regulatory networks. Multidrug transporters are often regulated by environmental signals and they are also required for bacterial virulence in addition to multidrug resistance. Because multidrug transporters have roles in drug resistance and virulence, multidrug transporters have greater clinical relevance than previously considered.

1SHA-1 微生物型ロドプシンに基づく光遺伝学ツール開発のためのボトムアッププアプローチ
Bottom-up approach for microbial rhodopsin-based optogenetic tools

Keiichi Kojima, Yuki Sudo (*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*)

Microbial rhodopsins are photoreceptive seven-transmembrane proteins containing retinal as a chromophore. Recent genomic advances have revealed that they are widely distributed in all three biological domains and show a variety of biological functions, such as ion transporters and light sensors. They recently become a focus of interest as tools for optogenetics, a technology to regulate biological phenomena by light. We are investigating them with the following strategies to develop optogenetic tools. (i) we explored novel microbial rhodopsins from nature and analyzed their functions and properties. (ii) we rationally modified their properties. (iii) we applied them to development of optogenetic tools. Combining with the results, we will also discuss future prospect.

1SHA-2 光遺伝学ツール開発につながる微生物型ロドプシン
Microbial rhodopsins leading to development of optogenetic tool

Masae Konno (*Grad. Sch. Eng., NIT*)

Microbial rhodopsin is a key molecule of a regulatory tool in optogenetics. Channelrhodopsin 2 (ChR2) is widely used for neural excitation by its ion transport properties. On the other hand, novel microbial rhodopsins have been found one after another in recent years. They act as light-driven ion transport, light sensor, light-activated enzyme, etc. In addition, we recently found novel rhodopsins (heliorhodopsins), whose sequences are far different from microbial and animal rhodopsins. Optogenetic application of these proteins can regulate various biological functions, such as membrane potential and second messenger's concentration. I will discuss molecular functions of the microbial rhodopsins that we study, and the benefit of these proteins for optogenetics.

1SHA-3 Anion channelrhodopsin-2 の構造モデリングと分子シミュレーションによる機能メカニズム解析
Structural modeling and molecular simulations provide insights into the functional mechanism of anion channelrhodpsin-2

Hiroshi Watanabe[1,2,3], Misaki Kato[2], Hiroshi Ishikita[1,2] ([1]*RCAST, Univ. Tokyo*, [2]*App. Chem., Grad. Sch. Eng., Univ. Tokyo*, [3]*JST, PRESTO*)

Anion channelrhodopsins (ACRs), derived from cryptophyte algae, lead to great advances in optogenetics, where they can be used for membrane hyperpolarization as a neural silencer. ACRs are grouped into ACR1 and ACR2, and the functional differences are of great interest in optogenetics. Although recent experiments have revealed the respective functional properties of ACRs, the cause of the differences still remain unknown, because the detailed structural information has not been available yet. Thus, we took computational approaches for ACR2, homology modeling and molecular dynamics simulations. Here, we present the useful insights into structural characters, which seem to be related to various molecular characters such as ion-binding, color-tuning, and kinetics.

1SHA-4 Dark-active and light-inactivated G protein-coupled receptors based on an animal opsin, peropsin

Takashi Nagata[1], Mitsumasa Koyanagi[1,2], Robert Lucas[3], Akihisa Terakita[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*, [3]*Fac. Biol. Med. Health, Univ. Manchester*)

Most animal opsins bind to 11-*cis*-retinal as a chromophore to form photopigments and serve as light-sensitive G protein-coupled receptors (GPCRs). Interestingly, an opsin called peropsin binds predominantly to all-*trans*-retinal, but it was unclear whether it activates G proteins. We revealed that an all-*trans*-retinal-bearing peropsin, of which intracellular domain was replaced with that of Gs- or Gi-type G protein-coupled opsin, activates Gs or Gi proteins, respectively, in the dark and is inactivated by light. Such dark-active, light-inactivated peropsin mutants could complement existing light-activated GPCR-based optogenetic tools to mimic various GPCR signaling, which regulates many aspects of animal physiology and behavior *in vivo*.

1SHA-5 アップコンバージョンを用いたファイバーレス光遺伝学の開発
The development of fiberless optogenetics using up conversion luminescence from lanthanide

Toh Miyazaki[1,2], Chowdhury Srikanta[1,2], Takayuki Yamashita[1,2], Hiromu Yawo[3], Hideya Yuasa[4], Akihiro Yamanaka[1,2] ([1]*Department of Neuroscience II Research Institute of Environmental Medicine Nagoya University*, [2]*CREST, JST*, [3]*Department of developmental biology and neuroscience, Tohoku University Graduate School of life Sciences*, [4]*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology*)

Optogenetics is a powerful tool to control neuronal activity with high temporal and spatial precision. However, the conventional optogenetics has problems such as high invasiveness. This is caused by low permeability to tissue of visible light which use to activate channel rhodopsin. To address these problems, we developed a new method to control neurons by near-infrared light (NIR) which permeates animal tissues, and lanthanide micro particle (LMP) which converts NIR to visible light. We activated and to inhibited the neuronal activity using up conversion optogenetics. Our data indicates that up conversion optogenetics is more powerful tool enable us to control neuronal activity without fiber insertion in freely behaving mice.

1SHA-6 光操作によるゼブラフィッシュ小脳高次機能の解析
Optogenetic manipulation of zebrafish neural circuits toward understanding higher order function of the cerebellum

Takashi Shimizu[1,2], Koji Matsuda[1], Masahiko Hibi[1,2] ([1]*BBC, Nagoya Univ.*, [2]*Grad. Sch. Sci., Nagoya Univ.*)

The cerebellum functions in wide range of motor coordination and motor learning. It is also involved in cognitive and emotional functions. We previously addressed roles of the cerebellum in classical fear conditioning using a delayed fear-conditioning paradigm with zebrafish larvae. The larval zebrafish is a good model for understanding neural functions with optogenetic approach because of translucency and small size of the brain and feasibility of genetic manipulation. In an initial attempt to reveal mechanisms for cerebellum-dependent adaptive motor learning and fear conditioning, we are trying to express newly developed optogenetic tools that can manipulate a variety of cytoplasmic signaling cascades in neurons that control locomotion. We shall report our progress.

1SIA-1 Regulation mechanisms of EGFR activity by ganglioside homodimer rafts as revealed by single-molecule imaging

Kenichi Suzuki (*Gifu Univ. G-CHAIN*)

Raft domains have been drawing extensive attention as signaling platforms. However, raft structure and function are still controversial due to lack of true raft lipid probes. By single-molecule tracking, we investigated dynamic organization of new ganglioside probes in the plasma membrane. All of the gangliosides were mobile, and continually formed transient (~200 ms) homodimers, which were induced by glycan-glycan interactions and stabilized by raft-lipid interactions. We call these entities “ganglioside homodimer rafts”. Furthermore, we found that GM3 homodimer rafts interacted with EGF receptors (EGFR), which inhibited EGFR dimerization and activation. The transient homodimer rafts are likely one of the basic units for the organization and function of raft domains.

1SIA-2 The function of the transmembrane-juxtamembrane region of EGFR

Takeshi Sato (*Kyoto Pharm Univ*)

Receptor tyrosine kinase (RTK) is involved in one of the most important signaling pathways for cell growth and differentiation. The presenter has been working on molecular characterization of the transmembrane-juxtamembrane region in lipid bilayers. This region has a crucial role in the transmembrane signaling for the receptor as the functional bridge between the extracellular and the intracellular regions. In this talk, the presenter will discuss about a possible role of the region in the activation mechanism.

1SIA-3 Dimerization-deficient opsin mutants: implications for disease

George Khelashvili, **Anant K. Menon** (*Weill Cornell Medical College*)

Rhodopsin is a light-sensing G protein-coupled receptor and phospholipid scramblase. Using in vitro reconstitution approaches coupled with a phospholipid scramblase activity assay we discovered that whereas wild type rhodopsin dimerizes during detergent-mediated reconstitution into liposomes, three independent retinitis pigmentosa (RP)-associated rhodopsin mutants (F45L, V209M, F220C) reconstitute as monomers. Preliminary results from molecular dynamics simulations indicate that the RP mutations also disrupt modes of rhodopsin dimerization in a phospholipid membrane. Our data suggest that the photoreceptor pathology associated with expression of these mutants in the retina may arise from their inability to dimerize via transmembrane helices 1 and 5.

1SIA-4 Computer simulations of complex membrane models

D. Peter Tieleman (*University of Calgary*)

Biological membranes have a complex composition with hundreds of lipid types and a high protein concentration. The nature of the lateral structure of membranes is hotly debated as both experiments and simulation converge on the relevant time and length scales. We are particularly interested in the principles that determine the structure of membranes, including domain formation and lipid-protein interactions. The local environment around membrane proteins is uniquely shaped by the protein surface, resulting in a local composition and membrane properties that differ significantly from the average lipid properties. This may play an important role in shaping the lateral structure and organization of biological membranes.

1SIA-5 Resolving the spatiotemporal organization of GPCRs in live cells with PIE-FCCS

Adam W. Smith (*The University of Akron*)

For G protein-coupled receptors (GPCRs), dimerization likely regulates protein stability and trafficking and could act as an allosteric modulator. These effects need to be directly assessed in live cells because the unique lipid composition of the plasma membrane influences structure and function in a way difficult to reconstitute in vitro. In this talk I will describe investigations of GPCR dimerization in live cells with pulsed interleaved excitation fluorescence cross-correlation spectroscopy (PIE-FCCS), which is sensitive to protein mobility, concentration, and monomer/dimer/oligomer distributions. With this approach we have quantified dimerization for representative GPCRs from the A, B and C families, including the visual opsins.

1SIA-6 Raftophilicity and aggregation of membrane proteins in the photo-transduction

Kenichi Morigaki[1,2], Yasushi Tanimoto[1], Hayato Yamashita[3], Akinori Awazu[4], Fumio Hayashi[5] ([1]*Kobe Univ. Biosignal*, [2]*Kobe Univ. Agrobioscience*, [3]*Osaka Univ. Eng. Sci.*, [4]*Hiroshima Univ. Sci.*, [5]*Kobe Univ. Sci.*)

Phototransduction is regulated by the membrane heterogeneity such as raft and molecular aggregation. To gain insight into the regulation mechanisms, we determine affinity of membrane proteins to raft (raftophilicity) using a model membrane with patterned liquid ordered- and liquid disordered-regions. The raftophilicity quantitatively predicts the influence of molecular segregation on the signal transduction efficiency, as supported by the kinetic simulation and microscopic observation of disk membranes. We also observe aggregation of rhodopsin to elucidate the roles of receptor clustering in phototransduction. These in-vitro studies provide the physicochemical basis to analyze the functional roles of dynamic and elusive molecular organization.

1SKA-1 DNA ナノテクノロジーと 1 分子計測技術の融合が拓く分子動態・力の高解像イメージング
High-resolution imaging of molecular dynamics and force pioneered by DNA nanotechnology and single molecule detection techniques

Mitsuhiro Iwaki[1,2] ([1]*RIKEN, BDR*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*)

Recent DNA nanotechnology (e.g. DNA origami) enables us to create nanoscale architectures. Due to its high degree of customization and spatial addressability, this technology provides a versatile platform useful for single molecule biophysics. Here we developed a programmable myosin filament (essential contractile unit of muscle) composed of DNA origami and myosin motor domains, and DNA nanospring, with which we can achieve high-resolution imaging of molecular dynamics and mechanical force. We'll present the machinery of muscle contraction, imaging of mechanical force and ultra-resolution imaging technique, DNA-PAINT (DNA-based point accumulation for imaging in nanoscale topography).

1SKA-2 高速 AFM による天然変性タンパク質 MeCP2 の一分子観察
Single-molecule visualization of intrinsically disordered Rett syndrome protein, MeCP2 by high-speed AFM

Noriyuki Kodera[1], Anna Kalashnikova[2], Mary E. Porter-Goff[2], Toshio Ando[1], Jeffrey C. Hansen[2] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Dept. Biochem. & Mol. Biol., Colorado State Univ.*)

MeCP2 is a transcriptional regulator essential for growth and synaptic activity of neurons and deregulated in the neurodevelopmental disorder, Rett syndrome (RTT). MeCP2 is an intrinsically disordered protein, and little is known about its molecular architecture. Here, we directly visualized MeCP2 molecules at the single molecule level by high-speed AFM. MeCP2 was composed of a small folded domain (the methyl DNA binding domain, MBD) from which the N-term short- and C-term long disordered tails protruded. The observations using missense and nonsense RTT mutants suggest that folding stability of the MBD is affected by not only point mutations in the MBD but also the interactions between the MBD and the C-term tail. The results would give hints for treating RTT.

1SKA-3 マイクロチップを利用した膜タンパク質の１分子機能分析
Single molecule analysis of membrane proteins by using microsystems

Rikiya Watanabe (*Department of Applied Chemistry, The University of Tokyo*)

The maintenance of an appropriate intracellular environment is a constant challenge for all living organisms. Intracellular homeostasis is maintained by membrane proteins transporting various compounds across the membrane. In this study, we developed a novel microsystem (ALBiC) that forms sub-million femtoliter reaction chambers, each sealed with an artificial membrane. Due to the infinitesimal volume of chambers, ALBiC can enhance the detection sensitivity, demonstrating the single-molecule analysis of membrane transport proteins, e.g., F-ATPase, and TMEM16F, in a high throughput manner. Importantly, the microsystem we have designed could also be used to investigate various transport by other membrane proteins, which would significantly impact in cell membrane biology.

1SKA-4 酵素活性の網羅的解析（Enzymomics）法による疾患関連タンパク質の探索
Development of enzymomics approach to search for disease-related alternation of enzymatic functions

Toru Komatsu[1], Jun Onagi[1], Yuki Ichihashi[1], Shingo Sakamoto[1], Rikiya Watanabe[2], Yi Zhang[2], Hiroyuki Noji[2,6], Tetsuo Nagano[4], Yasuteru Urano[3,5] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*Grad. Sch. Eng., Univ. Tokyo*, [3]*Grad. Sch. Med., Univ. Tokyo*, [4]*DDI, Univ. Tokyo*, [5]*AMED-CREST*, [6]*JST ImPACT*)

Fluorescent substrate probes that report enzymatic activities by fluorescence activation are a practical experimental platform to study enzyme functions in living samples with high sensitivity, and such probes have been used in biochemical/biological studies, inhibitor screening assays, disease diagnosis, and so on. With use of the fluorescent substrate techniques, we have developed the system to search for tissue-type-specific, cell-type-specific, and disease-related alternation of enzymatic activities by library of substrates. We used those approaches to discover and characterize novel disease-related enzymatic activities for future development of novel drug targets and biomarkers.

1SKA-5 生体高分子スマートシーケンサに向けた１分子電気計測法の開発
Development of Single-Molecule Electrical Identification Method For Smart Biopolymer Sequencer

Takahito Ohshiro (*Osaka University, ISIR*)

Single-molecule genome electrical sequencing is promising technology for personal genome uses. We have been proposed a tunneling-current based identification as a single-molecule sequencing by nano-gap electrode devices. In principle, this methodology is based on sequentially reading the tunneling-current across individual single-nucleotide in the sequence, resulting in a high-speed electrical discrimination of the individual nucleotides. In addition, we also applied this methodology to amino-acid molecules and peptide discrimination from the conductance-value and retention-time. The characteristic conductance values are found to be closely related to the highest occupied molecular orbital energy. This tunnel-current based single-molecule identification method would be potentially applicable for future nucleotide and peptide sequencing.

1SKA-6 細胞内全自動１分子解析と発展的応用
In Cell Automated Single-molecule Analysis and Its Extensive Applications

Michio Hiroshima[1,2], Masato Yasui[1], Jun Kozuka[1], Yasushi Sako[2], Masahiro Ueda[1] ([1]*RIKEN BDR*, [2]*Cellular Informatics Lab., RIKEN*)

Single-molecule analysis in cells provides spatiotemporal and quantitative information of behaviors of individual molecules responsible for cell signaling. Using the method, regulation mechanisms of signal transduction have been revealed from the aspects of dynamics and reaction kinetics of signaling molecules. However, conventional single-molecule imaging is dependent on a lot of specific expertise and hardly applicable to a comprehensive analysis of numerous molecular species in a signaling pathway. To establish an expertise-free operation, we automated all the procedures including focusing, searching cells, dispensing drug, and so forth. The demonstrated capability for comprehensive analysis enables single-molecule drug screening as a pharmacological application.

1SMA-1 生体運動システムの自律性：概観
Autonomy integrated in motility systems : An overview

Taro Uyeda (*Dept of Physics, Faculty of Sci and Eng, Waseda Univ*)

The control of the generation, directionality and transmission of force in cell motility is created by proteins that reversibly assemble into elaborate supramolecular motility machines. The dynamic assembly and disassembly of the components of these motility machines, as well as regulatory cooperative conformational changes, are dependent on autonomy of the proteins, rather than on chemical signals. I will briefly review such examples as an introduction for the following talks in this symposium, in which the molecular mechanisms behind such dynamic processes are discussed from the viewpoints of mechano-sensitivity, cooperativity, polymorphism and allostery. We will then attempt to highlight design principles that are common to apparently divergent motility systems.

1SMA-2 Collective cell movements driven by actomyosin contractility in vertebrate embryos

Asako Shindo[1], Yasuhiro Inoue[2], John Wallingford[2], Makoto Kinoshita[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Inst. Front. Life Med. Sci., Kyoto Univ.*, [3]*Univ. Texas*)

Actomyosin-mediated contractility drives tissue formation and repair in the embryos. We have focused on two collective cell movements, the convergent extension and wound closure, to understand how the contractile force is spatiotemporally regulated in each cell. We found that each collective cell movement establishes a distinct actomyosin behavior. During convergent extension, actomyosin oscillates asynchronous between the neighboring cells. In contrast, we observed the non-oscillating contraction of actomyosin during wound closure. In this talk, I will highlight the local behaviors of actomyosin as cellular machinery to alter tissue shape and discuss how the simple contractile force of actomyosin is utilized for shaping various tissues in vivo.

1SMA-3 Mechanical design principles of the cell division apparatus

Yuta Shimamoto (*Nat'l Inst Genetics*)

Spindles, required for faithful segregation of chromosomes during cell division, generate and respond to diverse mechanical and biochemical cues while maintaining overall integrity. We use microneedle-based quantitative micromanipulation and fluorescence speckle imaging to perturb local force and track relevant microtubule motility in the spindle. Using cell-free Xenopus egg extracts, we find considerable mechanical heterogeneity in the filament's motion responses that arise across the length of the bipolar structure. Together with our previous in vitro study on collective force generation of kinesin-5, a key mitotic motor protein crosslinking microtubules, I will discuss how this dynamic cytoskeletal machinery adapts to force while maintaining its robust function.

1SMA-4 Coulombic interaction network and novel allostery in molecular machines

Mitsunori Takano (*Dept Pure & Appl Phys, Waseda Univ*)

There are two types of energy storage that molecular machines can use to execute their functions: one is the energy stored in small molecules such as ATP, and the other is the energy stored across membrane. These energies are all Coulombic in nature. Therefore, one can suppose that molecular machines have evolved to acquire an exquisite system to fully utilize these Coulombic energies. In this talk, I will show our recent molecular dynamic simulation studies on several molecular machines, focusing on the Coulombic interaction network that exhibits loosely-coupled response to external inputs, which leads us to a novel idea of allostery due to dielectric and piezoelectric properties that may form a physical basis of autonomous functions of molecular machines.

1SMA-5 Directed Actin Cytoskeleton Self Organization, Contractility and Motility

Laurent Blanchoin (*Biosci. Biotechnol. Inst. Grenoble, France*)

The organization of actin filaments into higher-ordered structures governs eukaryotic cell shape and movement. The intracellular actin cytoskeleton forms such complex intricate networks in cells that it is difficult to identify the principles of their dynamic self-organization. We have developed a micropatterning method that enables the spatial control of actin nucleation sites for in vitro assays. Using this method, we generated a variety of actin templates and measured how defined actin structures modulate the contractile and motile response.

1SMA-6 Evidence for a functional actin cytoskeleton in Asgard archaea

Bob Robinson[1,2,3], Akil Caner[2,3] ([1]*Res Inst for Interdisciplinary Sci, Okayama Univ*, [2]*Institute of Molecular and Cell Biology*, [3]*Dept. of Biochem, Sch of Medicine, Natl Univ of Singapore*)

The origin of the eukaryotic cell is unresolved. Metagenomics sequencing recently provided evidence for the hypothesis that the source cell arose from the archaea domain through the identification of several potential eukaryotic gene homologs in the Asgard archaea. However, many of these eukaryotic-like sequences are highly divergent and the organisms have yet to be imaged or cultivated, bringing in to question whether these archaea exhibit eukaryotic characteristics. Here we explore the biochemical and structural properties of putative cytoskeletal proteins from Asgard archaea.

1SMA-7 バクテリアべん毛モーターの固定子再編成における自律的制御
Autonomous stator remodeling mechanism of the bacterial flagellar motor

Tohru Minamino (*Grad. Sch. Frontier Biosci, Osaka Univ.*)

The bacterial flagellar motor coordinates the number of active stator units around a rotor in response to changes in the environment. The peptidoglycan-binding (PGB) domain of the stator unit induces stator remodeling in the motor in response to environmental changes. When each stator unit encounters the rotor, the N-terminal potion of the PGB domain adopts a partially stretched conformation, allowing the PGB domain to bind to the peptidoglycan layer. The binding affinity of the PGB domain for the peptidoglycan layer is affected by force applied to its anchoring point and chemicals such as sodium ions and polysaccharides. In this symposium, I will present current understanding of autonomous remodeling mechanism of stator stoichiometry in the bacterial flagellar motor.

1SOA-1 多剤排出トランスポーター AcrB の薬剤排出メカニズムの解明
Elucidation of a drug efflux mechanism of multidrug efflux transporter AcrB

Tsutomu Yamane (*Graduate School of Medical Life Science, Yokohama City University*)

The multidrug transporter AcrB actively exports a wide variety of noxious compounds using the proton-motive force as an energy source in Gram-negative bacteria. AcrB adopts an asymmetric structure comprising three protomers with different conformations that are sequentially converted during drug export. This drug export process is called the functional rotation. However, the detailed structural change mechanisms of the functional rotation have been unclear. Here, we searched these mechanisms through results of the all-atom molecular dynamics simulations and the Motion Tree method, which is a new method to describe the structural change between two states.

1SOA-2 多剤排出トランスポーター AcrB の機能的回転における構造変化パスウェイとエネルギー
Energetics and conformational pathways of functional rotation in the multidrug transporter AcrB

Yasuhiro Matsunaga[1,2] ([1]*RIKEN Center for Computational Science*, [2]*JST PRESTO*)

The multidrug transporter AcrB transports a broad range of drugs out of the cell by means of the proton-motive force. The asymmetric crystal structure of trimeric AcrB suggests a functionally rotating mechanism for drug transport. Despite various supportive evidence from biochemical and simulation studies for this mechanism, the link between the functional rotation and proton translocation across the membrane remains elusive. Here, by simulating the conformational pathway of the functional rotation for the complete AcrB trimer, we studied the structural basis behind the coupling between the functional rotation and the proton translocation at atomic resolution.

1SOA-3 分子シミュレーションで探る ABC トランスポーターの構造的・機能的ダイナミクス
Structural and Functional dynamics of ABC transporters explored by molecular simulations

Tadaomi Furuta (*Sch. Life Sci. Tech., Tokyo Tech*)

ATP-binding cassette (ABC) transporters constitute one of the largest superfamilies of membrane proteins found in all living organisms, and harness the energy of ATP binding and hydrolysis to transport a wide variety of molecules across membranes. On the transport cycle of ABC transporters, the chemical energy of ATP generated on the nucleotide-binding domains (NBDs: engine) is converted into the mechanical and functional motion of the transmembrane domains (TMDs: pathway) via coupling helices (CHs: transmission), that is a typical example of "chemo-mechanical coupling". Here, we review recent advances in the structural and functional dynamics of ABC transporters as revealed by molecular simulations, and discuss the transport mechanism of these molecular machines.

1SOA-4 ヒトシスチン尿症関連トランスポーターにおける軽鎖遺伝子変異から重鎖グリコシレーションへの分子内情報伝達
Intramolecular information-transmission from light chain mutation to heavy chain glycosylation in human cystinuria-related transporter

Naohiko Anzai, Shinichi Sakamoto (*Grad. Sch. Med., Chiba Univ.*)

The heterodimeric transporter composed of rBAT, a single-membrane-spanning glycosylated heavy chain, and b(0,+)AT, a putative 12-membrane-spanning light chain, is an amino acid transporter that mediates the apical transport of cystine and dibasic amino acids in renal proximal tubule. Mutations in these genes result in cystinuria. The most frequent mutation in Japanese is P482L that affects a residue near the C-terminus of b(0,+)AT and causes loss of function. The deletion of its C-terminus resulted in the loss of function, owing to the failure of the plasma-membrane targeting of heterodimeric complex due to incomplete glycosylation. Mutation in one subunit causing change of glycosylation of another seems to be the example for "intramolecular information-transmission".

1SOA-5 重み付きアンサンブル法による生体分子のシミュレーション
Weighted ensemble simulation of biomolecules

Hiroshi Fujisaki (*Nippon Medical School*)

When we want to investigate and analyze kinetic properties of biomolecules including information transfer, we often employ the Markov state model (MSM), combining with long time molecular dynamics simulations. Though there have been many such studies using MSM, its limitations due to the state classification and Markovianity is well known, and as such the other methods should be devised. One such method is the weighted ensemble (WE) method, which is a simple but powerful nonequilibrium type simulations method for any dynamical systems, equipped with parallel computation. After reviewing the current situations of MSM and WE simulations, we discuss our recent application of the WE simulations to a small peptide, chignolin, and other large protein systems.

1SOA-6 Dynamic allostery in folded protein and intrinsically disordered protein (IDP)

Shin-ichi Tate (*Dept. Mathematical and Life Sciences*)

The role of dynamic allostery in protein will be described. Dynamic allostery communicates the distal residues in protein with unchanged structure but change in dynamics. Multiple-domain protein having the domains linked by unstructured linker shows interdomain dynamics in a large magnitude. Upon substrate binding to one of the domains will change the domain dynamics to alter the inter-domain communication. This is, thus, supposed to be an another type of dynamic allostery. The ensemble structures of multi-domain protein are determined by the combinatorial use of NMR and SAXS, which reveal the dynamic allostery within a multi-domain protein. We will demonstrate two types of dynamic allostery found in a folded protein and a multi-domain protein.

1SRA-1 紅色細菌の LH1-RC 複合体の構造：キノンゲートはどこにあるのか
Where is the quinone gate in purple photosynthetic bacterial LH1-RC complex?

Seiu Otomo[1], Yukihiro Kimura[2] ([1]*Fac. Sci., Ibaraki Univ.*, [2]*Grad. Sch. Agri. Sci., Kobe Univ.*)

Quinones are membrane-soluble redox molecules found in nearly all living organisms. They play important roles in photosynthetic and respiratory electron transport chains and function as electron and proton carriers to produce transmembrane proton gradients. Four types of quinone have been reported in anoxygenic photosynthetic bacteria: ubiquinone (UQ), menaquinone (MQ), rhodoquinone (RQ) and chlorobiumquinone (CQ). Based on a number of recently published structures of purple photosynthetic bacterial LH1-RC core complexes along with biochemical analysis of the quinone distribution in membranes and core complexes, we discuss the possible pathways of quinone molecules shuttled between reaction center and the so-called quinone pool through the LH1 rings.

1SRA-2 光合成反応中心蛋白質の電子移動経路におけるコファクターの酸化還元電位と電子移動反応機構
Redox potentials of cofactors in electron transfer branches in photosynthetic reaction centers

Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Tech., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*)

In photosystem I (i.e., a type-I reaction center), electron transfer occurs in both A- and B-branches, whereas in purple bacterial photosynthetic reaction centers and photosystem II (i.e., type-II reaction centers) electron transfer predominantly occurs along L- and D1-branches, respectively. The electron transfer pathways are formed by redox active cofactors, including (bacterio)chlorophyll, (bacterio)pheophytin, and quinone. Here we report redox potential values of the cofactors to understand the mechanisms of electron transfer [1-3]. **References** [1] Kawashima and Ishikita. *Chem. Sci. 9* (2018) 4083. [2] Ishikita et al. *Proc. Natl. Acad. Sci. U. S. A. 103* (2006) 9855. [3] Ishikita and Knapp. *J. Am. Chem. Soc. 127* (2005) 14714.

1SRA-3 What can the heliobacteria teach us about the evolution of photochemical reaction centers?

Gregory S. Orf (*Center for Bioenergy & Photosynthesis, ASU*)

The photochemical reaction center (RC) is the key enzyme enabling light-driven electron transfer in photosynthesis. All available evidence supports the hypothesis that the RC arose once, about 3 Gya, and diversified widely since that time. Here, I will present a fresh look at the evolution of RCs supported by recent structural and biochemical data from our group. We show that relying too heavily on sequence comparisons between RCs can be misleading, due to low sequence homology, so we instead turn to in-depth comparison between common structural and functional elements. The crux of our analysis relies on the new 2.2-Å X-ray structure of the heliobacterial RC (HbRC) and the observation that the HbRC can use both ferredoxins and quinones as terminal acceptors.

1SRA-4 X-ray structure of the type-I reaction center from *Heliobacterium modesticaldum* at 3.2 Å resolution

Tetsuko Nakaniwa[1], Risa Mutoh[2], Kokoro Fushimi[1,3], Aya Yasuda[1,3], Tadashi Mizoguchi[4], Hitoshi Tamiaki[4], Chihiro Azai[5], Hideaki Tanaka[1], Shigeru Itoh[6], Hirozo Oh-oka[3], Genji Kurisu[1] ([1]*IPR, Osaka Univ.*, [2]*Fac. Sci., Fukuoka Univ.*, [3]*Grad. Sch. Sci., Osaka Univ.*, [4]*Grad. Sch. Life Sci. Ritsumeikan Univ.*, [5]*Col. Life Sci., Ritsumeikan Univ.*, [6]*Grad. Sch. Sci., Nagoya Univ.*)

Light-dependent charge separation in photosynthesis is driven by the reaction center (RC) membrane protein complex that is classified into four types; the green bacterial or heliobacterial, the purple bacterial, the photosystem (PS) I and II RCs. Compared to the latter three types of RCs, the molecular architecture of heliobacterial RC is still poorly understood, in part due to the lack of high-resolution structural information. Structure of the RC from *Heliobacterium modesticaldum* has been solved to a resolution of 3.2 Å as described in this presentation, that is, implying the completion of the structural description of all-types of photosynthetic RCs.

1SRA-5 反応中心電子受容体として機能するキノン：原始的な光合成細菌から高等植物まで
Quinones serve as an electron acceptor in photosynthetic reaction center of primitive bacteria to higher plants

Toru Kondo[1,2] ([1]*MIT*, [2]*MIT-Harvard Center for Excitonics*)

Photosynthetic reaction center (RC), carrying out charge separation using solar energy, is mainly classified into four types: three heterodimeric RCs of purple bacteria and photosystem I and II (PS I and II) in plants and cyanobacteria, and homodimeric type-I RC of heliobacteria and green sulfur bacteria. Whereas the heterodimeric RCs are well known to employ quinones as a secondary electron acceptor, quinone functions have been ambiguous in the homodimeric RC despite of its importance as a more primitive type. Recently, we revealed quinone functions in a heliobacterial type-I RC by electron paramagnetic resonance. I will discuss a role of quinone in the RC, and provide a clue to understanding the evolutionary scenario of RC based on the quinone function.

1SRA-6 Symmetry or asymmetry? - Site-specific structural modification of the homodimeric photosynthetic reaction center of green sulfur bacteria

Chihiro Azai (*Dept. Bioinfo., Col. Life Sci., Ritsumeikan Univ.*)

Photosynthetic reaction center (RC) has dimeric core-protein (CP) while only bacterial type-1 RC (RC1) has homodimeric CP. Cofactors for a series of light-driven electron transfer (ET) reactions are arranged in an apparently C_2-symmetric fashion to form equal two pathways. However, its “perfect” symmetry has been hardly ever targeted by experimental research and not enough proved; it is thus still controversial that the homodimeric CP is asymmetry locally and functionally. The green sulfur bacterium *Chlorobaculum tepidum* is currently the only organism amenable to genetic modification on the homodimeric CP. Combined study of site-directed mutagenesis and molecular spectroscopy on RC1 is the most promising approach to elucidate structural and functional evolution of RC.

1SBP-1 PCDR 法による細胞質内 RNA 送達の原理と応用
Mechanism and Application of photoinduced cytosolic dispersion of RNA (PCDR) method

Takashi Ohtsuki[1,2], Tet Htut Soe[2], Kazunori Watanabe[2] ([1]*Grad. Sch. of ISEHS, Okayama Univ.*, [2]*Grad. Sch. of Nat. Sci. & Tech, Okayama Univ.*)

In many drug delivery strategies, an inefficient cytoplasmic uptake of the drug often occurs due to endosomal entrapment. One of the methods to overcome this problem is to use a photosensitizer and light for disruption of the endosomal membrane. By using this mechanism, we recently developed a method for light-directed RNA delivery using photosensitive RNA carriers. This method is referred to as photoinduced cytosolic dispersion of RNA (PCDR). In this presentation, we show molecular mechanism and application of PCDR method.

1SBP-2 濾胞樹状細胞による抗体の親和性成熟の制御機構の解明
Immunological functions of follicular dendritic cells on affinity maturation of antibody

Masaki Magari[1], Sayaka Ogawa[2], Yukiko Matsuoka[2], Miho Takada[2], Naoki Kanayama[1], Hiroshi Tokumitsu[1] ([1]*Grad. Sch. Interdiscip. Sci. and Eng. in Health Syst., Okayama Univ.*, [2]*Grad. Sch. of Natl. Sci. and Tech., Okayama Univ.*)

Follicular dendritic cells (FDC) play a crucial role in the differentiation of high-affinity antibody-producing B cells in germinal center (GC) during immune responses. Previously, we have established a mouse FDC line to investigate the role of FDCs in regulating GC reactions. Recently, we found that FDC line induced the differentiation of a novel class of monocytic cell, named as FDMC, with B-cell stimulating activity, in IL-34-dependent manner. Furthermore, we show that IL-34 expressed on FDC cell surface was associated with FDMC differentiation. Furthermore, a molecular chaperon, GRP78, regulated cell surface expression of IL-34. These results indicate a novel localization and specific function of IL-34, involving in monocytic cell differentiation and GC reactions.

1SBP-3 Cytokine expression and immune cell function in tumor growth

Junko Masuda (*Grad. Sch. Inter. Sci. & Eng. Heal. Sys., Okayama Univ.*)

Nests of tumor cells at primary and metastatic sites are usually infiltrated by a variety of cancer-associated fibroblasts, endothelial cells, tumor-infiltrating lymphocytes, and macrophages, which collectively produce cytokines and other mediators that have the potential to modulate both local and systemic anti-tumor immune responses. These cells may include both myeloid-derived suppressor cells and/or regulatory T cells, i.e., cells that suppress the proliferation of $CD4^+$ helper T cells and antigen-specific $CD8^+$ T cells, thus modifying anti-tumor responses by various distinct mechanisms. In the present study, we established syngeneic mouse tumor models and found that these tumors had different effects on systemic immunity, as assessed in the spleen.

1SBP-4 自然色、形状、奥行における脳情報処理機構に関する fMRI 研究
A fMRI Brain Imaging Study for Visual Contextual Process of Color, Shape and Depth

Qiong Wu[1], Chunlin Li[2], Shigeko Takahashi[3], Hongzan Sun[4], Qiyong Guo[4], Yoshio Ohtani[5], Yoshimichi Ejima[1], Jinglong Wu[1] ([1]*Grad. Sch. of Interdiscip. Sci. & Eng. in Health Systems, Univ. Okayama*, [2]*Sch. of Bio. Eng., Capital Med. Univ.*, [3]*Kyoto City Univ. of Arts*, [4]*Shengjing HP of China Med. Univ.*, [5]*Kyoto Inst. of Tech.*)

Context contributes to accurate and efficient information processing, and shapes perception, thoughts and actions. Contextual information allows for context-driven predictions or expectations, along with predictive coding, which is a guiding principle of efficient information processing in the brain. To reveal the dynamics of the neural mechanisms underlying the processing of the association context. We carried out fMRI experiments in which subjects were asked to judge contextual validity for the association context by color, shape and depth objects. Results showed that activation maps for each task. By the dynamic causal modeling (DCM) analysis, the dynamic nature of the neural connectivities in the contextual information processing was also revealed clearly.

1SBP-5 テラヘルツ工学による先端バイオセンシング
A terahertz technology for advanced bio-sensing

Toshihiko Kiwa, Kenji Sakai, Keiji Tsukada (*Okayama University*)

Terahertz is electromagnetic waves within the frequency band from 0.1 THz to 100 THz. Thanks to recent progress of ultrafast lasers and semiconductor fabricaiton technology, terahertz come to be the most atractive and exciting technology in scientific and/or industrial fields. In this talk, the principle and applications of terahertz technology will be briefly introduced. Then, possibility for bio-sensing will be described. Also, in our group, we have developed a terahertz chemical microscopy (TCM), which can visualize various types of chemical reactions in solutions. Here, we will introduce the mechanism of TCM and its applications for medical diagnosis.

1SBP-6 Speech Enhancement of Glossectomy Patient's Speech using Voice Conversion Approach

Masanobu Abe, Hiroki Murakami, Seiya Ogino, Sunao Hara (*Okayama Univ.*)

In this paper, we propose to apply voice conversion algorithm to improve intelligibility of speech uttered by a patient who has articulation disorders because of wide glossectomy and/or segmental mandibulectomy. The GMM-based algorithm was employed by frame-by-frame manner and the performance was compared with voice conversion among normal speakers. According to experiment results, mel-cepstrum distance is decreased by 40% in all pairs of speakers by comparing the difference with pre-conversion. Voice conversion algorithm successfully reconstructed high frequency spectrum in phonemes /h/, /t/, /k/, /ts/ and /ch/, and we confirmed improvement of speech intelligibility by informal listening test.

1SIP-1 大腸菌複製サイクル再構成系を用いたセルフリー長鎖環状 DNA 合成
Cell-free synthesis of large circular DNA using a reconstitution system of replication cycle of Escherichia coli

Masayuki Su'etsugu (*Col. of Sci., RIkkyo Univ.*)

We have developed a two-step reaction to synthesis very large circular DNA without relying on biological cloning. RCR (Replication Cycle Reaction) is an in vitro reconstitution system of chromosome replication cycle of E. coli, and can propagate large circular DNA (>200 kb) in an isothermal condition. RA (Recombination Assembly) is a DNA assembly reaction in which multiple fragments with overlapping ends are efficiently assembled in a single step. The RA product is subjected directly to RCR, so that the target circular DNA molecules, but not linear intermediate molecules, are selectively propagated. Using this RA-RCR system, we have successfully constructed a 27 kb plasmid from 50 fragments.

1SIP-2 ゲノムシミュレーターを目指した人工細胞リアクタの開発
Artificial cell reactor towards genome simulator

Hiroyuki Noji (*Graduate School of Engineering, The University of Tokyo*)

Synthetic Mycoplasma cell studies revealed that 473 genes are sufficient to sustain a self-replicating cell. The great achievement was accomplished by genome-sized DNA synthesis technology and the genome transportation protocol for Mycoplasma. To deeply understand how to design genome DNA, physical simulators are requisite that allows to test the functionalities of designed genomes even if not sufficient to sustain cell homeostasis and/or proliferation. With the aim to develop such physical simulators, we developed various types of artificial cell reactors in which a genome replication-cycle reaction system and/or a gene expression system are reconstituted. We will share the latest achievements of these developments.

1SIP-3 ゲノムサイズ DNA の脂質膜への自発的包埋
Spontaneous enveloping of genome-size DNA into lipid membrane

Hiroaki Suzuki[1], Mamiko Tsugane[1,2], Fumiko Sunaga[1], Taiji Okano[1] ([1]*Chuo University*, [2]*JSPS*)

The encapsulation of genomes in every cell is tightly regulated in eukaryotes. Prokaryotes also can partition single genomic DNAs into daughter cells during division without sophisticated mechanisms. Here we investigated the distribution of genome-size DNA (gDNA) encapsulated in giant unilamellar vesicles (GUVs) that deforms into the budding shape, to see if gDNA can be partitioned into daughter vesicles with no controlling factors. We found that the molecular crowding in GUV plays an important role; when the inner space of GUV was crowded by polyethylene glycol (PEG) with relatively high MW and concentration, gDNA spontaneously attached and enveloped by the lipid membrane. We presume that this peculiar phenomenon is caused by the tendency of the system to gain entropy.

1SIP-4 Synthetic Genomics for the Human Noncoding Regions

Yasunori Aizawa (*Tokyo Institute of Technology*)

With the notable achievements and progress in genome synthesis for bacteria and yeast, Genome Project-write (GP-write) now extends its reach to the synthesis of more complex genomes including the human genome, which has much larger intergenic as well as intronic regions. In light of attempts to redesign the human genome, it is critical to evaluate the dispensability of genomic segments residing outside of the annotated open reading frames (ORFs). We have been exploring the functional relevance of noncoding segments in mammalian genomes, recently by taking synthetic genomics approaches. In this presentation, I will share our latest data concerning the design of new noncoding regions of a synthetic human genome.

1SIP-5 人工細胞内で RNA ゲノムの協力性は持続し進化するのか？
Sustainability and evolvability of cooperative RNAs in an artificial cell-like system

Norikazu Ichihashi (*Osaka University*)

Cooperation among the primitive replicating molecules to form a large replication unit is the key step for the emergence of life. A major challenge to this phenomenon is the emergence of parasitic entities that are produced by mutations, because they uncontrollably replicate until they destroy the cooperative replication system. In this presentation, I show that the molecular cooperation between two gene-encoding RNAs is robust in artificial cell-like compartment and is spontaneously reinforced through Darwinian evolution. Our results present the first experimental evidence that supports the sustainability and robustness of molecular cooperation in an evolutionary timescale.

1SIP-6 遺伝暗号の改変による生物学的封じ込め
Biological containment through engineering of genetic code

Daisuke Kiga (*Waseda University*)

Emerging technology can pose an increased risk, but at the same time can aid in the development of safety technology. This topic has been discussed within Synthetic biology from its early days. Recently, engineering of genetic code has shown proof of concept in various containment technologies. One example is a designed auxotroph where a nonstandard amino acid encoded in an expanded genetic code is required for activities of essential proteins. Another example is orthogonality between pairs of genetic code and genes. Such orthogonality can reduce unintentional horizontal gene transfer among engineered and natural microbes. I would like to introduce discussion in a genome synthesis conference, and to discuss future safety engineering within artificial cell research.

2SAA-1 Non-invasive force measurement reveals the number of active kinesins on a synaptic vesicle precursor regulated by ARL-8

Kumiko Hayashi[1,2], Shin Hasegawa[1], Takashi Sagawa[3], Sohei Tasaki[4,5], Shinsuke Niwa[4] ([1]*Sch. Eng., Tohoku Univ.*, [2]*PRIME, AMED*, [3]*NICT*, [4]*FRIS, Tohoku Univ.*, [5]*BDR, RIKEN*)

Kinesin superfamily protein UNC-104 transports synaptic vesicle precursors (SVPs). In this study, the number of UNC-104 hauling a single SVP in the worm C. elegans was counted by using a non-invasive force measurement. The distribution of the force acting on a SVP was spread out over several clusters, implying the presence of several force-producing units (FPUs). We then compared the number of FPUs in the wild-type worms with that in arl-8 gene-deletion mutant worms. ARL-8 promotes unlocking of the autoinhibition of the motor in order to avoid unnecessary consumption of ATP when the motor does not bind to a SVP. There were fewer FPUs in the arl-8 mutant worms. It indicates that a lack of ARL-8 led to a decrease in the number of motors responsible for SVP transport.

2SAA-2 Accommodation of mRNA on the ribosome during translation initiation

Jin-Der Wen (*Institute of Molecular and Cellular Biology, National Taiwan University*)

Translation is a process of protein synthesis, which can be divided into the stages of initiation, elongation, and termination. In bacteria, the initiation reaction begins with the binding of the ribosomal small subunit 30S to mRNA at the ribosome binding site (RBS). Here we explore this dynamic process using two single-molecule approaches, optical tweezers and smFRET. We find that the 30S can tightly bind to a single-stranded mRNA containing a strong RBS. The initiator tRNA or initiation factors IF3 can greatly stabilize the complex. An mRNA with a downstream structure will impair its binding with 30S, but either the initiator tRNA or IF3 can facilitate their association. Our data provide great insight into the molecular mechanism of translation initiation.

2SAA-3 Single-Molecule Study of Swi5-Sfr1 Stimulation on Rad51 Recombinase Filament Assembly in Mouse and Yeast

Hung-Wen Li[1], Chih-Hao Lu[1], Peter HY Chi[1], Hiroshi Iwasaki[2] ([1]*National Taiwan University*, [2]*Tokyo Institute of Technology*)

Rad51 recombinase is essential for homologous recombination repair of DNA breaks. Rad51 first assembles onto single-stranded DNA to form a nucleoprotein filament. Swi5-Sfr1 (S5S1) has been shown to stimulate Rad51 recombination by stabilizing Rad51 filaments, but mechanism is not clear. We use single-molecule tethered particle motion and fluorescent resonance energy transfer experiments to show RAD51-S5S1 complex efficiently stimulates mRAD51 nucleus formation, and inhibits mRAD51 dissociation. Even though two S5S1 complexes from mouse and fission yeast appear to affect differently on kinetics, both act primarily by stabilizing Rad51 on DNA. This stimulation mechanism by S5S1 conserved from yeasts to mammals is a generally strategy for filament stabilization.

2SAA-4 Mechanics of the bacterial flagellar motor in vivo

Tsubasa Ishida[1], Taishi Kasai[2,3], Yong-Suk Che[4,5], **Yoshiyuki Sowa**[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Micro-Nano Tech, Hosei Univ.*, [3]*Dept. Life Sci., Rikkyo Univ.*, [4]*Dept. Frontier Biosci., Hosei Univ.*, [5]*Grad. Sch. Frontier Biosci., Osaka Univ.*)

The bacterial flagellar motor, embedded in the cell membrane, consists of a rotor and multiple stator units. It couples ion flux passing through the stator units to its rotation. To reveal how the motor works, we developed the techniques to measure its rotation in the range from stall to zero-load. We measured stall torque directly by an optical trap and linear relationship between speed and ion-motive force by a bead assay. These results give the minimum number of coupling ions required for motor rotation. We also succeeded in manipulating one of the two ion binding sites in each stator unit, leading to reveal kinetic cycle of motor rotation at molecular level. In this talk, we will present our recent progress and discuss the mechanochemical cycle of the motor.

2SAA-5 Measurement for the chemotaxis proteins and cellular behavior in single *E. coli* cell

Hajime Fukuoka (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

E. coli cell swims toward favorable environment by chemotaxis, which is a well-known signal transduction system. However, relation between the dynamics of each protein, such as activity and localization, and the magnitude of chemotactic response is not unclear at single cell level. To quantitatively understand this relation, the dynamics of chemotaxis proteins and the cellular response should be measured simultaneously at single cell. Therefore, we are trying to measure the change in the localization of CheY, the concentration of phosphorylated CheY, and/or the receptor's activity detected thorough FRET technique, with motor rotation. In this symposium, we will discuss the signaling process based on experimental results measured at a single *E. coli* cell.

2SAA-6 Probing bacterial flagellar growth by real-time fluorescence imaging

Chien-Jung Lo (*National Central University, Taiwan*)

Bacterial flagella are self-assembled external tubular filaments for swimming. We develop single-cell fluorescence imaging to monitor in real time the Vibrio alginolyticus polar flagellar growth. The flagellar growth rate is highly length-dependent. We characterized the key factors controlling the flagellar growth rate. We modeled the flagellar building process as a one-dimensional injection-diffusion process. Our results and mode shed new light on the dynamical process of this complex extracellular structure.

2SBA-1 Structural Insights into Light Harvesting and Its Regulation in Plants

Zhenfeng Liu (*Institute of Biophysics, Chinese Academy of Sciences*)

Plant photosystem II (PSII) is associated with peripheral antenna complexes, including the major (LHCII) and minor light-harvesting complexes II (CP29, CP26 and CP24), and receives photon energy from them. Recently, we have solved the structures of two different types of plant PSII-LHCII supercomplexes through single-particle cryo-electron microscopy method. The structures reveal the mechanism of specific assembly between PSII and the peripheral antennae. Numerous chlorophylls at the interfaces between adjacent complexes are connected closely, mediating the inter-complex energy-transfer processes. Insights into the dynamics of inter-complex assembly during light-harvesting regulation are obtained in the context of currently available structural and functional data.

2SBA-2 エボラウイルス・ヌクレオ蛋白質−RNA 複合体のクライオ電子顕微鏡構造
Structure of Ebola virus nucleoprotein-RNA complex by single-particle cryo-electron microscopy

Yukihiko Sugita[1,2], Hideyuki Matsunami[1], Yoshihiro Kawaoka[3,4], Takeshi Noda[5], Matthias Wolf[1] ([1]*OIST*, [2]*IPR, Osaka Univ.*, [3]*Inst. Med. Sci., Univ. Tokyo*, [4]*UW-Madison*, [5]*Inst. Front. Life Med. Sci., Kyoto Univ.*)

Ebola virus harbors linear, non-segmented, negative-sense, single-stranded, genomic RNA. The viral RNA is associated with multiple copies of viral nucleoprotein (NP) to form a helical complex. The NP-RNA complex functions as a scaffold for nucleocapsid (NC) formation and a template during the replication and transcription. Although recent studies have revealed the overall architecture of the NC core, detailed structure of NP-RNA complex has been unknown. Here, we report the first near-atomic resolution structure of an Ebola virus NP-RNA complex by single-particle cryo-electron microscopy. Our results describe the molecular architecture of the helical complex, revealing how it encapsidates RNA and assembles.

2SBA-3 Structure of Origin Recognition Complex Bound to Autonomously Replicating Sequence

Ning Gao (*School of Life Sciences, Peking University*)

Origin recognition complex (ORC) binds DNA to mark the site for replication initiation in eukaryotes. Here, we report a 3-Å cryo-EM structure of S. cerevisiae ORC bound to a 72-bp origin DNA containing the ARS consensus sequence (ACS) and B1 element. ORC encircles DNA through extensive interactions with both phosphate backbone and bases, and bends DNA at the ACS and B1 sites. Specific recognition of thymines in the ACS is carried out by a conserved basic amino acid motif of Orc1 in the minor groove, and by a species-specific helical insertion motif of Orc4 in the major groove. This work pinpoints a conserved role of ORC in modulating DNA structure to facilitate origin selection and helicase loading in eukaryotes.

2SBA-4 クライオ電子トモグラフィーを用いたゼブラフィッシュ繊毛における PIH タンパク質の機能解析
Cryo-electron tomography revealed zebrafish axonemal dyneins assembled by distinct PIH proteins

Hiroshi Yamaguchi[1], Toshiyuki Oda[2], Masahide Kikkawa[1], Hiroyuki Takeda[3] ([1]*Grad. Sch. Med., Univ. Tokyo*, [2]*Grad. Sch. Med., Univ. Yamanashi*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

Axonemal dyneins, huge motor molecules in cilia, are preassembled in the cytoplasm before transport into cilia. Axonemal dyneins have various subtypes, but the roles of each subtype and their assembly processes remain elusive in vertebrates. The PIH protein family has suggested to be implicated in the assembly of different dynein subtypes. Here, we established zebrafish mutants of all four PIH-protein genes: pih1d1, pih1d2, ktu, and twister. Our cryo-electron tomography enabled visualization of dyneins in zebrafish sperm for the first time. Mutations caused the loss of specific dynein subtypes, which was correlated with abnormal sperm motility. Therefore, our work revealed the roles of zebrafish dynein subtypes and their assembly processes through distinct PIH proteins.

2SBA-5 クライオ電子顕微鏡で明らかになったコフィリンによるアクチン線維分解機構
Structural basis of cofilin binding and disassembling of actin filaments revealed by cryo-electron microscopy

Akihiro Narita (*Nagoya University*)

ADF/cofilin family proteins play central roles in disassembling actin filaments in the cell. We have determined the 3.8 Å resolution cryo-EM structure of cofilactin (cofilin-decorated actin filament). The actin subunit in the cofilaction was distinct from F-actin and G-actin. The inner domain of actin (subdomains 3 and 4) and the majority of subdomain 1 move as two separate rigid bodies in the structural changes. The cofilin-actin interface consists of three distinct parts. Based on the rigid body movements of actin and the three cofilin-actin interfaces we could explain many features of ADF/cofilin functions. I also present our new cryoEM results and a few new electron microscopy techniques which might be helpful to overcome cryoEM limitations.

2SBA-6 Structure of phycobilisome

Sen-Fang Sui (*School of Life Sciences, Tsinghua University*)

Phycobilisomes (PBS) are the major light harvesting antennae of two very important groups of photosynthetic organisms on earth, the cyanobacteria and red algae. Ever since the discovery of PBS over 50 years ago, people have been trying to understand how this gigantic supramolecular complex is assembled and how the energy is delivered to photosynthetic reaction centers. Here, we report the cryo-EM structure of a 16.8-megadalton PBS from a red alga at an average resolution of 3.5 angstroms, leading to the atomic model of the entire complex. The results provide a firm structural basis for our understanding of complex assembly and the mechanisms of energy transfer within the PBS.

2SDA-1 創薬等ライフサイエンス研究のための相関構造解析プラットフォーム
Correlative Structural Analysis Platform for Drug Discovery and Life Sciences

Masaki Yamamoto (*RIKEN SPring-8 Center*)

In BINDS Project from AMED, we will establish the research infrastructure for “Correlative Structural Analysis” for biological macromolecules by combining complemental structural analysis technologies such as X-ray macromolecular crystallography, cryo-electron microscopy, Bio-SAXS and NMR. "Correlative Structural Analysis" can elucidate spatially and temporally abundant information not only on diverse three-dimensional structural information but also structural dynamics that is indispensable for drug discovery and life science research. This project promises development on new structural life sciences, including discovery of new active site of drug targets, functional analysis and physicochemical characterization of multicomponent systems, and so forth.

2SDA-2 創薬における実験化学と計算化学の融合
Integration of experimental and computational chemistry in drug discovery

Midori Takimoto-Kamimura (*Teijin Institute for Biomedical Research*)

SBDD strategy is most powerful and effective tool in drug discovery. SBDD is performed under the discussion among structural biologists, computer chemists and medicinal chemists. In drug discovery process, SBDD fits to the process in the scaffold conversion from hit to lead compound and lead optimization processes. The cycle consisted with the complex structure determination, the drug design and the compound synthesis and biological assays considering the compound ADME profiles are repeated. Drug discovery using SBDD that is carried out at pharmaceutical industries is almost possible at BINDS. Academia researcher should bring own specialized skill with the interesting target and combine multiple supports of BINDS that are not owned by yourself.

2SDA-3 蛋白質相互作用の物理化学的解析と次世代創薬
Physicochemical Analyses of Protein Interactions for Next Generation Drug Discovery and Development

Kouhei Tsumoto, Satoru Nagatoishi (*School of Engineering and Institute of Medical Science, The University of Tokyo*)

One of the major issues to be addressed for drug discovery is diversitification of targets, including protein-protein interactions and supramolecular complexes, which could have not been solved by traditional and/or conventional methods. We have investigated protein interactions, including protein-compound interactions, from physicochemical viewpoints. Recently, we have successfully incorporated several physicochemical methods into drug screening, hit validation of drug and target, and optimization of the drugs. Here we introduce recent progresses on physicochemical approaches for screening and/or validation of drugs.

2SDA-4 BINDS バイオロジカルシーズ探索ユニットにおける支援内容のご紹介
BINDS: supporting platform to explore biological activity of your seeds

Haruhiko Koseki (*RIKEN center for integrative medical sciences*)

Biological seeds exploring unit in BINDS is dedicated to accelerate drug discovery process by providing open access platforms for emerging sequencing technologies, disease model animals, and preclinical examinations to biomedical scientists affiliated to both academic and industrial institution. In this session, I will introduce accessible technologies at each platform and what you can by using those technologies. Briefly, at sequencing platform, many different types of libraries could be generated and some interpretation could be given upon demands. Disease model platform will provide genetically engineered models and other disease models.

2SDA-5 インシリコ創薬の展望
Perspective of in silico drug discovery

Shigenori Tanaka (*Kobe University*)

Recent progress of in silico drug discovery is reviewed in association with the activities of AMED-BINDS. Due to significant advances in high performance computing technologies, one can employ plethora of state-of-the-art computational techniques in molecular dynamics, quantum chemistry, cheminformatics, bioinformatics, data science, artificial intelligence, systems approach, and so on. Researchers can also utilize dependable experimental information concerning X-ray crystallography, NMR, neutron diffraction, cryo-EM, XFEL, genetic sequencing, mutagenesis, and many spectroscopies. In the AMED-BINDS activities for research support and development of novel technologies, examples of new types of collaborations among academia, industry and government are illustrated.

2SDA-6 生命科学データベースの接続をめざす VaProS から見えてくるあらたな知見
New knowledge and ideas found through VaProS, an application for life science database integration

Kei Yura[1,2] ([1]*Dept. Life Sci. & Med. Bio., Waseda Univ.*, [2]*Info. Bio., Ochanomizu Univ.*)

Life science research now heavily relies on all sorts of databases, such as genome sequences, protein structures, molecular interactions. A combinatory search of these databases has a chance to extract new ideas that can be examined by wet-lab experiments. By building a tool that virtually integrates the related databases, we enabled simultaneous access to different databases. The tool facilitates building new hypotheses of the research target based on different databases. This web application, named VaProS, puts stress on the connection between the functional information of genome sequences and protein structures. Here we will present the notion of VaProS, and an example of new knowledge that can be acquired through a keyword search on VaProS.

2SEA-1 The molecular clutch model as a framework to understand integrin-mediated mechanotransduction

Pere Roca-Cusachs (*Institute for Bioengineering of Catalonia*)

Cell proliferation and differentiation, as well as key processes in development, tumorigenesis, and wound healing, are strongly determined by the physical properties of the extracellular matrix (ECM). In this talk, I will discuss how the properties under force of integrin-ECM bonds, and of the adaptor protein talin, drive and regulate rigidity sensing. I will further discuss how this sensing can be understood through a computational molecular clutch model, which can quantitatively predict the role of integrins, talin, myosin, and ECM receptors, and their effect on cell response. Finally, I will analyze how this framework can explain cell sensing not only of substrate rigidity, but also of ECM ligand distribution.

2SEA-2 Single-molecule measurements of force transmission by integrin heterodimers in living cells

Alexander Dunn (*Stanford University*)

Integrins link the cytoskeleton to the extracellular matrix (ECM), and are required for both traction generation and mechanosensing. We used (FRET)-based molecular tension sensors to measure the tension experienced by individual integrins in living cells. We found that the force per integrin was predominantly determined by the nature of its connections to the actin cytoskeleton. In contrast, we found that the influence of integrin usage on traction generation, and by extension mechanotransduction, likely arises via indirect control of the collective properties of the adhesion as a whole. Our observations support a general model for how cells create regulated and dynamic adhesions to the ECM.

2SEA-3 α カテニンの張力応答性分子機構と上皮形態形成
Force-sensing device region of alpha-catenin and epithelial morphogenesis

Shigenobu Yonemura[1,2] ([1]*Tokushima Univ. Grad. Sch. Med. Sci.*, [2]*Riken BDR*)

We report the high-resolution structure of the force-sensing device region of an actin-binding adherns junction component, alpha-catenin, which shows the autoinhibited form comprised of helix bundles E, F and G (also called MI, MII and MIII, respectively). The cryptic vinculin-binding site is embedded into helix bundle E stabilized by direct interactions with the autoinhibitory region forming helix bundles F and G. Important residues mediating the autoinhibition are identified, resulting in production of mutated alpha-catenins that display variable force sensitivity and autoinhibition. When we form epithelial spheroids of cells expressing the mutants in 3D cultures, aberrant force sensitivity resulted in distorted shape of spheroids.

2SEA-4 細胞増殖における接触阻害のメカノバイオロジー
Mechanobiology of the contact inhibition in cell proliferation

Masahiro Sokabe, Hiroaki Hirata (*Mechanobiology Lab, Nagoya Univ., Grad., Sch., Med.*)

Confluence-dependent inhibition of cell proliferation, termed contact inhibition (CI), is crucial for tissue integrity; loss of CI is a typical feature of cancer. Although chemical and mechanical factors at cell-cell adhesions are considered to play a vital role in CI, the underlying mechanism remains to be solved. We found that proliferation of confluent keratinocytes was inhibited by contractile force of actomyosin cables connected to E-cadherin, suggesting that tensile force at cell-cell adhesions is crucial for CI. This sounds rather contradictory because cell proliferation is generally promoted by tensile force in actin cytoskeletons. Another intriguing problem may be how the tensile force is compromised in cancer cells. Those problems are under our investigation.

2SEA-5 Rigidity Sensing and Transformed cell growth

Michael Sheetz (*Mechanobiology Institute, Singapore, National University of Singapore*)

Rigidity-sensing is critical for growth and development. The depletion of many cytoskeletal proteins such as tropomyosin 2.1, alpha-actinin, and myosin IIA will block rigidity-sensing contractions. In addition, receptor tyrosine kinases, AXL and ROR2, are part of the rigidity sensing complex and control mechanical aspects of contractions without ligand activation. All transformed cancer cells tested lack rigidity sensing (Yang et al., BIORXIV-2017/221176) either because of Tpm2.1 depletion or Tpm3 overexpresion. Thus, we suggest that transformed growth in cancer results from the inability of the cancer cells to sense rigidity and restoration of rigidity sensors can restore normal growth behavior.

2SFA-1 細胞機能解析を目指した非標識神経伝達物質イメージセンサ
Non Label Nurotransmitter Image Sesnor for for Analysis of Cerebral Function

Kazuaki Sawada, Youna Lee, Tatsuya Iwata, Kazuhiro Takahashi (*Toyohashi University of Technology*)

Non Labeled Image Sensing technology is strategic research area in bio-medical field. By combining imaging sensors with chemical sensors has developed novel image sensor that can visualize specific neurotransmitters from cells in real time. They are crucial for sustaining the activities of living things, and understanding their behavior is critical for developing innovative drugs and devices based on chemical reactions. For spatiotemporal analysis of cerebral function, high spatial and time resolution neurotransmitter image sensor is developing by CMOS technology.

2SFA-2 オンチップ・セロミクス：「履歴・記憶」と「集団効果」から見た細胞ネットワークの後天的情報の理解
On-chip Cellomics: Reconstructive Understanding of Epigenetic Information in Cellular Networks from Algebraic and Geometric Perspectives

Kenji Yasuda (*Department of Physics, Waseda University*)

Exploiting the combination of latest microfabrication technologies and measurement technologies, which we call “on-chip cellomics assay”, we can select, control, and reconstruct the environment, interaction of single cells, and cell networks from “algebraic” and “geometric” perspectives. In this symposium, we explain our experimental results of the “community effect” of beating cardiomyocyte networks and firing neuronal networks as part of a series of cell-network-based “algebraic” and “geometric” studies of cellular systems after a brief explanation of the experimental set-up of on-chip cellomics microfabrication techniques regarding how the constructed approach of step-wise network formation of single cells was accomplished.

2SFA-3 Microfabricated Silicon Devices for Ion Channel Reconstitution

Ayumi Hirano-Iwata (*Advanced Institute for Materials Research, Tohoku University*)

Recording ion channel activities in artificially formed bilayer lipid membranes (BLMs) provides a well-defined system for screening the effects of drugs that act on ion channels. However, two major problems associated with the BLM systems reduce experimental efficiency, namely, instability of BLMs and a low efficiency of ion channel incorporation. Here, I will show you our recent approaches to address these issues based on silicon microfabrication techniques. The BLM system was then combined with a cell-free synthesized hERG channel, whose relation to drug-induced arrhythmia is well recognized. Such BLM system combined with a cell-free protein synthesis will be a potential platform for screening the effects of drugs that act on various ion-channel genotypes.

2SFA-4 High Sensitive Virus Sensing by Sugar Chain Modified Graphene FET

Kazuhiko Matsumoto (*Institute of Scientific & Industrial Research, Osaka University*)

Using the Field Effect Transistor with graphene layer as a channel, the highly pathogenic avian influenza virus could be judged whether it infects to humane or not within few minutes. Virus first connects to the sugar chain at the cell surface and invades into the human body. At this point, virus can distinguish the small structural difference of the human and the avian sugar chain. As graphene has a feature of an ultra high electron mobility of 200,000cm^2/Vs, the graphene FET can detect the small change of the charge on its surface when the virus connects to the graphene FET modified by the human and avian sugar chain. The present graphene FET can distinguish whether the virus infects to human or not within 30minutes, which so far takes more than 1 week.

2SGA-1 ハイブリッド分子シミュレーションによる光受容体タンパク質の分子機能ダイナミクスの解明
Functional Molecular Dynamics of Photo-Receptor Proteins Revealed by a Hybrid Molecular Simulation Technique

Shigehiko Hayashi (*Dept. Chem., Grad. Sch. Sci., Kyoto Univ.*)

Functional processes of photo-receptor proteins involve dynamic molecular conformational changes of complex protein systems triggered by electronic photo-activations at reaction centres. Complex electronic and molecular structures often found in the reaction centres of photo-receptor proteins have been obstacles to examine their functional molecular dynamics by conventional molecular dynamics (MD) simulations, which are not capable of accurately describing the complex reaction centres. In this talk, I will present our recent development of a hybrid molecular simulation technique allowing one to treat the reaction centres at the ab initio quantum chemistry level of theory in long-time MD simulations of the proteins as well as its applications to photo-receptor proteins.

2SGA-2 全原子分子動力学シミュレーションによるヌクレオソーム内・間相互作用の自由エネルギープロファイル
Free energy profiles of the intra- and inter-nucleosomal interactions by all-atom molecular dynamics simulations

Hisashi Ishida, Hidetoshi Kono (*National Institutes for Quantum and Radiological Science and Technology*)

Nucleosomes create the diverse of the conformation of chromatin by the intra- and inter-nucleosome interactions. We analyzed these interactions using all-atom molecular dynamics simulations. As for the intra-nucleosomal interaction, the free energy profile for unwrapping the outer superhelical turn of nucleosomal DNA revealed that there are many potential paths to outer superhelicdal turn unwrapping, but the dominant path is likely asymmetric. As for the inter-nucleosomal interaction, the free energy profile for separating two nucleosomes revealed that H4 histone tails diversify the two nucleosomes' orientation. These results provide insight into the construction, disruption, repositioning of nucleosomes to understand chromatin dynamics.

2SGA-3 大規模計算によるマルチコピーマルチスケールシミュレーションとその応用研究
Multicopy/multiscale simulations and their applications using massive computing

Kei Moritsugu[1], Tohru Terada[2], Ryuji Ishida[1], Akinori Kidera[1] ([1]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [2]*III, Univ. Tokyo*)

Characteristic timescale of biologically relevant processes of proteins far exceeds the feasible computational time of a single brute-force molecular dynamics (MD). However, recent advances in HPC have allowed a huge number of short-time MDs to be performed in parallel, leading to accurate and efficient calculations of the associated free energy landscape and kinetics on the basis of statistical mechanics. Here, the application studies of large proteins such as glucokinase and ABC transporter have been presented using three simulation techniques: our newly developed multiscale enhanced sampling, weighted ensemble, and string method. The illustrative results of these biological/pharmacological targets demonstrate the usefulness of HPC for elucidating functional dynamics.

2SGA-4 マルコフ状態モデルによるタンパク質の立体構造変化のダイナミクス解析
Analysis of the dynamics of protein conformational change using Markov state model

Tohru Terada[1,2], Tatsuki Negami[2] ([1]*III, Univ. Tokyo*, [2]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*)

Thanks to the high computational power of GPUs, it has become usual to perform molecular dynamics (MD) simulations for longer than one microsecond. However, there is still a large gap between the timescale on which biological phenomena occur (milliseconds to seconds) and the timescale accessible to a single MD run. Markov state model (MSM) constructed from multiple MD runs has been expected to bridge the gap. Here, we applied this method to study the dynamics of the conformational change of a protein. The free-energy landscape and the distribution of the first-passage time of the conformational change were calculated from the model. We will discuss the effect of the parameters of MSM on the results and will propose a method to reasonably determine the parameters.

2SGA-5 Quantitative Coarse-Grained Molecular Modeling of Biomembranes

Wataru Shinoda (*Nagoya Univ.*)

In this talk, I would like to illustrate our recent research activity on quantitative coarse-grained molecular modeling of lipid and protein self-assemblies to simulate a complex biomolecular structure and biologically relevant events including membrane domain formation and membrane fusion. Free energy analysis of topological and/or morphological changes of lipid membranes has also been carried out to reveal the effect of membrane geometry and lipid composition on the free energy barriers for these events. Large-scale molecular simulations reaching to submicron size will also be demonstrated to elucidate the power of chemically accurate coarse-grained molecular dynamics.

2SGA-6 Investigating Genome Organization and Regulation with Coarse-Grained Molecular Simulations

Cheng Tan, Shoji Takada (*Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.*)

Among the multiscale hierarchy of computational simulations of the biomolecular systems, coarse-grained (CG) molecular dynamics (MD) simulations are used to study long-time behaviors of large systems. Here we present our recent developments of CG models for protein-DNA interactions and applications to genomic systems. We designed hydrogen-bond-based models for both sequence-specific and nonspecific protein-DNA interactions. With these renovations, we investigated the dynamics of the target search process of transcription factors on the highly rugged landscapes and the different scenarios of genome compaction assisted by eucaryotic histone and prokaryotic histone-like protein. On top of these, we explored the binding of pioneer transcription factors to nucleosomal DNA.

2SGA-7 タンパク質の構造揺らぎを考慮したリガンド結合部位解析と創薬支援
Ligand binding site analysis with protein flexibility for drug design

Takatsugu Hirokawa (*molprof, AIST*)

Modeling of the receptor conformations optimized for ligand docking, lead optimization and virtual screening from the ensemble of MD conformation is a key technique for in silico structure-based drug design with protein flexibility. In this work, we expand the pre-docking processing of MD conformations starting from the apo structure by evaluating the shapes and druggability of the ligand binding sites in conformations resulting from MD simulations. Results from several benchmark using the drug target proteins, this pre-screening protocol combining MD and shape analysis allows us to find optimized receptor conformations for fragment ligand docking, hit-to-lead optimization and virtual screening.

2SHA-1 ゲノム科学により拡がる新奇微生物型ロドプシンの多様性と光化学
New diversity of microbial rhodopsins revealed by genome science

Keiichi Inoue[1,2] ([1]*Univ. Tokyo, Inst. Solid State Phys.*, [2]*JST PRESTO*)

Microbial rhodopsin is photoreceptive membrane protein diversely present in microbes. Before 2000, they were mainly found in haloarchaea. The recent progress of genomic and metagenomics analysis, however, revealed a number of new types of microbial rhodopsins in various archaea, eubacteria and even lower eukaryotes showing large variety of functions: pumps, channels, sensor, gene regulation, enzymatic reaction and so on. Many of them are also applied to control cellular activity by light (optogenetics). In this presentation, we will introduce the rhodopsin proteins identified by genome science in recent years, and also present about our recent research of a new rhodopsin family, “heliorhodopsin (HeR)”, completely distinct from all other microbial rhodopsins.

2SHA-2 PYP タンパク質における多様な分光学的性質と相互作用
Divergent spectroscopic features and interactions of PYP proteins

Yoichi Yamazaki (*Division of Materials Science, Graduate School of Science and Technology, NAIST*)

Photoactive yellow protein (PYP) is a blue light photo-receptor firstly obtained from, Halorhodospira halophila (Hh). PYP absorbs blue light by use of a covalently attached chromophore, p-coumaric acid. PYP proteins classified three types, the first group is represented by Hh-PYP which has an absorbance maximum around 440nm, and the second group is represented by PYP obtained from Rhodobacter capsulatus which shows two absorbance peaks at around 370 and 440nm. In the rest group, PYP is a part of multi domain proteins as a sensor domain. All these PYPs make a photoreaction cycle in common molecular mechanism, but each PYP owns different features in them. In this symposium spectroscopic features of photoreaction and interaction will be discussed in several PYP proteins.

2SHA-3 Flavin 結合タンパク質の光反応の多様性
Diversity of photochemical reactions of Flavin-based photoreceptors

Yusuke Nakasone (*Graduate school of Science, Kyoto University*)

LOV and BLUF proteins are blue light sensors containing flavin as a chromophore. The light sensing domains have high similarities in their structures and they show photocyclic reactions which have been characterized by specific absorption spectral changes. In order to understand the signal transduction mechanisms, we have investigated the reaction dynamics of several LOV and BLUF proteins by the transient grating method. At the symposium, we will discuss the diversity of their signaling mechanisms based on the photochemical reactions of several phototropins and BLUF-containing phosphodiesterases.

2SHA-4 Cyanobacteriochromes covering UV-to-FR region: Newcomers to the photoreceptor field potentially useful for bio-imaging and optogenetics

Rei Narikawa (*Dept. Biol. Sci., Shizuoka Univ.*)

Cyanobacteriochromes (CBCRs) are cyanobacterial linear tetrapyrrole-binding photoreceptors that are distantly related to classical red/far-red reversible phytochromes. The CBCRs have been identified to regulate some photo-acclimation processes such as phototaxis and chromatic acclimation. To date, diverse CBCRs have been characterized to show various reversible photoconversions such as red/green, blue/green, UV/orange and far-red/orange reversible photoconversions. Detailed spectral and structural studies have revealed general and diverse aspects of their color-tuning mechanisms. In this presentation, after brief summarization of these mechanisms, we focus on recently discovered biliverdin-binding CBCRs that should be advantageous for bio-imaging and optogenetics.

2SHA-5 オプトジェネティクス応用へ向けた酵素型ロドプシンの分子機構理解
Enzyme rhodopsins -molecular properties of potential optogenetics tools-

Satoshi Tsunoda[1,2] ([1]*JST PRESTO*, [2]*Nagoya Institute of Technology*)

Function of microbial rhodopsins involve ion pump, ion channel, light sensor for phototaxis response. Recent studies revealed novel rhodopsins with light-dependent enzymatic functions such as guanylate cyclase (Rh-GC) and phosphodiesterase (Rh-PDE). These molecules could be genetically targeted into various types of cells, serving as optogenetics tools for optical control of intercellular cyclic nucleotide-associated signal transductions. To get deeper insights into the light-activation mechanism of Rh-GC and Rh-PDE, we here investigate the spectroscopic property, enzymatic kinetics, and evaluate the light-dependent activity in mammalian cells. Mutation studies were performed to identify critical residues for enzymatic activation.

2SHA-6 脊椎動物の暗所視獲得プロセスを再考する
Revisit of the acquisition process of vertebrate scotopic vision

Takahiro Yamashita (*Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.*)

Most vertebrate retinas have rhodopsin for scotopic vision and cone pigments for photopic vision. The repertories of visual pigments found in the genomes and the variety of their molecular properties underlie the visual system. The typical phylogenetic analysis revealed that cone pigments diversified into four groups before branching of the rhodopsin group. This provided the possibility that color vision (tetrachromacy) under photopic conditions originated first and scotopic vision developed later. Recently, we found that pinopsin, which is most closely related with visual pigments in the phylogenetic tree, can also work for scotopic vision in lower vertebrates. We would like to revisit the acquisition process of vertebrate scotopic vision.

2SKA-1 XFEL analysis of light-mediated pyrimidine dimer repair by DNA photolyase

Yoshitaka Bessho[1,2] ([1]*Academia Sinica, IBC*, [2]*RIKEN SPring-8 Center*)

DNA photolyase is an enzyme that repairs DNA pyrimidine dimer damage caused by UV exposure. Visible light, especially purple or blue (400-450 nm), fuels this enzyme reaction. To clarify the molecular reaction mechanism of CPD (cyclobutane pyrimidine dimer) photolyase, we used the femtosecond pulse of the SACLA X-ray free-electron laser (XFEL) as a probe, to obtain the molecular structure before the crystal was damaged by radiation. The structure revealed the exact arrangement of the water molecule clusters adjacent to the U-shaped FAD cofactor. We also aimed to elucidate the dynamics of the light-mediated DNA-repair reaction via time-resolved serial femtosecond crystallography. At this symposium, we will report our latest results.

2SKA-2 細胞内結晶工学を利用したタンパク質結晶の機能設計
Functional design of protein crystals by in vivo crystal engineering

Satoshi Abe, Takafumi Ueno (*Sch. Life Sci. Technol. Tokyo Tech.*)

The development of biomaterials using protein assembly has attracted much attention in material sciences and bionanotechnology. Three dimensional (3D) protein crystals have great potential as solid biomaterials because they have highly ordered 3D arrangements of protein molecules. Here, we are investigating in vivo crystal engineering toward the development of functional crystalline materials. It is known that certain proteins can be crystallized in living cell. Cypovirus (cytoplasmic polyhedrosis virus) produces polyhedrin monomer (PhM) in the infected insect cells, and then PhMs are crystallized in the cells. In this presentation, I will discuss functional design of protein crystals by in vivo crystal engineering.

2SKA-3 X 線自由電子レーザーによる生体高分子 X 線溶液散乱
BioSAXS with X-ray Free Electron Lasers

Nobutaka Shimizu (*PF, IMSS, KEK*)

Small-angle X-ray scattering for solution samples of the biological molecules, BioSAXS is vigorously utilized in recent years to understand the structural mechanism of the biological system. The analytical method tightly combined with computational science gives images of molecules and complexes in solution. Moreover, technological innovation such as SAXS in line with size-exclusion chromatography, SEC-SAXS has extended the scope of application of SAXS analysis to samples up to higher difficulty level. On the other hand, new measuring techniques with XFEL such as SFX and the undamaged analysis have brought about innovation for protein crystallography. I would like to discuss the possibilities and prospects of BioSAXS measurement using XFEL in this presentation.

2SKA-4 QM/MM 法による金属酵素の構造活性相関の研究
QM/MM studies on structure-function relationships of metalloenzymes

Yasuteru Shigeta (*Center for Computational Sciences, University of Tsukuba*)

In recent years, real-time structure-function relationships of complicated systems have been elucidated due to technological innovations such as X-ray free electron lasers (XFEL). In theoretical analyses, detailed reaction mechanisms of metalloenzymes have been clarified using QM / MM methods. Thus, the distance between experiment and theory is getting closer and closer. In this presentation, we will discuss about geometrical and electronic structures of four different metalloenzymes, (1) cytochrome c oxidase (CcO), (2) alternative oxidase (AOX), (3) bilirubin reductase (BOD), and (4) oxygen-evolving complex (OEC) in photosystem II in relation to their functions.

2SKA-5 X 線自由電子レーザーによるタンパク質中で起こる化学反応の三次元動画
Three-dimensional movie of chemical reactions in proteins captured by X-ray free electron lasers

So Iwata (*Kyoto Univ. Grad.Sch.Med.*)

The advent of the X-ray free-electron laser (XFEL) has enabled visualization of movements and reactions in protein that could not previously be achieved using conventional crystallography. We are currently developing a data collection system focusing on time-resolved x-ray crystallography at the Japanese XFEL facility, SACLA. At the first target, we chose a light-driven proton pump, bacteriorhodopsin (bR) and uncovered structural changes throughout the protein during its proton transport occurring from nanoseconds to milliseconds following photoactivation using our pump-probe experimental device. Recently, we are successful in capturing enzyme reactions using a new-type injector that can mix substrates and microcrystals rapidly.

2SKA-6 フェムト秒ラマン分光による光受容タンパク質の超高速構造ダイナミクスの観測
Ultrafast structural dynamics of photoreceptor proteins revealed by femtosecond Raman spectroscopy

Tahei Tahara[1,2] ([1]*Molecular Spectroscopy Laboratory, RIKEN*, [2]*RIKEN Center for Advanced Photonics (RAP)*)

Time-resolved Raman spectroscopy is a very powerful method to study the dynamics of simple and complex molecules. Utilizing the stimulated Raman process in the time- or frequency-domain, we are now able to track femtosecond dynamics of the molecules with time-resolved Raman spectroscopy. A big advantage of femtosecond Raman spectroscopy over femtosecond IR spectroscopy is that we can selectively detect the change of a specific part of the large molecules (i.e., chromophore) owing to the resonance Raman effect, by tuning the Raman probing wavelength to the electronic transition of the chromophore. In this presentation, we report on our recent femtosecond Raman studies on the primary processes of photoreceptor proteins.

2SMA-1 ATP 結合部位の合理設計: 分子モーターを理解する試み
Rational Design of ATP Binding Site: An Attempt to Understand Molecular Motor

Takahiro Kosugi[1,2,3] ([1]*CIMoS, IMS*, [2]*SOKENDAI*, [3]*ExCELLS*)

Rotary molecular motors rotate by hydrolyzing ATP at each interface of subunit in order. Rational design of the binding and hydrolysis site leads to be a better understanding of the rotational mechanism and probably controlling the speed or scheme. First, we focused to create the binding site and designed De Novo ATP binding protein from scratch. In this study, several rules for ATP binding were found. Second, by using the rules for ATP binding, we introduced ATP binding site to non-catalytic interface, which does not bind ATP, of a molecular motor, V_1-ATPase. Researches for this redesigned V_1-ATPase revealed several reasons why non-catalytic interface of V_1-ATPase lost ATP binding affinity.

2SMA-2 生物分子モーターの再デザイン
Re-design of biomolecular motors

Ryota Ibusuki[1], Akane Furuta[2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[2], **Ken'ya Furuta**[2] ([1]*University of Hyogo*, [2]*National Institute of Information and Communications Technology*)

Despite the decades of studies, the essential mechanisms of linear biomolecular motors remain unclear. A limitation is that neither motors nor cytoskeletal tracks can be rationally re-designed for systematic research. To overcome this limitation, we constructed new variety of ‘possible’ molecular motor systems where new molecular motors and tracks are re-designed based on naturally-occurring protein building blocks. The tracks can be cytoskeletal tracks that are not compatible with original motors or even artificial DNA nanotubes. We successfully constructed new hybrid motors and show that they can walk along actin filaments or DNA nanotubes. Our strategy opens the way to systematic research on the mechanisms of motors and to nanotechnological applications.

2SMA-3 Design and evolution of synthetic nucleocapsids

Marc Lajoie (*Univ Washington, Molecular Engineering and Sciences*)

Nucleic acid encapsulation is a fundamental requirement of life, elegantly solving the challenges of evolution in a complex biochemical environment by coupling genotype to phenotype and protecting genetic material. In the simplest examples, viruses use capsids to surround their genomes, but they remain delicate systems that are difficult to re-engineer for therapeutic applications. Based on simple first principles, we have created synthetic nucleocapsids that encapsulate their own RNA genome, providing a “blank slate” to design and evolve desired properties for drug delivery, while avoiding the safety risks and engineering challenges associated with viruses.

2SMA-4 集積型遺伝子チップの構築
Construction of integrated gene chip

Hisashi Tadakuma (*IPR Osaka University*)

In synthetic biology, the design of gene expression requires devices that alter the output depending on the situation. Inspired by RNA viruses that contain both enzymes and substrate genes, and express specific genes through architectural modalities, we integrated a T7 RNA polymerase enzyme and genes onto a DNA-origami base scaffold. The integration approach allowed us to construct orthogonal and rational gene expression elements. We further integrated reprogrammable logic gates so that the nano-chip responds to water-in-oil droplets and computes their small RNA (miRNA) profiles, which demonstrates that the nano-chip can function as a gene logic-chip. Our approach of component integration on a nano-chip may provide the basis for an integrated gene expression circuit.

2SMA-5 Structural DNA Nanotechnology: Complex Self-Assembly and Applications

Yonggang Ke (*Emory University*)

A key challenge in nanotechnology is to design and fabricate nanostructures and nanodevices, for basic science and for practical applications. Bottom-up structural DNA nanotechnology has attracted significant attentions due to its programmability and its precise control of matter at nanoscale. I will discuss our most recent results of making complex DNA nanostructures and dynamic DNA devices: particularly, how we can construct fully addressable GDa nanostructures from modular DNA components called “DNA bricks”, and a new type of DNA structure transformation driven by information propagation. In addition, I will also share our works on single-molecule biosensors, drug delivery, and fabrication of functional nanoscale materials by using DNA self-assembly.

2SMA-6 RNA synthetic biology and nanotechnology to program cells

Hirohide Saito (*Kyoto University, CiRA*)

Gene delivery using RNA rather than DNA may be safer owing to a reduced risk of genomic integration. By designing microRNA (miRNA)-responsive synthetic mRNAs, (miRNA switches), we developed a method for high-resolution identification, separation, and purification of target mammalian cells.Possible applications using new RNA technologies will be discussed.

2SOA-1 脱窒菌の一酸化窒素還元酵素：反応機構と分子進化
Bacterial Nitric Oxide Reductases: Reaction Mechanism and Molecular Evolution

Yoshitsugu Shiro (*U. Hyogo*)

Bacterial nitric oxide reductases (NOR) are iron-containing membrane-integrated enzymes, which catalyze the nitric oxide (NO) reduction to generate nitrous oxide (N2O) in denitrification process. The enzymes share the same ancestor with cytochrome oxidases, O2-reductase, in molecular evolution of the respiratory enzymes. We have studied two bacterial NORs, cytochrome c dependent and quinol dependent enzymes (cNOR and qOR), to establish the reaction mechanism of the NO reduction, and the proton transfer coupled with the enzymatic reaction by using the crystallographic and time-resolved spectroscopic techniques. On the basis of these results, we will explore the molecular evolution of the respirator enzymes from NO-reductases to O2-reductases.

2SOA-2 Development of Raman spectroscopic measurement system for analyzing the enzymatic reaction with gaseous substrate

Koji Nishikawa, Yuka Nakagawa, Yoshiki Higuchi, Takashi Ogura (*Grad. Sch. Sci., Univ. Hyogo*)

Hydrogenases catalyze the reversible conversion of H2 to H+ and e- in vivo. To get an insight into the detailed mechanism of the reversible oxidation of H2 by hydrogenases, two reactions have been investigated as follows; H/D isotope exchange reaction and nuclear spin isomer conversion reaction. The Raman method enable us to trace the time course of the reaction continuously in a non-invasive way. Therefore, we have developed Raman spectroscopic system specialized to study the reaction whose substrates are gaseous molecules. Using the system, we measured the H/D isotope exchange reaction catalyzed by [NiFe] hydrogenase from Deslufovibrio vulgaris Miyazaki F. In this talk, I will discuss the kinetics of H/D isotope exchange reaction by [NiFe] hydrogenase.

2SOA-3 Picobiology of metalloproteins: Vibrational spectroscopic studies of cytochrome *c* and hydrogenase

Shun Hirota[1], Hulin Tai[1], Yoshiki Higuchi[2], Sachiko Yanagisawa[2], Takashi Ogura[2] ([1]*Grad. Sch. Sci. Tech., Nara Inst. Sci. Tech.*, [2]*Grad. Sch. Sci., Univ. Hyogo*)

Vibrational spectroscopy is a powerful method to investigate the properties and reaction intermediates of biomolecules. Cytochrome *c* (cyt *c*) transfers electrons in mitochondria, whereas the peroxidase activity of cyt *c* increases by the interaction with cardiolipin in the inner mitochondrial membrane. The resonance Raman spectra of cyt *c* are investigated to elucidate the reaction properties of cyt *c*. [NiFe] hydrogenase is a metalloenzyme that catalyzes one of the simplest molecular reactions, reversible oxidation of dihydrogen to two protons and two electrons. By combining infrared spectroscopy with light irradiation, we elucidated a new intermediate in the [NiFe] hydrogenase reaction cycle.

2SOA-4 時間分解振動分光法によるチトクローム酸化酵素のプロトンポンプ機構
Proton pumping mechanism of cytochrome *c* oxidase by time-resolved vibrational spectroscopy

Satoru Nakashima (*Nara Institute for Science and Technology*)

Dynamic behavior of protonated carboxyl groups involved in proton transfer for proton-pumping and oxygen reduction by cytochrome *c* oxidase (CcO) was investigated using a custom-designed highly sensitive time-resolved IR (TRIR) facility. TRIR spectra were measured as CO difference spectra of intermediates present from 100 ns to 4.5 ms after initiation of the reaction. The 1740 cm-1 peak, assignable to D51 at the exit of the proton pumping system of CcO, appears upon oxidation of the heme a, and gives experimental evidence for protonation of D51. The 1762 cm-1 peak observable in the **P** state is assignable to a carboxyl group coordinated to Mg2+ in the proposed pumping-proton storage structure. These data which clarify the dynamics of proton-pumping mechanism of CcO.

2SOA-5 Oxygen Activation Mechanism by Copper Monooxygenases and Models

Shinobu Itoh (*Osaka University*)

Dioxygen-activation mechanisms by copper enzymes have long been an important research subject in bioinorganic chemistry. Several types of copper/active-oxygen species have been developed in synthetic modeling studies to provide significant insights into the reactive intermediates involved in the biological systems. Using these copper active-oxygen complexes, we have explored detailed oxygenation mechanisms of aliphatic and aromatic compounds, providing important information to the enzymatic reaction mechanisms as well as catalytic oxidation/oxygenation mechanisms in synthetic organic chemistry.

2SOA-6 イオン液体中における小分子活性化の分光学的アプローチ
Spectroscopic study on the activation of CO_2 and N_2 in an ionic liquid

Hideki Masuda (*Nagoya Institute of Technology*)

The activation of small molecules, such as CO_2 and N_2, was electrochemically performed in an ionic liquid, which was studied by IR, resonance Raman and SEIRAS measurements. The electrochemical reduction of CO_2 on the ionic liquid-modified Au electrode containing imidazole gave methanol at a low over-potential, which was studied by SEIRAS measurement. The electrochemical oxidation of N_2-coordinated Mo(I) complex in organic solvent cleaved the N-N triple bond to afford the nitride molybdenum complex, although the N-N triple bond cleavage is usually carried out through the reduction reaction. The reaction behavior was followed by IR and resonance Raman spectroscopies.

2SOA-7 シトクロム *c* 酸化酵素における触媒反応のピコバイオロジー
Pico-biology in Catalytic Reactions of Cyotchrome *c* Oxidase

Teizo Kitagawa (*Grad.Sch.Sci.Univ.Hyogo*)

Ogura determined the resonance Raman spectra of all the intermediates in O2 reduction by cytochrome oxidase. The important point was identification of the P intermediate between the Fe(II)-O2 (A) and the Fe(IV)=O (F) intermediates. All the biochemists in this field had thought it to be Fe(III)-O-O-Cu(II), but Ogura denied it from his experiment with 18O16O. Its oxidation level of heme a3 should be Fe(V) and therefore, possibilities of Fe(V)=O, Fe(IV)=O of porphyrin cation radical or Fe(IV)=O coupled with an amino acid cation radical were present. In the last case it remained to be explained why its Fe(IV)=O stretching frequency is different from that of F intermediate. Ogura investigated Fe(IV)=O porphyrin model compounds and finally solved it in terms of picobiology.

2SBP-1 Deconstruction and reconstruction of cell polarity networks

Fumio Motegi[1,2,3] ([1]*Temasek Lifesciences Lab.*, [2]*Mechanobiology Institute*, [3]*National Univ. of Singapore*)

Cell polarity, the generation of cellular asymmetries, is necessary for diverse processes during animal development. A hallmark of polarized metazoan cells is the segregation of partitioning-defective (PAR) proteins into distinct compartments at the cell cortex. The design principle that governs local molecular interactions among PAR proteins into global cellular patterning remains elusive. Here we deconstruct the molecular circuits in the Caenorhabditis elegans cell polarity network and reconstruct them in a non-metazoan cell system. Our findings provide the simplest network that executes spatially self-organized polarization, and will permit synthetic control of cell polarity programs in living cells.

2SBP-2 微小管の構造変化による細胞内物質輸送の極性制御
Conformational switching of microtubule as the basis for the polarized intracellular transport

Yasushi Okada[1,2] ([1]*Center for Biosystems Dynamics Research (BDR), RIKEN*, [2]*Dept Phys & Univ Biol Inst (UBI), Univ Tokyo*)

Kinesin-1, the founding member of the kinesin superfamily of proteins, is known to use only a subset of microtubules for transport in living cells. This biased use of microtubules is proposed as the guidance cue for polarized transport in neurons, but the underlying mechanisms are still poorly understood. Here we report that there is positive feedback in the binding of kinesin to GDP-microtubule, which spontaneously produces high affinity microtubules from other low-affinity microtubules. X-ray fiber diffraction, fluorescence speckle microscopy and second harmonic generation microscopy collectively demonstrated that the binding of kinesin to GDP-microtubule changes the conformation of GDP-microtubule to a conformation resembling the GMPCPP-microtubule.

2SBP-3 The cytoskeleton as a smart composite material: A unified pathway linking microtubules, myosin-II filaments and integrin adhesions

Rafiq Nisha Bte Mohd[1], Yukako Nishimura[1], Sergey V. Plotnikov[2], Visalatchi Thiagarajan[1], Zhen Zhang[1], Meenubharathi Natarajan[1], Shidong Shi[1], Viasnoff Virgile[1,3,4], Gareth E. Jones[5], Pakorn Kanchanawong[1,6], **Alexander D. Bershadsky**[7] ([1]*Mechanobiology Institute, National University of Singapore*, [2]*Department of Cell and Systems Biology, University of Toronto*, [3]*CNRS UMI*, [4]*Department of Biological Sciences, National university of Singapore*, [5]*Randall Centre for Cell & Molecular Biophysics, King's College London*, [6]*Deparment of Biomedical Engineering, National University of Singapore*, [7]*Department of Molecular Cell Biology, Weizmann Institute of Science*)

Interrelationship between microtubules, actin cytoskeleton and integrin-mediated adhesions is insufficiently understood. Here, we show that apparently contrasting effects of microtubules on two major types of cell-matrix adhesions, focal adhesions and podosomes, are mediated by KANK family proteins connecting the adhesion protein talin with the microtubule tips. Myosin-IIA filaments function as effectors in the microtubule-driven regulation of integrin adhesions. Microtubule uncoupling from the integrin adhesions triggers a release of RhoGEF, GEF-H1, from microtubules, activation of Rho and ROCK and the assembly of myosin-IIA filaments. Subsequent actomyosin reorganization then remodels the focal adhesions and podosomes, closing the regulatory loop.

2SBP-4 3D micro-environmental control around single hepatocytes to induce apico basal polarization and lumenogenesis

Virgile Viasnoff[1] ([1]*National University of Singapore*, [2]*CNRS France*)

The influence of the microenvironment on cell behavior is increasingly recognized. New imaging techniques for cells in their 3D environment are essential to understanding the processes by which they probe and respond to the cues received from their microniches. Here, we present an approach that allows transforming microwells into artificial microniches where the chemical coating, the rheological properties, and the topographical properties are differentially controlled on the top, sides, and bottom of the wells and assembled in a combinatorial way. We show the benefits of this approach in terms of imaging cell polarity development in the context of liver regeneration.

2SBP-5 Collective cell movement driven by cellular torque generation

Takaki Yamamoto[1], Tetsuya Hiraiwa[2], **Tatsuo Shibata**[1] ([1]*RIKEN BDR*, [2]*The university of Tokyo*)

Accumulating evidences indicate that individual cells can exhibit chiral asymmetries, which depend on cytoskeletal structures. It has been also shown that molecular chiral behaviors can actually generate cellular chiral behaviors, such as cytoplasmic flow and torque generation. When such chiral cells form a multicellular system, how can the cellular chiral behavior affect tissue-scale behaviors? In this talk, we will particularly focus on the tissue-scale effect of chiral torque generation of individual cells. we will first discuss how the cellular torque generation can be mathematically described in a tissue scale model. Then, we will show the condition that a collective cell movement arises from cellular torque generation.

2SBP-6 多細胞の自己組織化と発生制御による in vitro での機能的な神経組織形成 Functional three-dimensional tissue formation by in vitro manipulation and multicellular autonomy

Mototsugu Eiraku (*Institute for Frontier Life and Medical Sciences, Kyoto University*)

In recent years, organoid technologies for forming a “mini organ” in a culture dish by recapitulating the development processes has been actively reported. These technologies are expected to be applied to substitution of animal experiments in drug discovery and a future regenerative medicine. In the case of a retinal organoid, the retinal neuroepithelial spontaneously forms a layered structure like the animal retina. In addition, optic cup morphogenesis are similarly recapitulated in vitro. So far, we have developed various neural organoid technologies and studied underlying mechanisms of multicellular self-organization. In this presentation, we will talk about recent progresses in our understanding of multicellular autonomy.

2SBP-7 Quantitative analysis of cellular dynamics in C. elegans embryo

Shuichi Onami (*RIKEN Center for Biosystems Dynamics Research*)

Quantitative information of cellular dynamics is crucial for mechanical modeling of embryogenesis. We developed image-processing based tools for quantitative measurement of cellular dynamics in C. elegans embryos and generated a large collection of quantitative data by using these tools. In this presentation, I will present data-driven modeling of C. elegans embryogenesis by using these data. Cluster analysis-based prediction of basic embryonic functions and quantitative analysis of asymmetric cell division will also be presented.

2SIP-1 Mechanism of Protein Dynamics Revealed by the Combination of Multiple Protein Analyses in Solution

Tadayuki Ogawa, Nobutaka Hirokawa (*Grad. Sch. Med., Univ. Tokyo*)

To describe the protein behavior accurately, multiple analyses should be performed on the target molecule. This talk focuses on the combination of multiple analyses: size-exclusion chromatography, multi-angle light scattering, small-angle X-ray scattering, analytical ultracentrifugation, atomic force microscopy and crosslink mass spectrometry. We discuss the comparison between the determined molar mass value of not only the standard proteins, but of our target molecules as an example. The comparison provides additional information about the target molecule, because the value reflects the dynamically changing states of the target molecule in solution. The combination and integration of multiple methods will permit a deeper understanding of protein dynamics in solution.

2SIP-2 Modern analytical ultracentrifugation for quantitative studies on intermolecular interactions

Susumu Uchiyama[1,2,3] ([1]*Grad. Sch. Eng. Osaka Univ.*, [2]*ExCELLS, NINS*, [3]*IPBS, Guangdong Univ. Tech.*)

Intermolecular interactions in biological systems are typically accompanied by Gibbs free energy changes ranging from 20 kJ/mol to 50 kJ/mol which corresponds to dissociation constant (KD) of mM and nM levels, respectively. Modern analytical ultracentrifugation (AUC) is one of the most powerful methods to estimate quantitative parameters related to intermolecular interactions. Very weak reversible interactions, typically KD of mM can be evaluated quantitatively as a parameter, secondary virial coefficient (B22), by AUC sedimentation equilibrium. Strong interactions such as KD in nM order can be now examined by AUC sedimentation velocity with a fluorescent signal detector. In this symposium, basics and applications of modern AUC will be comprehensively introduced.

2SIP-3 高速原子間力顕微鏡で観る機能中のタンパク質動態
Watching single proteins in action using high-speed AFM

Mikihiro Shibata[1,2] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*)

Structural biology accumulated our knowledge of how proteins function by solving their detailed structures. In addition to this, direct visualizations of single molecules in action could gain our understanding of how proteins function, because most of proteins undergo dynamic conformational changes. High-speed atomic force microscopy (HS-AFM) is a unique technique to directly visualize individual proteins under physiological conditions. HS-AFM studies performed in the last few years provided new mechanistic insight into the functional mechanism of proteins. In this symposium, we will present our latest HS-AFM studies of proteins including, a DNA endonuclease Cas9 [M. Shibata et al. Nat. Commun. 2017.] and calcium/calmodulin-dependent protein kinase II.

2SIP-4 Structural characterization of antibody interactions in situ

Saeko Yanaka[1,2,3], Hiroki Watanabe[4], Rina Yogo[1,3], Hirokazu Yagi[3], Takayuki Uchihashi[4], Koichi Kato[1,2,3] ([1]*Inst. for Mol. Sci.*, [2]*ExCELLS*, [3]*Nagoya City Univ.*, [4]*Nagoya Univ.*)

Antibodies are involved in specific and non-specific interactions with various biomolecular components in the heterogeneous and crowded blood environment. Such promiscuous interactions can significantly influence molecular processes in our immune system. However, little is known about the potential effects of the blood component interactions on the antibody functions. Thus, detailed characterization of antibody structure and interactions in such environment is necessary for understanding the immune system. We employed an integrative approach, including high-speed atomic force microscopy and nuclear magnetic resonance to characterize dynamic antibody interactions. Using these methods, we observed unique antibody-antibody interactions in membrane and blood environments.

2SIP-5 クライオ電子顕微鏡によるタンパク質複合体の構造解析
Structural Analysis of Protein Complexes by Cryo-Electron Microscopy

Akihisa Tsutsumi, Masahide Kikkawa (*Graduate School of Medicine, The University of Tokyo*)

The introduction of the direct electron detector and the development of methods for image analysis has resulted in the “resolution revolution”. Cryo-electron microscopy (cryo-EM) has now become a powerful technique that enables structural analysis at near-atomic resolution. In our laboratory, we installed the latest electron microscopes in last April, and started supporting researchers willing to solve the structures of their target protein (complexes). In this talk, we will explain the workflow of cryo-EM single particle analysis and discuss about its difficulties. We will also present some of the results we have recently obtained.

2SIP-6 連続滴定 SAXS 測定を利用した多成分混合溶液中のタンパク質の構造解析
Structural analysis of multiple-component systems using continuous titration SAXS

Hironari Kamikubo (*MS, NAIST*)

Biological systems contain multiple-components of protein, which sometimes associate and dissociate in a concentration-dependent manner. The amount of each component temporally changes upon external stimuli, resulting in adaptive responses. To investigate the dynamical behavior of the system, we have developed the continuous titration SAXS (tiSAXS) measurements by utilizing micro-fluidics based auto-sampler. Two examples of applications will be shown, where the method was subject to a light-induced signal transduction system and the molecular assembly system involving a multi-domain protein. Here, I would like to introduce how to extract the structural information of each complex in the mixed solution and evaluate the protein-protein interaction in the complex.

2SIP-7 人工タンパク質ナノブロックによる自己集合超分子複合体ナノ構造の創製と解析
Construction and analyses of self-assembling supramolecular complex nanostructures constructed from de novo protein nanobuilding blocks

Ryoichi Arai[1,2] ([1]*Appl. Biol., FTST, Shinshu Univ.*, [2]*CFMD, Shinshu Univ.*)

Recently, we produced a polyhedral protein nanobuilding block (PN-Block), WA20-foldon, to form self-assembling nanoarchitectures (JACS 2015). In this study, we developed extender protein nanobuilding blocks (ePN-Blocks) by tandemly fusing two de novo binary-patterned WA20 proteins with linkers. The ePN-Blocks were analyzed by native PAGE, SEC-MALS, SAXS, and TEM, indicating their formation of various homooligomers. Subsequently, we reconstructed heterooligomeric complexes from extender and stopper PN-Blocks (esPN-Blocks) by denaturation and refolding. The esPN-Block heterocomplexes formed different types of extended chain-like structures. Moreover, AFM imaging demonstrated that the esPN-Block with metal ions further self-assembled into supramolecular nanostructures.

3SAA-1 DNA binding and light-dependent DNA repair abilities of photolyases

Junpei Yamamoto (*Grad. Sch. Eng. Sci., Osaka Univ.*)

Photolyase/cryptochrome superfamily (PCSf) proteins harness blue light in sunlight for maintenance of genome integrity and/or signal transduction. They share common architectures and light-absorbing catalytic center flavin adenine dinucleotide (FAD), but have diverse functions. Photolyases (PLs) are DNA repairing enzymes targeting UV-damaged DNA, cyclobutane pyrimidine dimers (CPDs) and pyrimidine(6-4)pyrimidone photoproducts. In this study, DNA binding and repair abilities of (6-4)-PL, which is obviously distinct from those of CPD-PLs, has been illuminated. An amino acid residue that functions in the specific substrate binding of (6-4)PL would shed light on the molecular origin of the functional turning point of PCSf.

3SAA-2 Differences and similarities in (6-4) photolyase DNA repair pathways

Hisham Dokainish[1], Daichi Yamada[2], Hideki Kandori[2], Akio Kitao[3] ([1]*Theoretical Molecular Science Laboratory, Riken*, [2]*Nagoya Institute of Technology*, [3]*Tokyo Institute of Technology*)

(6-4) photolyase are evolutionally ancient enzymes that maintain genetic integrity. They repair DNA lesions, pyrimidine(6-4)pyrimidone, via a chemically challenging reaction. Despite this importance, the enzyme repair mechanisms is still elusive. Also, previous studies have mainly considered Thymine(6-4)Thymine photorepair mechanism, assuming the transferability to Thymine(6-4)Cytosine. Here, we investigated the repair pathway for both photolesions using unprecedentedly large quantum mechanics/molecular mechanics approach. We propose a new mechanism for both substrates, wherein 5`base and 3`base radicals are formed as reactive complexes in the case of Thymine and Cytosine respectively. Subsequently, water or free-NH3 formation mechanism leads to pyrimidine restoration.

3SAA-3 The undistorted photolyase: photoreduction stages revealed via serial femtosecond crystallography

Manuel Maestre-Reyna (*Inst. Biol. Chem., Academia Sinica*)

For more than two decades, it has been well documented that cryptochromes and DNA-photolyases suffer in-situ photoreduction during X-ray crystallographic data collection. Accordingly, all known crystal structures present ill-defined reaction intermediates. By combining damage free serial femtosecond crystallography (DF-SFX) with other biophysical techniques, here we reveal the structural changes in the undistorted reaction steps of the photoreduction of a class II CPD DNA-photolyase, i.e. oxidized, semiquinone, and hydroquinone, both in the presence and absence of the DNA substrate. These address in detail the stabilization mechanism for the FAD co-factor in its different isoforms, and how the protein moiety may lengthen one state's half-life above the others.

3SAA-4 Light-induced electron (and proton) transfer underlying the activation of cryptochromes and photolyases

Pavel Müller (*CNRS/I2BC*)

Flavoproteins cryptochromes (CRYs) are implied in the regulation of circadian rhythms of both plants and animals and they are evolutionarily derived from DNA repair enzymes photolyases (PLs). In order to perform their respective biological functions, some CRYs and likely all PLs need to be activated by light. Upon photoexcitation, their FAD cofactor abstracts an electron from a chain of three to four tryptophan (and/or tyrosine) residues. Deprotonation of the terminal Trp (or Tyr) cation radical and the subsequent quenching of the resulting neutral radical stabilizes the active semireduced or reduced form of FAD. Similarities and differences in the photoactivation mechanisms of several representative CRYs and PLs will be discussed.

3SAA-5 光回復酵素/クリプトクロムスーパーファミリーの機能転換研究
Functional conversion of photolyases/cryptochrome superfamily (PCSf): Toward finding the ancestor of PCSf

Daichi Yamada (*Nagoya Inst. Tech.*)

Photolyases (PHRs), DNA repair enzymes, belong to the same protein family with cryptochromes (CRYs). Two types of PHRs have been reported: CPD PHR repairs cyclobutane pyrimidine dimers (CPDs), while (6-4) PHR repairs (6-4) photoproducts (PPs). The features distinguishing the substrates of CPD and (6-4) PHRs are not well understood. We attempted functional conversion between PHRs, whose repair signals were monitored by FTIR spectroscopy. We found that a triple mutant of (6-4) PHR can repair the CPD. In contrast, the (6-4) PP was neither repaired by the reverse triple mutation of CPD PHR, nor by the eleven-fold mutant. We conducted further functional conversion experiments including CRY-DASH, and the ancestor of PCSf will be discussed based on these results.

3SBA-1 高圧力で誘起される細胞運動
Pressure-induced activation of the cell motility

Masayoshi Nishiyama (*Kindai Univ.*)

Hydrostatic pressure is an important physical factor to arrange the intracellular conditions. Applied pressures can increase the cell activity or induce cell differentiation. To understand the pressure-induced effects, we have developed a high-pressure microscope to monitor biological samples in real time. It was optimized both for the best image formation and for the stability to hydrostatic pressure up to 150 MPa. Application of pressure dynamically changed the morphology of cultivated cells and the polymerization dynamics of cytoskeletons. Furthermore, high hydrostatic pressure restores the rhythmical beating motion of paralyzed-flagella mutants of *Chlamydomonas*. The present techniques could be extended to study the pressure response of various research targets.

3SBA-2 心筋細胞伸展感受性のマクロ・ミクロ連関
Macro-micro linkages in cardiac response to stretch

Gentaro Iribe (*Grad. Sch. Med. Dent. Pharm., Univ. Okayama*)

When the cardiac muscle is stretched, it contracts more. This simple “Frank-Starling’s law of the heart” is the result of complex interactions among various load-dependent cellular responses. For instance, myocardial stretch activates NADPH oxidase 2 to produce reactive oxygen species, which stimulates ryanodine receptors to increase Ca^{2+} spark rate. These responses may facilitate Ca^{2+} recruitment for contractions against stretch. Also, myocardial stretch hyperpolarizes mitochondrial membrane potential, which is the driving force for ATP production. This response might be beneficial for efficient ATP production against increased load. These load-dependent responses may contribute to Frank-Starling’s law of the heart.

3SBA-3 Combined effects of microgravity and UVB radiation on plant

Jun Hidema[1], Akihisa Takahashi[2] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*Gunma Univ., Heavy Ion Med. Center*)

Plants play an important role in supplying nutrients and oxygen to humans under resource-recycling system in space. It is necessary to understand the short and long term combined effects of gravitational and space radiation including UV on plant. We previously found that repair-enzyme for UV-induced DNA damage or autophagy function play an important role for survival of plant grown under supplementary UVB radiation. So, we investigated the effects of UVB radiation on plant under microgravity condition using 3D clinostat, especially we focus the functions of repair for UVB-induced DNA damage and of autophagy. Mitochondria damage in leaf cells was more induced by microgravity treatment. I discuss about the effects of microgravity on UVB-induced damage in plant.

3SBA-4 線虫の物理的力に対する応答
Response to physical force in *C. elegans*

Atsushi Higashitani (*Grad Schl Life Sci. Tohoku Univ.*)

All living organisms are affected by the gravity of the earth. Furthermore, when the center of gravity changes due to the behavior of motion and movement, a large local force is applied. An individual's physique is shaped over long periods by both external physical stimuli and locomotory gaits. Bone and muscle wasting are inevitable pathophysiological adaptations in microgravity, e.g., spaceflight, and with inactivity, e.g., in the bedridden. The wasting of these tissues is a major obstacle for long-tern space exploration. In this presentation, I would like to introduce our spaceflight experiments, ground based experiments in response to fluid dynamic properties, increased hydrostatic pressure, and temperatures using the nematode C. elegans.

3SBA-5 骨格筋維持における重力の役割―ゼブラフィッシュの宇宙滞在から学ぶこと
Roles of the gravity in the maintenance of skeletal muscle—what we can learn from space stay of zebrafish

Atsuko Sehara (*Institute for Frontier Life and Medical Sciences, Kyoto University, Japan*)

Land animals maintain balanced postures and move opposing the gravity. Staying in the International Space Station causes a rapid decrease in the mass and strength of skeletal muscle of astronauts. In this symposium, we would like to introduce our project named "Zebrafish Muscle". Key questions of this project are whether skeletal muscle atrophy also occurs in zebrafish under the microgravity, and if so, how the microgravity causes skeletal muscle atrophy. Analyses of transcriptome data will illuminate progression of muscle atrophy in space from its initial phase towards the recovery phase after return to the earth for the first time. Based on these data, we will discuss roles of gravity in the maintenance / homeostasis of skeletal muscle.

3SDA-1 筋小胞体カルシウム ATP アーゼ SERCA2b の膜貫通ヘリックス相互作用による制御機構の構造基盤
Structural basis of Sarco/Endoplasmic reticulum Ca2+-ATPase 2b regulation via transmembrane helix interplay

Michio Inoue[1], Nanami Sakuta[1], Satoshi Watanabe[1], Yoshiki Tanaka[2], Ryo Ushioda[3], Yukinari Kato[4], Junichi Takagi[5], Tomoya Tsukazaki[2], Kazuhiro Nagata[3], Kenji Inaba[1] ([1]*IMRAM, Tohoku Univ*, [2]*Grad. Sch. Biol. Sci., NAIST*, [3]*Fac. of Life Sci., KSU*, [4]*Med., Tohoku Univ.*, [5]*IPR, Osaka Univ.*)

Sarco/endoplasmic reticulum (ER) Ca2+-ATPase 2b (SERCA2b) conducts Ca2+ uptake from the cytosol to the ER. In contrast to other SERCA family members, SERCA2b contains a characteristic 11th transmembrane helix (TM11). To elucidate molecular mechanisms of the TM11-mediated SERCA regulation, we determined a crystal structure of SERCA2b. Consequently, TM11 was found to interact weakly with a part of the L8/9 loop and the N-terminus of TM10, thereby inhibiting the SERCA2b activity. SERCA2b dimerises through intermolecular interactions between TM11 domains, of which the disruption enhanced SERCA2b activity. We propose that TM11 serves as a key modulator of SERCA2b activity by fine-tuning the intra- and inter-molecular interactions with neighbouring TM regions in the membrane.

3SDA-2 循環型電子伝達に関わる NDH-1 複合体の構造および相互作用解析
Structure and interaction studies on the cyanobacterial NDH-1 complex involved in the photosynthetic cyclic electron flow

Hideaki Tanaka[1], Keita Umeno[1], Yuko Misumi[1], Ju Yaen Kim[1], Matthias Rögner[2], Takahisa Ikegami[3], Marc Nowaczyk[2], Genji Kurisu[1] ([1]*IPR, Osaka Univ.*, [2]*Ruhr University Bochum*, [3]*Grad. Sch. of Medical Life Science, Yokohama City Univ.*)

The cyanobacterial NDH-1L (NADH dehydrogenase-like 1L) complex is one of the membrane protein supercomplex involved in respiration and CEF (Cyclic Electron Flow) around Photosystem I. Recent studies show that NDH-1L receives electrons from ferredoxin instead of NAD(P)H and one of the soluble subunit of NDH-1L, NdhS, may play a key role in interacting with ferredoxin by forming the acceptor domain. In this study, we have determined X-ray structure of NdhS in order to elucidate the interaction sites between NDH-1L and Fd. And we also identified the interaction sites by NMR measurements.

3SDA-3 てんかん関連リガンド-受容体複合体 LGI1-ADAM22 の構造基盤
Structural basis of epilepsy-related ligand-receptor complex LGI1-ADAM22

Atsushi Yamagata[1], Yuri Miyazaki[2], Hideki Shigematsu[3], Mikako Shirouzu[3], Yuko Fukata[2], Masaki Fukata[2], Shuya Fukai[1] ([1]*Institute for Quantitative Biosciences, Univ. of Tokyo*, [2]*Div. of Membrane Physiology, NIPS*, [3]*RIKEN Center for Biosystems Dynamics Research*)

Epilepsy is one of the most common neurological disorders, which affects 1-2% of the population. LGI1-ADAM22 complex plays critical roles to regulate neuronal excitability as their mutations and autoantibodies to LGI1 cause epileptic disorders. Crystal structures of LGI1 N-terminal leucine-rich repeat domain, the complex between LGI1 C-terminal EPTP domain and ADAM22, and that between full-length LGI1 and ADAM22 provide the detailed information of LGI1-ADAM22 interaction, and reveal the higher-order assembly of LGI1-ADAM22 complex, which is further supported by cryo-EM and SAXS analyses. A pathogenic mutation in LGI1 disturbs the higher-order assembly of the complex, supporting the notion that LGI1 and ADAM22 family proteins function as a trans-synaptic complex.

3SDA-4 電位依存性ホスファターゼ VSP の構造生物学的研究
Structural analysis of voltage-sensing phosphatase (VSP) on the electrochemical coupling

Hirotaka Narita[1], Makoto Matsuda[2], Yasushi Okamura[3], Atsushi Nakagawa[2] ([1]*Nagoya Inst. Tech.*, [2]*Inst. Protein Res., Osaka Univ.*, [3]*Gra. Sch. of Med., Osaka Univ.*)

The voltage-sensing phosphatase, VSP is the first protein to be described as having its catalytic activity controlled by changes in membrane potential. VSP consists of a transmembrane voltage sensor domain (VSD), an inter-domain linker, and a cytoplasmic enzyme region and catalyzes the dephosphorylation of phosphoinositides. However, the molecular mechanism of the coupling between the VSD and enzyme region in VSP is still unclear. In this study, we attempted to investigate the crystal structure of VSP and the effect of structural changes of the linker on substrate binding in VSP using ITC assays. Our findings suggest that conformational change in the inter-domain linker plays a key role in substrate-binding and coupling in membrane potential and phosphatase activity.

3SDA-5 [NiFe]ヒドロゲナーゼがもつ鉄硫黄クラスターの新規機能
Novel functions of the Fe-S clusters in the [NiFe]-hydrogenases

Yasuhito Shomura (*Grad. Sch. Sci. and Eng., Ibaraki Univ.*)

The NAD^+-reducing soluble [NiFe]-hydrogenase (SH) function as a redox regulator in the cytoplasm of some bacteria by coupling oxidation of NADH and reduction of two protons. Our recent X-ray crystallographic study has shown that the air-oxidized state of SH takes a unique coordination geometry that has never been observed for the other [NiFe]-hydrogenases. The detailed structure comparison between the air-oxidized (inactive) and H_2-reduced (active) states has suggested that the rearrangement of the coordination geometry of the Ni-Fe cluster is triggered by the repulsion between the side-chain of Arg58 and the proximal [4Fe-4S] cluster. The mechanism is likely to be beneficial to protect the Ni-Fe cluster from O_2 attack under prolonged oxidized environments.

3SDA-6 Toll 様受容体の構造生物学
Structural biology of Toll-like receptors

Umeharu Ohto, Toshiyuki Shimizu (*Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

Toll-like receptor (TLR) evokes a first line of defense mechanism called innate immunity against microbial infections by recognizing a wide range of microbial products. The extracellular domain of TLR consisting of leucine-rich repeat is responsible for ligand recognition and transduces signals into the intracellular compartment through the transmembrane and intracellular TIR domains. The structural biology of TLRs in this decade has mainly focused on their extracellular domain and revealed how each TLR recognizes the specific ligand and dimerizes in ligand-dependent manner. In this symposium, I will provide an overview of structural biology of TLRs and discuss the similarities and differences in the ligand recognition and activation mechanism of TLRs.

3SEA-1 Taste perception approached by biophysics and structural biology

Atsuko Yamashita (*Grad. Sch. Med. Dent. & Pharm. Sci., Okayama University*)

Chemical senses begin with interactions between environmental chemicals and chemosensory receptors. In the case of taste perception, taste substances in foods are recognized by taste receptors in the oral cavity. So far, studies of taste perception have been mostly limited in the field of physiology or molecular biology. Recently, we succeeded to prepare a recombinant protein of the extracellular ligand-binding domain of a taste receptor, T1r2a/T1r3 heterodimer from medaka fish. Our biophysical and structural-biological approaches to the protein deepened the understandings about the mechanisms of recognition of taste substances and subsequent signal transduction by the receptor, also explaining several characteristics of taste perception.

3SEA-2 甘味受容体のアゴニスト/アンタゴニスト特性
Agonistic/antagonist properties of sweet taste receptor

Keisuke Sanematsu[1,2], Noriatsu Shigemura[1,2], Yuzo Ninomiya[1,2,3] ([1]*Sect. Oral Neurosci., Grad.Sch. of Dent. Sci., Kyushu Univ.*, [2]*Div. Sensory Physiol. R & D TAOS, Kyushu Univ.*, [3]*Monell Chem. Senses Ctr.*)

Sweet taste is mediated by the sweet taste receptor, TAS1R2 + TAS1R3, with multiple biding sites for structurally diverse chemical substances. However, much remains unknown about the molecular mechanisms underlying agonistic/antagonistic properties of the sweet taste receptor. Using the sweet receptor assay, we examined the sweet-suppressing effect of gymnemic acids (GAs) and sweet-modifying effect of miraculin. As a result, GAs inhibited the sweet taste receptor through the interaction between glucuronosyl group of GAs and the transmembrane domain of human TAS1R3. Intracellular acidification was required for the effect of miraculin. In this symposium, we also show a novel finding of inactivating the sweet receptor.

3SEA-3 霊長類味覚受容体の機能多様性
Functional diversities of primate taste receptors

Hiroo Imai (*Primate Research Institute, Kyoto University*)

Most animals avoid bitter compounds and prefer sweet compounds. However, some primates ingest food items which are bitter to humans and/or not sweet to humans, suggesting a species-specific sense of taste. To reveal the mechanism of specific taste phenotypes, we conducted genetic and functional analysis of taste receptors in cultured cells along with behavioral analysis. We found species-specific sensitivities of bitter taste receptors, some of which are supported by the behavioral test. Interestingly, some of the receptors showed specific responses to natural ligands due to the amino acid substitutions. These differences in receptor sensitivities highlight the relevant tastes of compounds in the habitat of primates and contribute to their survival and adaptation.

3SEA-4 Taste cells lacking synapses open a wide pore channel for rapid neurotransmission of tastes

Akiyuki Taruno (*Dept. Mol. Cell Physiol., Kyoto Pref. Univ. Med.*)

Type II taste bud cells responsible for perception of sweet, bitter, and umami tastes, fire action potentials in response to taste stimuli and exhibit non-synaptic, conductive release of ATP (neurotransmitter) to the afferent nerves. However, the molecular mechanism underlying the conductive ATP release was unknown as the synaptic release was considered as the only mechanism for action potential-dependent ATP release. We have demonstrated that a CALHM1/CALHM3 hetero-hexamer is a novel fast-activating voltage-gated ATP-permeable channel, and it mediates the ATP release from type II taste cells required for neurotransmission of tastes. Our studies also provide the first demonstration of an ion channel-mediated mechanism of fast purinergic neurotransmission.

3SEA-5 光遺伝子操作による単一の糸球体の活性により誘因される恐怖行動の探索
Immobility responses are induced by photoactivation of single glomerular species responsive to fox odour TMT

Harumi Saito[1,2,3], Hirofumi Nishizumi[2,3], Satoshi Suzuki[3], Hideyuki Matsumoto[4], Nao Ieki[4], Takaya Abe[5], Hiroshi Kiyonari[5,6], Masahiko Morita[7], Masahiko Morita[7], Nozomi Hirayama[8], Takefumi Kikusui[8], Kensaku Mori[4], Hitoshi Sakano[2,3] ([1]*Brain Science Institute, Tamagawa University*, [2]*Department of Brain Function, Faculty of Medical Sciences, University of Fukui*, [3]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, [4]*Department of Physiology, Cellular and Molecular Physiology, Graduate School of Medicine, The University of Tokyo*, [5]*Genetic Engineering Team, RIKEN, Center for Life Science, Technologies*, [6]*Animal Resource Development Unit, RIKEN, Center for Life Science Technologies*, [7]*Image Processing Research Team, RIKEN,*, [8]*Department of Animal Science and Biotechnology, School of Veterinary, Medicine, Azabu University*)

Fox odour 2,4,5-trimethyl thiazoline (TMT) is known to activate multiple glomeruli in the mouse olfactory bulb (OB) and elicits strong fear responses. In this study, we screened TMTreactive odourant receptors and identified Olfr1019 with high ligand reactivity and selectivity. In the channelrhodopsin knock-in mice for Olfr1019, TMT-responsive olfactory-cortical regions were activated by photostimulation, leading to the induction of immobility, but not aversive behaviour. Our results demonstrate that the activation of a single glomerular species in the posterodorsal OB is sufficient to elicit immobility responses and that TMT-induced fear may be separated into at least two different components of immobility and aversion.

3SEA-6 Male glandular odorants evoke female attractive behavior among ring-tailed lemurs (*Lemur catta*): A putative pheromone in primates

Mika Shirasu[1,2] ([1]*Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences,*, [2]*ERATO Touhara Chemosensory Signal Project*)

Ring-tailed lemurs use olfactory cues for conspecific communications. Male lemurs mark their scent from the antebrachial gland. Our behavioral assay indicated that females sniff the males' antebrachial secretions longer during the breeding season than during the nonbreeding season. By examining seasonal changes in volatiles of antebrachial secretions using gas chromatography mass spectrometry, three C12 and C14 aldehydes significantly increased during the breeding season in a testosterone-dependent manner. Moreover, females were significantly interested in a mixture of these three aldehydes. This study suggest that these aldehydes are key male glandular odorants involved in the attractiveness of males to females during the breeding season among lemurs.

3SFA-1 シンギュラリティ生物学による神経変性疾患へのアプローチ
Approach to neurodegenerative disease by singularity biology

Hiroko Bannai[1,2], Misa Kanatani[3], Sumihiro Maeda[4], Matsumi Hirose[2], Akihiko Takashima[3], Katsuhiko Mikoshiba[2] ([1]*JST PRESTO*, [2]*RIKEN CBS*, [3]*Gakushuin Univ, Faculty. Sci.*, [4]*Keio Univ. Sch. Med.*)

"Tauopathies", including Alzheimer's disease (AD), are a class of neurodegenerative diseases characterized by aggregated pathological Tau protein. Working mechanism of pathological Tau protein has been well characterized. However, the function of physiological tau has not been fully clarified yet. Tau is soluble and is abundant in axons under physiological condition, while several lines of evidence suggest the involvement of Tau in synaptic function in dendrites. Using a "quantum dot-single particle tracking (QD-SPT)", we examined the effect of Tau knockout on the stability of synaptic neurotransmitter receptors. Here we report that the surface receptors on neurons from TauKO mice showed impaired diffusion dynamics compared with wild type.

3SFA-2 シンギュラリティ生物学を定量する情報理論的アプローチ
Information theoretic approach to quantify singularity in biology

Tamiki Komatsuzaki[1,2] ([1]*Hokkaido Univ. RIES MSC*, [2]*ENS de Lyon*)

Singularity in biology involves phase-transition-like behavior triggered by a small set of elements in the whole system. To characterize the singularity requires spatiotemporal information of the system and some scheme to measure causality between the event in question and the set to trigger the event. We present our recent information theoretic approach to identify the state of cells and address the possible scheme to reveal singularity in biology.

3SFA-3 シンギュラリティ細胞を探索する技術：散乱光を使った非染色細胞状態計測
A Challenges to use scattering lights for singularity biology

Tomonobu M. Watanabe (*RIKEN, BDR*)

In singularity biology, people have to explore a rare cell showing unique state that triggers the singularity phenomenon. There are a lot of ways to define the cellular state, such as omics information, expression/locations/movements of specific proteins, and so on. We have developed methods to do it based on scattering microscopy. This talk introduces our technologies by utilizing three types of scattering lights. For example, we are now challenging to predict gene expression patterns from spectral shapes of Raman scattering of cells in combination with machine learning techniques. Second harmonic generation enables to investigate structure on fiber proteins like microtubule and actmyosin, and Brillouin scattering reflects elasticity of observing sample.

3SFA-4 シンギュラリティ生物学へ向けて：１細胞の観察・分取とそのシークエンシング解析
An automated system of single cell picking and sequencing for singularity biology

Katsuyuki Shiroguchi[1,2,3] ([1]*RIKEN BDR*, [2]*RIKEN IMS*, [3]*JST PRESTO*)

Dynamic behavior of cells such as motility, activation, and cell-cell interaction may be observed using an optical microscope. But understanding molecular mechanisms behind these behaviors and/or cell states which may be investigated by whole gene expression analysis is often limited mainly due to technical difficulties. We have been developing a measurement system based on single-cell picking which enables whole gene expression analysis (RNA-seq) for each cells whose behaviors are observed under an optical microscope. This system is automated for high throughput measurements, and is useful to study the molecular mechanisms behind the dynamic behavior of cells. I will discuss advantages of this system for studying, e.g., rare cells focused in “Singularity biology”.

3SFA-5 高速・高拡張性全脳イメージングシステム FAST：アンバイアスで仮説フリーに脳内のシンギュラリティを検出する手法へ
High-speed and scalable whole-brain imaging system FAST: unbiased and hypothesis-free approach to detect singularity in the brain

Hitoshi Hashimoto[1,2,3,4], Atsushi Kasai[1], Kaoru Seiriki[1,5], Takanobu Nakazawa[1,6] ([1]*Lab. of Mol. Neuropharmacol., Grad. Sch. of Pharmaceutical Sci., Osaka Univ.*, [2]*Center for Child Mental Dev., United Grad. Sch. of Child Dev.*, [3]*Div. of Biosci., Inst. for Datability Sci.*, [4]*Dep. of Transdimensional Life Imaging, Open and Transdisciplinary Res. Initiatives*, [5]*Inst. for Academic Initiatives, Osaka Univ.*, [6]*Dep. of Pharmacology, Grad. Sch. of Dentistry, Osaka Univ.*)

Whole-brain imaging and systems analyses of entire brains at subcellular resolution are prerequisites for understanding the mechanisms for brain function and dysfunction. However, it is still challenging due to the trade-offs between imaging speed and spatial resolution. To overcome the issue, we have been attempting to increase the imaging throughput and relieve bottlenecks in the procedure, and recently developed an automated imaging system with unprecedented speed and no limitations related to size, FAST (block-face serial microscopy tomography). The FAST system provides new opportunities for unbiased and hypothesis-free approaches that would contribute to a better understanding of the anatomical and functional brain networks.

3SFA-6 シンギュラリティ生物学による自己免疫疾患制御機構の解明
Singularity cell research in autoimmunity

Taku Okazaki (*Div. Immun. Reg., Inst. Adv. Med. Sci., Tokushima U.*)

About a trillion of lymphocytes are strictly regulated not to attack self-tissues to cause autoimmune diseases in our body by the mechanism called immune tolerance. However, certain forms of autoimmune diseases are found in about 5% of people, indicating that immune tolerance can be broken at certain points in our long life. Because each lymphocyte expresses a different antigen receptor with different antigen specificity, the break-down of immune tolerance is likely initiated by a limited number of lymphocytes by unknown cue at unknown time point. We have been trying to identify and characterize causative lymphocytes that somehow escape from immune tolerance and cause autoimmune diseases, focusing on roles of inhibitory co-receptors.

3SGA-1 Single molecule fluorescence tracking at 10-μs resolution: Application to protein folding and functional dynamics

Satoshi Takahashi, Hiroyuki Oikawa (*IMRAM, Tohoku Univ.*)

Time series fluorescence information of single proteins has been combined with the results of molecular dynamics calculation to obtain realistic understanding of protein dynamics. However, the time resolution of the previous methods of fluorescence detection was limited to at most 100 μs. We recently developed a new method of single molecule fluorescence detection, and achieved the time resolution of 10 μs and the observation time of 5 ms. The method revealed significant structural heterogeneity for the unfolded state of the B domain of protein A as well as ubiquitin, suggesting the coupling of the local structures and the long range distance distribution. We will discuss the structural transition of F1-ATPase examined by the method.

3SGA-2 蛋白質の複雑なコンフォメーション変化の解明を目指して-ハイブリッドアプローチ Toward the elucidation of complicated conformational change in proteins by using a hybrid approach

Kenji Iwasaki[1], Atsushi Matsumoto[2], Atsushi Kawaguchi[3] ([1]*IPR, Osaka Univ.*, [2]*QST*, [3]*Grad. Sch. Comprehensive Human Sciences, Univ. of Tsukuba*)

Our cryo-EM facility at IPR, introduced by AMED's BINDS program, achieved 2.3-Å-resolution analysis, which is the highest resolution in Japan and a world-leading advance. Beyond the atomic-resolution analysis of static molecular structures, we are trying to determine heterogeneous structures by using SPA technique and computer simulations. The main target is an RNA-dependent RNA polymerase of influenza virus. Although the molecule's large and complicated conformational change, which is directly correlated with the transcription and relocation process, has been determined by crystal structure analysis and biochemical experiments, much uncertainty remains about how domain arrangements occur and how conformation change differs between transcription and replication.

3SGA-3 一分子ダイナミクス理解のための高速 AFM データの画像処理と定量解析 Image Processing and Quantitative Analysis of High-Speed AFM data for studying single-molecule dynamic

Takayuki Uchihashi (*Department of Physics, Nagoya University*)

Recent advance in high-speed atomic force microscopy (HS-AFM) has enabled us to directly visualize diverse dynamic events on biological molecules. Image processing and quantitative analysis are critical factors to accentuate the dynamic biological phenomena on the HS-AFM images and understand the biological significance of the dynamic events observed. Optimum image processing and analytical ways are highly dependent on the target molecules and, therefore, we need to develop an appropriate analytical method on a case-by-case basis. In this talk, I will discuss about basic image processing techniques handling HS-AFM data and demonstrate quantitative analysis in which we have ever succeeded for revealing single-molecule dynamics.

3SGA-4 Controlled Environment Nano-Imaging Free From Radiation Damage by X-ray Laser Diffraction

Yoshinori Nishino[1], Takashi Kimura[1], Akihiro Suzuki[1], Yasumasa Joti[2], Yoshitaka Bessho[3] ([1]*RIES, Hokkaido Univ.*, [2]*JASRI*, [3]*Inst. Bio. Chem., Academia Sinica*)

Coherent diffractive imaging (CDI) is a growing technique in photon science. CDI has been demonstrated to be a powerful tool for visualizing cells and organelles using synchrotron radiation. X-ray free-electron lasers (XFELs) with femtosecond pulse durations further extends the ability of CDI to achieve spatial resolution beyond the conventional radiation-damage limitation. We are developing a technique called pulsed coherent X-ray solution scattering (PCXSS), a form of X-ray CDI for solution sample using focused XFELs. We have demonstrated successful PCXSS experiments for live cells, gold nanoparticle self-assemblies, etc. We will present our recent studies toward imaging uncrystallized biomolecules in solution.

3SGA-5 Temporal hierarchy in the energy landscape of adenylate kinase folding/unfolding

J. Nicholas Taylor (*Research Institute for Electronic Science, Hokkaido University*)

We use information theory to quantify the folding and unfolding behavior of adenylate kinase at various denaturant concentrations. Single-molecule FRET trajectories were analyzed with a combination of change-point detection and rate-distortion theory, extracting a set of conformational states that naturally considers the effects of measurement and sampling errors. Energy landscapes are constructed as a function of observation time scale, revealing multiple partially-folded conformations at small time scales that merge into a single state at longer observation times. We also examine state-dependent photobleaching behavior in the trajectories and discuss nonequilibrium features that may arise from unbalanced photobleaching rates.

3SGA-6 Hybrid modeling approaches to study structures and dynamics of biological systems

Florence Tama[1,2] ([1]*Nagoya University*, [2]*RIKEN*)

Integrative approaches are becoming mainstream for structural biology. X-ray crystallography provides atomic detailed information that is necessary for biochemical understanding while others, such as cryo-EM, AFM, spectroscopy, and XFEL CDI, can provide near native or time resolved measurement in exchange of structural resolution. For data integration to take advantage of complementary information, computational modeling and data analysis play an essential role. I will present some new developments of modeling approaches utilizing these low-resolution data.

3SHA-1 Intramolecular vibrations complement robustness of the primary charge separation in Photosystem II reaction center

Akihito Ishizaki (*Institute for Molecular Science*)

Energy conversion of oxygenic photosynthesis is triggered by the primary charge separation (CS) in photosystem II reaction center (PSII RC). We investigated impacts of intramolecular vibrations on the primary CS in the PSII RC by combining quantum dynamic theories of condensed phase electron transfer with quantum chemical calculations to evaluate Huang-Rhys factors. We report that individual vibrational modes play a minor role in promoting the CS, contrary to the discussion in recent publications. However, such small contributions add up to make a big change of the rate, resulting in subpicosecond CS almost independent of the driving force. The intramolecular vibrations complement robustness of the CS against inherently large static disorder of the electronic energies.

3SHA-2 極低温顕微分光による光化学系複合体の単一分子分光
Single Molecule Spectroscopy of Photosystem Complex by Cryomicroscopy

Yutaka Shibata (*Tohoku Univ. Chemistry*)

We developed a cryogenic microscope in which an objective lens is set inside the cryostat heat-insulating vacuum chamber. This novel design enables us to use an objective lens with a high NA of 0.9. We have applied this system to observe fluorescence spectra of single photosystem I (PSI) trimers at 80-100 K. The study revealed that fluorescence from single PSI trimers show intermittent intensity fluctuations (blinking). The blinking is enhanced upon pre-oxidation of the primary electron donor, P700. Phylloquinone, the secondary electron acceptor in PSI, is inferred to be in different redox states depending on the P700 redox state, and responsible for the different blinking amplitudes. We will explain the molecular mechanism of the blinking based on the PSI structure.

3SHA-3 Crystal structure of PSII in the intermediate states and possible mechanism for the O=O bond formation

Michi Suga, Jian-Ren Shen (*Research Institute for Interdisciplinary Science*)

PSII catalyzes photo-oxidation of water into dioxygen through the S-state cycle of the OEC. This mechanism remains obscure owing to the lack of intermediate-state structures determined at atomic resolution. We prepared PSII in the S3 state by providing two-flash illumination into micro-sized crystals at room temperature and determined its structure at 2.35 Å resolution by using time-resolved SFX with an XFEL. An isomorphous difference map between the two-flash-illuminated and dark-adapted states revealed clear structural changes in both regions around the electron donor and acceptor sides. These structural changes allowed us to propose the mechanism of O=O bond formation between O5 and O6 and the proton exit path used when the S-state advances.

3SHA-4 光合成初期反応の電子スピン画像解析
Electron Spin Polarization Imaging Analyses of Primary Charge Separations in Photosynthesis

Yasuhiro Kobori[1,2], Hiroki Nagashima[1], Reina Minobe[2], Masashi Hasegawa[2], Hiroyuki Mino[3], James Norris[4] ([1]*Molecular Photoscience Research Center, Kobe Univ.*, [2]*Graduate School of Science, Kobe Univ.*, [3]*Graduate School of Science, Nagoya Univ.*, [4]*Dep. Chem. Univ. of Chicago*)

In initial events of the photosynthesis by higher plants, the photosystem II generates photoinduced primary charge-separated (CS) states, ultimately leading to the water oxidation. To understand mechanism of the efficient generation of the initial CS state, we have characterized cofactor geometries and electronic coupling of the photoinduced primary CS state by developing electron spin polarization imaging methodology by the time-resolved EPR method. It has been revealed that that the electronic coupling between the charges is significantly weak in the CS state, showing an importance of regulated cofactor-cofactor electronic interaction to inhibit the energy-wasting charge-recombination after the primary electron-transfer processes.

3SHA-5 光化学系 II における水分解酸素発生反応の分子機構
Molecular mechanism of the water-splitting and oxygen-evolving reaction in photosystem II

Keisuke Saito (*RCAST, Univ. Tokyo*)

In photosystem II (PSII), light-induced water-splitting reaction occurs at the Mn4CaO5 cluster. The reaction proceeds with oxidation states of the cluster called the Kok cycle: S0-S1-S2-S3-S4-S0, where the subscript represents the number of oxidation steps accumulated. In this study, we calculated molecular structures and their energy of the cluster at the S0-S4 states in the PSII protein environment by using the quantum mechanical/molecular mechanical approach. Assuming that the product dioxygen molecule originates from a corner-oxo O4 and a water molecule W1 ligating Mn1 of the cluster, we rationally explained molecular mechanisms of 1) proton releases from the substrate water, 2) dioxygen formation, and 3) substrate water incorporation.

3SHA-6 光合成光エネルギー変換におけるプロトン共役電子移動の赤外分光解析
Infrared analyses of proton-coupled electron transfer in photosynthetic light-energy conversion

Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

Light-induced electron transfer coupled with proton transfer is essential in the energy-conversion process of photosynthesis. In particular, water oxidation taking place in photosystem II (PSII), which is performed through a light-driven cycle of five intermediates (Si states: i = 0-4), consists of complex processes of electron and proton transfer, and hence its molecular mechanism remains to be clarified. Quinone reduction by the electrons from water is also coupled with proton transfer and shows reaction rates dependent on pH. Here, our recent researches using Fourier transform infrared difference and time-resolved infrared spectroscopies to resolve the regulation mechanisms of the proton-coupled electron transfer reactions in PSII are introduced.

3SIA-1 Watching single proteins dancing at biological membranes

Ming Li (*The Institute of Physics, Chinese Academy of Sciences*)

It is challenging to assess protein-membrane interactions because of the lack of appropriate tools to detect position changes of single proteins in ~4 nm space of biological membranes. We recently developed methods which we termed SIFA and LipoFRET, respectively, to track both vertical and lateral dynamic motion of singly-labeled membrane proteins in supported lipid bilayers and at liposome membranes. SIFA and LipoFRET are capable of monitoring three-dimensional movements of the fluorophore-labeled protein not only inside but also near the lipid membrane.

3SIA-2 1 分子イメージングを用いた GPCR の薬理学に向けて
Toward single-molecule imaging-based pharmacology of G protein-coupled receptors

Masataka Yanagawa (*Cell. Info. Lab., Riken*)

G protein-coupled receptors (GPCRs) are major drug targets. However, it is difficult to measure the effects of a drug by monitoring each receptor molecule in a living cell. Here, we show that single-molecule imaging analysis provides an alternative method for assessing ligand effects on GPCRs. First, we demonstrate that the diffusion coefficient of metabotropic glutamate receptor 3 is tightly coupled with its functional states including G protein binding and clathrin-dependent endocytosis. Then, we confirmed the generality of diffusion-function relationship to many GPCRs regardless of the coupling specificity to G proteins. We will discuss the future applicability of the single-molecule imaging in pharmacology and drug screening.

3SIA-3 Biophysics of intercellular nanotube

Minhyeok Chang[1], Jaeho Oh[1], **Jong-Bong Lee**[1,2] ([1]*Department of Physics, POSTECH*, [2]*Department of Interdisciplinary Bioscience & Bioengineering, POSTECH*)

A novel cellular bridge connecting cells, termed “intercellular nanotube (INT)”, has been recognized as a new pathway for the distant transport of cytoplasmic components, virus, and pathogenic substances between donor and acceptor cells. INT can be initiated by direct contact between the filopodia that are slender actin-rich plasma membrane protrusions. However, it is not yet known how such a fine structure can extend over several hundred micrometers and sustain robust for several hours in culture. We recently visualized filopodia that evolves into a single actin-based INT connecting two distinct cells via the intermediate state of a helical structure. We will introduce our biophysical studies of INT formation in living cells.

3SIA-4 Resolving nano-architectural dynamics of molecular assembly in living cells with emission dipole orientation imaging

Tomomi Tani (*Marine Biological Laboratory, Woods Hole*)

Fluorescent single molecule imaging provides spatial and temporal dynamics of individual biological molecules in living cells. Nano-precision positioning of fluorophores in single molecule imaging has helped break down the spatial resolution barrier of conventional light microscopy. Such super-resolution approaches, however, have missed the opportunity, and requirement, to consider the molecular orientation of fluorescent labels, which is important for studying the dynamics of protein structures. We have developed the Instantaneous FluoPolScope, which detects changes in the orientation and position of proteins of interest with single molecule sensitivity, based on the fluorescence intensity and polarization of fluorophores that are rigidly connected to those proteins.

3SIA-5 Single-Molecule fluorescence studies on cotranscriptional folding and intrinsic termination Dynamics

Sungchul Hohng (*Department of Physics and Astronomy, Institute of Applied Physics, and National Center of Creative Research Initiatives, Seoul National University*)

The dynamic nature of transcription has not been fully captured in conventional experimental approaches. I will present single-molecule fluorescence assays that can monitor the cotranscriptional RNA folding and intrinsic termination of E. coli.

3SIA-6 Single-molecule mechanical (un)folding of RNA: Unravelling mRNA structure's role in translational regulation

Gang Chen (*Division of Chemistry and Biological Chemistry, School of Physical and Mathematical Sciences, Nanyang Technological University*)

Ribosomal frameshifting is a translational recoding mechanism utilized by cells and viruses for the regulation of mRNA halflife and for the expression of multiple protein from one mRNA. We carried out single-molecule mechanical (un)folding studies of ribosomal frameshifting pseudoknots found in Simian Retrovirus type 1 (SRV-1). Cooperative mechanical unfolding rates of the seven SRV-1 pseudoknots studied are inversely proportional to frameshifting efficiency in a wide range of stretching forces, consistent with the fact that ribosome is a force-generating molecular motor with helicase activity. Frameshifting can be stimulated by enhancing through (i) directly improving the local base pairing interactions and (ii) indirect energetic coupling by triplex formation.

3SIA-7 Studies on the dynamics and regulation of 30-nm chromatin fiber by single molecule force spectroscopy

Wei Li[1], Ping Chen[2], Ming Li[1], Guohong Li[2] ([1]*National Laboratory for Condensed Matter Physics and Key Laboratory of Soft Matter Physics, Institute of Physics, Chinese Academy of Sciences*, [2]*National Laboratory of Biomacromolecules, CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences*)

In eukaryotes, the packaging of genomic DNA into chromatin plays a critical role in gene regulation. However, the dynamic organization of chromatin fibers and its regulatory mechanisms remain poorly understood. Using magnetic tweezers, we reveal that the tetranucleosomes-on-a-string appears as a stable secondary structure which is attenuated by histone chaperone FACT. Furthermore, we reveal that FACT's subunit SSRP1 is responsible for maintenance of the nucleosome integrity by holding H3/H4 tetramer on DNA. In contrast, the large subunit SPT16 destabilizes the nucleosome structure by displacing H2A/H2B dimers. Our findings provide mechanistic insights by which the two subunits of FACT coordinate with each other to fulfill its functions.

3SIA-8 Mechanical lifetime of biomolecules under physiological forces

Shiwen Guo[1], Qingnan Tang[2], **Jie Yan**[1,2] ([1]*Mechanobiology Institute, National University of Singapore*, [2]*Department of Physics, Faculty of Science, National University of Singapore*)

Current understanding of mechanical lifetime of biomolecules has mainly been based on data obtained at high force regime (> 100 pN), while how force affects the mechanical rate under physiological forces remains unclear. I will show that at physiological forces, the entropic conformational fluctuation of the molecules plays a crucial role in determining the mechanical rate, resulting in a strong dependence on the structural-elastic properties of the molecule. A new analytic theoretical framework is developed, which can be applied to understand mechanical rate over a much wider force range. We demonstrate the applications of this model by applying it to explain complex force-dependent lifetime data for several molecules reported in recent experiments.

3SKA-1 小さなスパイダーマン： 糸をひっぱるバクテリア
Tiny Spider-Man: Bacteria pulling fibers

Daisuke Nakane, Takayuki Nishizaka (*Dept. Phys., Gakushuin Univ.*)

Type IV pili (T4P) is a super-molecular machine observed in prokaryotes. Cells repeat the cycle of extension of T4P fibers, surface attachment and retraction to drive twitching motility. The dynamics was driven by two ATPases present at the base part of core complex, and PilT was thought to be responsible for disassembly of T4P fibers. Here we demonstrated that PilT activity is not required for the retraction of T4P in the thermophilic bacterium Thermus thermophiles. Even in the absence of PilT and its paralog, the T4P fiber showed the movement toward cell at a speed of 1 μm/s in response to physical property of the environment. This PilT-independent retraction provides insights into the mechanical sensing of T4P system that may common in bacteria.

3SKA-2 生命の根幹の理解に向けた ミニマムゲノム細菌における CRISPRi の開発
Toward understanding of the Fundamentals of Life: minimal bacterium and inducible CRISPRi

Shigeyuki Kakizawa[1,2] ([1]*JCVI, Synthetic Biology&Bioenergy*, [2]*AIST, Bioprocess*)

Recently a minimal genome bacterium was produced. This cell has only essential genes for growth, and its genome (531 kbp, 473 genes) is the smallest among all known culturable bacteria. This achievement would contribute our deeper understanding of the “fundamentals of life”, however there were still large amount of functional unknown genes (149/473 genes; 31%), suggesting that we still don’t know “how bacteria could grow” nor “how life is alive”. To tackle this problem, we developed inducible CRISPR-interference (CRISPRi) in the minimal bacterium. CRISPRi is a facile method for conditional gene repression that opens the door to analysis of protein function and systematic dissection of genetic programs at the core of cellular life.

3SKA-3 To use light or to avoid it? Light-adaptation strategies in marine bacteria

Susumu Yoshizawa[1,2] ([1]*AORI, UTokyo*, [2]*Grad. Sch. Front. Sci., UTokyo*)

Proteorhodopsin (PR) is a light-mediated proton pump that is found in diverse bacteria and archaea species, and is widespread in marine microbial ecosystems. To date, many studies have suggested the advantage of PR for microorganisms in sunlit environments. The ecophysiological significance of PR is still not fully understood however, including the drivers of PR gene gain, retention, and loss in different marine microbial species. To explore this question we sequenced 21 marine Flavobacteriia genomes of polyphyletic origin, which encompassed both PR-possessing as well as PR-lacking strains. Here, we show that the possession or alternatively the lack of PR genes reflects one of two fundamental adaptive strategies in marine bacteria.

3SKA-4 Investigating the Unique Swimming Style of *Campylobacter jejuni*

Eli J. Cohen, Morgan Beeby (*Department of Life Sciences, Imperial College London*)

In our lab, we study the flagellar motor of Campylobacter jejuni, a leading cause of gastroenteritis worldwide. In contrast to the well-studied flagellum of Salmonella enterica, the C. jejuni flagellum remains relatively poorly understood. In order to swim through the viscous mucus environments it normally colonizes, C. jejuni has evolved a more robust flagellar apparatus capable of generating greater torque than that of Salmonella. In my talk, I will discuss the evolutionary adaptations that have produced the more powerful C. jejuni flagellum. Additionally, I will describe ongoing projects aimed at elucidating the specific morphogenetic features of the C. jejuni flagellum that have given rise to the unique swimming style of this fascinating species.

3SKA-5 The second messenger signaling drives chromosome replication in the asymmetrically dividing bacterium *Caulobacter crescentus*

Shogo Ozaki[1,2], Christian Lori[1], Urs Jenal[1] ([1]*Biozentrum, University of Basel*, [2]*Kyushu University*)

Fundamental to life is the capacity to tune cell division cycle in time and space to generate appropriate numbers of specialized cells. Whereas eukaryotes use cyclins and cyclin-dependent kinases to govern cell cycle progression, equivalent regulatory systems have not been described in bacteria. Here we show that the alpha-proteobacterium *Caulobacter crescentus* uses oscillating levels of the second messenger cyclic diguanylate (cdGMP) to drive its cell cycle. We reveal cdGMP directly binds to the essential cell cycle kinase CckA to switch from the kinase into the phosphatase mode, thereby allowing chromosome replication and cell cycle progression. Thus, we propose cdGMP act as a cell cycle oscillator to drive the cell cycle in a eukaryotic cyclin-like manner.

3SKA-6 Bacterial surface motility and biofilm formation in motile and non-motile bacteria

Andrew Utada (*U of Tsukuba*)

Bacteria in the environment exist either as individual, planktonic cells, or as members of surface-adhered 3D communities, encased in a slimy extracellular matrix, called biofilms. The biofilm lifestyle is fundamental to bacterial ecology and it begins with the initial encounter a bacterium has with a surface. However, different bacteria engage and colonize surfaces differently, depending on their specific ecological niche. We utilize time-lapse microscopy, single-cell tracking algorithms, and microfluidics to control the local environment, image, and analyze the first stages of biofilm formation and to compare the strategies of motile and non-motile bacteria. A greater understanding of the biofilm lifestyle will possibly lead to strategies to control biofilms.

3SMA-1 *Corynebacterium glutamicum* によるヘム取り込み反応の構造基盤
Structural Basis for Heme Uptake Reaction in *Corynebacterium glutamicum*

Shigetoshi Aono[1,2] ([1]*NINS, ExCELLS*, [2]*NINS, IMS*)

Heme uptake machinery of Corynebacteria consists of heme binding proteins, HtaA and HtaB, and the heme transporter HmuTUV. In this work, we have studied the structural and functional relationships of HtaA, HtaB and HmuT in C. glutamicum. Sequence analysis identified a conserved region (CR) of approximately 150 amino acids that is duplicated in HtaA and present in a single copy in HtaB. We have determined the crystal structures of the N-, and C-terminal CR of HtaA (HtaA-N and HtaA-C, respectively) and HtaB. HtaA-C and HtaB show similar global structures to HtaA-N. The key residues for heme-binding and recognition including the axial ligand of heme and residues involved in the hydrogen bonding interactions with heme are conserved among HtaA-N, HtaA-C, and HtaB.

3SMA-2 anammox 反応を担う金属タンパク質
Metalloproteins responsible for anammox reaction

Daisuke Hira (*Fac. of Biotech. and Life Sci., Sojo Univ.*)

Efficient and economical removal of nitrogen compounds is being becoming a major issue in wastewater treatment. Anaerobic denitrification processes performed by bacteria, i.e., heterotrophic denitrification and anaerobic ammonium oxidation (anammox), are have providing provided some technological solutions. Anammox reaction mechanism composed of three redox reactions has been proposed. The metalloenzymes catalyzing these reactions have been investigated and called them nitrite reductase (NIR), hydrazine synthase (HZS) and hydrazine-oxidizing enzyme (HZO) also called hydrazine dehydrogenase (HDH), respectively. In this presentation, we present our biochemical studies on the metallproteins involved in these redox reactions of anammox.

3SMA-3 脱窒にみられる金属タンパク質複合体による効率的な連続化学反応
Effective consecutive chemical reactions catalyzed by metalloprotein complex in denitrification

Takehiko Tosha (*RIKEN SPring-8*)

Microbial denitrification is a part of global nitrogen cycle, and is a step-wise reduction process from nitrate to dinitrogen gas; nitrate => nitrite => nitric oxide => nitrous oxide => dinitrogen. These four consecutive chemical reactions are catalyzed by four metalloenzymes unique to denitrification. It is hypothesized that the metalloenzymes involved in denitrification concertedly work for effective consecutive chemical reactions. In fact, we found that NO-producing nitrite reductase (NiR) forms a complex with NO-decomposing nitric oxide reductase (NOR) to suppress the diffusion of NO. On the basis of the structure-guided mutagenesis on NOR, the mechanism of effective consecutive chemical reactions in denitrification.

3SMA-4 スーパーオキシドディスムターゼを通じたバクテリアにおける銅イオン動態の理解
A mechanism on copper acquisition of bacterial Cu/Zn-superoxide dismutase

Yoshiaki Furukawa (*Dept. of Chem., Keio Univ.*)

Cu/Zn-superoxide dismutase (SOD1) is an antioxidant enzyme that can eliminate superoxide radicals. The enzymatic activity of SOD1 requires the binding of copper and zinc ions and also known as an important factor to inhibit the development of several diseases such as cancer and diabetes. A bacterial counterpart of SOD1 (called SodC) can also eliminate superoxide radicals in vitro, but its physiological function remains obscure. Furthermore, eukaryotic SOD1 acquires its copper ion by a copper chaperone, CCS, but no CCS homologs have been identified in prokaryotes; therefore, the activation mechanism of SodC also remains unknown. In this symposium, I will present our recent data on the activation mechanism of SodC with its possible function in vivo.

3SMA-5 硫酸性環境に生息する単細胞性紅藻を利用した貴金属回収
Study on the effective and selective recovery of precious metal ions using a sulfo-thermophilic red alga, Galdieria sulphuraria

Ayumi Minoda (*Fac. of Life and Environ. Sci., Univ. of Tsukuba*)

Galdieria sulphuraria is a unicellular microalga, which is one of the few eukaryotes capable of adapting to a very acidic environment. G. sulphuraria cells efficiently absorbed precious metals from strong acids through biosorption. Single-cell analysis by using time-resolved inductively coupled plasma mass spectrometry and X-ray absorption fine structure showed the alteration of metal recovery mechanism in G. sulphuraria dependent on pH of the solution. We will report the recovery mechanism of precious metal ions in G. sulphuraria.

3SMA-6 微生物による金属腐食
Metal corrosion by microorganisms

Satoshi Wakai (*Grad. Sch. Sci. Tech. Innov., Kobe Univ.*)

Microbiologically influenced corrosion, also called microbial corrosion and biocorrosion, refers to the corrosion of materials caused or promoted by microorganisms. Recently, many novel causative microorganisms were isolated in various environments. Of these, iron-corrosive methanogen Methanococcus maripaludis KA1 was isolated from bottom water in an oil reservation tank, and can grow with metallic iron as sole electron donor. The iron-corrosive strain KA1 produced methane during the corrosion with carbon dioxide. In contrast, it generated molecular hydrogen during the corrosion without carbon dioxide. Interestingly, this strain has genes encoding hydrogenase with secretion signal. Probably, this extracellular hydrogenase relates to hydrogen-producing corrosion ability.

1A1330* *Spiroplasma eriocheiris* 遊泳運動に関係する 5 つの MreB の機能及び構造解析
Structural and functional analyses of five MreB proteins involved in swimming motility of *Spiroplasma eriocheiris*

Daichi Takahashi[1], Aya Kodama[1], Katsumi Imada[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Univ. Osaka City*, [2]*Grad. Sch. Sci., Univ. Osaka*, [3]*OCARINA, Univ. Osaka City*)

Spiroplasma eriocheiris swims by a unique mechanism, in which kinks propagate along its helical body. The helical shape is formed by at least six cytoskeletal proteins including Fibril, a *Spiroplasma* specific protein, and five MreB proteins (MreB1-MreB5), bacterial actin. To elucidate the role of the five MreB proteins, we individually expressed them as recombinants in *Escherichia coli*. The cells expressing MreB1, MreB2, MreB3 or MreB5 showed elongated cell morphology, and linear filamentous structures were observed in lysates of the cells. MreB1, MreB2, MreB3 and MreB5 were expressed in soluble form. MreB3 and MreB5 were purified and crystallized. The purified MreB3 formed filament in the presence of glycerol, indicating that MreB3 can polymerize alone.

1A1342* マイコプラズマ・ガリセプティカム滑走運動の詳細測定
Detailed measurements of gliding behavior in *Mycoplasma gallisepticum*

Masaki Mizutani[1], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*)

Mycoplasma gallisepticum, an avian pathogenic bacterium, glides on animal tissue surfaces by using a unique motility system. The gliding machinery of *M. gallisepticum* is totally different from that of *Mycoplasma mobile*, a well-studied system. To clarify *M. gallisepticum* gliding system, we focused on the gliding behaviors and direct energy source. We measured the gliding movements by using optical microscopy and analyzed them. *M. gallisepticum* straightly glided at a velocity of 0.27 μm/s without the rolling of cell body. A cytoadhesion inhibitor sigmoigally deceased the cell binding, indicating the drag force of cell. Peameabilized cells showed gliding movements only under ATP existing conditions, suggesting that the gliding movement is driven by ATP.

1A1354* 細胞内温度動態における微小管の寄与の検討
Investigating the contribution of microtubule on intracellular temperature dynamics

Takashi Yanagi[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ of Tokyo*, [2]*JST, PRESTO*)

Recent studies have shown that intracellular environmental possesses unique thermal dynamics, which might significantly influence cellular activities. However, the mechanism of this phenomenon is unclear. We hypothesized the contribution of microtubule to the intracellular energy dynamics. In this study, we performed temperature measurement in microtubule disrupted cells by using fluorescence thermometer under infrared laser irradiation or mitochondrial thermogenesis. We found that microtubule was essential in increasing of temperature of cell upon endogenous and exogenous heat souse application, and heat-dependent cell function such as mRNA granule formation. These results suggest that microtubule might be a mediator between intracellular heat source and biomolecules.

1A1406* A mechanical effect of oriented actin fibers on the nuclear morphology during osteogenic differentiation of mesenchymal stem cell

Masashi Yamazaki[1], Shota Iwakura[2], Manabu Numao[1], Hiromichi Fujie[1,2], Hiromi Miyoshi[1,2] ([1]*Grad. Sch. Syst., Tokyo Metro. Univ.*, [2]*Faculty Syst., Tokyo Metro. Univ.*)

It is known that actin cytoskeleton plays an important role in regulation of differentiation of mesenchymal stem cell (MSC). However, the details about the mechanical effect of actin fibers on the cell nucleus remain to be clarified. In this study, we indicated that orientation intensity of actin fiber on the top of nucleus increased as osteogenic differentiation. And the orientation angle of the actin fiber coincided with the direction of long axis of the nucleus in the initial stage of osteogenic differentiation. However, this tendency disappeared as culture time proceed. It could be suggested that tensile forces generated by the oriented actin fiber on the top of the nucleus affect the nucleus morphology during the initial stage of osteogenic differentiation of MSC.

1A1418* Helicity formed by actin homologs in swimming bacterium, Spiroplasma

Yuya Sasajima[1], Isil Tulum[1,2], Makoto Miyata[1,2] ([1]*Graduate School of Science, Osaka City University, Japan*, [2]*The OCU Advanced Research Institute for Natural Science and Technology (OCARINA), Osaka City University, Japan.*)

Spiroplasma swims by switching the cell helicity, based on its special internal structures involving five MreBs, a bacterial actin, and Fibril specific to genus Spiroplasma. To elucidate the role of MreBs in the swimming, we analyzed the effects of MreB depolymerization and energy depletion. The cell helicity switched into three different states according to the conditions. The isolated internal structure, helical ribbon, was a bundle of thin filaments, and its helicity was lost by MreB depolymerization. These results suggest that MreBs interacting with fibril forms helical ribbon which drives the helicity-switching with energy consumption. Structural analyses of isolated Fibril are undertaken.

1A1430 Focal adhesions of cells to the matrix are mediators and targets of cooperative activity of microtubules and actomyosin cytoskeleton

Yukako Nishimura[1], Nisha Bte Mohd Rafiq[1,5], Sergey V. Plotnikov[2], Visalatchi Thiagarajan[1], Zhen Zhang[1], Meenubharathi Natarajan[1], Shidong Shi[1], Virgile Viasnoff[1,3,4], Gareth E. Jones[5], Pakorn Kanchanawong[1,6], Alexander D. Bershadsky[1,7] ([1]*MBI, NUS*, [2]*Dept. of Cell and Syst. Biol., Univ. Toronto*, [3]*CNRS UMI*, [4]*Dept. of Biol. Sci., NUS*, [5]*Randall Center for Cell and Mol.Biophys., KCL*, [6]*Dept. of Biomed. Eng., NUS*, [7]*Dept. of Mol. Cell Biol., WIS*)

How microtubules regulate integrin-mediated adhesions during cell migration is poorly understood. Here, we show that the effects of microtubules on focal adhesions is mediated by KANK family proteins connecting the adhesion protein talin with microtubule tips. Microtubule trapping by focal adhesions modulates the release of the microtubule-associated RhoGEF, GEF-H1 from microtubules. GEF-H1 stimulates Rho/ROCK signaling axis, which augments formation of myosin-IIA filaments. Myosin-IIA filaments in turn operate as effectors controlling focal adhesions by generating mechanical forces that induce the growth of these structures. Thus, cross-talk between microtubules and myosin-IIA filaments via KANKs and GEF-H1 is essential regulator of focal adhesions.

1A1448 Mechanical stress modulates the homeostasis of periodontal ligament

Ayano Fujita[1], Masatoshi Morimatsu[1], Masayoshi Nishiyama[2], Shogo Takashiba[1], Keiji Naruse[1] ([1]*Grad Sch of Med, Dent and Pharma Sci, Okayama Univ*, [2]*Department of Physics, Kindai Univ*)

Periodontal ligament (PDL), which connects the teeth to the bone, is always exposed to mechanical stress such as occlusal force. We study the effects of stretch and pressure on PDL cells. We cultured PDL cells under uniaxial cyclic stretch. After 4 hours, PDL cells and actin fibers were aligned in the vertical direction to the stretch axis. These results suggested that mechanical stress regulate the orientation of PDL cells to support the teeth. We used high hydrostatic pressure microscope to observe PDL cells under the high pressure conditions. As a result, high pressure contracted PDL cells, but did not change the actin stress fibers. Our data suggested that excessive occlusal force induces the collapse of PDL.

1A1500* 肝線維症における肝星細胞活性化とメカノセンシング
Hepatic Stellate Cell Activation and Mechanosensing in Liver Fibrosis

Mutsuko Arimoto[1], Takaaki Sumiyoshi[2] ([1]*KIT*, [2]*Kansai Univ.*)

Hepatic stellate cells (HSCs) play a key role in liver fibrosis. Primary cultured HSCs isolated from normal rodents' liver show morphological change after 2-3-day cultivation on plastic culture dish. In 2011, Olsen et al. suggested the cause of this HSC activation is stiffness of plastic. Indeed, each organ has own proper stiffness: the stiffness of normal liver, fibrotic liver and culture dish are about 1kPa, 20kPa and 10x7kPa, respectively. Here we evaluated the involvement of integrin, TGF-beta and GPR91 in stiffness-induced HSC activation by using their inhibitors. We determined gene expression levels of alpha-SMA and type1 collagen both are marker of myofibroblast by qRT-PCR. Morphological change of HSCs and cell proliferation were observed under microscope.

1A1512* デスミン中間径フィラメントを包含する細胞サイズ液滴の変形と突出
Deformation and protrusion of cell-sized droplets containing intermediate filaments of desmin

Yoshiya Miyasaka, Koji Ito, Kuniyuki Hatori (*Grad. Sch. Sci. Eng., Yamagata Univ.*)

Although cytoskeletons play a key role in cell dynamics, the obvious role of intermediate filaments (IFs) remains unclear. We examined the assembly of the IF protein, desmin, inside water-in-oil droplets under a fluorescence microscope. Desmin assembly induced protrusion and deformation of the droplets in the absence of other substances. The probability of these changes increased up to 30% with an increase in desmin concentration up to 1 mg/mL. Actin assembly rarely induced such changes. The coexisting desmin and actin also exhibited similar deformations, wherein the assembled actin and desmin were co-located. These results indicate that assembly forces of IFs can induce morphological changes, like cell deformations, and desmin interacts with actin filaments.

1A1524* アクチン束化タンパク質 fascin の成長円錐ラメリポディアの弾性率に対する寄与
Contribution of actin bundling protein fascin to the elasticity of lamellipodial region in the growth cone

Minami Tanaka[1], Yuki Fujii[2], Ryoki Ishikawa[3], Kazumi Hirano[4], Takaharu Okajima[2], Kaoru Katoh[4] ([1]*Grad. Sch. Life & Env. Sci., Univ. Tsukuba*, [2]*Grad. Schl. Inform. Sci & Tech. Univ., Hokkaido*, [3]*Gunma Pref. Coll. Health Sci*, [4]*Bio Mes Res. Inst., AIST*)

Growth cone movements at the tip of growing neurites are controlled by dynamics of actin cytoskeletons (filopodial actin bundles and lamellipodial actin meshwork). Fascin is well known to bundle actin filaments in filopodia. Fascin is also present in actin meshwork in lamellipodia but is not well studied. Actin meshwork is too small to be observed with conventional optical microscopy. Here, we observed lifeact-labeled actin meshwork and GFP-fascin simultaneously with superresolution (two camera SIM) after application of drugs which enhanced phosphorylation of fascin. As the phosphorylated fascin was dissociated from actin bundles, actin bundles were separated into filaments. Furthermore, using AFM, we estimated contribution of the actin bundles to cell elasticity.

1A1536* クシクラゲの巨大複合繊毛を構成する新規タンパク質 CTENO64 の同定と櫛板繊毛の協調的運動における役割
Identification of a novel protein CTENO64 in giant compound cilia in the ctenophore and its role in the coordinated ciliary movement

Kei Jokura[1], Daisuke Shibata[1], Katsushi Yamaguchi[2], Shuji Shigenobu[2], Kogiku Shiba[1], Kazuo Inaba[1] ([1]*Shimoda Marine Res. Ctr., Tsukuba Univ.*, [2]*Functional Genomics Facility, NIBB.*)

Comb plates are giant compound cilia uniquely present in ctenophores. They are composed of tens of thousands of cilia, where all cilia have connected each other by the structures called compartmenting lamellae (CL). Although CL is thought to play an essential role in the synchronous movement of cilia, the molecular structure and function of CL are completely unknown. Here we isolated the comb plates and identified a ctenophore-specific novel protein CTENO64 as components of CL. Immunofluorescence and immunogold electron microscopy revealed that CTENO64 was localized at CL in the proximal region of the comb plates. Gene knockdown by morpholino oligonucleotides in the embryos showed that CTENO64 played an important role in the coordination of multiple cilia.

1A1548 細胞外環境のダイナミックリモデリングが支配する細胞集団行動解析
Spatio-temporal remodeling of microenvironment regulates the directionality of collective cell migration

Masaya Hagiwara[1], Moegi Marumoto[1,2], Hisataka Maruyama[3], Hideki Mori[2], Fumihito Arai[3] ([1]*NanoSquare Research Institute, Osaka Prefecture University*, [2]*Department of Biological Science, Osaka Prefecture University*, [3]*Department of Micro-Nano Systems Engineering, Nagoya University*)

Cells are exposed by physical force from surrounding microenvironments to expand their territory during collective cell migrations. However, little is known how surrounding niche are spatio-temporally remodeled and regulate the collective cell migration. By employing microfabrications and optical tweezers, we quantitatively demonstrated how extracellular matrix (ECM) were spatio-temporary degraded by enzyme secreted from cells as well as repetitive push-pull cellular movement. On the other hand, we revealed cells favorably stay in the site with footprint of other cells. Our study suggests that active remodeling of cellular microenvironments contribute to development of cellular territory as well as maintenance for the original form as a tissue.

1C1330 マスク付きガウス関数による電顕３次元密度マップ内のαヘリックスを認識する手法の開発
Detection of alpha-helices from the 3D EM density map using masked single Gaussian functions

Takeshi Kawabata, Haruki Nakamura, Genji Kurisu (*Inst. Prot. Res., Osaka Univ.*)

The electron microscopy (EM) now provides high resolution 3D density maps with 3-8 Å, which enable us to build a de novo atomic model. We developed the helix detection program using Gaussian mixture model using pre-defined single Gaussian functions corresponding alpha-helices. The strategy was the “multiple-helices global fitting”, however, we now introduced a new algorithm using the iteration of “single-helix local fittings”. The new algorithm employs the ellipsoidal masked region for each Gaussian function. The maximum likelihood method searches regions consistent with a predefined Gaussian function. Detected Gaussian functions of helices are transformed to poly-Ala atomic models, and refined their positions. The new algorithm is faster and more robust.

1C1342 Multiscale Modeling of Bacterial Lipid Recognition in Mammalian Immune Receptor Pathways, and Regulation by Novel Host Defense Peptides

Peter J. Bond (*BII A*STAR Singapore*)

Lipopolysaccharide (LPS) signals the presence of bacterial infection to the Toll-like receptor 4 (TLR4) pathway in the mammalian innate immune system. We have developed multiscale computational models allowing us to trace in near-atomic resolution the complete TLR4 cascade, from LPS extraction at the bacterial envelope, through co-receptor binding, to recognition at the terminal host surface receptor complex. Further, by integrating diverse biophysical data, we have uncovered several novel, multifunctional host defense peptides found naturally during wound healing. Collectively, our work provides insights into mechanisms of inflammatory disease, and could be leveraged to develop new ways to fight bacterial infections and sepsis, a leading worldwide cause of mortality.

1C1354 p53C 末端ドメインのエクストラ・ディスオーダー状態
Extra-Disordered State of p53 C-terminal Domain

Shinji Iida[1], Haruki Nakamura[2], Junichi Higo[3] ([1]*IPR, Osak Univ.*, [2]*DDBJ center, NIG, ROIS*, [3]*Grd. Sch. Sim., Univ. Hyogo*)

When recognizing a partner molecule, intrinsically disordered regions of a protein often employ a flexible binding mechanism. We investigated the disordered p53 C-Terminal Domain (CTD) and one of its partner molecules, S100B, via Multicanonical Molecular Dynamics (McMD) simulations. Our aim is to reveal the binding mechanism of CTD to S100B. We demonstrate that CTD and S100B form a variety of complex structures. Our computational results are supported by experimental results. Furthermore, we estimated the configurational entropic effect of CTD binding to S100B, from which we propose the hypothesis that CTD becomes an extra-disordered state upon binding to S100B.

1C1406 相互作用パターンと機械学習を用いたタンパク質-低分子化合物ドッキング手法の改良
A new method to improve the accuracy for protein-small molecule docking by using interaction pattern fingerprint and machine learning

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In the past decades, machine learning (ML) has been applied to molecular docking for discovery of lead compound from many candidates. A major problem to apply ML is how to define the feature vector. We developed a new docking method by using ML techniques based on our original interaction pattern fingerprint (IPFP) as a feature vector. IPFP was based on knowledge about the known structures of protein-ligand complexes, extracted from the PDB. In this method, we used “Auto-dock” program to predict the candidate structures of complex. Then, the ML technique with IPFP was applied to rearrange order of the ranking. We will evaluate our method by using DUD-E dataset and find an improvement of ROC curves compared with the original Auto-dock result.

1C1418 剛体ドッキングで得られた相互作用部位のアミノ酸配列情報の解析
Analysis of amino acid sequences of protein interaction surfaces by rigid-body docking for known and unknown protein complex pairs

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To understand a mechanism of protein-protein interactions, a profile method was proposed for analysis of protein-protein interactions using rigid-body docking process. Rigid-body docking process gives us a set of many candidate protein complex structures. We have developed a method of interaction fingerprints (IFPs). We used IFPs for investigating differences between protein-protein interactions involved in bacterial chemotaxis systems. Previously, we showed differences between protein pair surfaces of known and unknown interaction protein pairs with profile base information. For more details, in this work, amino acid sequences are used for analyzing protein-protein interaction surfaces. We will discuss properties of differences interaction protein pairs.

1C1430 分子動力学法を用いたタンパク質球状ドメイン外の相互作用メカニズムの解明
Elucidation of the mechanism of protein-protein interaction between regions out of globular domains with molecular dynamics simulations

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Elucidation of the mechanism of protein-protein interaction is a central issue in protein science. In particular, interactions between regions out of globular domains were rarely found and the nature of such interaction remains unknown. This study focused on serial region having more than 5 residues without intramolecular contacts. We defined the floating interaction segment (FIS) where the distance between the nearest heavy atoms of such regions is less than 5 Å. First, we obtained 35 protein complexes with FIS from PDB. We cut out only FIS from each protein and created structure composed of 2 peptides. To examine the stability of these FISs, we performed canonical molecular dynamics for 100 ns. As a result, the stable structure with FIS had beta-sheet and homo-dimer.

1C1448 スーパーコンピューティングによる網羅的タンパク質間相互作用予測法の開発と予測結果データベースの公開
Supercomputing-based exhaustive protein-protein interaction prediction and its open database

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Protein-protein interaction (PPI) plays a core role in cellular functions. We have developed an high-throughput PPI prediction system based on rigid-body protein-protein docking and supercomputing, named MEGADOCK. MEGADOCK can perform faster docking based on its original scoring function and implementation for heterogeneous supercomputers. We applied MEGADOCK to interactome analyses and constructed an integrated database of MEGADOCK predictions, named MEGADOCK-Web. The 7,564 proteins and predicted PPIs are registered. Each protein is annotated with PDB ID, chain, UniProt AC, KEGG Pathway and known PPI pairs. The users can visualize candidate of interaction with query protein on biochemical pathway and predicted complex structure by 3D molecular viewer.

1C1500 室温で凍るソフトマテリアル中の水
Water freezing in soft materials at room temperature

Hiroshi Murakami[1], Yuko Kanahara[2] ([1]*QST, KPSI*, [2]*Nara Women's Univ.*)

Does water freeze in cells ? Cytoplasm exhibits the glassy behavior around room temperature; the experiments, however, were not able to elucidate the state of individual molecules because cytoplasm is crowded with many types of biological macromolecules at high occupancy. This raises a question of how water behaves in cytoplasm and whether or not it exhibits the glassy behavior because the water is the main constituent of cytoplasm. We used a reverse micelle which is a microscopic water droplet covered with surfactant molecules in oil solvent; here, a single water-soluble probe molecule resides in the droplet. Moreover, hole-burning spectroscopy was used to confirm unambiguously whether or not the water surrounding the probe molecule is in a glassy state.

1C1512 細菌とリポソームの融合によるゲノム封入とリポソーム内ゲノムの精製法の開発
Investigation of encapsulation and purification of genome by fusion between liposome and bacteria

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Genome DNA is difficult to handling in vitro, because it can be easily damaged by shearing force of pipetting and also it is easily diffused or aggregated. In this study, we aimed to (1) encapsulate genome in lipid bilayer compartment, called liposomes, to prevent genome from damaging and (2) change inner environment of liposomes after liposome formation. As a result, we found that some liposomes (~15%) were encapsulated proteins and genome DNA after fusion. Also we established the method for forming pore on the liposome membrane temporally by adding streptolysin O (SLO). We showed that TA488 and TA647 proteins (80 kDa proteins) were pass through the membrane. We are now trying to combine these methods to investigate to encapsulate and purify genome in liposomes.

1C1524* 微小液滴内における 1 分子からの DNA 複製
DNA amplification from single molecule in micro-sized droplet

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There is a demand for amplifying large DNA *in vitro* from single molecule. Recently, replication-cycle reaction (RCR) which enables propagation of large circular DNA has been developed. Here we attempted to amplify single molecule DNA in micro-sized water-in-oil droplets. We encapsulated template DNA in the droplet containing the RCR components and incubated. Then, we introduced intercalator dye into droplets. As a result, many droplets show fluorescence, even in which 0 or 1 template DNA is encapsulated. These results indicate that large circular DNA is amplified from single molecule by RCR in micro-sized droplet. It would be extended for use in the application of *in vitro* and single molecule DNA amplification with high throughput.

1C1536* 三次元培養プラットフォームによる気管支分岐パターンの定量解析
Quantitative measurement of developed brunch pattern formation by using in vitro 3D culture platform

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The importance of in vitro 3D culture is emphasizing considerably in cell/tissue culture. However, the lack of experimental repeatability is one of the bottle necks. Here, we have achieved to obtain high repeatability of experimental result by controlling the initial cell cluster shape in Hybrid gel cube (HGC). HGC supplies multi-directional scanning by rotating the cube, which enables to obtain the high resolution imaging and capture whole tissue structure even though a low magnification lens is used. Normal human bronchial epithelial cells were employed to control and the repeatability of developed branch pattern was significantly improved. Then, the multi-scanning supplies quantitative analysis of developed branch pattern formation.

1C1548* 集光フェムト秒レーザー刺激による神経活動の時空間ダイナミクス
Spatio-Temporal Dynamics of Neuronal Spikes Induced by a Focused Femtosecond Laser

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Spatio-temporal dynamics of neuronal spikes in neuronal networks are essential for understanding brain functions. To identify the functional connections in neuronal network, we evaluated cell membrane and following dynamics in neuronal networks induced by femtosecond laser with simultaneous measurements of Ca^{2+} imaging and electrophysiological recoding. After femtosecond laser irradiation with 8 ms, lateral diffusion of cell membrane measured by FRAP was obtained to be 1.06×10^{-4} μm^2/ms, which did not depend on the laser power, suggesting that the mobility of cell membrane was maintained after laser irradiation. Moreover, spiking dynamics in neuronal networks were compared with femtosecond laser-induced stimulation and conventional electrical stimulation.

1C1600* 幅に依存したライン状心筋細胞ネットワークの伝導速度解析
Analysis of Conduction Velocity Depending Width of Line-Networked Cardiomyocytes

Tetsuro Yoshida, Koki Fujii, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

In actual hearts, cardiomyocytes are arranged regularly in line shape. However, dispersed culture of cardiomyocytes are randomly arranged and the conduction velocity is slower than actual hearts. In this study, we constructed different width of line-networked cardiomyocytes on the multi-electrode array system and measured conduction velocity. The narrower width of line-networked cardiomyocytes had the faster conduction velocity, and the wider had the larger fluctuation of conduction velocity. It was suggested that the larger width of line-networked cardiomyocytes had more complicated conduction pathways. Therefore, we expected that the line-networked cardiomyocytes at single cell level have the conduction velocity as actual hearts.

1D1330 Toward Automated Identification and Analysis of Cell Differentiation Stages using Bright Field Microscope Image by Artificial Intelligence

Archana Bajpai, Toutai Mitsuyama (*Artificial Intelligence Research Center, National Institute of Advanced Industrial Science and Technology (AIST)*)

Many researchers in the field of biology must deal with culturing cells which requires daily maintenance work that consumes substantial amount of time and cost. Whereas, bio-industries demand constant supply of a large number of cultured cells for regenerative medicine and novel drug discovery. Having these backgrounds, we are developing an automated cell culturing system using the MAHOLO lab-drodid which performs medium exchange and optic observation of cells. The latter requires an automated computational analyses of microscope images to identify conditions of cultured cells. We acquired cell differentiation time-lapse images of C2C12 and applied several artificial intelligence approaches to extract quantitative features to enable differentiation stage identification.

1D1342* Three-dimensional vesicle motion in complex cytoskeletal network revealed by numerical analysis method

Seohyun Lee, Hideo Higuchi (*Dept. of Physics, Graduate School of Science, The University of Tokyo*)

The mechanism of intracellular transport of a vesicle contains key information, especially for biomedical applications such as drug delivery. Here, we propose a novel numerical method for analyzing the three-dimensional movement of vesicles, and we report the observed detailed feature of vesicle dynamics in a cytoskeletal network structure in terms of the interaction between the vesicle and cytoskeleton. Particularly, when we analyzed the angular and translational dynamics of vesicle, we observed characteristic rotational movements of vesicles detected on the microtubules, which can be interpreted as an obstacle-avoidance movement of vesicle, as a reaction of the vesicle maneuvering its destination while navigating the cytoplasmic area.

1D1354* 演題取り消し

1D1406* mRNA の一分子観察を用いたストレス顆粒形成初期のメカニズム解明
Investigating initiation mechanism of stress granule formation in cells by observing single mRNA molecules

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mRNA is an essential gene product in cells and undergoes various regulations such as stress granule (SG) formation. SG is an mRNA granule formed under stress, inhibiting translation of house-keeping proteins. Previously, it was suggested that heat induces SG formation. However, its molecular mechanism is unknown. In this research, we directly tracked mRNA in COS7 cells after stress induction. mRNA trajectories showed a temporary increase in diffusion coefficient which indicated 60S ribosome dissociation. Furthermore, inducing 60S ribosome dissociation by adding puromycin results in SG formation. These result suggested that 60S ribosome dissociation was an important trigger of subsequent granulation of mRNA.

1D1418* 転写装置 RNA ポリメラーゼ II によるクロマチンの安定化
Chromatin stabilization regulated by transcription machinery

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Chromatin structure and dynamics are crucial factors for gene expression because both factors regulate accessibility of transcription factors to the target gene sequences to be expressed. Generally transcription is thought to occur at decondensed euchromatin. However a relationship between transcription and chromatin dynamics remains unclear. To elucidate their relationship, we performed single-nucleosome imaging in living cells and investigated effects of transcription inhibitors and a conditional rapid depletion of RNA polymerase II on the chromatin dynamics. We demonstrated RNA polymerase II, which binds to DNA, decreased the chromatin dynamics, suggesting chromatin become more stable upon transcription.

1D1430 高速 AFM による天然変性タンパク質 CAMP の構造動態観察
Structural dynamics of the intrinsically disordered protein CAMP revealed by high-speed AFM

Tomoyuki Narita[1], Masanori Ikeda[2], Masahiro Shimizu[3], Kozo Tanaka[2], Noriyuki Kodera[3] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Dept. Mol. Oncol., Inst. Dev. Aging Cancer, Tohoku Univ.*, [3]*WPI-NanoLSI, Kanazawa Univ.*)

Chromosome Alignment-Maintaining Phosphoprotein (CAMP) is an intrinsically disordered protein, and mitotic phosphorylation of CAMP is essential for accurate chromosome alignment. Last year, we directly visualized by high-speed AFM that CAMP molecules take on a shape of two globular domains linked by a long flexible string. To characterize their dynamic molecular features, we here performed the detailed image analysis. The results demonstrated that, upon phosphorylation, the flexible string and the height of the C-terminal globular domain tend to extend and decrease, respectively. This result gains the mechanistic insight into the functional regulation of CAMP induced by phosphorylation. Coarse-grained simulations to deeply interpret the results are currently applied.

1D1448 曲率を持った膜上のタンパク質の集合-解離現象の高速 AFM 観察
High-speed AFM imaging of protein assembly-disassembly on curved membranes

Daiki Ishikuro[1], Akane Goto[1], Takahiro Toyoda[1], Ayumi Sumino[2,3], Mikihiro Shibata[2,3], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ*, [3]*InFiniti, Kanazawa Univ*)

Some proteins recognize and bind to specific curvatures of cell membranes, and the resulting site specific biochemical reactions contribute to cellular functions. To directly observe these phenomena at high spatiotemporal resolution by high-speed AFM, we have been developing AFM-substrates with size-controlled convex and concave shapes. Last year, we reported that these substrates can be fabricated on glass by a Focused Ion Beam lithography and on PDMS by a nanosphere lithography, respectively. Here, we utilized the substrates to directly monitor assembly-disassembly of some membrane associated proteins depending on membrane curvatures. It was also demonstrated that the substrates can be used to induce deformation on biological macro-molecules placed on the substrates.

1D1500 L_p 正則化最尤推定による超解像画像再構成計算を用いた高生体適合性 SPoD-ExPAN 超解像イメージング
Highly-biocompatible superresolution imaging by SPoD-ExPAN with L_p-regularized image reconstruction

Tetsuichi Wazawa, Yoshiyuki Arai, Yoshinobu Kawahara, Takashi Washio, Takeharu Nagai (*ISIR, Osaka Univ*)

We have developed a superresolution imaging technique that is based on SPoD-ExPAN method but provides high biocompatibility and accurate image reconstruction. The present technique exploits a fast photoswitchable protein Kohinoor so that the power density of illumination light is several orders of magnitude lower than that used for conventional superresolution imaging. This reduces phototoxicity during observation, which has been a serious problem in many superresolution imaging techniques. Furthermore, we employ L_p-regularization in the image reconstruction calculation so as to mitigate overcorrection that has occurred in L_1-regularization algorithm used in conventional SPoD-ExPAN. We are trying to perform superresolution observation of dynamic processes in cells.

1D1512* マニピュレーター付き高速 AFM スキャナーの開発
Development of high-speed AFM scanner with manipulator

Jun Takano[1], Shinji Watanabe[2], Toshio Ando[2], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

It is known that protein functions are modulated by external forces (tension and compressive forces). If we can directly observe these modulations induced by the external forces at high spatiotemporal resolution, the mechanistic insight on them would be gained. To realize these observations, here we developed a new high-speed AFM scanner system, in which a manipulation scanner (M-scanner) was additionally installed just adjacent to the imaging scanner (I-scanner). The base of a manipulator needle was glued on the M-scanner, while the other sharp end was gently placed on the surface of the I-scanner. By this setup, we succeeded in applying external force to the targeted objects during high-speed AFM observation. Currently, we apply this scanner system to biomolecules.

1D1524 高速 AFM 観察結果を解析するための粗視化分子動力学計算手法の開発
Development of a method for analyzing high-speed AFM observations by coarse-grained molecular dynamics simulation

Masahiro Shimizu[1], Tomoyuki Narita[2], Noriyuki Kodera[1] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Grad. Sch. Math. & Phys., Kanazawa Univ.*)

While high-speed AFM (HS-AFM) enables direct observation of biomolecules on a substrate surface, the structures and functions of molecules are more or less affected by the surface. Quantitative assessment of the surface effect will greatly help to interpret the molecular behaviors seen in the AFM images. Coarse-grained molecular dynamics simulation (CGMD) is useful to analyze dynamic behavior of biomolecules. Here, we developed a method to reproduce HS-AFM experiment in CGMD where a substrate surface was represented by a charged plane. Using test proteins, we tuned simulation parameters to reproduce the AFM images and analyzed the surface effect on the biomolecules. This method would be also useful for optimizing the experimental condition of HS-AFM observations.

1D1536 Automatic single-neuron reconstruction from fluorescent images

Chi-Tin Shih (*Tunghai University*)

In order to process the fast growing amount of neuroimage data to construct the comprehensive brain networks of animals, we developed a new, fully automatic algorithm to segment single neurons from the fluorescent neural images. The algorithm "NeuroRetriever" contains the following parts: (1) a powerful tracing engine named FAST (Fast Automatically Structural Tracing), (2) the high-dynamic-rage (HDR) thresholding to segment the target neuron, (3) "NeuroSlim" and "Kaleido" algorithms for large scale visualization. NeuroRetriever was applied to the whole dataset of FlyCircuit (www.flycircuit.tw), the largest database for single neuron images of Drosophila. 28,125 single-neuron images were successfully segmented from 22,037 fluorescent raw images.

1D1548* Machine Learning Approaches to Raman Micro-spectroscopic Images

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Raman microscopy, combined with data analysis through machine learning, can be a powerful diagnostic tool for the detailed analysis of complex Raman spectra to detect the critical spectral changes of biomolecules at different states of tissue, especially for the case that the biomarker of a targeted disease is not identified. Dimension reduction (manifold learning) and ensemble-learning-based random forest classification are performed on the Raman hyperspectral images using rat models for predicting fibrosis in non-alcoholic fatty liver disease (NAFLD) and for enhancing the diagnostic capabilities to distinguish the states of tissues at early stages where histological characteristics have not yet been observed.

1E1330* 垂直力成分を決定する in vitro 滑り運動系による肥大型心筋症特異的なトロポミオシン変異体(V95A および D175N)の収縮機能異常の計測
Effect of HCM mutants of tropomyosin on actomyosin interaction by in vitro motility assay determining both horizontal and vertical forces

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Hypertrophic cardiomyopathy (HCM) is a heart disease caused by mutations in sarcomeric proteins in most cases. We have studied two human α-tropomyosin mutants V95A and D175N on the effect of actomyosin interaction with in vitro motility assay, in which the force vector horizontal to the glass surface as well as the vertical component are determined (Ishii et al., 2018, PLoS ONE 13(2); e0192558). In addition, sliding velocity was measured. The study was conducted at varying pCa in the range of 4.0 and 9.0, and 50 mM ionic strength at 24°C. While both mutations cause the same pathology and they increased sliding velocity at pCa 8-9 (relaxation), our results indicate that the maximum sliding force, cross-bridge duty ratio and cooperativity may be different for each mutant.

1E1342* 心機能に適した心筋ミオシンの集団的性質
Collective behaviors of cardiac myosins for effective cardiac function

Yongtae Hwang, Hideo Higuchi, Motoshi Kaya (*Univ. of Tokyo Dep. science*)

For effective heart contractions, it is extremely important to maintain high / stable ventricular pressure during systole and release the pressure immediately during the following relaxation. In this study, in order to reveal molecular properties of cardiac myosins for such functional demands in heart, forces generated by synthetic cardiac myosin filaments were measured by optical tweezers. Back and forth stepwise force curves were frequently observed at high ATP and ADP concentrations. Combined with simulation results, one key feature is the ADP state of myosin, which remains bound to actin and causes the reverse strokes and subsequent detachments more frequently at higher loads. These molecular properties appeared to be suitable for functional demands in heart.

1E1354* F_O 回転モーターの回転角と保存残基のプロトン化状態の連関
Coupling of protonation state of conserved residues and rotation angle in F_O rotary motor

Daiki Yamakoshi, Dan Parkin, Kota Tezuka, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

F_O is the membrane-embedded portion of ATP synthase, where the ring-like *c*-subunit assembly (*c*-ring) undergoes rotary motion relative to the *a*-subunit. The physical mechanism of this rotation is widely explained by the half-channel model, in which the protonation states of conserved acidic residues in the *c*-subunits play the key role. We previously analyzed rotation-angle dependent Brownian motion of the *c*-ring by molecular dynamics (MD) simulation. We here investigate rotation-angle dependent protonation state of the conserved acidic residues of the *c*-subunit by using a number of MD snapshot structures, and found that pKa is largely affected by the rotational angle. We show how the rotation-angle dependent pKa relates to the unidirectional rotation.

1E1406* ハイブリッド F_1-ATPase の 1 分子回転観察
Rotation of hybrid F_1-ATPases between bacterial and mammalian ones

Ryo Watanabe, Hiroshi Ueno, Toshiharu Suzuki, Ryohei Kobayashi, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

F_1-ATPase (F_1) is a rotary molecular motor which has the rotor γ subunit and the stator $\alpha_3\beta_3$-ring. Previous single-molecule studies revealed that F_1 from *Bacillus* PS3 (TF_1) and bovine mitochondrial F_1 (bMF_1) differ in rotation rate and step size. An arising question from these observations is 'Which subunit dominates the principal characteristics of rotation of F_1?'. To address it, we studied hybrid F_1's. The γ or β of bMF_1 was replaced with the corresponding subunit from TF_1 to create hybrid motors: $bMF_1(\gamma^{TF1})$ and $bMF_1(\beta^{TF1})$. While $bMF_1(\gamma^{TF1})$ showed rotation behaviors almost corresponding to those of genuine bMF_1, the rotation dynamics of $bMF_1(\beta^{TF1})$ are similar to those of TF_1. These results suggest the β is principally responsible for the rotation behaviors of F_1.

1E1418* シアノバクテリア ATP 合成酵素 ε サブユニットの N 末端側領域の機能
Function of the N-terminal region of the ε subunit of cyanobacterial ATP synthase

Kosuke Inabe, Ken-ichi Wakabayashi, Toru Hisabori (*CLS., Tokyo tech.*)

The ε subunit is an intrinsic inhibitory subunit of F_1-ATPase. In this study, we analyzed the inhibition of F_1-ATPase obtained from thermophilic cyanobacterium *Thermosynechococcus elongatus* BP-1 caused by the ε subunit. Two ε subunit mutants were generated; ε_N which lacks the C-terminal domain α-helices part, and ε_{SS} which cannot change its conformation of C-terminal domain. Surprisingly, both ε subunit mutants maintained the inhibition competency for the ATPase. The rotary motion of F_1-ATPase was also analyzed by way of the single molecule observation technique. ε_{SS} significantly stopped the rotation at around 80º.

1E1430* 電位駆動型モータープレスチン以外の SLC26 イオン輸送体も電位感受能を持つ。
Prestin, a membrane-based voltage-driven motor, is not the sole member of the SLC26 family that can sense voltage

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Prestin is unique among the SLC26 anion transporter family members in that it displays voltage-driven motor activity (electromotility). Since its anion transport activity is extremely low as compared to other SLC26 members, prestin-based electromotility has been presumed to have evolved from and taken over an ancestral ion transport mechanism. Here, we show that other SLC26 members exhibit indications of electromotility by using the whole-cell patch-clamp technique. These results suggest that prestin and other SLC26 members share a common molecular mechanism that responds to voltage, and imply that the voltage-sensing mechanism has evolved independently of the anion transport mechanism.

1E1448* 高速 AFM を用いたマイコプラズマモービレ滑走装置の可視化
Gliding machinery of *Mycoplasma mobile* visualized by high-speed AFM

Kohei Kobayashi[1], Noriyuki Kodera[2], Yuhei Tahara[1,3], Takuma Toyonaga[1], Taishi Kasai[1], Toshio Ando[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Bio-AFM FRC, Kanazawa Univ.*, [3]*OCARINA, Osaka City Univ.*)

Mycoplasma mobile, a bacterium lacking a cell wall, glides on substrate surfaces. In the gliding mechanism, the force is generated through ATP hydrolysis on an internal novel motor. In this study, we tried to visualize the gliding machinery in living cells by the high-speed AFM. The structures consistent with those of internal motors reconstructed by electron cryomicroscopy were found by the AFM on the living cells fixed onto substrate surfaces. We observed the "inside" of the living cell, probably because the internal motor exists just beneath the cell membrane, and the cell surface is flexible enough to allow detection of the internal motor. Now we are trying to observe behaviors of the internal motors involved in the gliding motility in the living cell.

1E1500* 細菌べん毛モーターの回転速度と構成ユニット数の関係
The dependence of the speed of the bacterial flagellar motor on the number of stator units

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The rotation of the bacterial flagellar motor is driven by multiple stator units. To reveal how the motor works, it is necessary to determine the dependence of its speed on the number of stator units. However, it is controversial whether its speed near zero load depends on the number of units or not. To resolve this controversy, we constructed an *E. coli* strain, which has a straight hook with Cys residues and has no filament. By attaching a 60 nm gold-nanoparticle directly to the hook, the motor rotation near zero load was monitored with back-scattering microscopy. As a result, we found that the maximum speed was ~300 Hz, and there were distinct speed levels. We are currently trying to test whether these levels reflect the change of assembled stator units in a motor.

1E1512* アーキアべん毛モーターが発生するトルクの精密測定
Measurement of the torque generated by the archaellar rotary motor in microscopic detail

Seiji Iwata, Yoshiaki Kinosita, Daisuke Nakane, Takayuki Nishizaka (*Department of Physics, Gakushuin Univ*)

Motile archaea swim using a rotary filament, the archaellum. We had previously characterized almost all archaellar function in the model organism *Halobacterium salinarum* under advanced microscopes that we had developed, but the direct measurement of the torque had not been completed. Here we imposed various loads on single archaella through markers with different sizes, and precisely quantified their trajectories by 3-D tracking method, combining with high-speed recording and show that the motor showed constant torque, 1.05-1.58×100 pN nm, despite of the rotation rate in the range from 0.5 to 30 Hz. This apparent contradiction gives a clue how archaellar motor proceeds mechano-chemical coupling, which is mechanistically different from other rotary molecular motors.

1E1524* 広い負荷領域の測定から明らかになったキネシン１分子のステップ運動
Kinesin's stepping motion clarified from wide range load measurement

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To understand vesicle/mitosis worked by multiple motors, the load dependent dwell time and step ratio of single kinesin molecule were measured in the wide load range (-20~+50 pN) by optical tweezers with high temporal resolution (~50 microseconds). We newly found that (1) kinesin's stepping was accelerated at large assisting load, dwell times decreased exponentially over 15 pN, (2) dwell times just before detachment were almost same as that of forward and backward steps and (3) surprisingly very fast backward step (~0.5ms) was observed at load of 3-50 pN. To explain the results, we constructed analytical model and determined load dependent rate constants of forward step, backward step and detachment.

1E1536 金ナノピラーへの選択的固定を用いた kinesin-1 および Ncd の協働性の計測
Investigating coordination of kinesin-1 and Ncd using their selective immobilization on gold nano-pillars

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Many cellular processes such as mitosis and flagellar motility are achieved by a team of motor proteins. However, the coordination of motors remains poorly understood due to the experimental difficulty in controlling the number and arrangement of motors, which are considered to affect the coordination. We developed a nano-patterning method of kinesin molecules that enables to control the number and spacing of motors transporting a single microtubule filament. Kinesin-1 or Ncd were specifically immobilized on Au nano-pillars by using selective grafting of PEG. In contrast to kinesin-1, the microtubule velocity on patterned Ncd was sensitive on both the number and spacing of motors. This result suggested kinesin-1 and Ncd have a different mechanism of coordination.

1E1548 コンデンシン複合体は分子モーターである
The condensin complex is a mechanochemical molecular motor

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Condensin plays crucial roles in chromosome organization and compaction, but the mechanistic basis for its functions remains obscure. Here, we used single-molecule imaging to demonstrate that Saccharomyces cerevisiae condensin is a molecular motor capable of ATP hydrolysis-dependent translocation along double-stranded DNA. Condensin's translocation activity is rapid and highly processive, with individual complexes traveling an average distance of >10 kilobases at a velocity of ~60 base pairs per second. Our results suggest that condensin takes steps comparable in length to its ~50-nanometer coiled-coil subunits. The finding that condensin is a mechanochemical motor has important implications for understanding the mechanisms of chromosome organization and condensation.

1E1600 滑走するフラボバクテリアの集団運動は予期せぬ渦格子と回転を伴う動的プレートを形成する
Collective motion of gliding Flavobacteria exhibits unforeseen vortex lattice and dynamic plate with rotation

Daisuke Nakane, Shouko Odaka, Kana Suzuki, Takayuki Nishizaka (*Dept. Phys., Gakushuin Univ.*)

We found an unforeseen new mode of a collective motion of bacteria, the dynamic circular plate accompanying one-directed rotation and development. Flavobacterium johnsoniae cells glide in random orientation on the glass surface, but they exhibited a vortex lattice during spreading on the agar plate with poor nutrition. This pattern is possibly due to the collision of cells that induces a nematic alignment of dense movable units. Subsequently, each lattice started to oscillate, and transformed to the rotating mode as a sole circular plate. Notably, the direction was counterclockwise without exception. The circular plates developed accompanying rotation with constant angular velocity, suggesting that the mode is an efficient strategy of bacteria for their survival.

1F1330 Cryo-EM structure of a supercomplex containing photosystem II and fucoxanthin chlorophyll binding proteins from a diatom

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Diatoms are dominant phytoplanktons in aquatic environments and have unique fucoxanthin chlorophyll a/c-binding proteins (FCPs) as their light-harvesting antennae different from light harvest complexes (LHCs) in green plants. FCPs bind to photosystem II (PSII) to form a PSII-FCP supercomplex for the efficient photosynthetic reactions. To understand the energy transfer from FCP to PSII, we determined the structure by cryo-electron microscopy at 3.3 Å resolution. The results showed that the PSII dimeric core is surrounded by FCPs at two opposite sides, and each side consists of a strongly associated tetrameric FCPs, a moderately strong associated tetrameric FCPs and three monomeric FCPs. This structure is significantly different from that of PSII-LHCII in green plants.

1F1342 FTIR study on the S-state cycle of water oxidation in the microcrystals of photosystem II

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To clarify the mechanism of water oxidation in photosystem II (PSII), the crystal structures of the S-state intermediates have recently been investigated by time-resolved crystallography. However, it remains unanswered whether the reactions efficiently proceed throughout the S-state cycle in PSII crystals. In this work, we studied the water oxidation reactions in PSII microcrystals using FTIR spectroscopy. FTIR difference spectra of the PSII crystals upon 4 flashes were obtained. Comparison with the FTIR spectra in solution showed that all the metastable intermediates in the crystals retain their native structures, and the S-state transitions advanced relatively efficiently, although the efficiencies of the S2-S3 and S3-S0 transitions were slightly lowered in crystals.

1F1354 Ca^{2+}除去した光化学系Ⅱの高酸化状態でのスピン構造
High spin state in Ca^{2+}-depleted photosystem II

Takahiro Sakai, **Hiroyuki Mino** (*Grad. School of Sci., Nagoya Univ.*)

Photosynthetic oxygen evolution is performed in the $CaMn_4O_5$ cluster of photosystem II (PS II), through five intermediates called Si state (S_0-S_4). It has been proposed that Ca^{2+}-depletion does not affect the electronic structure of Mn cluster in S_1 and S_2 state and does not advanced to in higher oxidation state. In order to clarify the effect of Ca^{2+} in high oxidation state, Q-band pulsed EPR was performed for Ca^{2+}-depleted Mn cluster. After illuminating for 1 minute at 273 K, the EPR signal around g = 3.2 was detected, indicating that Ca^{2+} directly affect spin structure of Mn cluster in high oxidation state. The results give a clue to clarify the electric structure of the higher oxidation state in manganese cluster.

1F1406 Proton transfer or H_3O^+ stabilization

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Water molecules can serve as the proton donor and acceptor in the hydrogen bond (H-bond) network of the protein interior, forming a proton transfer pathway with titratable residues. In particular, when water molecules are strongly H-bonded, the activation energy for proton transfer is the lowest, without involving formation of an isolated hydronium ion, H_3O^+. On the other hand, H_3O^+ was proposed to be present in H, K-ATPase or at the end of the proton transfer pathway in bacteriorhodopsin. Here, we clarified how the protein environment can facilitate proton transfer or stabilize an isolated H_3O^+ [1-3].
References [1] Saito et al. *Nat. Commun. 6* (2015) 8488. [2] Ikeda et al. *Angew. Chem. Int. Ed. Engl. 56* (2017) 9151. [3] Kawashima et al. *Nat. Commun. 9* (2018) 1247.

1F1418 単一分子蛍光寿命相関解析：光合成光反応を制御する複数のタンパク質ダイナミクス
Multiple protein dynamics regulating photosynthetic photoreaction revealed by single-molecule fluorescence lifetime correlation analysis

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Fluorescence intensity correlation analysis of single-molecule data has been extensively used to estimate protein dynamics, but the time resolution is restricted. Recently, the lifetime-based approach, two-dimensional lifetime correlation analysis, allowed the identification of fast dynamics even on the microsecond time scale. However, it is still difficult to investigate the system containing a number of fluorescence emitters, each of which is associated with discrete dynamics. Here, we developed a correlation analysis for multiple independent dynamics in single chromoproteins. The new approach revealed that three distinct dynamic components occurring at different time scales regulate the energy transport in photosynthetic light-harvesting complexes.

1F1430 人工色素を付加した光収穫系複合体の再構成膜系での超高速エネルギー移動
Ultrafast Energy Transfer of Light-Harvesting Complex 2 Covalently Attached Artificial Chromophores in Reconstituted Lipid Bilayer

Takehisa Dewa[1], Yusuke Yoneda[2], Akari Goto[1], Masaharu Kondo[1], Hiroshi Miyasaka[2], Yutaka Nagasawa[3] ([1]*Nagoya Inst. Tech.*, [2]*Osaka Univ.*, [3]*Ritsumeikan Univ.*)

Photosynthetic light-harvesting complex 2 (LH2) from a purple photosynthetic bacterium performs highly efficient light harvesting and excitation energy transfer (EET). In order to expand the available light of LH2, we have reported that an artificial fluorescence dyes covalently attached to LH2 can efficiently transfer excitation energy to bacteriochlorophylls in LH2. In this study, we report that the rate of EET is significantly enhanced when LH2-fluorophore conjugates are reconstituted into lipid bilayer. In addition, it was found that ultrafast EET from the fluorophore to light-harvesting-1/reaction center complex (LH1-RC) occur in the picosecond time range in the system of LH2-fluorophore/LH1-RC co-assembled in the lipid bilayer.

1F1448 Reconstitution and functional analysis of thylakoid membrane on a glass substrate

Takuro Yoneda[1], Yasushi Tanimoto[1], Daisuke Takagi[2], Kenichi Morigaki[1,3] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Grad. Sch. Agr., Univ. Tohoku*, [3]*Biosignal., Univ. Kobe*)

We reconstituted thylakoid membranes from spinach on a glass substrate as an experimental platform to evaluate the molecular mechanisms of photosynthesis. For facilitating the membrane formation, thylakoid membranes were mixed with phospholipid (DOPC) vesicles and reconstituted into the scaffold of patterned polymeric bilayer. The electron transfer activity of photosystem II was confirmed by the changes in chlorophyll fluorescence as the electron acceptor or the inhibitor was added. We also observed the generation of NADPH from NADP+, confirming the electron transfer activity. The results support the feasibility to evaluate the photosynthetic functions using reconstituted thylakoid membranes.

1F1500 フコキサンチン会合体のアセトン-水混合溶媒中での分光特性
Optical property of aggregated fucoxanthin in acetone-water mixture

Nami Yamano, Ritsuko Fujii (*Grad. Sch. Sci., Osaka City Univ.*)

Fucoxanthin is a carbonyl carotenoid having absorption band peaking around 450 nm in organic solvent. The absorption band shifts to red upto 550 nm when bound to the photosynthetic antenna proteins in marine algae, known as fucoxanthin-chlorophyll protein (FCP), although the mechanism of large bathochromic shift is not clarified yet. In this study, we investigate the fucoxanthin self-assemblies in acetone-water binary solvent system by using absorption and circular dichroism spectra. The excitonic couplings between fucoxanthin molecules assembled in close proximity will be discussed in relation to the fucoxanthin in FCP.

1F1512 Mutation study of heliorhodopsin 48C12

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Recently, through the use of functional metagenomics, we reported a previously unnoticed diverse family, heliorhodopsins (HeRs), which are abundant and distributed globally in archaea, bacteria, eukarya and their viruses. The sequential identity is less than 15% between HeRs and type-1 rhodopsins, so that many aspects of molecular properties of HeRs remain unknown. In this study, to gain information about the residues responsible for the interaction with chromophore, we applied Ala scanning to 30 candidate residues in HeR 48C12 and monitored the absorption spectra. Consequently, 12 mutants show identical absorption spectra, 8 exhibited a spectral blue shift, 6 exhibited a spectral red shift, and 4 did not form a pigment. Molecular properties of HeRs will be discussed.

1F1524 リン酸イオン結合による光駆動型硫酸イオン輸送体 SyHR の分光特性の調節
Phosphate ion binding modulates photochemical properties of a light-driven SO_4^{2-} transporter, SyHR

Keiichi Kojima[1], Masaki Nakama[2], Marie Kurihara[1], Susumu Yoshizawa[3], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*AORI, UTokyo*)

We have recently reported a novel rhodopsin named SyHR from *Synechocystis* sp. PCC 7509 as a light-driven divalent sulfate ion (SO_4^{2-}) transporter and showed its changes of photochemical properties by SO_4^{2-} [JACS 2017, 139, 4376]. In addition to SO_4^{2-}, SyHR also binds to a monoatomic monovalent chloride ion (Cl^-). In this study, we demonstrate phosphate ion binding to SyHR. Absorption maximum of SyHR is shifted from 540 nm to 550 nm in the presence of phosphate, indicating the phosphate ion binding to SyHR around the chromophore. The spectral shift allowed us to estimate the affinity of phosphate as 21 mM, which is comparable to that of the environment. Together with other spectroscopic characterization, we will discuss impact of phosphate ion binding to SyHR.

1F1536 膜電位モニタリングのための高蛍光性微生物型ロドプシンの実装に向けて
Towards implementation of highly fluorescent microbial rhodopsins for monitoring membrane potential

Rika Kurihara[1], Keiichi Kojima[1], Masayuki Skamoto[2], Haruhiko Bito[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Med., The Univ. of Tokyo*)

Archaerhodopsin-3 (AR3), a member of microbial rhodopsin, has been applied to a tool for visualization of membrane potential in the cells as a voltage-sensitive fluorescent protein. The AR3-based voltage indicators allowed to visualize the changes of membrane voltage below threshold with high temporal resolution (i.e., several milliseconds). In this study, to obtain the brighter microbial rhodopsin, we quantitatively analyzed the fluorescence properties of 17 rhodopsins including AR3. As a result, among them, the fluorescent intensities showed a wide variety. In addition to the results, we would like to present the applicability of the brightness rhodopsin and its variants in the cells.

1G1330 Single molecule observation of membrane proteins in a model biological membrane integrated with a nanometric gap structure

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Single molecule observation is a powerful tool to elucidate the functions of membrane proteins. However, observation of single molecules at high concentrations by the conventional total internal reflection fluorescence is difficult due to heightened background noise. We develop a single molecule observation technique of membrane proteins by integrating a model biological membrane and a nanometric gap structure (nanogap-junction). In nanogap-junction, the background noise is more effectively suppressed owing to its thin thickness (< 100 nm). We observe rhodopsin, a G-protein-coupled receptor, and some other membrane-bound molecules in the nanogap-junction. The technique opens a new avenue to observe membrane proteins at heightened concentrations.

1G1342 高速 AFM 解析により明らかになったグラム陰性菌及びグラム陽性菌の産生するメンブランベシクルの物性多様性
High-speed AFM imaging revealed the physical diversity of membrane vesicles produced from Gram-negative and Gram-positive bacteria

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Bacterial cells secret membrane vesicles (MVs) to environment for cell-cell communication. We isolated MVs from three species of Gram-negative bacteria and one species of Gram-positive bacterium. We examined MVs physical properties, such as elasticity, using the phase mode of high-speed AFM. By this approach, we succeeded in the assessment of physical properties of individual MV particles in PBS. We compared the distributions of physical properties of MVs between these four bacterial species. Interestingly, the single bacterial species produced several types of physically different MVs. Moreover, the distributions of MVs physical property were different between these four bacterial species, indicating MVs physical properties have the species specificity.

1G1354* リポソームの 1 粒子膜融合解析
Single particle analysis for membrane fusion of liposomes

Masato Yamada, Naoki Soga, Hiroyuki Noji, Rikiya Watanabe (*Dept. Appl. Chem., Univ. Tokyo.*)

Membrane vesicles mediate various physiological functions upon a fusion with biological membranes inside or outside cells. The vesicles are heterogeneous, i.e., only a few of them are involved in critical functions, and thus it has been highly awaited to develop analytical tools for measuring their functions at single particle level. In this study, we developed a novel microsystem for single particle analysis of membrane vesicles, which first enabled to visualize a fusion of fluorescently-labeled membrane vesicles at single particle level. Here, we would like to introduce current progress on single particle analysis of membrane fusion by using this microsystem.

1G1406* DNA ナノポアプローブを用いたナノ空間内溶液物性の評価
NANOPORE PROBE WITH DNA: ANALYSIS OF SOLUTION BEHAVIOR IN NANOSPACE

Masaki Matsushita, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

Several studies have reported that behavior of molecules in nanoscale is different from that in the macroscale. We have developed a “nanopore probe” to observe physicochemical properties in nanospace. This system has an α-hemolysin (αHL) nanopore containing a short hairpin-DNA (hpDNA). It has previously reported that the hpDNA fits exactly in the αHL vestibule and moves in the nanospace under applying voltages. The movement of hpDNA will reflect the states in the nano-environment. In this study, we evaluated the viscosity and ion effects in nanospace, and these effects suggested that these are closely related to water molecule hydration and structure. In the future, we believe that this system can evaluate the physicochemical properties of a solution in a real cell.

1G1418* 抗菌ペプチド・マガイニン２が誘起するポア形成の初期過程のメカニズム
Mechanism of Initial Stage of Pore Formation Induced by Antimicrobial Peptide Magainin 2 (mag)

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To elucidate the mechanism of mag-induced pore formation, we investigated the effect on pore formation of asymmetric lipid distribution in two monolayers (1). First, we investigated the interaction of mag with single GUVs with asymmetric distribution of lyso-PC (LPC), and found that the rate constant of mag-induced pore formation, k_p, decreased with increasing LPC concentration in the inner monolayer. We constructed a quantitative model of the initial stage of mag-induced pore formation. A theoretical equation defining k_p as a function of mag surface concentration, X, reasonably explains the experimental relationship between k_p and X. This model quantitatively explains the effect on k_p of the LPC concentration in the inner monolayer.
(1) Langmuir, 34, 3349, 2018.

1G1430* The effects of different alkali metal ions on KR2 structure revealed by multidimensional solid-state NMR

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Krokinobacter rhodopsin 2 (KR2), a light-driven Na+ pump [1], has characteristic non-transported Na+ at the extracellular side [2]. Here, we investigated the effects of different alkali metal ions on the KR2 structure by multidimensional solid-state NMR. When the buffer with alkali metal ions from Na+ to Cs+ or Li+ were exchanged, the several peak shifts of residues were clearly observed. Especially, the shifted cross peaks of Arg109, which plays a crucial role on Na+ pump process, suggest that alters the structure of hydrogen bonding network in the vicinity of Schiff base. Therefore, our NMR results are an evidence of the presence of long-distance interaction between the structure in the vicinity of retinal and extracellular Na+ binding site.

1G1448* 糖脂質 S-TGA-1 との特異的相互作用を通したバクテリオロドプシンの構造化および機能発現
Crucial Role of Specific Interactions with Archeal Glycolipid S-TGA-1 in Structuralization and Functionalization of Bacteriorhodopsin

Masataka Inada, Masanao Kinoshita, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ*)

It has been demonstrated the interaction between lipids and membrane proteins (MPs) is essential for structuration and functional expression of MPs. However, details on how the interaction is correlated with structure and function of MPs have yet to be fully understood. Here we first developed a method for quantitatively evaluating the interactions via surface plasmon resonance (SPR), and applied it to bacteriorhodopsin (bR), an MP that acts as a light-driven proton pump. As a result, the halobacterium-derived glycolipid S-TGA-1 was found to have the highest specificity to bR with a nanomolar K_d. Each spectrometry further suggested that this glycolipid affected formation of bR's stable structure through specific interactions, and consequently provided its full function.

1G1500* 脂質膜環境によるリン脂質輸送タンパク質 Sec14 の機能制御メカニズムの解明
Regulation of Sec14-mediated lipid transfer by lipid-membrane environment

Taichi Sugiura, Ukyo Yoshida, Hiroyuki Nakao, Keisuke Ikeda, Minoru Nakano (*Grad. Sch. Med. Pharm. Sci., Univ. Toyama*)

Sec14 is a phosphatidylinositol (PI)/phosphatidylcholine (PC) transfer protein, which is known to facilitate vesicle budding from the trans-Golgi network in yeast. Sec14 has a hydrophobic pocket and an amphipathic helix that covers a lipid captured into the pocket. However, lipid transfer mechanism of Sec14 has not been fully elucidated. In this study, we evaluated its lipid transfer by using fluorescence and small angle neutron scattering. In combination with binding assays, we revealed that Sec14-mediated lipid transfer is promoted by anionic phospholipids and membrane curvature. Acidic phospholipids are likely to accelerate lipid exchange step on membrane through electrostatic interaction. On the other hand, membrane curvature promotes Sec14-binding onto membranes.

1G1512* 細菌の排出システムにおける多剤認識の構造に基づく解析
Structure-based Analysis for Multidrug Recognition in Bacterial Efflux System

Kaori Nakao[1], Keisuke Sakurai[2], Seiji Yamasaki[1], Kunihiko Nishino[1], Akihito Yamaguchi[1], Ryousuke Nakashima[1] ([1]*ISIR*, [2]*GSIS, Tohoku Univ.*)

Antibiotic resistant bacteria cause untreatable nosocomial infections. Expressing efflux transporters, such as MexB in Pseudomonas aeruginosa, is a strategy to achieve resistance to various kinds of chemotherapeutic drugs. Here we report the crystal structures of MexB complex with high molecular mass molecules. MexB is known to have two connected multi-substrate binding pockets each to recognize high and low molecular mass substrates. The new structure was against our hypothesis based on this knowledge acquired from previously solved structures. Our study indicates MexB uses two different pockets inside according to many sides of characteristics of each substrate. These insights help develop global spectrum inhibitors to restore previously effective chemotherapy.

1G1524 Interrogation of a bacterial sugar transporter for novel biomedicines and biotechnologies

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Bacterial drug resistance has been a global grand challenge. I have initiated and led a research program that focused on the interrogation of a transporter of capsular polysaccharides Wza that is conserved in Gram-negative bacteria. Protein engineering of Wza enabled the application of single-molecule electrical channel recording to screen for blockers at the single-molecule level. Cyclic oligosaccharide am8γCD that binds to the barrel of Wza with nanomolar affinity was discovered. It is non-toxic to the bacteria but it enhances the vulnerability of bacteria to immune attacks. A novel vaccination strategy based on the Wza inhibitor has also been developed. Studies on the alpha-helix barrel have further led to the development of novel functional peptide pores.

1G1536* ミトコンドリアの電子伝達系の働きとクリステ構造の安定性について
Stability of cristae structures of mitochondria and the electron transfer chain activities

Mayu Yoneda, Takahiro Shibata, Yoshihiro Ohta (*Ohta. lab., Grad. Univ. Noko*)

Mitochondrial inner membrane has the highly folded structure, called cristae. The disruption and formation of the cristae is necessary when mitochondria change their shape and the volume. However, since the cristae structure has been observed mainly with electron microscopy, the dynamic changes in cristae structure has not been observed in the solution. Here, we examined the mitochondrial swelling which accompanies the disruption of the cristae structure by observing the changes in transmittance of light through individual isolated mitochondria. The effects of respiration substrates and inhibitors of FoF1-ATPase on the swelling were examined. The detailed mechanism underlying the stability of the cristae structure will be discussed.

1G1548 A unique respiratory adaptation in Drosophila independent of supercomplex formation

Satoru Shimada[1,2], Marika Oosaki[1], Ryoko Takahashi[1], Shigefumi Uene[1], Sachiko Yanagisawa[1], Tomitake Tsukihara[1], **Kyoko Shinzawa-Itoh**[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*KNC Lab Co., Ltd.*)

The formation of supercomplexes (SC) is thought to contribute to efficient electron transfer, stabilization of each complex, and inhibition of ROS generation. Mitochondria (Mit) from various organisms were solubilized with digitonin, which revealed a SC in Mit from bovine, porcine and mouse. However, SCs were barely detectable in Drosophila. Drosophila Mit exhibited the highest activities, and the concentrations of the electron carriers cyt c and quinone were higher than in other species. Respiratory chain complexes were tightly packed in the Mit membrane, which contained abundant PE with the fatty acid palmitoleic acid (C16:1), which is relatively high oxidation-resistant. These findings reveal the existence of a new biological adaptation independent of SC formation.

1H1330* レチニリデンシッフ塩基の対イオンの高い pK_a は Na^+ポンプロドプシン の効率的なイオン輸送に必須である
An elevated pK_a of the retinylidene Schiff base counterion is prerequisite for efficient ion transport in Na^+ pumping rhodopsins

Marie Kurihara[1], Misa Hashimoto[2], Susumu Yoshizawa[3], Keiichi Kojima[1,2], Takashi Tsukamoto[1,2], Takashi Kikukawa[4,5], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*AORI, UTokyo.*, [4]*Fac. Adv. Life Sci., Hokkaido Univ.*, [5]*GSS, GI-CoRE, Hokkaido Univ.*)

Microbial rhodopsins are widespread in microbial world as photoreceptive seven-transmembrane proteins with a chromophore retinal. Microbes utilize them for transporting ions and transducing light-signals. Light-driven Na^+ pumping rhodopsins (NaRs) have become a focus of interest, because of its functional novelty. Here we functionally and spectroscopically characterized four distinctive NaRs (Y-NaR, M-NaR, IaNaR and KR2) in the same experimental condition. Of note, Na^+ pumping activity of NaRs showed a large variety, and the activity was positively correlated with the pK_a of the retinylidene Schiff base counterion. Thus we demonstrated a high pK_a of the counterion as a functional determinant in NaRs. From the results, we proposed a model for Na^+ pumping mechanism.

1H1342* KR2 の水素結合ネットワークとナトリウム輸送メカニズムに関する構造解析
Structural analysis on the hydrogen bonding network in KR2 and its sodium pump mechanism

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The FTIR spectra of KR2 wild type, a light-driven sodium/proton pump, exhibit strongly hydrogen-bonded water vibrations, which were thought to be essential for proton pump function. Crystal structure of KR2 showed no water molecule between protonated Schiff base and its counter ion, unlike other microbial rhodopsins. In this study, we applied light-induced FTIR spectroscopy at 77 K to study hydrogen bonding network in the extracellular side of KR2. We successfully identified the location of the strongly hydrogen-bonded water near R109. Interestingly, R109K showed pump activity without strongly hydrogen-bonded water, indicating the strong hydrogen bond of water is not necessary for ion pump in KR2. Role of the charged residues near the Schiff base will be discussed.

1H1354* 微生物型ロドプシンで広く保存される波長制御に重要な２残基のアミノ酸変異による制御メカニズムの解明と光遺伝学への応用
Elucidation of wavelength regulation mechanism by widely-preserved amino-acid mutation in rhodopsins and its application to optogenetics

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Microbial rhodopsins mainly function as light driven ion transporter and have been used in optogenetics. Most rhodopsins have absorption maxima (λmax) around 500 nm, but it is demanded to achieve spectral red shift for higher tissue-penetration depth and expand the variation of λmax for visual regeneration. In this study, we conducted a comprehensive mutagenesis study on highly conserved amino-acid residues (P219 and S254) near β-ionone ring and protonated Schiff base of retinal in sodium pump rhodopsin, KR2. While some mutants showed significant red shift in λmax, further variants exhibiting larger shift was constructed by multiple mutations. In presentation, we will discuss the mechanism of spectral red shift and the possibility for optogenetic application.

1H1406* 霊長類緑感受性視物質の 100 K 以上での赤外分光解析
FTIR study of primate green-sensitive cone visual pigment at >100 K

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Cone pigments are photoreceptor proteins responsible for color vision, whose structural information is little known compared to rhodopsin for scotopic vision. We first reported structural information of monkey color visual pigments by FTIR spectroscopy, where photochromic properties were utilized to accumulate difference spectra with Batho-intermediate at 77 K. As visual pigments bleach, structural study for late intermediates is challenging. Here we extend the FTIR study for Lumi-intermediate of mokey green-sensitive pigment by use of insect cell expression and combination of illuminations. The first Lumi spectra at 200 K show relaxed structure from Batho as well as in rhodopsin, whereas different hydrogen-bonding alterations were detected including waters.

1H1418* 紅色細菌 strain 970 が最も大きいエネルギー勾配を遡って光合成を行うことができるのはなぜか
Origin of the anomalous uphill energy gap in the light-harvesting reaction center from purple photosynthetic bacterium strain 970

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In the light-harvesting 1 reaction center (LH1-RC) complex from purple photosynthetic bacteria, excited energies are transferred from LH1 to RC by an uphill energy transfer mechanism. However, factors responsible for the uphill energy transfer are largely unknown. The LH1-RC from strain 970 has the largest uphill energy gap among purple bacteria containing bacteriochlorophyll a. Our preliminary data demonstrated that the energy gap is regulated by calcium, similarly observed for *Tch. tepidum*, the thermophilic counterpart. In this study, the origin of the unusual uphill energy gap in the strain 970 LH1-RC complex was investigated by spectroscopic analyses. Based on the present result, the factors allowing the uphill energy transfer from LH1 to RC are discussed.

1H1430* 多孔質ガラス板内部における光化学系 I から白金ナノ粒子への光誘起電子移動反応
The light induced electron transfer reaction from photosystem I to Pt nanoparticles inside a nanoporous glass plate

Makoto Hirano[1], Tomoyasu Noji[2], Keisuke Kawakami[2], Teturo Jin[3], Masaharu Kondo[4], Hirozo Oh-oka[5], Nobuo Kamiya[1,2] ([1]*Grad. Sch. Sci., Univ. Osaka City*, [2]*OCARINA, Univ. Osaka City*, [3]*AIST*, [4]*Grad. Sch. Engi., Univ. Nagoya Institute of Technology*, [5]*Grad. Sch. Sci., Univ. Osaka University*)

A natural-artificial hybrid photocatalyst, PSI-PtNP, has been developed to use in an artificial photosynthesis that produces hydrogen utilizing sunlight energy. The natural photosynthetic membrane protein, PSI (photosystem I), is hybridized with PtNPs (Pt nanoparticles) as the hydrogen production co-catalyst. More recently, a new hydrogen production system was constructed by immobilizing the PSI-PtNP in a nanoporous glass plate (PSI-PtNP/PGP). In this study, we investigated flash-induced transient absorption changes of PSI and PSI-PtNP/PGP, and estimated the rate constant of the electron transfer from PSI to the PtNP by solving rate equations. Furthermore, we will discuss the relation between the electron transfer rate and the hydrogen production efficiencies.

1H1448* 過渡回折格子法と活性測定を用いた BlrP1 の光強度センサー機能
Non-linear light intensity sensing of BlrP1 studied by TG spectroscopy and enzymatic assay

Kosei Shibata, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

BlrP1 is a blue-light sensor from K. pneumoniae. It consists of an N-terminus BLUF domain (photosensor domain) and a C-terminus EAL domain (enzymatic domain). The catalytic activity of EAL is regulated by BLUF in light dependent manner. We investigated the photoreaction dynamics of BlrP1 by the transient grating method and found light-induced conformation change of the BlrP1 dimer depends on the intensity of excitation light. In addition, we performed enzymatic assay under different light conditions, and found the activity of BlrP1 also depends on the light intensity. These findings indicate BlrP1 acts as a non-linear light intensity sensor. To clarify the mechanism of signaling in detail, we are now examining the photoreaction and enzyme activity of several mutants.

1H1500* LOV ドメインに保存されるグルタミン残基の役割
The role of Gln residue conserved among the LOV domains

Itsuki Kobayashi, Osamu Hisatomi (*Grad. Sch. Sci., Univ. Osaka*)

Photozipper (PZ) is an engineered protein containing a basic region/leucine zipper (bZIP) domain and a light-oxygen-voltage-sensing (LOV) domain of Aureochrome-1. We have reported that blue light induces dimerization of PZ and increases its affinity for the target DNA. The Gln residue (corresponding to Gln317 of PZ) closely located at C(4a) of FMN was supposed to play a crucial role on the function of LOV domains. To elucidate the role of Gln317 on the conformational change of PZ, we prepared mutant PZs in which Gln317 was replaced to five amino acids, and investigated the DNA-binding of bZIP domain. Substitutions of Gln317 increased the affinity of PZ for DNA in the dark state. Our data suggested the Gln317 had the role on stabilizing the structure in the dark state.

1H1512 Crystallization of squid metarhodopsin

Midori Murakami (*Dept. Physics, Nagoya Univ.*)

Invertebrate metarhodopsins are thermally stable and hit back to rhodopsin by absorption of a second photon. We have investigated light-induced structural changes in squid rhodopsin using the P62 crystal in the dark-adapted state. When the illuminated crystal was warmed >250 K, the crystal quality was severely lowered, suggesting large helix rearrangements might occur to destroy the crystal lattice upon formation of metarhodopsin. We have performed crystallographic studies of squid rhodopsin in meta states. Using a sample of 100 % meta state, we obtained new crystals which diffracted up to 3.6 A. Low resolution structure suggests that helix architecture is unchanged whereas some aromatic rings of residues are somewhat moved to enlarge the active site.

1H1524 ハロロドプシンのイオン輸送におけるレチナール異性化反応
Retinal isomerization during the anion pumping cycle of halorhodopsin

Tsutomu Kouyama (*Nagoya University*)

A previous crystallographic study of halorhodopsin suggested that the N state with 13-cis/15-anti retinal decays into an N-like reaction state with 13-cis/15-syn retinal, which in turn relaxes to the initial state with all-trans/15-anti retinal; i.e., three different types of isomerization occur during the anion pumping cycle. Meanwhile, the protein moiety can take on three different conformations: i) the extracellular side is open and the cytoplasmic side is closed; ii) the extracellular side is closed and the cytoplasmic side is open; iii) the both sides are closed. We discuss the possibility that the unidirectional translocation of a halide ion is guaranteed by a restricted correlation between the retinal configuration and the protein conformation.

1H1536 光照射固体ＮＭＲとＤＦＴ計算によるファラオニスホボロドプシン中間体のレチナールの配座の解析
Retinal configuration of pharaonis phoborhodopsin intermediates revealed by photo-irradiation solid-state NMR and DFT calculation

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Pharaonis phoborhodopsin (ppR) from Natronomonas pharaonis is a transmembrane photoreceptor protein involved negative phototaxis. Structural changes in ppR triggered by the photoisomerization of retinal chromophore are transmitted to its cognate transducer protein (pHtrII) during a cyclic photo-reaction pathway through several photointermediates. We observed the 13C CP MAS NMR signals of late photointermediates such as M-, O- and N'-intermediates by illuminating with green light. Under UV light irradiation of the M-intermediate, the O-intermediate were appeared with the 13-trans, 15-syn configuration. Thus, photo-irradiation NMR studies revealed the photoreaction pathways from the M- to O- intermediates and the equilibrium state between the N'- and O-intermediate.

1H1548 脊椎動物の光受容体 Opn5L1 は逆行性・自己再生能をもつ新しいタイプのオプシンである
Vertebrate photoreceptor, Opn5L1, is the newcomer of opsin acting as a reverse and self-regenerating photoreceptor

Keita Sato[1], Takahiro Yamashita[2], Hideyo Ohuchi[1], Atsuko Takeuchi[3], Hitoshi Gotoh[4], Katsuhiko Ono[4], Misao Mizuno[5], Yasuhisa Mizutani[5], Sayuri Tomonari[6], Kasumi Sakai[2], Yasushi Imamoto[2], Akimori Wada[7], Yoshinori Shichida[2,8] ([1]*Grad. Sch. of Med., Dent. and Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Sci., Kyoto Univ.*, [3]*Div. of Anal. Lab., Kobe Pharm. Univ.*, [4]*Dept. of Biol., Kyoto Pref. Univ. of Med.*, [5]*Graduate School of Science, Osaka University*, [6]*Inst. of Tech. and Sci., Tokushima Univ.*, [7]*Dept. of Org. Chem. for Life Sci., Kobe Pham. Univ.*, [8]*Res. Org. for Sci. and Tech., Ritsumeikan Univ.*)

Opsin is a G protein-coupled receptor that uses retinal both as a ligand and as a chromophore. Here we revealed that opsin named Opn5L1 found in vertebrates has unique molecular properties. Opn5L1 exclusively binds all-trans-retinal and forms the active state. It is inactivated by photoisomerization of retinal into 11-cis form, which is followed by a covalent bond formation of the retinal with a nearby cysteine. This converts C11=C12 into a single bond. Lastly, thermal isomerization of C11-C12 to the trans-conformer, breakage of C-S bond, and the double bond reformation revert the retinal to its original all-trans form. In summary, Opn5L1 loses its activity upon light absorption and spontaneously regenerates the active state employing covalent chromophore modification.

1J1330 Structure-based analysis of ILEI/FAM3C activity to inhibit Aβ generation

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We identified the secretory protein ILEI (FAM3C) as a lead molecule of drug development for Alzheimer's disease. ILEI binds to Presenilin-1 and destabilizes APP-C-terminal fragment (CTF) to suppress A β generation. However, structural aspect of the binding between Presenilin-1 and ILEI remains unexamined. Our objective is to elucidate the structure-based mechanism underlying its ILEI activity.
We obtained candidate Presenilin-1-binding sites on ILEI by using 3D-RISM theory. Subsequently, we introduced amino-acid substitutions at each predicted site and evaluated the mutational effect on APP-CTF level and Aβ production. Using 2D NMR, we also analyzed ^{1}H, ^{15}N-HSQC spectra of Presenilin-1 C-terminal tail to identify amino-acid residues contributing to ILEI-binding.

1J1342 Domain motion of Fv-fragment in anti-dansyl immunoglobulin G controls conformation of its flexible antigen-binding region

Tomotaka Oroguchi[1,2], Masayoshi Nakasako[1,2] ([1]*Faclt. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 Center*)

Immunoglobulin G is a representative member of antibodies, and recognized antigens by the Fv-fragment in the Fab portion. The previous structural studies have revealed that the Fv-fragment is composed of VH and VL domains, and a flexible loop region (CDRH3) in VH domain plays important roles for multi-specificity to bind structurally distinct antigens. In this study, we investigated the conformational dynamics of Fv-fragment using molecular dynamics (MD) simulations and small-angle X-ray solution scattering (SAXS). The results suggests that the motions between VH and VL domains controls the flexibility of CDRH3 and also works as a switch for the conformational transition of CDRH3 from the state unable to bind antigen to the state able to bind.

1J1406 B 型肝炎ウイルスの薬剤の吸収に関する自由エネルギー計算
Free energy evaluation of drug absorption on Hepatitis B virus capsid

Ryo Urano, Noriyuki Yoshii, Wataru Shinoda, Susumu Okazaki (*Grad. Sch. Engnr., Univ. Nagoya*)

Hepatitis B virus (HBV) causes liver disease, and drugs for HBV such as entecavir can render the virus inactive. A new and more effective drug is required for HBV treatment to prevent HBV recurrence. For this purpose, researchers have made an effort to understand the fundamental mechanism of drug. For example, they confirmed tha entecavir inhibits reverse transcription. On the other hand, molecular understanding for drug and HBV is developed less. In this work, computer simulation is used to explore the mechanism of how drug interacts with HBV virus. Using free energy evaluation, we explore a possible mechanism of efficient drug adsorption into the HBV capsid. We will report results on the day.

1J1418 3D-RISM 理論と新しい溶媒和自由エネルギー表式を用いた蛋白質の構造安定性
Structural stability of proteins using 3D-RISM with new solvation free energy functional

Yutaka Maruyama[1], Ayori Mitsutake[2] ([1]*RIKEN R-CCS*, [2]*Dept. Phys, Meiji Univ.*)

We investigated the stability of the folded and unfolded structures of proteins obtained from Anton's long simulations. Protein stability is determined by the characteristics of the protein itself as well as the surrounding solvent. Thus the total energy is given by the sum of the conformational energy and the solvation free energy, and their balance results in the stabilization, as demonstrated by the correspondence between structures with the lowest total energy of all proteins to their native structures. These findings indicate that the total energy function is appropriate for evaluating the stability of protein folding systems. In addition, the solvation entropy is the main contributor to the process of folding from more extended structures to compact structures.

1J1430 生体高分子立体構造生成およびタンパク質間相互作用解析の高速処理について
Fast Processing of Biopolymer Structure Generation and Protein-Protein Interaction Analysis

Takanori Sugihara[1,5], Kota Kasahara[2], Junichi Higo[3,5], Ichio Shimada[4,5] ([1]*JBIC*, [2]*Ritsumeikan Univ.*, [3]*Univ. Hyogo*, [4]*Univ. Tokyo*, [5]*N2PC*)

At an early stage, small chemical compounds were mainly used in drug development. After that, natural chemical compounds have been widely used in candidate search for medicine since they are attractive due to various 3D structures. In these days, 20 to 50 % of the approved medicines come from natural chemical compounds. Besides, information contained in protein-protein interactions is important for understanding functions the proteins. For these reasons, we propose a method to generate a sufficiently large number of 3D structures of biopolymers and predict complexes composed of proteins and ligands using computers. As computational tools, we use myPresto software omegagene and sievgene_M for 3D structure generation and docking calculations, respectively.

1J1448 Accurate temperature evaluation in molecular dynamics for long time simulations of biological systems with large time step

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If temperature is estimated accurately, all motions share a single simulation temperature according to Tolman's equipartition theorem. However, this is not generally true in MD because of truncation errors using finite time step. Here, we show how to evaluate temperature more accurately that satisfies the equipartition theorem without any further computational cost in MD. Our new temperature estimation is tested for a hydrated 1,2-dispalmitoyl-sn-phosphatidylcholine (DPPC) lipid bilayer, showing that the physical properties does not change even if we increase the time step up to 5 fs.

1J1500 Computational design of symmetric protein scaffold and assembly with inorganics into hybrid materials

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One of the objectives of protein engineering is to design of functional protein materials. Recently, we developed the perfectly 6-fold symmetrical β-propeller Pizza using a RE3volutionary design approach. Next, we redesigned this protein to coordinate a CdCl2 nanocsytral. Now, we have also developed novel de novo designing β-propeller proteins with different symmetrical architectures as scaffold proteins. These proteins are highly suitable for the addition of symmetrically arranged metal binding sites for catalysis. While they exhibit interesting highly ordered, the addition of symmetric inorganic metal cluster catalysts induces the assembly of crystalline hybrid materials with very porous highly symmetric assembly in which the metal clusters glue the proteins together.

1J1512 量子化学計算を用いた催涙因子合成酵素の反応機構の解明
Elucidation of catalytic reaction mechanism of lachrymatory factor synthase using quantum chemical calculation

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An onion enzyme, lachrymatory factor synthase (LFS), is responsible for production of syn-propanethial S-oxide, which causes lachrymatory effect. Because its substrate and product are both transient, its reaction mechanism has been poorly known to date. Recently, the tertiary structure of onion LFS has been determined by X-ray crystallography. In this study, we have investigated the catalytic mechanism based on the crystal structure employing the molecular dynamics method and the quantum mechanics/molecular mechanics method. From the analysis of minimum energy paths and their energy profiles, a reasonable reaction mechanism, which is consistent with experimental results, was determined.

1J1524 酸化や酵素処理が LDL の硬さ変化を起こすメカニズムについて
Putative mechanism of the elastic modulus change of low density-lipoprotein by oxidation or enzyme treatment

Seiji Takeda[1], Toshihiro Sakurai[1], Shu-Ping Hui[1], Hirotoshi Fuda[1], Hitoshi Chiba[2] ([1]*Hokkaido University*, [2]*Sapporo University of Health Sciences*)

Oxidation of the low-density lipoproteins (LDLs) induce development of cardiovascular disease. We previously reported that elastic modulus of LDL is decreased after oxidation or phospholipase A2 treatment by using AFM. In this study, we investigated the mechanism of the elastic modulus change of the LDL. We measured the concentration of fatty acid of the PLA2 treated LDL and 2-thiobarbituric acid reactive substance (TBARS) of oxidized LDL. We found some amount of the free fatty acids and TBARS were removed from LDLs to the bulk solution even though the LDL size did not decrease. The results suggested that the disorder of the lipid might contribute to the elastic modulus change. We would like to suggest a putative mechanism of the elastic modulus change of the LDL.

1J1536 高速原子間力顕微鏡 1 分子計測データの粒子フィルタを用いたデータ同化によるヌクレオソームの動的構造解析
Dynamic structure analysis of nucleosome using particle filter data assimilation of single molecule measurement data by HS-AFM

Sotaro Fuchigami[1,2], Toru Niina[1], Shoji Takada[1,2] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*CREST, JST*)

High-speed atomic force microscopy (HS-AFM) has been developed and has made it possible to directly observe biomolecules in dynamic action at high spatiotemporal resolution. However, the resolution is not enough to reveal the molecular details of the structural dynamics of biomolecules. In the present study, we develop a four-dimensional structure analysis method of single molecule measurement data by HS-AFM combined with coarse-grained molecular simulation using data assimilation with particle filter. As a target biomolecule, we select a nucleosome with linker DNAs, which can be largely fluctuated. We validate this method using pseudo AFM images generated from molecular simulation results instead of experimental data, and will discuss its usefulness and limitations.

1J1548 口腔細菌グルカンスクラーゼのドメイン間屈曲運動
A hinge-bending domain motion in oral bacterial glucansucrase

Yudai Murata, Tomoichirou Kusumoto, Junichi Taira, Hiroshi Sakamoto, Hideyuki Komatsu (*Dept. Biosci. Bioinf., Kyushu Inst. Tech.*)

Oral streptococci glucansucrase (Glucosyltransferase-I (GTF-I)) consists of a Glucan-Binding Domain (GBD, 56kDa) and a Catalytic Domain (CD, 94kDa). The CD transfers glucose from sucrose to dextran (α-1,6 glucan) bound to GBD and synthesizes α-1,3 glucan. Crystal structures of glucansucrase have showed extended and bent conformations, in which GBD is distant from CD and close to CD, respectively (Pijning et al. *FEBS J.* 2014). This bending motion may be related to the transfer of glucose to dextran. The hinge site of GTF-I was predicted by homology modeling based on other glucansucrases. The structural polymorphism of GTF-I was confirmed by using dry AFM. The effect of dextran and sucrose on the polymorphism will be investigated to examine the induced fit bending motion.

1K1330* TnaC の翻訳停止に依存したフレームシフトの解析
Analysis of the frameshift depending on TnaC-mediated ribosome stalling

Tomoki Shinozawa, Ryo Iizuka, Takashi Funatsu (*Grad. Sch. Pharm. Sci., Univ. Tokyo*)

The *Escherichia coli* TnaC is a leader peptide of the tryptophanase operon and regulates the expression of downstream genes in response to the cellular concentration of tryptophan. Under low concentration of tryptophan, translation of TnaC is terminated at the stop codon UGA by the action of release factor 2 (RF2). In contrast, when the concentration is high, the ribosome is stalled at the stop codon and peptide release by RF2 is inhibited, resulting in expression of downstream genes. Interestingly, in *in vitro* translation assays, we found that the ribosome stalling induces +1 frameshift, which generates the second stop codon UAG recognized solely by RF1 in the 3' UTR of *tnaC*. We speculate that the +1 frameshift is used to rescue TnaC-mediated ribosome stalling.

1K1342* 演題取り消し

1K1354* ラン藻由来アルデヒド脱ホルミル化オキシゲナーゼによる炭化水素合成の向上に重要なアミノ酸残基の同定
Identification of amino acid residues essential for high production of hydrocarbons in aldehyde deformylating oxygenase from cyanobacteria

Hisashi Kudo[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

Aldehyde deformylating oxygenase (ADO) is a key enzyme involved in cyanobacterial synthesis of hydrocarbons that can be used as biofuels. There are two types of ADOs, those having high and low activities, depending on derived cyanobacteria. To identify residues essential for high production of hydrocarbons in ADO, we introduced various single amino acid substitutions into the less active ADO, to make its sequence close to that of the highly active ADO. We succeeded in identifying the non-conserved residues of ADO important for high activity and high expression level of soluble protein and could improve hydrocarbon production of the less active ADO. Our data will be useful for improving the ADO activity for biofuel production.

1K1406* ジョロウグモ牽引糸の配列に基づく合成ペプチドの β 構造の繊維形成性の評価
Potential Fiber-Forming Regions in the Dragline Silk of Nephila clavata Possess a β-Structure

Yuki Yamawaki, Shinji Hashimoto, Masatoshi Saiki (*Department of Applied Chemistry, Faculty of Engineering, Sanyo-onoda City University*)

Nephila clavata dragline silk, which consists of proteins, is a high-performance fiber possessing both high strength and elasticity. To develop a method for biomaterial production, it is necessary to explore the fiber-forming regions in the spider silk. In this study, synthetic peptides derived from spider dragline silk were prepared by a solid-phase peptide method, based on predictions using the hydrophobic parameter of each individual amino acid residue. Furthermore, to explore the potential regions with fiber-forming ability, the precipitated peptides were chemically modified with the 9-fluorenylmethyloxycarbonyl (Fmoc) group and Arg residues. The results suggested that the sequences 28-41, 59-72, and 76-89 can be potential fiber-forming regions.

1K1418* 転写因子 c-Myb と転写コアクチベーター CBP の KIX ドメインとの相互作用を阻害するペプチドの合理的設計
Rational design of peptides that inhibit interaction of the transcription factor c-Myb with the KIX domain of CBP

Shunji Suetaka[1], Yoshiki Oka[1], Tomoko Kunihara[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

The transcriptional activator c-Myb interacts with the KIX domain of CBP and regulates hematopoiesis. However, aberrant expression of c-Myb causes leukemia. Here, we designed peptide inhibitors of the c-Myb-KIX interaction by introducing mutations into the transactivation domain of c-Myb (c-Myb32). Because c-Myb32 is intrinsically disordered and interacts with KIX by the confirmation selection mechanism, one strategy to develop the inhibitor was to stabilize the helical structure of c-Myb32 by mutations using theoretical predictions of helical propensity. However, binding affinity has been little improved by this method. Another strategy is to optimize the c-Myb-KIX binding interface using the Rosetta software. We will show our progress in the meeting.

1K1430* ショウジョウバエ Argonaute2 の N 末端はアミロイド繊維形成能を持つ
N-terminal residues of Drosophila Argonaute2 possess the ability to form amyloid fibrils

Haruka Narita, Makoto Kuwabara, Tomotka Komori, Ryo Murakami, Tomohiro Shima, Mikiko Siomi, Sotaro Uemura (*Grad. Sch. Sci., Univ. of Tokyo*)

Argonaute plays a crucial role in RNA silencing. Drosophila Argonaute2 (DmAgo2) contains an unusual N-terminus insertion of about 400 amino acid (DmAgo2-Nter) with unclear function. DmAgo2-Nter has a glutamine- and glycine-rich sequence, which is a well-known property of prion-like domain (PrLD). To clarify whether DmAgo2-Nter is a PrLD, we predicted the possibility of amyloid fibril formation based on its amino acids sequence in silico. Upon finding a high score, we confirmed that DmAgo2-Nter aggregates are SDS-resistant, which is consistent with canonical amyloid, using SDD-AGE. Finally, we directly observed fibrils constituted of mCherry-tagged DmAgo2-Nter using fluorescence microscopy. These results suggest that DmAgo2-Nter is indeed a PrLD.

1K1448* 天然変性タンパク質 c-Jun の構造解析と転写コアクチベータ CBP の KIX ドメインとの相互作用
Structural analysis of the intrinsically disordered c-Jun and its interaction with the KIX domain of the transcriptional coactivator CBP

Satoru Yoshizaki[1], Yuma Suematsu[1], Shunji Suetaka[1], Tomoko Kunihara[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

Intrinsically disordered proteins play important roles in cellular signaling and transcriptional regulation. However, their structures and target recognition mechanisms are poorly understood. To solve these problems, we studied the interaction of N-terminal activation domain of c-Jun (c-Jun43) with the KIX domain of the transcriptional coactivator CREB-binding protein (CBP). Using circular dichroism (CD) and NMR spectroscopy, we show that c-Jun43 is intrinsically disordered in isolation but changes its structure upon binding to KIX. NMR chemical shift perturbations suggest that the region around Leu76 of c-Jun43 binds to KIX, concomitant with possible α-helix formation. Detailed structural characterization of c-Jun43 upon binding to KIX is under way.

1K1500* システイン残基の酸化修飾が制御する SOD1 の分解メカニズム
Roles of cysteine oxidation as a signal for degradation of SOD1

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Cu/Zn-superoxide dismutase (SOD1) is a copper and zinc-binding protein catalyzing the conversion of superoxide into hydrogen peroxide and molecular oxygen. Because of the oxidizing ability of both substrate and products, SOD1 itself is thought to be a major target of oxidative damage, which potentially leads to loss of the bound copper and zinc ions. Such metal-dissociated, damaged forms of SOD1 is supposed to be degraded in the cell but is known to exhibit high tolerance to proteasomal degradation reconstituted in vitro. Here, we propose a new mechanism of SOD1 degradation that is facilitated by oxidation of a cysteine residue via monomerization and destabilization of SOD1.

1K1512* *Mycoplasma mobile* の滑走に必須な Gli123 タンパク質の構造変化
Structural change of Gli123 protein, essential for *Mycoplasma mobile* gliding

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M. mobile, a fish pathogen glides on solid surface by a unique mechanism. Three huge proteins clustering on the surface of gliding machinery are essential for this mechanism. We focused on the structure of Gli123, a 123 kDa protein responsible for the assembly of surface gliding proteins. SAXS analyses suggested that the rGli123 is a globular protein with its radius of gyration about 8.7 nm. Light scattering and rotary-shadowing electron microscopy showed rGli123 changed their conformations to globular and filamentous structures under high and low ionic strength condition, respectively. Limited proteolysis showed rGli123 had the flexibility of N-terminal 450 amino acid residues in the whole 1132 residues. Based on these findings, we discuss the role of Gli123.

1K1524* 糖はタンパク質の溶媒和と構造安定性にどのように影響するのか？ ：WAXS 及び SANS によるタンパク質の化学変性及び熱変性の研究
How do sugars affect protein solvation and structure stability? : WAXS and SANS studies of chemical and thermal denaturation of proteins

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Sugars are well known to retain protein structures. Despite many studies devoted to clarifying protective actions by sugars, the mechanism has not been clearly understood. Recently, we have revealed that preferentially hydration (exclusion) of sugar molecules is dominant at the sugar concentration lower than ~25% w/w, and neutral solvation is dominant at more higher concentration. In the present study, we observed effects of sugars on the denaturation process of myoglobin by chemical agents (guanidine hydrochloride (GdnHCl)) or heating. We have found that sugars suppress the unfolding in GdnHCl solution by preservation the hydration-shell of the protein, and sugars evidently suppress aggregations and helix-to-sheet transitions of myoglobin by heating.

1K1536* マイクロフロー・フラッシュ赤外分光法を用いた膜内在性 NO 還元酵素の触媒反応の直接観測
Direct observation of the enzymatic reaction catalyzed by an integral membrane NO reductase using microflow-flash IR spectroscopy

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NO reductase (NOR) is a membrane protein that reduces NO to N_2O at the active site, composed of heme and non-heme irons. The NO reduction mechanism in the unique metal environment has received great attention; however, it is yet to be defined because this reaction proceeds very fast. In this study, we tried tracking the catalytic reaction of NOR using microflow-flash IR spectroscopy. As a result, we succeeded in observing a NO stretching band derived from the substrate NO bound to the metal site at 10 μs. This 1st intermediate gave an NO stretching frequency of 1683 cm^{-1}, indicating that one NO first binds to the non-heme iron with a weak interaction to the heme iron. Currently, we are trying to observe a sub-ms reaction process to reveal how the N-N bond can be formed.

1K1548* all-α タンパク質のデザイン
Design of all-α proteins

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Many α-helical proteins have been designed but most of the structures were bundles or coiled-coils so far. The structural diversity of all-α structures yet remains to be explored by protein designers. Our goal is to comprehensively design more complex all-α structures like Globin from scratch. We computationally generated myriad all-α backbone conformations by combining ideal α-helices with typical 18 helix-loop-helix motifs. Then we designed amino acid sequences and experimentally investigated their foldability. As for the backbone structure named fold-0, NMR spectroscopy and X-ray crystallography revealed the native conformation of the designed proteins well agrees with the target structure. We will also report design of other all-α topologies named fold-C and fold-Z.

1L1330* Theoretical Study on the Contribution of Spin Structure to Redox Potential of [2Fe-2S] Core Cluster from Iron-Sulfur Proteins

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Iron-sulfur proteins play a vital role in several processes of biomolecular systems. These proteins have a broad range of redox potential and thus can interact with many substrates. Hence, the redox potential is important for this protein to support those processes. The aim of this study is to investigate the redox potential of iron-sulfur proteins containing [2Fe-2S] cluster. Calculations are performed by using two DFT functionals, i.e. B3LYP and M06, combined with several spin approximations, i.e. high spin, low spin, approximated spin projection (AP), and J coupling approximation. With absolute error of 0.01V, the best results are obtained for AP UM06/6-31++G(d,p).

1L1342* 分子動力学計算を用いた 4 つの蛋白質ファミリーによるリン酸化認識機構の解明
How proteins recognize a phosphoserine residue: diversity and heterogeneity in different protonation states revealed by MD simulations

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Phosphorylation plays critical roles in a wide range of cellular processes. To understand these processes and the related diseases, molecular dynamics (MD) simulations have been exploited to analyze proteins' recognition mechanisms of phosphorylated amino acids. However, most of the previous studies assumed that the protonation state of a phosphorylated amino acid was PO_3^{2-}. We performed MD simulations of 4 different proteins-phosphorylated peptide complexes both in the PO_3^{2-} and PO_3H^- states. Our study suggested PO_3^{2-} was more preferable to PO_3H^- in the interactions due to the larger mobility of the phosphate group in the PO_3^{2-} state. This study suggests strategies to design proteins that can recognize phosphorylated amino acids.

1L1354* 誘電アロステリーによるシトクロム P450 還元酵素の酸化還元状態と構造状態のカップリング
Coupling of redox and structural states in cytochrome P450 reductase via dielectric allostery

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Cytochrome P450 reductase (CPR) regulates the electron transfer from NADPH to various heme-containing proteins. CPR is composed of two flavin-containing domains and considered to regulate the electron transfer by the interdomain motion that is dependent on the redox state of the flavin cofactors. The physical mechanism of the coupling, however, has not yet been firmly established. In our previous molecular dynamics (MD) study, we found that the coupling of the redox and the structural states could be caused by the dielectric allostery. In this study, by employing the accelerated MD technique, we explore the redox-state dependent structural dynamics occurring on a longer time scale and clarify the involvement of the dielectric allostery.

1L1406* Crystal Molecular Dynamics Simulations to study the dynamics of presequence peptide in Crystal Contact-Free Space

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X-ray crystallography provides snapshots of protein conformational ensembles but does not reveal dynamic motions within protein molecules. A new fusion protein method has been devised to create crystal contact-free space (CCFS) within the protein crystals where the mobile parts of the target molecule may remain in dynamic motion. A maltose binding protein (MBP) was fused to Tom20 of the Tom20-presequence complex to create CCFS in protein crystals to study the motions of presequence within protein molecules. We have performed crystal molecular dynamics (MD) simulations for this fused protein complex to correlate dynamics of presequence and experimental data from CCFS method.

1L1418* Molecular dynamics coupled with virtual system for effective conformational sampling

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We developed virtual-system coupled canonical molecular dynamics (VcMD), which is an enhanced conformational sampling method free from estimation of a canonical distribution function along the reaction coordinate. Furthermore, we proposed multidimensional VcMD (mD-VcMD), which is an extension of VcMD to multiple reaction-coordinate axes. We applied these methods to systems consisting of several short peptides of Alanine (VcMD: 2 peptides, mD-VcMD: 3 or 4 peptides) in an explicit solvent. The VcMD provided quicker association/dissociation motions of peptides than a conventional molecular dynamics simulation did, and resultant snapshots produced a canonical ensemble. These methods are applicable to various complicated systems because of its methodological simplicity.

1L1430* 翻訳伸長因子 EF-1α 及び EFL のインシリコモデル構造解析
In silico structural analysis of Elongation factor-1 alpha and Elongation factor-like

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Translation elongation factor-1 alpha (EF-1α) or its paralog Elongation factor-like (EFL) interact with an aminoacyl-transfer RNA (aa-tRNA) to play its essential role in elongation during protein synthesis. Homology modelling and surface analysis of EF-1α and EFL in the eukaryotes with both EF-1α and EFL were performed to examine the hypothesis that the divergent EF-1α does not strongly interact with aa-tRNA compared to the ordinary EF-1α. The subsequent molecular dynamics simulations were carried out to confirm the validity of modelled structures and to analyse the stability of them. It was found that the molecular surfaces of the divergent ones were negatively charged partly, and thus they might not interact with negatively charged aa-tRNA.

1L1448* 統計力学モデルの拡張によるマルチドメインタンパク質のフォールディング機構の予測
Prediction of folding mechanisms of multi-domain proteins by an extended statistical mechanical model

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The Wako-Saitô-Muñoz-Eaton (WSME) model is a coarse-grained statistical mechanical model and has succeeded in explaining folding mechanisms of small, single-domain proteins by calculating free energy landscapes. To apply the model to large, multi-domain proteins, we introduced another energy term, corresponding to a virtual linker between non-local residues, to the WSME model. By introducing these linkers to disulfide bonds, we could obtain free energy landscapes of disulfide-containing, multi-domain proteins, such as lysozyme and α-lactalbumin, consistent with experimental results. We are now working on developing a general method for introducing virtual linkers in multi-domain proteins, to enable calculation of free energy landscapes of any proteins by the WSME model.

1L1500* NMR study of N-terminal SH2 domain of phosphatidylinositol 3-kinase and its interaction with CD28

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For activation of T cells, co-stimulatory signals via CD28 receptors are required in addition to signals via T cell receptors. Following Tyr phosphorylation in the intracellular region of CD28, CD28 recruits adaptor molecules via their SH2 domains. We recently reported the crystal structures of SH2 domains in complex with CD28 phosphopeptide (J. Biol. Chem. 292, 1052, 2017). In this study, to analyze the site-specific contribution of structural dynamics for the CD28 recognition by N-terminal SH2 of phosphoinositide 3-kinase, we applied NMR and assigned about 90% of main-chain signals. Upon the addition of CD28 phosphopeptide, we observed the signal shifts, corresponding to not only the residues involving the CD28 binding but also those outside the interface.

1L1512* caged-GTP を用いた時間依存的な NMR 信号変化のモニタリングによるガン遺伝子産物 Ras の GTP 加水分解過程における構造変化の解明
Conformational changes on GTP hydrolysis of oncogene product Ras revealed by monitoring of time-dependent NMR signal using caged-GTP

Chika Hagihara[1], Yoshiteru Makino[1], Shigeyuki Matsumoto[2], Takashi Kawamura[3], Eriko Nango[4], Ichiro Mori[1], Tohru Kataoka[2], Takashi Kumasaka[3], Fumi Shima[1] ([1]*Grad. Sch. Sci. Tec. Innov., Kobe Univ.*, [2]*Grad. Sch. Med., Kobe Univ.*, [3]*SPring-8, JASRI*, [4]*RSC., RIKEN*)

Small GTPase Ras functions as a molecular switch by cycling between GTP-bound (Ras-GTP) and GDP-bound (Ras-GDP) forms in cell signaling pathways. Ras-GTP adopts two interconverting conformational states, in active State 1 and active State 2, and effecter-binding to Ras-GTP induces its equilibrium shift toward State 2. To reveal the structural changes on GTP hydrolysis making completely inactive Ras-GDP, we monitored the time-dependent signal changes on 1H-15N HSQC NMR spectra of photo-responsive caged GTP-bound Ras. The results indicated that caged GTP-bound Ras exhibits State 1 same as its crystal structure, and that on GTP hydrolysis process induced by near-UV irradiation, Ras-GTP conformation transiently adopts State 2, subsequently leading to conversion to Ras-GDP.

1L1524* An Initial Interaction Difference between Bombinin H2 and H4 on Leishmania mimetic membrane

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Bombinin H2 (H2) and H4 (H4) are stereochemical isomers. H4 contains a D-allo-isoleucine as the second residue in its sequence. It is the most active among the bombinin family peptides against many bacteria, and fungi as well as the parasite Leishmania. H4 exhibits 5-times stronger binding affinity than H2 does. We analyzed structural dynamics and the membrane interactions of H2 and H4 on a Leishmania mimetic membrane using solid-state NMR, VCD spectroscopy, and MD simulations. The specific arrangement of L-Ile1 and D-allo-Ile2 of H4 rapidly form a cis conformation which plays an anchoring role in the initial deposition and penetration of H4 into the membrane. In contrast, H2 could gradually attach to the membrane because trans conformation dominates in these residues.

1M1330 真空紫外円二色性分光による α1 酸性糖蛋白質の生体膜相互作用機構の研究
Interaction Mechanism between α_1-Acid Glycoprotein and Membrane Characterized by Vacuum-Ultraviolet Circular-Dichroism Spectroscopy

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α_1Acid glycoprotein (AGP) interacts with membrane, inducing the decrease of its drug-binding capacity and the β→α conformational change. To clarify the interaction mechanism, the vacuum-ultraviolet circular-dichroism spectra of AGP were measured down to 170 nm in the presence of six types of liposomes with different surface charges. The secondary structure analyses showed that the helical regions of AGP increase upon interacting with the negatively-charged liposomes and both neutral and positively-charged helix regions are involved in the interaction. The neutral helix region was amphiphilic and its interaction was retained even in NaCl solution, suggesting that the AGP and membrane interacts under a delicate balance between electrostatic and hydrophobic interactions.

1M1342 時計タンパク質 KaiC の C1 リングの構造変化が KaiB との結合のタイミングを計る
Conformational rearrangements of the C1 ring in KaiC measure the timing of assembly with KaiB via a conformational selection mechanism

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KaiC, the core oscillator of the cyanobacterial circadian clock, forms a hexamer composed of an N-terminal C1 ring and a C-terminal C2 ring. KaiC assembles/disassembles with other clock proteins, KaiA and KaiB in a circadian fashion. Recent studies have revealed that the C1 ring not only binds with KaiB but also plays a crucial role for determining the cycle period. Accordingly, a dynamical aspect linking the two functions is important as a key step to transmit slowness from intra-molecular to inter-molecular scales. In this study, we performed a dynamic analysis of the C1 ring using fluorescence spectroscopy. We demonstrated that the structural transition of the C1 ring triggered by ATP hydrolysis recruits KaiB and limits the overall rate of slow complex formation.

1M1354 RXRα リガンド結合ドメイン四量体と新規合成パーシャルアゴニストとの複合体結晶構造
Crystal structure of the tetrameric ligand binding domain of RXRα complexed with a novel synthetic partial agonist

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Retinoid X receptor (RXR) has been studied as a major nuclear receptor, and various agonists, antagonists, and partial agonists have been developed followed by the structural studies of its complexes. However, the detailed model of the complex of RXR and partial agonists, which show intermediate activities, is hardly elucidated. We have determined the crystal structure of the complex of the ligand binding domain of human RXRα and a novel synthesized partial agonist CBt-PMN (Kakuta et al, ACS Med Chem Lett., 3, 427, 2012). The structure reveals a novel binding mode of the partial agonist, and the molecular mechanism of the partial agonistic activity induced by the multiple conformation of the bound ligands.

1M1406 植物硝酸輸送体 NRT2-NAR2 複合体の結晶構造
Crystal structure of plant high affinity nitrate transporter NRT2 in complex with the accessory protein NAR2

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Nitrate is a major nitrogen source for higher plants, in which several nitrate transport systems with different affinity for nitrate have been evolved and developed. Previous studies suggested that the plant high affinity nitrate transporter NRT2 interacts with the accessory protein NAR2, however the molecular mechanism of how NAR2 regulate the activity of NRT2 remains elusive. Here we report the crystal structure of plant NRT2-NAR2 hetero-complex at 2.1 Å resolution. The accessory protein NAR2 possess single transmembrane helix and beta-sheet-rich large extracellular domain, both of which are interacted mainly with the N-bundles of NRT2 transporter. This structure will facilitate the understanding of the molecular mechanism of nitrate uptake in plants.

1M1418 動的核偏極タンパク質中性子結晶解析に向けた高圧凍結最適化と新たなラジカルドーピング
Optimization of high-pressure freezing and new radical doping for neutron protein crystallography by dynamic nuclear polarization

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To improve the sensitivity of hydrogen detection using neutrons, a dynamic nuclear polarization (DNP) technique together with high-pressure freezing (HPF) method would be necessary [Tanaka et al., 2018; DOI = 10.1007/978-981-10-8459-1]. The high pressure frozen crystals diffracted up to nearly the same resolution as that of flash cooled small crystals soaked with cryoprotectants and the preliminary DNP experiment of protein crystals had already been succeded [Tanaka et al., Acta Cryst. D (in press)]. Here, as an advanced development of these techniques, the optimization of HPF method to make it easier to manipulate (large) single crystals and new radical doping for higher temperature DNP realization.

1M1430 中性子準弾性散乱及び動的光散乱による蛋白質のマルチスケールダイナミクス測定
The multiscale dynamics of proteins measured by quasielastic neutron scattering and dynamic light scattering

Satoru Fujiwara[1], Tatsuhito Matsuo[1], Fumiaki Kono[1], Kaoru Shibata[2] ([1]*QuBS, QST*, [2]*J-PARC Center*)

Proteins have a hierarchy of dynamics from local side-chain motions, through segmental and domain motions, to diffusion of the entire molecules. Elucidating how the dynamics at these different scales are related to each other is important for elucidation of the mechanisms of the protein functions. The dynamics at the different scales thus needs to be measured under the same condition. Here we propose a new method to measure the multiscale dynamics of the proteins. Combination of neutron and light scattering distinguishes the local motions, segmental motions, and diffusion of the entire molecules. We applied this method to ribonuclease A in the folded, molten-globule, and unfolded states, and showed that the degrees of the segmental motions are different in these states.

1M1448 チトクロム酸化酵素によるプロトンポンプは、酸素結合によって誘起されるタンパク質内構造変化によって厳密に制御されている
Structure changes induced by O_2-binding tightly regulate the proton-pumping of cytochrome c oxidase

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Cytochrome *c* oxidase (CcO) pumps protons by employing the electrostatic repulsion between protons incorporated through the water channel and net positive charges created by oxidation of heme *a* to reduce O_2 binding at O_2 reduction center composed of heme a_3 and Cu_B. To guarantee high efficient proton-pumping, CcO prevents pumping proton back-leakage by timely closure of the water channel. We directly observed the opening process of the channel coupled to the CO (O_2 analogue) release from O_2 reduction center using XFEL time-resolved crystallography. The opening process reveals that Cu_B senses completion of proton collection and binds O_2 prior to binding to Fe_{a3} to close the water channel using a conformational relay system among Cu_B, heme a_3 and a transmembrane helix.

1M1500 Finding potential 3D biological shapes for a small number of XFEL diffraction patterns

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Single particle X-ray Free Electron Laser (XFEL) scattering is a method that promises to probe biomolecules that have eluded us. However, in addition to the challenges faced in 3D reconstruction, XFEL diffraction patterns are in Fourier space. To overcome such issues, we propose an efficient yet accurate method to find 3D shapes to serve as a starting point. In our proposed strategy, a few XFEL diffraction images are matched against a library of simulated diffraction patterns from 1628 EM models, to find potential matching 3D shapes. In general, we find that defining matching regions on the diffraction patterns is critical for finding accurate matches, as well as the uniqueness of the shape and its availability in the library.

1M1512 単粒子解析における X 線自由電子レーザー回折像の定量的評価
Quantitative evaluation of the diffraction images for single particle analysis by X-ray free electron laser experiment

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Single-particle analysis by X-ray free electron laser (XFEL) is a novel method that can observe biomolecules and living tissue difficult to crystallize in a state close to nature. However, even with the strong beam of XFEL, the diffraction intensity obtained from single particles of biomolecules is weak, and the SN ratio of the diffraction image is extremely small. So, we have to identify the experimental diffraction images suitable for 3D reconstruction. In this presentation, we show the quantitative investigation that how the resolution of the reconstructed 3D structure depends on the amount and quality of the diffraction images, and discuss the requirement for experimental condition to restore molecular structures of a few nanometer resolution.

1O1330* 微小管の滑り運動における進行方向の長時間シミュレーション
Long-time simulation for the traveling direction of a microtubule in motility assays

Ryota Shinagawa, Kazuo Sasaki (*Grad. Sch. Eng., Tohoku Univ.*)

In vitro motility assays using protein filaments and molecular motors show collective behaviors of the filaments at the high density of them. Microtubules form vortex structures in the system consisting of microtubules and inner-arm dyneins (Y. Sumino *et al.*, Nature (2012)). To form vortices it is necessary that the traveling direction of a protein filament is maintained for a long time. However, it has not been clarified what physical properties maintain the direction of filaments. In this study, we constructed a mathematical model of a filament driven by molecular motors and calculated the relaxation time of the traveling direction of a filament by simulation analysis. We discuss what physical properties affect the relaxation time.

1O1342* キネシン駆動微小管の集団運動における立体障害相互作用の役割
The role of steric interaction in collective motion of microtubules driven by kinesins

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Collective motion is ubiquitous in biological system. To investigate mechanism of collective motion, we observed collective motion of microtubules driven by kinesins focusing on the relation between microscopic interaction and macroscopic pattern. We found that strong steric interaction produces strong alignment of a pair of colliding filaments but nonetheless prevents global alignment and rather forms clusters. Numerical simulations were also performed, which reproduced this observation. Furthermore, our experimental system showed various other collective behaviors, including order-disorder coexistence, global rotation, and looping. This study may provide new insights into dynamic ordering by self-propelled particles interacting with each other.

1O1354 境界に拘束されたアクトミオシンゲルの周期的な収縮現象と位置対称性の破れ
Periodic contraction of actomyosin gel and nucleus-like cluster positioning in a confined geometry

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Nucleus positioning is essential for cell division, polarization, and normal embryogenesis. It has been known that the centrosome controls geometric positioning of nucleus but several species of mammalian oocytes that lack centrosome structure can place nucleus at the center with the help of actomyosin. However, little is known about how actomyosin controls spatial positioning. Here, we study an artificial cell model which consists of nucleus-like object and actomyosin molecular motors in a confined space. We find that symmetry breaking of the object positioning occurs as the size of artificial cell decreases. Periodic actomyosin contraction is involved in this spatial positioning. We further construct active gel theory to reveal the mechanism of nucleus positioning.

1O1406 生化学反応における情報幾何と熱力学的な不確定性関係
Information geometry and thermodynamic uncertainty for biochemical process

Sosuke Ito (*Hokkaido Univ. RIES*)

The unified theory of information and thermodynamics reveals that information theory would be useful to understand small systems such as biochemical systems. We here discuss a new link between thermodynamics and information theory well known as information geometry. By applying this link, information geometric inequalities can be interpreted as thermodynamic uncertainty relationship between speed and thermodynamic cost. We have numerically illustrate this thermodynamic uncertainty relationship to a thermodynamical model of biochemical reaction.

1O1418 Chemical potential formalism for polymer entropic forces

Hong-Qing Xie, **Cheng-Hung Chang** (*Institute of Physics, National Chiao Tung University, Taiwan*)

Despite entropy plays an essential role in the behaviors of polymers in confined systems, it lacks a simple way to estimate its magnitude. Here, we derive an entropic force formula for partly confined polymers and show its mathematical correspondence to the widely used chemical potential formula for solutions. This formalism clarifies the force magnitudes inferred in several recent polymer and granular experiments and more generally predicts the force strengths in a variety of polymer systems in single molecule experiments and biological systems. This simple reference-based approach may largely ease an instantaneous quantitative description on that elusive force in scientific discussions.

1O1430* A new measure of the interrelation of cellular phenotypes in cellular reproductive systems

Shunpei Yamauchi, Yuichi Wakamoto (*Graduate School of Arts and Sciences, University of Tokyo*)

It is known that even when cells with the same genotype are in the same environment, phenotypes such as growth rate and gene expression level are greatly heterogeneous among cells. In this study, we propose a new measure of interrelation between phenotypes, considering two types of statistics on cellular populations: Retrospective statistics, which emphasizes cellular lineages that reproduce more descendants; and Chronological statistics, which dismisses such bias. We first define selection strength of phenotype based on those statistics, and introduce mutual selection strength as the intersection of the selection strength of two phenotypes. We show that mutual selection strength represents the gain of the correlation of phenotypes caused by cellular growth.

1O1448 A robotic system for combining single-cell RNA-seq with live cell imaging

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Single-cell RNA-seq provides a large volume of information about the states of individual cells. Although this method has been developed to study many biological processes, targeted cells are killed before sequencing, then time-course analysis of whole transcriptome expression is impossible. On the other hand, live cell imaging is useful to follow dynamic biological events. Here, we established a robotic system for combining single-cell RNA-seq with live cell imaging. This makes it possible to perform sequencing for individual cells observed under a microscope in a high throughput manner, which may link the information of dynamic behavior and whole transcriptome expression for a few thousand cells. We will discuss applications and future plans using this system.

1O1500* 糖摂取後のヒト血中分子濃度の時間変動解析
Time-series analysis of metabolic responsiveness to the oral glucose intake

Suguru Fujita[1], Yohei Sumitomo[1], Yasuaki Karasawa[2], Masashi Fujii[1], Shinsuke Uda[3], Kaoru Ohashi[1], Akiyoshi Hirayama[4], Tomoyoshi Soga[4], Shinya Kuroda[1] ([1]*Grad. Sch. of Sci., Univ. of Tokyo.*, [2]*Rehab. Med., Univ. of Tokyo. Hosp.*, [3]*Med. Inst. of Bioreg., Kyushu Univ.*, [4]*Inst. for Adv. Biosci., Keio Univ.*)

There are many kinds of metabolomes and hormones in human blood, whose metabolic homeostasis are mainly kept by organ. However, it was difficult to clarify those homeostasis since it is still unclear the blood concentration fluctuation of many kinds of molecules after meal intake. At first, we obtained a blood sample over time up to 4 hours from oral glucose intake in 20 healthy individuals and measured the molecular concentrations. Next, we found that the "magnitude of fluctuation" and "speed of fluctuation" of blood molecule concentration are necessary for classification into 13 clusters by principal component analysis and hierarchical clustering of a fluctuation index we defined.

1O1512* 線虫の Lifespan 解析に向けたマイクロ流体デバイスの構築
A two-story structured microfluidic device (WormFlo) toward recording of C. elegans motion during lifespan at the video-rate

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After the fertilization, animals develop, grows and ages, and eventually die. During lifespan, animals move in a mode characteristic in each lifestage. However, the statistical rule that governs the mode transition during lifespan remains unknown. In this study, we report a new microfluidic device (WormFlo). WormFlo has a two-story structure, where the flow path for buffer or medium is located at the first floor and 108 microchambers for culturing worms are located at the second floor. This structure minimizes physical stress when introducing worms to the device, and maximizes the chamber density. Using WormFlo, we successfully cultured worms and recorded their motions at the video rate for 6 days. We also report a plan to improve WormFlo for life-long observation.

1O1524* 細胞内微小環境における高分子と熱ダイナミクスの関係の解明
Study on the relationship between macromolecules and thermodynamics in intracellular microenvironment

Masaharu Takarada[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Graduate School of Pharmaceutical Science, The University of Tokyo.*, [2]*PRESTO, JST*)

Previous studies have shown that intracellular local temperature increase initiates stress granule (SG) formation, which is inhibited by excess amount of fluorescent polymer thermometer (FPT). However, thermodynamic mechanism of this phenomenon has not yet been revealed. By observing the temperature distribution by FPT, we have shown the followings; firstly, temperature gradient under local heating becomes low and broad in the FPT concentration-dependent manner, and secondly, the FPT accumulates in the heat source by the Soret effect. These results suggest that FPT accumulation-dependent interference of local heat inhibits SG formation, highlighting the interaction of thermodynamics and macromolecule in single cell.

1O1536* 単一細胞におけるミトコンドリアの４つのプロトンポンプ活性の連続計測
Sequential imaging of four proton pump activities of mitochondria in a single cell

Hiroko Kashiwagi, Yoshihiro Ohta (*Ohta. lab., Grad. Sch., Univ. Noko*)

For oxidative phosphorylation in mitochondria, three proton pumps and one H+-ATPase are included. Since the decrease in activities of these proteins has the deleterious effect on the cellular functions, the activities of these proteins are extensively examined. However, most measurements have been performed with a lot of cells. The aim of this study is to measure the activities of all of these proteins in a single cell. By the combination of specific substrates and inhibitors for these proteins, we successfully observed the mitochondrial membrane potentials generated by these proteins in a single cell with fluorescence microscopy after permeabilizing plasma membrane. After incubating cells with H2O2, the activities significantly decreased in the protein-dependent manner.

1O1548* 一粒子軌跡解析による洗浄工程を必要としないタンパク質のデジタル検出技術
Wash-free digital protein detection method by single particle tracking analysis

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Digital enzyme-linked immunosorbent assay (Digital ELISA) is a single molecule counting technology and one of the most sensitive immunoassay methods. However, since Digital ELISA needs many washing steps, the protocol is so complicated to apply for clinical use. Here, we propose the novel digital protein detection method that does not require washing steps. For a wash-free assay, the key challenge was to trigger signal generation only when target protein exists. In our method, we identified target by analyzing the motion of nanoparticles. The limit of detection of this method for PSA, a kind of cancer biomarker, detection was 12 fM. Our method is high sensitive and does not need for washing steps, so this method would be suitable for clinical diagnostics.

1Q1330* DNA 整列固定技術を用いた構造的 DNA 結合タンパク質のスライディング運動の単分子観察
Single-molecule investigation of the sliding dynamics of architectural DNA-binding proteins along crowded DNA using DNA garden technique

Kana Ouchi[1,2], Reid C. Johnson[3], Satoshi Takahashi[1], Kiyoto Kamagata[1] ([1]*IMRAM, Tohoku University*, [2]*Grad. Sch. Life Science, Tohoku University*, [3]*UCLA*)

Architectural DNA-binding proteins assist the function of other DNA-binding proteins by bending DNA and sliding along DNA. However, the surface of DNA in cells is crowded by the binding of other DNA-binding proteins, which may affect the sliding of the architectural DNA-binding proteins. We investigated the sliding dynamics of three architectural DNA binding proteins, Nhp6A, HU, and Fis along crowded DNA using DNA garden technique and single-molecule fluorescence microscopy. As the concentration of other proteins on DNA increased, the diffusion coefficient of Nhp6A along DNA decreased; however, the movement of Nhp6A was not restricted between two neighboring molecules. This suggests that the sliding of Nhp6A is slowed down by the collision with other molecules.

1Q1342* 人工細胞デバイス内に封入した長鎖 DNA 1 分子からの遺伝子発現
Gene expression from a single large DNA encapsulated in artificial cell device

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Reconstitution of autonomous artificial cells requires encapsulation of a large DNA and components for gene expression and replication into cell-sized reactors. In this work, we developed the artificial cell device system, in which cell-free protein synthesis from a large DNA was implemented. This device contains cell-sized reactors (φ=5 μm) encapsulating 200 kbp DNA of which hydrodynamic diameter is about 2 μm. Without chemical modification of reactors, DNA wasn't entrapped into reactors. Supposing the electrostatic repulsion between DNA and reactors, reactors were modified with cationic polymer, and DNA was successfully encapsulated into reactors. A fluorescent protein was synthesized from encapsulated DNA with comparable yields of that from short DNA fragments.

1Q1354* シスプラチンとトランスプラチンによる DNA への異なる作用：DNA 高次構造と遺伝子発現
Different effect between cisplatin and transplatin on the higher order structure of DNA and gene expression

Toshifumi Kishimoto[1], Yuko Yoshikawa[1], Seiji Komeda[2], Kenichi Yoshikawa[1] ([1]*Grad. Sch. Life Med. Sci., Univ. Doshisha*, [2]*Fac. Pharm., Univ. Suzuka. Med. Sci*)

Cisplatin is widely used as an anticancer drug. On the other hand, transplatin has been regarded as clinically ineffective. In this study, we compared the effects of cisplatin and transplatin on gene expression in vitro by luciferase assay. We found that inhibitory effect of cisplatin on gene expression is ca. 6 times higher than that of transplatin. As for the higher order structure of DNA, transplatin tends to cause intermolecular aggregation, whereas both compounds induce shrinking on DNA. We will discuss the mechanism of inhibitory effect on gene-expression in terms of the structural change of DNA. This study is expected to contribute to the development of rapid, quantitative and in vitro screening methodology for evaluating the candidate of new anticancer drugs.

1Q1406* Elucidating transcriptional mechanisms of NF-kB target gene expression based on various sequence data

Minami Ando, Shigeyuki Magi, Kazunari Iwamoto, Mariko Okada (*Institute for Protein Research, Osaka University*)

Upon TNF-α stimulation, transcription factor NF-kB enters nucleus and transcribes genes including its inhibitor IkBα. This negative feedback generates oscillatory dynamics of nuclear NF-kB. However, the biological significance of NF-kB oscillation is still unclear. To elucidate this, we analyzed timecourse RNA-seq data obtained from MCF-7 cells stimulated with TNF-α. Our developed method identified 29 genes showing oscillation as well as NF-kB. The analysis of NF-kB ChIP-seq revealed that NF-kB was highly enriched at promoters of the oscillating genes, compared to non-oscillating genes. In addition, the binding pattern of NF-kB to oscillating gene promoters also showed oscillation. We will investigate how its binding is regulated by chromatin structure and modification.

1Q1418 海洋性細菌 *Vibrio alginolyticus* 4 株 (138-2, VIO5, YM4, YM19)のゲノム構造比較解析
Comparative analysis of whole genome structure of marine bacteria *Vibrio alginolyticus* spp. strains 138-2, VIO5, YM4 and YM19

Kunio Ihara[1], Keita Inaba[1], Kazuma Uesaka[1], Masayuki Nakamura[1], Noriko Nishioka[2], Seiji Kojima[2], Michio Homma[2] ([1]*Nagoya University Center for Gene Research*, [2]*Nagoya University Graduate School of Science*)

In order to study the dual flagellar system (polar and lateral) in a marine bacterium Vibrio alginolyticus, we constructed mutant strains from a wild type strain 138-2 (Pof^{+}, Laf^{+}) about 20 years ago. A strain VIO5 (Pof^{+}, Laf^{-}) was created by natural mutation, and two strains YM4 (Pof^{+}, Laf^{-}) and YM19 (Pof^{-}, Laf^{+}) were created by UV-mutagenesis. Now, we have determined the whole genome structure of these 4 strains and picked up all genomic variations including SNVs and indels. The number of the genomic variations were consistent with the method for creating mutants and the order of isolation. Putative responsible genes for different flagellation were found in three mutants and discussed in detail in the meeting.

1Q1430 Discovering novel functional genome structures in Dengue and Zika viruses through experiment and multi-scale modeling

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Viral genomes are highly dynamic and undergo structural changes throughout a complex life cycle. We apply biophysical techniques to study structural features of Dengue and Zika viral RNA. In addition to known regulatory structural elements in the 5' and 3' UTRs we show that the coding regions contain structures that are highly conserved within and across serotypes and that these structures are functionally important for viral replication. To this end, we employ chemical structure probing techniques in conjunction with next-generation sequencing to derive information on the fold of the viral genomes. We use coarse-grained molecular simulations to create 3-dimensional models that allow us to understand the spatial arrangement of structural elements within the viral RNA.

1Q1448* モデルペプチドを用いた MD シミュレーションによる膜タンパク質複合体形成にコレステロールが及ぼす影響の検討
Influence of cholesterol on membrane protein complex formation by molecular dynamics simulations with model peptides

Hayato Itaya[1], Kota Kasahara[1], Katumi Matsuzaki[2], Yoshiaki Yano[2], Takuya Takahashi[1] ([1]*Coll. Life Sci., Ritsumeikan Univ*, [2]*Grad. Sch. Pharm.Sci., Kyoto Univ*)

Membrane proteins play important roles in living organisms. Whereas it is known that their dynamics is closely related to the nature of lipids, the mechanisms of this relationship has not been fully clarified yet. Therefore, this study aims to clarify how lipid affects the structural dynamics of membrane protein complex using computer simulation. A complex of two model peptides that are Ala-based single-helix and 2-helix-bundle is created by homology modeling and embedded into membranes with/without cholesterol. We simulated these system and analyzed how closely interacting and their bindings modes. As a results, cholesterol modulates their binding modes and gains tightness of the intermolecular contacts.

1Q1500 Chiral selectivity mechanism on aminoacylation of an RNA minihelix examined by molecular dynamics simulations

Tadashi Ando[1], Koji Tamura[2] ([1]*Dept. Appl. Elec., Tokyo Univ. of Sci.*, [2]*Dept. Biol. Sci. & Tech. Tokyo Univ. of Sci.*)

The origin of homochirality in L-amino acid in proteins is one of the mysteries of the evolution of life. Experiments show that a non-enzymatic aminoacylation reaction of an RNA minihelix by aminoacyl phosphate oligunucleotides has a clear chiral preference for L-amino acids over D-amino acids. In this study, by employing molecular dynamics simulations, we explored the possible mechanisms that determine the chiral selectivity of the RNA minihelix. With the same force field parameters except chirality of alanine, the simulation system adopts a geometry required for the chemical reaction to occur more frequently with L-alanine than that with D-alanine. The preference was likely explained by simple chemical principles.

1Q1512* タンパク質 FUS の液滴・凝集形成に関する分子動力学シミュレーション
Molecular dynamics simulations of liquid droplet and aggregation formations of protein FUS

Hiroki Terazawa, Kota Kasahara, Takuya Takahashi (*Coll. Life Sci., Ritsumeikan Univ*)

Liquid droplet and aggregate formations cause various kinds of biological effects. However, little is known for these microscopic processes and effects because it is difficult to perform molecular simulations for these processes due to insufficiency for methodological developments. In this study, we developed our original molecular dynamics simulation software and analyzed the phase diagrams which are reported in previous experiments. As a model case, we conducted a molecular dynamics simulation of FUS using myPresto/Omegagene software and coarse-grained model. Then we discuss reproducibility of the simulated phase diagram and effects of simulation models and parameters.

1Q1524 深層学習を用いたゲノムシークエンスのクラスター解析
Graphical Classification of DNA Sequences of using Deep Learning

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We are developing a method to outlook the nature of genomic sequences as mitochondria DNA. Usual ORF sequences are too long to recognize for human intelligence. Some special part of the genes are used as nameplates. Such part (as SNPs) might not represent the whole structure of entire sequence. Deep learning is a method to project a complex system to another complex system, which human intelligence can recognize easier. DNAs are classified and expressed graphically by using artificial intelligence "Deep Learning/Autoencoder". The two-dimensional plot of DNAs gives a clear outlook for characterizing the genes.

1Q1536* ニューラルネットワークを用いたタンパク質 N-gram 配列間相互作用の予測
Predicting interactions between N-gram sequences in proteins by using Neural Network

Ryohei Kondo[1], Kota Kasahara[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

Elucidating principle of protein sequence-structure-function relationship is a key issue in biophysics. Toward this, it is important to analyze enormous data of protein structure accumulated in Protein Data Bank (PDB). We first focused on the effects of subsequences on conformations and functions of proteins. Specifically, we decomposed sequences of many proteins in PDB into short sequences consisting of six residues (called Hexa-gram). The interactions between Hexa-grams were analyzed by using neural network. As a result, it was possible for the prediction of interactions between Hexa-grams in same chain with about 64.3 % accuracy. Interactions between Hexa-grams in other chains were predicted with about 62.3 % accuracy.

1Q1548 蛋白質立体構造と機能に影響しうるゲノムバリアントの選択と解析
Extraction and analysis of missense variants with possible impact on protein structure and function

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Recent population genomics studies have been discovering a huge number of missense variants in human genome, a large proportion of which remain functionally unannotated. The information from three-dimensional (3D) structures of proteins plays important roles in estimating the functional impact of these missense variants, but a comprehensive application of Protein Data Bank structures to genome-wide vairants remain challenging. In this study, a genome-wide annotation system for missense variants with protein structure information was developed. Using this method, missense variants of unknown significance were assessed with their possible impact on protein structure and function.

2A1400 Cell-size dependent polarity dynamics revealed by high-throughput imaging and machine learning analysis

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To understand the nature of cell-to-cell heterogeneity in cell migration and chemotaxis, we developed parallel arrays of linear channels of several micrometers wide for high-resolution image acquisition from several hundred isolated cells in a single run. We utilized machine learning for the feature extraction and clustering of the leading-edge signaling dynamics obtained from the high-throughput imaging. From the analysis, we show that the migration speed of Dictyostelium and neutrophil-like HL60 cells depends on cell-size and that there are distinct modes of cell polarity dynamics. Our results suggest that there is a reaction-diffusion based mechanism of actin assembly organization that underlies the polarity dynamics.

2A1412 Elucidating pathogenesis of congenital muscular and neuronal diseases caused by defective membrane remodeling of dynamin GTPase

Tetsuya Takeda, Kenshiro Fujise, Yuta Nobunaga, Hiroshi Yamada, Kohji Takei (*Grad Sch Med Dent Pharm Sci, Okayama Univ*)

Dynamin is a mechanochemical GTPase essential for membrane fission in endocytosis. Dynamin forms helical complexes at the neck of endocytic pits and their structural changes upon GTP hydrolysis drive membrane fission. Our recent HS-AFM study revealed a novel mechanism of the dynamin mediated fission (Takeda et al., Elife 2018). Dynamin is also known to be a responsible gene for centronuclear myopathy (CNM) and early infantile epileptic encephalopathy (EIEE) that are congenital diseases in muscles and in neurons, respectively. In this study, we will present our recent findings about the impact of the disease-related mutations in dynamin on its membrane remodeling activity in vitro and in cellulo aiming to understand pathogenesis of these intractable diseases.

2A1424 イノシトールリン脂質代謝系の細胞内自己組織化現象の超解像イメージングによる解析
Super-resolution imaging analysis of self-organization mechanism in phosphoinositide signaling system on the cell membrane

Satomi Matsuoka[1,2], Hiroaki Takagi[1,3], Seiya Fukushima[2], Yukihiro Miyanaga[1,2], Masahiro Ueda[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. Frontier Biosciences, Osaka Univ.*, [3]*Sch. Med., Nara Med. Univ.*)

Phosphatidylinositol 3,4,5-trisphosphate, $PI(3,4,5)P_3$, is a signaling molecule that determines direction of locomotion in eukaryotic cell movement. $PI(3,4,5)P_3$ accumulates in a self-organized manner on the inner leaflet of cell membranes as a consequence of the reaction and diffusion of the relevant molecules such as Ras, PI3K, PTEN, $PI(4,5)P_2$ and $PI(3,4,5)P_3$. We performed statistic analysis of their spatial distribution on the membrane revealed under photo-activation localization microscopy (PALM) in fixed Dictyostelium discoideum cells. It has been suggested that the molecules were concentrated to submicron-sized domains on the membrane, which will be discussed in relation to the self-organization mechanism.

2A1436 Ras 依存的に作られる PIP3 局在パターン形成の観察とモデル化
Observation and modeling of Ras dependent PIP3 localization pattern formation

Seiya Fukushima[1], Satomi Matsuoka[2], Masahiro Ueda[2,3] ([1]*Grad. Sch. of Sci., The Univ. of Osaka*, [2]*Riken BDR*, [3]*Grad. Sch. of Frontier Bio-Sci., The Univ. of Osaka*)

Eukaryotic cells show the polarization corresponds to cell migration. Some signaling molecules accumulate in an anterior part of a cell, especially, Ras small GTPase and PIP3 Phosphatidylinositol lipid show localization pattern on a cell membrane. In this study, by using high-sensitive multi-color TIRFM, we succeed in comprehensive observation of components of PIP3 synthesis (PIP2 and PI3K) and degradation (PTEN). From the result, we found Ras GTPase is a key regulator of PIP3 domain formation through membrane translocation of PI3K. PI3K accumulates on a membrane before PIP3 accumulation in a Ras-GTP dependent manner. We demonstrate that Ras is dominant in the self-organized localization pattern of signaling molecules.

2A1448 走化性 G タンパク質共役受容体は濃度依存的に三量体 G タンパク質の制御機構を切り替えて走化性レンジを拡張する
Chemoattractant receptor-mediated activation, membrane recruitment and capture of G proteins enable wide range chemotaxis

Yukihiro Miyanaga[1], Yoichiro Kamimura[2], Hidekazu Kuwayama[3], Masahiro Ueda[1,2] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*RIKEN Center for Biosystems Dynamics Research*, [3]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

The wide range sensing of extracellular signals by living cells has been explained by negative feedback mechanisms such as the chemical modification and down-regulation of receptors. Here we report an additional but essential regulation on the cognate G protein for wide range chemotaxis. Receptor-mediated activation, recruitment, and capturing of G protein mediate chemotactic signaling at the lower, middle and higher concentration ranges, respectively, in Dictyostelium cells. Especially, the capturing of activated Gα by the receptor formed an unexpected complex specifically at the higher range and prolonged the membrane-binding lifetime of Gα leading to its local accumulation along the chemical gradient and thus extending the chemotaxis range.

2A1500 CLIP-170 は細胞接着表面でタンパク質をプラス端へ運ぶことにより免疫 T 細胞活性化における中心体の細胞表面への移動を制御している
CLIP-170 is essential for MTOC repositioning during T cell activation by recruiting proteins to the plus-end tracking on the cell surface

Wei Ming Lim[1], Yuma Ito[1], Kumiko Sakata-Sogawa[1,2], **Makio Tokunaga**[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Grad. Sch. Agr. Sci., Tohoku Univ.*)

Microtubule-organizing center (MTOC) repositioned to the center of the contacted cell surface, the immunological synapse, during T cell activation. However, our understanding of the underlying molecular mechanism remains limited. We investigated how the microtubule plus-end tracking cytoplasmic linker protein 170 (CLIP-170) regulates MTOC repositioning. Simultaneous dual-colour fluorescence live-cell microscopy enabled us to obtain plenty of findings on molecular interactions and localisations. Inhibition of CLIP-170 phosphorylation impaired both MTOC repositioning and full activation of T cells. We found that CLIP-170 plays a novel role in MTOC repositioning by recruiting proteins to the plus-end tracking and by regulating localization of the proteins.

2A1518 大腸菌走化性応答適応過程の CW bias タイムトレースを記述するパラメータは、培養停止時の OD600 値に相関する
Parameters describing CW bias time traces of adaptation of chemotaxis of cells of E. coli correlate to OD 600 value at cell culture stop

Hiroto Tanaka[1], Yasuaki Kazuta[1], Risa Tsubomoto[1,2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[1] ([1]*KARC, NICT*, [2]*University of Hyogo*)

We have developed a chemical substance identification method by using E. coli tethered assay. Our method is based on statistical speculation of input chemical species (stimulus by attractants) from response output, CW bias Time traces of Adaptation of Chemotaxis Averaged over hundreds of Cells (CW-TACAC) of E. coli. We had acquired a large amount of data for statistical analysis of input/output relation, and then, we found that shapes of CW-TACAC vary depending on OD600 value at cell culture stop even if species and concentration of chemicals are same. Here, we report quantitative analysis of correlation between CW-TACAC and OD600 value in case of attractant amino acids. We will discuss chemical type-dependent correlation in accordance with signaling system.

2A1530 ヒト精子運動性に影響を与える静水圧負荷の閾値
Hydrostatic pressure threshold for the reduction of human sperm motility

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Hydrostatic pressure (HP) can potentially be used for human sperm freezing. We evaluated the motility parameters of human sperm treated with HP of 20 and 40 MPa for 90 min. Treatment with 40 MPa decreased the average curvilinear velocity to half of that observed in a static control. After 60 min of incubation at atmospheric pressure, the average recovery rate reached 80% of the control. Treatment with 20 MPa did not alter the average curvilinear velocity. Motility of sperm after 20-MPa treatment was 60%-70% but decreased to 20%-30% after 40-MPa treatment. Results suggest that excess HP induces structural changes in motor proteins and inhibits flagellar beating.

2A1542 カルシウムイオンを介した精子鞭毛波形制御における cAMP の調整効果
cAMP modulates Ca^{2+}-mediated regulation of sperm flagellar waveform

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To elucidate the roles of Ca^{2+} and cAMP on the regulatory mechanism of sperm flagellar motility, we performed the experiments using membrane permeable caged cAMP in the ascidian *Ciona intestinalis*. Transient increase of cAMP by UV uncaging induced a highly asymmetric flagellar waveform and a subsequent symmetric waveform, which appeared analogous to the waveform change during sperm chemotactic turn. Live imaging revealed a transient increase of intracellular Ca^{2+} concentration when the flagellar waveform was converted to a highly asymmetric one. On the other hand, UV photolysis of caged cAMP in low Ca^{2+} conditions induced only symmetric flagellar waveforms. These results suggest that cAMP has a role in the symmetrization of Ca^{2+}-induced asymmetric flagellar waveform.

2A1554 緑藻クラミドモナスの走光性における鞭毛運動調節
Regulation of flagellar motion for phototactic turning in *Chlamydomonas*

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The unicellular green alga *Chlamydomonas reinhardtii* detects environmental light conditions with the eyespot. It displays both positive and negative phototaxis. However, how they change the swimming direction upon photodetection was unclear. By high-speed observation of phototactic turnings cells, we found that one of the two flagella ("dominant" flagellum) beats stronger than the other upon photodetection for reorientation. Dominant flagellum in a positively phototactic strain is the trans flagellum (the flagellum farthest from the eyespot) and that in a negatively phototactic strain is the cis flagellum (the other one). We identified the responsible gene of a negatively phototactic strain, and its product is localized in the cell body, not in flagella.

2A1606 細菌べん毛繊維の成長端の構造
Structure of the growing end of the bacterial flagellar filament

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The bacterial flagellum is a long filamentous organelle for locomotion. The flagellar filament is a helical assembly of about 20,000 flagellin subunits. The subunits are exported through the central channel to the distal end of the filament and incorporated into the growing structure beneath the cap complex attached at the tip of the filament. The cap is a pentameric assembly of FliD and essential for the filament growth. To understand the filament growth mechanism, we have determined the crystal structure of the FliD pentamer and analyzed the flagellar tip structure by cryo electron microscopy. On the basis of the structures, we will discuss the interaction between the cap and the filament tip and how the cap promotes the flagellin assembly.

2A1618 FliF 構造から見出された細菌べん毛と III 型ニードル複合体の構造類似性
Similarity between the bacterial flagellum and the type III injectisome revealed by the X-ray crystal structure of FliF fragment

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The bacterial flagellar MS-ring is composed of FliF, a two-transmembrane protein with a large periplasmic region. FliF interacts with various flagellar components and serves as an assembly base for flagellar formation. Here we determined the crystal structure of a periplasmic fragment of FliF, $FliF_{58\text{-}213}$, at 2.3 Å resolution. The structure of $FliF_{58\text{-}213}$ consists of two domains, and the domains show structural similarity with periplasmic domains of PrgH and PrgK in the type III injectisome, and SpoIIIAH in the spore-forming complex. Structural comparison and mutational analysis suggest that the domain II forms a ring around the central pore of the MS-ring, and a loop in FliF domain II interacts with FlhA, a secretion apparatus component.

2C1400 細胞分化への現象論的アプローチ：エピジェティクスによる安定細胞タイプの形成
Phenomenological approach to cell differentiation: generation of stable cell type by epigenetics

Yuki Matsushita, Kunihiko Kaneko (*The University of Tokyo Department of Basic Science*)

Cell differentiation is an interesting phenomena that a cell specialize to another specialized cells during development. Each specialized cells have same DNA sequence, but they take different protein composition as their own stable state. Since Waddington invented epigenetic landscape, it is considered that epigenetic regulation, such as DNA methylation, is important for cell differentiation. But it is unknown that how epigenetic regulation works for cell differentiation. For phenome- nological understanding, we introduce a model gene expressions are determined by genetic regulation and epigenetic regulation. We found oscillation of gene expression is important for cell differentiation and specialized process appear as dimension reduction in gene expression space.

2C1412 ヒト iPS 細胞由来の原腸形成期の中胚葉と内胚葉はランダムに動く
Random Migration of Induced Pluripotent Stem Cell-Derived Human Gastrulation-Stage Mesoderm and endoderm

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In this study, we show that the intrinsic cell movement (isolated single cells, 2-dimensional, no chemical cues) during early human body formation (gastrulation-stage) is random.
Because of ethical limitations, the early dynamics of forming the human body are unknown. To overcome this limitation, we used human pluripotent stem (iPS) cells, which correspond to epiblast (future baby). We focused on the mesoderm and endoderm cells (future muscle and gut) during the gastrulation stage, which is the initial systematic deformation of the embryo.
A random walk analysis of time-lapse images of dispersed single mesoderm and endoderm cells showed that the migration modes are both random. The random migration might help to form homogeneous germ layers of the human.

2C1424 肺上皮シートの分岐形態形成における ERK 活性を介したメカノ応答
ERK activity-mediated mechanoresponse in branching morphogenesis of lung epithelial sheet

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In developing lung, an epithelial monolayer sheet changes its shape via cell-cell mechanical interactions, and requires extracellular signal-regulated kinase (ERK). However, underlying mechanisms bridging the ERK and the cellular activities are poorly understood. In this study, we employed mouse embryos expressing FRET biosensors for ERK activity, and performed multi-photon live imaging using organ culture systems. Through imaging analysis, we found that spatiotemporal distribution of ERK activity changes according to the curvature of epithelial sheet. Moreover, mechanical stimuli assay revealed that the ERK activity is regulated by cellular mechanical state in the sheet. We discuss ERK activity-mediated mechanoresponse system for the epithelial sheet morphogenesis.

2C1436 流体力学における「クラミドモナスのモデル種」の重力走性
Gravitaxis of "*Chlamydomonas* model species" in hydrodynamics

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Unicellular green alga *Chlamydomonas* is now known as a puller-type microswimmer as well as a leading model organism for basic biology. Early investigators in hydrodynamics used *Chlamydomonas nivalis*, a snow alga, for their experiments. This species is not the same as *Chlamydomonas reinhardtii*, a common model species for biology, that recently is also popular among physicists to study low Reynolds number hydrodynamics. Despite its potential importance, the difference in motility between these two species of "*Chlamydomonas*" has not been clarified to my knowledge. Here, I would like to compare the swimming characteristics of *Chlamydomonas reinhardtii* and "*C. nivalis*" (strain SAG26.86, now renamed *Chloromonas typhlos*) with emphasis on gravitaxis.

2C1448 走化性受容体クラスター形成に対するヒスチジンキナーゼとアダプターの影響
Effects of the histidine kinase and the adaptor protein on chemoreceptor clustering in the bacterial cytoplasmic membrane

Tomoya Yamazaki[1], Nana Ito[1], Masatoshi Nishikawa[1], Yoshiyuki Sowa[1,2], **Ikuro Kawagishi**[1,2] ([1]*Dept. Frontier Biosci., Hosei Univ.*, [2]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

The chemoreceptors of *Escherichia coli*, together with the histidine kinase CheA and the adaptor protein CheW, forms a huge cluster at a cell pole that has been implicated in signal amplification. It has been shown that the aspartate chemoreceptor Tar fused to GFP is first inserted into the lateral region of the cytoplasmic membrane and then migrates toward the cell pole via lateral diffusion. Here we examined how CheA and CheW influence migration and/or clustering of Tar-GFP molecules using TIRF microscopy. Intensities and mean square displacements of single fluorescent foci suggest that Tar-GFP molecules cluster upon lateral diffusion and that CheW plays a critical role in the formation and/or stability of the receptor cluster.

2C1500 コレラ菌新規アミノ酸走性応答系の同定
The novel chemotactic transducer Mlp3 of *Vibrio cholerae* mediates serine chemotaxis via a putative periplasmic binding protein

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Vibrio cholerae, the etiological agent of cholera, has two MCP-like proteins (MLPs), Mlp24 and Mlp37, that serve as major chemoreceptors for amino acid taxis. However, the mutant lacking both of them showed weak but significant responses to amino acids in capillary assay. We found that additional MLPs, Mlp2 and Mlp3, mediate attractant responses to serine. Isothermal titration calorimetry measurements detected no direct binding of serine to Mlp2 or Mlp3. Among the five putative amino acid-binding proteins of ABC transporters, one named SatA, when co-expressed with Mlp3, enhanced an attractant response to serine. These results suggest that Mlp3 is a transducer that requires this putative binding protein as a soluble serine receptor.

2C1518 マウス脳スライスの温度イメージング法の開発と虚血性脳浮腫のメカニズムの解明
Imaging temperature of mouse brain slice reveals the mechanism of ischemic brain edema

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Temperature influences many physiological functions of organisms. Previously, we demonstrated the first intracellular temperature imaging based on a fluorescent polymeric thermometer (FPT). Here, we have developed a method of imaging of temperature of mouse brain slice to study the biological significance of intracellular temperature variations. By utilizing cell-permeable FPT and fluorescence lifetime imaging microscopy, we were able to observe the temperature-dependent change in the fluorescence lifetime of FPT in cells of brain slice. We also detected ischemic stimulation-dependent temperature increase in cellular temperature of brain, showing the feasibility of our new method in investigating the function of thermal signaling in brain physiology.

2C1530 生体神経回路網における連続入力刺激に対する応答パターンの再現性と階層性
The hierarchical feature and reproducibility of electrical response patterns induced by sequential inputs in a living neuronal circuit

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The electrical activity patterns in a living neuronal circuit are fundamental elements of code for information processing in a brain. To observe the characteristic of neuronal response pattern, a living neuronal circuit is useful. In this study, we cultivated rat hippocampal cells on a multi-electrode array(MEA) dish and applied hierarchical clustering to spatiotemporal patterns of electrical responses induced by electrical stimulus via randomly selected one of three stimulation electrodes. We found response patterns from the same stimulation electrode formed a cluster and the patterns were modified by hysteresis of sequential inputs. These results indicates that the living neuronal network separates and classifies the sequential inputs influenced by the hysteresis.

2C1542 Voltage-sensitive dye imaging of the interhemispheric neural activity across the anterior cingulate cortex (ACC) via corpus callosum

Pooja Gusain, Makiko Taketoshi, Yoko Tominaga, Takashi Tominaga (*Tokushima Bunri University*)

Abstract: The anterior cingulate cortex controls higher-order functions between the interhemispheric brain activities via callosal projection. To investigate the functional connection, we studied neural activity propagation in mice slice preparations containing intact corpus callosum ACC using voltage-sensitive dye (VSD). To acquire entire activation, we constructed a new imaging system. The neural activity evoked by a brief electrical stimulation spread not only in the vast areas of the ipsilateral side but also in the contralateral side. We here report the functional connectivity between the hemispheres before and after micro-surgical section near corpus callosum. We discuss that deep layer of the cingulate cortex two is crucial for the interhemispheric connectivity.

2C1554 海馬 CA1 でペアドバースト促通（PBF)はフィードバックとフィードフォワードの異なる GABA 作動性制御を使う
The paired burst facilitation (PBF) of the hippocampus employ the distinct feedforward- and feedback- GABAergic controls in the circuit

Takashi Tominaga, Yoko Tominaga (*Inst. Neurosci., Tokushima Bunri Univ.*)

The theta oscillation (5-8 Hz) is the critical oscillatory activity in the hippocampus. We have found that the pair of the burst of the theta activity induced a novel type of facilitation (PBF). Since the PBF was apparent in the sub-threshold stimulation, we thought that the feedforward GABAergic inhibition should be involved. To examine this possibility, we divided Schaffer collateral fibers into two groups with micro-surgery and applied stimulation separately. The PBF appeared when we delivered a burst stimulation into the same pathway. On the other hand feedback- control suppress both inputs. The PBF may act to control the input pathway's specific amplification while to inhibit different pathways for oscillatory calculations in the circuit.

2D1400 Multimodal persistence of antibiotic-stressed Escherichia coli

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Under antibiotic-drug treatment, a small fraction of cells in isogenic population survive without genetic mutation. It has been considered that these surviving cells termed as persisters are dormant cells in the population. Here we report the coexistence of various persistence modes in Escherichia coli exposed to lethal dose of β-lactam antibiotics. We studied persistence of E. coli at the single-cell level under several physiological conditions (exponential or late-lag phase; in rich or minimal media), finding that the persistence modes strongly depend on those conditions. In most cases, the persisters were growing normally before drug exposures, which suggests that dormancy is only one of the possible physiological courses for survival in persistence.

2D1412 β1, 3 インテグリンの接着斑形成・分解における機能：超長時間蛍光 1 分子追跡法による解明
β1 and 3 integrin function in focal adhesion formation and disintegration: unraveling by super-long single-fluorescent molecule tracking

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Newly developed super-long single-fluorescent molecule tracking revealed that β1 and β3 integrins entered and exited from the focal adhesion (FA) region readily and, in addition, diffused inside the FA, with intermittent stationary periods (0.5-80-s lifetime), probably due to their binding to the FA protein islands. β1 tended to undergo longer stationary periods when FAs grow and to move away from the FA upon FA disintegration. Meanwhile, β3 arrived later when FAs grow and also exited later from disintegrating FA, than β1. Consistently, loss of tension induced earlier β1 disappearance than β3. These results suggest that β1 integrin is responsible for initiating the FA formation and disintegration, whereas β3 integrin is for FA maintenance.

2D1424 生理的 RNA 顆粒形成過程の細胞内温度測定
Intracellular temperature measurement during RNA granule formation for thermal biology

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RNA granules are non-membranous ribonucleoprotein aggregates that spatially and temporally regulate translation. Previously, we showed that temperature variation inside mammalian cells is essential for initiating RNA granule formation. However, the contribution of temperature to RNA granule formation on the physiological level is uncertain. In this study, we performed temperature imaging during this phenomenon by introducing a fluorescent polymeric thermometer and an antisense RNA probe into the gonads of C. elegans. We succeeded in observing P granule while visualizing temperature distribution in germ line cells and finding the relation between temperature and P granule assembly. This technique will help to clarify the mechanism of physiological RNA granule formation.

2D1436 Genetically encoded photoswitchable indicators towards super-resolution calcium imaging

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In fluorescence microscopy, photoswitchable proteins are exploited to resolve nanostructures at spatial resolution beyond the diffraction limit. To image calcium dynamics at increased resolution, we describe genetically encoded calcium indicators possessing photoswitching capability. Upon calcium binding to the indicators, fluorescence resonance energy transfer (FRET) was enhanced between a photoswitchable donor and its acceptor by closing of distance. We constructed such indicators comprised of various combinations of FRET pairs and calcium-binding linker domains. Their photophysiology and calcium response were compared in mammalian cells, which leaned towards compatibility with several super-resolution microscopy techniques.

2D1448 遺伝子コード可能な HyperCEST MRI 造影剤の開発
Multiplexed HyperCEST detection of genetically-reconstituted gas vesicle nanoparticles in human cancer cells in vitro

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Gas vesicle nanoparticle (GV) is the gas-containing protein assembly expressed in part of bacteria and archaea. Recently, it attracts much attention on their biotechnological application as genetically-encoded contrast agent for MRI and ultrasonography. However, the lack of methodology for induction of gas vesicle nanoparticles in mammalian cells has hindered its practice. Here we report the genetic reconstitution of GV in a human breast cancer cell line KPL-4 and genetic control of their size and shape by combinatorial expression of humanized GV genes referencing the natural GV gene clusters of planktothrix rubescenes / agardhii. We also demonstrated their utility as multiplexed, ultra-sensitive and genetically-encoded HyperCEST MRI contrast agent.

2D1500 回折限界内に位置するミオシン複数分子の動態計測
Measuring dynamics of individual skeletal myosin molecules located within diffraction limit space

Motoshi Kaya, Yuto Ashida, Masahito Ueda, Hideo Higuchi (*Graduate School of Science, The University of Tokyo*)

In in-situ sarcomere, ~20 myosin molecules aligned along one-half side of myosin filament (~700 nm) can interact with a single actin filament. We found that force generations among these myosins are potentially coordinated. Hence, in order to investigate coordinated force generations among myosins, we applied the multi-emitter localization (MEL) method to detect the positions of individual myosin molecules located within diffraction limit on myosin filaments. The scattered images of gold nanoparticles attached to myosin heads were recorded by high speed camera at 10000 fps. The MEL method detects movements of two myosin molecules from scattered images and revealed occasionally synchronized displacements of these molecules when actin filament slides past myosin filament.

2D1518 Microtubule defects, self-healing, and tubulin bond energies with high-speed AFM

Christian Ganser, Takayuki Uchihashi (*Nagoya University, Department of Physics*)

Defects in microtubules (MTs) impede their functions by reducing the MTs stiffness and hampering the movement of the motor proteins kinesin and dynein. Studying the creation of defects or their impact on the movement of motor proteins requires a fast measurement technique as defects can change size within seconds. Using high-speed atomic force microscopy (HS-AFM) based force measurements it is possible to create a defect and record topography about 100 ms after force application. This opens the possibility to study the self-healing of tubulin defects, which happens within a few seconds after damage occurs. Further, we present quantitative force measurements during defect creation and subsequent determination of tubulin bond energies.

2D1530 光ピンセット・探針走査型高速 AFM 複合装置を用いた外力印加中の一分子ライブイメージング
Live Imaging of Single-Molecules under External Force using Tip-Scan High-Speed AFM Combined with Optical Tweezers

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Tip-scan type high-speed AFM (HS-AFM) has recently been developed, in which the sample stage is fixed, while the cantilever tip is scanned over the sample. Since all the mechanical and optical components of this system are positioned above the sample stage, the tip-scan HS-AFM setup can make a good combination with an inverted optical microscope. In this study, we combined the HS-AFM system with optical tweezers (OT) to observe dynamic behavior of a biomolecule while it is being pulled with the OT via a long λDNA. In this talk, we will discuss the potential applications of this combined system.

2D1542 高速イオン電導顕微鏡を用いた脂質膜の表面電荷密度のナノ解像マッピング手法の開発
Development of nanoscale mapping of surface charge density of lipid membranes by high-speed ion conductance microscopy

Shusei Kaihatsu[1], Kazuki Shigyo[2], Toshio Ando[2], Shinji Watanabe[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

The surface charge density (SCD) of lipid membranes is important for understanding and designing the membrane binding mechanism, liposome formation, and biological drug delivery systems. However, the detection of SCD of lipid membranes is known to be difficult in a physiological liquid environment. Very recently, it has been discovered that scanning ion conductance microscope (SICM) has the capability of measuring the SCD of lipid membranes with nanoscale spatial resolution even in the physiological condition. In this study, we will discuss the mechanism of the SCD detection measured by SICM and show the spatial distribution of the SCD of lipid membranes on a substrate. In addition, our improvement on the detection speed of the SCD will be reported.

2D1554 高速イオン伝導顕微鏡による生細胞表面の観察
Observation of Morphological Changes in Nanostructures on Live Cell Surfaces by High Speed Ion Conductance Microscopy

Satoko Kitazawa[1], Ayako Housaka[2], Takahiro Watanabe-Nakayama[2], Hiroki Konno[2], Shinji Watanabe[2] ([1]*Grad.Sch.Math.& Phys.,Kanazawa Univ.*, [2]*WPI-NanoLSI,Kanazawa Univ.*)

Various nanostructures forming on living cell surfaces exhibit morphological changes. These changes are likely to be correlated with cell functions. However, due to the lack of the spatiotemporal resolution in existing observation techniques, these changes can be only partially captured. To investigate how the morphological changes correlate with cell functions, we have developed scanning ion conductance microscope (SICM). Our SICM has the capability for non-invasively visualizing the morphological changes with a spatial resolution of 10 nm (lateral) and 1 nm (vertical), and a temporal resolution of 100 microsecond per one pixel. In this study, we will discuss SICM performances that are important for visualizing nanostructures on live cell surfaces.

2D1606 平行光走査型 4 次元顕微鏡法
Parallel Light Scanning 4-Dimensional Microscopy

Kuniaki Nagayama (*Nagayama Microsc. Lab., LisCo*)

Four-dimensional microscopy (4DM) is a non-interferometric phase observation method using the incidence deflection through the object refraction. While the first proposal adapted to STEM dates back to 1979, its full-scale application has recently begun as STEM 4DM. By extending the reciprocity theorem between STEM and TEM that claims an equivalence of images obtained by two methods to cover the 4DM regime, we got an idea of a TEM version of 4DM using parallel light instead of convergent one, which was filed in 2017. The advantages in the TEM 4DM are 1) dimension reduction to 2- or 3-dimension and 2) adaptation of the dark field method for the sensitivity improvement. The novel paradigm for phase microscopy is overviewed together with preliminary experimental results.

2E1400 1 分子偏光 FRET 法により検出した F_1-ATPase α-β 間の遂次的な構造変化
Single-molecule polarized FRET measurements revealed sequential conformational changes between α and β of F_1-ATPase

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Rotation of the central shaft γ in F_1-ATPase is driven by cooperative conformational changes in the stator $\alpha_3\beta_3$. The crystal structures showed that the three αβ pairs take different conformational states according to their nucleotide binding states. Yet the αβ interface motions coupled to the rotation remain still unclear. Therefore, we developed a novel method for single-molecule polarized FRET measurements. In this method, FRET probes are bifunctionally labelled to the α-helices of the α and β so that not only the distance but also the orientation between the donor and acceptor are reflected to FRET efficiency. We observed two-state transitions in the presence of ATP or ATPγS in contrast to ADP. The dwell times of the FRET states are consistent with turnover rates.

2E1412 X 線結晶構造解析により明らかになった回転分子モーター F_1-ATPase の力発生の仕組み
Physical power generation mechanism of rotary molecular motor F_1-ATPase by X-ray Crystallographic Study

Toshiharu Suzuki[1,2,3], Eiki Yamashita[4], Seiki Baba[5], Kunio Hirata[6], Naoya Iida[7], Toshiya Endo[3], Takashi Kumasaka[5], Toru Hisabori[2], Masasuke Yoshida[3], Hiroyuki Noji[1] ([1]*Dept of Applied Chem, Graduate School of Eng, The Univ of Tokyo*, [2]*CLS, Inst of Innovative Res, Tokyo Tech*, [3]*Dept of Mol Bioscience, Kyoto-Sangyo Univ*, [4]*Inst of Protein Res, Osaka Univ*, [5]*Japan Synchrotron Radiation Research Inst (JASRI)*, [6]*SPring8-center, Riken*, [7]*Dept of Physics, Waseda Univ*)

Molecular motors can generate physical power by ATP hydrolysis, but its detailed mechanism is still obscure. F_1-ATPase (F_1) is a rotary molecular motor driven by ATP hydrolysis. To know the mechanism, we have determined several X-ray crystallographic structures of bovine F_1. The Pi-releasing interim structures identified stepwise displacements in Pi-mimicking waters, arginine finger, and p-loop Lys residues at the pocket which led to stepwise rotation of the rotor shaft *via* global rearrangement of subunits. In addition, the ADP-releasing intermediates revealed significant changes in the catalytic site during ADP-releasing without rotation. These results supported the rotation scheme of human F_1 and provided detailed power-generating mechanism of F_1 at atomic level.

2E1424 結晶構造との対応付けを目指したミトコンドリア F_1-ATPase の回転解析
Single-molecule analysis of bovine mitochondrial F_1-ATPase for direct assignment of crystal structures and rotational pausing states

Ryohei Kobayashi, Hiroshi Ueno, Toshiharu Suzuki, Mayu Hara, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

F_1-ATPase (F_1), one of the best-characterized molecular motors, has been studied by both single-molecule studies and structural analysis. However, the model F_1's for single-molecule studies and structural analysis have been different. So, the correlation between crystal structures and rotational pauses has been still unclear. Here, we conducted single-molecule rotation assay of bovine mitochondrial F_1 (bMF_1) of which many crystal structures are available. In order to determine the angular position of ATP hydrolysis, we adopted 3 systems; ATPγS, AMP-PNP, and catalytic-site mutant (βE188D). We found that ATP hydrolysis reaction occurs at ~80 degrees after ATP binding pause, which is consistent with the crystal structures considered to be ATP hydrolysis waiting state.

2E1436 Thermodynamic Efficiency of F_1-ATPase at High Temperature

Tomoaki Okaniwa, Yohei Nakayama, Eiro Muneyuki (*Dept. Phys., Faculty of Science and Engineering, Chuo Univ.*)

We investigate the thermodynamic efficiency of F_1-ATPase in single molecule experiment at high temperature. It has been already found that the thermodynamic efficiency in converting free energy released by ATP hydrolysis to mechanical work by F_1-ATPase reaches nearly 100% at 25℃ [PNAS. 108, 17951(2011)]; however, the robustness of the high thermodynamic efficiency to environmental condition has been elusive. Thus, we estimate the maximum work which is generated by F_1-ATPase against external torque and compare it with the literature values of the free energy difference of ATP hydrolysis at 37℃ in order to elucidate temperature dependence of the thermodynamic efficiency.

2E1448 Chemomechanical Coupling of the Paracoccus denitrificans F1-ATPase

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Biophysical studies of the bacterial and eukaryotic F1-ATPases have shown differences in their chemomechanical coupling schemes; however, the structural basis of that divergence remains unclear. P. denitrificans (Pd) is a bacterium phylogenetically related to the protomitochondria. The PdF1 has a canonical bacterial composition but displays a unique inhibitor, named the ζ subunit that resembles the eukaryotic IF1. We analyzed the rotation of PdF1 using different substrates and inhibitors, unveiling that the PdF1 angles for ATP cleavage and binding appear to be the same, in contrast to the F1-ATPases reported. Finally, We studied the inhibitory mechanism of the ζ subunit in the PdF1 rotation. This work could provide insight into the evolution of the ATPase machinery.

2E1500 Na+駆動型べん毛モーター PomA/PomB の Thr 残基のイオン透過における役割: MD シミュレーション結果
Role of Threonine residues in ion permeation for the Na+ driven flagellar motor PomA/PomB: insights from MD simulations

Yasushiro Onoue[1], Masayo Iwaki[2], **Ai Shinobu**[3], Yasutaka Nishihara[4], Hiroto Iwatsuki[1], Hiroyuki Terashima[1], Akio Kitao[3], Hideki Kandori[2], Michio Homma[1] ([1]*Nagoya Univ.*, [2]*Nitech*, [3]*Tokyo Tech*, [4]*UTokyo*)

The stator complex of the Na+ driven flagellar motor in vibrio is composed of two membrane proteins, PomA and PomB that form two transmembranal channels. In this work we show the essential role of T158 and T186 of PomA and the conserved PomB-D24 in ion permeation and selectivity. We focus on results from MD simulations of the WT and T158A, T186A mutants. Our results confirm that D24 is a favorable binding site for Na+, and is further stabilized by interaction with T158. Steered MD simulations show increased force in the mutants, suggesting that Na+ will experience a high energy barrier for transfer in the mutants. Inspection of the molecular architecture during the simulations shows that T158 and T186 assist in creating the water solvation layer around Na+.

2E1518 光ピンセットを用いた細菌べん毛モーター回転計測系の確立
Measuring the bacterial flagellar rotation with optical trap nanometry

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Swimming of bacteria is powered by rotating their flagella like screws. Their rotation is driven by flagellar rotary motors embedded in the cell membrane. Studies of single flagellar motors by a bead assay have been applied for only limited bacterial species, such as *Escherichia coli*. In this study, we have built a system to monitor the flagellar rotation of swimming bacteria by an optical trap. We applied this method to measure the rotation of Na^+-driven single polar flagellum of *Vibrio alginolyticus* cells. The maximum speed of Vibrio motor was ~800 Hz at r.t., which is consistent with the previous report. By changing viscosity, we could estimate its torque-speed curve. In principle, our method can be applicable for any flagellar motors of swimming bacteria.

2E1530 Visualization of the motor switching and subcellular localization of chemotaxis proteins in a halophilic archaeon, *Haloferax volcanii*

Yoshiaki Kinosita, Nagisa Mikami, Zhengqun Li, Tessa Quax, Sonja-Verena Albers (*Freiburg University*)

Archaea swim by rotating a helical filament called the archaellum. Here, to clarify the switching mechanism of archaeal motors, we applied the biophysical techniques and genetics to *Haloferax volcanii*. We detected the reversal motion in WT cells, whereas ΔCheY strain only showed the straight movement. Next, we monitored the motor switching thorough the beads rotation attached to the filament, demonstrating that the archaeal CheY induced CW rotation as seen in bacterial flagella. Finally, we detected CheY-GFP clusters at cell pole where formed the archaellar filament, whereas we didn't see GFP-CheY clusters and the switching behavior in GFP-CheY strain. It suggested that the N-terminal region of CheY was essential for the interaction with and switching of motors.

2E1542 トラジェクトリから多エネルギー面を乗り移る拡散モデルの推定：生体分子モーターへの応用
Estimating a diffusion model hopping on multiple energy surfaces from trajectories: Toward application to biomolecular motors

Kei-ichi Okazaki, Akihiko Nakamura, Ryota Iino (*Inst. for Mol. Sci.*)

Single-molecule experiments have been used to investigate mechanism of biomolecular motors by visualizing their motions. However, it is challenging to build a physical model that consistently explains observed trajectories. Here, we estimate a diffusion model from trajectories by Bayesian inference. We particularly focus on nonequilibrium trajectories with some periodicity in one direction, which is the case for many biomolecular motors. We develop a novel procedure that considers switching among multiple energy surfaces depending on chemical states of the motors. This novel procedure based on hidden Markov model allows us to bridge a gap between microscopic chemical states and unidirectional motion of the biomolecular motors.

2E1554 Characterization and engineering of chitin-hydrolyzing Brownian linear motor from marine bacteria

Akihiko Nakamura[1,2], Veda Boorla[1], Hiroki Watanabe[3], Takayuki Uchihashi[3], Ryota Iino[1,2] ([1]*IMS*, [2]*SOKENDAI*, [3]*Nagoya Univ.*)

Serratia marcescens Chitinase A (SmChiA) is a Brownian linear motor hydrolyzing crystalline chitin. In this study, a unique chitinase from marine bacteria Vibrio species (VpChi1) was characterized. Predicted structure of VpChi1 was similar to SmChiA, but additional carbohydrate binding domain was connected to the C-terminal. In biochemical assay, VpChi1 showed twice higher hydrolysis activity than SmChiA at low chitin concentration. On the other hand, hydrolysis activity decreased to the level similar to SmChiA at high chitin concentration. In high-speed AFM observation, VpChi1 showed similar moving velocity to SmChiA, suggesting other parameters will be a key for high activity. Mechanism of VpChi1 will be examined in detail to engineer non-natural efficient chitinases.

2F1400 Molecular simulation on light-activation mechanism of LOV photoreceptor protein

Masahiko Taguchi, Cheng Cheng, Chika Higashimura, Shigehiko Hayashi (*Kyoto Univ.*)

LOV domain which exists in light-receptor site of plants and bacteria is a protein complex with FMN as a chromophore. Light absorption of FMN leads to an adduct formation between FMN and a cysteine group nearby FMN, followed by dissociation of an a-helix called Jα, which initiates the signal transduction. We carried out free energy geometry optimizations with QM/MM RWFE-SCF method and obtained both optimized dark- and light-state structures. We clarified new molecular mechanism from local structural changes around FMN to large conformational changes of Jα.

2F1412 光遺伝学ツールとして用いられる植物クリプトクロム２の分光研究
Spectroscopic analysis of AtCRY2 used in optogenetics

Kazuya Agata, Daichi Yamada, Hideki Kandori (*Nagoya Inst. Tech., Dept. Life Sci. Appl. Chem.*)

Cryptochrome (CRY) is a photosensor protein having flavin adenine dinucleotide (FAD) as a chromophore. CRY2 from Arabidopsis thaliana (AtCRY2) exhibits light-induced interaction with a signaling protein and homo-oligomerization, by which AtCRY2 is used as a tool of optogenetics. However, as little is known about the molecular mechanism, we studied protein-protein interaction of AtCRY2 by various spectroscopic methods such as UV-vis, FTIR and DLS. Consequently, we observed increase in scattering upon photoreduction of flavin, suggesting that AtCRY2 is homo-oligomerized in vitro by light. We will discuss the molecular properties of AtCRY2 based on the present results.

2F1424 プロトンによって調節されるシアノバクテリオクロム型光受容体の光感知機構
Proton-mediated spectral tuning in a cyanobacteriochrome photoreceptor family

Yuu Hirose, Teppei Sato, Chinatsu Yonekawa, Toshihiko Eki (*Toyohashi Univ. of Tech, Dep. Env. and Life Sci.*)

Cyanobacteriochromes (CBCRs) are phytochrome-related photoreceptor family that are distributed only in cyanobacteria. They bind a linear tetrapyrrole choromophore within the conserved GAF (cGMP phosphodiesterase/ adenylyl cyclase/FhlA) domain, but their absorbing light colors are significantly diverse spanning UV to near far-red. Previously, we discovered that a green/red CBCR subfamily tunes the chromophore protonation to cause its absorption shift upon photoperception (Hirose et al 2013 Proc. Natl. Acad. Sci.). Here, we identified another CBCR subfamily tuning the chromophore protonation to absorb orange light. We will discuss a possible molecular mechanism of the CBCR subfamily.

2F1436 QCM による bZIP 型転写因子の basic 領域に存在する Asn 残基の解析
The role of Asn residue conserved among the basic region of bZIP transcription factors studied by QCM

Samu Tateyama, Itsuki Kobayashi, **Osamu Hisatomi** (*Grad. Sch. f Sci., Osaka Univ.*)

Photozipper (PZ) is a light-activatable transcription factor consisting of a basic/region leucine zipper (bZIP) domain and a light-oxygen-voltage-sensing (LOV) domain of Aureochrome-1. Asparagine residues in the basic region (corresponding to Asn131 of PZ) highly conserved among bZIP transcription factors were suggested to plays an important role on DNA-binding of PZ. We prepared site-directed mutant PZs whose Asn131 (N131) were substituted to Ala and Gln. The affinities of N131 mutants for the target sequence were lower than that of wild-type PZ, although N131 mutants showed almost the same spectroscopic and dimerization properties as wild-type PZ. Our quartz crystal microbalance (QCM) data suggested the N131 contributed to the stabilization of bZIP/DNA complex.

2F1448 光回復酵素/クリプトクロムスーパーファミリーにおける FAD 酸化還元状態の FTIR 研究
FTIR study of FAD redox state in photolyase/cryptochrome superfamily

Yui Sakai[1], Daichi Yamada[1], Tatsuya Iwata[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Toho Univ.*)

Photolyase/cryptochrome superfamily (PCSf) is FAD binding proteins that perform different functions in different organisms, despite structural homology. Their different functions are related to the redox states of FAD, which are controlled by protein environments. Our FTIR study showed that the hydrogen bond between the FAD N5-H group and the proximal Asn is strongest in the semiquinone form. In this study, we performed FTIR measurement of cryptochrome-DASH and (6-4) photolyase to examine their hydrogen-bonding environments. In addition, we compared the spectra of the four FAD redox states obtained among the PCSf. Mechanism of the redox control of FAD will be discussed based on the present vibrational identifications.

2F1500 Class II CPD 光回復酵素の電子移動反応の理論研究
Theoretical Study on Electron Transfer Reactions in Class II CPD Photolyases

Hirotaka Kitoh-Nishioka[1,2], Ryuhei Harada[2], Ryuma Sato[3], Yasuteru Shigeta[2] ([1]*JST-PRESTO*, [2]*CCS, Univ. of Tsukuba*, [3]*RIKEN BDR*)

We study the photoactivation process in class II CPD photolyases by using the combined method of molecular dynamics simulations and quantum chemical calculations. It has been believed that the photoactivation processes in DNA photolyases and cryptochromes involve the electron transfer (ET) reactions through a conserved triad of tryptophan (TRP) residues between an oxidized flavin adenine dinucleotide (FAD) cofactor and protein surface. Recent X-ray crystal structure analyses revealed that the conserved TRP triad of class II CPD photolyases is quite different in the localization from that of other DNA photolyase/cryptochrome families. Our simulation examines the molecular mechanism regulating the ET reactions through the unusual TRP triad in class II CPD photolyases.

2F1518 二光子顕微鏡によるマウス単離網膜での一細胞キナーゼ活性測定
Single-cell kinase activity measurements of the mouse retina by two-photon ex vivo imaging

Shinya Sato[1], Michiyuki Matsuda[1,2] ([1]*Grad. Sch. Biostudies, Kyoto Univ.*, [2]*Grad. Sch. Med., Kyoto Univ.*)

We previously generated mouse strains those ubiquitously express protein-based fluorescent probes to visualize the activity of kinases based on fluorescent resonance energy transfer (FRET biosensor). Here, we show two-photon ex vivo imaging studies from retinas isolated from those mice. First, we studied distribution of biosensors designed for extracellular signal-regulated kinase (ERK), protein kinase A (PKA) and AMP-activated protein kinase (AMPK), in the respective retina. Biosensors were detected from all layers of retinas. Next, we validated functions of biosensors by drug stimulation experiments. Finally, we studied if kinase activity is modulated by light. The presence of a novel photo-regulatory mechanism of PKA was suggested.

2F1530 イエロープロテインの 115 ループの構造揺らぎと光反応サイクル
Conformational Fluctuation of 115 Loop during the Photocycle of Photoactive Yellow Protein

Yasushi Imamoto[1], Yi-Chung Shen[1], Yuji Furutani[2] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Inst. Mol. Sci.*)

Photoactive yellow protein is a water-soluble blue-light receptor protein. Its 115 loop, connecting beta-strands, is flexible due to Gly115. The mutation of Gly115 to Pro significantly accelerated the decay of pB (recovery of dark state), while the pR-to-pB transition was not largely affected. Time-resolved FTIR spectroscopy demonstrated that amide I mode in pR/pG difference spectrum is sharpened in G115P, suggesting that 115 loop of pR of WT is flexible. Thermodynamic analysis of pB decay kinetics demonstrated that activation heat capacity change shows negative value, suggesting the ordered transition state structure. Rigid 115 loop would shift the structural ensemble to ordered conformation, resulting in the acceleration of photocycle.

2F1542 アゾベンゼン架橋タンパク質の光異性化反応による変性温度変化
Photoisomerization of azobenzene-crosslinked protein switches its denaturation temperature

Tosho Nagashima, Keisuke Ueda, Toshio Yamazaki (*RIKEN RSC*)

Azobenzene (AB)-crosslinked protein GB1 was swung between native and denatured structure by *cis-trans* photoisomerization. The large geometry change of AB is assumed to be a major cause of the denaturation of protein, but the driving force of denaturation is unclear. In *cis*-AB state of crosslinked GB1, which includes an improper distance between two cysteine residues, the structure was distributed into two isolated conformations depended on the sample temperature. At lower temperature, structure of *cis*-protein GB1 was distorted native structure, on the other hand, at higher temperature, was partially unfolded structure. The photoisomerization of the AB-crosslinker possesses the ability for switching the denaturation temperature of local structures in a protein.

2F1554 脂肪細胞のトリアシルグリセロールにおけるレーザーエネルギーの選択的吸収
Selective delivery of laser energy to ester bonds of triacylglycerol in 3T3-L1 adipocyte

Noritaka Masaki, Shigetoshi Okazaki (*Department of Medical Spectroscopy*)

The recent development of quantum cascade lasers (QCLs) has facilitated the irradiation of a mid-infrared laser beam that is specifically absorbed by a target molecular bond. Aiming for a selective delivery of laser energy to a specific absorption at 1738 cm^{-1} by the ester bonds of triacylglycerol, a QCL beam with a wavenumber of 1710 cm^{-1} was irradiated to adipocytes differentiated from 3T3-L1 cells. Neutral red staining assay revealed the occurrence of adipocyte-specific cell death 24 h after QCL irradiation. Adipocyte 24 h after QCL irradiation was revealed as late apoptotic or necrotic with annexin V and ethidium homodimer-III assays. The selective delivery of laser energy could affect endogenous molecules in a living organism.

2G1400 細胞透過ペプチド・トランスポータン 10 のベシクル内腔への侵入の連続的な検出法の開発
Continuous Detection of Entry of Cell-Penetrating Peptide (CPP) Transportan 10 (TP10) into Single Vesicle Lumens

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CPPs can translocate across plasma membranes and lipid bilayers (1). To elucidate the mechanism of the translocation, we have developed a method for the quantitative detection of the entry of fluorescent probe-labeled CPPs (e.g., CF-TP10) into single GUVs containing LUVs (2). When low concentrations of CF-TP10 interacted with single GUVs, first the fluorescence intensity (FI) of the GUV membrane increased with time, and then after some lag time the FI of the GUV lumen increased continuously without leakage of AF647. This result indicates the time course of the entry of CF-TP10 into the GUV lumen without pore formation. We discussed the kinetics of entry of CF-TP10 into single GUVs.
(1)Appl. Microbiol. Biotechnol., 102, 3879, 2018, (2) Chem. Phys. Lipids, 212,120, 2018

2G1412 両親媒性ポリマーによる脂質膜パッキングの認識
Recognition of lipid packing in membrane by amphiphilic polymers

Kazuma Yasuhara, Ryo Yamanaka, Jun-ichi Kikuchi (*Division of Materials Science, Nara Institute of Science and Tecnology*)

Biomembranes have highly curved regions, which recruit specific proteins to express various cellular functions. In this study, we designed synthetic polymers inspired by the amphipathic helix found in the membrane curvature sensing motif of some proteins. We synthesized a molecular library of amphiphilic polymers having a fluorophore at the polymer terminal by varying the ratio between hydrophobic and hydrophilic monomer units. Curvature recognition by the polymer was evaluated by a microscopic observation of giant vesicles and the following image analysis. We found that the polymer recognizes curvature of GUVs depending on its hydrophilic/hydrophobic balance. In addition, the polymer found to be able to recognize the highly curved region of E.coli membrane.

2G1424 バナナ状たんぱく質の集合による膜チューブ形成：キラリティの効果
Membrane tubulation induced by assembly of chiral banana-shaped protein rods

Hiroshi Noguchi (*ISSP, Univ. Tokyo*)

BAR superfamily proteins have a banana-shaped domain and bend the membrane along the domain axis. We have studied tubulation by these banana-shaped protein rods using meshless membrane simulations. The helical arrangement of BAR domains on the membrane tubules was observed by electron microscopy. To clarify the chirality effects, we added a chirality to our banana-shaped protein rods. Without the chirality, the protein rods deform a tubular membrane into an elliptical tube and assemble on two ends of the ellipse. We found that the chirality induces the transition from the elliptical tube to a circular tube where the chiral protein rods are helically aligned. Thus, the chirality is essential for the formation of tubules with a constant radius.

2G1436 Surface Enhanced IR study of insertion and folding process of membrane protein on the solid supported lipid bilayer

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We present an application of Surface Enhance Infrared Absorption spectroscopy (SEIRAS) to in-situ investigation for following insertion and folding process of membrane proteins on the solid supported lipid bilayer, a) in-vitro expression of LacY on various type of the lipid bilayer, b) folding process of translocon-unassisted membrane protein folding process of GlpG and DsbB

2G1448 Molecular dynamics simulations of domain formation in mixed lipid bilayers

Sangjae Seo, Wataru Shinoda (*Grad. Sch. Eng., Nagoya Univ.*)

Lipid raft plays an important role in biological function. Molecular dynamics simulation has been used to elucidate the characteristics of the lipid raft. We have recently developed coarse-grained force field for the membrane phase separation simulation. Various lipid compositions were simulated and showed the coexistence of liquid ordered and disordered phase similar to the experimental results. We further investigated the underlying mechanism of domain formation, such as the effect of asymmetric composition and hydrophobic mismatch. The findings of this research may provide insights for the deep understanding of the lipid rafts.

2G1500 全原子分子動力学シミュレーションによる静止膜電位に関する理論的研究
Theoretical study on a resting membrane potential by using all-atom molecular dynamics simulations

Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

A resting membrane potential across the cell membrane is in the range from -50 to -100 mV and is regulated by concentration gradient of various ions. The net flux of K+ is zero, and the membrane potential is calculated by using the Nernst equation in the resting state. The membrane potential can be also calculated by using the Poisson equation in molecular dynamics simulations. The membrane potential calculated by the Nernst equation should be equal to that calculated by the Poisson equation in the resting state. In this study, we present all-atom molecular dynamics simulations of POPC bilayer in the resting state. We show ion density profile and water and lipid ordering at the membrane surface from the results of molecular dynamics simulations.

2G1518 脂質膜環境の変化は細菌機械受容チャネル MscL のゲーティングにどのような影響を与えるか？
How can the change in membrane environment affect Mechano-Gating of the Bacterial Mechanosensitive Channel MscL?

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The bacterial mechanosensitive channel MscL is constituted of homopentamer of a subunit with two transmembrane helices. One of the major issues on MscL is to understand the gating mechanism driven by membrane tension. To get insights into the detailed mechanism of the mechano-gating including the effect of changes in membrane environment, we performed MD simulations for opening of MscL embedded in high/low-density membrane with two ratios of mixture of DPPG and POPG. As a result, MscL in the low-density membrane containing DPPG and POPG with mixing ratio of 1:1 showed spontaneously opening without membrane stretch, thus it is suggested that a combination of the 1:1 mixing ratio and low-density can change its mechanical property for easier opening of MscL.

2G1530 “Force-From-Lipids” (FFL) gating of mechanosensitive channels of Corynebacterium glutamicum

Yoshitaka Nakayama[1], Kosuke Komazawa[2], Navid Bavi[1,3], Ken-ichi Hashimoto[2], Hisashi Kawasaki[2], Boris Martinac[1,3] ([1]*Victor Chang Cardiac Research Institute*, [2]*Tokyo Denki University*, [3]*University of New South Wales*)

Mechanosensitive (MS) channels are gated in response to a variety of mechanical stimuli and how they sense the mechanical force in cell membranes is still not fully understood. The diversity of the bacterial MscS channel superfamily provides an excellent paradigm towards understanding structural and functional relationship. We have developed the patch-clamp technique of C. glutamicum and succeeded to identify activities of endogenous MscCG, MscCG2, and MscL-like channels. Here, we demonstrate the importance of “soft” properties of the C. glutamicum membrane for the MscCG gating by bilayer tension characterized by a voltage-dependent hysteresis. Like MS channels of E. coli the MS channels of C. glutamicum are designed to sense the FFL in their membrane environment.

2G1542 四量体型ナトリウムチャネルにみられる透過イオンや阻害剤との非対称な相互作用
Asymmetric interaction of permeating cation and local anesthetic with homo-tetrameric sodium channel

Katsumasa Irie[1,2], Yukari Haga[2], Shun Nakamura[1], Yoshinori Fujiyoshi[1,3] ([1]*CeSPI, Nagoya univ*, [2]*Grad. Pharm. Med. Sci., Nagoya univ.*, [3]*CeSPIA Co., Ltd*)

Voltage-gated sodium channel (Nav) plays a central role in the transition of the action potential on the axons of nerve cells. Prokaryotic homotetrameric Nav (BacNav) shows high sodium ion selectivity and is inhibited by local anesthetic as same as that of mammalian Navs, which contain four repeats of homologous sequence.
Asymmetric electron density was observed in selectivity filter of BacNav in crystal structure. Mutation of residues involved in this interaction to bulky amino acids lost channel activity, but if one wild type subunit remains in tandem tetramers, the activity is retained. Similar asymmetric interactions were also observed in blockage of local anesthetics.
It is suggested that these asymmetric interactions are conserved in homotetramaric Nav.

2G1554 Na^+イオンは KcsA K^+チャネルを遅いが透過する
Na^+ ions permeate through the KcsA K^+c channel slowly

Takashi Sumikama[1], Kenichiro Mita[2], Shigetoshi Oiki[2] ([1]*Kanazawa University, WPI Nano Life Science Institute*, [2]*University of Fukui, Faculty of Medical Sciences*)

Selectivity of the K^+ channels is critical to maintain the resting potential. The x-ray crystal structure of the KcsA K^+ channel has shown that the structure is well fitted to K^+ but not to Na^+, thereby the K^+ channels select K^+. Many researchers likely believe this explanation and think that Na^+ do not permeate through the K^+ channels. However, we show Na^+ currents through the KcsA channel here. The low conductance of Na^+ was electrophysiologically measured, which was then quantitatively reproduced by the molecular dynamics simulation. The analysis on the ion trajectories indicates that there exist large free energy barriers at both intracellular and extracellular entrances. These barriers lead to slow permeation rate, which contributes to keep the resting potential.

2G1606 Functional roles of Mg^{2+} binding sites in ion-dependent gating of a Mg^{2+} channel, MgtE, revealed by solution NMR

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Mg^{2+} homeostasis is maintained through Mg^{2+} channels such as MgtE, a prokaryotic Mg^{2+} channel whose gating is regulated by intracellular Mg^{2+} levels. Our previous crystal structure of MgtE in the Mg^{2+}-bound, closed state revealed the existence of seven crystallographically-independent Mg^{2+}-binding sites, Mg1-Mg7. The role of Mg^{2+}-binding to each site in channel closure remains unknown. Here, we investigated Mg^{2+}-dependent changes in the structure and dynamics of MgtE using nuclear magnetic resonance spectroscopy. This study revealed the role of each Mg^{2+}-binding site in MgtE gating, underlying the mechanism of cellular Mg^{2+} homeostasis.

2G1618 膜ータンパク間の協同性による上皮成長因子受容体の膜近傍ドメイン二量体形成機構
Membrane-protein interplay in the dimerization of juxtamembrane domains of epidermal growth factor receptor

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Transmembrane (TM) helix and juxtamembrane (JM) domains bridge the extracellular and intracellular domains of single-pass membrane proteins, including epidermal growth factor receptor (EGFR). JM dimerization plays a crucial role in regulation of EGFR kinase activity at the cytoplasmic side. Although the interaction of JM with membrane lipids is thought to be important to turn on EGF signaling, the underlying kinetic mechanisms remain unclear. Here, combining single-pair FRET imaging and nanodisc techniques, we showed that electrostatic interactions between basic residues and negatively charged lipids facilitated JM dimerization effectively. Furthermore, we examined the effect of cholesterol and found that cholesterol in the membranes can help the assembly of JM domains.

2H1400 Distinctively small distortion of retinal chromophore in K intermediate of proteorhodopsin observed by low-temperature Raman spectroscopy

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Proteorhodopsin (PR) is a microbial rhodopsin that functions as the light-driven proton pump in many aquatic bacteria. We carried out the low-temperature Raman measurement of PR to obtain the structure of the primary photoproduct, i.e., K intermediate. The Raman spectrum of the K intermediate of PR presented the much smaller intensities of the HOOP (hydrogen-out-of-plane) modes relative to those of bacteriorhodopsin, which is the representative archaeal light-driven proton pump. The present result indicates the significantly relaxed structure of the chromophore in the K intermediate of PR. This chromophore structure of the K intermediate suggests the loose packing in the retinal biding site of PR, which may couple to the kinetic property of K intermediate.

2H1412 Structural changes in retinal-binding site of the *Krokinobacter* rhodopsin 2 mutant H30A

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Krokinobacter rhodopsin 2 (KR2) has both light-driven Na^+ and H^+ pump functions with depending on the buffer condition. A specific mutation in helix A near the extracellular non-transported Na^+ binding site, H30A, eliminates its H^+ pumping. Here, we investigated the interaction of Schiff base-counterion by solid-state NMR, FTIR and flash-photolysis. Our results showed that strong electrostatic interaction with counterion and torsion around Schiff base induced by replacement of His30 and bound ion at extracellular binding site precluded the re-isomerization of retinal and proton transfer to counterion which corresponds to the result from flash-photolysis showing less formation of K-intermediate.

2H1424 赤外分光法を用いた酵素型ロドプシン Rh-PDE の反応機構解析
Reaction mechanism of enzymatic rhodopsin Rh-PDE analyzed by infrared spectroscopy

Masahito Watari[1], Tatsuya Ikuta[2], Daichi Yamada[1], Wataru Shihoya[2], Kazuho Yoshida[1], Satoshi Tsunoda[1,3], Osamu Nureki[2], Hideki Kandori[1] ([1]*Life Sci. Appl. Chem., Nagoya Inst. Tech.*, [2]*Grad. Sch. Sci., Univ. Tokyo.*, [3]*PREST, JST*)

Rh-PDE is a novel type of microbial rhodopsin, containing C-terminal cyclic nucleotide phosphodiesterase (PDE) enzyme domain which degrades ubiquitous second messengers cGMP and cAMP. Although light-dependent enzyme activity was demonstrated by biochemical experiments, reaction mechanism of Rh-PDE has not been elucidated. Here, we attempted to monitor the structural changes of Rh-PDE for understanding the light-regulated mechanism by using FTIR spectroscopy. We obtained light-induced difference spectra of intermediates which are supposed to reflect structural changes of the enzyme domain. In addition, we argue key photo-intermediates which allow activation of the enzyme domain, by comparing the results between Rh-PDE full length and without PDE domain.

2H1436 新たに発見された TAT モチーフを持つ微生物型ロドプシンの分光研究
Spectroscopic study of newly discovered microbial rhodopsin with TAT motif

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SAR11 TAT is a new member of microbial rhodopsin, which was recently identified in SAR11 HIMB114 strain. To investigate the photoreaction, we expressed SAR11 TAT in E.*coli* and purified the protein. Interestingly, it showed two absorbance maxima at UV (398 nm) and visible region (561 nm) at neutral pH. SAR11 TAT has no ion transport activity for both UV and visible illumination. Upon excitation of the visible band, we did not observe any transient absorption changes representing the photocycle at >40s. In contrast, we observed transient absorption changes upon excitation of the UV band. We will discuss the photoreaction mechanism and the functional role of SAR11 TAT in more detail in the presentation.

2H1448 クリプト藻由来カチオンチャネルロドプシン Gt_CCR4 のパッチクランプ法によるイオン輸送特性評価
Electrophysiological characterization of cation channelrhodopsin Gt_CCR4 from cryptophyte algae

Shunta Shigemura[1], Shouko Hososhima[1], Satoshi Tsunoda[1,2], Hideki Kandori[1] ([1]*Grad. Sch. Eng., NIT*, [2]*JST PRESTO*)

We recently reported a new light-gated cation channelrhodopsin, Gt_CCR4 from a cryptophyte algae Guillardia theta. Because of close sequence homology to proton pumping rhodopsins and poor homology to a well-known channelrhodopsin2 (ChR2) from green algae, the channel gating and ion transport mechanism of Gt_CCR4 could be distinct from ChR2. Actually Gt_CCR4 exhibits large photocurrent without considerable inactivation and desensitization which are disadvantageous in ChR2. Thus Gt_CCR4 serves as a new optogenetics tool. We here explore a putative channel pore region on a basis of ion permeation properties of Gt_CCR4 by patch-clamp measurement and study photocurrent kinetics, ion selectivity and the maximal absorption.

2H1500 Substrate anion concentration significantly affects the fast channel function of *Proteomonas sulcata* anion channelrhodopsin-1

Takashi Tsukamoto[1,2,3,4], Chihiro Kikuchi[3,4], Hiromu Suzuki[3], Tomoyasu Aizawa[1,2,3,4], Takashi Kikukawa[1,2,3,4], Makoto Demura[1,2,3,4] ([1]*Fac. Adv. Life Sci., Hokkaido Univ.*, [2]*GSS, GI-CoRE, Hokkaido Univ.*, [3]*Sch. Sci., Hokkaido Univ.*, [4]*Grad. Sch. Life Sci., Hokkaido Univ.*)

The purpose of this study is to reveal the effect of substrate anion concentration on the fast anion channel function of *Psu*ACR1. From the Cl^- concentration dependency on static absorption spectra, we demonstrated that *Psu*ACR1 bound Cl^- in the initial state at a K_d of 5.5 mM. We revealed that the photoreaction kinetics and the equilibrium states of several photo-intermediates of *Psu*ACR1 were significantly changed with increasing in the Cl^- concentration. Because the accumulation of M involving in the channel closing was significantly suppressed in the presence of high Cl^- concentrations, the Cl^- conducting state became protracted by one order of magnitude. Therefore, we concluded that the fast channel function became impaired in the presence of high Cl^- concentrations.

2H1518 アニオンチャネルロドプシン 2(ACR2)の機能及び分光特性に与える R129 の影響
Impact of R129 on the functional and spectroscopic properties of anion channelrhodopsin-2 (ACR2)

Natsuki Miyoshi[1], Satoko Doi[1], Keiichi Kojima[1], Hiroshi Watanabe[2], Hiroshi Ishikita[2], Yuki Sudo[1] ([1]*Grad. Sch. Of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. Of Eng., The Univ. Of Tokyo*)

We have previously succeeded in the functional expression of light-gated anion channelrhodopsin-2 (ACR2) in *E. coli* cells [Sci. Rep 2017]. Taking advantage of the system, we performed here site-directed mutagenesis to understand the functional and photochemical properties of ACR2. For three characteristic residues near retinal. We prepared the mutants (R129M, G152S, C233A) and measured light-induced pH changes of the cells in terms of channel function. The multiple mutants including R129M showed red-shifted absorption maxima and long lived ion conductance state. Similar results were also observed for ACR2 expressed in HEK293 cells. In a model structure, R129 formed a hydrogen bond with E159. Thus, we concluded that R129 plays key roles in ACR2.

2H1530 アニオンチャネルロドプシンによる線虫の超高感度光神経抑制
The hypersensitive optical neural silencing by anion channelrhodopsins (ACRs) in the nematode *C. elegans*

Taro Yamanashi[1], Misayo Maki[1], Keiichi Kojima[1], Atsushi Shibukawa[1], Shin Takagi[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Sci., Nagoya Univ.*)

A light-driven outward proton pump archaerhodopsin-3 (Arch) has been utilized as a neural silencer, while high light intensity (tens of mW/cm^2) was required. Anion channelrhodopsin-1 and -2 (ACR1 and ACR2) have been recently discovered as monovalent anion transporters. In cultured mammalian cells, the photocurrents of ACRs were about 1000 times larger than that of Arch. In this study, to demonstrate the neural silencing activity of ACRs in living animal, we employed *C. elegans*. We generated transgenic worms expressing ACRs in neurons, and they showed locomotion paralysis in response to visible light. Expectedly, ACRs induced locomotion paralysis at about 1000-hold lower intensity (tens of $\mu W/cm^2$) than Arch, indicating hypersensitive neural silencing activity of ACRs.

2H1542 ナトリウムポンプロドプシンの初期中間体における発色団の構造変化に対して極低温ラマン分光法を用いた研究
Chromophore structural change in the primary photointermediate of sodium-pump rhodopsin studied by low-temperature Raman spectroscopy

Yushi Nakamizo[1], Takashi Kikukawa[2], Tomotsumi Fujisawa[1], Masashi Unno[1] ([1]*Fac. Sci. Eng., Saga Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

Sodium pump rhodopsin (NaR) is a microbial rhodopsin which was recently identified from marine bacteria. Since its discovery in 2013, NaR has been studied intensively to understand the molecular mechanism of the light-driven Na+ pump. In this study, we carried out the low-temperature Raman measurement of the K intermediate (initial photointermediate) of NaR to examine the primary structural change for Na+ pumping. The Raman spectrum shows the multiple large HOOP (hydrogen-out-of-plane) vibrational modes of the K intermediate, which indicates the significant structural distortion of chromophore about the retinal Schiff base. We show that the chromophore distortion is induced by Na+ binding, and discuss the relevance in initial process of the Na+ transport.

2H1554 Photochemical analysis of sodium ion-pumping rhodopsin from Indibacter alkaliphilus

Tomoya Kato[1], Keisuke Murabe[1], Takashi Kikukawa[1,2], Takashi Tsukamoto[1,2], Tomoyasu Aizawa[1,2], Makoto Demura[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*GI-CoRE, Hokkaido Univ.*)

Na+-pumping rhodopsin (NaR) is a microbial rhodopsin that pumps Na+ outwardly. Here we analyzed NaR from Indibacter alkaliphilus (IaNaR) focusing on the differences between O1 and O2 intermediates, which appear sequentially in the long wavelength region (Kajimoto et al., 2017, J. Phys. Chem. B). We observed the flash-induced Na + concentration changes using a Na+ selective membrane. The results indicated that IaNaR captures Na+ along with O1 formation, and releases it during O2 decay. Then we examined the transient absorption changes under various conditions. Na+ concentration dependence suggested O1 appears to have a Na+ binding site exposed to the cytoplasmic medium, while that of O2 seems to be isolated. We will discuss the molecular details of O1 and O2.

2H1606 ビニレン基挿入レチナール誘導体による光開閉型プロトンチャネルの創成
Production of a Light-gated Proton Channel by Replacing the Retinal Chromophore with Its Synthetic Vinylene Derivative

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Rhodopsin is widely distributed in organisms as a membrane-embedded photoreceptor protein, consisting of the apoprotein opsin and vitamin-A aldehyde retinal. Modifications of opsin (i.e., mutations) have provided insights into the molecular mechanism of the functions of rhodopsins as well as providing tools to control cellular activity by light. In this study, we focused on the retinal chromophore and synthesized three vinylene derivatives. One of them named 14V-A2 was successfully incorporated into the opsin of a proton pump archaerhodopsin-3. Electrophysiological experiments revealed that it functions as a light-gated proton channel, indicating conversion into a proton channel by replacing the chromophore. Its characteristic properties are also presented.

2J1400 Structural and dynamical insights into functional differences in mammalian cryptochromes

Ashutosh Srivastava[1], Christin Rakers[2], Tsuyoshi Hirota[1], Florence Tama[1,3,4] ([1]*Inst. of Trans. Bio-Mol., Nagoya Univ.*, [2]*Grad. Sch. Pharm. Sci., Kyoto Univ.*, [3]*Dept. of Phys., Sch. of Sci., Nagoya Univ.*, [4]*Riken Center for Comp. Sci.*)

The physiology and behavior of mammals is synchronized to a 24-hour solar cycle by a well-regulated molecular clock mechanism. The regulation of this internal biological clock (circadian clock) involves several transcriptional activators, kinases and dedicated “clock” proteins. Cryptochromes (CRY1 and CRY2) are important clock proteins that participate in circadian rhythm regulation. Here, we have explored the structure and dynamics of mammalian CRY proteins using molecular dynamics simulations. The results reveal crucial difference in the dynamics of two types mammalian cryptochromes. We have further explored the conformational dynamics of highly dynamic loops lining two pockets on the surface of these proteins and their role in interaction with other clock proteins.

2J1412 酸素センサータンパク質の情報伝達機構のコンピューターによる研究
Computational study on the signal transduction mechanism of oxygen sensor protein

Kunitaka Ota[1], **Takahisa Yamato**[1,2] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*IGBMC, Univ. Strasbourg*)

The kinase activity of FixL is suppressed by O2 binding to its oxygen-binding sensor domain, FixLH. To evaluate the effect of O2 binding, we performed molecular dynamics simulations of deoxy- and oxy states of FixLH, and analyzed the difference of residue-residue interactions between the two states. As a result, we identified distinct clusters of surface residues that experienced significant changes of residue interactions, indicating these clusters mediates the crosstalk between FixLH and the kinase domain of FixL. Refs: [1] Gong W. et al., PNAS, 95, 15177-15182 (1998). [2] D. Leitner, T. Yamato, Rev. Comput. Chem. (in press) [3] T. Ishikura, Y. Iwata, T. Hatano, T. Yamato, J. Comput. Chem. 36, 1709 (2015). [4] CURP: http://www.comp-biophys.com/yamato-lab/curp.html

2J1424 アミロイドペプチド高次複合体形成に関する高次元自由エネルギー地形の分子動力学的解析
Molecular dynamics study on high-dimensional free-energy landscape of amyloid peptide higher-order complexes

Kota Kasahara[1], Junichi Higo[2], Tomonori Hayami[3,4], Takuya Takahashi[1] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Sim. Studies, Univ. Hyogo*, [3]*IPR, Osaka Univ.*, [4]*Grad. Sch. Fro. Bio., Osaka Univ.*)

Molecular mechanisms of formation of peptide higher-order complexes are largely unknown. Whereas the generalized ensemble approach with the molecular dynamics (MD) method provides the free-energy landscape of molecular systems, analysis of multimeric molecular assembly is not still straightforward. We developed a new conformational sampling scheme termed multi-dimensional virtual-system coupled MD (VcMD), which can conformational sampling along multiple reaction coordinates. By taking advantages of this new method, we analyzed the free-energy landscape of tetramer of 8-residue amyloid peptide. As a result, the four-stranded β-sheet was confirmed as a stable conformation, and many other sub-stable states were found.

2J1436 分子動力学シミュレーションを用いたモジュール型 CRISPR/CAS システムの核酸切断ダイナミクス
Dynamics of the cleavage of DNA/RNA in module type CRISPR/CAS system by using molecular dynamics

Naoyuki Miyashita, Ryo Ohashi, Reiwat Takeuchi, Yui Taketomo (*BOST KINDAI Univ.*)

CRISPR/Cas system is an immune system in a prokaryote, and it works as antiviral defenses like acquired immunity. CRISPR/Cas system usually contains the module proteins and the crRNA which has the complementary nucleotide sequences of a part of targeted RNA/DNA sequences. It usually binds to the targeted RNA/DNA specifically and also cut the targeted nucleotide specifically. Thus, some of them, CRISPR-Cas9 and so on, have been known as a genome editing tools. However, the detailed mechanism of the cleavage of RNA/DNA has known yet. We performed micro-second molecular dynamics simulation of module type CRISPR/CAS system to understand the dynamics in the cleavage of DNA/RNA.

2J1448 ColDock: Concentrated ligand Docking method for an efficient protein-ligand complex structure prediction using all-atom MD

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

We have developed a simple but efficient and accurate method to generate protein-ligand complex structures using MD simulation at high ligand concentration, called Concentrated ligand Docking (ColDock). In ColDock, we distribute ligands randomly around the target protein and conduct multiple independent MD simulations. Ligands at relatively high concentration efficiently explore the protein surface, then spontaneously bind to the correct binding site. The predicted structures are the representatives of the largest clusters after RMSD clustering of ligands in contact with the target protein. Although the procedure is quite simple, CoLdock successfully predicted complex structures including a big ligand and accurately captured effects of mutations on ligand bindings.

2J1500 Extensive molecular dynamics sampling characterizes ligand binding pathway to Src kinase

Suyong Re[1], Hiraku Oshima[1], Motoshi Kamiya[2], Yuji Sugita[1] ([1]*RIKEN BDR*, [2]*RIKEN R-CCS*)

Ligand binding to a target protein is essential for biological processes as well as diseases. While many advances in the binding affinity measurements and computations, the binding pathway remains unclear. Here, we investigate the binding/unbinding pathway of inhibitor PP1 to Src kinase through molecular dynamics simulations with enhanced sampling technique. A modified two-dimensional replica-exchange approach, with local temperature scaling of a ligand and binding site residues, allows sampling of more than hundred binding/unbinding events. The known binding structure and hydration states are well reproduced. Free energy landscapes from the simulations characterize the binding pathway including a crucial intermediate governing the binding.

2J1518 自由エネルギー計算による hERG イオンチャネルと薬剤分子の結合親和性予測
Prediction of hERG-drug binding affinities by free energy calculation

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All drug candidates are tested for cardiotoxicity. It is well known that binding of drugs to the hERG potassium ion channel can cause severe cardiac arrhythmia. We are developing a method to predict interactions between the hERG channel and drugs based on molecular simulation methods. In this method, we first performed docking simulations of drugs to the experimental structure of the hERG channel. Then we calculated the binding free energies for top ranked poses with the MP-CAFEE method. The calculated values of 12 drugs were well correlated with the experimental data. The result suggests that our method is useful to accurately predict the affinities of drugs to the channel. We will discuss the accuracies of the docking simulation and the free energy calculation.

2J1530 分子動力学シミュレーションによる単一ドメイン抗体に対する安定性の評価
Estimation of Single Domain Antibody Stability by MD Simulations

Gert-Jan Bekker[1], Benson Ma[2], Narutoshi Kamiya[3] ([1]*IPR, Osaka Univ.*, [2]*Georgia Tech.*, [3]*Grad. Sch. Sim., Univ. Hyogo*)

Single domain antibodies, sdAbs consist of only one chain. Because of their low weight, sdAbs have advantages to production and delivery. We chose two sdAbs and two engineered antibodies consisting of only the heavy chain, which have a wide range of melting temperature (Tm) values and known structures. We then applied MD simulations to these four antibodies to estimate their relative stability and compare them with the experimental data. High temperature MD simulations were executed. The fraction of native atomic contacts, Q, showed a fair correlation, and so the Q values classified by hydrophobicity and size were subsequently analyzed. Interestingly, the Q value between hydrophilic residues exhibited good correlation with the experimental Tm.

2J1542 Go モデルを用いた GA・GB ドメイン関連タンパク質のフォールディングシミュレーション
Folding simulations of GA / GB domain related proteins based on coarse-grained go-model

Shoya Hamaue, Takeshi Kikuchi (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

It is known that proteins showing an amino acid sequence identity of 30% or more exhibit a similar 3D-structures. However, despite showing more than 30% sequence identity, there are several proteins with completely different structures. In this study, we target artificial proteins with 3α structure (GA) and 4β+α structure (GB) derived from albumin binding domain and IgG binding domain, respectively. In order to clarify how such proteins are folded into different structures, we conducted a simulation based on a coarse grained Go model. As a result, it is possible to confirm the difference in residues with frequent contacts in the transition state of each protein.

2J1554 蛋白質のフォールディングシミュレーションに関する緩和モード解析
Analysis of a protein folding simulation by using relaxation mode analysis

Ayori Mitsutake[1], Hiroshi Takano[2] ([1]*Dept. of Physics, Meiji Univ.*, [2]*Dept. of Physics, Keio Univ.*)

Molecular simulation is a powerful method for describing the stability, dynamics, and function of proteins at atomic resolution. As longer MD simulations are performed, it is more important to develop analysis methods to investigate dynamics and kinetics. We have developed dynamical analysis method, relaxation mode analysis, to investigate “dynamic” properties of structural fluctuations of proteins (for review, see [1]). In RMA, slow relaxation modes are extracted from molecular simulations. We apply RMA to folding trajectories. We obtained several characteristic states by using RMA. [1]A. Mitsutake and H. Takano, Biophysical Review, 10, 375-389 (2018).

2J1606 中サイズの酵素の立体構造上で４つのイントロン位置が形成する平面
The planes formed with the 4-intron-positions in an enzyme of medium size

Michiko Nosaka, Vongsaksid Phonexay, Masato Rikitake (*National Institute of Technology, Sasebo College*)

Understanding the interaction of an enzyme with its substrate is important for protein research. We present a novel approach for the analysis of enzyme-substrate complexes. Previously, we showed how two single domains of enzymes form a plane around their respective ligands. Here, we report the formation of two planes within the larger enzyme. We express the relationship between the planes and the ligand molecule. Simulations showed that the planes were formed by combinations of four intron positions (exon-junctions)in the enzyme, even as the exons connected to them move at random. We discuss about the significance of the formation of such planes around the ligand.

2K1400 Destabilizing effects of residues in the hydrophobic core of three helix-bundle peptide

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In order to analyze protein structural dynamics and thermodynamics with conformational changes in protein folding and interaction, we designed simple model peptides which formed three helix-bundle structures induced by metal-ion binding. In this study, we analyzed the destabilizing effects of residues in the hydrophobic core of three helix-bundle peptide by substitution with alanine (HA), isoleucine (HI), and leucine (HL). Isothermal titration calorimetry experiments revealed that the Zn^{2+} binding process was mainly driven by enthalpy term. The enthalpy change of HA was larger than those of HI and HL, which was in good correlation with the difference in Zn^{2+} induced conformational change of each peptide analyzed using circular dichroism experiments.

2K1412 Structure elements are building blocks of protein tertiary structure responsible for protein stability

Yasumichi Takase, Yugo Hayashi, Yoichi Yamazaki, Hironari Kamikubo (*Div. Mat. Sci., NAIST*)

Structure elements determined by comprehensive Ala-insertion mutation analysis are indispensable units to form the tertiary structure. We previously reported that overlapped contact volume (CV) in every residue-residue contacts calculated from crystal structures allows us to predict the structure elements. The fact also implies that the CV would be closely related to the protein stability. In order to confirm this idea, we examined the relationship between the loss of stability due to a mutation (ddG) and difference in the CV between WT and the mutant (dCV). In the result, we found good correlation between ddG and dCV in several proteins, indicating that intra-molecular contacts among the structure elements quantitatively regulate the protein stability.

2K1424 The reaction mechanism of RSC-mediated nucleosome remodeling

Hsiu-Fang Fan, Kuan-Wei Hsu, Sih-Yao Chow, Bo-Yu Su (*National Yang-Ming University*)

Chromatin structure remodeling complexes (RSC, Remodel the Structure of Chromatin) can hydrolyze ATP to perturb DNA-histone contacts, leading to nucleosome sliding and ejection. With tether particle motion (TPM) experiments, we observed the ATP-dependent RSC-mediated DNA looping and nucleosome ejection. For mononucleosomes, Nap1 suppressed RSC-mediated DNA looping and nucleosome ejection. On the contrary, Nap1 enhanced RSC-mediated nucleosome ejection in a two-step disassembly manner from di-nucleosomes. Based on this work, we provide the whole reaction scheme of RSC-mediated nucleosome remodeling process including DNA looping, nucleosome ejection, the influence of adjacent nucleosomes and the coordinated action between Nap1 and RSC.

2K1448 ファージ宿主認識蛋白質の構造と機能
Structure and function of phage receptor binding protein

Shuji Kanamaru (*Dep. of Life Science & Tech., Tokyo Inst. of Tech.*)

T2-like phages have unique receptor binding protein (RBP), gp (gene product) 38, at the distal tip of the long tail fiber. Mutational analysis has been shown that the RBP recognize and identify host bacteria surface LPS and/or outer membrane proteins. From the amino acid sequences of various phage RBPs, gp38 has 5 hypervariable regions. It is most likely that these regions are responsible for host recognition. However, the structure of the RBP nor recognition details are still unknown. Here I will discuss the structure and function relationship of RBP of one of T2-like phage.

2K1500 SecM 翻訳アレスト安定化機構の解析
Analysis of the stabilization mechanism of SecM-mediated translation arrest

Mikihisa Muta, Ryo Iizuka, Takashi Funatsu (*Laboratory of Bio-Analytical Chemistry Graduate School of Pharmaceutical Sciences The University of Tokyo*)

SecM, a bacterial secretion monitor protein, contains a specific amino acid sequence at its C-terminus, called arrest sequence, which interacts with the ribosomal tunnel and arrests its own translation. It has been widely believed that the sequence is sufficient and necessary for translation arrest. However, we have found that the nascent SecM chain outside the ribosome stabilizes the translation arrest. In this study, we performed alanine-scanning mutagenesis to identify residues responsible for the stabilization. Of these residues, positively-charged (His84, Arg87 and Arg91) residues significantly contribute to the stability of the translation arrest, suggesting that these residues associate with negatively-charged ribosomal surface.

2K1518 鶏卵白リゾチームに対する一本鎖抗体の作製と抗原認識機構の解明
Generation of single-chain Fv antibody against hen egg lysozyme and analysis of its antigen recognition mechanism

Takanori Yamaoka[1], Yuji Kamatari O[2], Takachika Azuma[3], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*Life Sci. Res. Center, Gifu University.*, [3]*Antibody Eng. Res. Center.*)

A monoclonal antibody, HyC1, distinguishes the native form of hen egg lysozyme from partially reduced from, both of which have similar 3D structures revealed by X-ray crystallography. In this study, a single-chain Fv (scFv) antibody of HyC1 was designed to comprise the variable regions of light and heavy chains connected by a linker peptide. This scFv was expressed in *E. coli* in the insoluble fraction, solubilized in the presence of Guanidine hydrochloride, and refolded by stepwise dialysis. The antigen binding ability of purified scFv was analyzed using isothermal titration calorimetry, showing that the binding stoichiometry to antigen is 1. In the presentation, we will discuss the structural and functional properties of HyC1 scFv analyzed using Biacore and NMR.

2K1530 不凍タンパク質は低温環境下における線虫の細胞を保護し、生存率を上昇させる
The ice-binding proteins protect the cells and contribute to increase the survival rate in Caenorhabditis elegans under cold environments

Masahiro Kuramochi[1,2,3], Chiaki Takanashi[1,3], Akari Yamauchi[4], Sakae Tsuda[4], Motomichi Doi[2], Kazuhiro Mio[3], Yuji Sasaki[1,3]
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Ice-Binding protein (IBP) can inhibit the growth of ice crystal, and protect the cells and organs from cold environments. Although many physical characteristics of IBP are identified, it is poorly understood how does IBP within living animals contribute to the cold tolerance behavior. Here we characterize the IBP function for cold tolerance by using the nematode Caenorhabditis elegans. Using transgenic worms expressing IBP at cell-specifically, we showed that IBP can protect the cells from several cold shocks, and works for cold tolerance. We also found out that a fungus IBP contributes for the strong cold tolerance, and suggesting that adsorption site and thermal hysteresis in antifreeze activity are important functions for in vivo function.

2K1542 哺乳類概日時計における温度補償されたリン酸化反応の再構成
Reconstitution of Temperature-compensated Phosphorylation in the Circadian Clock

Yuta Shinohara[1], Yohei Koyama[1], Hiroki Ueda[1,2] ([1]*Center for Biosystems Dynamics Research, RIKEN*, [2]*Graduate School of Medicine, University of Tokyo*)

The circadian clock, which coordinates key cellular functions in organisms ranging from bacteria to warm-blooded mammals, is remarkably resilient to changes in temperature. This is surprising since it relies on enzymatic reactions that become slower at lower temperatures and faster at higher temperature. But despite this, the body clock remains largely unperturbed by temperature changes (known as temperature compensation). Previously, we have determined that phosphorylation by the CK1δ stabilizes the circadian clock against the effects of heat. CK1δ controls the cycle time by introducing multiple phosphorylation onto a target circadian protein. Here we investigate biochemical mechanisms underlying temperature compensated CK1δ-dependent phosphorylation in mammals.

2L1400 溶液条件の違いから EGFR C-tail 天然変性ドメインの構造情報を得る
Structural information of intrinsically disordered C-terminal domain of the EGFR revealed by changing solution condition

Kenji Okamoto, **Yasushi Sako** (*RIKEN*)

The epidermal growth factor receptor (EGFR) has an intrinsically disordered (ID) C-terminal domain (CTD), which contains binding sites for various downstream adapter proteins and possibly regulates those binding kinetics. However, little is known about its structure and dynamics. We conducted circular dichroism (CD) and single-molecule Förster resonance energy transfer (smFRET) measurements to investigate its structural components with various concentration of ions (KCl) and denaturant (guanidinium chloride, urea). The results indicated that significant fractions of β-sheet component was contained and the local structure was broken by denaturant but not affected by ions. It suggests that the CTD has quite different structural properties from typical ID proteins.

2L1412 インスリン B 鎖における多段階的なアミロイド核形成および阻害の解析
Investigation of multi-step nucleation of insulin B chain amyloid fibrils and its inhibition

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Amyloid fibrils are a specific type of protein aggregates, the formation of which typically follows a nucleation-dependent polymerization. Here, we have investigated early stages of the formation of insulin B chain amyloid fibrils. As a result of time-lapse monitoring, the formation of prefibrillar intermediates with rod-like structure has been revealed, indicating a multi-step nucleation scheme in which metastable intermediates serve as a precursor of amyloid nuclei. Furthermore, fibrinogen, typically known as a major blood plasma protein, inhibited the fibril formation by a strong interaction with the intermediates, which suggests that the intermediate-targeted inhibition of the nucleation step is an efficient way to prevent amyloid fibril formation.

2L1424 An RNA aptamer disrupts the interaction of prion protein with Amyloid β

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Amyloid β (Aβ) protein forms various types of oligomers and fibrils. Recent studies proposed that Aβ oligomer binds to prion protein (PrP), which is acts a receptor of the Aβ oligomer, causing the Alzheimer's disease. Thus, the compounds which can disrupt the interaction of PrP with Aβ oligomer have a therapeutic potential as to Alzheimer's disease. In the present study, we demonstrate that PrP and even PrP-derived peptides interact with Aβ and inhibits the fibrillization of Aβ. We also demonstrate that the Aβ fibrillization restarts when an anti-prion RNA aptamer (R12) is added. These results indicate that R12 suppresses the inhibitory effect of PrP on Aβ fibrillization via disruption of PrP-Aβ complex and that thereby R12 induces restarting of the Aβ fibrillization.

2L1436 ナノスペースビデオイメージングによる食品関連因子アミロイド凝集抑制作用機序の解明
Nano-space video imaging reveals structural dynamics of amyloidogenic protein aggregation inhibition by food components

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Amyloid aggregation accompanied by structural conversion of amyloidogenic proteins are associated with neurodegenerative diseases including Alzheimer's disease, Recently, some of food components are identified to inhibit the aggregation. However, their inhibition mechanisms have been unclarified. Various aggregation intermediates with different structures exist simultaneously, which prevents isolation and biochemical analysis of each intermediate. To solve this problem, we use high-speed atomic force microscopy to identify structural dynamics of individual aggregates without purification of each intermediate. We discuss structural dynamics of amyloid protein aggregates in the presence/absence of food components.

2L1448 Protein Structures Define Misfolding and Prion-like Propagation of Alzheimer's Amyloid-β: Solid-state NMR Studies

Yoshitaka Ishii[1,2], Yiling Xiao[2], Brian Yoo[2], Isamu Matsuda[1], Dan McElheny[2] ([1]*Ti Tech*, [2]*Univ. Illinois at Chicago*)

Misfolded fibrillar aggregates of Aβ are a primary component of senile plaque, a hallmark of Alzheimer's disease (AD). Increasing evidence suggests that formation and propagation of misfolded aggregates of 42-residue Aβ42, rather than the more abundant 40-residue Aβ40, provokes the Alzheimer's cascade. Our group recently presented the first detailed atomic model of Aβ42 amyloid fibril based on solid-state NMR (SSNMR) data (Xiao et al. NSMB 22 499, 2015). In this study, we discuss how amyloid fibril structures affect "prion-like" propagation across different Aβ isoforms based on the results. We also present our ongoing efforts to analyze a structural conversion in misfolding of Aβ42 from oligomeric intermediates to fibrils by SSNMR.

2L1500 EPR 法による Shewanella 由来無機ピロフォスファターゼにおける複核 Mn サイトの構造解析
Structural analysis on di-Mn ion site for Shewanella inorganic pyrophosphatase by EPR

Masaki Horitani, Yuki Sakakibara, Keiichi Watanabe (*Saga Univ., Fac. Agr.*)

Inorganic pyrophosphatase (PPase) catalyzes the hydrolysis reaction of inorganic pyrophosphate to two phosphate ions and plays an essential role for all living organisms. PPase from Shewanella sp. AS 11 (Sh-PPase), lives in Antarctic Ocean, is found to be a family II PPase which has di-Mn2+ ions in the active-site. We have previously isolated Sh-PPase and reported that Mn-activated Sh-PPase had the maximum enzymatic activity at 5 Celsius. To elucidate of the mechanism for this characteristic activity, we have collected electron paramagnetic resonance signals and analyzed the structure of active site on Sh-PPase. We will discuss the detail of analytical method and relationship between structure and functions in this presentation.

2L1518 Kinetics of reversible NADP$^+$/H reduction/oxidation reaction catalyzed by a ferredoxin-NADP$^+$ oxidoreductase from *Rhodopseudomonas palustris*

Daisuke Seo (*Div. Mat. Sci., Grad. Sch. Nat. Sci. Tec., Kanazawa Univ.*)

Ferredoxin-NAD(P)$^+$ oxidoreductase (FNR) is a soluble flavoprotein catalyzing the redox reaction between NAD(P)$^+$/H and small iron sulfur protein ferredoxin. In this presentation, kinetics of the pre-steady state reaction between NADP$^+$/H and FNR from purple non-sulfur bacterium *Rhodopseudomonas palstris* (RpFNR) was investigated with stopped-flow spectrophotometry. Mixing with NADP$^+$/H gave rapid formations of the charge transfer complexes followed by the rate limiting hydride transfer in both directions. RpFNR was reduced in part at the equilibrium and the presence of excess NADP$^+$/H increased the amount of oxidized/reduced species. The rates for the hydride-transfer in both directions were comparable in contrast to the other homo-dimer type FNRs.

2L1530 シトクロム c-シトクロム c 酸化酵素間電子伝達反応における特異的脱水和の機能的役割
Functional role of specific dehydration from cytochrome c in electron transfer to cytochrome c oxidase

Wataru Sato[1,2], Takeshi Uchida[1], Tomohide Saio[1], Koichiro Ishimori[1] ([1]*Fac. of Sci. Hokkaido Univ.*, [2]*Sci. Acad. Area Stockholm Univ.*)

In respiratory chain, cytochrome c (Cyt c) donates an electron to cytochrome c oxidase (CcO). Our docking simulation predicted that the Cyt c-CcO complex is formed by the increase in entropy owing to dehydration near the heme periphery of Cyt c, but the contribution of the dehydration on its reaction activity was unknown. Here, we explored the influence of dehydration of Cyt c on its function by addition of polyethylene glycol, causing dehydration from the surfaces of proteins. Various spectroscopic measurements found that the dehydration near the heme periphery caused a slight shift in the heme position (1.0 Å), leading to the downshift of redox potential. These results suggest the heme-displacement upon the Cyt c-CcO complexation, contributing to electron transfer.

2M1400 高圧力 NMR 法による蛋白質水和に関する研究
High-pressure NMR reveals water-protein interactions coupled with protein conformational transition

Soichiro Kitazawa[1], Yu Aoshima[2], Takuro Wakamoto[2], **Ryo Kitahara**[1] ([1]*Pharmaceutical Sciences, Ritsumeikan University*, [2]*Graduate School of Life Sciences, Ritsumeikan University*)

Although motions of proteins on nanosecond-to-second timescales can be revealed by solution NMR spectroscopy, the location and dynamics of hydrated water in many proteins have not been fully understood. Here, we used phase-modulated clean chemical exchange (CLEANEX-PM) NMR approach to investigate pressure-induced changes in water-to-amide proton exchange occurring at sub-second time scale. With the transition of ubiquitin from its native conformation (N1) to an alternative conformation (N2) at 250 MPa, proton exchange rates of residues located at the C-terminal side of the protein were significantly increased. These observations can be explained by the destabilization of the hydrogen bonds in the backbone and partial exposure of those amide groups to solvent in N2.

2M1412 PDZ ドメインと低分子リガンドの分子認識機構の NMR 法による解析
Molecular recognition of PDZ domains and their non-peptidic ligands revealed by NMR

Takeshi Tenno[1,2], Shotaro Yasukochi[1], Misaki Hisada[1], **Hidekazu Hiroaki**[1,2] ([1]*Graduate School of Pharmaceutical Sciences*, [2]*BeCellBar LLC.*)

PDZ domain is a modular domain that mainly recognizes the C-termini of cytosolic regions of membrane proteins. We already reported that some non-steroid anti-inflammatory drugs (NSAIDs) weekly bound to the several PDZ domains. Accordingly, N-substituted anthranilic acid analogs can bind some PDZ domains more strongly, and some of them show several cellular activities. For example, our group discovered NPL-4011 is a more potent dishevelled PDZ inhibitor. NPL-3004 and 3013 are the other anthranilic acid analogs that inhibit ZO1-PDZ1 domain, resulting down regulation of barrier function of epithelial cells. NMR chemical shift perturbation studies clarify the key residues of the PDZ domains that contributed to the molecular recognition.

2M1424 NMR characterization of conformational dynamics of cyclic and linear Lys48-linked ubiquitin chains

Methanee Hiranyakorn[1,2,3], Saeko Yanaka[1,2,3], Maho Yagi-Utsumi[1,2,3], Koichi Kato[1,2,3] ([1]*Exploratory Research Center on Life and Living Systems, National Institutes of Natural Sciences*, [2]*Institute for Molecular Science, National Institutes of Natural Sciences*, [3]*SOKENDAI*)

Ubiquitin (Ub) can be connected through (iso)peptide linkages, giving rise to a variety of assembly forms, which, however, remain to be fully characterized in terms of conformational dynamics. We prepared a series of cyclic and linear Lys-48-linked Ub chains composed of two to four ubiquitin proteins and carried out NMR studies for characterizing their conformational dynamics. Our NMR results showed that the Ub chains exhibited temperature-dependent conformational equilibria between closed and open states mainly through the hydrophobic interactions at the inter-subunit interface. Particularly, we found slow conformational dynamics of linear tri-Ub, suggesting that its unique multiple domain rearrangement.

2M1436 NMR による天然変性アルファーシヌクレイン蛋白質の残存構造解析
Residual structure of alpha-synuclein mutants elucidated by NMR

Chiaki Nishimura (*Teikyo Heisei University*)

Alpha-synuclein is one of the intrinsically disordered proteins, which adopts no characteristic secondary and tertiary structures. Its residual structure which is related to the function was studied using NMR. Two mutants (A30P and A53T) were analyzed by the chemical shift, signal intensity, and amide-proton exchange. CLEANEX-PM and signal intensity data revealed that the C-terminal region (C-region) has the most significant residual structure for all constructs. Furthermore, A53T indicated more residual structures at the N- and C-regions than wild-type. By contrast, A30P revealed less residual structure at the C-region as well as 50-region. Thus, the tendency of the amount of the residual structure is consistent with the kinetics of the amyloid formation.

2M1448 解鎖タンパク質の全アミノ酸残基の構造分布情報を化学シフトから得る方法の開発
Method for deriving information of the structural distribution of amino acid residues of unfolded proteins from their chemical shifts

Yasutaka Seki (*Molec. Biophys., Kochi Med. Sch., Kochi Univ.*)

It is necessary to explicitly consider the probability distribution of different conformations, in the case of structural analysis of unfolded proteins including IDPs. It was revealed by simulating peptide chains that chemical shifts (CSs) of NMR for unfolded proteins are reflected in the probability distributions of the structure of their amino acid residues (*Ozenne, V., et al., JACS*, 2012). We developed previously a method to generate chain conformation of the unfolded protein, using the main-chain dihedral-angle distribution (MCDAD) for each amino acid residue derived from PDB (*Seki, Y., et al., JCTC*, 2011). Based on this, we propose a new algorithm to determine the MCDAD of a structural ensemble reproducing experimental CSs of an unfolded protein.

2M1500 クライオ電子顕微鏡で解き明かす細菌べん毛モーターのトルク伝達に重要な回転対称構造
Rotational symmetry structure of the bacterial flagellar motor for torque transmission revealed by electron cryomicroscopy

Akihiro Kawamoto[1,2], Tomoko Miyata[2], Miki Kinoshita[2], Tohru Minamino[2], Katsumi Imada[3], Takayuki Kato[2], Keiichi Namba[2,4] ([1]*IPR, Osaka Univ*, [2]*Grad. Sch. Frontier Biosci, Osaka Univ*, [3]*Grad. Sch. Sci, Osaka Univ*, [4]*BDR, RIKEN*)

The bacterial flagellum is a motility nanomachine with a rotary motor and a helical propeller. The MS ring of the flagellar basal body is a major rotor component composed of a single membrane protein, FliF, and acts as the base for flagellar assembly and rotation. The MS ring structure previously analyzed by electron cryomicroscopy (cryoEM) showed the 26-fold rotational symmetry. However, the resolution was limited to show the structural detail to confirm it. We report a high-resolution cryoEM structure of the Salmonella MS ring at 3.9 Å resolution, which clearly shows the 34-fold rotational symmetry in the S ring region, disproving a widely believed hypothesis on the symmetry. We will discuss the mechanism of torque transmission in the flagellar motor.

2M1518 Gwatch: クライオ電顕におけるハイスループット評価システムの構築と評価
Gwatch: the pipeline program for quick evaluation of sample quality in CryoEM

Fumiaki Makino[1], Takayuki Kato[1], Tatsuo Fukagawa[1], Keiichi Namba[1,2] ([1]*Graduate School of Frontier Bioscience, Osaka University*, [2]*BDR and SPring-8, RIKEN*)

In recent years, the structural analysis technique of biomolecules by a cryo-electron microscope (CryoEM) has developed. The background is the development of a direct detector camera and advance of single particle image analysis software represented by Relion. However, the challenges remain. We are not sure whether it is necessary to analyze a large number of images until it finish image analysis. It is important to increase the speed screening including data collection and image analysis. Gwatch: A pipeline program for the screening of the CryoEM image was developed. Here, we show how many images are required and what two dimensional average images should be obtained. Now, we also have developed the program, YOLOpick to pick-up particles by AI and show them.

2M1530 The near-atomic resolution cryo-EM structure of the infectious Staphylococcus bacteriophage S13'

Naoyuki Miyazaki[1], Jumpei Uchiyama[2], Shigenobu Matsuzaki[3], Kazuyoshi Murata[4], Kenji Iwasaki[1] ([1]*IPR*, [2]*Azabu Univ.*, [3]*Kochi Univ.*, [4]*NIPS*)

Cryo-EM single particle analysis has been dramatically developed for the last decade and has been used for structure determination of supramolecular complexes in physiological conditions without crystallization. Here, we determined the overall structure of infectious Staphylococcus bacteriophage S13' at near-atomic resolution by cryo-EM single particle analysis and investigated the structure to understand the detailed mechanism of the phage infection and replication. The bacteriophage S13' has a quasi-icosahedral head of approximately 50 nm in diameter and a short non-contractile tail of approximately 40 nm in length. This bacteriophage structure is one of the largest supramolecular complexes determined at near-atomic resolution.

2M1542 Structural analysis of Type V pilus by Cryo-electron microscopy

Satoshi Shibata[1], Mikio Shoji[2], Kodai Okada[3], Katsumi Imada[3], Koji Nakayama[2], Matthias Wolf[1] ([1]*OIST Molecular Cryo-Electron Microscopy Unit*, [2]*Grad. Sch. BioMedical Sci., Nagasaki Univ.*, [3]*Dept. MacroMol Sci., Osaka Univ.*)

Adhesive pili are known to be one of the virulence factors in pathogenic bacteria. The periodontal pathogen *Porphyromonas gingivalis*, which belongs to the class Bacteroidia, has newly discovered type V pili. Crystal structures and biochemical studies of type V pili have suggested that a protease-mediated donor strand-exchange mechanism is involved in pilus assembly. However, the precise molecular mechanisms of the assembly are not clear. Using cryo-EM and a single particle approach, we have generated a 4 Å resolution structure of type V pilus. Consistent with the assembly model, the cryo-EM structure reveals that the C-terminal strand of a former pilin subunit has been inserted into the groove of next subunit. We will discuss the mechanism of assembly of Type V pilus.

2M1554 クライオ電子顕微鏡を用いた高分解能構造解析による軸糸ダブレット微小管の構築・安定化機構の解明
Cryo-electron microscopy revealed a high-resolution structure of doublet microtubule and its assembly and stabilization mechanisms

Muneyoshi Ichikawa[1], Dinan Liu[1], Panagiotis L. Kastritis[2], Kaustuv Basu[3], Tzu Chin Hsu[1], Shunkai Yang[1], Khanh Huy Bui[1,4] ([1]*Dept. of Anat. and Cell Biol., McGill Univ.*, [2]*Struct. and Comput. Biol. Unit, EMBL*, [3]*FEMR, McGill Univ.*, [4]*GRASP*)

Doublet microtubules in eukaryotic cilia and flagella are highly stable structure. The doublet microtubule structure has been studied in ~20-40 Å resolution using cryo-electron tomography and subtomogram averaging and microtubule inner proteins (MIPs) have been characterized inside the doublet microtubule tubulin lattice. However, the biological functions of the MIPs have not been clearly understood mainly because of no existing high-resolution structure of the MIPs interacting with the tubulin lattice of the doublet. Here, by single particle analysis, we obtained first subnanometer-resolution structure of doublet microtubule. From the obtained structure, we will discuss the functions of the MIPs and how the doublet microtubule is assembled and stabilized.

2M1606 クライオ電子顕微鏡における高分解能構造解析のためのスクリーニング法の検討
Screening method for samples for high resolution structural analysis by cryoEM

Takayuki Kato[1], Naoya Terahara[1], Tomoko Miyata[1], Keiichi Namba[1,2] ([1]*Grad. Sch. Front. Bio., Osaka univ.*, [2]*BDR & SPring-8, RIKEN*)

The single particle image analysis by the electron cryomicroscope(cryoEM) is dramatically improved in several years, and it became indispensable technique in structural biology. To high-resolution structural analysis, finding of sample conditions with less conformational variation is most important. The screening in cryoEM is a much longer process than crystallization in X-ray crystallography, because all samples with different conditions have to be observed by cryoEM. Differential scanning fluorimetry is a simple evaluation method for the temperature stability of proteins, it can evaluate 96 conditions at once within an hour. We will discuss whether this method is suitable as a screening method for high-resolution structural analysis by cryoEM.

2M1618 Structure of a prehandover mammalian ribosomal SRP·SRP receptor targeting complex

Kan Kobayashi[1], Ahmad Jomaa[1], Jae Ho Lee[2], Sowmya Chandrasekar[2], Daniel Boehringer[1], Shu-ou Shan[2], Nenad Ban[1] ([1]*ETH Zurich*, [2]*Caltech*)

Signal recognition particle (SRP) and its receptor (SR) are universally conserved and play a central role in co-translational targeting of nascent proteins to the membrane for their insertion into membrane or secretion. The mechanism of this process has been understood in bacteria, but not in eukaryotes mainly because eukaryotic SRP and SR have eukaryotic-specific components whose roles were unclear. Here, we present the cryo-EM structure of the mammalian ribosome in complex with SRP and SR in a conformation primed for the binding of ribosome onto the membrane. This structure visualizes all eukaryotic-specific components of SRP and SR and, combined with our biochemical data, revealed their roles in stabilizing this conformation by forming a large protein assembly.

2N1400 アクチン繊維の極性揃えた配向はミオシンとの相互作用により引き起こされる
Self-organization of actin filaments of the same polarity by myosin

Kohei Yoshimura[1], Nobuyoshi Koie[1], Takeshi Haraguchi[1], Motoki Tominaga[2,3], Yuichi Hiratsuka[4], **Kohji Ito**[1] ([1]*Dept. Biol. Grad. Sch. Sci., Chiba Univ.*, [2]*Fac. Edu. and Int. Arts and Sci., Waseda Univ.*, [3]*Grad. Sch. Adv. Sci. and Eng., Waseda Univ.*, [4]*Sch. Mat. Sci., JAIST*)

In plant cells, there occurs active circulation of the entire fluid, a process known as cytoplasmic streaming. To induce cytoplasmic streaming in one-direction, actin filaments are arranged with the same polarity. How is actin arranged in one-direction? We made ring-shaped groove that resemble cytoplasm of plant cells using photopolymer. Myosin was attached to it. Then actin filaments whose concentrations are similar to those in plant cells were put on the substrate in the presence of methylcellulose. One hour after the addition of actin filaments, the direction of movements of actin filaments became the same direction. Our results suggest that actin filaments can be autonomously arranged in one-direction by interacting with myosin in cell sized-confinement.

2N1412 心筋・骨格筋のサルコメア集団が生み出すメカニカルな波動特性
Mechanical wave characteristics generated by sarcomere group of cardiac / skeletal muscle

Seine Shintani (*Dep. Biomed. Sci., Col. Life and Health Sci.*)

Cardiac and skeletal muscles are made up of contraction units called sarcomeres. In order to investigate the characteristics of cardiac and skeletal muscle by having this sarcomere aggregated structure, we developed a method to analyze the wave characteristics of the sarcomere group. Sarcomeres have the property of oscillating at a constant calcium concentration solution condition. Examining the nature of the waves generated by this sarcomere group, it was possible to clarify that nonlinear wave properties are provided. In this meeting, we will introduce the nature of this wave, which is unknown from the analysis of one sarcomere's oscillation.

2N1424 *In vivo* マウス心筋における単一サルコメア動態のナノイメージング
Nano-imaging of individual sarcomere dynamics in the beating mouse heart *in vivo*

Fuyu Kobirumaki-Shimozawa[1], Togo Shimozawa[2], Kotaro Oyama[3,4], Shin'ich Isiwata[5], Norio Fukuda[1] ([1]*Dept Cell Physiol, The Jikei Univ Sch of Med*, [2]*Tech Div, Sch of Sci, The Univ of Tokyo*, [3]*QST*, [4]*PRESTO, JST*, [5]*Waseda Univ*)

We developed a high-speed (100 fps), high-resolution (20 nm) spinning disc confocal-imaging system for the beating mouse heart *in vivo* (*J Gen Physiol* 2016). In the present study, we analyzed physiological sarcomere dynamics in a single myofibril consisting of 30 sarcomeres in a ventricular myocyte, simultaneous with hemodynamic parameters. The sarcomere length (SL) values were 1.88±0.29 and 1.66±0.19 μm, respectively, in diastole and systole, and the individual SL values varied markedly during the cardiac cycle. Likewise, the correlation (R) between the dynamics of an individual sarcomere and that of a whole myofibril varied markedly, i.e., from -0.2 to 0.8. We will discuss how myofibrillar contractions are organized in the beating heart *in vivo*.

2N1448 クシクラゲの櫛板はほぼ完全な動く巨大蛋白単結晶である
The comb plate of ctenophore is a nearly perfect giant single protein crystal that moves

Hiroyuki Iwamoto[1], Kei Jokura[2], Kazuo Inaba[2] ([1]*SPring-8, JASRI*, [2]*Shimoda Marine Research Center, Univ. Tsukuba*)

Ctenophores are marine animals that swim means of the beat of comb plates, each of which consists of a large number of closely packed motile cilia. We recorded X-ray diffraction patterns from intact comb plates isolated from a ctenophore, Bolinopsis mikado. In general, the diffraction patterns were basically similar to those recorded from the flagellar axonemes of Chlamydomonas or sea urchin sperm. However, the equatorial reflections were very finely sampled into a series of discrete spots characteristic of a crystal. Its lattice constant was ~290 nm, and the peaks were recognized up to ~40th order. This indicates that the packing of the cilia is enormously regular, and the entire comb plate can be regarded as a nearly perfect giant single protein crystal.

2N1500 ダイニン・微小管・DNA 折り紙複合体の運動および構造の解析
Motility and structure of the dynein-microtubule complex crosslinked with DNA-origami

Shimaa A. Abdellatef[1], Hisashi Tadakuma[2], Yuichi Kondo[3], Kangmin Yan[1], Hideo Higuchi[3], **Keiko Hirose**[1] ([1]*Biomed. Res. Inst., AIST*, [2]*Inst. Protein Res., Univ. Osaka*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

The oscillatory movement of cilia and flagella is produced by regulated force generation of axonemal dynein. In order to understand its mechanism, we analyzed the motility and structures of axonemal outer-arm dynein molecules bound to microtubules (MTs). To prevent disassembly of the complex during movement and observe the structures of force-producing dynein, we designed rod-shaped DNA-origami structures and used them to cross-link the MTs of the complex. DNA rods bound to the complex were clearly observed by negative-stain electron microscopy. Fluorescent microscopy and optical trapping nanometry showed that relative sliding of the MTs of the complex was limited to a certain distance in the presence of DNA rods. Some traces showed bidirectional movement of the MTs.

2N1518 細胞質ダイニンの不活性化状態から活性状態への新規遷移構造
Novel intermediate structures of cytoplasmic dynein between shutdown and active states

Takuma Shioi, **Akira Fukunaga**, Rieko Shimo, Ryousuke Yamamoto, Hiroshi Imai, Takahide Kon (*Dep. Biol. Sci., Grad. Sch. of Sci., Osaka Univ*)

Cytoplasmic dynein is a homodimeric protein that transports various cargoes along microtubules (MTs) in eukaryotic cells. *In vivo*, most of dynein molecules are in a shutdown state, while only a small portion of dynein steps along MTs. Dynein AAA+ rings are in a parallel orientation during stepping, whereas two of dynein AAA+ rings are in a side-by-side orientation under the shutdown state. Dynein is expected to have transitional structures from the shutdown state to the actively stepping state but there were no such experimental observations. We observed novel fluctuation structures of dynein seemingly between shutdown and actively stepping structures using GST-dimerized 380 kDa *Dictyostelium* cytoplasmic dynein motor domains. We propose a novel transition hypothesis.

2N1530 Cell-like movement of self-organized microtubule aster

Takayuki Torisawa[1,2], Shuji Ishihara[3], Kazuhiro Oiwa[2] ([1]*Cell Arch Lab., NIG*, [2]*Adv. ICT Res. Inst., NICT*, [3]*Grad. Sch. Arts and Sciences, Univ. Tokyo*)

Spontaneous directed movement is an essential characteristics of living things. We recently observed cell-like persistent motion of the radial microtubule (MT) array formed by MT and kinesin (aster). When the aster attached to the surface of the glass chamber, the traction force by the surface-adsorbed kinesins drove the movement of the aster. As the aster started to move, the symmetry of aster shape broke in the direction of motion. By changing the crosslinking property of kinesin, we found that the strength of crosslinking affects the aster shape and changes the nature of motion. Our results together with theoretical modeling demonstrate the simple self-organized system without complex regulatory system can lead to the complex dynamics like cell movements.

2N1542 ダイニン c 尾部先端の糸状構造
The String-Like Structure on the Tip of Dynein-c Tail

Hitoshi Sakakibara, Hiroaki Kojima (*Adv. ICT Res. Inst., NICT*)

We observed string-like structure on the tail tip of the single headed axonemal dynein, dynein-c. The string-like structure was observed with the high-speed AFM (Sakakibara et al., BP annual meeting 2009). However, no such structure of the dynein tail tip is observed on the averaged images of the electron micrographs. Here, we observed the detail of the dynein c tail tip in the negative staining electron microscopic images of individual molecules. For each electron micrograph, CTF correction was performed to reduce CTF aberration (Sakakibara, BP annual meeting 2017). The string-like structure was clearly observed in approximately 30% of the dynein c molecules which the form of the tail tips were able to be clearly seen.

2O1400 Predicting gene expression of living cells from a label-free spectral imaging technique

Arno Germond[1], Vipin Kumar[1], Takaaki Horinouchi[1], Chikara Furusawa[1,2], Hideaki Fujita[1], Yuichi Taniguchi[1], Toshio Yanagida[1], Taro Ichimura[1], Tomonobu M. Watanabe[1] ([1]*RIKEN BDR*, [2]*Tokyo Univ.*)

The measurement of gene expression is an invaluable source of information in cellular biology. However, this information cannot be accessed from living cells. Raman spectroscopy is a label-free imaging technique that give information about the molecular compounds of living cells. Using a statistical model, we demonstrate the possibility to predict the gene expression of living cells from spectral measurements in a fast, accurate, and systematic manner, using Escherichia coli strains resistant to antibiotic drugs. Our model exhibits an excellent performance and biological relevance, as genes selected by the model exhibit functions of stress resistance and antibiotic resistance phenotypes. Our recent analysis of 17 cell lines of human iPS cells will also be introduced.

2O1412 Quantifying heterogeneity of stochastic gene expression

Keita Iida[1], Nobuaki Obata[2], Yoshitaka Kimura[1] ([1]*Grad. Sch. Med., Univ. Tohoku*, [2]*Grad. Sch. Sci., Univ. Tohoku*)

The heterogeneity of stochastic gene expression has attracted considerable interest from biologists and physicists. The dynamics of protein production and degradation have been modeled as random processes. However, there is a gap between theory and phenomena, particularly in terms of analytical formulation and parameter estimation. In this study, we propose a theoretical framework in which we present a fairly general model of a gene regulatory system, derive a novel solution, and provide a Bayesian approach for estimating the model parameters from single-cell experimental data. Our framework is demonstrated to be applicable for various scales of single-cell experiments at both the mRNA and protein levels.

2O1424 対称性の自発的破れにより生起する分子生物学のセントラルドグマ
The origin of the central dogma of molecular biology through spontaneous symmetry breaking

Nobuto Takeuchi, Kunihiko Kaneko (*Grad. Sch. Arts and Sci. UTokyo*)

Molecular biology embodies three asymmetries between genomes and enzymes. Information flows from genomes to enzymes, but not from enzymes to genomes: informatic asymmetry. Genomes serve as templates, whereas enzymes serve as catalysts: functional asymmetry. Genomes are less abundant than enzymes per cell: numerical asymmetry. How did these asymmetries originate? Here, we theoretically show that all these asymmetries can spontaneously arise from conflict between evolution at the molecular level and evolution at the cellular level. We find that this conflicting multilevel evolution forms a positive feedback loop with the asymmetric flow of information between molecules, a mechanism that induces spontaneous symmetry breaking of the molecules into genomes and enzymes.

2O1436 変異生成と増殖阻害のトレードオフとしての最適変異率モデル
An optimal mutation rate model as a trade-off between mutation generation and growth inhibition

Atsushi Shibai[1], Minako Izutsu[2], Chikara Furusawa[1] ([1]*RIKEN BDR*, [2]*Michigan State University*)

Mutation is the ultimate source of genetic diversity which drives biological evolution. There should be an optimal value of mutation rate for each situation. Here, we considered a model for explaining how the optimal mutation rate is determined in bacterial populations. We focused on two aspects of mutation; (1) generating beneficial mutations to the population, and (2) inhibiting the cell growth. The former contributes positively to the evolutionary speed, while the latter affects negatively. These reciprocal effects elevate as the mutation rate raise, forming a peak of evolvability. We showed that, in our model, the optimal mutation rate is determined by the coefficient of growth inhibition, and the preliminary experimental results are consistent with that.

2O1448 Mathematical Analysis of Copper Efflux System in Escherichia coli

Jun-ichi Ishihara[1], Tomohiro Mekubo[2], Chikako Kusaka[2], Suguru Kondou[2], Naotake Ogasawara[2], Taku Oshima[3], Hiroki Takahashi[1,4] ([1]*Medical Mycology Research Center, Univ. Chiba*, [2]*Grad. Sch. Bio. Sci., NAIST*, [3]*Grad. Sch. Eng., Univ. Toyama Pref.*, [4]*Molecular Chirality Research Center, Univ. Chiba*)

Copper is essential for all life, but also toxic in excess. Thus the amount of internal copper must be tightly controlled. In E.coli, Cue efflux system is primarily expressed, and Cus efflux system is activated following addition of copper. To systematically address the copper homeostasis, we derived a mathematical model using ODEs in which two-component system (TCS) mediates a signal transduction between the both efflux systems. By integrating experimental data with the mathematical model, we found that reversible phosphorelays in the TCS are crucial for regulating amount of the phosphorylated response regulator, i.e. the TCS operon itself and Cus system. A stochastic simulation revealed the homeostasis of internal copper amount independently of the outside copper.

2O1500 Model-based prediction of ErbB signaling activities on cell cycle entry

Hiroaki Imoto, Kazunari Iwamoto, Shigeyuki Magi, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

In MCF-7 breast cancer cells, the activation of ErbB receptors by epidermal growth factor (EGF) and heregulin (HRG) induces proliferation and differentiation, respectively. To elucidate how the different dynamics of ErbB signaling activities controls distinct cell-fate decisions, we developed a novel mathematical model integrating the processes of ErbB signal transduction, early transcriptional regulation and cell cycle. Our integrated model was validated against a wide range of experimental data and accounted for the mechanism of ligand-specific response. The model provides insights into previously unobserved cellular systems, including how the amplitude and duration of ErbB signaling activities affect cell-cycle entry.

2O1518 孤立した遊走細胞の集団での挙動の理論
Theory on collective behavior of migrating eukaryotic cells

Tetsuya Hiraiwa (*Grad. Sch. Sci., Univ. Tokyo*)

Eukaryotic migration is a ubiquitous kind of cell motility. Cells migrate according to intracellular signals that localize at their front or back. Such localization occurs even without extracellular cues. In light of this, we established a theoretical model for single eukaryotic cell migration with intrinsic polarity. In this presentation, I will explain our work extending this to the multicellular case. We found that, incorporating the contact inhibition of locomotion into the model with volume exclusion, collective directional migration occurs without any explicit alignment interaction. We also studied the case with interaction by which two colliding cells try to reorient their polarities to each other, which we found leads to cell clusters.

2O1530 C. elegans の遊泳運動は、フラクタルノイズを介した状態遷移による
C. elegans swimming motion is a fractal process

Yukinobu Arata[1], Yusaku Ikeda[1,2], Hiroshi Kimura[2], Yuki Shindo[1], Peter Jurica[1], Zbigniew Struzik[3,4], Hiroaki Takagi[5], Yasushi Sako[1] ([1]*Cell Info, Riken*, [2]*Biomed. Microfluidic System Lab., Tokai Univ.*, [3]*Grad. Sch. of Ed., Univ. of Tokyo*, [4]*ACCC, RIKEN*, [5]*Dept. of Phys., Nara Medical Univ.*)

After the fertilization, animals develop, grow, age, and eventually die. During lifespan, animals move in a mode characteristic in each life stage. However, the statistical rule that governs the mode transitions during lifespan remains unknown. Here, we cultured 108 of individual nematode C. elegans in microfluidic device, WormFlo, and recorded motions during 6 days at video rate. Swimming and resting states are pronounced at multiple time scales. Detrended Fluctuation analysis showed that swimming and resting activities were scaled over the range from minutes to a day. Thus, C. elegans swimming motion is a fractal process.

2O1542 境界形状が誘起するバクテリア集団運動と転移現象
Geometry-driven collective ordering of bacterial vortices

Kazusa Beppu, Ziane Izri, **Yusuke T. Maeda** (*Dept. Phys., Kyushu Univ.*)

Collective motion organized by motile elements is ubiquitously observed from motor proteins to flagellated sperms. Here, we investigate collectively ordered phase of vortices of bacteria inside microwells with designed geometries. When swimming bacteria are confined in a circular microwell, a rotational mode of vortex arises from the guiding interaction between the bacteria and the wall. In a doublet of microwells, two vortices emerge but their spinning directions show two distinct phases. The transition of collective ordered vortices can be explained by theoretical model of confined self-propelled particles with polar interaction. This mechanism allows us to construct coexisting vortices in a quadruplet of microwells, revealing a design principle of active vortices.

2O1554 変形菌 Physarum polycephalum の微小変形体にみられる間欠的細胞運動
Emergence of intermittent break in cell motion for tiny plasmodium of Myxomycete Physarum polycephalum

Yasutaka Kakiuchi, Nobuaki Nishiyama (*Kanazawa Univ.*)

Plasmodium of the Myxomycete Physarum polycephalum shows continuous cell shape changes, accompanying vigorous protoplasmic shuttle streaming. Whereas, tiny plasmodia, with a diameter of about 20-50 um, do not show stable protoplasmic stream. Here we report characteristic cell shape change in tiny plasmodia, where cell motility is not continuous but accompanied by ‘intermittent break’. In typical cases, the breaks appear every 5-10 minutes and continue around several ten seconds. During the break, plasmodia almost completely cease cell shape change, but protoplasm still continue its flow. Emergence rate of the break roughly depends on the cell size, and we try to explain such dependence with simple coupled oscillator model.

2O1606 一分子時間分解 FRET データの三次元解析：生体高分子の構造不均一性をモデルフリーで定量する方法の開発
Third-order correlation analysis of single-molecule time-resolved FRET data: a new method for quantification of heterogeneity

Miyuki Sakaguchi[1], Kunihiko Ishii[1,2], Tahei Tahara[1,2] ([1]*Molecular Spectroscopy Lab., RIKEN*, [2]*RAP, RIKEN*)

Structural heterogeneity is an important issue for biomolecules. In this study, we have developed a new model-free method, three-dimensional fluorescence correlation spectroscopy (3D FCS), for visualizing the heterogeneity using single-molecule time-resolved FRET data. Firstly, we applied 3D FCS to an artificially synthesized photon data and confirmed that it can determine as many as 5 FRET components. Next, we applied 3D FCS to real experimental data of model FRET systems and found that 3D FCS detected not only the major FRET species but also minor impurities. We expect that 3D FCS becomes a powerful quantitative analysis tool, because it is model-free and in principle it has a better time resolution than conventional analysis methods.

2O1618 分子数絶対定量に向けた認証標準物質による蛍光相関分光装置の校正
System calibration of fluorescence correlation spectroscopy for absolute quantification of molecular number

Akira Sasaki[1], Johtaro Yamamoto[1,2], Masataka Kinjo[2], Naohiro Noda[1] ([1]*BMRI, AIST*, [2]*Faculty Adv. Life Sci., Hokkaido Univ.*)

Direct quantification of molar concentration is one of the best way to quantify biomolecules. Fluorescence correlation spectroscopy (FCS) is powerful tool to determine molecular number in solution and in living cells. However, metrological aspect has not been considered sufficiently. To achieve accurate and precise FCS measurement, calibration of the FCS system (i.e. confocal volume characterization) is important. We performed the calibration of the FCS system by measuring the primary standard, the concentration of which is surely determined and certified. Furthermore, the calibrated system was validated using another primary standard. The work can improve an assurance of FCS measurement and serve a universal method for absolute quantification of molar concentration.

2Q1400 Chromatin remodelers couple inchworm motion with twist-defect formation to slide nucleosomal DNA

Giovanni Brandani, Shoji Takada (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

ATP-dependent chromatin remodelers are molecular machines that control genome organization by repositioning, ejecting, or editing nucleosomes, activities that confer them essential regulatory roles on gene expression and DNA replication. We investigated the molecular mechanism of active nucleosome sliding via MD simulations of the Snf2 remodeler in complex with a nucleosome. During its inchworm motion driven by ATP consumption, Snf2 overwrites the original nucleosome energy landscape through steric and electrostatic interactions to induce sliding of nucleosomal DNA via the generation of twist defect deformations. Our results offer a detailed mechanistic picture of remodeling necessary for the complete understanding of this important biological process.

2Q1412 単一ヌクレオソームイメージングによる生細胞中の分裂期染色体の局所ゆらぎ計測
Local nucleosome dynamics in mitotic chromosomes in living cells

Kayo Hibino[1,2], Kazuhiro Maeshima[1,2] ([1]*NIG*, [2]*SOKENDAI*)

Mitotic chromosomes are essential structures for the faithful transmission of copied genome information. The chromosome condensation requires large proteins including Condensin and topoisomerase IIα. However, how a long DNA is assembled into mitotic chromosomes remains unclear. Here, we measured local nucleosome dynamics in mitotic chromosomes by single nucleosome imaging in living cells. Nucleosomes in the chromosome fluctuated slowly but relatively freely on sub-second time scale. By contrast, apoptotic chromatin, which is also highly condensed, showed much less nucleosome movements, implying the functional difference(s) of their condensed organizations. We will discuss significance of the fluctuation in terms of chromosome functions.

2Q1424 リンカー DNA によって大きく決まるポリヌクレオソームの局所構造
Local structures of poly-nucleosome largely restricted by linker DNA

Hiroo Kenzaki[1], Shoji Takada[2] ([1]*Info. Sys. Div., RIKEN*, [2]*Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.*)

Nucleosomes are connected by linker DNA, but how linker DNA affects the local structure of nucleosomes has not been clarified. The length dependence of linker DNA should be very large, because linker DNA rotates about 36 degrees around double helical axis per base pair. Previously, we had performed coarse-grained model simulations of di-nucleosome and tri-nucleosome with various length of linker DNA. We have analyzed the trajectories such as clustering methods and PCA. The local structure of poly-nucleosome was largely restricted by the linker DNA. In particular, tri-nucleosome takes some characteristic structures depending on the length of the linker DNA.

2Q1436 Investigating the influence of Argine Dimethylation on Nucleosome Dynamics using All-atom Simulation and Kinetic Analysis

Zhenhai Li, Hidetoshi Kono (*QST*)

Post-translational modification (PTM) of nucleosome regulates gene activity. To study impact of a single PTM on the nucleosome structure, we performed all-atom replica-exchange molecular dynamics simulations with and without a single PTM, either symmetric (R42me2s) or asymmetric (R42me2a) dimethylation. With the aiding of comprehensive kinetics analysis, our simulations showed R42me2a nucleosome promoted the DNA opening rate and adopted a more opened conformation, but not R42me2s. This study unravels the mechanism for distinct gene-regulation induced by a subtle, different dimethylation.

2Q1448 大腸菌非六量体型 DNA ヘリカーゼ UvrD 変異体の 1 分子イメージング
Single-molecule imaging of mutants of the non-hexameric *Escherichia coli* helicase UvrD

Hiroaki Yokota (*Biooptics Lab, Grad. Sch. Creation Photon. Indust.*)

Escherichia coli UvrD protein is a non-hexameric superfamily I DNA helicase which plays a crucial role in nucleotide excision repair and methyl-directed mismatch repair. We performed direct single-molecule fluorescence visualization of the helicase and reported that the helicase unwinds DNA in the form of an oligomer (dimer or trimer) (*Biophys. J.* 2013). Although the oligomeric form is responsible for efficient DNA unwinding, only monomeric structures of the helicase are available (*Cell* 2006). To address the relationship between the oligomer dynamics and helicase activity, single-molecule visualization of several mutants of the helicase has been performed. Recent results of the single-molecule visualization will be presented in the meeting.

2Q1500 in vitro と in vivo での DNA 結合タンパク質の単分子蛍光測定
Single-molecule fluorescence imaging of architectural DNA-binding proteins in vitro and in vivo

Kiyoto Kamagata[1], Eriko Mano[1], Sridhar Mandali[2], Yuji Itoh[1], Reid Johnson[2] ([1]*IMRAM, Tohoku Univ.*, [2]*UCLA*)

Architectural DNA-binding proteins (ADBP) bind to and bend DNA, and assist the reactions by other proteins. However, the fundamental question how they behave on DNA and in cell remain unclear. Here, we first characterized the dynamics of three ADBPs along DNA using single-molecule fluorescence microscope and DNA garden. Three ADBPs exhibit rotation-coupled sliding along DNA with high free energy barrier. Mutational analysis identified a key residue/part for sliding ofADBPs. Second, we examined the dynamics of ADBPs at single molecule level in bacteria using the fluorescence microscope. Slow dynamics of three ADBPs in bacteria may attribute for the slow sliding and dissociation. Overall, the slow dynamics by ADBPs may be important to stand by other proteins on DNA.

2Q1518 クライオ電顕フィッティングによる RNA ポリメラーゼ-DNA 複合体の構造精密化
Cryo-EM structure refinement of RNA polymerase by molecular dynamics simulations

Takaharu Mori[1], Haruhiko Ehara[2], Shun-ichi Sekine[2], Yuji Sugita[1,2,3] ([1]*RIKEN Theor. Mol. Sci. Lab*, [2]*RIKEN BDR*, [3]*RIKEN R-CCS*)

Cryo-electron microscopy (cryo-EM) is a powerful tool to determine three-dimensional structures of biomolecules with near atomic resolution. Prediction of high-resolution structures from cryo-EM density maps is challenging, because there are usually low local-resolution regions due to large fluctuation of flexible domains. In this study, we perform molecular-dynamics-based flexible fitting for structure refinement of RNA polymerase to elucidate detailed interactions between the polymerase, DNA, RNA, and elongation factors.

2Q1530 種々のポリアミンによる遺伝子発現活性制御
Effect of polyamines on in vitro gene expression

Hiroko Tanaka[1], Yuko Yoshikawa[1], Naoki Umezawa[2], Takahiro Kenmotsu[1], Kenichi Yoshikawa[1] ([1]*Lab. Life Phys., Grad. Sch. Life Med. Sci., Doshisha Univ.*, [2]*Grad. Sch. Phar. Sci., Nagoya City Univ.*)

Polyamines exist in almost all living cells and are known to play important roles on various biological functions. We examined the effect of linear-chain polyamines with a valency from 2+ to 5+, on the gene expression activity by adapting an in vitro luciferase assay. As a result, maximum acceleration of gene expression was observed at certain concentration of each polyamine, being critically dependent on its valency. In addition, we investigated the effect of the carbon chain length (from C3 to C6) of divalent polyamines on gene expression. It was found that gene expression was markedly enhanced in the presence of diamines having C3, C4 and C5 carbon chains. We will discuss structural factors of polyamines affecting gene expression in relation to DNA conformation.

2Q1542 選択的な DNA ライゲーションと情報成長の分子的起源：「富むものはより富む」モデル
Molecular origin of selective DNA ligation and information growth: The rich-get-richer model

Takaharu Shiraki[1], Ken-ichiro Kamei[2], Yusuke T. Maeda[1] ([1]*Dept. Phys. Kyushu Univ.*, [2]*WPI-iCeMS, Kyoto Univ.*)

Enzymatic ligation catalyzes the growth of DNA or RNA, which could be involved in the origin of protocell genome. However, randomly ligation cannot selectively connect larger molecules and thus longer DNA occurs at very low probability. How can simple enzymatic reaction acquire selective ligation, even at early stage of chemical evolution? To solve this fundamental question, we study the ligated growth of DNA out of equilibrium by newly developed qPCR method. We find that the coexistence of another polymer drives non-random, size-selective ligation of DNA and it facilitates longer DNA storing much information. Theoretical analysis tells that selective ligation is mediated by entropic depletion attraction, implying the emergence of the rich-get-richer growth.

2Q1554 転写因子 NF-κB がつくる核内クラスターと転写応答の解析
Analysis of NF-κB clusters and transcriptional initiations

Takehiko Inaba[1], Kazunari Iwamoto[2], Mariko Okada[2], Yasushi Sako[1] ([1]*RIKEN Cellular informatics*, [2]*Laboratory of Cell Systems, Institute for Protein Research, Osaka U.*)

The transcription factor NF-κB is a hub of signaling networks and is responsible for various gene expressions. The translocation of NF-κB into the nucleus is one of the critical steps in its functions. We have observed the GFP fusion of NF-κB in chick DT40 cells to study its behavior in response to B-cell receptor activation. Single-cell observation showed that NF-κB in the nucleoplasm forms clusters. These cluster sites might regulate the transcriptional responses. In fact, the clusters were partially co-localized with the signal of RNA polymerase II immunofluorescence. This result indicates the NF-κB clusters are associate with the transcriptional initiation.

2Q1606 Biopolymer self-assembly and combinatorial evolution at the origin of life

Tony Z Jia[1], Charalampos G Pappas[2], Ankit Jain[2], Daniela Kroiss[2], Nadeesha K Wijerathne[2], James M Aramini[2], Ayan Pal[3], Jack W. Szostak[3], Rein V Ulijn[2], Kuhan Chandru[1], Rehana Afrin[1], Yayoi Hongo[1], Henderson J Cleaves[1] ([1]*Earth-Life Science Institute, Tokyo Institute of Technology*, [2]*Advanced Science Research Center, City University of New York*, [3]*Massachusetts General Hospital, Harvard Medical School*)

Modern life uses DNA and proteins for genetics and metabolism. Early life did not have these biopolymers, but genetic replication and metabolism are necessary for life. Supramolecular self-assemblies and combinatorial evolution of simple small molecules or short oligomers available on the early Earth have been studied to assist in these reactions. We have discovered a variety of self-assembled systems with emergent properties relevant to the origin of life, including small peptide nanofibers and hydrogels that interact with RNA, dynamic combinatorial evolving libraries of small peptides, and polyester microdroplets that segregate small molecule dyes and are useful for drug delivery applications.

2Q1618 アクチン線維封入巨大リポソームからの光応答性の膜チューブの伸張短縮は自身の移動を引き起こす
Photoresponsive elongation and retraction of membrane tubes from F-actin-encapsulating giant liposome can move its cell body

Masahito Hayashi[1], Shunsuke Tanaka[2], Kingo Takiguchi[2] ([1]*RIKEN CBS*, [2]*Grad Sch of Sci, Nagoya Univ*)

We have reported that F-actin-encapsulating giant liposomes (FAGLs) can reversibly change their shape between spindle-like and spherical one due to turning ON/OFF of stimulation light. In this cycle, two membrane tubes elongated and retracted from apexes of the spindle. The tubes included F-actin and more rigid than empty membrane tubes. The tubes elongated to 100 μm long and retracted to original length at the rate of 30 μm/min and 15 μm/min, respectively. If the tip of elongating tube attached on a substrate, the body of an FAGL moved by the tube retraction. These results indicated that morphological change of FAGLs can realize living cell-like motion; they need just only lipid membrane and F-actin and need not motor proteins such as myosin or kinesin.

1Pos001 分子動力学法を用いた Hras-GTP/GDP 複合体の各部の構造変化と各部の水素結合との動的関連性の研究
Molecular dynamics study of dynamical relationship between structures and the hydrogen bonds of some parts in the Hras-GTP/GDP complexes

Takeshi Miyakawa[1], Ryota Morikawa[1], Masako Takasu[1], Kimikazu Sugimori[2], Kazutomo Kawaguchi[3], Hidemi Nagao[3] ([1]*Sch. of Life Sci, Tokyo Univ. of Pharm. and Life Sci.*, [2]*Inst. of Liberal Arts. and Sci., Kanazawa Univ.*, [3]*Coll. of Sci. and Eng., Kanazawa Univ.*)

In order to understand the role of hydrogen bonds in the Hras-GTP/GDP complexes, we study the structures of the Hras-GTP/GDP complexes in water solvent by molecular dynamics (MD) simulations. We evaluated the potential parameters around Mg2+ in Hras-GTP/GDP complexes by quantum chemical calculations. We performed MD simulations of the Hras-GTP/GDP complexes in water solvent using parameters of AMBER03 and our parameters around Mg2+. We found that the positions and orientations of water molecules near GTP are different from those near GDP. In this study, we analyze the dynamical property of the structural deformation of various parts and the hydrogen bonds of various parts in the Hras-GTP/GDP complexes using Ralaxation Mode Analyses.

1Pos002 分子シミュレーションを用いた複数ドッキングポーズからの正しい結合ポーズの特定―自動デザインに向けて
Identifying correct ligand binding pose out of multiple docking poses by MD simulations toward AutoDesign

Hironori Kokubo (*Axcelead, Inc.*)

Docking software has been widely used to predict a binding mode of a ligand. However, it is often difficult to identify the correct pose from putative docking poses. We have recently examined the stability of binding modes to proteins by MD simulations systematically and showed that about 95 % of the native poses were maintained stable during the simulations, while only 56-74 % of decoy poses were stable. It suggests that equilibrium MD simulations can serve as an effective filter to exclude some decoy poses. We next performed absolute binding free energy calculation for the survived poses to identify the correct pose. The concept of automatic drug design tool will be introduced, which produces rational design by automatically interpreting simulation data.

1Pos003 α シヌクレインフラグメントの 2 量体形成過程の解明に向けた定温定圧レプリカ置換分子動力学シミュレーション
Isothermal-isobaric replica-permutation molecular dynamics simulation to reveal dimerization process of α-synuclein fragments

Masataka Yamauchi[1,2,3], Hisashi Okumura[1,2,3] ([1]*SOKENDAI*, [2]*IMS*, [3]*ExCELLS*)

α-synuclein is an intrinsically disordered protein consisting of 140 amino-acid residues, which has no specific structure in aqueous solution. This protein is present at the nerve terminal and its amyloid fibrils are principal components of Lewy bodies, hallmarks of Parkinson's disease. In order to elucidate the molecular mechanism of the disease, it is necessary to reveal the fibril formation process. In this study, we focus on the early process that takes the longest time in the fibril formation process. Especially, we focus on the dimerization process. We applied the isothermal-isobaric replica-permutation method toα-synuclein fragments. We will show probability of the dimer structures and discuss molecular mechanism of the dimerization process.

1Pos004 Cryo-tomography and sub-tomogram averaging of dimeric F type ATP synthase at bovine sub-mitochondrial particle

Jun-chi Kishikawa[1], Atsuko Nakanishi[1], Masatoshi Murai[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. Mol. BioSci., Kyoto Sangyo Univ.*, [2]*Div. Appl. Life Sci., Grad. Sch. Agrci., Kyoto Univ.*, [3]*Res. Ctr. UHVEM, Osaka Univ.*)

Cryo-tomography and its sub-tomogram averaging using cryo-EM are powerful techniques to solve the *in vivo* structures of macromolecules. In this study, we attempted to obtain the structure of dimeric F_oF_1 in mitochondrial inner membrane by sub-tomogram averaging. The tilt series of bovine sub-mitochondrial particle for reconstruction of the cryo-tomograms were recorded by Titan Krios. To obtain the high-resolution structures of dimeric F_oF_1, 3D regions including F_oF_1 (sub-tomograms of F_oF_1) were extracted from the reconstructed tomograms and classified using RELION software. After classification, the selected sub-tomograms were used for structural refinement. We introduce the reconstituted dimeric F_oF_1 and discuss about the technical problems of sub-tomogram averaging.

1Pos005 クライオ電子顕微鏡による好熱菌 *Thermus thermophilus* 由来 V 型 ATP 合成酵素の単粒子解析
Cryo EM structure of intact rotary H^+-ATPase/synthase from *Thermus thermophilus*

Atsuko Nakanishi[1], Jun-ichi Kishikawa[1], Masatada Tamakoshi[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. of Mol. Biosci., Kyoto Sangyo Univ.*, [2]*Dept. of Mol. Biol., Tokyo Univ. of Pharm. and Life Sci.*, [3]*Res. Ctr. for UHVEM, Osaka Univ.*)

The *Thermus thermophilus* V_oV_1 (*T. th* V_oV_1) is a rotary enzyme that mediates the coupling between ATP synthesis/hydrolysis in V_1 and proton translocation across membranes through V_o. To understand the molecular mechanism of *T. th* V_oV_1, the whole structural information of the enzyme at atomic resolution is required. Here we report the structures of intact *T. th* V_oV_1 by single particle analysis using Cryo-EM. The maps provided a detailed molecular basis for how the rotary ATPase maintain structural integrity of the peripheral stator apparatus, and confirming the existence of clear proton translocation paths from both sides of the membrane.

1Pos006 Startup of Laboratory-scale SEC-SAXS (La-SSS) system

Rintaro Inoue, Ken Morishima, Nobuhiro Sato, Masaaki Sugiyama (*Institute for Integrated Radiation and Nuclear Science, Kyoto UniversityInstitute for Integrated Radiation and Nuclear Science, Kyoto University*)

Small-angle X-ray (SAXS) technique offers the opportunity for structural analyzes on various biomolecules. Only the subtle contamination of aggregation of bio-molecules significantly deteriorates the SAXS profiles since the intensity is roughly proportional to the square of the molecular weight. As a result, the detailed structural analyses of concerned biomolecules are strongly hindered. Recently, the combination of size exclusion chromatography (SEC) and SAXS, SEC-SAXS, provides much superior opportunity for structural analyses on unstable biomolecules. At present, a SEC-SAXS system is only limited to be installed at a synchrotron facility despite of its high applicability. To tackle such situation, we start up the Laboratory-scale SEC-SAXS (La-SSS) system.

1Pos007 Determination and Comparsion of the Structural Ensemble of Molten Globule State of Proteins by Computer Simulations

Masahiro Shimizu, Yuko Okamoto (*Grad. Sch. Sci., Univ. Nagoya*)

We have used computer simulations to investigate the structural nature of the molten globule (MG) state of lysozyme, α-lactalbumin, and myoglobin. In order to sample the conformational space efficiently, we performed replica-exchange umbrella sampling simulations with the radius of gyration as a reaction coordinate. We got some clusters of similar structures corresponding to local minima in the free energy surface. The representative structures obtained in this way are in accord with the characteristics of the MG state reported previously by experimental studies.

1Pos008 GPI アタッチメントシグナルの二次構造解析
Secondary structural analysis of GPI attachment signal

Keiya Inoue[1], Daiki Takahashi[1], Tatsuki Kikegawa[1], Kenji Etchuya[2], Yuri Mukai[1] ([1]*Dept. Electronics, Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Biomed. Res. Inst., AIST*)

In the premature GPI-anchored proteins (GPI-APs), the specific structures around GPI attachment signals (GPI-ASs) are recognized and digested by GPI transamidase. However, even though the tertiary structural data of mature GPI-APs have been reported in the PDB, the structures of GPI-ASs are not included because the GPI-ASs are separated from the mature proteins. The purpose of this study is to uncover the recognition and digestion mechanisms of GPI transamidase based on analyzing the secondary structures. The secondary structures of GPI-ASs which were fused GFP proteins and were expressed in E.coli, were analyzed by circular dichroism. The secondary structure of GPI-ASs were predicted based on several programs and analyzed the overall trend of the secondary structure.

1Pos009 位相差クライオ電子顕微鏡単粒子解析法を用いた腸球菌 V-ATPase の構造解析
Single Particle Analysis of *Eh*V-ATPase by Phase-Plate electron cryo-microscopy

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V-ATPases are large membrane protein complexes to transport ions through cell membranes. *Eh*V-ATPase isolated from *Enterococcus hirae* consists of 24 subunits from 9 different proteins, and especially transports Na^+ using energy of ATP hydrolysis. So far, the entire structures of several H^+-type V-ATPases and the partial subunit structures of *Eh*V-ATPase have been revealed, however the overall structure of the *Eh*V-ATPase is still unclear. In this study, we applied phase plates cryo-electron microscopy to visualize the detergent-solubilized *Eh*V-ATPase and successfully obtained the 3D structure. Furthermore, we used PA tag system to fix the flexible structure and successfully obtained the detailed structure at higher resolution.

1Pos010 マルチスケールシミュレーションと構造比較を用いた、シグナル蛋白質カルモジュリンの研究
Multiscale simulation and Structural comparison of Calmodulin

Hiromitsu Shimoyama (*Kitasato University*)

Calmodulin (CaM) is an intermediate calcium-binding messenger protein which regulates many enzymes. CaM has two globular domains and acts via structural changes; these domains cooperatively wrap the target enzyme through a large conformational change in a calcium ion dependent manner. However, the regulation mechanism is still unclear. In order to understand the mechanism, experimentally obtained CaM-structures were analyzed, and then, a relationship between conformation and domain-domain interactions was clarified. CaM-bindin domain (CaMBD) structures of an enzyme are studied using a multiscale simulation. The CaM-CaMBD interactions are also studied by docking simulation.

1Pos011 Investigation of the common sequence-structural patterns in different protein folds using cross-profile analysis and simulation

Yu Yamamori, Kentaro Tomii (*AIST*)

Structurally similar segments can be occurred in different protein folds. Combining the database analysis and molecular simulation, we investigated the evolutionary meaning of the existence of those segments. Previously, using cross-profile analysis, we found that the clusters of structural segments detected from structural-profiles show the strong correlation between particular sequence profiles. In this study, in order to validate the sequence-structure relationship, folding simulations of the peptides derived from those sequence profiles were performed using the replica-exchange molecular dynamics. It was indicated that the peptides can have stable folded structures.

1Pos012 Modeling three-dimensional (3D) volume of protein from Atomic-Force Microscopy (AFM) images

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Hybrid structural modeling uses multiple experimental and computational techniques to obtain reliable 3D model of biomolecules. We intent to use two-dimensional molecular surface images from AFM in hybrid structural modeling. Such images can also reveal multiple conformational states. We are developing computational tools utilizing such images to obtain low-resolution 3D models of biomolecules. As a test case, simulated AFM data were generated from one of the conformations of Elongation factor2 and its another conformation was deformed by Monte-Carlo (MC) sampling. In each MC step an AFM-like projection from the latter was matched to the simulated AFM data of the former. Here we discuss the computational approaches used and preliminary results on 3D models prediction.

1Pos013 結合ヌクレオチド依存的なチューブリン C 末端テイルの構造分布に関する分子動力学計算解析
The bound-nucleotide (GDP or GTP) effects on C-terminal tails of tubulins investigated by molecular dynamics simulation

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The microtubule cytoskeleton is formed by assembling the heterodimer consisting of α-tubulin (αTUB) and β-tubulin (βTUB). Each of αTUB and βTUB contains a structurally-flexible C-terminal tail (CTT) and has a nucleotide binding site. The bound-nucleotide (GTP or GDP) state is known to contribute to the stability of microtubule. However, although CTT is also related to the microtubule assembly, the relationship between the nucleotide state and the CTT conformation remains unclear. Then, we have studied the nucleotide-dependent CTT conformational change by using molecular dynamics simulation. The results showed the conformational ensemble of CTT of βTUB was affected by the nucleotide state, which may provide a new insight into microtubule assembly mechanism.

1Pos014 クライオ電子顕微鏡によるグルタミン酸脱水素酵素ドメイン運動の可視化
Visualizing the domain motion of Glutamate Dehydrogenase by using cryo-electron microscopy

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Hexameric glutamate dehydrogenase (GDH) is a large enzyme (Mw 280k). Each subunit comprises two functional domains forming a large active-site cleft between them. X-ray crystal structure analysis and molecular dynamics simulation of unliganded GDH have revealed several metastable conformations in the domain motion to open/close the cleft. More importantly, the hydration structure changes suggest a cooperative variation of hydration in coupling with the domain motion. By using cryo-electron microscopy, we visualized the structures of GDH at several conformational states indicating the domain motions to open/close the cleft. In this report, we will show the result of this study and discuss the correlation between the domain motion and the function of GDH.

1Pos015 クライオ電子顕微鏡単粒子解析法を用いた KcsA の構造解析
Structural Analysis of KcsA by Cryo-EM Single Particle Analysis

Hiroko Takazaki[1], Hirofumi Shimizu[2], Kaoru Mitsuoka[3], Takuo Yasunaga[1] ([1]*Grad. Sch. Comp. Sci. Syst. Eng., KIT*, [2]*Fac. Med. Sci., Univ. Fukui*, [3]*Research Center for UHVEM, Univ. Osaka*)

KcsA is a potassium channel. It has open and closed conformations under acidic and neutral conditions, respectively. Both of open and closed structures of full-length KcsA have been solved by X-ray crystallography. However, the structural change between open and closed conformations is predicted more dynamic by diffracted X-ray tracking. In this study, we try to elucidate the structures of KcsA under open and closed conditions by cryo-electron microscopy (EM) and single particle analysis. We prepared samples under different pH conditions, observed them and reconstructed their 3D structures. Under acidic conditions, the structure around 'Bulge helix' is more flexible than under neutral conditions. This structural flexibility would reflect the open conformation.

1Pos016 *Porphyromonas gingivitis* の線毛蛋白質 FimA の構造
Structure of FimA, a major component protein of fimbriae of *Porphyromonas gingivitis*

Kodai Okada[1], Koji Nakayama[2], Mikio Shoji[2], Satoshi Shibata[3], Katsumi Imada[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Biomedical Sci., Nagasaki Univ.*, [3]*OIST*)

Porphyromonas gingivitis is a gram-negative anaerobic bacterium known as a major periodontal pathogen. *P.gingivalis* cell adheres to its host cells using fimbria, hence the fimbria is a major virulence factor of *P.gingivalis* and is involved in biofilm formation. FimA is a major component of the fimbriae of *P.gingivalis* and is classified into five different subtypes (FimA1-FimA5) based on sequence and immunogenic properties. The virulence highly depends on the type of fimbriae expressed on bacteria. To elucidate the molecular basis of fimbriae virulence, we determined the crystal structure of FimA1 at 2.1 Å resolution and compared it with those of FimA2 and FimA4. We will discuss the structural differences that may determine the virulence of *P.gingivalis*

1Pos017 好熱菌 V1-ATPase の単粒子解析
Single particle analysis of V1-ATPase from Thermus thermophilus

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The V1-ATPase is a ATP driven molecular motor composed of central rotor DF and the surrounding stator cylinder A3B3 responsible for ATP hydrolysis. To understand the mechanisms of V1-ATPase, we attempted to determine the structure of V1 by single particle analysis using cryo-EM. V1-ATPase exhibited strong preferred orientation in cryo grid without any modification. To overcome this problem, the poly-lysine modified cryo grid with thin carbon backing was used. In addition, we used LMNG solubilized V1 for preparation of cryo-grids. These trials enabled us to improve distributions of particle images orientation. These particle images were extracted by RELION 2.1, then subjected to 2D and 3D classification. We finally obtained 3D reconstruction of V1 at 5.8 Å resolution.

1Pos018 マベガイ由来 PPL3 の構造解析
Structure analysis of PPL3 regulating pearl shell biomineralization

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Jacalin-related lectins, including PPL3 isoforms, are known to regulate pearl shell biomineralization of *Pteria penguin*. The PPL3 crystal structures were determined partly by utilizing microgravity environments for three isoforms, namely, PPL3A, PPL3B, and PPL3C. The structures revealed a tail-to-tail dimer structure established by forming a unique inter-subunit disulfide bond at C-termini. The complex structures with trehalose and isomaltose indicated that the novel specificity originated from the unique α-helix of PPL3 isoforms. Docking simulations of PPL3B to various calcite crystal faces suggested the edge of a β-sheet and the carbohydrate-binding site were the interface to the biomineral, and implied that the isoforms differed in calcite interactions.

1Pos019 Application of the solution technique to identify a binding site and mode of a ligand in a protein

Masataka Hamano, Masatake Sugita, Takeshi Kikuchi, Fumio Hirata (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

Solution map analysis is a method for predicting the plausible position and orientation of a solvent molecule based on the distribution of the solvent inside and around a solute in solution. That distribution of solvent molecule is determined by the three-dimensional reference interaction site model (3D-RISM) theory which is a statistical mechanics theory of molecular liquids. This 3D-RISM based method will realize the identification of ligand binding site in a protein. For the purpose to examine the accuracy of this method, we apply to some protein-ligand systems, T4 Lysozyme-benzene, IGG-KAPPA protein-isopropanol and SH3 domain-imidazole.

1Pos020 MM/3D ー RISM 法を用いた水・エタノール混合溶液中における小分子間における結合エネルギー予測
Cosolvent effect on the binding affinity between small molecules in a water-ethanol mixture : MM/3D-RISM study

Kazuma Kondo[1], Masatake Sugita[1], Takeshi Kikuchi[1], Fumio Hirata[2] ([1]*Dept. of Bioinf., Col. Life Sci., Ritsumeikan Univ.,*, [2]*Toyota Phys. & Chem. Res. Inst.*)

A biomolecule exhibits its function in a mixture-solution containing cosolvent molecules such as ions. Therefore, to accurately predict the affinity between molecules, it is necessary to calculate binding free energy considering the effect of cosolvent. This time, we calculate binding free energy using MM / 3D-RISM method for inclusion reaction of fluosterone by cyclodextrin in ethanol-water solution and verifie whether binding free energy calculation in mixed solution is possible. We report the calculated results of binding free energy and each distribution functions. It is demonstrated that the trend of experimental data and effect of cosolvent can be reproduced.

1Pos021 MD シミュレーションを用いた BAF の野生型と変異体の揺らぎの解析
Analyses of fluctuations of wild type and mutant of BAF using MD simulation

Chiaki Yamaguchi[1], Siyao Li[2], Masatake Sugita[1], Toshiya Hayano[2], Takeshi Kikuchi[1] ([1]*Dept. of Bioinf., Col. Life Sci., Ritsumeikan Univ.*, [2]*Dept. of Biomed., Col. Life Sci., Ritsumeikan Univ.*)

Barrier-to-autointegration factor (BAF) is a 10 kDa conserved protein. It localizes to nuclear lamina and binds double-stranded DNA as a homodimer. A coding mutation (A12T) in BANF1 gene was reported as the genetic basis of Nestor-Guillermo progeria syndrome (NGPS), a so-called rare disease that involves premature aging, however the mechanism underlying NGPS remains unclear and no effective treatment has been found. In this study, MD simulations of BAF are performed. As a result, it is predicted that the fluctuation of the structure, particularly the α1 helix, in the mutant became larger. This result is compared to the nuclear morphology experiments.

1Pos022 Bio-SAXS を活用したタンパク質相関構造解析
Hybrid Approach of the Protein Structure Analysis utilizing Biological Small-Angle X-ray Scattering

Kento Yonezawa, Keiko Yatabe, Masatsuyo Takahashi, Yasuko Nagatani, Nobutaka Shimizu (*Photon Factory, IMSS, KEK*)

The biological small-angle X-ray scattering (Bio-SAXS) is the highly effective method to analyze the structure of biological macromolecules in the solution. The hybrid approach which combined Bio-SAXS with the crystallography, NMR, Cryo-EM, etc. is actively utilized in order to clarify the structure mechanism of the biological systems. We, Photon Factory promote a national platform project for the life science research, BINDS (http://www.binds.jp/), and not only improve and develop the equipment and the beamline about the Bio-SAXS technique but also support the beginner users as collaborative work. We will introduce the latest status of Bio-SAXS technique at the PF in this presentation.

1Pos023 Chk1 阻害剤系の分類と自由エネルギー変分原理に基づく相対的結合自由エネルギー予測
Classification of Chk1 inhibitor system and Prediction of relative binding free energy based on a free energy variational principal

Daichi Kondo, Takeshi Ashida, Takeshi Kikuchi (*Dept. Bioinf. Col. Life Sci. Ritsumeikan Univ.*)

It is important to predict accurate binding free energy of a ligand to a target protein in drug discovery process. There are many methods to predict it. This time, we calculate relative binding free energy to use free energy variational principal method. It is needless to set parameters and requires much computational cost. This point is superior to other methods. We apply this method to check point kinase1 (Chk1) inhibitor system. There are 39 ligands with known experimental values. However, our results provide poor prediction for some of those ligands. Therefore we try classification to ligands. If characteristic of ligands are found, we can improve this method and increase the accuracy. We will present the details in this meeting.

1Pos024 Sensitivity to radiation dose of buried waters in Green Fluorescent Protein

Hoang Anh Dao, Kiyofumi Takaba, Yang Tai, Nagayuki Hasegawa, Kazuki Takeda (*Kyoto University Graduate School of Science*)

Though waters in protein cavities can form hydrogen bonding network, they sometimes possess non-tetrhedral coordination. In the course of accurate crystallographic studies of Green Fluorescent Protein (GFP) at ultra-high resolution, we investigated the X-ray radiation dose limit. Several datasets were collected at different cryogenic temperatures 15 K, 50 K and 100K under radiation doses ranging from 20 kGy to 200 kGy. Water molecules in the victiny of the chromophore are very sensitive to the radiation damage. These detailed and systematic investigations reveal the limit of radiation dose. In addition, we discuss about the relationship between the radiation sensitivity and chemical and geometrical features of these waters.

1Pos025 ジスルフィド結合はβ-ストランドを逆平行に会合することに関与している？
Do disulfide bonds involve in β-strand assembly in anti-parallel manner ?

Hiromi Suzuki (*Sch. Agri., Meiji Univ.*)

We selected 21,312 protein chains showing less than 30% sequence identity from PDB and analyzed DSSP data. In total, 14,283 of 54,127 (26.4%) cysteines (Cys) formed disulfide (SS) bonds. In the secondary structure, 30.8% (5,017 of 16,302) and 13.0% (1,637 of 12,598) of Cys made SS bonds in β-strand and α-helix regions, respectively. More precise analysis of β-strand regions showed that 38.0% (4,561 of 12,012), 8.9 % (279 of 2,109) and 12.1% (90 of 743) of Cys formed SS bonds in anti-parallel, parallel and mixed sheets, respectively. In addition to higher ratio of SS bonds in anti-parallel sheets, 2,014 of 4,561 SS forming Cys were concerned in intra- or inter-sheet SS bonds, suggesting that SS bonds involved in β-strand assembly in anti-parallel manner.

1Pos026 単粒子コヒーレント回折パターンを用いた粗視化分子モデリングのためのテンプレートマッチング法
A template matching method for coarse-grained molecular modelling using a noisy single particle coherent diffraction pattern

Atsushi Tokuhisa[1,5], Ryo Kanada[1], Shuntaro Chiba[2], Yuta Isaka[3], Biao Ma[3], Shigeyuki Matsumoto[2], Kei Terayama[4,6], Narutoshi Kamiya[7], Yasushi Okuno[1,2,3,4] ([1]*RIKEN. RCSTI. RCH*, [2]*RIKEN. RCSTI. MIH*, [3]*FBRI. CCD*, [4]*Grad. Sch. Med., Univ. Kyoto*, [5]*RIKEN. R-CCS*, [6]*RIKEN. AIP*, [7]*Grad. Sch. Sim., Univ. Hyogo*)

We developed a hybrid modeling method to determine conformations of a target biomolecule based on its noisy coherent diffraction pattern. The method, called the XFEL template matching, consists of two procedures, conformational sampling of the candidates and similarity calculation between diffraction patterns derived from the sampled conformations and the target pattern. Improving calculation efficiency in the both procedures is indispensable for utilizing the method. We achieved 90% cost reduction by employing a coarse-grained model and advanced MD methods. We applied the XFEL template matching to elucidate multiple conformations of a part of chromatin. As a result, the incident X-ray intensity necessary for the multi-conformation analysis of the molecule was revealed.

1Pos027 テンプレートの MD シミュレーションを利用したタンパク質モデリングツールの開発
Development of Template-based Protein Structure Modeling Software using Molecular Dynamics Simulations of Template proteins

Masaya Furue, Naoyuki Miyashita, Mitsutaka Nemoto (*BOST, KINDAI Univ.*)

Homology modeling often has been used to constructing the unknown tertiary structure of a protein using the homologous proteins, which have been known the tertiary structure by experiments. Although the shape of modeled structure was often reasonable, the dynamics of the modeled structure sometimes wrong. Recently, deep learning methods have applied to Image analysis and so on. The methods also have potent to construct the similar structure of the protein. It would be possible to include the information of the protein dynamics by using datasets for learning. We have developed template-based protein structure modeling program using a the deep auto-encoder and the trajectories of the molecular dynamics simulation of template proteins.

1Pos028 Hsp90 をターゲットとするペプチドアプタマーの構造と、シミュレーションのための力場作成支援プログラムの開発
Dynamics of peptide aptamer which targeting Hsp90 and the development of supporting program for modification of force field parameters

Lisa Matsukura[1], Kazuto Mochizuki[2], Masumi Taki[2], Naoyuki Miyashita[1], Shinichi Watanabe[2] ([1]*BOST, KINDAI Univ.*, [2]*GSIE, UEC.*)

Recent experimental research has explained that cryptand-aptamer (aptamer) in which cryptands are bound to a specific amino acid sequence (peptide) suppress the action of Hsp90. The experimental results have suggested that both have a turn structure. However, the dissociation constant between the aptamer and Hsp90 is much smaller than that between the peptide and Hsp90. Thus, we investigated the structure and fluctuations of the aptamer and the peptide using molecular dynamics simulations. We also have developed a semi-automatic supporting program, which modifies the force field parameters. We found that these have identical type I beta-turn structure in the middle of the peptide region of both, while these dynamics and fluctuations are different from each other.

1Pos029 A skewed distribution of psi-loop motifs in the protein structure database

Koki Fukuda, George Chikenji (*Dept. Appl. Phys. ,Grad. Sch. Eng. , Nagoya Univ.*)

The psi-loop motifs, defined by consecutive three beta strands on the amino acid sequence that include "+2" connection, have four possible connecting patterns. Although these four psi-loop patterns are structurally similar to each other, it has been repeatedly confirmed in many publications that distributions of these patterns in the protein structure database are highly skewed: only the two of them frequently observed and the others are rare. Addressing a question why the distributions are highly skewed is important for protein structure prediction and design, but a consensus has not been reached. Here we study the origin of the skewed distributions of psi-loop motifs by physics based folding simulations and the database analysis.

1Pos030 The protein structure database analysis of the greek key motif and its similar structures

Ryuichiro Ueda, George Chikenji (*Dept. Appl. Phys. , Grad. Sch. Eng. , Nagoya Univ.*)

The Greek key motif consists of four antiparallel b-strands with two b-hairpins and one '+3' loop, which traverses two strands. Whereas the motif is prevalent among various proteins, its similar structures, which have four stands and one '+3' loop, are little or none in a protein structural database. To better understand factors behind appearance frequency of the Greek key, here we focused on features which have not been studied and analyzed a difference between the motif and the similar ones. In addition, we carried out physics based folding simulations and compared with the results of database analysis.

1Pos031 Observation of the dynamics associated with ubiquitination of HECT E3 ubiquitin ligase using High speed AFM

Ikumi Muro[1], Huminori Kobayashi[1], Takahiro Nakayama[2], Noriyuki Kodera[2], Toshio Ando[2], Hiroki Konno[2]
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Ubiquitin ligase (E3) is the most important factor selecting target proteins for ubiquitination and determining the poly-ubiquitin chain type on the target proteins. The previous studies led to the hypothesis that large conformational rearrangement via the flexible hinge loop connecting the C-lobe and N-lobe of the HECT domain is essential for ubiquitin transfer by the HECT-type E3s. In this study, we observed wild type and hinge loop mutation of HECT domain using high-speed atomic force microscopy (HS-AFM), and verify that the effect of the flexibility of hinge loop gives movement of domain C-lobe. We also provide the possibility that the HECT domain transiently promotes the formation of homo-oligomers only when the HECT domain contains ubiquitin.

1Pos032 転写制御因子 LmrR および QacR における多剤認識メカニズムに関する分子シミュレーション研究
Molecular simulation study of the underlying mechanism of multidrug recognition in transcriptional regulators LmrR and QacR

Kazuho Cryershinozuka, **Tadaomi Furuta**, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

Multidrug (MD) binding regulators can recognize various drugs and thus bacteria expressing them become MD resistant by efflux transporters. The elucidation of the molecular mechanism of MD recognition (MDrec) is essential for drug design targeting MD resistance. Two plausible mechanisms of MDrec have been proposed: 1) entropy-driven MDrec: a single substrate-binding pocket (SBP) can recognize many substrates due to its flexibility, and 2) enthalpy-driven MDrec: there are many SBPs, each of which binds a different substrate enthalpically. In this work, we investigated the difference of these mechanisms using various molecular simulation methods. We revealed that transcriptional regulators, LmrR and QacR, recognize various drugs by the mechanisms 1) and 2), respectively.

1Pos033 Attempts at CA-type formal analysis of fibrous assembly of particles

Takashi Konno (*Mol. Physiol. Med. Univ. Fukui*)

In the framework of 2D and 3D cellular automata (CA), transition rules leading to fibrously assembled "structures" were constructed and analyzed. The elements could represent proteins in an abstractive form. The analysis in high dimensional CA systems could naturally be unexhaustive, but careful choice of the CA transition rules gave valuable insights into the physical reality. The rules could also be translated into the "energy" term. "Fibrous" pattern of a state in the CA lattice could directly be regarded as "fibers", but more abstractive definitions of "structure" were also challenged. This study is an initial step towards elucidating hidden logics unconsiously employed for recognizing "structures" in daily and/or scientific life.

1Pos034 ファーマコフォア解析を用いたビタミン D 受容体のアゴニスト/アンタゴニスト活性調節機構の研究
Regulation mechanism of agonistic / antagonistic activities of vitamin D receptor studied by pharmacophore analysis

Takafumi Kudo, Toru Ekimoto, Mitsunori Ikeguchi (*Grad. Sch. Medical Life Sci., Yokohama City Univ.*)

Vitamin D receptor (VDR) is one of the nuclear receptors and important target for drug discovery. In order to clarify the regulation mechanism of agonistic/antagonistic activities of VDR ligands, pharmacophore analysis was performed. By creating pharmacophore models from crystal structures and MD trajectories, the analysis was extended to dynamic pharmacophore analysis considering structural fluctuation. As a result of dynamic pharmacophore analysis, VDR agonistic activities are influenced by the hydrophobic interaction between VDR ligands and helix 12. On the other hand, VDR antagonistic activities are influenced by the hydrophobic interaction between VDR ligand and helices 7 and 10/11, and the absence of the interactions of antagonists between helix 12.

1Pos035 基準振動のネットワーク解析による TCR-pMHC 複合体の動的構造
Dynamic structures of TCR-pMHC complexes studied by a network analysis of normal modes

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Normal mode analysis (NMA) can reveal dynamic aspects of a protein molecule from PDB data. In order to characterize dynamic structures derived from NMA we have developed a method based on a network analysis. Here the network is defined for each of the 20 lowest-frequency normal modes by connecting a pair of spatially neighboring residues that move in a coherent manner. We focused our attention to one of the centrality measures, betweenness (BTWN). A residue with higher BTWN would have more control over the network, because more residues communicate each other passing through that residue. In this study we analyzed various TCR-pMHC complexes. Not only common residues with higher BTWN among them but also the differences in such residues are interesting to be discussed.

1Pos036 サルモネラ菌べん毛タンパク質 FliC と FljB で構成された繊維構造の比較と機能の違い
Structural comparison between Salmonella flagellar filaments consisting of FliC and FljB and the implication for their functions

Tomoko Yamaguchi[1], Takayuki Kato[1], Naoya Terahara[1], Shoko Toma[1], Keiichi Namba[1,2] ([1]*Osaka University FBS*, [2]*BDR & SPRING-8, RIKEN*)

Salmonella typhimurium cells swim by rotating 6-8 peritrichous flagella. The cell expresses two distinct flagellins, FliC and FljB, in different phase. The second phase flagellin FljB is for the emergency, such as escaping from immune recognitions. The FliC filament structure has been solved, but the FljB filament has not been well studied, and why salmonella has two flagellin proteins is still unclear. We solved the FljB filament structure at 5.6 Å resolution by cryoEM helical image analysis. The structure is mostly the same as that of FliC, except that the most outer domain D3 was different. Also, domain D3 appears to be more flexible in the FljB filament than FliC. We will discuss how these structural difference affects the function of the filament as a propeller.

1Pos037 溶液 NMR 法を用いた MAPK p38α によるストレスシグナル伝達最適化の構造機構の解明
Structural Basis for the Optimum Stress Signal Transduction via MAPK p38α under the ATP-depleted, Low pH Condition Elucidated by NMR

Yuji Tokunaga[1,2], Koh Takeuchi[1], Hideo Takahashi[3], Ichio Shimada[1,4] ([1]*molprof, AIST*, [2]*JBIC*, [3]*Grad Sch Med Life Sci, YCU*, [4]*Grad Sch Pharm Sci, UTokyo*)

The MAPK p38α phosphorylates specific substrates within the stressed cells, where ATP severely decreases. To elucidate its structural basis, we investigated the effects of a stress-associated environmental change, pH decrease, on p38α's structure and activity by solution NMR spectroscopy. We found that p38α in the apo state forms an ATP-high affinity conformation in an equilibrium under the low pH condition to compensate for the ATP depletion, upon the protonation of sensory histidine residues. In addition, an acidification-induced protonation of another histidine residue of p38α attenuated the binding of non-specific proteins. These findings reveal how the p38α-mediated stress signal concomitantly achieves its robustness and substrate specificity.

1Pos038 自由エネルギー地形による T686A 変異 AMPA 受容体の部分作動メカニズムの解明
Free-energy landscapes reveal partial agonism at T686A mutation of AMPA receptor

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AMPA ionotropic glutamate receptors mediate fast excitatory neurotransmission in the central nervous system. T686A mutation reduces the efficacy of full-agonist glutamate. However, crystal structures of the ligand-binding domains (LBDs) show little difference. To elucidate the effect of the mutation, we computed the free-energy landscapes for GluA2 LBD closing using replica-exchange umbrella sampling simulations. We observed a semi-closed state, in which the LBD cleft opens slightly due to a break of inter-lobe hydrogen bonds. T686A mutation changes interactions within the cleft, shifting the major population from the closed to the semi-closed state. The flipping of S652 peptide bond is shown to be significant in partial agonism at AMPA receptors.

1Pos039 糖転移酵素の基質特異性メカニズムの解明
Clarify of the substrate specificity mechanism of glycosyltransferase

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The elucidation of the protein sugar modification mechanism of glycosyltransferases is essential to understand the complicated sugar chain structure. Therefore, this study aimed to clarify the mechanism of substrate specificity in glycosyltransferases by the sequence and structural analysis. The family members of glycosyltransferases registered in the Protein Data Bank (PDB) was analyzed. Especially in the beta-1,4-galactosyltransferase (B4GALT) superfamily, the substrate specificity at the position of arginine appearance was found by comparing the sequences and tertiary structures of two enzyme groups their substrates are xylose (Xyl) and N-acetylglucosamine (GlcNAc), respectively.

1Pos040 Pin1 由来のタンパク質分解酵素の触媒部位の変異解析
Mutational analysis on the catalytic site of a protease derived from Pin1

Teikichi Ikura, Nobutoshi Ito (*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

A peptidyl-prolyl isomerase, Pin1, functions as a switch in the cell cycle, a regulator for the Alzheimer's disease, and so on. Several years ago, we found that some mutations like C113A deactivated the catalytic activity but created a proteolytic activity. Since then, we have investigated the catalytic mechanism of the novel protease derived from Pin1. So far, we have elucidated that this protease recognizes a proline residue and cleaves the peptide bond of the amino acid four residue earlier by mass spectrometry and site-directed mutagenesis analysis. The major catalytic site was composed of typical triad seen in some serine proteases. In the present study, we introduced mutations into the triad and evaluated their effects on the catalytic activity.

1Pos041 酵素 PHBH の 2 つの没食子酸産生変異体の違いについての理論的考察
Theoretical insight into differences in two PHBH mutants that can produce gallic acid

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p-Hydroxybenzoate hydroxylase (PHBH) catalyzes the hydroxylation of *p*-hydroxybenzoate (*p*-OHB) to 3,4-dihydroxybenzoate (3,4-DOHB). Recently, two novel mutants, L199V/Y385F and T294A/Y385F, have been shown to have the ability to convert 3,4-DOHB into gallic acid, while the wild type cannot catalyze this reaction. To get insight into the mechanism underlying the substrate specificity, we performed MD simulations and QM/MM calculations for the wild-type and mutant proteins. We found that the mutations altered the H-bond network between the reaction center and the solvent and the conformation of the peroxide group bound to FAD. We will discuss the reason for the difference in the efficiency of the gallic-acid production between the two mutants.

1Pos042 LysW・LysY・LysZ 三者複合体仮説のモデリング
Modeling of a hypothetical ternary complex of LysW, LysY, and LysZ

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LysW, LysY, and LysZ are the major components of the lysine synthesis pathway of the bacterium Thermus thermophilus. The carrier protein LysW carries the substrate (α-aminoadipate; AAA) by attaching it to its C-terminal flexible extension (LysW-γ-AAA). The substrate is then phosphorylated by LysZ and reduced by LysY to form LysW-γ-aminoadipic semialdehyde. The crystal structures of the LysW-LysZ and LysW-LysY binary complexes suggest that they may form a LysW,Z,Y ternary complex and the C-terminal extension of LysW may facilitate the transfer of the substrate from LysZ to LysY. To assess the validity of this hypothesis, we constructed a model of the LysW,Z,Y complex. By using the PaCS-MD method, we succeeded in getting the substrate transferred from LysZ to LysY.

1Pos043 How Toll-like receptor 4 dimerization is activated in lipid raft studied by molecular simulations

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Lipid raft is known as a platform that facilitates membrane protein reactions, but detailed mechanisms are still unknown. TLR4, a single transmembrane(TM) sensor protein in the immune system, is suggested to localize and dimerize in raft. Our purpose is to reveal how raft supports human TLR4 activation. For TLR4, structural information for the cytoplasmic and intracellular domains are available. Recently, a structure model for the TM domain dimer was proposed by NMR and a simulation. Based on it, we can model the full length of TLR4 dimer and simulate its activation. Here, using Martini coarse-grained model in Gromacs software, we simulate TLR4 dimerization process both in DPPC and in various mixtures of lipids including cholesterol and sphingomyelin.

1Pos044 全反射赤外分光法による電位依存性タンパク質の構造研究
The chemistry-induced structural changes in voltage-sensing proteins studied by ATR-FTIR

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The voltage-gated proton channel (Hv1/VSOP) is composed of only four membrane spanning helices corresponding to the voltage-sensor domain (VSD). The channel activity is inhibited by Zn^{2+}. X-ray crystallography proposed the binding site in the extracellular region although the detail coordination geometry is uncertain. To elucidate the Zn^{2+} inhibition mechanism at a molecular level, metal ion-induced structural changes in Hv1/VSOP were studied by ATR-FTIR spectroscopy. Recent progress in the study of ligand recognition by voltage-sensing phosphatase (VSP), which consists of a voltage sensor transmembrane domain followed by a phosphatase and tensin homolog domain at the cytoplasmic site, will be also presented.

1Pos045 タンパク質の局所構造のサンプリングと構造コンプライアンス特性の解析
Sampling of Localized Structures of Proteins and Analysis of their Structural Compliance Properties

Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

Amino acid chains having mutually different sequences were extracted from the data stored in PDB. Similarities of the sequences were evaluated based on the minimum edit distance. The localized structures were extracted from the amino acid chains. Structural compliance (SC) properties of the extracted structures were analyzed by creating elastic network models. The SC was defined based on the relations between the applied forces and the changes in the distances between alpha carbons. Sorting by the criteria defined based on the calculated SC properties, the localized structures with specific properties, e.g., soft or hard structures and SC isotropic or anisotropic structures, can be enumerated.

1Pos046 実験と計算で明らかにした β-1,2-グルコオリゴ糖結合タンパク質の構造機能相関
Structure-function relationships of β-1,2-glucooligosaccharide-binding protein revealed by experimental and computational methods

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β-1,2-Glucan and β-1,2-glucooligosaccharide (SopN, where N denotes the degree of polymerization) are natural carbohydrates, composed of β-1,2-linkded glucose units. Although a number of β-1,2-glucan-degrading enzymes have been characterized, it is little known how β-1,2-glucan and SopN are captured and imported into cells. Here, we focused on a SopN-binding protein (SO-BP) of an ABC transporter from the Gram-positive bacterium *Listeria innocua*. We determined its binding thermodynamics and the crystal structures of the ligand-free open form and of the closed complexes with Sop3, Sop4, and Sop5. Molecular dynamics (MD) simulation and free energy calculation supported the thermodynamic data. We discuss the mechanism of the interactions with Sopn based on the MD results.

1Pos047 Wide-angle x-ray scattering study on cyanobacterial circadian clock system

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Wide-angle x-ray solution scattering (WAXS) is one of the powerful methods to characterize hierarchical structures of bio-molecular systems. In a typical experiment, a sample solution containing quasi-monodispersed bio-macromolecule is irradiated by a focused x-ray beam, and then the intensity of the scattered x-ray is recorded using a 2D-detector as a function of the momentum transfer (Q) up to 2.5 $Å^{-1}$ (d = ~ 2.5 Å). We developed a software to reduce scattering images into one-dimensional WAXS curve with exact geometrical- and polarization-corrections of each pixel on the detector. In this presentation, we will present a recent application to cyanobacterial clock system with some future perspectives.

1Pos048 Minimum free energy path of the conformational change in multidrug ABC transporter

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Multidrug ABC transporter is a member of the ABC transporter superfamily and transports stereochemically diverse compounds through the cell membrane. While its function is of pharmacological importance, the molecular mechanism of how the transporter recognizes and extrudes the substrate has not been well understood yet. Since the transport is driven by the structural transition from the inward-facing to the outward-facing, the atomic details of the conformational change is crucially important to understand the transport mechanism. In this study, we tried to computationally evaluate the minimum free energy path of the transition in a multidrug ABC transporter using the string method.

1Pos049 シクロスポリン A の CHARMM 力場の開発
Development of the CHARMM force field for Cyclosporine A

Tsutomu Yamane, Yuta Watanabe, Toru Ekimoto, Mitsunori Ikeguchi (*Graduate School of Medical Life Science, Yokohama City University*)

Cyclosporine A (CsA), which has used as an immune suppressor, is a compound of an 11-residue cyclic peptide, and shows biomembrane permeability, despite high molecular weight (M. w. ~ 1200). It caused by the structural change between "open" and "closed" conformation, which are hydrophilic and hydrophobic structure, respectively. In addition, seven of CsA residues are methylated backbone amide group (N-methyl amino acids), which play a role in the structural change of CsA. In the present study, we developed the CHARMM force field for CsA and obtained the backbone conformational energy of N-methyl amino acids (alanine and glycine) through QM calculation and decided the CMAP, which included the crystal structures of CsA in the minimum energy area.

1Pos050 Evaluation of tau's effects on flexural rigidity and growth rate of microtubule under nanometer-level precision

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Tau mutations have been linked to kinds of neurodegenerative conditions, like Alzheimer's disease (AD). Although enormous advances have been taken in the pathogenesis of these tauopathies, the relation of microtubule (MT) molecular mechanical behavior to tauopathies is still a controversial issue. Moreover, the reported results about whether tau will soften or stiffen MT vary significantly. Here we gave reasonable explanations for the discrepancy and measured the flexural rigidity of modified MTs via tubulin concentration and tau under nanometer-level localization precision. Further evaluation of tau's effects on MT persistence length and growth rate will lead new insight into tau's function in neurons and may reveal new potential treatments for tauopathies.

1Pos051 4-ヒドロキシイソロイシン脱水素酵素（ＨＩＬＤＨ）変異体における特異的反応に関する計算化学的研究
Computational investigation of the selective reaction in the 4-hydroxyisoleucine dehydrogenase (HILDH) mutant

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The 4-hydroxyisoleucine (4-HIL) dehydrogenase (HILDH) produces all of the eight diastereomers of 4-HIL from a mixture of the four diastereomers of AMKP. Recently, it has been reported that its E144K/W242Q mutant selectively produces (2S, 3R, 4S)-4-HIL from the mixture. To investigate the mechanism of the selectivity, we modeled the complex of the HILDH mutant bound to each of the AMKP diastereomers. Although none of the complexes were stably maintained in conventional MD runs, it was found that the C-terminus of one subunit of the tetrameric HILDH mutant moved into the substrate-binding pocket of another subunit, making some interactions with the substrate, in an accelerated MD run. These interactions may play an important role in the selectivity of the HILDH mutant.

1Pos052 重水素化支援中性子小角散乱と超遠心分析を協奏的に用いた αB-クリスタリンの構造と動態
Structure and kinetics of αB-crystallin by complementary use of deuteration-assisted SANS and AUC

Ken Morishima, Yusuke Sakamaki, Rintaro Inoue, Nobuhiro Sato, Masaaki Sugiyama (*Institute for Integrated Radiation and Nuclear Science*)

We have observed subunit-exchanges between oligomers of αB-crystallin, which is one of eye lens proteins, under dilute and dense concentration conditions by deuteration-assisted small-angle neutron scattering. Interestingly, the exchange rates are almost identical under the both conditions. It is important to clarify the distribution of oligomers for elucidation of the mechanism of the subunit-exchange, and then we also performed analytical ultracentrifugation (AUC) measurements under both conditions. The AUC indicated that monomers exist in addition to the oligomers. It is suggested that the liberated monomers are responsible for the subunit exchange and the functions.

1Pos053 タンパク質ダイナミクスに対する多様体学習の適用
Applications of a manifold learning technique to protein dynamics

Hiroto Kikuchi, Hiroshi Fujisaki (*Dept. of Phys. Nippon Med. Sch.*)

When proteins function, they often use collective motions, but it is difficult to characterize them both computationally and experimentally. With this respect, for analyzing trajectory data from molecular dynamics simulations, principle component analysis has been a method of choice but it only characterizes large amplitude motions without time information and is only applicable to simple data sets. Here we try to apply a diffusion map method, one of the manifold learning techniques which are applicable to much complicated data sets, to several protein systems including adenylate kinase, PIN1 enzyme, and xanthine redoxidase. We will use the diffusion map method for whole proteins and parts of proteins and analyze the connections between the global and local motions.

1Pos054 培養細胞に一過性発現されたヒトヘアケラチン K85 と K35 の中間径フィラメント形成
Intermediate filament assembly of transiently expressed human hair keratins K85 and K35 in cultured cells

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Hair keratins belong to the intermediate filament (IF) protein family. Human hair keratins consist of 11 type I and 6 type II hair keratins, and their complex expression patterns in the hair-forming compartments of hair follicles have been determined. However, the significance of their multiplicity and the molecular mechanism of hair formation remain obscure. In this study, we forced co-expression of human hair keratins K85 (type II) and K35 (type I) as fusion proteins with fluorescent proteins in cultured cells and examined IF assembly competence by fluorescence microscopy. K85 mutant proteins related to ectodermal dysplasia of hair and nail type were also co-expressed with K35 in cultured cells. The effects of the mutations on the function of K85 will be discussed.

1Pos055 ヤナギマツタケ（Agrocybe cylindracea）の子実体特異的蛋白質 PRI4 の免疫組織化学と分子物性
Immunohistochemistry and molecular property of a fruiting body-specific protein, PRI4, of the basidiomycete Agrocybe cylindracea

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Mushrooms are widely cultivated and are well known for their high medicinal and nutritional values. However, molecular mechanisms underlying their growth and fruiting body morphogenesis still remain obscure. Pri4 is initially identified as a gene that is specifically expressed during fruiting initiation of the edible mushroom Agrocybe aegerita. Recently we have identified the Pri4 gene product as a fruiting body-specific protein through the proteomic analysis of A. cylindracea. We have carried out the cDNA cloning, Northern blotting and in situ hybridization analysis of Pri4 from A. cylindracea. Here we report the unique intracellular localization of the PRI4 protein revealed by immunohistochemistry and the molecular property of the recombinant protein.

1Pos056 Crystal structure of human oxidative nucleotide hydrolase in complex with a newly found substrate

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Human oxidative nucleotide hydrolase has broad substrate specificity for oxidative nucleoside triphosphates such as 8-oxo-dGTP and 2-oxo-dATP. We determined crystal structures of the enzyme in complex with these oxidative substrates and elucidated the structural basis for broad substrate specificity of the enzyme. As the substrate binding modes showed that the enzyme might recognize 2-amino-dATP, which was previously reported not as a substrate, we determined the crystal structure of the enzyme bound to 2-amino-dATP and found that its binding mode of 2-amino-dATP is quite similar to those of the major substrates. Then, we confirmed the hydrolysis activity for 2-amino-dATP by hydrolysis reaction both in crystal and in solution.

1Pos057 細菌 9 型分泌装置蛋白質 PorM の構造
Structure of PorM, a core component of bacterial type IX secretion system

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Porphyromonas gingivalis is a major periodontal pathogen. The virulence factors are secreted through the type IX secretion system (T9SS). The core complex of T9SS consists of, at least, four proteins, PorK, PorL, PorM and PorN, but their stoichiometry is unknown. PorM is the largest component of the core complex and believed to span the periplasm and connect the outer membrane component with the inner membrane component. We have determined the crystal structure of PorM at 3.7 Å resolution. PorM consists of four domains and forms a dimer with unique domain swapping structure. The domains are arranged vertically with a kink between domain 1 and 2. We will discuss the structural details of PorM and possible arrangement of PorM in the T9SS complex.

1Pos058 高速 AFM による IV 型線毛 ATPase-PilB の観察
Observation of the type IV pilus assembly ATPase PilB by using High-Speed AFM

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Type IV pili (T4P) are thin protein filaments for bacterial motility and virulence. They extend, attach to the surface, and then retract to move the bacteria forward on a solid surface. The extension and retraction are driven by the secretion ATPase. The PilB promotes the polymerization of PilA filament. It is assumed that PilB forms the two-fold symmetric hexamer ring and functions as a rotary motor driving PilC at the central pore due to ATP hydrolysis. However, cooperative structural changes producing the rotational motion has not been experimentally evidenced. We try to observe conformational dynamics of the PilB hexamer using high-speed atomic force microscopy. The HS-AFM images showed cooperative conformational changes in the PilB hexamer driven by ATP hydrolysis.

1Pos059 3D−RISM 理論を応用した溶液中における Met−enkephalin の構造揺らぎの解析
Analysis of structural fluctuations of Met-encephalin in the solution phase by means of 3D-RISM theory

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Recently, B. Kim and F. Hirata derived a generalized Langevin equation to describe the structural dynamics of protein in water. In this formulation, variance-covariance matrix is expressed as an inverse matrix of the hessian matrix of the free energy surface that can be defined by the sum of the potential energy and solvation free energy of the solute molecule. In this study, we analyze structural fluctuation of Met-enkephalin immersed in water by calculating the second order derivative of the solvation free energy in addition with the potential energy, and diagonalizing the hessian matrix. After that comparing the results with those from the Normal Mode analysis and MD simulation.

1Pos060 Design of peptides to hasten actin depolymerization

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Actins are highly conserved across all eukaryotes. This 42 kDa protein is found as a monomeric form and has the capacity to polymerize in cellular conditions to form non-covalent linear filaments. The competences to form filaments and depolymerize in a dynamic manner confer on actin key roles to play in a number of cellular processes. Fragmenting actin filaments into smaller pieces is a key process as it drastically reduces the time needed for complete depolymerization. In this project, we study the two key components of gelsolin, a 6-domain F-actin severer, that are required for the severing activity. The goal in this project is to design, model, express and purify optimized WH2 peptides in order to create an actin-severing peptide that recapitulates gelsolin activity.

1Pos061 残基間コンタクトプロファイルに基づく MD 計算トラジェクトリの比較手法：PDZ3 ドメインと CypA タンパク質への応用
Comparing two MD simulation trajectories in terms of residue-residue contact: detection of allostery in PDZ3 domain and CypA protein

Chie Motono[1], Takatsugu Hirokawa[1,2] ([1]*molprof, AIST*, [2]*Fac Med., Univ. Tsukuba*)

It is an essential task to compare the two Molecular Dynamics (MD) simulation trajectories with different conditions (ex. with or without mutations, binding other molecules) and to detect the fundamental differences. We propose a new approach to compare the fluctuations of residue-residue interactions of two MD trajectories. We introduced the new index which shows with which residues and how long a specific residue interacts throughout a simulation. For each residue, the index is calculated, and then compared with that from another trajectory to provide the similarity. We applied the procedure to the MD trajectories of a wild-type PDZ3 domain protein, CypA protein and their mutants. The analysis detected some allosteric comunication pathways in those proteins.

1Pos062 細胞骨格タンパク質であるビメンチンの細胞膜上への出現機構の解明
Elucidation of recruitment mechanism of vimentin to cell surface

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Recently, vimentin, a cytoskeletal protein, has been reported to possess GlcNAc-binding activity on cell surface. However, the mechanism of the cell surface expression of vimentin is unclear. In this study, to elucidate the cell-surface expression mechanism, we examined the affinity of vimentin to lipid bilayers by using surface plasmon resonance (SPR). Just after refolding, recombinant vimentin formed tetramer and thereafter the multimeric structure was formed. SPR showed that tetrameric vimentin interacted with lipid bilayer but multimeric vimentin (filamentous structure) not. These results demonstrated that tetrameric vimentin has high affinity to lipid bilayer. We suggest that tetrameric vimentin depolymerized from filamentous vimentin is recruited to cell membrane.

1Pos063 酵素の触媒塩基におけるプロトンの配座転移に関するアンブレラ・サンプリング
Umbrella sampling on proton shift in catalytic base of enzyme

Kyosuke Sato (*Dept. Mol. Phys., Fac. Life Sci., Kumamoto Univ.*)

During the acyl-CoA dehydrogenase catalysis, an αH of substrate acyl-CoA is abstracted by a catalytic base Glu as proton and a βH is transferred to FAD as hydride. Crystal structure of substrate-bound acyl-CoA shows that the Glu-abstracted H must be located at first in the conformation where the dihedral angle for H-O-C-O of the carboxy is 180°. The later life of the proton is presently unclear. QM/MM molecular dynamics simulation with umbrella sampling method revealed the profile of potential of mean force along the H-O-C-O dihedral angle. The profile indicated that the proton at the initial 180° position moves to the 0° position by way of -90° not 90° transition state. The 0°/180° equilibrium constant was estimated to be 20,000.

1Pos064 滴定 X 線溶液散乱を用いた GGA の構造と相互作用の解析
Structure and interaction analysis of GGA by using titration SAXS measurement

Yugo Hayashi[1], Natsumi Endo[1], Yoichi Yamazaki[1], Kazuhisa Nakayama[2], Soichi Wakatsuki[3], Hironari Kamikubo[1] ([1]*Div. Mat. Sci., NAIST*, [2]*Grad. Sch. Pharm., Kyoto Univ.*, [3]*Stanford Univ.*)

The GGAs are a family of clathrin coat adaptor proteins involved in vesicular transport. GGA is composed of three domains, an N-terminal VHS domain, a GAT domain, and a C-terminal GAE domain. GAT acts as a platform for multiple interaction partners, such as Arf, Ub, and so on. However, because there is no structural information of the full length of GGA, how GGA as an interaction platform regulates the binding with the partners is still unclear. In this study, we prepared a GGA fragment composed of VHS and GAT and carried out titration SAXS measurements. In the results, we revealed the GGA fragment takes a compact form in which VHS and GAT tightly packed with each other (closed form) and VHS is released from GAT upon binding MPR (open form).

1Pos065 Ragulator-Rag GTPases 複合体構造における p18 の重要性
Crucial role of p18 component in assembly of Ragulator-Rag GTPases complex

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The mechanistic target of rapamycin complex 1 (mTORC1) plays a central role in regulating cell growth and metabolism. The activity of mTORC1 is mediated by Rag GTPases, which are tethered to lysosomes via Ragulator, a pentameric complex consisting of membrane-anchored p18 and two roadblock heterodimers. To understand the molecular basis, we determined the crystal structures of Ragulator and its complex with the roadblock domains of RagA-C. In these structures, p18 wraps around the three pairs of roadblock heterodimers. Cellular and in vitro analyses demonstrated that complete p18 is required for the assembly and function of Ragulator-Rag GTPases. Our results establish p18 as a critical organizing scaffold for the Ragulator-Rag GTPases complex.

1Pos066 植物ホルモン「ブラシノステロイド」の生合成の鍵酵素 CYP90B1 の結晶構造解析
Structural insights into a key step of brassinosteroid biosynthesis

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Brassinosteroids (BRs) are essential plant steroid hormones that regulate plant growth and development. CYP90B1 catalyzes the 22(*S*)-hydroxylation of campesterol and is the first and rate-limiting enzyme in BR biosynthesis. We determined the crystal structure of *Arabidopsis thaliana* CYP90B1 complexed with cholesterol, which is also 22(*S*)-hydroxylated, as was found for campesterol. The substrate-binding conformation found in the crystal structure helps explain the stereoselective introduction of a hydroxy group at the 22*S* position. The resultant 22*S*-OH moiety, instead of 22*R*-OH, on BR allows hydrogen-bonding interactions with the BR receptor. Thus, the substrate-bound CYP90B1 structure unveiled the mechanism of the key step in the functionalization of phytosterol to BR.

1Pos067 分子動力学シミュレーションを用いた抗 HIV 中和抗体 PG9 と PG16 の CDR-H3 についての構造揺らぎの比較
Molecular dynamics study of structural Fluctuations in CDR-H3 of anti-HIV antibodies PG9 and PG16

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Monoclonal antibodies PG9 and PG16 neutralize 70 to 80% of circulating human immunodeficiency virus 1 (HIV-1) isolates. X-ray crystallographic studies of these antibodies suggest a structural similarity between them. Both PG9 and PG16 have a 28-residue third complementarity-determining region of the heavy chain (CDR-H3), which forms a unique subdomain referred to as “hammerhead.” In this study we compared the structural fluctuations of the CDR-H3s of these antibodies by using molecular dynamics simulations. Principal component analysis (PCA) of each CDR-H3 revealed the difference in the structural fluctuation between them. The “hammerhead” tended to bend form the root of CDR-H3 in PG9, while the CDR-H3 of PG16 showed a partial bending of “hammerhead.”

1Pos068 Crystal analysis investigates signaling molecule for general response protein RsbQ in Bacillus subtilis

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Energy stress response of Bacillus subtilis begins with signaling molecules captured and digested by RsbQ; the products were transferred to RsbP. We aims to identify the signaling molecules. From results of preliminary studies of enzymatic activity of RsbQ in alcohols, in silico ligands screening, sequence alignment, expression of RsbQ in B. subtilis, we hypothesize a group of single chain lipid: monoacylglycerols (MAGs) might act as ligands. We successfully solved crystal structures of MAGs and RsbQ showing open conformation, binding to the catalytic sites, possibly mode of entry of the ligands. We are conducting biochemical analyses such as enzymatic activity of RsbQ and RsbP, microbial inhibition test, mass spectrometry, SAXS to confirm functional relevance of MAGs.

1Pos069 部位特異的スピンラベル EPR 分光法による ABC トランスポーター; BhuUV の構造変化の実時間測定
Real-time measurements of the conformational changes in ABC transporter; BhuUV, revealed by site-directed spin-labeling EPR spectroscopy

Kizashi Onishi, Motonari Tsubaki, Yasuhiro Kobori, Tetsunari Kimura (*Grad. Sch. Sci., Kobe Univ.*)

ATP-binding cassette (ABC) transporters are membrane proteins, which transport allocrites across the membrane along the conformational changes driven by ATP. Although the transport cycle has been proposed based on the nucleotide-free and -bound structures, the relationships between the reactions in ATP, the conformational change and the allocrite transport are still unresolved. The unpaired electrons were incorporated into the residues locating the “gate” of allocrite channel in the transmembrane domain of a heme importer, BhuUV. The time-courses of the local structure or dynamics of motion interrogated by the unpaired electrons are compared with those of heme transport, and the molecular mechanism of transport cycle will be discussed.

1Pos070 SR-Ca^{2+}-ATPase におけるリガンド解離の分子動力学法シミュレーション
Molecular dynamics simulations for dissociation of ligands in SR-Ca^{2+}-ATPase

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Sarco(endo)plasmic reticulum Ca^{2+}-ATPase is a P-type ATPases, which transports Ca^{2+} across membrane against a large concentration gradient by utilizing ATP hydrolysis. Crystal structural analyses have revealed large conformational changes of the protein on reaction steps, and biochemical studies have suggested that the conformational change plays an important role in Ca^{2+} transport. In this study, we focus on dissociations of ADP and Ca^{2+} on a reaction step between E1 and E2. We performed molecular dynamics simulations and sampling simulations with string method to find how the conformational changes affect the dissociation. We discuss relation between the coupled motions between domains and the dissociation.

1Pos071 Molecular simulation of protein conformational transition using a two-structure based model

Mashiho Ito, Ryota Mori, Tomoki P. Terada, Masaki Sasai (*Nagoya Univ.*)

Coarse-grained molecular dynamics simulation has been widely used for biomolecular simulation. In particular, structure-based models such as the Go potential are useful for computing dynamics of proteins. To compute conformational transition of proteins, we introduce a simulation model that is based on two reference structures called "chameleon model" (Terada et al., J. Phys. Chem. B, 2013). In an improved version of the model, configurational switching is represented by the switching of microenvironment around interacting particles under the influence of the knowledge-based angle potentials. We analyze the conformational transition of adenylate kinase (AdK) and other proteins by free energy landscape analysis.

1Pos072 網羅的構造解析によって示された基質結合蛋白質の天然変性領域の動的役割
Dynamic roles of intrinsically disordered regions of ligand binding proteins suggested by the comprehensive structural search

Satoshi Omori, Hafumi Nishi, Kengo Kinoshita (*Grad. Sch. of Info. Sci., Tohoku Univ.*)

Intrinsically disordered regions (IDR) are protein regions that lack the stable three-dimensional structures. Some of IDRs invoke disorder-order transitions after the binding to other proteins or small ligands. In such cases, the dynamic properties of IDRs seem to be highly relevant to the protein functions. However, the relations between such structural dynamics and their functions are still unknown. In this study, we tried the comprehensive structural search of IDRs using Natural Ligand Database (NLDB), the structural database of protein-ligand complexes. Information about SNPs strengthened the biological importance of the dynamic IDRs. Molecular dynamics simulations of some proteins were performed to explore the dynamic property of IDRs in their ligand-free states.

1Pos073 時計タンパク質 KaiC に組み込まれたアロステリック制御
Allosteric Regulation Designed in Clock Protein KaiC

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A core protein of the cyanobacterial circadian clock, KaiC, changes its phosphorylation states with a period of 24 hours in a test tube including KaiA, KaiB, and ATP. The rate of ATPases and the speed of phosphorylation rhythms of KaiC are tightly coupled and temperature-compensated. A hexamer of KaiC adopts duplicated ring structures called as C1 ring and C2 ring. Because the ATP hydrolysis in C1 ring occurs 40 Å apart from the phosphorylation sites of C2 ring, some unknown allosteric regulations work inside KaiC. In the presentation, the influences of various mutations at the interface between C1 ring and C2 ring are discussed based on biochemical experiments and crystal structures newly obtained.

1Pos074 全原子および粗視化シミュレーションによるバクテリアフリッパーゼ Pg1K の動作機構研究
Flipping mechanisms of bacterial flippase Pg1K studied by all-atom and coarse grained simulations

Yutaka Murata, Toru Niina, Shoji Takada (*Biophys. Sci. Kyoto Univ*)

Lipid flipping is an important cellular process so that it is tightly regulated by protein transporters called flippase. The bacterial flippase Pg1K transports lipid-linked-oligosaccharide from the cytoplasm to the cellular surface contributing to form the cell wall. Here, we try to uncover the mechanism of lipid flipping in Pg1K. In a previously proposed mechanism, the hydrophilic head of the substrate lipid directly enters into the flippase pocket which is open to the opposite side of the membrane. To evaluate this process, we estimated free energies of the substrate across the membrane via all-atom simulations. We then constructed a coarse grained model and used it for dynamic simulations of the lipid flipping and for clarifying the flipping mechanisms

1Pos075 タンパク質の折れ畳みの協同性が語るトポロジーの選択性
Cooperativity of protein folding tells us about topology selectivity in genome

Nobu C. Shirai[1], Shintaro Minami[2] ([1]*Center for Info. Tech. and Networks, Mie Univ.*, [2]*NINS, ExCELLS*)

In the previous study, we reported that the combination of folding temperature and cooperativity of protein folding can explain the number of families with 2α-4β topologies defined in the SCOP database. Since we used a hydrophobic core of a specific topology to model coarse-grained structures, we still needed to confirm the generality of the result using different structures. In this study, we remodeled the coarse-grained model and added new topologies and multi-layer structures. We will discuss the scope of the application of the found result.

1Pos076 銅イオン結合したプリオンペプチドのレドックスポテンシャル
Redox potential of copper-binding prion peptide

Shuhei Murakami, Yukihaya Watanabe, Wakako Hiraoka (*Grad.Sch.of Sci.& Tech.,Meiji Univ*)

Prion protein (PrP) which misfolding leads to neurodegenerative diseases has metal-binding sites. Its redox and metal-reservoir potentials are considered to be significant for maintaining both the integrity of normal PrP and the tissue homeostasis. We focused on the octapeptide (PHGGGWGQ) acting as the copper-binding site located in the octarepeat region of human PrP in order to know whether binding copper still had the reactivity with hydrogen peroxide or not. Here we present the data of ESR-spin trapping for copper-binding octapeptide with hydrogen peroxide and hydroxyl radical. We also report the antioxidant property of octapeptide against cytotoxicity of copper ion in myeloid leukemia PLB-985 cultured cells.

1Pos077 酸化ストレスによるミトコンドリア電子伝達系機能異常の ESR 分析
ESR analysis of ROS-induced dysfunction of electron transport chain of mitochondria

Yukihaya Watanabe, Syuhei Murakami, Wakako Hiraoka (*Grad. Sch. of Sci. & Tech., Meiji Univ*)

A mitochondrial electron transport chain (mETC) is a validated target of cancer therapy and drug treatment. To estimate the dysfunction of mETC in whole cells, hydrogen peroxide treated human myeloid leukemia PLB-985 cells and human cervical carcinoma HeLa cells were analyzed with electron spin resonance (ESR). Growth inhibition, apoptosis and necrosis were analyzed with flow cytometer. Harvested cells (-10^8) were resuspended into 200 µl PBS(-) containing 30% glycerol. Cell suspension was transferred to 5 mm µ cylindrical quartz cell for experiment (20K-300K). Our results showed that the oxidative stress made the transition of ESR spectra from Fe-S, complex I, and semi quinone radical in whole cells.

1Pos078 NHEJ pathway mainly repairs lethal damage caused by the direct action of X-irradiation

Ryoichi Hirayama, Akiko Uzawa, Motofumi Suzuki, Sumitaka Hasegawa (*QST NIRS*)

Cell lethality is induced by direct action and indirect action (OH radical) from ionizing radiation. CHO cells, its NHEJ repair mutant (xrs6) and HR repair mutant (51D1) were exposed to X-rays. 51D1 cells showed approximately twice the sensitivity of the wild-type CHO cells. Furthermore, xrs6 cells were more sensitive than 51D1 cells. After 2 Gy X-irradiation, the lethal effects for 51D1 cells by both direct and indirect actions were about 1.7 times larger than that of CHO cells. However, in xrs6 cells, it was found that the lethal effect by direct action was about 3.5 times larger than that of CHO cells. It was suggested that xrs6 cells showed high radiosensitivity against X-rays because the lethal damage by direct action was not repaired by NHEJ pathway.

1Pos079 Evaluation of correlation between fluctuation of enzyme activity and evolvability by single enzyme activity measurement

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Organisms flexibly adapt to environmental change by evolution. At the processes, fluctuation of phenotypic plasticity play an important role, but the correlation between the fluctuation and evolution is largely unknown. As a further questionable point, do enzymes also have fluctuation? Single enzyme activity measurement could be applicable to elucidate the correlation between fluctuation of enzyme activity and evolvability. In this experiment, enzymatic activity was measured in a supper-arrayed reactor. Fifty thousand of 50 fL of droplets could be formed in the array, and single enzyme activity was quantitatively evaluated in them. From the ensemble of single enzyme measurement, activity and coefficient variance (CV) of mutated enzyme was evaluated.

1Pos080 High-throughput Laboratory Evolution of E. coli to Unveil Phenotypic Plasticity and Constraint

Chikara Furusawa[1,2], Takaaki Horinouchi[1], Tomoya Maeda[1] ([1]*BDR, RIKEN*, [2]*UBI, Univ. Tokyo*)

Biological systems change their state to evolve and adapt to changes in environmental conditions. To unveil universal characteristics in adaptation and evolution, we performed a high-throughput laboratory evolution of E. coli under various stress environments. Then, changes in transcriptome profile and genomic sequence of the resistant strains were analyzed by high-throughput sequencing. The results of these comprehensive analyses demonstrated that the expression changes were constrained to a relatively low-dimensional dynamics. Based on these experimental results and theoretical analysis, we will discuss the nature of phenotypic plasticity and constraint in bacterial evolution, and possible strategies to predict and control the evolutionary dynamics.

1Pos081 Natural Peptide-Oligomerization under Aqueous Condition

Muneyuki Matsuo[1,2], Kensuke Kurihara[2,3] ([1]*The Univ. of Tokyo*, [2]*Institute for Molecular Science*, [3]*Exploratory Research Center on Life and Living Systems*)

Sharov (2009) and Francis (2015) proposed that organic compounds induced the formation of peptides which could work as templates for RNA or DNA ligation in the prebiotic environment. The spontaneous polymerization played a key role to emerge primitive information of protocells. Here we report natural peptide oligomerization based native chemical ligation (NCL) involving amide bond formation through thiol-thioester exchange and S to N acyl-shift under the mild aqueous condition. In the presence of reductant, a synthesized cystine derivative was converted into two monomers which can generate oligo-peptides by NCL. Peptide oligomerization was analyzed by NMR and MS spectrometry. We will discuss how oligomerization is induced by aggregates of organic compound.

1Pos082 鋳型ライゲーションにおいて頻度依存的な選択がエラーカタストロフィーを抑制する
Suppression of error catastrophe by frequency-dependent information selection in template-directed ligation

Yasuhiro Magi, Shoichi Toyabe (*Appl. Phys., Tohoku Univ.*)

Template-directed ligation is one of the simplest replication reaction of information polymers such as RNA and DNA. When driven at nonequilibrium, frequency-dependent selection of sequence information based on a molecular cooperativity arises, and stable retention of complex information is realized (Toyabe and Braun, 2018). This selection could be a key for the origin of molecular species. We experimentally tested if this mechanism can suppress the error catastrophe and enhance the information retention. We performed template-directed ligation of DNA strands under a thermal cycling and serial dilutions. We will present our measurements of the net error rate by the ligation under controlled nonequilibrium strength.

1Pos083 Experimental demonstration of information retention against diffusional mixing in templated ligation

Kazuki Hata, Shoichi Toyabe, Yasuhiro Magi (*Tohoku University*)

In the previous study, we experimentally demonstrated that (i) the templated ligation of information polymers such as DNA and RNA copies information not exponentially but hyper-exponentially,(ii) this growth selects information in a frequency-dependent way. However, the effect is not very strong and might be seen in a narrow range of parameters. Our numerical calculations suggest that length-dependent dilution promotes frequency-dependent selection, and information can be sustained at different locations against diffusional mixing.For the experimental verification, we constructed a replication system in which length-dependent dilution and diffusional mixing are performed. We used a templated ligation reaction in a polyacrylamide gel in contact with buffer.

1Pos084 せん断変形と狭窄変形における細胞粘弾性の負荷時間依存性
Loading-time dependence of cellular viscoelasticity under shear and squeezing deformation

Hiroaki Ito[1], Atsushi Kirimoto[1], Naoki Takeishi[2], Makoto Kaneko[1] ([1]*School of Engineering, Osaka University*, [2]*School of Engineering Science, Osaka University*)

Squeezing deformation of a single cell during the passage through a narrow path is an important living phenomenon for various blood cells and circulating tumor cells. To quantify the nonlinear viscoelasticity involved in the squeezing deformation, we performed the measurement of these deformability of a cell flowing in a microfluidic channel, which is equipped with a robotic pump that enables on-chip high-speed manipulation. Using this technique, we imposed shear flow and geometric constriction for the cell. Combining the image analysis and finite element simulations of the channel flow and deformation, we determined nonlinear viscosity and constant elasticity, which have been difficult to measure under high-throughput microfluidic platform.

1Pos085 Effect of lateral phase separation on mechanical stability of lipid membrane

Mika Terada, Yukihiro Tamba (*Natl. Inst. of Tech., Suzuka Coll.*)

We investigated the stability of giant unilamellar vesicles (GUVs) with coexisting liquid-disordered (La) and liquid-ordered (lo) phases of lipid membranes. Using micropipet aspiration, we applied constant tension σ to GUVs composed of DOPC/DPPC/cholesterol membrane (3/4/3; molar ratio). After some time passed, the GUV was suddenly ruptured and aspirated into the micropipet, because of a pore formation in the membrane. The fraction of intact GUVs among all of the GUVs followed a single-exponential decay function, and the rate constants of pore formation k_p were obtained. According to the pore formation theory, we estimated the line tension of a pore Γ. The Γ value of DOPC/DPPC/ cholesterol (3/4/3) membrane was almost the same as that of DOPC membrane.

1Pos086 抗菌ペプチド・PGLa と単一 GUV との相互作用とそれが誘起するポア形成
Interaction of Antimicrobial Peptide PGLa with Single Giant Unilamellar Vesicles and its Induced Pore Formation

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To elucidate the mechanism of PGLa-induced pore formation, we examined the interaction of PGLa with single GUVs. The binding of PGLa to the GUV membrane increased its fractional area change, δ. At high PGLa concentrations, the time course of δ showed a two-step increase;δ increased to a steady value, δ_1, which remained constant for an extended period, before increasing to another steady value, δ_2, that persisted until aspiration of the GUV. We also investigated the interaction of a mixture of PGLa and CF-PGLa with single GUVs. The time course of the rim intensity, I, showed a two-step increase from a steady value, I_1, to another, I_2, before membrane permeation of AF647. Based on these results, we discuss the elementary process of the PGLa-induced pore formation.

1Pos087 脂質分子のフリップ・フロップに対する膜張力の効果
Effect of Membrane Tension on Transbilayer Movement of Lipids

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We examined the effect of membrane tension on the rate constant of the transbilayer movement (k_{FF}) of fluorescent probe-labeled lipids using a new technique (1) that employs GUVs with asymmetric lipid compositions in two monolayers. We found that the k_{FF} greatly increased with tension without leakage of water-soluble fluorescent probes from the GUV lumen (i.e., without the formation of pores in the GUV membrane). We discussed the plausible mechanisms for the effect of tension on the transbilayer movement of lipids. As one of the mechanisms, we hypothesized that the transbilayer movement of lipids occurs through the lateral diffusion of lipids in the walls of hydrophilic pre-pores.

(1) Langmuir, 34, 3349, 2018.

1Pos088 リン脂質フリッパーゼ発現による細胞膜の粘度への影響
Effect of flippases expression on viscosity of plasma membranes

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Phospholipid flippases, P4-ATPase family, regulate the transbilayer asymmetric distributions of phospholipids in biomembranes. However, the transport mechanism of phospholipids by flippases and the impact on the plasma membrane dynamics by flippase activities are poorly understood. We previously estimated the viscosity of the plasma membrane by using fluorescent amphiphilic probes. In this study, we attempt to evaluate the viscosity of the plasma membrane in HeLa cells expressing phosphatidylcholine (PC) or phosphatidylserine flippases. The viscosity of the plasma membrane are smaller when PC-flippases are expressed in HeLa cells. The result suggests that transbilayer movements of lipids link to membrane viscosity and may affect the plasma membrane dynamics.

1Pos089 バクテリアの推進力によるリポソーム膜の形態変化
Morphological changes of liposomes by bacterial propulsion force

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To provide the motility to liposomes, we attempted to apply the bacterial propulsion force to liposomes. E. coli was encapsulated into the liposome by inverted emulsion method using POPC mainly. At first, it was difficult to encapsulate E. coli, however, improving preparation method made encapsulation efficiency dramatically increased. As a result, it was observed that some membranes of liposomes were extended and morphologically changed by inside pressure from bacterial propulsion force, although E. coli couldn't give motility to the liposome. As this morphological changes of liposomes were considered to occur due to membrane fluidity, we will try to encapsulate E. coli to liposomes made of various lipid composition of higher membrane fluidity.

1Pos090 抗菌ペプチド・マガイニン２が誘起するポア形成に対する膜界面疎水性の効果
Role of Interfacial Hydrophobicity in Antimicrobial Peptide Magainin 2 (mag)-Induced Pore Formation

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We investigated the effect on mag-induced pore formation of the mutation of mag based on its interfacial hydrophobicity. First, we investigated the interaction of mag mutants with single GUVs containing calcein using the single GUV method, and found that the rate constant of mag-induced pore formation, k_p, increased with an increase in the number of Phe of the mutants. Second, we investigated the effect of mutation on mag-induced fractional change in the area of the membrane, δ. The mutants with more Phe induced the larger δ. We examined the relationship between k_p and δ, and found that k_p increased as δ increased.On the basis of these results, we discuss the role of interfacial hydrophobicity on mag-induced pore formation.
(1) Langmuir, 31, 3391, 2015.

1Pos091 モデル膜を用いたコレステロール依存性細胞溶解毒素の膜結合活性評価
Evaluation of binding activity of cholesterol-dependent cytolytic toxin using model membranes

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Suilysin (SLY) is a cholesterol (Chol)-dependent cytolytic toxin secreted by *Streptococcus suis* and its toxic nature derives from its ability to bind specifically to Chol in cell membranes to create pores within them. We examined the binding activity of SLY to Chol-phospholipid binary bilayers by means of surface plasmon resonance (SPR) and the observation of leakage behavior of vesicle contents using uranine as a fluorescent tracer. Our SPR results showed that SLY can bind to saturated phosphatidylcholine (PC) bilayer membranes in the presence of 40 mol % Chol or higher, which may suggest that 1:1-Chol/PC regions with a sufficient size are needed for SLY to bind to the binary bilayers. This was also suggested by the results of the uranine leakage behavior.

1Pos092 コレステロールによる薬剤クロルゾキサゾン脂質膜結合抑制効果のリン脂質種依存性
Phospholipid species dependence of cholesterol inhibition effect on the bind of chlorzoxazone to lipid membrane

Hiroshi Takahashi, Shosei Kano (*Biophys. Lab. Gunma Univ.*)

High cholesterol concentrations (~30mol%) tend to inhibit the bind of chlorzoxazone (CXZ) to phosphatidylcholine bilayers (*Biochemistry* **55** (2016) 3888). The cholesterol inhibition effect should also be investigated for other phospholipid species, taking consideration of the fact that biomembranes contain extremely numbers of various lipid species. In this study, we investigated the cholesterol effect by using the lipid bilayer consisting of phosphatidylethanolamine (PE). To estimate the bind of CXZ to the PE bilayers, we performed dialysis analysis, calorimetry, and X-ray diffraction measurements. Almost the same tendency found for PC systems was observed for PE systems. Additional study using a charged lipid, phosphatidylglycerol (PG), is now in progress.

1Pos093 気液界面における脂質単分子膜へのコレステロールと人工肺サーファクタントタンパク質 B の影響
Effect of cholesterol and synthetic lung surfactant protein B on a lipid monolayer at the air-water interface

Hideyuki Nagatsuka, **Masahiro Hibino** (*Div. Sustain. Environ. Eng., Muroran Inst. Tech.*)

Lung surfactant is a complex mixture of lipids and proteins at the air-water interface of the alveolus and responsible for reducing the surface tension. The reduction makes the process effortless during the process of inhalation. The surfactant protein B (SP-B) is mainly involved in enhancing the surface activity of the surfactant film during compression and expansion. However, the function of SP-B and cholesterol, a neutral lipid, in the monolayer is not well understood. Here we investigate the combined effects of SP-B and cholesterol on a model surfactant monolayers containing phosphatidylcholine (PC) and phosphatidylglycerol (PG), using isotherms, surface elastic modulus and fluorescence microscopy. The details of the results will be discussed.

1Pos094 粗視化モデルによる二成分脂質膜の構造安定性に関する理論的研究
Theoretical study on the conformational stability of binary lipid membrane by a coarse-grained model

Tetsu Matsuura, Tomoya Maeda, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Nat. Sci. Tech. Kanazawa Univ.*)

Self-assemble dynamics of various lipid membrane has been investigated by using coarse-grained simulations. We have investigated conformational stability of binary lipid membrane induced by changing both size of molecules and hydrophobic interactions compared with another kind of molecule by using a coarse-grained model. The purpose of this study is to investigate conformational stability induced by either molecular size or hydrophobic potential parameter . By the change of only molecular size compared with another kind of molecule, we found bicelle and random distribution of two kinds of molecules in vesicle. By the change of only potential parameters, we found random distribution in vesicle, phase separation and vesicle devision.

1Pos095 抗菌ペプチド・ラクトフェリシン B と単一大腸菌や大腸菌由来の脂質の GUV との相互作用
Interaction of antimicrobial peptide lactoferricin B (Lfcin B) with single *E. coli* cells and single vesicles of extract lipids

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Antimicrobial peptide Lfcin B induced leakage of calcein from single DOPG/DOPC-GUVs as a result of local rupture of the GUV membrane (1). Here we investigated the interaction of Lfcin B with living *E. coli* cells containing calcein using CLSM. Lfcin B induced a rapid leakage of calcein from *E. coli* cells, concomitant with a decreased in the cell length. Next we examined the interaction of Lfcin B with single GUVs composed of *E. coli* polar extract lipids containing AF647. Lfcin B induced a rapid leakage of AF647 from GUVs stochastically; statistical analysis of this result provided a rate constant for pore formation. On the basis of these results, we discuss the mechanism of antimicrobial activity of Lfcin B.
(1) Biochemistry, 54, 5802, 2015.

1Pos096 膜透過ペプチド・オリゴアルギニンの抗菌活性と単一大腸菌との相互作用
Antimicrobial activity of cell-penetrating peptide oligoarginine and its interaction with single cells of *Escherichia coli*

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The mechanism of translocation of oligoarginine(R_9) across plasma membrane is not clear. Previously, we found that CF-R_9 entered the GUVs of various lipid compositions without any leakage (1). Here, we investigated the interaction of R_9 with *E. coli* cells which do not have endocytotic pathway. We found that R_9 and Rh-R_9 had antimicrobial activity. To elucidate this mechanism, we examined the interaction of Rh-R_9 with single *E. coli* cells. Rh-R_9 induced leakage of calcein from single *E. coli* cells, and subsequently entered their cytoplasm. Rh-R_9 also entered the single GUVs composed of *E. coli* extract polar lipids and then pore formation occurred. Based on these results, we discuss the mechanism of the antimicrobial activity of Rh-R_9.
(1) Biochemistry, 55, 4154, 2016

1Pos097 脂質二重膜の組成が EGFR JM 領域の二量体構造に与える影響
Investigation of the correlation between lipid composition and the dimer structure of EGFR JM region

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Epidermal growth factor receptor (EGFR) is a member of receptor tyrosine kinase (RTK) and it is involved in cell proliferation. The transmembrane (TM) and juxtamembrane (JM) regions of EGFR has a critical role to regulate EGFR activation. Recently, through single-pair FRET experiments, it was indicated that lipid composition and phosphorylation of T654 residue affect the dimeric state of EGFR JM region. However, the detail mechanisms of the conformational changes are still unknown. To examine how the lipid composition or the phosphorylation state affects the dimer structure of the JM region, we performed MD simulations for each system. In the presentation, we will discuss the interaction between lipid and the peptide, and its effect on the JM dimer structure.

1Pos098 Substrate-supported model biological membrane with controlled two-dimensional and three-dimensional structures

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Single molecule observation of membrane proteins is important to elucidate their functions. However, it is generally difficult to observe membrane proteins with a high signal-to-noise ratio. Here, we develop a substrate-supported model biological membrane with controlled two-dimensional and three-dimensional structures. A patterned membrane was lithographically generated, and dense brush of hydrophilic polymer was grafted on the surface of polymeric bilayer. The polymer brush suppresses nonspecific adsorption of proteins, and enables to construct three-dimensional structures by attaching to a silicon elastomer. The model membrane gives opportunity to quantitatively study the molecular behaviors of membrane proteins.

1Pos099 非対称膜組成の小胞封入ベシクルの作製
Formation of giant vesicle containing small vesicles with asymmetric lipid membranes

Koki Kamiya[1], Toshihisa Osaki[1,2], Shoji Takeuchi[1,2] ([1]*Kanagawa Institute of Industrial Science and Technology*, [2]*IIS, university of Tokyo*)

Plasma membranes in eukaryotic cells have an asymmetric lipid distribution. The asymmetric lipid distribution of the intracellular vesicles, which have a function of protein trafficking, is completely opposite from the asymmetric lipid distribution of the plasma membranes. Recently, to generate well-defined artificial cell models, use of microfluidic technologies facilitates the formation of lipid vesicles which mimic the asymmetric lipid distribution. In this study, we develop a giant vesicle containing small vesicles, which emulates the asymmetric distribution of phospholipids in the intracellular vesicle membranes and the plasma membranes of the eukaryotic cells, using an improved asymmetric lipid vesicle formation method.

1Pos100 逆相遠心法による巨大リポソームの迅速形成・精製とその特性
Giant vesicles rapidly prepared and purified using a reverse-phase/centrifugation method

Kanta Tsumoto, Kohei Nakano, Yuki Hayashi, Masahiro Tomita (*Grad. Sch. Eng., Mie Univ.*)

Referring to a classic protocol, the reverse-phase evaporation method developed by Papahadjopoulos for large unilamellar vesicle (LUV) preparation, we invented a simple protocol for rapid preparation/purification of giant liposomes (reverse-phase/centrifugation) by replacing an evaporation procedure by serial centrifugations (Tsumoto K, et al., Colloid Surf A, 546 (2018) 74). The giant vesicles possessed diameters of 10-20 μm and spherical unilamellar morphologies (i.e., GUV). By adapting lipid compositions and species of solvents, we could obtain many giant vesicles 1) in physiological buffered saline and 2) with microdomains on their membranes. We will also show entrapped esterase reaction and efficient formation of vesicle-in-vesicle liposomes using this method.

1Pos101 Development of a polarized coarse grained water model and its application in lipid membrane systems

Yuusuke Miyazaki, Susumu Okazaki, Wataru Shinoda (*Grad. Sch. Eng., Nagoya Univ.*)

A new polarized coarse-grained (CG) water model has been developed. The CG model reproduces several thermodynamic properties of bulk water such as density, surface tension, and electric permittivity. Based on the new water model, we have further developed a CG force field for lipid membranes, which precisely predicts molecular area, surface tension, line tension, and distribution functions comparable to those obtained by all-atom molecular dynamics simulations. The polarized CG water model enabled us to successfully simulate an electroporation process and a water string formation due to a polar molecule insertion into membrane core.

1Pos102 ニック DNA のナノポアへのつまりと特異的挙動
Clogging and returning of nicked DNA at nanopores

Kento Lloyd, Seiya Minato, Tomoya Kubota, Toshiyuki Mitsui (*Grad. Sch. of Sci. & Eng., Aoyama Gakuin Univ.*)

We focused on the issue that the DNA clogging occurs at a nanopore without passing through the pore. We have investigated the cause of the clogging by directly observing how DNA passes through a nanopore by using fluorescence microscopy. Our observation indicated DNA clogging is generated due to the counter flow by electro-osmosis depending on the DNA shape inside a pore. Here we prepared DNA with nicks by restriction endonucleases. As a result, the DNA nicks significantly increased the clogging probability. In addition, the nicked DNAs, clogged at pores once, returned back to the cis side where the DNA's were introduced. We will discuss these results with the density of DNA contour inside a pore.

1Pos103 A datamining approach for genotype-phenotype correlation of *SCN1A*-related epilepsies based on physico-chemical properties changes

Shuichi Yoshida, Takuhiro Nishio (*Dept. of Physics, Hamamatsu Univ. Sch. Med.*)

Mutations in *SCN1A* encoding the neuronal voltage-gated Na^+ channel α1 subunit are most common genetic cause of inherited and idiopathic epilepsy. *SCN1A* missense mutations were identified in two clearly distinct epilepsy syndromes; the generalized epilepsy febrile seizures plus which is a benign syndrome, and the *SCN1A*-related infantile epileptic encephalopathy which is a severe syndrome with delayed psychomotor development and refractoriness to drug therapy. However, the reason why similar missense mutations in *SCN1A* resulting in different phenotypes has not been fully clarified yet. In this study, we describe a datamining approach for genotype-phenotype correlation of *SCN1A*-related epilepsies based on physico-chemical properties changes effect of missense mutations.

1Pos104 数理モデルとライブイメージングデータを用いた分裂酵母間期核内構造の解析
Analysis of fission yeast interphase intranuclear structure by mathematical model and live imaging data

Yuki Takayama[1], Hiroaki Ito[2], Hisamichi Senda[2], Hiraku Nishimori[1], Masaru Ueno[2], Akinori Awazu[1] ([1]*Grad. Sch. Sci., Univ. Hiroshima*, [2]*Grad. Sch. Advanced Sciences of Matter, Univ. Hiroshima*)

Eukaryote genome dynamics are closely related to nuclear functions, such as gene expressions and DNA repairs. For fission yeast that is one of the simplest eukaryote, some models of interphase chromosome were proposed. These models assumed that spindle pole body (SPB) that anchors the centromeres of all chromosomes is fixed opposite to nucleolus. On the other hand, recent live imaging analysis suggested SPB moves dynamically along the microtubule. In this study, we proposed and simulated a model of interphase chromosome structures considering relative positional change between SPB and nucleolus. We also analyzed live imaging data and found our model exhibits similar SPB-nucleolus and inter-loci positional relationships to live imaging data than recent models.

1Pos105 ヌクレオチド組成空間におけるハビタブルゾーンの生物的意味
Biological meaning of “habitable zone” in nucleotide composition space

Shigeki Mitaku[1], Ryusuke Sawada[2] ([1]*Emeritus Prof. Nagoya Univ.*, [2]*Med. Inst. Bioregulation, Kyushu Univ.*)

We studied on the question of how genome sequences describe "life" where a large number of biomolecules are harmonized. We found that all organisms are plotted in a narrow region called habitable zone of the nucleotide composition space from the genome sequence. We discussed the biological significance of the habitable zone from three aspects: the great reduction of the number of possible sequences, the relationship between the second letter and the distribution of membrane proteins, and the relationship between the first letter and molecular recognition units. Hypotheses for the mechanism of the habitable zone formation were also discussed.

1Pos106 Dynamic changes in the interchromosomal interaction of early histone gene loci during development of sea urchin

Masaya Matsushita, Hiroshi Ochiai, Ken-ichi Suzuki, Sayaka Hayashi, Ayaka Sugiyama, Takashi Yamamoto, **Akinori Awazu**, Naoaki Sakamoto (*Dept. of Math and Life Sci. Hiroshima Univ.*)

Chromatin positioning and dynamics of eukaryotic genes are closely related to the regulation of gene expression. In this study, we focused on the early development of the sea urchin Hemicentrotus pulcherrimus (HP) and performed three-dimensional fluorescence in situ hybridization of gene loci encoding early histones. There are two non-allelic early histone gene loci per HP genome. We found that during the morula stage, when the early histone gene expression levels are at their maximum, interchromosomal interactions were often formed between the early histone gene loci on separate chromosomes and that the gene loci were directed to locate to more interior positions. Furthermore, these interactions were associated with the active transcription of the early histone genes.

1Pos107 大腸菌における走化性関連タンパク質のコドン使用傾向
Pattern of codon usage for chemotaxis related protein genes in E.coli

Serika Taga[1], Nobuyuki Uchikoga[2], Takanori Sasaki[3] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ*, [2]*Catalyst*, [3]*Grad. Sch. Adv. Math. Sci., Meiji Univ*)

Chemotaxis of bacteria is controlled by Che proteins related to the chemotaxis signal transduction. Because the kinds of Che proteins are common in many bacteria with different habitats, it is expected to be similar tendencies for gene sequences in the whole of chemotaxis system. In this study, we standardized and compared the number of each codon usage in che genes of E.coli to conform the presence of specific codons used. As a result, there were 9 of frequently used codons (Z-score > 2) in the che genes, and 8 of those codons were also frequently used even compared with the codon usage of all of E.coli gene. In addition, 7 of those codons had synonymous codons, suggesting the specific codon selectivity in the che genes.

1Pos108 遅発性アルツハイマー病に関連する新規ゲノム領域の網羅的探索
Comprehensive Search of Novel Genome Regions Related to Late-Onset Alzheimer’s Disease

Yudai Hirose, Hiraku Nishimori, Akinori Awazu (*Department of Mathematical and Life Sciences, Hiroshima University*)

Recently, as main causes of Alzheimer's disease (AD), the neuronal cell death by the aggregation of proteins such as amyloid β (Aβ) and tau has been considered. However, no successful therapeutic agents targeting these proteins have been reported in clinical trials. In this study, to search other causative factors, in particular new disease-related region on the genome (DRR), we performed the comprehensive analysis of single nucleotide polymorphism (SNP), RNA-seq, and Chip-seq data of human hippocampus. We mainly focused on regions where the transcription frequency was increased and SNP was found significantly in the AD patient group. As AD risk factors, we found genome regions involved in UNC13A and PDE4, and suggested these genes may influence on AD progression.

1Pos109 核膜変形と核内流体を考慮した分裂酵母染色体動態の物理モデル
Physical model of fission yeast chromosome dynamics considering nuclear envelope deformation and intranuclear hydrodynamics

Kazutaka Takao, Hiraku Nishimori, Akinori Awazu (*Dept. Math and Life Sci., Hiroshima Univ.*)

Homologous recombination (HR) in meiosis provides genetic diversity among identical organisms. To realize HR, homologous chromosomes (HC) pairing must be formed correctly. However, the mechanism why HC can recognition with each other is still unclear. Fission yeast nuclear exhibits the oscillatory motion with large deformation in cell in meiotic prophase. During this process, chromosomes interact with other chromosomes and nuclear envelope (NE) through the intranuclear fluid. In this study, we constructed a model of chromosome, NE, and intranuclear fluid dynamics. As a result, we found three dimensional oscillatory motion of nucleus is necessary for correct HC pairing formation. Additionaly, we examined interphase chromosome dynamics by using the constructed model.

1Pos110 Dynamics and organization of slow nucleosomes in live mammalian cells

Ashwin Selvarajan S[1], Tadasu Nozaki[2], Kazuhiro Maeshima[2], Masaki Sasai[1] ([1]*Department of Applied Physics, Nagoya University, Nagoya, Japan*, [2]*Structural Biology Center, National Institute of Genetics, Mishima, Japan*)

Understanding the genome packing structure is one of the fundamental challenges in biology since it is intrinsically linked to gene regulation. Single nucleosome tracking in live mammalian cells has shed light in this regard. In this work, we use single nucleosome tracking data to analyze distributions of diffusive movement of nucleosomes in a live mammalian cell. This helps us categorize nucleosomes as fast and slow. Analysis of the nucleosome-nucleosome correlation functions along with the vibrational density of states reveals that the slow nucleosomes form dynamically correlated amorphous regions, we extract the size distribution of these regions.

1Pos201 心筋の調節タンパク質トロポニンは構造多型をカルシウムとリン酸化により部分的にシフトさせる：二量子遷移(DQC)ESR 距離測定による研究
Calcium and phosphorylation partially shifts multiple conformations of cardiac troponin: Distance study by double quantum coherence ESR

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Ku-band DQC ESR was used to measure the inter-domain distances of double cys mutants labeled with nitroxide spin labels to investigate the spatial relationship of 4 helices of N lobe relative to C lobe of cardiac troponin (cTn) C in cTnC-cTnI complex. The Gaussian functions were grouped into short and long components, 1 and 2, separated by ~1 nm. The fractions of comp. 2 were 0.2 even without Ca^{2+} and increased by 0.3 on Ca^{2+} addition, suggesting a Ca^{2+}-induced partial (not all-or-none) shift in multi-conformations of cTn that will lead to multi-conformations of tropomyosin in the thin filaments ± Ca^{2+}. This does not support conventional 2-state steric block model. The phosphomimic S23/24D of cTnI caused Ca^{2+}-induced increases in the distance of the comp. 2 by ~1.5 nm.

1Pos202 FRET で捉えたアクチン繊維末端付近の構造ゆらぎ
B- or P-ends of actin filament can be determined by measuring the fluctuation of FRET efficiencies

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We have developed a novel system to visualize the flexibility of the longitudinal portion of an actin filament using the fluctuation of inter-monomer FRET efficiency. This system can visualize the distribution of flexibility along the filament on a real-time basis. At first, we have focused on the both ends of a filament first. The fluctuations from both ends were found to be larger than those from middle part. Furthermore, the length of portion with considerably large fluctuation was found to be differ from either end of a filament. Uni-directional polymerization experiments indicated that fluctuation of B-end was absolutely larger than P-end. These result suggest that this system can distinguish B-end from P-end of the single filament of actin in solution.

1Pos203 細胞クラスター構成法を用いた心筋細胞の拍動同期化における集団効果の解明
Community effect of cardiomyocytes in synchronous behavior of beating by constructing cell cluster (1): Experimental approach

Naoki Takahashi[1], Akihiro Yamashita[2], Kazuhumi Sakamoto[3], Masao Odaka[4,5], Akihiro Hattori[4,5], Kenji Matsuura[4,5], Kenji Yasuda[1,3,4,5] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Adv. Sci. & Eng., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [4]*Org. Univ. Res. Initiatives, Waseda Univ.*, [5]*WASEDA Biosci. Res. Ins. in Singapore*)

We examined a mechanism of synchronized interbeat interval (IBI) formation of cardiomyocytes during their network formation. We investigated the IBI synchronization properties of three kinds of cardiomyocytes, mouse primary, human iPS and ES, cultivated from isolated single cells to clusters formed in agarose concave structures. The large variety of IBIs and their fluctuations in isolated single cells were synchronized to stable IBIs after their clustering. Formed synchronized IBIs were not followed to the fastest beating component of single cells and were much slower than them in all these three species and species-dependent. Mathematical modeling also supported these results with fluctuation-reduction oriented synchronization hypothesis.

1Pos204 アクチン分子の構造多様性について
Polymorphism of actin molecules

Toshiro Oda[1], Shuichi Takeda[2], Akihiro Narita[2], Yuichiro Maeda[2,3] ([1]*Fac. Health and Welfare, Tokaigakuin Univ.*, [2]*Struct. Biol. Res. Center, Grad. Sch. Sci., Nagoya Univ.*, [3]*TOYOTA RIKEN*)

For understanding of a mechanism of protein function at the atomic level, information on polymorphism of the target protein is essential. Actin studies have accumulated much information on polymorphism of actin molecule for a long time. Recently, structure of cofiactin (cofilin-decorated F-actin) was determined, and a new conformation of actin was discovered. We have now distinguished several actin forms: F-form in naked F-actin, C-form in cofiactin, O-form in profilin-actin and G-form in almost all of crystal. A new parameter is necessary for clear distinction of these conformations. In this study, we propose simple, visible, and sharply-defined parameters on the basis of the rigid body concepts for actin molecule.

1Pos205 表面プラズモン共鳴を用いた β-アドレナリン刺激に関わる心筋トロポニン分子内相互作用の研究
Surface plasmon resonance studies of the intramolecular interaction in cardiac troponin concerned with β-adrenergic stimulation

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β-adrenergic stimulation and following phosphorylation of N-terminal extension of cardiac troponin I (cTnI) regulate the calcium sensitivity of troponin C (TnC). It is considered that the phosphorylation weaken the interaction between the N-terminus of cTnI and the N-domain of TnC. This study is intended to identify the residues in TnC concerned with the interaction. We prepared TnC mutants substituted the acidic residues with alanine in N-domain of TnC. Then, we measured the dissociation constants of the interactions between these TnC mutants and the N-terminal peptides of cTnI by surface plasmon resonance spectroscopy. It was found that Asp25 residue of TnC is strongly contributed to the interaction with N-terminus of cTnI.

1Pos206 高静水圧下におけるマウス心筋細胞への影響
High hydrostatic pressure induces cardiomyocyte contraction

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Cardiac muscles contract iteratively for their life, producing mechanical force to circulate the blood. Its force subjects cardiomyocytes to several types of mechanical stress such as stretch, shear stress, and pressure. The effect of pressure in cardiomyocytes has never been observed due to the lack of quantitative measurement system. In the present study, we firstly developed a novel high-hydrostatic pressure system to quantitively measure the hydrostatic pressure to apply to cardiomyocytes. Our results showed that high hydrostatic pressure drives contraction of cardiomyocytes. The contraction might be caused by actomyosin interaction regulated by high pressure. The contraction is a reversible response without the collapse of intracellular structure.

1Pos207 *Bacillus* PS3 F_oF_1-ATP 合成酵素の H^+輸送活性の顕微鏡 1 リポソーム解析
Microscopic single liposome analysis of H^+-translocating activity of *Bacillus* PS3 F_oF_1-ATP synthase

Naoya Iida[1], Yuzo Kasuya[1], Naoki Soga[2], Taro Uyeda[1], Masasuke Yoshida[3], Kazuhiko Kinosita[1], Toshiharu Suzuki[2,3,4] ([1]*Dept. Physics, Waseda Univ.*, [2]*Dept. Eng, Univ. of Tokyo*, [3]*Dept. Mol Biochem, Kyoto Sangyo Univ*, [4]*CLS, Tokyo Inst of Tech*)

ATPase activity has been extensively investigated in F_oF_1-ATP synthase (F_oF_1), but H^+-translocation activity driven by the energy of the ATP hydrolysis are still obscure. To understand it, we established analytical system for H^+-translocating activity of *Bacillus* PS3 F_oF_1-reconstituted proteoliposomes (PLs) by utilizing pH-indicative fluorescent lipid, and analyzed the functional coupling with ATPase activity. To analyze in detail, the PLs were subjected to microscopic fluorescent analysis. Interestingly, ΔpH in each of the PLs linearly increased with frequent pauses. The behavior was obviously different from the result from its balk-phase analysis. The analysis simultaneously suggested that the pauses correspond to the MgADP-inhibiton state of ATPase in F_1 part.

1Pos208 Rotation of the engineered F_1-ATPase with non-catalytic α-type P-loops

Hiroshi Ueno[1], Rie Koga[2], Tomoko Masaike[3], Nobuyasu Koga[2], Hiroyuki Noji[1] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*ExCELLS, NINS*, [3]*Grad. Sch. Sci. Tech., Tokyo Univ. of Sci.*)

The rotation scheme of F_1-ATPase (F_1) has been investigated in detail by extensive single-molecule studies. However, its design principle, e.g., the origin of conformational change of F_1, remains elusive. To reveal it, we focused on the P-loops in non-catalytic α and catalytic β subunits that undergo little and large conformational changes during catalysis, respectively. Interestingly, the P-loop sequences of α and β subunits are similar (GxxxxGKT) but distinctly different at x residues. Thus, we substituted x residues of β subunit with that of α subunit and analyzed the rotation of engineered F_1s. Surprisingly, the engineered F_1 with all α-type P-loops showed ~1,000 times slower rotation. We report the details of how such β-α conversion influences the rotation of F_1.

1Pos209 ヒンジ領域を非触媒型に置換した触媒サブユニットをもつ F_1-ATPase の回転トルクと反応速度
Rotational torque and kinetics of F_1-ATPase containing the catalytic subunit with a non-catalytic hinge

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F_1-ATPase shows rotation of the central shaft γ inside the $\alpha_3\beta_3$ hexamer ring. The α and β subunits have structural similarities, but they have distinct roles; the β subunits make intra-subunit domain motions upon nucleotide binding and dissociation to support ATP hydrolysis, while the α subunit is involved mainly in regulation of catalysis through limited local conformational changes. Here we focused on the conformational difference between the hinge region in β and the corresponding region in α. We replaced the sequence of hinge loop region in β with those of α, QKDQNM. Rotation assay suggested possible unique features of this mutant: either decreased rotary torque or load dependent reaction kinetics.

1Pos210 好熱菌 F1 による ATP 加水分解におけるリン酸解離のタイミング
On the timing of phosphate release in the ATPase reaction by TF1

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During ATP hydrolysis by TF1, whether product Pi releases before ADP or ADP releases before Pi has been a matter of debate. Shimo et al supported the former possibility (Biophys. J. 2010) and Watanabe et al supported the latter possibility (Nat. Chem. Biol. 2012). Now we employed a Trp mutant and examined the effect of Pi on the nucleotide binding. We also employed another mutant which seems to have low Pi release rate and analysed it by single molecule rotation assays. Both analyses favored the scheme in which Pi releases from TF1 before ADP.

1Pos211 F1-ATPase の構造変化に α と β の P-loop 配列の違いが及ぼす影響
Impact of the sequence difference of P-loop on the conformational changes of F1-ATPase

Rie Koga[1], Hiroshi Ueno[2], Tomoko Masaike[3], Hiroyuki Noji[2,4], Nobuyasu Koga[1] ([1]*ExCELLS, NINS*, [2]*Dept. Appl. Chem., The Univ. Tokyo*, [3]*Dept. Appl. Biol. Sci., Tokyo Univ. of Sci.*, [4]*ImPACT, JST*)

F1-ATPase is a rotary molecular motor using ATP as an energy source. F1-ATPase is a hexamer ring consisting of alternate α and β subunits, of which γ subunit penetrates the center. The α and β subunits have similar structures and have ATP binding abilities with P-loop motif, GxxxxGKT/S (x: arbitrary residue). But β subunits change their conformations hydrolyzing ATP, while α subunits do not and only bind ATP. What makes such a difference? We focused on the sequence differences of xxxx region of P-loop. We replaced the sequence of β with that of α, and explored the effect on the conformational change and the rotation via molecular dynamics simulations, single molecule measurements and so on. We will report how xxxx region of P-loop gives impact on conformational change.

1Pos212 Assignment of subunit components in motor evolved from F-ATPase for *Mycoplasma mobile* gliding

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M. mobile, a fish pathogen, glides on solid surfaces by a unique mechanism. The gliding force is believed to be generated by the motor evolved from F-ATPase, in which two hexamers similar to F1-ATPase are paired by a frame and then assemble through eight arm-like extensions to form a sheet. To elucidate the subunit components, we isolated the motor consisting of only hexamer without the frame and arm by using sodium cholate. The protein profile showed that the amounts of two constituent proteins, MMOB1620 and MMOB4530, were reduced, suggesting that the frame and arms for the pair and sheet formations consist of these two proteins. We will discuss the components and functions of all the subunits of the motor in combination with sequence information previously reported.

1Pos213 Half channels and unidirectional rotation in the F_O sector of *E. coli* ATP synthase observed by molecular dynamics simulation

Dan Parkin, Daiki yamakoshi, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

F_O , the membrane-embedded part of ATP synthase, is a molecular motor composed of multi-subunit stator and rotor. F_O couples the ion translocation with the rotation of the rotor relative to the stator. The coupling mechanism is explained by the half-channel model that assumes two distinct ion channels at the interface of the stator and the rotor. We previously elucidated the half channels in the bovine F_O by molecular dynamics simulation. We here studied the *E. coli* F_O, and found two distinct half-channels and unidirectional rotation in the presence of the electrochemical potential, as was observed in the bovine F_O. We discuss the coupling mechanism and make comparisons with mutational experiments.

1Pos214 細菌べん毛モーターの回転方向変換制御機構の解明
Elucidation of the directional switching mechanism of the bacterial flagellar motor by electron cryomicroscopy

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Many bacteria swim by reversibly rotating flagella. The three switch proteins, FliG, FliM and FliN, form the C-ring on the cytoplasmic face of the MS ring and control counterclockwise-clockwise (CCW/CW) switching of the motor rotation. To understand the switching mechanisms in detail, we analyzed the C ring structures of the wild type (CCW form) and CW-locked mutants (CW form) by electron cryomicroscopy. We obtained high-resolution 3D density maps of the C-ring in the two states and built pseudo-atomic models of the C-ring. We will report the structural changes of the C-ring between the CCW and CW forms including the interactions of component proteins and discuss the switching mechanism of flagellar motor rotation.

1Pos215 Effect of pH on rotation of the proton-driven bacterial flagellar motor under near zero load

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The bacterial flagellar motor is a rotary nanomachine. The motor converts an electrochemical gradient of proton into torque, but the energy coupling mechanism is not fully understood. Here we measured rotation of the *Salmonella* flagellar motors under various external pH conditions by labeling a 100-nm gold nanosphere to a solid, cysteine-introduced, 115-nm hook without a filament. Rotation traces obtained at high pH contained long pausing events with the order of seconds and relatively shorter ones with the order of milliseconds. The long pauses would be caused by detachment of stators from the motor because overexpression of stator proteins decreased the events; short pauses imply the dwell time for proton binding to the stator.

1Pos216 Feedback regulation of the ion channel activity of the flagellar motor stator complex

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The bacterial flagellar motor consists of two distinct rotor and stator parts. Torque for motor rotation is generated by rotor-stator interactions that is coupled with the ion flow through an ion channel in the stator. However, the energy coupling mechanism remains unclear. Here, we isolated up-motile mutants from a Salmonella slow-motile strain expressing the *Bacillus* Na^+-type MotPS stator complex. A point mutation that considerably enhanced the motor function was found in FliG. This FliG mutation activated the Na^+ channel activity of the MotPS complex, thereby increasing the maximum speed of the motor from 50 to 200 Hz. Based on the available information, we will discuss the mechano-chemical reaction cycle of the flagellar motor.

1Pos217 海洋性ビブリオ菌べん毛モーター固定子 PomA タンパク質の Cys 変異導入を用いた細胞質領域荷電残基の構造解析
Analysis of charged residues by Cys mutagenesis in cytoplasmic loop of flagellar motor protein PomA of marine *Vibrio*

Taira Mino, Tatsuro Nishikino, Hiroto Iwatsuki, Seiji Kojima, **Michio Homma** (*Nagoya Univ, Sch Science, Biological Sci*)

The polar flagella of the marine *Vibrio* are rotated by a Na^+-driven motor. The stator, which is an energy conversion complex, is composed of PomA and PomB. Torque is generated by interacting with FliG of C ring rotor and the cytoplasmic region, $Loop_{2\text{-}3}$, of PomA. The charged residues in the Loop region are thought to play an important for the interaction. In this study, we made the mutants replacing the charged residues (K89, E96, E97 and E99) of PomA and labeling cysteine with biotin maleimide. In Na^+ buffer, E96C mutant was less labeled among these mutants, E97C and E99C mutants were labeled moderate, and K89C mutant was strongly labeled. However, all mutants were similarly labeled in K^+ buffer, suggesting that sodium ion binding affects the loop structure.

1Pos218 Stator-units distribution and dynamics of E. coli sodium-driven chimera flagella motor

Tsai-Shun Lin[1], Michio Homma[2], Seiji Kojima[2], Chien-Jung Lo[1] ([1]*National Central Univ.,Taiwan*, [2]*Grad. sch. of Sci., Nagoya Univ.*)

Bacteria flagellar motor (BFM) is crucial to bacteria motility for swimming. A BFM composes of a rotating part known as a rotor and about a dozen of torque generating protein complex known as stator-units. Many researches indicated the stator-units are dynamically exchanging between the membrane and BFM. Interestingly, recent studies found the number of recruited stator-units on a motor is depend on motor's external load. However, the mechanism of this mechanic sensing is still unknown. Here, we use optical approaches to measure the recruiting process of the stator-units. Combing with biochemistry technology and fluorescent microscopy, we try to understand dynamical exchanging mechanism in a functional motor at high load conditions.

1Pos219 *Paenibacillus* sp. TCA20 がもつ二価カチオン駆動型べん毛モーター固定子 MotA1MotB1 の機能解析
Characterization of ion specificity of MotA1/MotB1 in *Paenibacillus* sp. TCA20

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Bacterial flagellar motor consists of a rotor and multiple stator complexes. Stator complex functions as ion channel and generates the torque gained the energy from the flux of coupling ions. Most stator complexes couple monovalent cations, however, MotA1^{TCA}/MotB1^{TCA} in *Paenibacillus* sp. TCA20 couples divalent cations, such as Ca^{2+} (Imazawa *et al*. 2016). To characterize the properties of MotA1^{TCA}/MotB1^{TCA}, we constructed a chimera stator protein MotB1^{TCA}B^{Ec} from MotB1^{TCA} and MotB of *Escherichia coli*. Chimeric stator complex of MotA1^{TCA} and MotB1^{TCA}B^{Ec} restored the motility of Δ*motAmotB E. coli* strain. Surprisingly, we found that the strain had motility without divalent cation, whereas membrane spanning segments of the chimeric stator are derived from MotA1^{TCA}/MotB1^{TCA}.

1Pos220 Investigating the Growth Mechanism of Bacterial Flagella by Real-time Fluorescencet Imaging

Xiang-Yu Zhuang, Chien-Jung Lo (*Department of physics, National Central University*)

Bacterial flagella are thin helical hollow filaments which length are several micrometers long and only 20 nanometers wide. During flagellar growth, flagellin delivers to the distal end of the filament and folded into flagellum. Many Vibrio species (e.g. Vibrio alginolyticus and Vibrio fischeri) have sheathed flagella which are covered by a layer membrane-like structure. Therefore, we develop a labelling and visualization method using FM4-64(lipophilic dye) to monitor flagellar growth in real-time. Combing our fluorescent labeling protocol, the injection-diffusion model, and mutagenesis approach, our results will shed new light of understanding bacterial flagella self-assembly mechanism.

1Pos221 線毛を使って運動する桿菌とその走化性に関するシミュレーション
Simulation study of bacillus moving with pili and its chemotaxis

Ryota Morikawa, Masatada Tamakoshi, Takeshi Miyakawa, Masako Takasu (*School of Life Sciences, Tokyo University of Pharmacy and Life Sciences*)

We modeled a bacterium moving on a medium with viscous resistance using pili and have studied the features and chemotaxis. This motion is called “twitching motility” whose physical aspects have been experimentally investigated on P. aeruginosa, N. gonnorrhoeae, T. thermophilus, etc. Especially in the case of bacillus, two kinds of movement of the cell by twitching motility are observed: “horizontal crawling” and “vertical walking”. We investigate dynamical properties of our bacterial model by computer simulation and explore some conditions to switch between walking and crawling. Furthermore, we check the influence of the twitching motility on chemotaxis in our model and predict that walking could not fully utilize the chemotaxis ability of the bacillus.

1Pos222 Rng2 のアクチン結合部位は、HMM で駆動されるアクチン運動を強くかつ協同的に阻害する
Potent and highly cooperative inhibition of actin movement on HMM by actin binding domain of Rng2

Yuuki Hayakawa[1], Kien X Ngo[2], Noriyuki Kodera[2], Taro Uyeda[1] ([1]*Grad. Sch. Faculty of Sci. and Eng., Waseda Univ.*, [2]*WPI NanoLSI., Kanazawa Univ.*)

Rng2 is an IQGAP protein essential for the formation of contractile rings in fission yeast. In in vitro motility assays, calponin-homology actin-binding domain of Rng2 (Rng2CHD) strongly inhibited sliding of actin filaments on HMM surfaces. At IC50, the proportion of bound Rng2CHD molecules to actin protomers was estimated to be 1%. We have reported that the half helical pitch of actin filament became 5% shorter by bound Rng2CHD. We thus hypothesize that structural changes of actin protomers induced by each bound Rng2CHD molecule inhibit interaction of many neighboring actin protomers with myosin II motors. We are currently measuring the effect of Rng2CHD on acto-S1 ATPase kinetics and performing TIRFM observation to reveal the mechanism of this cooperative inhibition.

1Pos223 Molecular Structures of Actin Filaments Bound with α-Actinin, Tropomyosin-Troponin and Myosin II Analyzed by High Speed AFM

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We analyzed the molecular structures of actin filaments bound with α-actinin or tropomyosin-troponin (TmTn) in the presence and absence of myosin II (S1) and ATP using high-speed AFM. During ATP hydrolysis cycles of actomyosin, we reported that S1 repetitively interacted with actin filaments and extended the helical pitch (HP) by ~8%. Here, the HPs of actin filaments bound with either TmTn or α-actinin remain unchanged. When these filaments underwent the repetitive binding of S1, only HPs of filaments bound with α-actinin are extended by ~4% as compared with the normal HPs. We also analyze the molecular structures of actin monomers inside the filaments bound with α-actinin and S1 to understand the mechanism of lengthening of HPs (i.e., untwisting or stretching actin).

1Pos224 Myosin minifilament-driven fragmentation of actin filaments triggers contraction of a disordered actin network

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Contraction of the actomyosin network is essential for muscle contraction, cell migration, and division. The contraction is driven by myosin, which exerts a force on actin filaments. While the contraction mechanism has been well studied in the muscle, little is known about the molecular mechanism by which myosin executes network contraction in the disordered actomyosin network in cells. We provide insights into how myosin activity triggers contraction of a mechanically stable disordered actomyosin network. We show that contraction of the network is controlled by a myosin-driven actin-severing activity, which can weaken the network connectivity and thence, stresses redistribute within the network, rather than by myosin-driven actin sliding and buckling activities.

1Pos225 歩行運動中のミオシン VI の前足のブラウン運動の自由エネルギーランドスケープ
Free energy landscape for the Brownian motion of the leading head of myosin VI during the stepping motion

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Myosin VI, a two-headed member of the myosin superfamily, walks towards the minus end of the actin filament with a large and variable step size. This stepping movement cannot be fully accounted for with the lever arm model, and therefore Brownian motion should be playing a significant role. Here we calculate the free energy landscape for the Brownian motion of the leading head connected with the trailing head, using a same method as we have used for myosin II (Nie et al., PLoS Comput. Biol. 2014). Comparison of the landscapes obtained with different models for the inter-head connection suggests that the stiffness of the single alpha helix region is important for the strong bias of free energy landscape consistent with the observed large and variable step size.

1Pos226 DNA オリガミ-ミオシン II モーター混合システムの 1 分子解析
Single molecule analysis of DNA origami-myosin II motor hybrid system

Hiroki Fukunaga[1], Masashi Ohmachi[2], Keisuke Fujita[2], Keigo Ikezaki[3], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*FBS, Univ. Osaka*, [2]*BDR, Riken*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

Muscle contraction is generated by a coordinated motion of myosin II motors in thick filaments. While mechanical motion of isolated single myosins and ensemble motion of the filament are well characterized, how individual myosins in an assembly are coordinated together is unclear. Previously we have developed an artificial myosin filament composed of DNA origami, which gives us an analytical platform to clarify both single and ensemble myosin II dynamics. Due to its high programmability and spatial addressability, we can robustly control probe labeling position. For now, we monitor both single and ensemble myosin dynamics during sliding motion by attaching different color Qdots, In this meeting, we will present the current progress of our experiments.

1Pos227 アクチンフィラメントに対するヘビーメロミオシンの協同的結合の方向性の解析
Analysis of the direction of cooperative binding of heavy meromyosin to actin filaments

Naoyuki Muratsubaki[1], Rika Hirakawa[1], Taro Q.P. Uyeda[2], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Sustain, Environ. Eng., Muroran Inst. Technol.*, [2]*Waseda Univ.*)

The cooperative binding between actin filaments (F-actin) and myosin is caused by the propagation of the conformational change of the actin subunit induced by the binding of myosin head to F-actin. Recently, we found that cooperative binding between F-actin and heavy meromyosin (HMM) often grows in one direction. In this study, therefore, we tried to analyze the direction of propagation of conformational change of F-actin evoked by HMM binding. Binding of HMM-GFP to polarity-marked F-actin loosely immobilized on the lipid membrane was observed over time using a fluorescence microscope. The results suggested that HMM-GFP clusters bound on F-actin spreads to the barbed end side along F-actin.

1Pos228 高速原子間力顕微鏡による人工ミオシンフィラメントでのミオシン II モーターの可視化
Direct visualization of individual myosin II motors in artificial myosin filaments by high-speed AFM

Masashi Ohmachi[1], Keigo Ikezaki[3], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*BDR, Riken*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

Muscle contraction is driven by mechanical motions of myosin II motors on the actin filaments. While various theoretical models and experimental studies have proposed the myosin behaviors in myofilaments, direct monitoring of how individual myosin molecules work in the molecular assembly still remains challenging. To achieve the direct visualization of individual myosins, here, we applied high-speed atomic force microscopy to the programmable artificial myosin filaments developed using DNA origami technology. Our experimental system has captured the structural and dynamical changes of myosin molecules, which will provide direct evidence for the working mechanism of skeletal myosins in the myosin filaments of muscle.

1Pos301 アミロイドβ（1-40）ペプチドと人工 GM1 糖鎖クラスターの複合体形成シミュレーション p
Binding Simulations of an Amyloid-β (1-40) peptide to an Artificial GM1 Glycan Cluster

Yuhei Tachi[1,2], Yuko Okamoto[1], Hisashi Okumura[2,3,4] ([1]*Graduate school of Science, Nagoya University*, [2]*Institute for Molecular Science*, [3]*The Graduate University for Advanced Studies*, [4]*Exploratory Research Center on Life and Living Systems*)

Binding of amyloid-β (Aβ) peptides to GM1 glycan clusters is an early process of amyloid fibril formations. An artificial glycan cluster, in which 24 GM1 glycans are transplanted to a metal-ligand complex, was developed to observe the interaction between glycan clusters and proteins by NMR analysis. In this study, molecular dynamics (MD) simulations were performed to elucidate the Aβ recognition mechanism of the artificial glycan cluster. As a result, we found that the Aβ frequently interact with the artificial glycan cluster on the N terminal side. We also observed that the Aβ stepwise binds to GM1 glycans on the complex in this binding process. These results give an understanding of the Aβ recognition of the GM1 glycan cluster at atomic level.

1Pos302 アミロイドβの凝集はアクチンに富む細胞辺縁部で凝集が促進される
Aggregation of amyloid β was induced at the actin-rich cell periphery

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Alzheimer's disease is caused by aggregation and accumulation of amyloid β (Aβ) in the brain. To understand the toxic mechanism of Aβ for neurons, we attempted real-time imaging of aggregation of Aβ added to the medium seeded PC12 cells using quantum dot nanoprobes. The result showed that Aβ aggregates were formed at the cell periphery that many actin filaments were localized. When cytochalasin D was added to the culture, the aggregation was remarkably decreased, suggesting that the Aβ aggregation at the cell periphery was related to cell movement. On the basis of results, we considered that the ruffling of cell membranes enhance Aβ aggregation.

1Pos303 シナプス後肥厚部タンパク質群の自己集積のメソスケール分子シミュレーション研究
Mesoscopic Molecular Simulation for Self-assembly of the Postsynaptic Density Proteins

Hana Slevin Ohama, Diego Ugarte, Shoji Takada (*Dept. Biophysics, Div. Biology, Graduate School of Science, Kyoto University*)

Postsynaptic density (PSD) is a protein-dense structure lies just underneath a postsynaptic plasma membrane. The structure and molecular components of PSD change dynamically during neuronal activities such as synaptic plasticity change. The structures and functions of many PSD proteins have been revealed. However, the mechanism of the PSD formation that involves hundreds of proteins has not been fully understood. In this study, we made a mesoscopic molecular model that represents a protein with domains and flexible linkers. Each domain is represented by a few beads. The model enables to simulate a large-scale protein network. Our current main focus is to elucidate the mechanism of multimerization of a scaffold protein PSD-95, and its binding to other scaffold proteins.

1Pos304 AFM 細胞間接着力測定技術を用いた腫瘍内細胞間接着力の in vitro 解析
Measurements of intercellular adhesions of tumor microenvironment cells in vitro by using AFM

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A portion of macrophages (MΦ) is recruited into tumor microenvironments and promotes cancer progression by applying chemical stimulations, however, the mechanism is not clear. As a model of the stimulation, cancer cells were incubated in a MΦ cultured medium for a day, and intercellular adhesion forces between two cancer cells were measured by using cup-attached AFM chip. In results, the intercellular adhesion forces increased 1.5 folds by the stimulation, and in addition, both Young's modulus and cell migration velocity decreased. One possible explanation of these results could be MΦs promote cluster formations of cancer cells to upregulate the success of metastasis, indicate that MΦs play a key role to regulate tumor metastasis.

1Pos305 全身麻酔薬プロポフォールによる蛙坐骨神経の複合活動電位抑制とその化学構造
Inhibition by general anesthetic propofol of frog sciatic nerve compound action potential and its chemical structure

Nobuya Magori, Tsugumi Fujita, Kotaro Mizuta, **Eiichi Kumamoto** (*Department of Physiology, Faculty of Medicine, Saga University*)

Although the intravenous general anesthetic propofol (2,6-diisopropylphenol) has an ability to inhibit nerve conduction, this has not been fully examined. To determine propofol's chemical structure responsible for nerve conduction inhibition, we examined the effects of propofol and its related compounds on fast-conducting compound action potential recorded from the frog sciatic nerve by using the air-gap method. Propofol and other phenols reduced its peak amplitude; these activities were correlated with the logarithm of their octanol-water partition coefficients. It was concluded that propofol inhibits nerve conduction, possibly owing to the isopropyl and hydroxyl groups bound to the benzene ring of propofol and to its lipophilicity.

1Pos306 Chemosensing-neuron regulates cold tolerance via Ca2+-dependent endoribonuclease with apoptotic signaling in C. elegans

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Acclimating to environmental temperature is essential for animals, yet its mechanisms are poorly understood. We show here that regulation of cold tolerance in C. elegans involves a chemosensory neuron in which Ca2+-dependent endoribonuclease (EndoU) functions. Deletion of EndoU results in abnormalities of cold tolerance, aging and behaviors. The cause of these abnormalities was defects in the pair of chemosensory-neurons (ADL) receiving aversive cues. Ca2+ imaging elucidated that ADL are responsive to temperature stimuli. RNA-sequencing for EndoU revealed that EndoU is involved in expression of apoptotic signaling that is coupled with synaptic remodeling. Thus, EndoU governs temperature tolerance and aging in a single type of chemosensory neuron.

1Pos307 ミミズ繰り返し体壁刺激による慣れの神経機構
Mechanism of habituation by repeated tactile stimulus in earthworm

Yoshiichiro Kitamura, Haruya Fujita, Yoshiki Funahashi (*Department of Mathematical Sciences and Physics College of Science and Engineering, Kanto Gakuin University*)

Repeated tactile stimulus to the body wall decreases number of action potentials (APs) in the earthworm *Eisenia fetida*. We previously reported that habituation by repeated tactile stimulus to the body wall in the earthworm is induced assumedly due to via serotonin (5-HT)-nitric oxide (NO)-cGMP signaling. In this study, we investigated effect of 5-HT receptor antagonists and cyclic nucleotide analogues on establishment of habituation and recovery process. From these results, it is revealed that 5-HT_3 antagonist delayed establishment habituation, and only cGMP but not cAMP induced habituation.

1Pos308 エピカテキンはヨーロッパモノアラガイの味覚嫌悪学習による長期記憶形成を増強する
Epicatechin enhances the long-term memory formation for taste-aversive conditioning in the pond snail

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Flavanoids enhance long-term memory (LTM) formation in pond snail, *Lymnaea stagnalis*. In our present study, we investigated the effects of epicatechin (EC), which is abundant in green tea, on LTM formation for a taste-aversive conditioning (TAC) in snails. When snails were conditioned in EC (15 mg/L) the TAC training session, which typically results in memory lasting 24 h, they now formed LTM lasting at least 72 h. This result shows that EC can enhance the LTM formation. We next measured the activities of the central giant cell (CGC), which is involved in the feeding behavior, by intracellular recording. As a result, the firing rate of CGC decreased in the snail in which the formed LTM lasted. We will also examine its excitability in the snail exposed to EC.

1Pos309 インビボでの周波数依存性シナプス可塑性の数学的解析
Mathematical analysis of the frequency-dependent synaptic plasticity in vivo

Katsuhiko Hata[1,2,3,4,5], Osamu Araki[6], Osamu Yokoi[2,4], Toshiaki Kaminaka[2,4], Tatsuya Saka[2,4], Izumi Kuboyama[1], Susumu Ito[3], Tetsuro Nikuni[5] ([1]*Sch. Emerg. Med. Sys. Kokushikan Univ.*, [2]*DPEMS, Kokushikan Univ*, [3]*High-Tech Res. Cent., Kokushikan Univ*, [4]*Res Cent for Math Med*, [5]*Dept of Phys TUS*, [6]*Dept of Ap Phys TUS*)

In the brain, many neurons transmit signals to each other via synaptic connections. The change in this connection strength is called “synaptic plasticity”, which is essentially involved in memory and learning. Synaptic plasticity is generally classified into long-term potentiation (LTP) and long-term depression (LTD). LTP/LTD is a long-lasting strengthening/ weakening in synaptic signal transmission. In the hippocampus of the brain, stimulation of synaptic input fibers with a frequency of 10-100 Hz triggers LTP. LTD, on the other hand, is induced by low frequency stimulation of 1-5 Hz. In this study, we investigate numerically and analytically the synaptic plasticity dependent on the frequency of stimulation.

1Pos310 Reinforcement learning using Deep Deterministic Policy Gradient (DDPG) with image input

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Reinforcement learning is a reward system-based framework that acquires optimal behavior through trial and error. In 2016, DeepMind proposed the algorithm called Deep Deterministic Policy Gradient (DDPG) that has an actor-critic structure. Previous studies has used distance sensors as inputs in the DDPG experiment, however information from these sensors alone could be insufficient to detect people and/or obstacles that emerges non-stationarily in the scene. Therefore, we performed automobile control simulation in The Open Racing Car Simulator (TORCS), using DDPG employing images as input. So far we observed that learning in our scheme allowed the agent running along the track in a circuit. We will further improve the model by preprocessing images.

1Pos311 光ファイバー集束光加熱光学系を用いた高精度・非侵襲オンチップアガロースパターン構築技術の開発
A 1064/1480-nm photo-thermal etching system with fiber optics for an accurate and non-invasive micropatterning of an agarose thin layer

Takahito Kikuchi[1], Shota Aoki[1], Yuhei Tanaka[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

For fabricating accurate width-controlled microchannels on a cultivation dish, we improved an in situ photothermal microfabrication assay, which we have developed to fabricate patterns in an agarose thin layer with a focused 1064/1480-nm dual infrared laser. To improve the accuracy and non-invasiveness of the assay, we replaced optical set-up from the focused beam of objective lens to the direct irradiation of the tip of the μm-sized optical fiber. Two kinds of laser beams irradiated from the tip of an optical fiber were scanned on a surface of an agarose layer, and accurate micropatterns were formed according to the trace of the optical fiber within the resolution of about 8 μm, which is the diameter of optical fiber.

1Pos312 プラズモニックチップ上の増強蛍光による培養神経細胞の自発活動計測
Spontaneous activity in cultured neurons measured with the enhanced fluorescence on the plasmonic chip

Wataru Minoshima[1], Chie Hosokawa[2], Suguru Kudoh[1], Keiko Tawa[1] ([1]*Kwnasei Gakuin University*, [2]*National Institute of Advanced Industrial Science and Technology*)

Spontaneous activity of neurons is known to involve in brain function. Spontaneous activity has been measured by voltage sensitive dye (VSD) at single cell resolution in the cultured neuronal network. However, signals to noise ratio (SNR) of VSD is very small for measurement of spontaneous activity. In this study, VSD imaging was performed on the plasmonic chip to improve SNR. As a result, only a few spikes were detected on the cover slip. On the other hand, dozens of fluorescence spikes were frequently detected on the plasmonic chip, suggesting that SNR of VSD imaging was improved due to the fluorescence excited by the grating coupled-surface plasmon resonance field. Furthermore, we will also discuss the pharmacological effects for neuronal activity in VSD imaging.

1Pos313 神経突起伸長速度に対する細胞集団サイズとチャネル幅の効果
Effect of cell cluster size and channel width to neurite elongation rate

Hayato Toriumi, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ*)

Neurons communicate each other by having specific structures such as axons and dendrites. To understand neuronal communication, we try to construct the artificial neuronal network. To control the neurite elongation, a width of channels was changed for the neurite elongation and we measured straight elongation rate of the neurites that elongated from a cell cluster. As a result, we found that the average elongation rate in large cell cluster is greater than one in small cell cluster under the condition of the narrow width. This study suggested the possibility of control the elongation rate with cell population and channel width. To construct the artificial neuronal network, we are set to design narrow channel width and configure large cell cluster in future.

1Pos314 外部からの磁気刺激に対する神経細胞の応答 - 刺激強度依存性
Response of nerve cells to external magnetic stimulation - Stimulation intensity dependence

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Transcranial magnetic stimulation (TMS) method is a non-invasive means of stimulating nerve cells. It is based on electromagnetic induction, using a time-varying magnetic field to induce an electric field in brain tissues. TMS is able to modify neuronal activity locally and at distant sites when delivered in series or trains of pulses (so-called rTMS). rTMS can be applied as continuous trains of low frequency (>1Hz) or bursts of higher frequency (

1Pos315 オンチップ多電極システムによる孤立神経１細胞自発発火の電位変化の解析
Extracellular field potential change analysis of spontaneous firing of an isolated neuron by an on-chip multi-electrode array system

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For understanding electrical characteristics of phenotypes in neurons and of network size dependence in neuronal circuit, we measured extracellular field potentials (FPs) of an isolated single neurons and its networks. First, we developed a culture condition of isolated single neurons for causing spontaneous firing for simultaneous FPs and calcium imaging. Then, we optimized the multielectrode chip design to be able to observe a neuron on the electrode. Finally, we measured FPs changes of single neuron on an agarose micro chambers to be able to isolate single neurons and to position single cells on a microelectrode and succeeded in measurement of spontaneous firing of single neuron. The results showed single neuron has many types of spontaneous firing characteristics.

1Pos316 神経活動電位系列の生成解読様式とその情報伝送容量について
Encoding and decoding of neural pulse code system and its channel capacity

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Neural network system uses action potentials as its communication tool. Action potentials can convey information by their mutual time intervals. Amplitude of signal is usually converted into frequency of the action potentials. Loss of information mainly occurs during encoding process, where amount of information conveyed as spike train par unit time is limited by the maximum spike frequency, the accuracy of spike interval and, as the most significant feature, stochastic property of spike generation. In this study, we construct a simple neuron model which stochastically encodes EPSP and IPSP inputs into spike train outputs and estimates channel capacity of the system in various spike generation patters including simple, realistic and general cases.

1Pos317 線虫のシナプス結合経路と全中枢神経細胞活動データから推定したシグナル経路の頑健性
Robustness of synaptic pathway and signaling pathway estimated from the whole-brain activity data in C. elegans

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High-speed 4-dimensional imaging system enables us to measure the neural activity in the whole central nervous system of C. elegans. Since synaptic wiring is completely identified in C. elegans, synaptic structure of the whole nervous system is subject to mathematical analysis. We study robustness of synaptic pathway and signaling pathway (information flow). The former is a static property of neural network, the latter is a dynamical property. Signaling pathway between neurons is evaluated by causality analysis on our whole-brain activity data. Our previous study suggests that many signaling pathways are caused by detour routing synaptic pathways. Furthermore, the module of signaling pathway is slightly different from the structure of synaptic connectivity.

1Pos318 海馬で合成される男性・女性ホルモンやストレスホルモンによる記憶シナプスの non-genomic な制御
Non-genomic modulation of synapses by hippocampus-synthesized androgen, estrogen and stress steroid

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Neurosteroids (sex steroids and stress steroids) are synthesized in the hippocampus, center for learning and memory. Rapid action of neurosteroids has been extensively studied in the hippocampus over more than decades, and a significant progress has been achieved in clarification of essential molecular mechanisms. We describe synaptic (classic) sex steroid receptors which trigger rapid modulation of dendritic spinogenesis in rat hippocampal slices, including dihydrotestosterone (DHT), testosterone (T), estradiol (E2) and corticosterone. We also describe the role of kinase-dependent signaling mechanisms which can well explain non-genomic modulation of dendritic spinogenesis by not only sex-steroids but also stress steroids.

1Pos319 アガロース微細構造を用いた二つの海馬細胞から伸長する２つの神経突起の反発相互作用の解析
Repulsive interactions of two neurites elongated from two isolated hippocampal cells in agarose width-length-controlled microchannels

Yuhei Tanaka[1], Takahito Kikuchi[2], Shota Aoki[2], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We investigated the interactions of two neurites elongated from different hippocampal cells in the width-length-controlled agarose microchannels. We fabricated two microchambers and two width-length-controlled microchannels crossing perpendicularly in a thin agarose layer on a cultivation dish with a focused 1480 nm infrared laser. We arranged a hippocampal cell into each microchamber, and observed elongations and interactions of two neurites. When two neurites contacted at the intersection of two microchannels, they hesitated to contact and slowed their elongation speed significantly without following but crossing each other. This result indicates that the contact of neurites from different cells influences repulsively each other during their elongation.

1Pos320 小脳核ペリニューロナルネットによる GABA シナプス伝達修飾と運動学習制御
Perineuronal nets in the deep cerebellar nuclei modulate GABAergic transmission and regulate motor learning

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Perineuronal nets (PNNs) are the extracellular matrix of CNS neurons and regulate brain functions. We found that PNN depletion by chondroitinase ABC in the mouse deep cerebellar nuclei (DCN) reduced the paired-pulse ratio of inhibitory postsynaptic currents (IPSCs) and increased the miniature IPSC frequency without changing the amplitude, suggesting that PNN depletion enhances GABA release from presynaptic terminals. Mice having received the enzyme in the interpositus nuclei exhibited a higher conditioned response rate in delay eyeblink conditioning than control mice. These results suggest that PNNs regulate presynaptic functions of Purkinje cell terminals and functional plasticity of synapses in the DCN, which influences the flexibility of adult cerebellar functions.

1Pos321 どのように神経突起は軸索および樹状突起へと個性化するのか？ ～微小管配向動態の観点から～
How neurites acquire identity of axon and dendrites through microtubule orientation dynamics?

Naoki Honda (*Grad. Sch. Biostudies., Kyoto Univ.*)

The identities of axons and dendrites are acquired through the self-organization of distinct microtubule orientations during neuronal polarization. However, how microtubule orientations are developed in the axon and dendrites is largely unknown. To investigate its mechanism, we constructed a biophysical model of microtubule kinetics within growing neurites. Through the model simulation, we showed that all microtubule orientation patterns observed in the axon and dendrites could be generated depending on the speed of neurite growth and the hydrolysis rate, which provides a unified understanding of how neurites are specified into axon and dendrites via microtubule orientation dynamics.

1Pos322 細胞性粘菌の細胞分化に伴う細胞質 pH 変化
Changes in cytoplasmic pH following the cell differentiation in *Dictyostelium*

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Intracellular pH plays a key role in a wide range of biological processes. Cytoplasmic pH change is important for signal transduction in the social amoebae *Dictyostelium discoideum*. Previous reports suggest that decrease in cytoplasmic pH caused cell differentiation into stalk cells in *Dictyostelium* cells. However it remains unclear how the intracellular pH change works in the cellular functions. To investigate the role of intracellular pH, we constructed *Dictyostelium* strains expressing a highly pH-sensitive fluorescent protein and observed the cytoplasmic pH change associated with cell dynamics in both unicellular and multicellular stages. Then we could observe the dramatic pH changes following the prestalkcell differentiation.

1Pos323 ヒト誘導多能性幹細胞由来の内胚葉および中胚葉による原腸形成期の移動
Migration of Endoderm and Mesoderm Derived from Human Induced Pluripotent Stem Cells during Human Gastrulation Stage

Kenshiro Maruyama[1], Ryo Kobayashi[2], **Kiyoshi Ohnuma**[1] ([1]*Grad. Sch. Eng., Univ. Nagaoka Tech.*, [2]*Dept. BioEng., Univ. Nagaoka Tech.*)

Gastrulation is the initial systematic deformation of embryo, hence is a critical stage for forming human body. Although, the dynamics are unknown because of ethical and technical limitations. Here we used human induced pluripotent stem cells (hiPSCs) to study the migration during human gastrulation in vitro. Human iPSCs correspond to epiblasts, differentiate into mesoderm/endoderm cells and undergo gastrulation. In this report, hiPSCs was differentiated into endoderm and mesoderm respectively. Single-cell time-lapse imaging showed that mesoderm and endoderm differentiation increased their migration speed, and their speed acceleration were difference. Random walk analysis showed random migration of both mesodermal cells and endodermal cells.

1Pos324 細胞分裂、分化、発生過程を細胞内小器官の 3D 構造モデルから読み解くための試み
Attempt to understand cell division, differentiated, developmental process from 3D structural model of intracellular organelle

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Sequential 2D-EM images and 3D reconstruction will provide us several information not only to the 3D-structural shape and connection. Last annual meeting we had selected *C. merolae* , as a model organism for mitosis, presented the interaction between individual several organelles during mitosis cycle and using FIB-SEM and 3D-reconstruction tech. Applying this tech., we selected C2C12 cell for muscle differentiation and Zebrafish for developmental process of bone formation, presented the interaction between individual several organelles during these important process using FIB-SEM/ SBF-SEM in this meeting. Although these are still preliminary results, we will want to discuss you the important life phenomena from 3D structural models obtained by using these tip EMs.

1Pos325 線虫 *C. elegans* 胚発生における細胞形状ダイナミクスの定量解析
Quantitative analysis of cell shape dynamics in *C. elegans* embryogenesis

Yusuke Azuma, Shuichi Onami (*RIKEN BDR*)

C. elegans is unique among multicellular model organisms because its embryogenesis proceeds through a stereotypical pattern of cell divisions, enabling single cell level comparison of developmental dynamics among embryos. To achieve this, we developed an image processing method to extract cell shape dynamics. The method automatically finds optimal segmentation of fluorescently labeled cell membrane by solving an optimization problem under biological constraints. We applied the method to more than 50 embryos and computed cell volumes. By calculating volume ratio between daughter cells at each cell division, we found asymmetric cell divisions that are not previously known. We plan to analyze the cell volume in more detail and other cell shape features.

1Pos326 初期胚発生における力学モデルの解析
Analyzing and modeling of early embryo development

Takaaki Matsui[1], Tetsuya Kobayashi[2] ([1]*Grad. Sch. Eng. EEIS, Univ.Tokyo*, [2]*IIS, Univ.Tokyo*)

Advancement in the live imaging enables us to observe processes of development of early embryos. Modeling the cell mechanics and combining the imaging data with it for inference are vital for understanding the dynamics of embryogenesis. In this research, we develop a simplified mechanical model of a mammalian preimplantation embryo and its simulation aiming at comparing it with the live imaging data to infer what factors operate during development. The result simulated by using our model suggests that the repulsive and attractive forces play an important role in the dynamically cell's movement.

1Pos401 紫外可視光変換システムとゲル固体電気化学素子のセンサーへの応用と水素化アモルファスシリコン薄膜の効果
Ultra violet visible light conversion system and gel electrochemical element for sensor and the effect of hydrogenated amorphous silicon

Koki Shimanaka[1], Makoto Horigane[1], Shotaro Minato[1], Miku Kaneta[1], Norimi Takahashi[1], Shota Murakami[1], Hiroshi Masumoto[2], Takashi Goto[3], **Yutaka Tsujiuchi**[1] ([1]*Material Science and Engineering, Akita University*, [2]*Frontier Research Institute for Interdisciplinary, Tohoku University*, [3]*Institute for Materials Research, Tohoku University*)

For the purpose of fabrication of functional biosensor, photo-controlled film system, by using ionic conduction in laminated gels, ultra violet visible light conversion system, and the effect of hydrogenated amorphous silicon film, have been studied. Firstly Langmuir Blodgett films of different fluorescent molecules were fabricated. And an emission spectrum analysis of films was conducted. As the result ultra violet visible light conversion system functions as the detection of sample properties. Secondly rectification properties in gel electrochemical element were influenced and induced to be controllable by light irradiation. Thirdly, the effects of hydrogenated amorphous silicon film on the sensor samples are discussed.

1Pos402 マイクロ流路を用いた連続滴定用オートサンプリングシステムの改良
Improvement of the micro-fluidics based auto sampling system designed for continuous titration experiments

Shinji Amano, Yugo Hayashi, Yoichi Yamazaki, Hionari Kamikubo (*Div. Mat. Sci., NAIST*)

We have developed a micro-fluidics based auto-sampling system designed for titration SAXS experiments, by using which we can prepare several hundreds of microL-solution mixed with desired dispensing ratios of different solutions. The ratio can be controlled by the flow rates of micro-syringe pumps. However, because of the capacity of the syringe, the total amount of the solution applied once and the maximum pressure are limited. To improve the specification, the pumps were replaced by high accuracy HPLC pumps, and the material of the micro-fluidics was also changed from PDMS to stainless steel. The new device potentially enables us to perform long-time measurement and apply viscous solution at the higher concentration of protein, such as antibody drugs.

1Pos403 HPD による広視野多色蛍光 1 分子検出
Wide-field single-molecule multicolor fluorescence detection by hybrid photo-detectors (HPDs)

Atsuhito Fukasawa[1], Gaku Nakano[1], Hiroaki Yokota[2], Minako Hirano[2], Toru Ide[3] ([1]*Hamamatsu Photonics K.K.*, [2]*Grad. Sch. Creation Photon Indust.*, [3]*Grad. Sch. Nat. Sci. Technol., Okayama Univ.*)

We have presented that the Hybrid photo-detector (HPD) (Hamamatsu Photonics) consisting of a photocathode and an avalanche photodiode enables low-background wide-field single-molecule fluorescence detection with high temporal resolution. Here, we demonstrate that HPDs enables simultaneous wide-field single-molecule multicolor fluorescence detection. We will present time courses of fluorescence of single-molecule fluorophores whose fluorescence images were simultaneously monitored by an EM-CCD. The HPD based time-resolved single-molecule fluorescence detection, which is unlike conventional single-molecule detection, provides us with innovative approaches to dynamics of single biomolecules.

1Pos404 水溶液中における蛍光タンパク質発色団の赤外スペクトル−過渡蛍光を利用した新規手法の開発−
IR spectrum of fluorescent protein chromospheres in water -Development of a transient fluorescence-detected resonance IR spectroscopy-

Hirona Takahashi, Tomoya Miyake, Tatsuya Oue, Makoto Sakai (*Okayama University of Science*)

IR spectroscopy is one of powerful tools for the investigation of structure of biological molecules including proteins. However, it is difficult to measure IR spectra of biological molecules in aqueous solution because of strong IR absorption of water. In this study, we have developed a novel transient fluorescence-detected resonance IR spectroscopy, which detect IR absorption of fluorescent molecules selectively. We have succeeded in measuring the IR spectrum of flavin mononucleotide (FMN) in aqueous solution. The IR spectrum of FMN is compared with the spectrum measured in sound Raman spectroscopy, and the similarity of those spectra will be discussed. In the presentation, we will report the IR spectrum of fluorescent protein chromospheres in aqueous solution.

1Pos405 偏光蛍光相関分光法(Pol-FCS)による回転拡散成分振幅の配向依存性の研究
Study of the orientation dependency of fraction of rotational diffusion in Polarization-dependent Fluorescence Correlation Spectroscopy

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Polarization-dependent Fluorescence Correlation Spectroscopy (Pol-FCS) can obtain information of rotational and translational diffusion. Previous our simulation indicated the fraction of rotational diffusion in Pol-FCS depends on the orientation of fluorophores. This study reports orientation dependency in Pol-FCS measurement with several different orientation protein molecules. In this study, Pol-FCS measurements were performed on YYm Series, which was modified from Yellow Chameleon Calcium-ion sensor. YYm have two fluorescence proteins Venus and circular permutated (cp) mVenus, and its conformation can be contralled by Calcium-ion. It was confirmed the fluctuation of the fraction of rotational diffusion were changed by different orientation of fluorophores.

1Pos406 赤外超解像顕微鏡による羽毛内ケラチンタンパク質の分布・配向観察
Orientation-sensitive molecular imaging of feather keratin proteins by an IR super-resolution micro-spectroscopy

Hirona Takahashi, Masanobu Miyoshi, Takeshi Fujimoto, **Makoto Sakai** (*Faculty of Science, Okayama University of Science*)

Feather is generally known to consist of rachis, barb and barbule regions from the root to the tip, and it has been reported that main components of feather are keratin proteins with β-sheet structures (β-keratins). On the other hand, the spatial inhomogeneity of β-keratins, such as the distribution and orientation, could not be disclosed because of a lack of the spatial resolution of previous analytical methods. In this study, we aim to elucidate the spatial distribution and orientation of β-keratins at each region of rachis and barb of feather and verify those differences at each region by an IR super-resolution micro-spectroscopy based on non-linear optical process. In the presentation, the results of polarization dependent measurement will be also discussed.

1Pos407 マイクロデバイス中の単一酵素活性検出による病態診断法の開発
Development of Novel Disease Diagnosis Platform based on Enzyme Activity Detection at Single Protein Level

Shingo Sakamoto[1], Toru Komatsu[1,5], Rikiya Watanabe[4,5], Zhang Yi[4], Hiroyuki Noji[4], Yasuteru Urano[1,2,3] ([1]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [2]*Grad. Sch. Med., The Univ. Tokyo*, [3]*AMED CREST*, [4]*Grad. Sch. Eng., The Univ. Tokyo*, [5]*JST PRESTO*)

This research aimed to develop a novel disease diagnosis system by directly monitoring the single molecular enzymatic activities of disease-related proteins in serum. We focused on alkaline phosphatase (ALP); the high activity of individual ALP isozymes in serum is known to reflect various diseases. We have developed fluorescent ALP probes for single molecular activity detection with multiple colors and reactive moieties. By using them, we achieved the discriminative single molecular counting of different ALP isozymes in multi-well chamber type microdevice. We also tried to detect and count multiple ALP isozymes in serum derived from diabetes patients.

1Pos408 Highly sensitive detections of protein-nucleic acid interactions and redox enzyme reactions using nanostructured electrode

Yasuhiro Mie, Yasuo Komatsu, Yoshiaki Yasutake, Tomohiro Tamura (*Bioproduction Res. Inst., AIST*)

Nanoporous gold (NPG) structure has received great attention and they are widely used in many applications including biosensors owing to its large surface area, catalytic activity, high conductivity, and easiness for surface modification. Although the conventional preparation of NPG by alloy/dealloying method is largely used, more simple anodizing method has been recently reported. We previously demonstrated that NPG surface is very effective to detect drug metabolism reactions. In the present study, we have applied the NPG electrochemical system for monitoring 1) protein-nucleic acid interactions and 2) bacterial P450 reactions, and exhibited highly-sensitive detection of both biochemical processes.

1Pos409 フォトクロミック分子を利用した蛋白質の高時間分解拡散観測手法
Protein diffusion probed by the transient grating method with a photochromic molecule

Shunki Takaramoto, Yusuke Nakasone, Masahide Terazima (*Dep. Chem., Sch. Sci, Kyoto Univ.*)

The transient grating (TG) method is a powerful technique to study reaction dynamics of a protein from a view point of the diffusion coefficient (D). In order to detect the TG signal, however, the reaction must be triggered by light, and consequently, the target had been limited to photosensor proteins. In this study, we labeled proteins with a photochromic molecule to detect the TG signal. We have selected a spiropyran as a labeling molecule, which has a high reaction yield and exhibits a significant change in absorption spectrum. These properties are important for obtaining a strong TG signal. Utilizing this labeling method, we determined the D values of non-photoreactive proteins within 10 ms and confirmed that D is sensitive to the size and structure of proteins.

1Pos410 リン酸結合タンパクを封入した水滴チャンバーアレイによるリン酸検出系の高度化
Advanced phosphate detection method by phosphate binding protein encapsulated in droplet chamber arrays

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Elucidating molecular mechanisms of enzymes involved in inorganic phosphate (Pi) production such as phosphatases and ATPases necessitates highly sensitive detection of Pi. As a primary step toward single-molecule Pi detection, we have tested application of a fluorescent biosensor, rhodamine-labeled phosphate binding protein (Rho-PBP) which shows high affinity to Pi, to a single-molecule enzyme assay utilizing femtoliter droplet chamber arrays. Here we revisited this system and improved conditions for labeling PBP and separation from unreacted dyes that lead up to 6-fold fluorescence increase in response to Pi binding in bulk-phase measurements. In addition, composition of droplets and coating of the device are also explored for stable performance of the system.

1Pos411 細胞内高分子クラウディング状態モデル検証と細胞周期研究への応用
Verification of macromolecule species in intracellular macromolecular crowding condition application to cell cycle study

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Pol-FCS (Polarization-dependent fluorescence correlation spectroscopy) is a method to measure translational and rotational diffusion of molecules. In this research, we have developed a new Pol - FCS with four detectors, which has been improved to eliminate optical noise in two detectors system. The new Pol-FCS was applied to evaluate of macromolecular crowding. Solution of polyethylene glycol (PEG), bovine serum albumin (BSA), Ficoll which is used to simulate translational and rotational diffusion of GFP were compared in macromolecular crowding solutions. Finally, we will propose to evaluate the macromolecular crowding condition with different composition of molecules and evaluate the cell cycle dependence of crowding by Pol-FCS.

1Pos412 マクロファージにおける貪食効率の評価のための抗原 free-flow 法の開発
Development of free-flow assay for precise evaluation of phagocytosis efficiency of macrophages

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For understanding a recognition and a response mechanism of phagocytosis for antigens in macrophage, we have developed the assay to maintain the circumstances of antigen concentration surrounding each macrophage. The assay contains the function of continuous free flow of antigens on a slightly tilted dish. For more than 3 h of 0.55 μm/s antigens' flow was accomplished, that is desirable speed to maintain the antigen concentration constant during phagocytosis. Combined with time lapse observation, the relationship between elapsed time and phagocytosis rate was measured. Experimental results under the constant antigen concentration was acquired and show that there was no hysteresis in phagocytosis and that macrophages don't have a mechanism to retain antigen information.

1Pos413 オンチップ１細胞計測におけるマクロファージの同一点連続貪食の履歴効果評価
Hysteresis of single point sequential phagocytoses in macrophages using on-chip single cell measurement assay

Toshki Azuma[1], Yoshiki Nakata[2], Yuya Furumoto[2], Amane Yoshida[1], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

For understanding whether macrophage can memorize the information of phagocytosis experience, we investigated the change of the manner of phagocytosis caused by hysteresis. We observed a series of phagocytosis continuously by contacting 2-μm IgG/BSA coated polystyrene beads as model antigens on a single identical point of macrophage using optical tweezers. We focused on the earlier series of phagocytosis from first to 10th phagocytosis, and found no obvious acceleration nor delay of phagocytosis was observed. The difference of each phagocytosis time was within a range of fluctuation. Hence, we conclude that macrophages have no function to memorize the phagocytosis experience on the contact point and each phagocytosis is independent reaction.

1Pos414 オンチップ１細胞計測系によるマクロファージの貪食限界の測定
Identifying the maximum size of phagocytosis in macrophages using on-chip single cell measurement assay

Amane Yoshida[1], Yoshiki Nakata[2], Yuya Furumoto[2], Toshiki Azuma[1], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

For identifying capacity for phagocytosis, we observed phagocytosis of macrophages (J774.2; mean size 15 μm) in a variety of sizes of IgG/BSA coated polystyrene beads from 2 μm to 45 μm in diameter as antigens. Antigens were attracted on a macrophage by optical tweezers or capillary needles, and recorded the engulf dynamics by a time lapse system. Macrophages phagocytosed 2, 4.5, 6, and 20 μm antigens, whereas, did not engulf 45-μm beads. Regarding the volume, macrophages engulfed up to 50 in 2-μm beads, 12 in 4.5-μm, and three in 20-μm. These results suggest that macrophages have an ability of engulfment of antigens larger than their own sizes in the range from 20 to 45 μm, indicating membrane of macrophage can be expanded depending on antigens.

1Pos415 血管内皮細胞のダイナミクス解明に向けた集束光によるゼラチン三次元微細加工技術の評価
Evaluation of photo-thermal three-dimensional gelatin-gel microfabrication technology for clarification of endothelial cells' dynamics

Hiromichi Hashimoto[1], Kento Iida[2], Yuki Yamanaka[2], Ryuji Takano[1], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We evaluated an ability and limitation of the flexible three-dimensional microfabrication technology of gelatin-gel quantitatively to analyze the behavior of endothelial cells in capillary blood vessels. Microstructures in gelatin were fabricated by melting a portion of gelatin due to spot heating generated by a permeable 1064 nm infrared laser irradiating to the μm-sized absorption tip on the microneedle to convert permeable light into the spot heat. Correlation of resolution of microtunnel size control with diameters of microneedle's tip, laser power, difference of materials for coating of microneedle's tip, and thickness of coating materials were examined. The size control of microtunnels were linearly correlated with laser power in the range of 50 μm to 300 μm.

1Pos416 アガロースマイクロチャンバーを用いた多電極アレイによる心筋細胞小細胞群における細胞外電位の測定
Measurement of extracellular potential in small cluster of cardiomyocytes by multi electrode array with agarose microchamber

Naoki Tadokoro, Tomoyuki Kaneko (*LaRc, FB, Hosei Univ.*)

Drugs have side effects and toxicity testing is indispensable at the preclinical testing as it takes a huge amount of time and cost. To improve these problems, we try to construct a high-throughput cardiotoxicity testing using multi electrode array (MEA) system with agarose microchamber. Refining the agarose microchamber technique, we could make the agarose microchamber on the electrode directly at once laser irradiation. Hence, by using this technique, individual cardiomyocyte cluster adhered to only around each 64 electrode on MEA chip. The extracellular potential on each electrode was simultaneously measured at multiple points. In the future, we will validate to efficacy of this high-throughput cardiotoxicity testing with applying the several drugs.

1Pos417 細胞のマクロな特徴量とラマンスペクトルの間に対応はあるか
Is There A Correspondence between Cellular Macroscopic Quantities and Raman Spectra?

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Raman spectra from a cell reflect non-destructively the abundances of various biomolecules in the cell. Recently, we showed that cellular Raman spectra and transcriptomes are linked in S. pombe and E. coli (Kobayashi-Kirschvink et al., Cell Syst., in press). Considering that omics information, which can characterize cellular states microscopically, is linked with Raman spectra, we are next examining whether Raman spectra can also be linked with macroscopic quantities of cellular states. Our analysis so far suggests that growth rate differences among single-gene knock-out strains of E. coli are predictable from Raman spectra. This approach has the potential to integrate macroscopic and microscopic characterizations of cellular states through Raman spectra.

1Pos418 オンチップ 1 点連続貪食計測系によるマクロファージの貪食飽和停止現象の解析
Analysis of neglecting phase in phagocytosis of macrophages using on-chip sequential single-point phagocytoses measurement assay

Yoshiki Nakata[1], Yuya Furumoto[1], Toshiki Azuma[2], Amane Yoshida[2], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We investigated phagocytic response and changes during sequential stimulation of antigens on a pin-point surface of macrophages by contacting non-digestible IgG/BSA coated microbeads as antigens on the identical position of isolated macrophages using optical tweezers. Macrophages engulfed antigens until they reached to the critical number of them, which was related to their sizes. Then, 36% of macrophages induced to apoptosis or necrosis, whereas 64% remained. These results indicate the maximum number of engulfing microbeads exists, and suggests that phagocytosis was classified as three distinct phases depending on their number or volume of total antigens remaining in the cell; phagocytosis phase, neglecting phase even though antigens contact, and cell death phase.

1Pos419 集束光によるゼラチンの 3 次元微細加工技術を用いた毛細血管形成のダイナミクス計測
Direct observation of blood vein formation dynamics exploiting flexible three-dimensional gelatin-gel microfabrication technology

Kento Iida[1], Yuki Yamanaka[1], Hiromichi Hashimoto[2], Ryuji Takano[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We have developed a method to fabricate capillary microtunnels to observe the behavior of vascular endothelial cells in capillary blood vessels. Microstructures in gelatin-gel were formed by a melting a portion of gelatin due to spot heating generated by a permeable 1064 nm infrared laser irradiating to the μm-sized absorption tip on the microneedle. We found that the endothelial cells moved and spread two dimensionally on the inner surface of cylindrical capillary microtunnels as monolayer instead of filling the capillary inside. We also found that three types of motions of cells during their spreading: straight forward to the boundary, backward to the source of cell supply, and rotation to circumferential direction around the boundary of the leading edge of spreading.

1Pos420 Model comparison for inverse tissue mechanics of epithelial spreading

Yohei Kondo[1], Kazuhiro Aoki[1], Shin Ishii[2] ([1]*ExCELLS*, [2]*GSI, Kyoto Univ.*)

Morphogenesis of living tissues requires accurate regulation of force generation and mechanical properties of tissues themselves. This previously motivated us to propose a passive measurement technique for rigidity of moving epithelial monolayer. The method allowed a non-invasive inference without directly perturbing spontaneous cellular motion, but the simplistic modeling strategy caused unphysical results such as negative rigidity in some cases. Here, in the same inference framework, we compared a few rheology models, including a Maxwell-fluid model which can represents stress relaxation due to cell rearrangement. Based on those results, we tried to clarify minimal requirements to capture the mechanics of epithelial spreading.

1Pos421 High precision single-molecule techniques for molecular biophysics

Ying Lu, Chun-Hua Xu, Shu-Xin Hu, Ming Li (*Institute of Physics, Chinese Academy of Sciences*)

Single-molecule FRET is widely used to study helicases by detecting distance changes between a fluorescent donor and an acceptor anchored to overhangs of a forked DNA duplex. However, it has lacked single-base pair (1-bp) resolution required for revealing stepping dynamics in unwinding because FRET signals are usually blurred by thermal fluctuations of the soft overhangs. We designed nanotensioners in which a short DNA is bent to exert a force on the overhangs, just as in optical/magnetic tweezers. The strategy improved the resolution to 0.5 bp, high enough to uncover the differences in DNA unwinding by yeast Pif1 and E. coli RecQ whose molecular mechanisms cannot be differentiated by currently practiced methods.

2Pos001 Substrate analogue-induced folding of staphylococcal nuclease analyzed by statistical mechanical model

Shunta Furuzawa, Kosuke Maki (*Grad. Schl. Sci., Nagoya Univ.*)

Although many proteins spontaneously fold into the native state, some proteins such as intrinsically disordered proteins are folded coupled with binding to partner proteins or ligands even under physiological conditions. We aim at understanding underlying mechanisms of the coupled folding and binding using a model protein, staphylococcal nuclease (SNase). We make use of difference in stability between ligand-bound and unbound forms of SNase, where the ligand is a substrate analogue, adenosine-3', 5'-diphosphate (prAp) (K_d ~ 3 μM). We measured folding coupled with prAp binding under denaturing conditions of the unbound form. We will discuss the physical chemical mechanisms by quantitatively analyzing the folding/binding behavior using a statistical mechanical model.

2Pos002 Analysis of pH, salt and mutation effects on folding of the N-terminal domain of ribosomal protein L9 using statistical mechanical model

Takuya Mizukami[1,2], **Kosuke Maki**[1] ([1]*Schl. Sci., Nagoya Univ.*, [2]*Fox Chase Cancer Ctr.*)

Although pH and salts play major roles in stability and folding of proteins, underlying physical chemical mechanisms remain to be elucidated. Here we quantitatively analyzed factors associated with pH-/salt-induced folding by using a statistical mechanical model. We used the N-terminal domain of ribosomal protein L9 with 56 residues as a model protein. The previous experimental results were fully reproduced on stability and folding as a function of pH and salt in addition to amino acid substitution. Our analysis suggested that (i) specific native-like structures are formed only after the rate-limiting step with nonspecific electrostatic interactions dominant in early steps and (ii) salt effects are fully accounted for by the Debye-Huckel screening for this protein.

2Pos003 Theoretical study on the structural stability of alanine dipeptide in supercritical carbon dioxide

Satoshi Nakagawa[1], Tatsuki Kataoka[1], Tomoya Maeda[1], Kazutomo Kawaguchi[1], Francesca Ingrosso[2], Marilia Martines-Costa[2], Manuel F Ruiz-Lopez[2], Hidemi Nagao[1] ([1]*Grad. Sch. Nat. Sci. Tech., Kanazawa Univ.*, [2]*Laboratoire de Physique et Chimie Theoriques, UMR CNRS 7019, Universite de Lorraine, 54506 Vandoeuvre-les-Nancy, France*)

Supercritical carbon dioxide is a promising green-chemistry solvent for many enzyme-catalyzed chemical reactions. However, the stability of some enzymes in such unconventional environments is not well understood. In this study, we investigate the structural stability of alanine dipeptide. The dipeptide is a biomolecule often used as a model system for biomolecular simulation. We perform molecular dynamics simulation and quantum mechanics/molecular mechanics molecular dynamics simulation for the system consisted of an alanine dipeptide, carbon dioxide solvent, and some water molecules. We discuss the structural stability of the dipeptide by using free energy profile and show that the dipeptide in carbon dioxide has the stable structure different from that in aqueous.

2Pos004 Ribosome-assisted co-translational folding of a CFTR domain and its deletion mutant studied by molecular simulations

Suguru Kato, Kazushi Mochizuki, Shoji Takada (*Kyoto University*)

Cystic fibrosis, a genetic disorder, is caused by misfolding of the cystic fibrosis transmembrane conductance regulator (CFTR) protein. The most common mutation of the CFTR gene which induces the misfolding is the deletion of Phe508 (Δ508). Recently, it was suggested that the co-translational folding assisted by the ribosome surface contributes to the folding process of the wildtype CFTR protein. Motivated by this experiment, we here addressed how the interaction of ribosome surface facilitates the folding of CFTR N-terminal domain and how the mutation Δ508 causes the misfolding using coarse-grained molecular dynamics simulations.

2Pos005 回転拡散より見積もられるリゾチーム間相互作用に対するホフマイスター効果
Hofmeister effects on lysozyme-lysozyme interaction estimated by rotational diffusion analysis

Akane Kato[1], Yudai Katsuki[1], Etsuko Nishimoto[2] ([1]*Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ.*, [2]*Fac. Agr., Kyushu Univ.*)

Hofmeister series is known as the ranking of ions influencing physicochemical properties of protein in solutions although the elucidation is still indefinite at sub-molecular level. We found that Hofmeister series is completed in lysozyme-lysozyme interaction, described by the virial coefficients of rotational diffusion coefficient (D_{rot}). D_{rot} was determined using the steady-state fluorescence anisotropy of fluorescent labeled lysozymes in the solution including monovalent cation and anion salts. The virial coefficients, estimated from the quadratic dependence of relative rotational diffusion coefficient (D_{rot}/D^0_{rot}) on lysozyme concentration, showed the attractive and repulsive interactions were induced by cations and anions in the order of inverse Hofmeister series.

2Pos006 改良カメレオンモデルによるアデニル酸キナーゼの構造転移の解析
A study on conformational transition of adenylate kinase with an improved chameleon model

Ryota Mori, Mashiho Ito, Tomoki P. Terada, Masaki Sasai (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

We have previously developed the chameleon model, a coarse-grained model which explicitly represents the interdependence of local structural changes during conformational transition of proteins (Terada et al., J. Phys. Chem. B, 2013). We here report an improved version of this model which is aimed to better mimic the real situation. Free energy landscape analysis using Langevin dynamics simulation is performed for adenylate kinase, which is a model protein of conformational transition with a large-scale domain movement. Conformational transition pathway between open and closed structures is compared with the preceding experimental and computational studies, and temperature dependent change of the free energy landscape is also discussed.

2Pos007 A thermodynamic model of amyloid-β protein oligomerization on negatively charged lipid bilayers

Keisuke Ikeda, Yuuki Sugiura, Minoru Nakano (*Graduate School of Medicine and Pharmaceutical Sciences, University of Toyama*)

Aggregation of amyloid-β protein on biomembranes is a critical step for the formation of neurotoxic aggregates. In this study, the association and oligomerization of Aβ on negatively charged liposomes were investigated by spectroscopic techniques and calorimetry. The Aβ-(1-40)[Y10W] mutant exhibited the three-state transition from a monomer with random coil structure to β-sheet-rich or α-helix-rich conformations along with the titration of lipid vesicles. The helix-to-sheet transition is well explained by a thermodynamic model of micelle formation. The Gibbs free energy, enthalpy, and entropy changes of the oligomerization were determined. We have found that the oligomerization is driven by entropic forces such as hydrophobic interactions.

2Pos008 タンパク質フォールディングにおける自由エネルギー面の理論的解析
Theoretical analysis of free energy profile for folding of chignolin

Tomonari Sumi, Kenichiro Koga (*Res. Inst. Interdisciplinary Sci., Okayama Univ.*)

We developed a new computational method for extracting predominant factor in protein folding by use of a liquid-state density functional theory and investigated folding and unfolding mechanisms for a small designed protein, chignolin. We demonstrate that the driving force in the folding is the intramolecular interactions rather than the solvent-induced interactions including hydrophobic one and a balance between the opposing factors, the intramolecular and solvent-induced interactions, determines the native structure.

2Pos009 天然変性ペプチド pKID は高圧力下でフォールドするか
Do an intrinsically disordered peptide, pKID fold under high pressure?

Minoru Kato, Soichiro Kubota, Tubasa Yamamoto (*Dept. Applied Chem., Ritsumeikan Univ.*)

Our previous experimental studies have shown that pressure induces or stabilizes helix structure of peptides and proteins having the helix forming ability. If this is a universal nature of peptides and proteins, applying pressure can be used for prediction of the helix forming ability of peptides and proteins. In this work, we performed high pressure study on the secondary structure of pKID, which is an intrinsically disordered peptide (IDP) to form helix on binding to the KIX domain of CREB binding protein. FTIR measurements up to 1058 MPa showed that pressure induced helix formation of pKID. This result supports that applying pressure can be used for prediction of helix forming ability of IDP without using the target protein.

2Pos010 Ultra-fast dynamics of simple polyalanine peptides by using nanosecond region fluorescence correlation spectroscopy

Supawich Kamonprasertsuk[1,2], Hiroyuki Oikawa[1,2], Satoshi Takahashi[1,2] ([1]*IMRAM, Univ. Tohoku*, [2]*Chem, Grad. Sch. Sci., Univ. Tohoku*)

We observed the ultra-fast dynamics of simple polyalanine peptides by using statistics of photon emission modulated by Forster resonance energy transfer (FRET). We constructed fluorescence correlation spectroscopy based on time-correlated single-photon counting board that detects intervals time between arrival photons and calculates the correlation functions. We labeled alanine-based polypeptides with Alexa488 and ATTO633. We confirmed that the sample showed different FRET efficiencies in solutions at different GdmCl concentrations, suggesting that the efficiency changes reflect the helix formation of the sample. We detected ~500 ns dynamics that likely corresponds to helix-coil transition of the sample peptide.

2Pos011 蛋白質-蛋白質相互作用面の二次構造に着目した分類手法の開発
Development of classification method of protein-protein interfaces based on their secondary structures

Takashi Fujii, Kazuo Fujiwara, Masamichi Ikeguchi (*Grad. Sch. of Eng., Soka Univ*)

Protein-protein interactions play crucial roles in many biological functions. It is also known that structurally unrelated complexes have occasionally similar interface. As a tool for evaluating the similarity of the interface structures, we developed a new method based on the number of contacting residues included in various secondary structure pairs such as αhelix-αhelix, αhelix-βsheet, etc. First, we analyzed 5867 dimer interfaces, and evaluated the similarity of the interfaces for all combinations. By grouping the interfaces with similar sequences, we identified 3803 different interface structures. By comparing the interface for 14 million group pairs, interface similarities were found in 10289 group pairs with different CATH Class.

2Pos012 水溶性および膜貫通 β-バレル構造における β-ストランドのねじれ/曲がり
β-strand twisting/bending in soluble and transmembrane β-barrel structures

Nobuaki Kikuchi, **Kazuo Fujiwara**, Masamichi Ikeguchi (*Dept. Bioinfo., Grad. Sch. Eng., Soka Univ.*)

The dominant driving force for β-strand twisting is thought to be inter-strand hydrogen bonds. We previously showed that both the twisting and bending of β-strand are suppressed by the polar side chains of serine, threonine and asparagine residues for soluble proteins. In this study, we statistically analyzed twist and bend angles of short frames of β-strands in transmembrane and soluble β-barrel proteins with known structures. We found that the suppressive effect of the polar side chains within a frame propagates to the neighboring, hydrogen-bonded strands under the restriction for the closed barrel structure. Furthermore, in transmembrane β-barrel proteins, the glycine-aromatic ring motif is important for generating the β-strand bending.

2Pos013 アクチンフィラメントの圧電・誘電アロステリーがコフィリンの選択的結合に与える影響
Piezoelectric and dielectric allostery of an actin filament and its effect on binding preference of cofilin

Jun Ohnuki, Akira Yodogawa, Takato Sato, Taro Q.P. Uyeda, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

Binding of cofilin to an actin filament depends on mechanical and chemical states of actin. By molecular dynamics simulation, we previously showed that the changes in mechanical and the chemical states induce allosteric response of actin due to its piezoelectric and dielectric properties. We here investigate the effect of the piezoelectric allostery on the binding preference of cofilin by calculating the interaction energy between cofilin and the tension-applied and tension-free actin filaments. Consistent with previous *in vitro* measurements, we found that the applied tension destabilizes the cofilin-actin electrostatic interaction. We are also investigating the dielectric allostery of an actin filament induced by ATP hydrolysis and its effect on cofilin binding.

2Pos014 The effect of a soft/discontinuity driveshaft on the rotation of F_1-ATPase

Shou Furuike[1], Naoki Soga[2], Yasushi Maki[1], Hideji Yoshida[1] ([1]*Osaka Med. Col.*, [2]*Sch. Eng., Univ. Tokyo*)

F_1-ATPase ($\alpha_3\beta_3\gamma$) is well known as an ATP-driven rotary molecular motor. The shaft of rotor (γ) consist of an antiparallel α-helical coiled coil of the N- and C-ter of the γ subunit, and that is set and fitted in the central cavity of the cylinder-like stator ($\alpha_3\beta_3$-ring). We constructed F_1 mutants in which the shaft would retain nearly genuine shape but has a soft/discontinuity driveshaft. For example, both C-ter and N-ter α-helices of a mutant were cut at the middle (the portion would not interact with the $\alpha_3\beta_3$-ring), and jointed together each by three helix-breaker amino-acids. The torque cannot be transmitted from N- and C-ter side to the other side of the shaft. The rotation rates both with and without drag were still ~1/3 of wild type.

2Pos015 Investigation on the structural properties of proteins included in non-membraneous granule droplets

Saya Nakano[1,2], Hiroyuki Oikawa[1], Satoshi Takahashi[1] ([1]*IMRAM*, [2]*Grad. school of Life Science, Tohoku Univ.*)

Non-membranous cytoplasmic and nucleoplasmic granules are formed as aggregates of proteins having intrinsically disordered regions and include various other proteins and RNAs. We are interested in the structural properties of the proteins included in the granules droplets made by the disordered arginine/glycine-rich (RGG) domain of Laf -1, which is one of RNA helicases in C. elegans and plays an important role in the embryo development. We expressed the N-terminal RGG domain of Laf-1, and will observe whether other proteins such as ubiquitin and the B-domain of protein A doubly labeled by fluorophores can be included into the granules or not. We will also investigate the included proteins by using the FRET measurements.

2Pos016 フェリチン変異体の帯電限界
Charge limit of ferritin mutants

Takumi Kuwata[1], Daisuke Sato[2], Atushi Kurobe[1], Satuki Takebe[1], Kazuo Fujiwara[1,2], Masamichi Ikeguchi[1,2] ([1]*Grad. Sch. of Eng., Soka Univ.*, [2]*Fac. of Sci. and Eng., Soka Univ*)

Ferritin (Ftn) is a spherical protein consists of 24 identical subunits. Ftn can incorporate Fe(II) ion into its central cavity and form a mineral core with about 5nm diameters. In this study, we prepared a series of Escherihia coli ferritin (EcFtnA) mutants in which Glu and Gln residues on the outer surface was replaced with Gln (Glu>Gln) and Glu (Gln>Glu), respectively. The net charge of these mutants was analyzed by native-PAGE at pH 8. The electrophoretic mobilities of Glu>Gln mutants decreased with the number of replacements, but those of Gln>Glu mutants didn't change. This result indicated the carboxyl groups is not charged, that is, protonated even at pH 8 if the number of carboxyl groups increase beyond the native one.

2Pos017 蛍光寿命計測によるアシル CoA 結合タンパク質のフォールディング機構の研究
Folding dynamics of acyl-CoA binding protein revealed by fluorescence lifetime measurements

Koichi Fujii, Motonari Tsubaki, Tetsunari Kimura (*Grad. Sch. Sci., Kobe Univ*)

The folding intermediates of proteins are generally compact and contain some secondary structures, but it is unclear whether compaction promotes secondary structure formation or vice versa. In this study, we aimed to experimentally clarify such cooperativity. We prepared the double-Cys mutants of acyl-CoA-binding protein(ACBP), which were chemically labeled with the fluorescent donor-acceptor (D-A) pair. Their folding/unfolding reactions were investigated by the fluorescence energy transfer, which allowed us to calculate D-A distances. We will follow the time-courses of the compaction and the helix formation by using the time-resolved fluorescence lifetime measurements equipped with a microchannel mixer, and discuss their correlation.

2Pos018 Influence of ligand binding on the glass transition temperature

Alexander Krah[1], Peter John Bond[2,3] ([1]*School of Computational Sciences, Korea Institute for Advanced Study (KIAS)*, [2]*Bioinformatics Institute, A*STAR*, [3]*Department of Biological Sciences, National University of Singapore*)

The biochemical function of proteins can be modulated at the protein glass transition temperature (Tg), which has been proposed to be dependent on protein-water interactions. To our knowledge, the molecular mechanism has not been described by which ligand binding to well-shaped binding sites influences Tg. To this end, we carried out simulations of the ε subunit from Bacillus PS3 from 20 to 300 K in the ligand-free and ligand-bound states, and measured Mean Square Deviation (MSD) to quantify Tg. We find that the transition temperature is hardly affected by ligand binding, but the MSD beyond Tg increases faster in the ligand-free than in the ligand-bound state, which is based on reduced water - binding site interactions, as site residues are shielded by the ligand.

2Pos019 回転対称軸周辺における相互作用の摂動による球殻状超分子のアセンブリ・メカニズムへの影響
Change in the assembly mechanism by disrupting of local interactions around symmetry axes of a spherical shell-shaped supermolecule

Daisuke Sato[1], Takumi Kuwata[2], Eriko Aoki[1], Kazuo Fujiwara[1,2], Masamichi Ikeguchi[1,2] ([1]*Fac. of Sci. and Eng., Soka Univ.*, [2]*Grad. Sch. of Eng., Soka Univ.*)

Ferritin (Ftn) is a spherical shell-shaped supermolecule consisting of 24 identical subunits arranged with 4/3/2 symmetry. Ftn reversibly dissociates into dimers under acidic conditions. We have investigated Ftn assembly mechanism by time-resolved small-angle X-ray scattering and clarified that the initial step is a mixture of the second- and third-order reactions. To know the influence of elimination of local interactions on the assembly mechanism, we produced 18 variants, which have mutations around symmetry axes. H128A showed increased reaction order in the assembly reaction, and its disassembly was decelerated despite elimination of a stabilizing interaction (salt bridge). H128F and H128V mutations led to further deceleration of the disassembly.

2Pos020 ポリミアン優先取込システムに関与する好熱菌由来 PotA の結晶構造解析
Crystal structure of PotA, a membrane-associated ATPase of the spermidine-preferential uptake system in Thermotoga maritima

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Polyamines, such as putrescine, spermidine (SPD) and spermine, are essential for cell growth and are distributed widely from prokaryotic to eukaryotic cells. There are several polyamine-transport systems in Escherichia coli. One of them constitutes the SPD-preferential (PotABCD) uptake system, which consists of a periplasmic substrate-binding protein (PotD), two transmembrane proteins (PotB and PotC) and a membrane associated ATPase (PotA). ATPase activity of PotA was inhibited by SPD, suggesting that uptake inhibition by spermidine may function during this process. To clarify the SPD inhibition mechanism of PotA, we carried out the structural studies of PotA. Here, we report the crystallization and crystallographic analyses of PotA from Thermotoga maritima.

2Pos021 ヨツヒメゾウリムシ由来アルギニンキナーゼの構造学的研究
Structural studies of arginine kinase from Paramecium tetraurelia

Yumeto Otsuka[1], Junko Tanaka[1], Daichi Yano[2], Koji Uda[2], Tomohiko Suzuki[2], Shigeru Sugiyama[2] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*Fac. Sci. & Tec., Kochi Univ.*)

Arginine kinase (AK) is the enzyme that catalyzes the reversible transfer of phosphoryl groups from ATP to arginine, yielding ADP and arginine phosphate. The ciliate Paramecium tetraurelia has four AKs (AK1-4). Recombinant AK1-4 were expressed in Escherichia coli and their kinetics parameters determined. Interestingly, AK3 showed typical substrate inhibition toward arginine, and enzymatic activity markedly decreased when arginine concentration increased. This is the first example of substrate inhibition in wild-type AKs. To elucidate the substrate inhibition mechanism of AK3, we performed a crystallographic study of AK3 with the bound arginine. In this presentation, we will report on the results of our preliminary crystallographic studies of AK3.

2Pos022 FABP3 の低分子薬剤に対する分子認識機構の解明
Elucidation of the molecular recognition mechanism of FABP3 in complex with low-molecular medicines

Junko Tanaka[1], Yumeto Otsuka[1], Daisuke Matsuoka[2], Osamu Hiraoka[3], Shigeru Matsuoka[4], Masashi Sonoyama[5], Michio Murata[2], Shigeru Sugiyama[6] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*Grad. Sch. Sci., Osaka Univ. & JST ERATO*, [3]*Sch. Pharm., Shujitsu Univ.*, [4]*Fac. Med., Oita Univ*, [5]*Sch. Sci. & Tec., Gumma Univ.*, [6]*Fac.Sci & Tec.,Kochi Univ*)

Long-chain fatty acids (FAs) with low water solubility require fatty-acid-binding proteins (FABPs) to transport them from cytoplasm to the mitochondria for energy production. FABP3 is one of the subtypes of human FABPs. Recently, we demonstrated the recognition mechanism of FABP3 to saturated FA with different chain-length by the accurate crystal structures and the WaterMap analysis. The FA chain-length adaptability was supported by the disposition of the water molecules. To further verify the role of these water molecules, we analyzed the crystal structures of FABP3 in complex with three low-molecular compounds [ANS, (S,R)-Ibuprofen], and studied those by isothermal titration calorimetry. We will dispute the recognition mechanism of FABP3 based on these analyses.

2Pos023 Conformational fluctuations and diffusive dynamics of small proteins

Eiji Yamamoto[1], Takuma Akimoto[2] ([1]*Dept. System Design Engineering, Keio Univ.*, [2]*Dept. Phys., Tokyo Univ. Sci.*)

Internal fluctuations of protein conformation have key roles for their function. The protein structural fluctuations are highly complex and correlated, which is attributed to multiple mechanisms, including trapping on a rugged energy landscape and fractional noise, etc. In addition, diffusivity of proteins is fluctuating due to their correlated dynamics. In this work, using all-atom molecular dynamics simulations, we investigate relationship between diffusivity and conformational fluctuations of small proteins, such as chignolin, villin, and, Pin1. Using a method [T. Miyaguchi, Phys. Rev. E 96, 042501 (2017)], we analyze a magnitude correlation and an orientation correlation of the fluctuating diffusivity of proteins.

2Pos024 カロテノイド結合とアミノ酸変異による微生物型ロドプシン TR の熱安定化
Thermostabilization of the microbial rhodopsin TR by carotenoid binding and amino-acid mutation

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Thermophilic rhodopsin (TR) has been obtained from the hotspring in US as a light-driven proton pump with exceptional high thermostability (Its denaturation temperature = >80 ℃). Here, we created the further thermostabilized TR by carotenoid binding and amino-acid mutation. In the crystal structure of TR, a binding site for carotenoid has been estimated. The binding is expected to make TR more thermostabilized one. Toward the thermostabilized mutant, we employed a theoretical method (EBM) which uses morphometric approach and integral equation theory. Then we coexpressed the theoretically estimated TR mutant and carotenoid in Escherichia coli cells, and successfully obtained the thermostabilized TR-carotenoid complex. We will discuss its molecular mechanism.

2Pos025 多糖モノオキシゲナーゼ，CBP21 の熱安定性に対する金属イオンの効果
Effects of metal ions on the thermal unfolding of lytic polysaccharide monooxygenase, CBP21

Hayuki Sugimoto, Ayaka Motoyama, Erina Katagiri, Takeshi Watanabe, Kazushi Suzuki (*Fac. Agri., Niigata Univ.*)

Lytic polysaccharide monooxygenase from *Serratia marcescens*, CBP21, catalyzes an oxidative cleavage of glycosidic bonds on crystalline chitin. CBP21 has an intrinsic copper ion. Effects of the copper ion (Cu^{2+}) and of metal substitution with zinc ions (Zn^{2+}) on the thermal unfolding of CBP21 were elucidated by DSC. Addition of Cu^{2+} to apoCBP21 increased the unfolding temperature $t_{1/2}$ by 9°C (pH 5). Increasing Cu^{2+} concentration did not increase $t_{1/2}$. These suggested that CBP21 was stabilized by Cu^{2+} binding and that the dissociation of Cu^{2+} was not involved during the unfolding. Metal substitution with Zn^{2+} suggested that the unfolding reaction differed in the two concentration regimes. This seemed to be due to lower binding affinity of unfolded CBP21 with Zn^{2+}.

2Pos026 水棲哺乳類ミオグロビンの分子進化：二つの適応戦略
Tracing evolution of aquatic mammal myoglobins: the two adaptation mechanisms

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Extant aquatic mammals, such as sperm whale and elephant seal, acquired the great ability to dive into the ocean depths during the evolution from their terrestrial ancestor that lived about 50 million years ago. Myoglobin (Mb) is highly concentrated in the myocytes of these diving animals, in comparison with those of land animals, and is thought to play a crucial role in their deep sea adaptation. We have resurrected ancestral cetacean and pinniped Mbs. The experimental and theoretical analyses demonstrated that aquatic mammal Mb adopted two distinguished strategies to increase the protein concentration in vivo along the evolutionary history; gaining precipitant tolerance in the early phase of the evolution, and increase of folding stability in the late phase.

2Pos027 スピンラベル ESR によるヘテロクロマチンタンパク質 HP1 の動的構造の研究
Structural dynamics of heterochromatin protein HP1 studied by site-directed spin labeling ESR spectroscopy

Toshiaki Arata[3,4], Yuichi Mishima[4], Shigeaki Nakazawa[5], Kazunobu Sato[5], Takeji Takui[5], Toshimichi Fujiwara[4], Makoto Miyata[3], **Isao Suetake**[1,2,4] ([1]*Koshien Univ.*, [2]*Twin Research Center, Osaka Univ.*, [3]*Dept. Biol., Grad. Sch. Sci., Osaka City Univ.*, [4]*IPR, Osaka Univ.*, [5]*Dept. Chem., Grad. Sch. Sci., Osaka City Univ.*)

HP1 plays a central role in the inactive heterochromatin. It has the chromo (CD) and the chromoshadow (CSD) domain, which are linked by hinge region (HR). The cw-ESR from the nitroxide spin label fixed at a cysteine of the CD or CSD of human HP1 indicated a rotational diffusion in agreement with free CD monomer or CSD dimer. Pulse electron double resonance showed the CSD-CSD and CD-CD interspin distance were 2.6 nm and >8nm, respectively. Therefore, HP1 dimerizes via CSD but does not show CD-CD interaction unlike yeast HP1(swi6). Flexible HRs allow free rotation of CD monomer and CSD dimer. The rotational correlation time of the CD increased due to complex formation when DNA or histone H3K9me3 peptide was added. Spin label will be mapped over the entire molecules.

2Pos028 TALE 蛋白質の新規構築法と応用
A simple and accurate construction of TALEs and its applications

Kazuho Ikeda, Yoko Terahara, Yasushi Okada (*RIKEN, BDR*)

A plant pathogen protein, transcription activator-like effector (TALE), is a “designable” DNA binding protein, which is promising platform for editing and manipulating of specific genome sequence in vivo. We recently developed highly active TALEs by inducing amino acid mutations at specific residues that might participate in conformational stability. In this study we further improved the utility of TALE based molecular applications by developing a novel method for assemble of TALE repeats. This method enables accurate TALE assemble within a day, and highly stable integration of TALE sequence into genome of cultured cells. We also reported nucleotide-free genome editing methods by introducing active TALE proteins rather than mRNA or DNA.

2Pos029 標的 RNA の切断前後の CRISPR-CMR の動力学
The dynamics of CRISPR-CMR before/after the cleavage of targeted RNA

Tomohiro Yamaguchi, Ryo Ohashi, Naoyuki Miyashita (*BOST, KINDAI Univ.*)

CRISPR/Cas system can specifically cleave the targeted RNA/DNA. Some of them, CRISPR-Cas9 and so on, have been known as a genome editing tools. CRISPR-CMR complex, is one of a family of CRISPR/Cas system, works as an antiviral defense's immune system in Thermus thermophilus. It has three active sites, and it cut the targeted RNA at three sites by 6-nt intervals. We have investigated the cleaving mechanisms of RNA in CRISPR-CMR using micro-second molecular dynamics simulations. We found that the CRISPR-CMR has the intrinsic fluctuations of the active domains for cleaving to the RNA, and the fluctuation of another module inhibits the fluctuation of the first active domain after the first cut.

2Pos030 Distinct binding of nuclear proteins to non B-type DNA studied by molecular simulations

Mami Saito, Shoji Takada (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

Cruciform structure is a non-canonical DNA formed by inverted repeat DNA sequences. It plays an important role in replication, regulation of gene expression, nucleosome structure and recombination. They are targets for many architectural and regulatory proteins, such as HU protein, histone proteins, HMG and p53. These proteins are suggest to recognize the junction DNA with high-affinity and also plays a role in regulation of gene expression. However, the interaction between cruciform and these proteins are unclear. We address how these nuclear proteins such as HU favorably bind the cruciform to the canonical B-type DNA, performing coarse-grained molecular dynamics simulations

2Pos031 Theoretical Studies on Stability of RA-VII for Anti-Cancer Agent by Docking and Molecular Dynamics Simulations

Muhammad Arwansyah Saleh[1], Yoh Noguchi[2], Takeshi Miyakawa[2], Kazutomo Kawaguchi[1], Yukio Hitotsuyanagi[3], Satoshi Yokojima[3], Ryota Morikawa[2], Masako Takasu[2], Hidemi Nagao[1] ([1]*Division of Mathematical and Physical Sciences, Kanazawa University*, [2]*School of Life Sciences, Tokyo University of Pharmacy and Life Sciences*, [3]*School of Pharmacy, Tokyo University of Pharmacy and Life Sciences*)

RA-VII peptide is one of a series of bicyclic hexapeptides which has been reported to have anti-tumor activity by inhibiting the protein synthesis in the ribosome. In this research, we performed docking and molecular dynamics (MD) simulations to predict the stable conformation and the binding energy of RA-VII in complex with the 60S ribosomal subunit. From the docking simulation, we obtained nine complex molecules represented as mode 1 to mode 9, where the mode 1 is the lowest of docking score energy as -16 kcal/mol. All complex molecules are simulated for the stability by using MD simulation. Our results may contribute to better understanding of the stable binding form of RA-VII molecule as a promising drug for anti-cancer agent.

2Pos032 Combinatorial DNA Binding of Sox/Oct Transcription Factors Studied with Molecular Dynamics Simulations

Cheng Tan, Shoji Takada (*Department of Biophysics, Kyoto University*)

The combinatorial DNA binding of proteins from the Sox and Oct transcription factor (TF) families are known to be crucial for the pluripotency of stem cells. Experiments have revealed that the Sox/Oct TF pairs bind to different DNA sequences with divergent cooperativities. However, an underlying mechanism of this binding specificity is lacking. Here we use coarse-grained molecular dynamics simulations to study the heterodimerization of Sox2 and Oct4 on designed DNA sequences with a different length of the gap between the individual consensus binding sites. Our results provided a structure-based model to explain the DNA sequence specificity of the Sox/Oct TF pair. With the same model, our results revealed a possible stepwise recognition mechanism for the Sox/Oct dimer.

2Pos033 蛍光相互相関分光法による単量体/二量体グルココルチコイド受容体の DNA 結合様式解明に向けた研究
Single-oligonucleotide mutated GRE impacts on glucocorticoid receptor binding studied by FCCS

Daisuke Yamashita[1], Sho Oasa[2], Jhotaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Grad. Shc. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [3]*Biomed. Res. Inst. AIST*)

Glucocorticoid receptor (GR) is one of the nuclear receptor. GR homodimer regulates gene transcription via binding to glucocorticoid response element (GRE). In contrast, GR monomer binds to so called half GRE and regulates other genes. However, DNA binding mechanism between GR homodimer and monomer and their correlation with transcriptional regulation are still unclear. To reveal this, we performed Fluorescence Cross-Correlation Spectroscopy (FCCS) to determine the dissociation constant (Kd) in purified EGFP-GR and Alexa647-GRE mixture. Interestingly, Kd analysis using single-oligonucleotide mutated GRE indicates the difference of substantial bases for monomer or homodimer binding. We also report the results of the transcriptional activity on deferent sequence GREs.

2Pos034 Comparing Nucleoprotein Filament Assembly of Yeast Dmc1 and Rad51 Recombinases at the Single-Molecule Level

Wei-Hsuan Lan[1], Sheng-Yao Lin[1], Wen-Hsuan Chang[1], Chih-Yuan Kao[2], Peter Chi[2,3], Hung-Wen Li[1] ([1]*Dept. of Chemistry, NTU*, [2]*Inst. of Biochemical Sciences,NTU*, [3]*Inst. of Biological Chemistry, Academia Sinica*)

Dmc1 and Rad51 are essential to homologous recombination repair of DNA double-strand breaks. Only Rad51 is required in mitotic cells, but both Rad51 and Dmc1 participate in meiotic recombination. The mechanism of differential requirement is unknown. Here, we compared the kinetics of the nucleoprotein filament assembly of S. cerevisiae Rad51 and Dmc1 using single-molecule method and in vitro biochemical assay. ScRad51 nucleoprotein filaments are better protected because of kinetically much faster nucleation step. Single-molecule experiments on DNA substrates of various ssDNA lengths showed the higher ssDNA affinity of ScRad51. Surprisingly, nucleation rates of ScDmc1 depend on number of duplex DNA/ssDNA junctions, suggesting ScDmc1 prefers to nucleate in these locations.

2Pos035 がん抑制タンパク質ｐ５３の標的探索ダイナミクスの一分子観察
Single-molecule observation of the target search dynamics of a tumor suppressor p53

Yuji Itoh, Agato Murata, Satoshi Takahashi, Kiyoto Kamagata (*IMRAM*)

A protein p53 recognizes the target DNA sequence to trigger the expression of downstream products responsible for the tumor suppression. One significant but unanswered question is how p53 searches for the short target in vast genome DNA within a physiological time. To answer the question, we aimed to characterize the target search process of p53 by single-molecule fluorescence microscopy. First, we revealed that p53 frequently passes over the target sequence and that the target recognition probability is ~7%. Second, we demonstrated that p53 transfers from one DNA strand to another with an ultrafast rate of ~10^8 M^{-1} s^{-1} and observed the transfer at the single-molecule level. Physiological roles of those two processes will be discussed in the presentation.

2Pos036 Using Single-Molecule Optical Microscopy to Study How PriA Helicase Restarts replication

Han Lin Yang[1], Hung-Wen Li[1], Min Guan Lin[2], Chwan-Deng (David) Hsiao[2] ([1]*Dept. Chem, NTU*, [2]*IMB, Academia Sinica*)

PriA which is responsible for restarting stalled DNA replication forks unwinds DNA to generate single-stranded DNA and loads other replicative proteins to form a primosome, so DNA polymerase can restart DNA replication. We used single-molecule tethered particle motion experiments and single-molecule Fluorescence Resonance Energy Transfer experiments to directly visualize how individual GstPriA and SpPriA unwind DNA. Analysis of Brownian motion time-courses offers kinetics and dynamics of GstPriA binding process. smFRET traces showed that SpPriA is a low efficiency helicase. Interaction with other primosome-associated proteins is required for PriA for efficient primosome assembly.

2Pos037 二面角系疎視化モデルによる巨大核酸分子の立体構造ゆらぎ—X線構造の温度因子との比較
Structure fluctuations of large nucleic acids with a corse-grained model in torsional angle space–A comparison with temperature factors

Shigeru Endo[1], Hiroshi Wako[2] ([1]*Dept. Phys., Sch. Sci., Kitasato Univ.*, [2]*Sch. Socical Sci., Waseda Univ.*)

We have developed a computer program that performs normal mode analysis (NMA) based on an elastic network model. Taking advantage of the relatively small number of degrees of freedom required to describe a molecular structure in dihedral angle space, we aim to develop the program applicable to a full-atom system of any molecule in PDB. In order to further reduce the number of independent variables, we adopted a corse grained model in which a phosphorus atom was directly connected to C3' in the previous residue and C4' in the same residue by rotatable pseudo bonds. Atomic fluctuations from NMA of large RNA molecules were compared with X-ray temperature factors.

2Pos038 SAXS および SANS プロファイルに基づくオーバーラッピングダイヌクレオソームのモデル構築
Model building of overlapping dinucleosome based on SAXS and SANS profiles

Atsushi Matsumoto[1], Hidetoshi Kono[1], Rintaro Inoue[2], Masaaki Sugiyama[2], Yasuhiro Arimura[3], Hitoshi Kurumizaka[3] ([1]*QST*, [2]*Kyoto U.*, [3]*U. Tokyo*)

We built the atomic models of the overlapping dinucleosome in solution based on the experimental profiles of the small-angle X-ray scattering (SAXS) and the small-angle neutron scattering (SANS) by the computational approach. Recently, the X-ray crystal structure of the overlapping dinucleosome was solved. However, the structure in the crystal may be different from those in solution, which are the ones we really need to know. In this study, we first generated a lot of atomic models of the dinucleosome with different conformations by computer simulations using the crystal structure as the initial model. Then, the SAXS and SANS profiles are computed for each model. Finally, these computed profiles are compared with the experimental ones to find the appropriate models.

2Pos039 分子輪投げによる環状 DNA1 分子のトラップ
Trapping of Single Circular DNA Molecules by Molecular Ringtoss

Ken Hirano[1], Taiki Dohi[1,2], Kyohei Terao[2] ([1]*Health Res. Inst., AIST*, [2]*Dep. Eng., Kagawa Univ.*)

In this study, we propose ‘ringtoss technique’ for trapping single circular DNA molecules to micropillars under an optical microscope to observe their dynamics with high-spatial resolution. By introducing huge circular DNA molecules (208 kbp) into a microfluidic channel with micropillars, the circular DNA molecules hang on the micropillar like ringtoss simply. From this result it is shown that single circular DNA molecules realized observation directly with high spatial resolution by developing by flow. This ringtoss technique for single circular DNA molecules can be used for observing dynamics change of DNA structure induced by enzymes (topoisomerase and gyrase), DNA-binding proteins and condensation reagents, and we are currently developing their analysis.

2Pos040 siRNA を安定化するカチオン性分子と二本鎖 RNA の NMR による相互作用解析
NMR analysis of interactions between dsRNA and cationic oligomers that stabilize small interfering RNA

Taiichi Sakamoto[1], Rintaro Hara[2], Yusuke Maeda[2], Takeshi Wada[2] ([1]*Fac. Adv. Eng., Chiba Inst. Tech.*, [2]*Fac. Pharm., Tokyo Univ. Sci.*)

Small interfering RNA (siRNA) drugs have been studied as promising therapeutic agents. For the effective transfection of siRNAs, a variety of drug delivery systems have previously been reported. We have developed various cationic oligosaccharides and oligopeptides which can stabilize RNA duplex structure. In this study, we analyzed the interaction between cationic oligomers and double-stranded RNA (dsRNA) by using NMR. When we measured NOESY spectra of the cationic oligomer-RNA complexes, lots of intermolecular NOEs were observed between base protons of the dsRNA and the cationic oligomers. Thus, it was suggested that the cationic oligomers bind to major groove of dsRNA.

2Pos041 DNA の構造の揺らぎへの溶媒粘性の影響
Effect of solvent viscosity on configuration fluctuations of DNA

Masato Tanigawa, Takafumi Iwaki (*Biophysics, Faculty of Medicine, Oita University*)

We studied the autocorrelation function of linear and circular DNA by measuring the relaxation time of the end-to-end distance of the DNA. Although the relaxation times of linear and circular DNA are different, there is no difference in autocorrelation function. However, when the viscosity of the solvent was changed, a difference was found in the autocorrelation function. In one molecule observation, DNA show a considerably different profile according to an individual molecule. We carefully analyzed the experimental results, and the effect of viscosity to the correlation time to elucidate whether a molecule-solvent interaction is analiticaly modeled.

2Pos042 Structural effect of spermine analogues on inducing DNA compaction

Tomoki Kitagawa, Tkashi Nishio, Yuuko Yoshikawa, Takahiro Kenmotsu, Kenichi Yoshikawa (*Faculty of Biological and Medical Sciences, Doshisha University Laboratory of Life Physics*)

Polyamines are found in many living organisms and are known to play important roles in various biological functions including DNA packaging and gene expression. We investigated the potentiality of naturally occurring tetravalent polyamines, spermine and thermospermine, which are structural isomers of each other, to induce DNA compaction by using fluorescence microscopy and atomic force microscopy. Result in single molecule observations of DNA revealed that thermospermine is more efficient at promoting DNA compaction than spermine. We also evaluated gene expression by in vitro luciferase assay. We will discuss the contribution of different structure of both isomers to DNA compaction in relation to their effects on genetic activity.

2Pos043 1-propanol causes reentrant transition on DNA whereas 2-propanol does not: Experimental verification through single molecular observation

Yue Ma, Yuko Yoshikawa, Koichiro Sadakane, Kenichi Yoshikawa (*Grad. Sch. Life Med. Sci, Doshisha Univ.*)

In the present study, we have measured the change of the higher-order structure of genomic DNA molecules in the presence of alcohols by use of single DNA observation with fluorescence microscopy, by focusing our attention to unveil the different effect between 1-propanol and 2-propanol. We found that, with 1-propanol, the long-axis length exhibits minimum at 60% and then tends to increase with the increase of alcohol content. On the other hand, with 2-propanol the long-axis length exhibits almost monotonous decrease with the increase of alcohol content. These results indicate that DNA undergoes reentrant transition of coil-globule-coil with 1-propanol, whereas such reentrance phenomenon does not appear with 2-propanol.

2Pos044 Direct Observation of the Protein-DNA Interaction Using Passive Force-Clamp Optical tweezers

Yen Chan Chang, Hung Wen Li (*Department of Chemistry, National Taiwan University, Taipei, Taiwan*)

Optical tweezers has been widely used to study protein-DNA interaction. By applying pico-Newton forces on individual DNA molecules, the variation of DNA extension (force-extension curve) allows to analyze protein bounds to DNA based on the worm-like chain model. To study the protein-DNA assembling dynamics with high spatiotemporal resolution, we implemented the existing optical tweezers platform with a passive force clamp. The passive force-clamp operates in a nearly zero trap-stiffness region and therefore, removes the needs to actively feedback the system while maintaining a constant force throughout the experiments. We showed that this implemented passive force-clamp platform can be used to characterize the protein-DNA interaction.

2Pos045 X 線小角散乱法による RecA タンパク質ーDNA 複合体フィラメントの構造解析とシミュレーションモデルとの比較
Structural changes of RecA protein/DNA complex filament promoted by Mg ions analyzed using SAXS and compared with its models

Satomi Inaba[1], Chantal Prevost[2], Tsutomu Mikawa[3], Hiroshi Sekiguchi[1], Masayuki Takahashi[4] ([1]*JASRI/SPring-8*, [2]*CNRS*, [3]*RIKEN BDC*, [4]*Tokyo Inst. Technol.*)

RecA protein promotes DNA strand exchange for homologous recombination. For the reaction, RecA binds at first single-stranded DNA with ATP and forms a filamentous complex. Its structure was modeled from X-ray crystal structure of RecA oligomer. We like to know if the model fits well with the structure of long filament in solution and how ATP affects the structure. Furthermore, we recently observed Mg^{2+}, which is required for the activation of RecA, also affects the RecA structure. In order to elucidate this structural change, we investigate the filament structure by measuring SAXS pattern and comparing with computed scattering profile from the model. The scattering profile of RecA-DNA filament clearly depends upon ATP, which is good agreement with the theoretical one.

2Pos046 DNA インターカレーションと光応答
DNA intercalation and optical response

Satoshi Yokojima (*Tokyo University of Pharmacy and Life Sciences*)

We computationally investigated intercalation of some molecules into DNA and its optical response by molecular dynamics and quantum chemical calculations. Effect of the intercalation on the optical response in comparison to the optical response in water solution was examined based on the interaction between the molecules and DNA.

2Pos047 転写開始複合体における DNA 開裂の粗視化分子シミュレーション研究
DNA Opening in Transcription Initiation Complex Studied by Coarse-grained Molecular Simulation

Genki Shino, Masahiro Shimizu, Shintaroh Kubo, Toru Niina, Shoji Takada (*Dept. of Biophys., Div. of Bio. Sci., Grad. Sch. of Sci., Univ. of Kyoto*)

The molecular mechanism of transcription initiation process has been actively studied by using cryo-electron microscopy and biochemical experiments. The transcription of eukaryotic protein-coding genes results from forming transcription initiation complex on the promoter DNA, consisting of RNA polymerase II and the six general transcription factors, and DNA opening. However, the details of DNA opening is unknown. We make the coarse-grained molecular dynamics simulation, representing each amino acid as one particle and a nucleotide as three and using as force fields AICG2+ for protein and 3SPN.2 for DNA, and aim to elucidate the molecular mechanism of DNA opening in transcription initiation complex.

2Pos048 光照射で構築した DNA マイクロ構造体の熱力学的特性の解析
Analysis of the thermodynamic property of DNA microstructures formed by photo-irradiation

Yu Kasahara, Masahiro Takinoue (*Tokyo Institute of Technology/School of Computing/Computer Science.*)

DNA nanotechnology allows us to construct self-assembled DNA nano/microstructures such as DNA origami and DNA hydrogels. They are expected to be applied to the system that control its function by structural change such as gene expression control. It is considered to control the transcription amount by volumetric shrinkage of DNA microgel. Since the shrinkage rate is related to the DNA microgel's pattern, in this research, we develop light patterned DNA microgel and analyze the pattern dependence of shrinkage rate. Currently, we succeeded in binding the Y-motif DNA units by light designed based on the base sequence dependence of DNA microgel structure. We believe that this system can be used as a gene expression control system that mimics the cell nuclear mechanism.

2Pos049 細胞核様 DNA ゲルカプセルの形成のシミュレーション
Numerical simulation of phase separation-based formation of cell nucleus-like DNA gel capsule

Tetsuro Sakamoto, Masamune Morita, Masahiro Takinoue (*Department of Computer Science, Tokyo Institute of Technology*)

We are focusing on the programmability of DNA molecules to control a formation of cell nucleus-like DNA gel capsule. Recently, we reported a DNA gel capsule formed on a water-in-oil microdroplet interface, and experimental data suggest that there are two types of formation mechanisms. According to our previous research, one of the mechanisms is explained by cluster-cluster aggregation model. However, the other mechanism has never been completely revealed yet. In this study, we consider a more general model and it's simulation method that explains both mechanisms and compares simulation results and experimental results to evaluate the validity of the model. We believe the model helps to control the shapes and functions of the capsule.

2Pos050 Heterogeneous chromatin accessibility establishes human nuclear organization

Shin Fujishiro[1,2], **Masaki Sasai**[1,2] ([1]*Dept. Comp. Sci. & Eng., Nagoya Univ.*, [2]*Dept. Appl. Phys., Nagoya Univ.*)

Spatial organization of chromosomes in mammalian nuclei is closely linked to gene expression. Recent studies suggested the nuclear organization through phase separation, the mechanism of which remains elusive. We developed a computational polymer model of chromosomes with biophysically plausible assumptions: Active chromatin regions keep high accessibility, allowing overlaps of polymer segments, whereas repressed chromatin regions bear meshworks of HP1 or PcG proteins, preventing overlapping of segments. Langevin dynamics simulations quantitatively explained the experimentally observed distribution of A/B compartments, LADs and NADs in human fibroblast nuclei. Thus, heterogeneity in local chromatin accessibility is sufficient to establish the phase separation in nuclei.

2Pos051 ヌクレオソーム排他的領域のインスレーター機能の解析
Analysis of insulator function of nucleosome exclusive genome regions

Yuki Matsushima, Hiraku Nishimori, Naoaki Sakamoto, Akinori Awazu (*Dept. of Math and Life Science, Hiroshima Univ.*)

Insulator sequence is known to play a role of genome domain boundary. CTCF binding site is one of the typical insulators that forms chromatin individual loop domain by binding CTCF and cohesion. Recently, also nucleosome exclusive sequences like Poly-A or CCGNN repeat sequences and Ars-insulator identified in Sea Urchin were reported to show insulator activity. In this study, we consider the mechanism of the insulator activity of such nucleosome exclusive regions (NER) in human genome. We analyzed the binding distribution of RPB1 around NERs and the contact frequency with Hi-C data. The results showed that RPB1 binds to one side of NER, and decreases the contact frequency between regions on both side of NER.

2Pos052 過渡的に生じる中間体ヌクレオソームにおけるヒストンテール動態
Histone Tail Dynamics in Transient Intermediate Single Nucleosomes

Takeru Kameda, Yuichi Togashi, Akinori Awazu (*Department of Mathematical and Life Sciences, Hiroshima University*)

The positioning of nucleosomes on DNA and their structural stability influence chromosome dynamics and functions. Nucleosomes often change their positions through their reconstitution. Here, the binding and dissociation of different types of histone are regulated by different proteins, and the exchange of H2A/H2B complex occurs more frequently than that of the other. From these facts, the presence or absence of each histone may contribute to the stability of nucleosome. In this study, we performed fully-atomic molecular dynamics simulation of various types of nucleosomes that contain all histones, that lacks one H2A/H2B hetero-dimer, and that lacks H3/H4 hetero-dimer, to analyze the contribution of each pair of core-histones to the nucleosome structure stability.

2Pos053 アミロイドβ凝集の初期過程に対するQM/MM法を用いた解析
QM/MM analysis of the initial aggregation of amyloid-β peptides

Hiroaki Nishizawa[1,2], Hisashi Okumura[1,2,3] ([1]*ExCELLS*, [2]*IMS*, [3]*Sokendai*)

An amyloid fibril of amyloid-β (Aβ) peptides is well known as the cause of the Alzheimer's disease. A part of the Aβ, i.e. Aβ(1-16) fragments, is considered to be important for initial formation of the amyloid fibrils. Furthermore, some experimental researches indicate that the Aβ aggregation is accelerated under existence of metal ions. We have studied the Aβ aggregation using the classical molecular dynamics (MD) simulation. However, because the classical MD method cannot reproduce the chemical bond, we did not obtain the results of acceleration of Aβ peptide aggregation. In this study, we investigate the initial aggregation of Aβ using the molecular mechanical theory and density-functional tight-binding method, which is one of the electronic structure theories.

2Pos054 Relative stability between hydroxide models and oxo models of S1 state of the OEC of PSII by DFT and beyond DFT methods

Koichi Miyagawa[2], Takashi Kawakami[1], Hiroshi Isobe[3], Mitsuo Shoji[4], Shusuke Yamanaka[1], Kazuhiko Nakatani[2], Mitsutaka Okumura[1], Kizashi Yamaguchi[2,5] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*ISIR, Osaka Univ.*, [3]*Grad. Sch. Nat. Sci. and Tech., Okayama Univ.*, [4]*CCS, Tsukuba Univ.*, [5]*Inst. Nanosci. Design, Osaka Univ.*)

Relative stability between hydroxide models and oxo models of S1 state of the Kok cycle for the oxygen evolving complex(OEC) of photosystem II (PSII) were investigated by hybrid DFT, double-hybrid DFT and beyond DFT methods like as (Domain-based(D)) Local Pair Natural Orbital(LPNO)-Coupled Cluster (CC) SD and CCSD(T) methods. In all cases, the hydroxide models' stability was indicated. But this relative stability's tendency was something different for DFT results and post-DFT results. This difference was caused by a dynamical electron correlation effect and by a solvent effect indicating the importance of such effects. Furthermore, the implications of present results are discussed to elucidate scope and applicability of hybrid DFT methods.

2Pos055 DASH型クリプトクロムにおける電子移動反応に関する理論的解析
Theoretical Analysis of Electron Transfer Reaction for Cryptochrome-DASH

Ryuma Sato, Makoto Taiji (*RIKEN*)

Cryptochromes (CRYs) are a group of flavoproteins, and photolyases (PHRs) and CRYs constitute a family. PHRs exert the DNA repair function, while CRYs exert versatile function. However, CRYs do not exhibit photorepair activity. Recently, a new type cryptochrome (Cryptochrome-DASH: CRY-DASH) has been identified, and exhibits a weak photorepair activity. We investigated the reason why the photorepair activity of CRY-DASH is weaker than that of PHRs in terms of the electron transfer reaction. We estimated the electronic coupling matrix elements for PHRs and CRY-DASH. The value of CRY-DASH was almost the same value as PHRs. Therefore, we think that the weakness of its photorepair activity is attributed to a mechanism other than the electron transfer reaction.

2Pos056 光電子放出を用いた TR の電子構造の観測 2：RxR との比較
Electronic structure of a film with TR observed by technique using photoelectron emission 2: Comparison with RxR

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Electronic structures of bio molecules are important for understanding bio-related processes. Techniques using photoelectron emission as UV photoelectron spectroscopy (UPS) are useful for examining them. In the last meeting, we investigated electronic structures of Thermophilic Rhodopsin(TR) film with high-sensitivity UPS. Photoelectron emission from retinal was successfully observed. In this study, we tried to observe electronic structures of Rubrobacter xylanophilus Rhodopsin(RxR), which is more stable than TR. They have similarities such as microbial origin, but different electronic structures were confirmed at the top region of valence state of them; Shallower state than EF level was observed in TR, but not in RxR. Details will be discussed with results.

2Pos057 高感度紫外光電子分光を用いたリゾチーム薄膜のギャップ内準位の観測
Gap state of lysozyme thin film observed by high-sensitivity UV photoelectron spectroscopy

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For understanding the function of molecule, it is important to evaluate not only HOMO and LUMO but also gap state between them. Our group has observed the gap state of organic semiconductors by high-sensitivity UV photoelectron spectroscopy (HS-UPS) and discussed the correlation between gap state and device characteristics. In the field of bio-molecule, gap state has not been so far recognized. In this study, we chose lysozyme as a very stable protein and tried to measure the gap state by HS-UPS while suppressing sample charging using low energy and high purity light source. As a result, we have observed the exponentially decaying gap state of a lysozyme film prepared by spray deposition. Such gap state can work as trap, affecting electron transfer among molecules.

2Pos058 各種溶質周囲の水分子ダイナミクスの分子動力学計算と解析
MD simulations and analysis of hydration dynamics around several types of solute molecules

Takuya Takahashi, Kota Kasahara, Ryoi Ashida, Nobuya Hasegawa, Daigo Itsuji, Tomomi Kura (*College of Life Science, Ritsumeikan University*)

To investigate relationship between dynamic feature of hydration water and protein structure, we examined differences in hydration dynamics among several different conformations with model peptides as well as mutated proteins and monovalent ions by using molecular dynamics simulations. As a result, in the first hydration layer, the hydration dynamics around the helix was the fastest in the tested structures. Moreover, to reproduce “fast water dynamics” around ions with the conventional water models. We modified the conventional TIP5P water model. We introduced a new Lennard-Jones (LJ) potential between ion and water and examined a wide range of parameter values. As a result, the new model improved the water dynamics compared with the conventional water models.

2Pos059 細胞混雑中の蛋白質間相互作用に及ぼす代謝物とイオンの影響:分子動力学法による理論的研究
Influence of metabolites and ions on the protein-protein interactions in cellular crowding: Theoretical study with MD simulations

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Inside of a cell is highly crowded with a large number of macromolecules together with solvents and metabolites. How variable interactions within dense cellular environments may affect the structure and dynamics, and ultimately function is one of the most fundamental questions in life science. We constructed full atomistic models of cytoplasm by changing the metabolite or ion concentration. Using these model, we performed all-atom molecular dynamics (MD) simulation with the high-performance MD simulator GENESIS on super computer K. Influence of non-specific interaction between macromolecule and metabolites/ions on the protein dynamics and aggregation was analyzed at the atomic level.

2Pos060 機械学習アプローチによる物理化学量の予測
Classification and prediction of physicochemical properties by machine-learning approach: molecular dynamic study of hydration water

Taku Mizukami[1], Viet Cuong Nguyen[3], Tien Lam Pham[2], Heui Chi Dam[2] ([1]*JAIST, Materials*, [2]*JAIST, Knowledge*, [3]*HPC.Inc*)

Water plays an important role in biology. Many kinds of biomolecules activate their functions in a hydrated environment, via mechanisms that are strongly influenced by interactions with water. In this study, we demonstrate a machine-learning approach to classify and to predict the features of water surrounding solute quantitatively. We modeled the “behavior” of all water molecules in classical MD simulations of solute-solvent system. The behavior of water molecules was then categorized by classification techniques. The sparse modeling techniques, like lasso or lars, were applied to leaning and prediction process on the physicochemical features. We will report the prediction of local potential energy, and will discuss on the application for free energy.

2Pos061 MDM2-p53NTD と MDM2-MIP の結合自由エネルギーに見られる大きな差の物理起源
Physical origin of the large difference between MDM2-p53NTD and -MIP complexes in binding free energy

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The oncoprotein MDM2 binds to a tumor suppressor protein p53 and inhibits its anticancer activity. We have recently identified a peptide MIP exhibiting very high affinity for MDM2 (PLoS One, 6, e17898, 2011; ibid., 9, e109163, 2014). Using our theoretical method based on statistical mechanics of hydration, we calculate the binding free energy (BFE) and its physically insightful energetic and entropic components for each of MDM2-p53NTD and -MIP complexes. We show that the BFE is much lower for MDM2-MIP, which is in accord with the experimental result. The main reason for this is that a more complete shape complementarity at the atomic level is achieved within the binding interface, leading to a larger gain of the translational, configurational entropy of water.

2Pos062 溶媒の種類が蛋白質の安定構造に及ぼす効果
Effects of solvent species on the stabilized structure of a protein

Tomohiko Hayashi[1], **Masao Inoue**[1], Satoshi Yasuda[1,2,3], Emanuele Petretto[4], Tatjana Skrbic[4], Achille Giacometti[4], Masahiro Kinoshita[1] ([1]*Inst. Adv. Energ., Kyoto Univ.*, [2]*Grad. Sch. Sci., Chiba Univ.*, [3]*MCRC, Chiba Univ.*, [4]*Dept. of Molecular Sciences and Nanosystems, Venezia Univ.*)

We study the dependence of the stabilized structure of a protein on the solvent species using our free-energy function (FEF) which accounts for the solvent-entropy gain, formation of protein intramolecular hydrogen bonds (HBs), break of protein-solvent HBs, and recovery of solvent-solvent HBs upon the folding. Applying the FEF to the native folds of α-helix-rich and β-sheet-rich proteins and to a number of misfolded decoys, we identify the stabilized structures in different model solvents: water, methanol, ethanol, and cyclohexane. We find that the most stable structures in water are the native folds for both of the two proteins. However, those in the other solvents are characterized as associated α-helices, which is probably independent of the amino-acid sequence.

2Pos063 セロビオースとマルトースの水への溶解度の大きな差に関する統計熱力学
Statistical thermodynamics on the large difference between maltose and cellobiose in terms of solubility in water

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It is a subtle subject to elucidate the differences in physical properties originating from the stereoisomerism. Here we analyze the origin of the large difference between cellobiose and maltose, which consist of two β-1,4 and α-1,4 linked D-glucose units, respectively, in terms of the solubility in water. The disaccharide structures are taken into account at the atomic level and a molecular model is employed for water. We show that their solubility ratio calculated from the key free-energy function defined in our thermodynamic theory is in good accord with the experimental value. Interestingly, the much lower solubility of cellobiose is ascribed to the effects of conformational entropy of a disaccharide and translational, configurational entropy of water.

2Pos064 The analysis of Housekeeping Gene Expression Variations During iPS Reprogramming Process

Yulia Panina, Arno Germond, Tomonobu Watanabe (*RIKEN BDR*)

iPS cell state is evaluated by gene expression analysis. RT-qPCR is the most sensitive technique available for such analysis, and relies on normalization of PCR data against housekeeping genes, such as Actin, GAPDH etc., which are presumed to have constant level. We have analysed the behaviour of 12 housekeeping genes during iPS reprogramming and revealed strong variations in their stability. Atp5f1, Pgk1 and Gapdh were the most stable genes, while the least stable genes were Rps18, Hprt, Tbp and Actb. Nevertheless, the variation in housekeeping genes' expression during the iPS reprogramming reached up to 250% even in the case of best genes. We conclude that the use of reference genes is unsuitable for normalization procedures during pluripotency-state investigations.

2Pos065 エピジェネティックな状態変化と遺伝子相互作用が細胞のがん化に及ぼす影響のランドスケープ理論による解析
Landscape analyses of coupled dynamics of epigenetic state change and gene interaction in carcerization

Yutaro Kameyama, Masaki Sasai (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

Recurrence of cancer cells makes complete cure of cancer diseases difficult. It was suggested that cancer stem cells (CSCs) are responsible for the recurrence; therefore, it is important to analyze whether CSCs are generated from normal stem cells or normal differentiated cells. We develop a model of transitions among CSCs, stem cells, differentiated cells and cancer cells by extending the gene network model developed by Li and Wang (Cancer Res. 2015) to include epigenetic degrees of freedom such as histone modification and DNA methylation patterns. We simulated the epigenetic state change with the Gillespie algorithm and calculated the dynamical change of gene expression landscape to analyze the transition mechanism of cancerization.

2Pos066 細胞膜アンカーを目指したαヘリックス型ペプトイドの合成
Synthesis of an α-helix peptoid for cell-membrane anchoring

George Mogami, Wato Oba, Masaya Yamamoto (*Grad. Sch. Eng., Tohoku Univ.*)

In this study, we designed and synthesized a membrane-anchored molecule as a cell-labeling probe. Lipids or glycoproteins modified with fluorescent dye or antibody are often inserted to visualize a cell membrane, but this method has a problem that observation time is limited due to desorption of the probe molecule from the membrane. Then, based on a transmembrane peptide with α-helix motif, a **"peptoid"**, *N*-substituted glycine, was synthesized using solid phase submonomer method, which is a peptide-like oligomer with biodegradability enabling the labeling for a long time. Also molecular dynamics simulation and free energy calculation of peptide/peptoid interacting with membrane were carried out, and thermodynamics of membrane-anchor was considered.

2Pos067 Implicit Solvent Coarse-Grained Lipid Model for Molecular Simulations of Multicomponent Membrane Systems

Diego Ugarte, Shoji Takada (*Dept. Biophysics, Div. Biology, Graduate School of Science, Kyoto University*)

This work presents the extension of our coarse-grained lipid model to multicomponent membrane systems. In our model, lipids are represented as single-tail molecules, intramolecular interactions are parameterized following a bottom-up approach and intermolecular interactions are top-down parameterized in order to reproduce experimental values of area per lipid and membrane thickness. Finally, using simple combination rules we tested the interactions between different lipids by analyzing the physical properties and the phase behavior of binary and ternary systems composed of DPPC, DOPC, and cholesterol.

2Pos068 細胞模倣系における蛍光相関分光法による分子拡散測定
Molecular diffusion in cell-mimicking system measured by fluorescence correlation spectroscopy

Chiho Watanabe, Yuta Kobori, Miho Yanagisawa (*Tokyo Univ. Agri. Technol.*)

Molecular diffusion in cells deviates from that in bulk solutions due to micrometric confinement by lipid membrane as well as macromolecular crowding. Previously, we have reported that these physical conditions induce anomalous diffusion by using cell-mimicking confinement (Watanabe, Yanagisawa, PCCP, 2018). To understand the effect in deep, we have investigated diffusion dependence on the distance from a bulk interface measured by fluorescence correlation spectroscopy. We employed non charged linear flexible polymer poly(ethylene)glycol (PEG) for crowder and a small fluorophore for tracer. We will compare this behavior with a system using a globule protein as a crowder molecule.

2Pos069 Single molecule analysis of transport protein using small liposome with size uniformity

Naoki Soga[1], Rikiya Watanabe[1,2], Hiroyuki Noji[1] ([1]*Dept. of Appl. Chem., The Univ. of Tokyo*, [2]*AMED-PRIME, JST*)

Transport proteins play pivotal roles by transporting molecules across bio-membrane. Single molecule analysis of transport protein on a single liposome revealed the existence of the several functional states in transport reaction, contributing the understanding of its working principle, however, a drawback of liposome, i.e. size heterogeneity, has prevented from the highly quantitative analysis. To address this issue, we developed a method to produce liposomes with size uniformity, whose diameter of liposome can be modulated down to sub-micron within ~15% deviations. Using this liposomes, we quantitatively measured the activity of a transport protein at single molecule level. Thus, our liposomes would offer a basic tool to understand their working principles.

2Pos070 高速 AFM を用いた光受容体ロドプシンクラスターとトランスデューシンとの相互作用観察
Observing the interaction between rhodopsin cluster and transducin by high-speed AFM

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Rhodopsin (Rh) molecules form supramolecular structures, such as dimer and cluster. Recent simulation studies indicated that G-protein transducin (Gt) can be activated by Rh cluster more efficiently owing to scanning on the row of Rh dimers. However, interactions between dark-state Rh cluster and Gt has not been observed. In order to elucidate the functional role of Rh cluster, we observed Rh clusters and Gt in the planer membrane by high-speed AFM. Rh cluster was prepared by depleting lipids in the disk membrane with detergent. We observed activation-dependent dissociation of Gt from Rh. Observation in the darkness should reveal the interaction between dark-state Rh and Gt and give insight of the functional role of Rh cluster.

2Pos071 全反射赤外分光法によるGタンパク質共役受容体-リガンド間相互作用の解析
Investigation of ligand-protein interaction in a G protein-coupled receptor via ATR-FTIR spectroscopy

Hisao Tsukamoto[1,2], Yuji Furutani[1] ([1]*Institute for Molecular Science*, [2]*PRESTO, JST*)

Various biological processes including vision, olfaction, and neural transmission are mediated by G protein-coupled receptors (GPCRs). We have revealed molecular properties of various animal opsins, light-sensitive GPCRs, but most of GPCRs are activated (or inactivated) by binding of diffusible ligands. ATR-FTIR spectroscopy is a powerful technique to analyze interaction manner of membrane proteins with exogenous ligands, and we have applied this technique to ion channels. In this study, we prepared GPCR samples suitable for ATR-FTIR spectroscopy and successfully measured IR spectral changes upon ligand binding to a GPCR. We will discuss how ATR-FTIR spectroscopy helps to understand structure-function relationship in GPCRs.

2Pos072 細胞骨格封入巨大リポソームの繰返し屈伸運動
Repetitive stretching of cytoskeleton-encapsulating giant liposomes

Masahito Hayashi[2], Shunsuke Tanaka[1], Masayoshi Nishiyama[3], Taro Toyota[4], **Kingo Takiguchi**[1] ([1]*Grad Sch of Sci, Nagoya Univ*, [2]*CBS, RIKEN*, [3]*Dept of Phys, Kindai Univ*, [4]*Graduate School of Arts and Sciences, The University of Tokyo*)

Giant liposomes encapsulating cytoskeletons have been constructed to further understand the mechanisms of cell movement. However, no one has succeeded in generating repetitive motions controlled by external stimuli. Here we show that if their concentration in liposomes is comparable to that of cytoplasms of living cells, the liposomes can be deformed depending on the type/nature of cytoskeleton. The liposomal shapes can be changed reversibly by changing temperature, applying hydrostatic pressure, adjusting osmotic pressure, or light irradiation of fluorescent-labeled filament. These results indicate that native filamentous polymer of variable length, such as microtubule or actin filament, itself is a potential material for the generation of cell movement.

2Pos073 アガロースマイクロチャンバー内でのマクロファージの運動の観察
Observation of Macrophage Migration in Agarose Microchamber

Nami Morizono, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ*)

Macrophage migration is known to be important for immune cell function. However, characteristics of macrophage migration have not been known in detail, especially the differences at single cell and cell cluster. In this study, we observed the migration of individual macrophage placed on an agarose microchamber (AMC) using time-lapse imaging and measured the average movement velocity of macrophages. As a result, inactive and active macrophages migrated at 2.8 μm/min and 0.12 μm/min, respectively. The result of inactive macrophages movement velocity on AMC was similar to already known previous data on glass-bottom dishes. These result offered that AMC could be observed the difference of macrophage migration at single cell and cell cluster with changing the shape of AMC.

2Pos074 *In vitro* reconstitution system for traveling waves of PIP3

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Phosphatidylinositol (PtdIns) signaling system exhibits excitability to self-organize traveling waves of PtdIns 3,4,5-trisphosphate (PIP3)-enriched domain on the cell membrane, providing an anterior-posterior polarity in eukaryotic motile cells such as Dictyostelium discoideum. We have tried to reconstitute the dynamics by purified PtdIns 3-kinase and PtdIns 3-phosphatase, PTEN, in giant unilamellar vesicles (GUVs). By anchoring GUVs to coverslips via an avidin-biotin interaction and making pores on GUVs with α-hemolysin, we succeeded in measuring temporal changes in PIP3 levels in the inner leaflet of GUVs with Pleckstrin homology domain (PHD)-GFP in response to ATP added to the external buffer. We will discuss the dynamics in the presence of both enzymatic reactions.

2Pos075 クラミドモナスの機械反応における TRP11 の役割
Roles of TRP11 in Mechanoresponces in Chlamydomonas

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When a Chlamydomonas cell collides with an obstacle and receives a mechanical stimulus, it temporarily reverses swimming direction. The mechanoreception in this avoiding reaction requires TRP11, a TRP channel that is located in the proximal region of flagella. We investigated the influence of the knockout and overexpression of TRP11 on the ability to perceive gravity, direct stimulation to flagella, and an increase in medium viscosity using TRP11 mutants. The expression level of TRP 11 affected avoiding reaction and gravitaxis, but not the responses to direct stimulation to flagella or an increase in viscosity. The result suggests that TRP 11 is involved in the response to gravity.

2Pos076 ナノポアによる一分子 AND ゲートの構築とリポソームへの搭載
Single molecule AND gate with a biological nanopore integrated into a liposome

Ping Liu, Keisuke Shimizu, Masayuki Ohara, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

This paper describes logic operation system using DNA and biological nanopore which is integrated into a liposome. DNA computing has been applied to biological systems owing to its biocompatibility and programmability. In the conventional DNA computing, the operation is implemented in solution with mixing molecules as the random solution whereas most of the information processing is localized in the living biological system. We have previously reported that DNA operation at artificial cell membrane: AND logic gate using Three-way junction DNA and biological nanopore. In this study, we attempted to integrate DNA logic gate into liposome as a molecular robot, which is a recently emerging biological robot in micron size.

2Pos077 A simple method for single ion channel recordings

Kota Kaneko[1], Huimin Ma[1], Minako Hirano[2], Toru Ide[1] ([1]*Okayama University*, [2]*The Graduate School for the Creation of New Photonics Industries*)

We previously reported that bilayers are formed at a gel surface and ion channel proteins immobilized on the gel can be incorporated into the bilayers. The purpose of our study is to develop this technology to make a method for channel recordings. Methods: A hydrogel bead was fixed at an opening by suction. Bilayers were made by moving the bead through the lipid solution layered on the recording solution to the lipid/water interface. Ion channel proteins immobilized on the bead were incorporated into the bilayer spontaneously. Results: Bilayers were formed on the gel promptly and almost simultaneously channel proteins were incorporated into the bilayer. Using this method, we measured single channel currents of several types of channel proteins such as KcsA and MthK.

2Pos078 イオンチャネルの特性の改変
Modifications of K^+ channel property

Tomoya Ishido[1], Toru Ide[1], Minako Hirano[2] ([1]*Okayama University*, [2]*GPI*)

To modify the property of KcsA channel, we made chimeric mutant channels which consisted of KcsA and OaPAC, photoactivated adenylyl cyclase from *Oscillatoria acuminate*. We investigated their channel activities by measuring growth activities of K^+ transport deficient yeasts transformed with the mutants. The yeasts with a mutant composed of full-length KcsA and a photoreceptor domain of OaPAC, BLUF domain, showed higher growth activity than those with the wild type KcsA. By contrast, yeasts with mutants in which KcsA or the BLUF domain were truncated did not grow well. These results indicate that the interaction between truncated portions of KcsA and the BLUF domain in truncated mutants is important to change the properties of KcsA channel.

2Pos079 ステロールによる膜張力を介した KcsA カリウムチャネル活性の制御
Regulation of the activity of the KcsA potassium channel via bilayer tension-mediated sterol action

Masayuki Iwamoto, Shigetoshi Oiki (*Dept. Mol. Physiol. Biophys., Univ. Fukui Facul. Med. Sci.*)

In this study effects of membrane sterols on the activity of the KcsA potassium channel were evaluated by using the contact bubble bilayer (CBB) method. Various types of membrane sterol were transiently administered into the KcsA-embedded CBB. The activation gate of the channel closed upon administration of all the sterols tested, indicating that the sterol action was non-stereospecific. Subsequently, physical properties of CBB were analyzed in the presence of sterols. We found that the closure of the activation gate correlated well with reduction of the bilayer tension. Our results showed that the KcsA channel changes its activity by sensing the change in bilayer tension induced by the membrane sterols.

2Pos080 ATP 合成阻害時の細胞内ミトコンドリアの膜電位モニタリング
Monitoring of mitochondrial membrane potential upon addition of oligomycin

Emika Shida, Yshihiro Ohta (*Tokyo University of Agriculture and Technology*)

Mitochondrial membrane potential (MMP), an index of the cellular metabolic states, has been extensively monitored. MMP is balanced between proton pumping by respiratory complex and proton influx through FoF1-ATPase. To monitor MMP in cells, MMP sensitive fluorescent dyes, which accumulate in mitochondria in membrane potential-dependent manner, are usually used. When we added the inhibitor of FoF1-ATPase (oligomycin) to intact cells, the increase in the fluorescence signal was observed, indicating the mitochondria were further polarized in cells. However, contrary to expectations, oligomycin increased the fluorescence in intact cell even when we inhibited proton pumping with KCN. We will explain the detailed behavior of MMP upon addition of oligomycin.

2Pos081 多剤輸送担体 EmrE の多剤認識における熱力学
Thermodynamics of multidrug recognition in multidrug transporter, EmrE

Kazumi Shimono[1,2], Keisuke Matsuda[2], Shoko Suzuki[2], Kaho Yajima[2], Sakiyo Yamamoto[2], Seiji Miyauchi[2] ([1]*Fac. Pharm. Sci., Sojo Univ.*, [2]*Fac. Pharm. Sci., Toho Univ.*)

Multidrug transporters recognize a wide range of substrates. The interaction between *Escherichia coli* small multidrug transporter, EmrE, and its substrate is known that depend on environmental pH. We reported previously the pH dependent entropic contribution to substrate binding energy with EmrE, and the pH independent heat capacity. In this study, to elucidate the thermodynamics-based molecular mechanism of multidrug recognition in EmrE, we analyzed an enthalpy-entropy compensation and the release water molecule causing large entropic contribution with substrate binding. These results might suggest that multidrug recognition of EmrE is primarily due to desolvation entropy by release of water molecules from the protein upon binding rather than conformational entropy.

2Pos082 移動性細胞における $PI(3,4,5)P_3$ の非対称分布を安定化する PTEN-$PI(4,5)P_2$ ポジティブフィードバック機構
PTEN-$PI(4,5)P_2$ positive feedback mechanism for stabilizing asymmetric $PI(3,4,5)P_3$ localization in migrating cell

Daisuke Yoshioka[1,3], Hiroyasu Koteishi[3], Daichi Okuno[3], Satomi Matsuoka[3], Toru Ide[4], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*Grad. Sch. of Front. Biosci., Osaka Univ.*, [3]*RIKEN*, [4]*Grad. Sch. of Nat. Sci. and Tech., Okayama Univ.*)

The posterior localization of PTEN, a 3-phosphatase of $PI(3,4,5)P_3$, is the basis of cell polarization in migrating cells, but its mechanism remains unclear. To elucidate the mechanism of the interaction between PTEN and the membrane, we developed a new in vitro single molecule imaging assay system. As a result, it was found that $PI(4,5)P_2$, the enzyme product of PTEN, induces stabilized membrane binding and limited diffusion of PTEN via electrostatic interaction with basic amino acid residues. This result suggests a positive feedback mechanism composed of PTEN and $PI(4,5)P_2$. Furthermore, live-cell imaging revealed that the PTEN-$PI(4,5)P_2$ positive feedback loop stabilize $PI(3,4,5)P_3$ asymmetric distribution and lead to efficient cell migration.

2Pos083 Simulation of Shape Transformation of Vesicle Including Particles

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It is known that the shape of giant vesicle including particles changes to pearl-necklace shape from various shapes when volume fraction of particles is high and excess area of the membrane is rich. To investigate the transformation, we constructed two models. One is rigid spherical shell and particles. The other is closed triangulated lattice and particles (TLP). The energy of repulsion for particles is proportional to distance^{-n}. We performed MC simulations with various conditions of the number of particles N_p and n. Then, we evaluated the distribution and the local diffusion coefficient of particles, and also the stiffness of the membrane for TLP model. For TLP model, we investigated the phase diagram (N_p,n) when external osmotic pressure becomes larger.

2Pos084 機械刺激がゾウリムシの逃走反応を誘導するしくみ
Molecular mechanism of escape response induced by mechanical stimulation in Paramecium

Mutsumi Kawano[1], Ayaka Seto[1], Takashi Tominaga[2], Masaki Ishida[3], **Manabu Hori**[1] ([1]*Fac. Sci, Yamaguchi Univ.*, [2]*Inst Neurosci, Tokushima BUNRI Univ.*, [3]*Sch. Sci. Edu., Nara Univ. Edu.*)

In Paramecium, a mechanical stimulus applied to the posterior part increases permeability to potassium ions and cause hyperpolarization, and they show rapid forward swimming, so-called Escape response. The molecular mechanism of the mechanoreceptor-behavior linkage is not clear, therefore we analyzed the function of Adenylate cyclases (ACs) and Stomatin-like proteins (SLPs) in mechanoreception with RNAi method. The results we obtained in the present study suggested the possibility that SLPs is a mechanoreceptor. Additionally, we obtained results demonstrating that AC1 and AC2 are essential for escape response induced by mechanical stimulation.

2Pos085 三次元空間における真正粘菌変形体の管ネットワーク形成
Tubular network formation in three dimensional space by the true slime mold

Seiji Takagi (*Future University Hakodate*)

Tubular network formation in a three dimensional object by plasmodium of true slime mold was investigated. For example, complete graphs with more than four vertices cannot be embedded in a two dimensional plane, in the case of four it depends on the arrangement of vertices, but they can be embedded in a three dimensional space without edge crossing. If the plasmodium is placed in a three dimensional object, it is expected to form networks that cannot be embedded in a plane. When four food sources were placed at the positions of the regular tetrahedron vertices, two types of network were formed; one is the complete graph and the other is a network having branching points other than the nodes. The networks more than six nodes will be reported.

2Pos086 珪藻および渦鞭毛藻由来の真核生物型 H^+ポンプロドプシンの機能・光化学的解析
Characterization of eukaryotic H^+ pumping rhodopsins from the diatom *Pseudo-nitzschia granii* and dinoflagellate *Oxyrrhis marina*

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Microbial rhodopsins are widely distributed in all three biological domains (i.e., archaea, bacteria and eukarya). Among them, archaeal and bacterial rhodopsins have been studied well. Here, we functionally and spectroscopically characterized two eukaryotic rhodopsins from the diatom *Pseudo-nitzschia granii* and dinoflagellate *Oxyrrhis marina*. The function of the proteins named PngR and OmR was determined by light-induced pH changes of the cells expressing them as a light-driven outward H^+ pump. The purified PngR and OmR showed absorption maxima at 511 and 533 nm, respectively, and possess all-trans retinal predominantly. Together with other spectroscopic analysis, we will discuss the similarities and dissimilarities of archaeal, bacterial and eukaryotic H^+ pumps.

2Pos087 スチレンマレイン酸 (SMA) コポリマーを用いた微生物型ロドプシンの可溶化とその分光学的解析
Solubilization and spectroscopic analysis of microbial rhodopsins in styrene-maleic acid (SMA) copolymers

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Microbial rhodopsins receive attention as a model of membrane proteins because their activities can be easily judged by visible colors. Purified proteins in detergent micelles are used to characterize their properties, but the instability occasionally hampers their spectroscopic analysis. Recently, the styrene-maleic acid (SMA) copolymers have been reported to be a media for solubilization of the membrane proteins. In this study, we employed the SMA for extraction and solubilization of two microbial rhodopsins, a proton pump (RxR) and a light-sensor (*Sr*SRI). The spectroscopy properties of the RxR and *Sr*SRI in the SMA copolymers were compared with those of detergent-solubilized ones. From the results, we will discuss the advantages and disadvantages of this approach.

2Pos088 光駆動ナトリウムポンプ KR2 における Ser70 の役割
Role of Ser70 for transport activity of a light-driven sodium ion pump

Rei Abe-Yoshizumi[1], Aki Nemoto[1], Keiichi Inoue[1,2,3], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*ISSP Univ. of Tokyo*, [3]*JST PRESTO*)

Light-driven outward sodium pump KR2 was found in marine bacteria. KR2 has a conserved NDQ (N112, D116 and Q123) motif and pumps H^+ in KCl solution. For the ion-uptake, the proton acceptor D116 moves and newly forms hydrogen bonds with N112 and S70. We studied the role of Asn112 (Abe-Yoshizumi et al. 2016), but the role of Ser70 is unclear. In this study, we expressed the 19 mutants of S70 in *E. coli* and examined molecular properties of these mutants. We found that the mutations of Ser70 affect color more largely than those of N112. We will discuss the structure and functional roles of Ser70 in the light-driven sodium/proton pumps.

2Pos089 光駆動 SO_4^{2-}輸送体（SyHR）のアニオン輸送と選択性への塩基性アミノ酸残基の役割
Role of basic amino acid residues on the anion transport and its selectivity in a light-driven SO_4^{2-} transporter SyHR

Masaki Nakama[1], Keiichi Kojima[1,2], Marie Kurihara[2], Susumu Yoshizawa[3], Yuki Sudo[1,2] ([1]*Fac. of Pharm. Sci. Okayama Univ*, [2]*Grad. Sch. of Med. Dent. & Pharm. Sci. Okayama Univ*, [3]*AORI, UTokyo*)

Most microbial rhodopsins act as ion transporters using solar energy. So far, the substrate ions identified have been confined to monovalent ions. Recently, we have demonstrated a novel rhodopsin named SyHR as a light-driven polyatomic divalent anion (SO_4^{2-}) transporter [JACS, 2017, 139, 4376]. To investigate anion transport mechanism in SyHR, we performed here alanine-scanning mutagenesis of 12 basic amino acid residues. Among the mutants, Cl^- and SO_4^{2-} transport activities showed a wide variety (0.36 - 2.4 and 0.07 - 1.7, respectively : Wild-type as 1). Of note, R71A decreased SO_4^{2-} transport activity by 93%, suggesting change of the ion selectivity. Based on the results, we will discuss the mechanism both in the anion transport and its selectivity in SyHR.

2Pos090 出芽酵母を用いたアニオンチャネルロドプシンの発現と分光学的解析
Expression and spectroscopic analysis of anion channelrhodopsins using a eukaryotic yeast, *Saccaromyces cerevisiae*

Ryota Ono[1], Taro Yamanashi[2], Keiichi Kojima[1,2], Hisao Moriya[3], Yuki Sudo[1,2] ([1]*Div. of Pharm. Sci., Okayama Univ.*, [2]*Grad. Sch. of Med., Dent. & Pharm. Sci., Okayama Univ.*, [3]*Res. Core for Interdiscip. Sci., Okayama Univ.*)

Microbial rhodopsins are photoreceptive membrane proteins for light-dependent biological functions. They have been mainly investigated using prokaryotic organisms as hosts (e.g., *E.coli*). Although a large number of novel rhodopsin genes have been identified, difficulty of recombinant protein expression hampers the functional and photochemical characterization of the rhodopsins. As an alternative choice for the protein expression, we constructed here expression system of anion channelrhodopsins in a eukaryotic yeast, *Saccaromyces cerevisiae*. Cultured cells harboring the rhodopsin genes showed visible colors, indicating their successful expression. With the results of spectroscopic analysis, we discuss potentials of this system for microbial rhodopsins.

2Pos091 海洋性真核藻類 *Guillardia theta* における 44 種類の微生物型ロドプシン様タンパク質の遺伝子発現解析
Gene expression analysis of 44 microbial rhodopsin-like proteins from marine algae *Guillardia theta*

Yumeka Yamauchi[1], Masae Konno[1,2], Keiichi Inoue[1,3,4], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*PRESTO, JST*)

Microbial rhodopsins are light-sensitive proteins working as light-driven ion transporters, light sensors or light-activated enzymes. *Guillardia theta* (*G. theta*) has 44 microbial rhodopsin-like genes on their genome. Some of their molecular functions were revealed by *in vitro* studies, but their physiological roles remain unknown. Here we investigated expression of the rhodopsin-like genes in native *G. theta* cells. We found 29 genes being expressed, and the gene expression patterns in native cell were analyzed in different light conditions and various nutrient conditions. The expressions of 6 genes were induced but those of the other 6 genes were reduced under nitrogen depletion. We will discuss physiological roles of the rhodopsin-like proteins in *G. theta*.

2Pos092 円石藻ウイルス由来のヘリオロドプシンの分子物性解析
Molecular characterization of heliorhodopsin from Emiliania huxleyi virus

Ritsu Mizutori[1], Masae Konno[1,2], Keiichi Inoue[1,2,3,4], Oded Beja[5], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*PRESTO, JST*, [5]*Technion-Israel Inst. Tech.*)

Recently, we identified a new group of rhodopsins by functional metagenomic analysis. Interestingly, their sequence identities are considerably low (less than 15 %) to both of microbial and animal rhodopsins suggesting they form a distinctively new family. These rhodopsins were named “heliorhodopsin (HeR)”. In this study, we investigated HeRs that are derived from viruses that infect Emiliania huxleyi (EhV). To understand the molecular property of HeR from EhVs, we attempted to express five HeRs from EhVs in yeast, and purified the proteins. Then, we performed laser-flash photolysis, HPLC analysis and so on to reveal the photocycle and molecular properties of them. We will discuss the difference and similarity between EhVs HeRs and other HeRs in the presentation.

2Pos093 Mutational analysis of amino acid residues surrounding the electron-transferring terminal Trp of plant (6-4) photolyase

Yuhei Hosokawa[1], Ryuma Sato[2], Shigenori Iwai[1], Junpei Yamamoto[1] ([1]*Grad. Sch. Eng. Sci., Univ. Osaka*, [2]*Riken*)

(6-4) photolyases ((6-4)PLs) are flavoproteins that can repair the ultraviolet-induced (6-4) photoproduct in DNA using blue light. To achieve the repair, their flavin adenine dinucleotide (FAD) cofactors need to be reduced to an $FADH^-$ form through a Trp chain in a light-dependent manner, called photoreduction. Previously, we showed that animal (6-4)PLs have four Trps involving photoreduction, and the fourth Trp is important to stabilize the radical pair generated during the photoreduction. Although plant (6-4)PLs have only three Trps, they successfully perform photoreduction. In this study, we investigated the circumstance of the terminal Trp in plant (6-4)PL by using the bacterial survival assay. The stabilization mechanism of the radical pair will be discussed.

2Pos094 Analysis of binding of light-harvesting secondary chromophore to animal and plant (6-4) photolyase

Ayaka Morimoto, Kumar Rajiv, Yuhei Hosokawa, Yuma Terai, Shigenori Iwai, Junpei Yamamoto (*Grad. Sch. Eng., Univ. Osaka*)

(6-4) photolyases ((6-4)PLs) are flavoproteins able to repair the (6-4) photoproduct in a light-dependent manner, by using a reduced from of flavin adenine dinucleotide (FADH-) as a catalytic center, which absorbs

2Pos095 過渡回折格子法を用いた orange carotenoid protein の光反応ダイナミクスの研究
Study on photoreaction dynamics of orange carotenoid protein using transient grating method

Takatoshi Ohata, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

Orange carotenoid protein (OCP) is a blue-green light sensor in cyanobacteria, and has a biological function relating with the photoprotection. OCP contains a carotenoid molecule as a chromophore and the active form is characterized by the red shift of the absorption spectrum. The signaling mechanism, however, has not been clear, because the reaction dynamics has not been clarified yet due to its very low quantum yield. In this study, we investigated the reaction of OCP using the transient grating method and found a light induced dimerization reaction besides the photochemistry of the chromophore. Interestingly, it was found that the dimerization occurs not only between holo-proteins but also between holo- and apo-protein.

2Pos096 ビリベルジン結合型シアノバクテリオクロムの遠赤／橙色光変換過程での構造変化の検出
Detection of structural change during far-red/orange reversible photoconversion of biliverdin-binding cyanobacteriaochrome

Yuka Takeda, Keiji Fushimi, Rei Narikawa (*Grad. Sch. Integrated Science and Technology, Univ. Shizuoka*)

Cyanobacteriochromes (CBCRs) are linear tetrapyrrole-binding photoreceptors to sense wide spectral range from ultraviolet to far-red. Recently, we have discovered biliverdin (BV) -binding cyanobacteriochromes showing far-red/orange reversible photoconversion. Because BV is an intrinsic chromophore in mammalian cells and absorbs far-red light that deeply penetrates into mammalian tissues, BV-based tools should be advantageous for optogenetic control of mammalian cells. In this study, we analyzed the BV-binding CBCR with various native-PAGEs and detected photo-reversible structural change. Further, site-directed mutagenesis based on structural information resulted in modifying the structural change. We are now trying to develop optogenetic tools based on these findings.

2Pos097 Application of electron spin polarization imaging method to obtain geometries of photoinduced charge-separated states in cryptochrome

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Cryptochrome has been thought to play an important role on sensing geomagnetism in some animals and insects. The light excitation of flavin adenine dinucleotide (FAD) as a pigment in this protein leads to sequential charge-separation processes though a series of tryptophan residues, resulting in a long distance charge-separated (CS) state. It is however required that the electrostatic stabilization in the primary charge-separated states needs to be overcome for the generations of the distant charge-separated states, whose mechanism is unknown in cryptochrome. In this study, we have utilized an electron spin polarization imaging method to characterize the geometries of the charge-separated states of FAD-W324(H)+ in Xenopus laevis cryptochrome.

2Pos098 Rc-PYP(K72Q)を用いた複合体形成過程の解析
Elucidation of the complex formation process using Rc-PYP mutant K72Q

Natsuki Oka, Yoichi Yamazaki, Yugo Hayashi, Hironari Kamikubo (*Nara Institute of Science and Technology*)

Rhodobacter capsulatus PYP (Rc-PYP) is a light receptor protein which binds to PYP binding protein (PBP) in a light-dependent manner. Our previous titration SAXS experiments revealed that Rc-PYP and PBP exhibit various oligomeric forms, and also implied that PYP has two distinct binding sites against PBP which have not been identified. We would like to show K72 is one of the candidates for the binding sites here. The UV-Vis spectrum of K72Q is almost identical to that of wild-type at the dark state, while under continuous irradiation, the amount of the light state was decreased by the mutation. Furthermore, the mutant partially lost its binding ability to PBP. These results suggest the K72 influences only the light state and would be involved in the binding site.

2Pos099 膜脂質環境が G タンパク質トランスデューシンの活性化効率に及ぼす影響
The effect of lipid environment of outer segment membranes on the activation of photoreceptor specific G protein, Transducin

Kyoko Kadomatsu[1], Keiji Seno[2], Yuki Ito[1], Satoru Kawamura[1], Shuji Tachibanaki[1] ([1]*Grad. Sch. of Frontier Biosci., Osaka Univ.*, [2]*Department of Biology, Faculty of Medicine, Hamamatsu University School of Medicine*)

Vertebrates have two types of visual photoreceptor cells, rods and cones. Both cells have a cellular region, called outer segment (OS), responsible for generation of photoresponses. The mechanism is homologous and mediated via trimeric G protein, Transducin (Tr). It is known that the efficiency of the reaction driven by a visual pigment is 5 times higher in rods than in cones. However, the molecular basis of the differences is not known yet. In this study, we focused on the lipid composition of the OS membranes, which would affect the efficiency of the reaction. It is found that the molar ratio of cholesterol is 10 times lower in rod OS membranes than in cone OS. Here, we will discuss whether this difference in cholesterol ratio affects Tr activation efficiency or not.

2Pos100 色覚視物質の結晶構造解析に向けたユニークな戦略
Unique approaches towards cone opsin crystallization

Kota Katayama, Hideki Kandori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

Color vision is achieved by three cone pigments, blue, green, and red. Each cone pigment consists of a different opsin protein bound to a common chromophore, 11-cis-retinal; differential chromophore-protein interactions allow preferential absorption at a selected range of wavelengths. Structural determination of cone pigments is needed for a precise understanding of spectral tuning. The principle obstacle to solving the structures is their innate instability in detergent micelles. Here, we demonstrate successful optimization for the expression, purification, and stabilization of chicken green cone pigment (cG) for further structural determinations. FTIR spectroscopic analysis also provides an evidence that recombinant cG still maintains its function as light absorbing.

2Pos101 フーリエ変換赤外分光法によるロドプシンと錐体視物質の発色団／蛋白質相互作用の比較
Comparison of chromophore/protein interaction between rhodopsin and cone pigment using Fourier transform infrared spectroscopy

Naoto Noguchi[1], Takahiro Yamashita[1], Yoshinori Shichida[2], Yasushi Imamoto[1] ([1]*Kyoto University*, [2]*Ritsumeikan University*)

Rod pigment rhodopsin and cone pigments work in dim and daylight conditions, respectively. In accordance with the difference in functions, rhodopsin shows low thermal isomerization rate, which is relevant to the low dark noise of rod cells. In the difference Fourier transform infrared (FTIR) spectra between batho and rhodopsin, characteristic OH stretching mode of Thr118 is observed. This band was substantially affected in E122Q/I189P mutant of rhodopsin, which shows cone-like high thermal isomerization rate, suggesting that the altered chromophore/protein interaction regulates the thermal isomerization. Based on the difference FTIR spectra of mutants, the difference in the chromophore/protein interactions between rhodopsin and cone pigments will be discussed.

2Pos102 網膜桿体細胞内円盤膜上の脂質-光受容タンパク質の秩序形成の数理モデル
A mathematical model of pattern formation of lipid-photoreceptor proteins on disk membranes of retinal cells

Yukito Kaneshige[1], Akinori Awazu[1], Hiraku Nishimori[1], Humio Hayashi[3], Kenichi Morigaki[2], Taishi Tanimoto[2] ([1]*Grad. Sci. Univ. Hiroshima*, [2]*Grad. Agri. Univ. Kobe*, [3]*Grad. Sci. Univ. Kobe*)

Phototransduction of vertebrate starts from the disk membrane in outer segment of rod cells in the retina. Disk membrane consists of raft lipid, non-raft lipid (NR), and rhodopsin (Rh) with 8 helices. Recent live imaging studies reported the clusters of aligned Rh are formed around the center of disk membrane and NR tends to localize on the outside. Although these studies suggested the importance of the interaction among Rh and lipids on disk membrane, the mechanism of such pattern formation is still unclear. In this study, we constructed a mathematical model to clarify the mechanism of aligned Rh clusters formation in disk membrane. We found Rh can form and maintain the straight aligned structure if only 8-th helix of Rh contains the affinity with raft.

2Pos103 バクテリオロドプシンにおける１段階目のプロトン移動を対象とした大規模量子分子動力学シミュレーション
Large-scale quantum-mechanical molecular dynamics simulations for the primary proton transfer in bacteriorhodopsin

Junichi Ono[1], Minori Imai[2], Yoshifumi Nishimura[1], Hiromi Nakai[1,2,3] ([1]*RISE, Waseda Univ.*, [2]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [3]*ESICB, Kyoto Univ.*)

The large-scale quantum-mechanical molecular dynamics simulations based on the divide-and-conquer density-functional tight-binding (DC-DFTB) method were performed to clarify the microscopic mechanism of the primary proton transfer in the L state of bacteriorhodopsin. From the recent snapshots of the L state obtained from time-resolved serial femtosecond crystallography, it is found that the deprotonation of the specific internal water (W452) results in the protonation of Asp85 via Thr89, followed by the reprotonation of the resulting hydroxide ion from the retinal Schiff base. This proton transfer process is found to be triggered by the strong hydrogen bond between W452 and Thr89, which is assisted by two different internal water molecules in the active site.

2Pos104 大規模励起状態計算手法の開発と光活性イエロータンパク質に対する応用研究
Development of large-scale excited-state calculation method and applied research on photoactive yellow protein

Nana Komoto[1], Takeshi Yoshikawa[1], Junichi Ono[2], Hiromi Nakai[1,2,3] ([1]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [2]*RISE, Waseda Univ.*, [3]*ESICB, Kyoto Univ.*)

In order to perform quantum molecular dynamics for large systems, divide-and-conquer based density functional tight-binding molecular dynamics (DC-DFTB-MD) method has been developed. DC-DFTB-MD method has been demonstrated for proton diffusion, mechanisms for CO2 absorption, and proton transfer in bacteriorhodopsin. In this study, the extension of DC-DFTB method to excited-state theory based on time-dependent (TD) formalism, as denoted by DC-TDDFTB-MD, has been examined to treat excited-state dynamics of large systems. Illustrative applications of proposed method have been performed for the potential energy of hydrogen bonding between Glu46 and p-coumaric acid (pCA) in photoactive yellow protein (PYP) in the ground and excited states.

2Pos105 ポリリジン残基の付加は、DNA オリガミへの SNAPf 融合蛋白質の結合速度を向上させる
Poly-lysine tag increase the binding rate of SNAPf-fused protein to DNA origami

Kodai Fukumoto[1], Yuya Miyazono[2], Hisashi Tadakuma[1], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

Cargo transport is central to the cellular phenomena, where multiple motors orchestrate their function. To elucidate the coordination mechanism, construction of protein integrated complex is useful. We have made transport complex, where kinesin motors were integrated onto DNA origami through covalent bond between tag-protein and its ligand (e.g. SNAP-system). However, the binding rate of the tag-protein fused kinesin onto the DNA origami is slow, which might be attribute to the negative charge of the DNA scaffold. Here, we added positively charged Lys-tag to C-terminal of kinesin-SNAPf protein. We observed the increase of binding rate of Lys-tagged protein onto the DNA origami, suggesting the usefulness of the Lys-tag for protein integration and transporter formation.

2Pos106 希少糖生産に関わる単糖間異性化反応の熱力学的研究
Thermodynamic investigation on the isomerization of monosaccharides for rare sugar production

Akihide Yoshihara, Mitsuki Murakami, Ryoko Iwata, Taro Kozakai, Kimi Fujiwara, **Kazuhiro Fukada** (*Fac. Agric., Kagawa Univ.*)

Rare sugars are the group of monosaccharides rarely exist in nature. Recent biotechnological advances have increased possibility of large scale production of rare sugars via enzymatic reactions. In this study, equilibrium constants for the isomerization between aldohexose and ketohexose were measured to estimate thermodynamic parameters concerning conversion of monosaccharides to give rare sugars. The reaction Gibbs free energy, enthalpy, entropy, and heat capacity difference between the reactants and the products were obtained for the enzymatic isomerization between psicose-allose, psicose-altrose, tagatose-galactose, tagatose-talose, and sorbose-gulose. Based on these thermodynamic parameters, efficient conditions for rare sugar production will be discussed.

2Pos107 試料環境による eGFP の電子誘起変換の依存性
The environmental dependence of the "electron-induced" conversion of eGFP

Koki Matsui, Keiichirou Akiba, Hiroki Minoda (*TUAT*)

Green Fluorescent Protein (GFP) has been used as an in-vivo fluorescent marker for the fluorescent microscopy. The electron irradiation damage on the GFP during electron microscope observation has been evaluated by measuring the fluorescence intensity. Contrary to the reports which showed degradation of proteins by electron irradiation, fluorescence intensity from the GFP increased with glycerol but it decreases without glycerol. And also, the fluorescence peak wavelength shifted from green to red. Since this suggests the importance of ambient environment of proteins, we studied environmental dependence of the electron-induced conversion of the GFP by observing the fluorescent intensity during electron irradiation under several environments.

2Pos108 A model for analyzing phenomena in multicellular organisms with multivariable polynomials: Polynomial-life model

Hiroshi Yoshida (*Grad. Schools of Math. & Systems Life Sci. Kyushu Univ.*)

Most of life maintains itself through turnover, namely cell proliferation, movement, and elimination. Inspired by such a biological fact, and together with various operations of polynomials, I here propose polynomial-life model towards analysis of some phenomena in multicellular organisms. Polynomial-life is multicells that are expressed as multivariable-polynomials. A cell is expressed as a term of polynomial, in which point (m,n) is described as a term x^my^n and the condition is as its coefficient. Starting with a single term and following reductions by set of polynomials, In this framework I present various patterns through the polynomial-life model and discuss patterns maintained through turnover.

2Pos109 The ancient gods of the modern cytoskeleton

Caner Akil[1,2], Robert C. Robinson[1,2,3] ([1]*Institute of Molecular and Cell Biology, A*STAR (Agency for Science, Technology and Research)*, [2]*Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore*, [3]*Research Institute for Interdisciplinary Science, Okayama University*)

The origin of the eukaryotic cell is unresolved. The recently discovered archaeal superphylum “Asgard” remains the closest kin with eukaryotes according to phylogenetic analysis (Spang *et al.*, 2015, Zaremba *et al.*, 2017). Further, the metagenomics sequencing explicated the hypothesis that the source cell arose from the symbiotic relationship between an archean and an alphaproteobacterium (the future mitochondrion) through the identification of several potential eukaryotic gene homologs in the archaeal superphylum. However, many of these eukaryotic like sequences are highly divergent and the organisms have yet to be imaged or cultivated, bringing in to question whether these archaea exhibit eukaryotic characteristics. Our hypothesis is that the determination of the atomic structures and biochemical properties of Asgard eukaryotic-like hypothetical proteins will enhance our understanding of the origin of eukaryotes

2Pos110 Structural characterization of ALP37, a potential chromosome segregating ParM

Samson Ali[1,2], N Akihiro[3], D Popp[1], Robert C. Robinson[1,2,4] ([1]*Institute of Molecular and Cell Biology*, [2]*National University of Singapore, NUS, Yong Loo Lin School of Medicine*, [3]*Nagoya University Graduate School of Science, Structural Biology Research Center and Division of Biological Sciences*, [4]*Research Institute for Interdisciplinary Science (RIIS), Okayama University*)

The mechanism of bacterial chromosome segregation has been subject of speculation and investigation for years. Over 65% of all sequenced bacterial genomes contain a chromosomally encoded partitioning (*par*) locus with the exception of *E. coli* and its close relatives. Only the Par ABS system has been shown to segregate chromosomes of *B. subtilis* and *Caulobacter crescentus*. Other types of active plasmid partitioning systems especially ParCMR system may be involved in this function. ALP37 showed to polymerize with different nucleotides including ATP. A 4 Å resolution map of the ParM filament showed it has a short pitch and highly twisted. Its features may be implicated in providing enough force to segregate chromosomal DNA. Thus ALP37 could be a potential chromosome segregating ParM.

2Pos201 アクトミオシンの運動を利用した抗原抗体反応の促進
Acceleration of antigen-antibody reaction by actomyosin motility

Shohta Takamori[1], Kaito Kobayashi[1], Takashi Ishiguro[2], Hajime Honda[1] ([1]*Nagaoka Univ. Tech.*, [2]*Taiyo Yuden Co., Ltd.*)

The function of actomyosin complex has been utilized for actuating macroscopic structures or concentrating some target molecules. We have been coming up an analysis kit for the molecules of various biomarkers by combining the antibody for the biomarker with the movement of actin filament attached to it. For conjugating antibody molecules with an actin filament, we have developed a standard procedure using a specific complex, MAC (Multiple-antibody Adapting Complex). This complex enabled the specific and stable binding of antibody-filament carriers. We have recently found that the concentration speed of MAC-actin system was much faster than that of simple diffusion system in conventional ELISA methods.

2Pos202 水晶振動子微量天秤によるアクチン繊維とミオシンの見かけの質量変化
QCM revealed the changes of apparent mass of actin filaments and myosin molecules

Kaho Yokomuro[1], Shota Takamori[1], Kazuya Soda[1], Takashi Ishiguro[2], Hajime Honda[1] ([1]*Nagaoka Univ. Tech.*, [2]*Taiyo Yuden Co., Ltd.*)

Quartz Crystal Microbalance method (QCM) can detect the change of mass on the metal-surface at the level of nano-gram order even in aqueous solution. We have combined this methods to fluorescence microscope, QCM-microscope, to quantify the mass-change of actomyosin complexes when emerging their sliding movement. Surprisingly, the apparent mass of actin filaments was measured about 200 times larger than that estimated by direct fluorescence microscopy. Even more surprisingly, this large apparent mass decreased sharply on the addition of Mg-ATP. At the same time, actin filaments were confirmed to be moving over the QCM metal surface under fluorescence microscopy. This unusual phenomena might be explained by changes of viscoelasticity of water molecules.

2Pos203 Single-molecule fluorescence imaging analysis of Serratia marcescens ChitinaseA (SmChiA) Trp-active mutant

Akasit Visootsat[1,2], Paul Vignon[3], Akihiko Nakamura[1,2], Ryota Iino[1,2] ([1]*SOKENDAI*, [2]*Institute for Molecular Science*, [3]*ParisTECH*)

Chitinases are crucial enzymes that are used for hydrolysis of chitin both in nature and industry. In the previous study, turnover rate of Serratia marcescens chitinaseA (SmChiA) increased by introducing two tryptophan mutations in the cleavage cleft (F232W and F396W). However, its molecular mechanism is still unknown. In this study, we aim to investigate kinetic properties of the F232W/F396W mutant by using single-molecule fluorescence imaging. We found that the binding and dissociation rate constant were almost similar between the wild-type and the mutant, suggesting that the mutations affect the chitin binding surface of SmChiA but the motility. In this poster we will show the results of detailed analysis and discuss the mechanism.

2Pos204 DNA ナノチューブに沿って移動する生体分子モーターの設計
Engineering motor proteins to move along DNA nanotubes

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Among several kinetic models of biomolecular motors, the Brownian ratchet models have recently been the focus of interest, especially for kinesin and dynein. However, the asymmetric nature of motor-filament interface, which might be the key of these models, cannot be rationally re-designed, making it difficult to test these models. We overcame this limitation by combining dynein and DNA-binding proteins to create novel motors that move along synthetic DNA nanotubes. Furthermore, taking advantages of programmable DNA nanostructures, we successfully reversed the direction of movement by reversing the direction of binding sites for novel motors on the DNA nanotubes. Our strategy opens the way to systematic studies on the mechanisms of motors.

2Pos205 高速 AFM を用いた DNA terminase の構造と動態の研究
Study of structure and dynamics of DNA terminase using high-speed AFM

Hirotaka Ariyama, Toshio Ando (*WPI-NanoLSI, Kanazawa Univ.*)

During large dsDNA virus assembly, DNA is translocated into a preformed prohead by the complex formed by a motor and connector, which is located at a specific prohead vertex. The motor, called terminase, converts ATP hydrolysis into mechanical movement of DNA and the connector supports the structure of the terminase. The terminase is composed by two proteins; the small protein recognizes DNA, whereas the large protein provides chemical energy for translocation using ATP. Gp19 is the large protein of T7 phage. It is expected to rotate, when DNA translocates. We studied gp19 with high-speed AFM (HS-AFM) which can visualize conformational change at submolecular spatial and sub-100 ms time resolution. We observed ring-shaped gp19 and its conformational change by ATP.

2Pos206 プロセッシブダイニンモータードメインのマイクロ秒時間分解能、ナノメーター位置決定精度１粒子トラッキング
Single-particle tracking of motor domain of a processive dynein at microsecond time resolution and nanometer localization precision

Jun Ando[1,2], Tomohiro Shima[3], Akihiko Nakamura[1,2], Akasit Visootsat[1,2], Mayuko Yamamoto[1], Takahide Kon[4], Ryota Iino[1,2] ([1]*IMS, NINS*, [2]*SOKENDAI*, [3]*Univ. Tokyo*, [4]*Osaka Univ.*)

Dynein is an ATP-driven dimeric molecular motor which moves along microtubule (MT). To follow fast dynamics of dynein by using gold nanoparticle (AuNP), we constructed annular illumination total internal reflection dark-field microscopy with axicon lens. At 33 μs time resolution with 30-nm AuNP, localization precision of 1.7 nm was achieved. We used a chimeric molecule which has motor domains from Dictyostelium discoideum cytoplasmic dynein and stalkheads from human axonemal dynein. One of two motor domains in the dimer was labeled with AuNP and movement was observed at 1 mM [ATP]. As results, 8-nm forward/backward steps and side steps were observed without clear unbound states along the MT long and short axes respectively, suggesting the uncoordinated inchworm motion.

2Pos207 中間鎖点変異による外腕ダイニンモーター活性の低下
A point mutation in intermediate chain gene reduces motor activity of outer-arm dynein

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Ciliary outer-arm dynein (OAD) is a large complex composed of heavy chains, intermediate chains (ICs) and light chains. ICs are thought to anchor OAD to MT. We recently identified a novel Chlamydomonas mutant (oda6 (E279K)) with a point mutation in the IC2 gene, which retains the normal amount of OAD but swims at ~60% velocity of wild type (WT). To understand how the mutation affects the OAD function, we examined ATP-induced MT sliding in protease-treated axonemes. In oda6 (E279K), the number of axonemes undergoing sliding in the presence of ATP was reduced to ~20% of the number in WT. However, it increased to the WT level under the conditions that apparently enhance dynein activities (e.g., in ATP plus ADP). It is likely that IC2 also regulates the activity of OAD.

2Pos208 単一軸糸ダイニンを欠失した新規クラミドモナス変異株９種の単離と解析
Identification of nine kinds of Chlamydomonas mutants missing single axonemal dynein heavy chains

Tomohiro Komatsu, Yusuke Kondo, Natsuki Tanaka, Kohei Fujimoto, Kazuhiro Takeshima (*Dept. Life Sci., Pref. Univ. of Hiroshima*)

Axonemal dyneins are composed of multiple subunits, of which the most important are dynein heavy chains (DHCs). Chlamydomonas axoneme has 15 different DHCs. Each DHC is thought to perform a unique role in axoneme beating. To understand the in vivo roles, isolation and characterization of mutants lacking single DHCs is important. 6 mutants lacking single different DHCs had been identified. In this study, we isolated 9 mutants lacking single remaining DHCs. Motility analysis showed that 3 mutants were slower than wild type (WT), but 6 mutants displayed WT-like motility. Further studies at various viscosities showed that 4 of 6 mutants were slower than WT especially at high viscosities, suggesting that the DHCs contribute to axoneme motility at high viscosity.

2Pos209 X 線繊維回折法で明らかにするクラミドモナス鞭毛軸糸構成要素の Ca2+濃度依存的らせん対称性の変化
Ca^{2+} dependent changes in helical symmetry of axonemal components of *Chlamydomonas* flagella studied by X-ray fiber diffraction

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The mechanism of waveform changes coupled with intracellular Ca^{2+} concentrations found in *Chlamydomonas* flagella has remained a long-standing unresolved issue. We investigate this mechanism using continuous shear-flow for alignment of flagellar axonemes and X-ray fiber diffraction in the synchrotron radiation facility SPring-8, BL40XU. We explored the spatial arrangement and dynamics of axonemal components under various concentrations of Ca^{2+}. In the high Ca^{2+} concentrations (pCa 4), 24-nm layer lines reduced their intensities and the meridian reflection increased its intensity, suggesting changes in helical nature of nine doublet microtubules in the axoneme.

2Pos210 Behavior of polymerized microtubules interacted with dyneins still attached on a doublet microtubule detected by laser tweezers

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Cyclical beating of eukaryotic flagella is caused by orchestrated activity of dyneins to produce sliding among nine doublet microtubules (DMT). It has been reported that skeletal myosin molecules work with coordination under load (Kaya et al., 2017). To study whether similar coordination is involved in the regulation of dyneins on a DMT, behavior of polymerized microtubules interacted with dyneins was examined by laser tweezers. Individual DMTs with dyneins were obtained by disintegration of protease-treated axonemes. Microtubules interacted with dyneins at 0.02-1 mM ATP sometimes changed the direction of movement. For more precise analysis, the displacement and force measurement of the microtubule is carried out under the photolysis of 1 mM caged ATP.

2Pos211 細胞質ダイニンの二足歩行メカニズムに関するマルコフ状態モデリング
Bi-pedal motions of cytoplasmic dynein via Markov state modeling

Shintaroh Kubo, Shoji Takada (*Takada Lab., Grad. Sch. of Sci., Kyoto Univ.*)

Cytoplasmic dynein consists of two motor-domains, each of which hydrolyzes ATP, and the tail region that connects the two motor-domains. For non-diffusive and uni-directional motions, how two motor-domains communicate each other is of crucial importance. However, the mechanism of interaction between them is largely unknown. In this research, we make a theoretical model of dynein and simulate it by using a Monte-Carlo method. In our model, each motor domain has four discrete states corresponding to the nucleotide state (Apo/ATP) and the binding state to microtubule. To model interactions between two motor-domains, we introduce several coupling parameters. As a result, we could estimate what kind of effect of the tail region is expected for dynein's motion.

2Pos212 高速原子間力顕微鏡により観察されたクラミドモナス軸糸ダイニンの調整機構
High-speed atomic force microscopic observations on demembranated Chlamydomonas axonemes and dynein arms

Kenta Ishibashi[1,2], Kazuhiro Oiwa[2,3] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ*, [2]*Advanced ICT Inst., NICT*, [3]*Grad. Sch. Sci., Univ. Hyogo*)

In a Chlamydomonas axoneme, precisely-aligned dynein arms on the outer-doublet microtubules are regulated in a coordinated fashion to produce periodic flagellar beating. To understand the coordination, we have performed imaging of demembranated flagellar axonemes and dynein arms under an aqueous environment using a high-speed atomic force microscope. AFM images clearly highlighted details of demembranated axonemes and difference between wild-type and the outer-dynein arm-less mutant oda1 axonemes. The structual repeat of 24nm of outer dynein arms was confirmed in the phase images which provide information about surface stiffness variations. The high-speed AFM images thus defined detailed positions of axonemal components and will provide the dynamics of these components.

2Pos213 Step sizes and rate constants of single-headed cytoplasmic dynein

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Cytoplasmic dynein is a motor protein moving along microtubules by utilizing free energy of ATP hydrolysis. From single-molecular assay, we measured and analyzed the displacement and microtubule-binding time of monomeric dynein. 8.3-nm displacement was generated by the power stroke. The transition rate via the power stroke and product release was 12 /s. To evaluate that the calculated rates are reasonable, we examined the microtubule-binding time of dimeric dynein. The dissociation rate of dimeric dynein was comparable to double of the turnover rate of monomeric dynein. We proposed the walking model of dimeric dynein with the step size of 8-nm to address the contribution of the power stroke.

2Pos214 DNA-templated assembly of axonemal outer arm dynein complexes in vitro

Yuka Matsuda[1], Akane Furuta[2], Hiroaki Kojima[2], Kazuhiro Oiwa[1,2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ Hyogo*, [2]*Adv ICT Res Ins, NICT*)

The beating of cilia and flagella is spontaneously generated by cooperative operation of many axonemal dynein motors aligned along the axoneme. How such beating waveform is generated has been extensively studied; however, the axonemes are composed of hundreds of different components, making it difficult to address the key question. Here we set out to build a simplified model system that can beat in vitro. To do this, we introduced a his-tag and a SNAP-tag to the outer arm dynein of Chlamydomonas reinhardtii and purified them on a Ni-IMAC resin. We show that the purified dynein molecules were successfully aligned along a DNA nanotube. The force response of axonemal dynein upon changing the number, spacing, and geometric arrangement of dynein molecules are being measured.

2Pos215 クライオ電子顕微鏡画像解析により明らかになった細胞質ダイニンの新たな歩行パターン
Cryo-EM observation of stepping patterns of cytoplasmic dynein on microtubules with new freezing conditions

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Dynein is a gigantic protein complex that drives intracellular transport by stepping along microtubules (MTs) using ATP as an energy source. In this study, we used cryo-electron microscopy to reveal the structure of dynein molecules stepping along MTs. We purified Dictyostelium GST-dimerized dynein molecules and observed their stepping behaviour on MTs in the presence of a physiological ATP concentration after freezing them in new conditions. The micrographs were analysed with an automated MT-polarity determination procedure that we have newly developed for this study, and drastically accelerates the image processing. Intriguingly, we have observed new distributions of dynein AAA+ rings along MTs, which let us to propose a novel model of dynein stepping sequences.

2Pos216 細胞質ダイニンが運動活性を示す蛍光 ATP の合成
Synthesis of fluorescent ATP to elucidate coordination of multiple ATPase sites in cytoplasmic dynein

Karibu Sakai, Tomotaka Komori, Tomohiro Shima, Sotaro Uemura (*Dep. of Bio. Sci., Grad. Sch. of Sci., The Univ. of Tokyo*)

Cytoplasmic dynein drives retrograde intracellular transport using the energy from ATP hydrolysis. A unique feature of dynein among cytoskeletal motor proteins is its 4 ATPase sites in each motor domain. Coordination and regulation between the ATPase sites have been proposed, yet details of the coordination remain poorly understood. To visualize ATP binding on each ATPase site, we synthesized a fluorescently labeled ATP that retains the ability to drive dynein motility. Based on the data using this fluorescent ATP, we will discuss the ATP binding process.

2Pos217 粘弾性溶液中におけるキネシンによる微小管の運動についての研究
Investigation of motility of microtubules driven by kinesins in viscoelastic media

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Microtubules (MTs) with kinesin motor-proteins perform diverse works in a highly viscoelastic media. However, only few experiments related to motility of MTs in viscoelastic condition has been reported. In this work, we have investigated the motility of MTs by changing kinesin concentrations, in presence of a crowding agent; methyl-cellulose. We observed a back and forth motility of MTs in viscoelastic solution, especially at low kinesin density. Our analysis suggests that such bi-directional motility of MTs comprised of two systems, active transport by kinesin and diffusion of MT. In future, to investigate specifically how the number of motors affects MTs motility in viscous solution, we will employ Au-nano pillars to selectively immobilize kinesins.

2Pos218 糸状菌キネシンへの１残基置換が低温適性をもたらす代わりに熱安定性を損なう
Single amino acid substitution for the fungal kinesin offers possible cold-adaptation but impairs thermal stability

Youske Shimizu, Toru Togawa, Shigeru Chaen (*Dept. Biosciences, Nihon Univ.*)

Two motor domains of kinesin-1 members, AnKinA from Aspergillus nidulans (growing optimally at 37C) and SbKin1 from the snow mold Sclerotinia borealis, were compared. Two glycine residues proximal to nucleotide in the SbKin1 motor domain, of which the corresponding residues of AnKinA were non-glycine ones (P60 and S323), would be responsible for cold-adaptation through the augmented flexibility. We made AnKinA recombinant kinesin along with P60G and S323G mutants. For S323G mutant, the signs of deterioration were detected from the basal ATPase activity at only slightly high temperature, and relatively low activation energy was shown from the motile activity. The point mutation S323G would offer possible cold-adaptation in compensation for thermal stability.

2Pos219 細胞分裂に関わるキネシン５の高速一分子観察
High-speed single molecule observations of the stepping motion of mitotic kinesin-5

Taiga Yamada, Kohei Matsuzaki, Michio Tomishige, Yoko Sakai (*Aoyamagakuinuniversity Tomishige lab.*)

Kinesin-5 (also called Eg5) is a motor protein that is essential for mitotic spindle assembly and chromosome segregation. Compared to the well-studied kinesin-1, the detailed motility mechanism of kinesin-5 is still unknown. Here, we employed a total-internal reflection-based dark field microscopy to observe the gold particle attached to a head of kinesin-5 with 50 us temporal resolution. We found that kinesin-5 frequently took off-pathway transitions: the leading head detaches before the trailing head detaches, or the detached trailing head rebinds to the backward-binding site. These results indicate that two heads of kinesin-5 is less coordinated compared to that of kinesin-1, which may arise from the difference in the cellular functions.

2Pos220 遺伝性痙性対麻痺を引き起こす変異型ヒト KIF1A の神経細胞内 Run-time 分布
Run-time distributions of human KIF1A mutants in hippocampal neurons in relation to hereditary spastic paraplegia

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The kinesin 3 family member KIF1A is a molecular motor that transports synaptic vesicle precursors (SVPs) in the axons. In this study, we investigated the SVPs in mouse hippocampal neurons, carried by human KIF1A mutants, which cause hereditary spastic paraplegia. The genes of mutant KIF1A-GFP were transfected into the hippocampal neurons: the motion of SVPs was observed by fluorescence microscopy. We found that run-time (the time for a SVP vesicle to keep moving) for the mutants was longer than that for the wild-type. The reason of this increased run-time was clarified by physical quantities such as force, velocity, and number of motors involved in the SVP transport.

2Pos221 キネシン１二量体の前頭部における微小管からの解離抑制の直接観察
Direct observation of the suppression of the leading head of kinesin-1 dimer from detachment from microtubule

Kohei Matsuzaki, Michio Tomishige (*Dept. Math. Phys., Col. Sci. Eng., Aoyama Univ.*)

Kinsin-1 is a motor protein that moves processively along microtubule. To move in a hand-over-hand manner, the trailing head should detach from the microtubule before the leading head detaches, however there is still no quantitative evidence whether the detachment of the leading head is suppressed or the detachment of the trailing head is accelerated. In this study, we observed binding/unbinding of the leading head by using a heterodimer composed of wild-type and E236A mutant heads. High-speed dark-field microscopic observations showed that the detachment rate of the leading head was 16 times slower than that of the trailing head of wild-type homodimer, supporting the idea that the leading head is suppressed from ATP hydrolysis by a tension posed to the neck linker.

2Pos222 Selective nano-patterning of kinesin motor-proteins and its effect on collective motion of microtubules

Tamanna Ishrat Farhana, Taikopaul Kaneko, Ryuji Yokokawa (*Dep. of microengineering, Kyoto university*)

In nature, a large-scale pattern arises from the collective motion of motile objects. The cytoskeletal microtubule (MT) driven by kinesin has been envisioned as a model system to study the collective motion in vitro. The effects of different physical parameters including the kinesin density on the coordinated behavior of MTs has been studied. Perhaps the reported results are inadequate to understand how the arrangement and number of motor proteins influence the collective motion. Recently, our group has developed a novel method which offers selective patterning of kinesins in nanometer scale using gold nano-pillars fabricated on silicon substrate. Our object is to study the collective motion of MTs driven by selectively nano-patterned kinesins.

2Pos223 Does giraffe kinesin move faster than mouse?

Taketoshi Kambara[1], Yasushi Okada[1,2] ([1]*RIKEN BDR*, [2]*Univ of Tokyo, Grad. Sci.*)

Many neurodegenerative diseases are known to be caused by impaired axonal transport due to decreased velocity of kinesin. For example, various point mutations of KIF5A is known to be causative for hereditary spastic paraplegia (HSP), which mainly affects the distal part of the long motor tracts in the spinal cord. The HSP mutations slightly decreased the velocity of KIF5A that would explain why neurons with longest axons are affected. If fast velocity is important for the survival of neurons with long axons, large animals with longer axons would require faster kinesin. Here, we address a simple question; is kinesin of giraffe faster than small animals such as mice?

2Pos224 Photoregulation of kinesin Eg5 using photochromic compound composed of azobenzene and spiropyran which forms three isomerization states

Md Alrazi Islam, Kei Sadakane, Shinsaku Maruta (*Soka University*)

Kinesin is an ATP drive motor protein move along with microtubule. Kinesin Eg5 is essential for bipolar cell division. Therefore, mitotic kinesin Eg5 has been considered as a potential target for cancer therapy. In this study, to control mitotic kinesin Eg5, we have synthesized a novel photochromic inhibitor (SP-AB) composed of photo-responsive azobenzene and Spiropyran, and 2,3-dimercaptosuccinic acid derivatives. The photochromic compound SP-AB formed Merocyanine-Cis, Spiro-Trans and Merocyanine-Trans states upon ultraviolet(UV) irradiation, Visible (Vis) Light irradiation, and in the dark respectively. The basal and microtubules stimulated ATPase activity of Eg5 are inhibited by SP-AB with different inhibitory activities among the three isomerization states.

2Pos225 2 つのアゾベンゼンを持つ新規フォトクロミック阻害剤を介したキネシン Eg5 の光制御
Photo-regulation of mitotic kinesin Eg5 using a novel photochromic inhibitor composed of two azobenzene

Kei Sadakane, Kenichi Taii, Alrazi M.D. Islam, Shinsaku Maruta (*Dept. Bioinfo., Soka Univ.*)

Mitotic kinesin Eg5 is a target of anti-cancer therapy. Previously many inhibitors of Eg5 have been developed as anticancer drugs. Interestingly, although the inhibitors have no conserved structure, they bind to the common pocket composed of L5,α2 and α3 in Eg5 motor domain. In this study, we synthesized novel photochromic Eg5 inhibitor composed of two azobenzene derivatives (BDPSB). BDPSB exhibited cis-trans isomerization with UV and VIS light irradiation. The trans form of BDPSB significantly inhibited microtubule-dependent ATPase activity of Eg5. Cis BDPSB showed weak effects on the microtubule-dependent ATPase activity. The results suggest that the novel photochromic Eg5 inhibitor BDPSB exhibits highly efficient photoswitching.

2Pos226 Photo-control of Ras GDP-GTP exchange using the peptide modified with spiropyran derivative

Kenichi Taii, Nobuyuki Nishibe, Shinsaku Maruta (*Dept. of Bioinfo, Grad. Sch. of Engin, Soka Univ.*)

GDP-GTP exchange of Small GTPase Ras is induced by binding of GEF to Ras. Recently some kinds of peptide which interfere binding of GEF resulting in inhibition of GDP-GTP exchange, were reported. Photochromic molecule, spiropyran isomerize between spiro (SP) and merocyanine(MC) forms photo reversibly upon visible and ultraviolet lights. It is known that MC form of spiropyran exhibit dimerization. In this study, we designed and synthesized the inhibitor peptides of Ras composed of two cysteine residues. The cysteine residues were modified with SP-maleimide stoichiometrically. The secondary structural change of the peptide induce by photoisoerization were examine by CD and the photo-control of GDP-GTP exchange of Ras was studied using fluorescently labeled GDP analogue.

2Pos227 鞭毛軸糸再構築系における微小管の繰り返し座屈運動の観察
Repetitive buckling of microtubules driven by axonemal dynein arrays reconstituted on a microtubule

Misaki Sagawa[1], Misaki Shiraga[2], Hitoshi Sakakibara[3], Kazuhiro Oiwa[3] ([1]*Sch. Sci, Univ. Hyogo*, [2]*Grad. Sch. Sci, Univ. Hyogo*, [3]*Adv. ICT Res. Inst., NICT*)

The complexity of the eukaryotic flagellar axoneme is studied by reconstructing modular building blocks to the axonemal structure *in vitro*. Tubulins were polymerized into microtubules from fragmented axonemes and we added crude outer-arm dynein extract from *Chlamydomonas* axonemes to these bundles. Negative-staining electron microscopy showed that these dyneins formed regular arrays (24nm-repeat) on the microtubules in a self-organized manner. On addition of Mg^{2+}-ATP, a pair of microtubules occasionally displayed the repetitive buckling at a few Hz. These repetitive interactions between dyneins and microtubules were derived from the intrinsic nature of dyneins. The features could be the essence of the beating mechanism working in an axoneme.

2Pos228 Identifying actin regulators from complex cellular lysates through profilin pull down

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Profilin is an actin-binding protein that is involved in various cellular processes such as cell motility through its ability to regulate actin polymerization in the cell. The role of profilin in regulating actin cytoskeleton relies on its capacity to interact and cross-talk with other proteins and molecules in the cell. In addition to actin, profilin is also known to bind polyproline motifs and PIP_2. In this study, profilin binding partners are completely mapped from cell culture lysates SILAC and quantitative mass spectrometry. Our results indicate that profilin interacts with actin regulators with polyproline motifs. In addition, the results of this study could establish a basis for identifying novel actin regulators.

2Pos301 Cellular localization of SAS6-L, a paralog of a flagellar basal body protein that self-assembles into a 9-fold symmetrical structure

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SAS-6 is a basal body protein that plays an essential role for fixing the triplet microtubule number to 9. It self-assembles into a 9-fold symmetrical structure through forming a dimer with two globular heads and a coiled-coil tail. A paralog of this protein, SAS6-L, has a homology to the N-terminal domain of SAS-6, which domain functions in the self-assembly. However, it is unknown whether it actually form dimers and how it functions in the cell. X-ray crystallography of Chlamydomonas SAS6-L revealed that it forms dimers like SAS-6. Immunofluorescence microscopy of Chlamydomonas cells showed that SAS6-L is associated with a 9-fold symmetrical structure located in the flagellar transition zone. Thus SAS6-L may function through exerting its self-assembling property.

2Pos302 ビブリオ菌の極べん毛本数制御における FlhG の ATPase モチーフおよび ATPase 活性の役割
The role of ATPase motif and ATPase activity of FlhG in flagellar number regulation at cell pole of Vibrio alginolyticus

Yoshino Imura, Seiji Kojima, Michio Homma (*Grad. Sch. Sci., Univ. Nagoya*)

The number and location of flagella vary among bacterial species, and are strictly controlled. Vibrio alginolyticus has a single flagellum at cell pole and its formation is controlled positively by FlhF and negatively by FlhG. Here, we focus on the FlhG function in flagellar number regulation. FlhG is known to have ATPase activity, and mutations in the ATPase motif affected the FlhG function. In this study, we aim to clarify the function of FlhG in cells by examining biochemical properties of purified FlhG protein. However, despite the fact that FlhG is a soluble protein, the purified protein tends to aggregate so hampers further analysis. We could overcome the aggregation problem, and sizing column chromatography revealed that FlhG exists as a monomer.

2Pos303 ビブリオ菌細胞の極に局在するタンパク質 FlhF による極べん毛形成促進機構の解析
Role of FlhF localized at cell pole on initiating the polar flagellar formation of Vibrio alginolyticus

Yuna Inoue, Seiji Kojima, Michio Homma (*Division of Biological Science, Graduate School of Science, Nagoya University*)

Vibrio alginolyticus has a single polar flagellum at the cell pole. Its number is positively regulated by FlhF. However, how and which step FlhF facilitates during the flagellar assembly remains unknown. We presumed that the formation of MS ring, consisted of FliF, is the first step on the flagellar formation and FlhF may act on this step by recruiting FliF to the cell pole. To test this idea, we investigated dependence of FlhF on FliF ring assembly. We found that GFP-fused FliF did not form a fluorescent dot at cell pole in the ΔflhF strain. Moreover, GFP-fused FliF could localize at cell pole in the strain devoid of flagellar proteins when FlhF was co-expressed, consistent with our hypothesis that FlhF recruits FliF to the pole to facilitate flagellar assembly.

2Pos304 ナトリウムイオン透過における、べん毛モーター固定子タンパク質 PomA のペリプラズムループ領域の構造機能解析
Structural and functional characterization of periplasmic loop regions of PomA, a stator protein of flagellar motor, in sodium ion flux

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In V. alginolyticus, the stator of the flagellar motor is composed of PomA and PomB, and is driven by sodium ion flow through the stator. The two loops located in the periplasmic region of PomA are involved in the Na+ flux in the stator channel. By in vitro labeling experiment, we found that only residues in loop3-4 were labeled, consistent with the previous in vivo observation. Our results suggest that loop1-2 is buried but loop3-4 is exposed in the PomA/PomB complex. In order to characterize the function of loop1-2, we analyzed PomA D31, whose Cys replacement raised threshold concentration of Na+ to drive motor, using FTIR and double mutation with PomB plug deletion. We will discuss how the PomA periplasmic loops is involved in the Na+ flux.

2Pos305 細菌べん毛モーター形成の中心となる超分子膜構造体 MS リングの形成メカニズムの解明
Assembly mechanism of supramolecular membrane structure of bacterial flagellar MS-ring composed of FliF

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A bacterial flagellar motor consists of rotor and stator. The rotor part is composed of MS-ring and C-ring. The MS-ring embedded in the cytoplasmic membrane has important roles for both the flagellar assembly and rotation. MS-ring is a supramolecular membrane complex which consists of 26 copies of FliF molecules. FliG has the two transmembrane helices. In a previous study, Salmonella FliF overexpressed in E. coli cells was assembled into MS-ring by itself, whereas Vibrio FliF was not., It is unclear what factors are needed for the MS-ring assembly. Here, we purified the Vibrio MS-ring from Vibrio or E. coli cells producing Vibrio FliF with FliG, which is a C-ring component. It seems that the formation of MS-ring for Vibrio FliF needs the assist of FliG.

2Pos306 細菌べん毛 III 型分泌装置のある構成因子は翻訳後多段階プロセシングを受ける
A component of the bacterial flagellar type III secretion apparatus receives multistep post-translational processing

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Rhomboid family intramembrane proteases are found among a wide range of organisms from bacteria to human and known to be involved in various important cellular events. Recently we have shown that FliO, one of the components of the flagellar type III secretion apparatus, receives proteolytic cleavage by the rhomboid protease homologue GlpG in *Escherichia coli*. To understand the molecular details of this proteolytic cleavage, we performed mass spectrometric analysis of purified FliO species. Surprisingly the results revealed that FliO receives not only proteolytic cleavages by GlpG but several N-terminal modifications. We are now trying to elucidate physiological importance and molecular mechanisms of these multiple processings of FliO.

2Pos307 バクテリアべん毛輸送ゲート複合体の構造機能解析
Structural and functional analyses of the bacterial flagellar type III export gate complex

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The transmembrane export gate complex of the flagellar type III protein export apparatus is composed of FlhA, FlhB, FliP, FliQ and FliR and acts as a proton-protein antiporter to couple proton flow through a proton channel with protein translocation through a peptide channel. FlhA and FliP are postulated to act as the proton and peptide channels, respectively. Here, to carry out high-resolution cryoEM image analysis of the export gate complex, we developed a purification procedure of the entire export gate complex incorporated into the basal body MS ring. We show that FlhA, FlhB, FliP, FliQ and FliR are associated with the MS ring and that FliQ interacts with FlhA and FliP. We will discuss a possible energy coupling mechanism of the export gate complex.

2Pos308 海洋性ビブリオ菌の極べん毛本数制御機構における FlhG の N 末端領域の解析
Role of N-terminal region of FlhG in polar flagellar number regulation in Vibrio alginolyticus

Seiji Kojima, Akira Mizuno, Michio Homma (*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

FlhF and FlhG are involved in flagellar number regulation of Vibrio alginolyticus. FlhG is a paralog of Escherichia coli cell division regulator MinD, and has the longer N-terminal region than MinD with a unique sequence. The Q9A mutation in the conserved DQAxxLR motif of this N-terminal region lost the ability of FlhG to activate FlhF GTPase. Expression of FlhG-Q9A conferred multiple flagellar phenotype, but the amount of FlhG was remarkably reduced compare to that of wild type. When the amount of mutant FlhG was regulated to the same level of wild-type FlhG, there were no difference in the number of flagellum. These results suggest that the N-terminal region of FlhG may control the number of flagellum by adjusting the amount of FlhG in vivo.

2Pos309 Quantitative observation of CheY-GFP binding to a flagellar motor in the presence of external load by electrorotation

Kenta Morishima, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front Biosciences, Osaka Univ*)

E. coli regulates the rotational direction of flagellar motor by CheYp binding, and we proposed different binding affinity to CheYp between motors rotating CCW and CW direction. In order to investigate whether the environmental perturbation applied to a motor rather than the receptors affects to chemotactic response, we developed the electrorotation system to apply the external load to a motor. Furthermore, we are simultaneously observing the binding of CheY-GFP to a motor with electrorotation to investigate whether the external load applied to a motor affects to the binding affinity of a motor to CheYp. We would like to discuss about the relation among the direction and the magnitude of external load and the change in CheY-GFP binding at the annual meeting.

2Pos310 Difference on chemotaxis response of E.coli derived from the dependency of flagellar motor

Akinori Nagataki, Yong-Suk Che, Akihiko Ishijima, Hajime Hukuoka (*Grad. Sch Front Biosciences, Osaka Univ.*)

The function of bacterial flagellar motor is affected by the external load. However, it is not unclear whether the load dependency of motor affect to chemotaxis response. To understand this, we measured the motor switching under several load conditions when the violet laser was applied as repellent. After giving strong stimuli to *E. coli*, CW bias increased in both high and low load conditions. The reaction was different depending on the load; CW rotation continued at high load, but frequent switching still observed at low load. From this the result, the load applied to a motor affects chemotaxis response. Now we are trying to quantitatively evaluate the relationship among the magnitude of load , stimuli, and the degree of chemotaxis response. Details will be discussed.

2Pos311 モーターの回転方向の同調的制御における CheR, CheB の役割
The role of CheR and CheB in coordinated switching of flagellar motor in *Escherichia coli*

Tatsuki Hamamoto, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

Recently we proposed that the spontaneous oscillation of receptor array's activity regulates the switching of flagellar motors coordinately, and our simulation demonstrated this oscillation was triggered by methylation of receptors. So, we measured the switching coordination of motors in the cells which have the receptors fixed in several methylation level. The switching coordination was not detected in any methylation level, whereas the coordination recovered by the complementation of *cheR*,*cheB* into these cells. These results suggest that the dynamic change of methylation level in receptor array is required for the oscillation of receptor array's activity. Thus, we are now trying to simultaneously observe the activity of CheR or CheB and their coordinated switching.

2Pos312 Quantitative analysis for the ratio of WT and mutant receptors that collapses receptor cooperativity in chemotaxis in *Escherichia coli*

Shin Koguchi, Hajime Fukuoka, Akihiko Ishijima, Yong-Suk Che (*Grad.Sch. Frontier Biosci., Osaka Univ*)

In *E. coli* under steady-state, the switching of flagellar motors is highly coordinated, therefore, we proposed the dynamic change in phospho-CheY concentration derived from cooperative activity of receptor array regulates its coordination. To evaluate our proposal, we investigated whether the insertion of receptor mutant (mTsr), lacking the cooperative response to serine, to receptor array made with wild-type receptor (wtTar) inhibits the switching coordination. The insertion of mTsr inhibited the switching coordination. Furthermore, in this condition, the expression level of mTsr was very low compared to that of wtTar. These results suggest that the receptor activity is highly cooperative under steady-state and this cooperativity is required for switching coordination.

2Pos313 Probing cell-wall synthesis dynamic using bacterial membrane protein-complex

Yi-Jen Sun, Chien-Jung Lo (*Department of Physics and Graduate Institute of Biophysics, National Central University, Zhongli, Taiwan 32001*)

When bacterial cells grow, new cell-wall (peptidoglycan, PG) synthesize and insert into the old cell-wall. However, technical difficulties prevent the further understanding of the spatial-temporal rearrangement of cell-wall. Bacterial flagellar motor is a protein complex anchored on the cell-wall firmly. We use BFM as land markers to study the cell-wall synthesis dynamics. When the new PG strand been inserted, the original cell-wall will be pushed away from its original location. Therefore, by observe the movement of the BFMs as cells reproduce, we can observe the spatiotemporal coordination of the PG insertion. We have successfully tracked the movement of the BFM with high resolution to probe the cell-wall synthesis dynamics quantitatively.

2Pos314 らせん形細菌スピロヘータの推進力測定
Force measurement of the spirochete *Leptospira* swimming

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Leptospira is a spirochete bacterium distinguished by a short-pitch coiled body and intracellular flagella. It is known that the spirochete cell swims in liquid while rotating the cell body with an asymmetric morphology, but the motility mechanism is not fully understood. Although we have theoretically estimated force of the spirochete swimming from the swimming speed and cell-body rotation rate, direct force measurement deepens understanding of the motility mechanism. In this study, we measured the propulsive force of *Leptospira* by trapping a microbead attached to the cell body using an optical tweezer, showing the propulsive force of about 2 pN. Based on the results, we discuss energetics of the *Leptospira* swimming.

2Pos315 細胞性粘菌や好中球の基質の硬さ感知
Rigidity sensing of fast-moving cell types

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Crawling cells can be classified into two categories: slow-moving and fast-moving cell types. Slow-moving cell types, such as fibroblasts, move toward rigid areas on the substratum in response to a rigidity gradient. However, rigidity sensing has hitherto not been recorded in fast-moving cell types. Here, we show that fast-moving *Dictyostelium* cells exert larger traction forces on more rigid isotropic substratum, and *Dictyostelium* cells and HL-60 cells migrate in the "soft" direction on the anisotropic substratum that is rigid on the x-axis but soft on the y-axis, although myosin II-null *Dictyostelium* cells migrated in random direction. Rigidity sensing of fast-moving cell types differs from that of slow types.

2Pos316 アクチンフィラメントに結合した MAPs の微小管重合促進活性の評価
Microtubule assembly-promoting activity of MAPs bound to actin filaments

Chihiro Doki[1], Miyuki Siga[1], Syoma Saitou[1], Susumu Kotani[2], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Sustain, Environ. Eng., Muroran Inst. Technol.*, [2]*Fac. Sci., Kanagawa Univ.*)

We recently reported that a part of the Pro-rich region in the microtubule-binding domain (MBD) of microtubule-associated protein (MAP) 4 bound to actin filaments (F-actin). Subsequently, we found that two MAP4 isoforms and MAP2 bound to F-actin retained microtubule-binding ability. In this study, we examined whether MAPs bound to F-actin retain microtubule assembly-promoting ability. MAPs were introduced flow chamber immobilized F-actin and incubated for 5 min at 25 ℃. And then, the flow chamber was introduced tubulin containing each MAP and observed by fluorescence microscopy at 37 ℃. The results revealed that MAP2 and MAP4 , but not tau induced microtubules along F-actin.

2Pos317 アクチン繊維の集団運動により形成されるベルト状パターン
The shape of belt-like patterns with millimeter size emerged from actomyosin motility

Kentaro Ozawa[1], Hirotaka Taomori[1], Itsuki Kunita[2], Shigeru Sakurazawa[3], Hajime Honda[1] ([1]*Dept. Bioeng., Nagaoka Univ. Tech.*, [2]*Univ. Ryukyus*, [3]*Future Univ. Hakodate*)

At the conventional gliding assay of actin filaments on the HMM-coated glass surface, we have found that the moving actin filaments at an intermediate concentration demonstrate the belt-like patters. Within the belt-structure, inter-filament distance were rather constant at about 35 nm. The curvature-radius was found to depend on the average length of actin filaments, the shorter the smaller. Furthermore, the patterns were found to transform into ring-shape when the ionic strength of solution was further decreased. The average outer diameter of the ring were about 60 μm, and the inner diameter decreased as the concentration of actin increased. This phenomenon might have close relation to the physiological functions, such as contractile ring.

2Pos318 重力下での形態形成に対する YAP 依存のアクトミオシンネットワークの寄与
Theoretical study of contribution of YAP-dependent actomyosin network to morphogenesis under gravity

Kazunori Takamiya, Seirin Ri, Hiraku Nishimori, Akinori Awazu (*Grad. Sch. Sci., Univ. Hiroshima Dept. Math and Life Sci*)

Multicellular organisms form their specific body shapes against the gravity. Recently, YAP protein was reported as a key transcriptional regulator to keep their body shape under gravity, where the YAP knockout mutant of medaka exhibits flattened body shape and misalignment of the organ. Furthermore, YAP knockout spheroid formed group of retinal cell cultured in human also showed the flattened body shape. Then, we construct a model of spheroid considering the dynamics of YAP-dependent actomyosin network and interactions among cells to unveil the mechanism of the abovementioned phenomena. We particularly focus on the roles of the interplays among intra-molecular dynamics and the translation and deformation of cells for their body shape regulations.

2Pos319 中心体アクチンネットワークによる微小管の形成制御
Regulation of microtubule growth by centrosomal actin network

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The centrosome is the main microtubule (MT) organizing centre. Recently, we reported that centrosome can nucleate and organize actin filaments as well. However, the precise function of the centrosomal actin network remains obscure. Here, we show that the density of actin filaments and MTs at the centrosome were negatively correlated in B lymphocyte and in vitro reconstitution assays based on (i) purified centrosomes and (ii) on the co-micropatterning of microtubule seeds and actin filaments. We also found that cell adhesion and spreading lead to lower densities of centrosomal actin thus resulting in higher microtubule growth. Hence, we propose a novel mechanism by which the number of centrosomal microtubules is regulated by cell adhesion and actinnetwork architecture.

2Pos320 FilGAP PH ドメインの構造と機能の解析
Structural and functional analysis of FilGAP PH domain

Koji Tsutsumi[1], Yurina Suzuki[1], Shunsuke Sato[2], Go Watanabe[2], Yasutaka Ohta[1] ([1]*Div. of Cell Biol., Sch. of Sci., Kitasato Univ.*, [2]*Div. of Biophysics., Sch. of Sci., Kitasato Univ.*)

Pleckstrin homology (PH) domain is a lipid binding domain, specifically recognizes phosphoinositide head group, allowing them to be recruited to cell membrane in response to extracellular stimulus. FilGAP is a negative regulator of Rac, containing PH domain in its N-terminal region. In this study, we found that FilGAP self-associates via PH domain. By biochemical experiment and in silico analyses, we revealed that FilGAP PH domain forms a trimer. FRET imaging analysis revealed the self-association of FilGAP via PH domain in the tip of the lamellipodia. These data suggest that self-association of FilGAP via PH domain is involved in the regulation of lamellipodia of migrating cell.

2Pos321 微小管結合蛋白質が微小管の強度と曲がりやすさに与える影響
Influence of microtubule-associated protein on strength and flexibility of microtubules

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Microtubule-associated proteins (MAPs) bind to the microtubules (MT), but the effect on the properties of microtubules has remained unknown. In this study, we examined the influence of MAP2, MAP4, and Tau on strength and flexibility of microtubules. Stretching test showed that MAP2-MT was most resistant in the presence of 200 nM MAPs and 100 nM MT. Interestingly, Tau-MT was most resistant to stretching when in the presence of 10 nM MAPs. We also estimated flexibility of MAPs-MT from fluorescence microscopic images. Bending ratios (distance between the ends of microtubule/length of microtubule) of MT, MAP2-MT, MAP4-MT, and Tau-MT were 81.6 ± 21.4, 82.8 ± 18.5, 92.5 ± 8.9, and 93.2 ± 5.8 %, suggesting that MAP4 and Tau have the effect of straightening the microtubules.

2Pos322 アメーバ運動中の ABP 局在形成機構の解明のためのアクチンと ABP からなる in vitro 系の構築
A new, actin and ABP-based in vitro system for elucidating the mechanism of intracellular ABP localization during amoeboid movement

Yosuke Yamazaki, Taro Q.P. Uyeda (*Dept. Physics, Waseda Univ.*)

Amoeboid cell movement depends on proper intracellular localizations of actin binding proteins (ABPs), particularly segregation of myosin II and cofilin. The segregation mechanism remains unclear, but we have been studying possible involvement of the autonomy of the actin/ABP system. Myosin and cofilin form segregated patches along individual actin filaments, due to mutually exclusive, cooperative actin binding of the ABPs (Ngo et al., 2016), but each patch is much smaller than the cells. We thus reasoned that crosslinking of actin filaments by myosin filaments would create larger, cell-sized myosin-rich areas, where cofilin is excluded. To test this hypothesis, we are constructing a simple in vitro system to recapitulate cell-sized segregation of myosin and cofilin.

2Pos323 Examining force regulation of anaphase cell

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The process of partitioning sister chromatids into daughter cells during cell division is mediated by spindle- and cell-elongation. It is not known how applied mechanical forces affect the physical processes involved in chromosome separation and cytokinesis. Using the micromanipulation technique, we found that a mechanical force externally applied to anaphase cells alters the dynamics of cell division as previously reported for the metaphase cell. Under the condition that actomyosin functions are inhibited, we quantified the force of cell elongation and the modulation of the period of time from the beginning of chromosome segregation to the completion of cytokinesis. Finally, we discuss the current progress in the biophysical approach on the cell division machinery.

2Pos324 C 型インフルエンザウイルスの直進的運動
Directional motility of influenza C virus

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Influenza virus motility is based on cooperation between viral hemagglutinin (HA) and neuraminidase (NA), and is a major determinant of virus infectivity. To translocate a virus, HA molecules exchange receptors and NA molecules accelerate the receptor exchange. This type of virus motility was recently identified in influenza A virus (IAV). To determine if other influenza virus types have a similar motility, we investigated influenza C virus (ICV) motility on a receptor-fixed glass surface. Like IAV, ICV was observed to move across the receptor-fixed surface. However, in contrast with the random movement of IAV, ICV moved straight, in a directed manner, and at a constant rate. Consequently, ICV has a unique motility that is highly regulated in both direction and speed.

2Pos325 紡錘状細胞集団の示す配向秩序と牽引力
Traction Force and Dynamics in Orientation Order of Spindle-shaped Cells

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Collective migration of spindle-shaped cells are observed as phenomena such as rostral migratory stream and cancer invasion after epithelial-mesenchymal transition, but remains to be understood quantitatively. A simple model from Active Matter field is proposed to describe these collective migrations using its orientation order, but is still to be checked by experiments. We observed the dynamics of the orientation field and measured the traction force in adhesive culture system of neural stem cells, to check if the simple models is suitable for real cell culture systems. As a result, these properties were consistent to the prediction and assumption of the model. We also tried to determine a coefficient in the model, which was introduced as a phenomenological parameter.

2Pos326 ARF1 activation initiates a regulation circuit for ARF1 and RAC1 activities in GPCR-mediated neutrophil chemotaxis

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The small GTPase ARF1 is essential for the GPCR-mediated chemotaxis of neutrophils. In this process, ARF1 is activated by the guanine nucleotide exchanger GBF1. Here, we investigated the association between ARF1 and RAC1/CDC42 during chemotaxis of HL60 cells. We found that the silencing of GBF1 significantly impaired the recruitment of RAC1 to the leading edges. A significant population of RAC1 colocalized with ARF1 at the leading edges in stimulated cells, whereas fMLP activated both ARF1 and ARF5. Consistently, the silencing of ARF1, but not ARF5, impaired the recruitment of RAC1. Our results indicated that the activation of ARF1 triggers the plasma membrane recruitment of RAC1 in GPCR-mediated chemotaxis, which is essential for cortical actin remodeling.

2Pos401 Investigation of binding mechanism of E-cadherin by high-speed atomic force microscopy (HS-AFM)

Hiroki Watanabe[1], Sivasankar Sanjeevi[2], Takayuki Uchihashi[3] ([1]*RIBM Co., Ltd.*, [2]*Dept. of Phys. and Astron., Iowa State Univ.*, [3]*Dept. of Phys., Nagoya Univ.*)

Cadherin, which is a Ca^{2+}-dependent cell adhesion protein, plays a key role in development and maintenance of tissue architecture. Especially, E-cadherin categorized as a classical cadherin has extracellular region; this region is composed of five domains (EC1 to 5) arranged in tandem. Previous study showed that the molecules could bind in two types of conformations called “X-dimer” and “S-dimer” during adhesion. Although the analysis of the two-binding states was carried out by various techniques, the shuttling between the two states was not directly visualized. To elucidate the relation between the shuttling behavior of E-cadherin and cell adhesion, observation of the Ca^{2+}-dependent structure and dynamic analysis of two-states transition were performed by HS-AFM.

2Pos402 ホウレンソウ由来ストロマラメラに内在する F0 c-リングの原子間力顕微鏡による観察
Observation of the c subunit ring of F0 in stroma lamellae membrane from spinach by atomic force microscopy

Daisuke Yamamoto, Risa Mutoh (*Fac. Sci. Fukuoka Univ.*)

The synthesis of ATP by the chloroplast ATP synthase (cF0F1) is driven by the proton motive force across the membrane. This process is accompanied by the tightly coupled action of the catalytic F1 head and the F0 motor that is embedded in the membrane. In plant chloroplast, cF0F1 is mainly located in stroma lamellae membrane. Here, atomic force microscopy (AFM) was applied to directly observe the c subunit ring of F0 (c-ring) in the stroma lamellae from spinach. The ring structure with outer diameter of about 7 nm was clearly observed in the membrane. The dimensions of the observed ring were consistent with those of the c-ring estimated by previous studies. The detail of the structure of the c-ring in the stroma lamellae observed by AFM will be discussed.

2Pos403 Simultaneous observation of a living COS7 cell using high-speed atomic force microscopy and fluorescence microscopy

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High-speed atomic force microscopy (HS-AFM) is a powerful technique to visualize dynamics of a single proteins and morphology of a single living cells with nanometer resolution under physiological conditions [1]. However, it is difficult to recognize a specific protein in a complex system like cell. In contrast, fluorescence microscopy is able to distinguish specific proteins by labeling of fluorescence dyes. Thus, the combination of HS-AFM with fluorescence microscopy could complement their spatial resolution and molecular recognition. In this study, we combined HS-AFM with confocal microscopy and observed morphological dynamics of a living COS7 cell. [1] M. Shibata et al. 2017 Biophys. Physicobiol. 14, 127-135.

2Pos404 マウスノロウイルス MNV-S7 のクライオ電顕単粒子構造解析
Capsid Structure of Murine Norovirus S7 revealed by cryo-electron microscopy

Chihong Song[1], Reiko Todaka[2], Kei Haga[2], Akira Fujimoto[2], Masaru Yokoyama[3], Naoyuki Miyazaki[4], Kenji Iwasaki[4], Kazuhiko Katayama[2], Kazuyoshi Murata[1] ([1]*National Institute for Physiological Sciences*, [2]*Kitasato University*, [3]*National Institute of Infectious Diseases*, [4]*Institute for Protein Research, Osaka University*)

Human norovirus (HuNoV) is the major cause of epidemic nonbacterial gastroenteritis. However, little is known about the mechanism leading to antigenic diversity. In this study, we generated murine norovirus type S7 (MNV-S7) VLPs as a surrogate of HuNoV using baculovirus expression system, and investigated the capsid structure by single-particle cryo-electron microscopy. The structure of MNV-S7 was then compared with that of murine norovirus type 1 (MNV-1). Amino acid differences were only 6% between two genotypes, but the structures of each capsid were totally different, where residues linking adjacent protruding (P) domains have been switched from the residues between the lower P1 domains in MNV-1 to the upper P2 subdomains in MNV-S7 by rotation of the P domains.

2Pos405 銀、金、銀金合金ナノ粒子を用いたマルチカラー 1 分子イメージング
Multi-color single-molecule imaging with silver, gold, and silver/gold-alloy nanoparticles

Jun Ando[1,2], Akihiko Nakamura[1,2], Mayuko Yamamoto[1], **Ryota Iino**[1,2] ([1]*IMS, NINS*, [2]*SOKENDAI*)

We applied silver, gold, and silver/gold-alloy nanoparticles (AgNP, AuNP, and AgAuNP) for multi-color imaging of single-biomolecules. AgNP and AuNP showed peak wavelength of scattering spectra around 410 nm and 530 nm, respectively. Furthermore, AgAuNP showed peak wavelength in between 410 nm and 530 nm, which could be tuned depending on the composition ratio of silver and gold. By combining lasers at the wavelengths of 404 nm, 473 nm, 520 nm, and a spectrophotometer with wide-slit, we developed an optical microscope system for multi-color single-particle tracking of AgNP, AuNP, and AgAuNP. With this system, motions of lipids in membrane, labeled with AgNP, AuNP, and AgAuNP, were simultaneously observed at 19 ms time resolution and 0.5 nm localization precision.

2Pos406 細胞内自発的発熱の検出と生理的意義の解明
Investigating the detection and the significance of spontaneous intracellular thermogenesis

Cuiyuan Cai[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*PRESTO, JST*)

Temperature is a fundamental physical parameter, having important effects on life. Cancer cells have higher temperature than normal cells. These suggest that temperature has a profound effect on cell functions. But the spontaneous intracellular thermogenesis and its significance on cell functions have been unknown. In this study, we used three kinds of media with different nutrients in culturing COS7 cells, and use fluorescent nanogel thermometer to investigate the intracellular temperature change during mitochondrial stimulation and at the steady-state, showing the nutrient-dependent thermogenesis. With this study focused on the significance of intracellular thermogenesis on cell functions, new discoveries of cell mechanisms and disease are expected.

2Pos407 Fluorescence correlation spectroscopy analysis of RNA degradation in cells

Naotaka Shimada[1], Kazunori Watanabe[1], Takashi Ohtsuki[1,2] ([1]*Grad. Sch. Nat., Univ. okayama*, [2]*Grad. Sch. Int., Univ. okayama*)

RNAs have a variety of roles in cells and it has been reported that RNA function is closely related to RNA degradation. Therefore, to clarify RNA functions, it is important to study RNA degradation in cells, preferably, in each subcellular localization. However, there have been limited methods for monitoring RNA degradation in cells. Thus, the purpose of this study is to analyze RNA degradation in cells using fluorescence correlation spectroscopy (FCS). In this study, we focused on initiator tRNAMet (iMet), which is degraded and accumulated into the nucleus under heat stress. Half-life of iMet is thus presumed to differ depends on subcellular localization. The results of FCS analyses of iMet will be shown on each subcellular location under heat stress.

2Pos408 The fast reporter system for quantification of the transcription by using BRET and the split luciferase complementation

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Fluorescent proteins are commonly used as reporters for quantification of gene expression. Although fluorescent proteins are useful to analyze the dynamic behavior of gene expression, there is intrinsic difficulty to interpret the fluctuating fluorescence because of the temporal gap between actual gene expression and emitting fluorescence, which is caused by chromophore maturation of fluorescent proteins. In this research, we developed the maturation less reporter system which is combining BRET and the split luciferase complementation. The performance of our new reporter system was validated in vitro and in vivo, and showed the significant improvement of the response time to the induction of gene expression. Our strategy can be applied to those dynamics is crucial.

2Pos409 高次粒子数輝度解析法を用いたタンパク質オリゴマー分布解析：多成分系への応用に向けて Protein Oligomer Distribution Analysis by High Order Number and Brightness Analysis: towards the Application to Multiple Components

Ryosuke Fukushima[1], Johtaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [3]*Biomed. Res. Inst., AIST*)

Several studies suggest that protein aggregations trigger cell death in neurodegenerative diseases. The aggregations include many species which have different number of molecules. This large heterogeneity hampers our ability to determine the aggregation state. We previously developed a method to visualize protein oligomers in living cells, named “Two-detector N&B”. The method based on statistical analysis for fluorescence images obtained by a confocal laser scanning microscopy. However, its application is restricted to homogeneous system. In order to apply to heterogeneous system, we developed “High order N&B” by introducing high order cumulants analysis. This method will facilitate the understanding of heterogeneity in oligomer formation.

2Pos410 Single fluorophore imaging using a DIY microscope with high extensibility

Takashi Sagawa, Wataru Nakashima, Kazuki Nakajima, Shin Yamaguchi, Tomohiro Masuda, Yuichi Inoue (*SIGMAKOKI Co.,LTD.*)

We developed a DIY fluorescence microscope, called “Core Unit”, as a future foundation in the advanced research of biological sciences. With a new additional laser unit, which can be switched from Koehler illumination to TIRF illumination (as well as optical tweezers), rhodamine-labeled tubulin molecules were observed at single molecular level using a high sensitive EMCCD. To our surprise, single fluorophore can be also observed using a digital camera for home use at video rate. More trials to reduce initial cost for the single molecular imaging would be discussed at the meeting. The low-priced system of Core Unit with high extensibility will open various applications in biosciences especially for young scientists and students.

2Pos411 A multi-emitter fitting algorithm for potential live cell super-resolution imaging over a wide range of molecular densities

Tomochika Takeshima[1], Teruo Takahashi[1], Jiro Yamashita[1], Yasushi Okada[2], **Shigeo Watanabe**[1] ([1]*Hamamatsu Photonics K.K., System division*, [2]*RIKEN Center for Biosystems Dynamics Research*)

Multi-emitter fitting algorithms have been developed to improve the temporal resolution of single-molecule switching nanoscopy. Here, we propose a computationally fast method, wedged template matching (WTM), an algorithm that uses a template matching technique to localize molecules at any overlapping molecular density from sparse to ultra-high density with sub-diffraction resolution. WTM achieves the localization of overlapping molecules at densities up to 600 molecules/μm^2 with a high detection sensitivity and fast computational speed with reasonable localization precision. WTM resolved protein dynamics from live cell images with sub-diffraction resolution and a temporal resolution of several hundred milliseconds or less. http://dx.doi.org/10.17632/bf3z6xpn5j.1

2Pos412 単一細胞 ATP イメージングにより明らかになった不均一な代謝状況下での頑健なエネルギー量調節
Single-cell ATP imaging reveals robust energy level control despite unequal metabolic contexts

Hideyuki Yaginuma, Yasushi Okada (*BDR, RIKEN*)

Adenosine triphosphate (ATP) is required to provide energy for various intracellular reactions. How the ATP concentration in living cells is maintained is not clear. We developed a fluorescent ATP indicator, “QUEEN-37C”, for visualization of absolute ATP concentrations in mammalian cells at 37℃. Since QUEEN-37C is based on single fluorescent protein, it circumvents the signal bias originating from maturation kinetics, which is common in previous FRET-type indicators. Using QUEEN-37C in MDCK cells, we found that total ATP level was nearly constant despite the heterogeneous dependency on oxidative phosphorylation. In addition, in many cell lines, ATP concentration was between a certain range even at single-cell resolution, suggesting a robust energy control.

2Pos413 Development of programmable RNA-binding protein and its application for live-cell imaging and manipulation of authentic RNAs

Akira Takai[1], Yasushi Okada[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. of Sci., Univ. of Tokyo*)

Here, we report the development of designable RNA-binding protein (dRBP), which is programmable to bind to the RNA of interest. We first established an ELISA-like assay using our bright bioluminescent protein, Nano-lantern (Takai et al., PNAS 2015), and showed our dRBPs have high affinity (1-10 nM) specifically to the target RNAs. We also showed our dRBPs can be used for the visualization of the authentic RNAs including Actb mRNA or lncRNA Neat1_2 in living cells. Furthermore, manipulation of the localization of the Actb mRNA using the dRBP fused to constitutively active kinesin resulted in the elongation of cellular processes. These data collectively suggests our dRBP would serve as a powerful tool for the imaging and manipulation of authentic RNAs in living cells.

2Pos414 共焦点画像解析による新規 FCS/FCCS 法の開発とその応用
A new FCS/FCCS method based on the image processing of a confocal laser scanning microscope and applications for it

Kazunari Mouri[1], Yasushi Okada[1,2] ([1]*BDR, RIKEN*, [2]*Univ. Tokyo, Grad. Sch. Sci., Dept. Phys.*)

Fluorescent correlation spectroscopy (FCS) is an established method for estimating the diffusion coefficient and the concentration of molecules using a confocal microscopy with special equipments. Here we developed a new FCS method with a conventional confocal microscope. We carefully selected the scanning conditions, and succeeded in getting the time-series data of the number of photons at a detector, which is comparable to those with FCS. Applying this, we can perform biochemical experiments in living cells. For example, we quantified the enzyme reaction rate constants of nuclear pore proteins which transport ERK proteins. In addition, this FCS method can be easily extended to FCCS. We show the maturation efficiency and brightness of more than 20 fluorescent proteins.

2Pos415 Single-molecule detection of combinatorial histone modifications for key genes in Epithelial-Mesenchymal-Transition

Jen-Chien Chang[1], Ye Liu[1], Kazuhide Watanabe[1], Prashanti Jeyamohan[1], Haruka Yabukami[1], Yuko Sato[2], Hiroshi Kimura[2], Akiko Minoda[1] ([1]*RIKEN IMS*, [2]*Tokyo Tech, Dept. Life Sci. Tech.*)

Epigenome, including histone modifications and DNA methylation, represents the unique signature of a cell type. Probing multiple modifications can be informative in revealing cell states. However, traditional bulk assays measure only the average, making delineating accurate epigenome during a heterogeneous cell process like differentiation or reprogramming difficult. To attack this challenge, a new method for simultaneously imaging many histone modifications on single nucleosomes isolated from specific genomic loci is under development. We will apply this method to key genes involved in Epithelial-Mesenchymal-Transition using a cell line model to reveal the intermediate epigenome states in this cell process related to cancer metastasis.

2Pos416 X 線自由電子レーザーを用いた低温 X 線回折イメージングによる異なる細胞周期にある酵母細胞核の構造解析
Structural analyses of yeast nuclei in different cell phases by X-ray diffraction imaging at cryogenic temperature using XFEL

Takahiro Yamamoto[1,2], Amane Kobayashi[2], Mao Oide[1,2], Koji Okajima[1,2], Tomotaka Oroguchi[1], Masaki Yamamoto[2], Masayoshi Nakasako[1,2] ([1]*Grad. Sci. Tech. Keio Univ.*, [2]*RSC, RIKEN*)

X-ray diffraction imaging (XDI) is a technique for visualizing internal structures of sub-micrometer-sized biological particles without sectioning and chemical labeling. A 2D electron density map of a particle projected along the direction of the incident X-ray is obtained by XDI. Furthermore, a 3D map averaged over particles can be reconstructed by applying the single particle analysis to a number of 2D electron density maps of various oriented particles, which they have similar structures. Here, we report 2D electron density maps and averaged 3D maps of yeast nuclei in the G1 and G2/M phases revealed by XDI experiments using X-ray free electron laser (XFEL) pulses at SACLA.

2Pos417 High-speed imaging of muscle myosin and super-resolution imaging of epidermal growth factor receptor with DNA origami technique

Keisuke Fujita[1,2], Michio Hiroshima[1], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*BDR, RIKEN*, [2]*Grad. Sch. of Front. Bioscience., Osaka Univ.*)

We have been developing single molecule measurement systems for many years, to understand how a complex biological phenomenon can be caused by single molecules. Now, we are trying to expand the capability of the single molecule measurement systems by combining DNA origami techniques, which are capable of constructing DNA nanostructures in a programmable way. To demonstrate the feasibility, we revisited the molecular mechanisms of two different biological phenomena, muscle contraction and multimerization of membrane proteins, which have been studied by the conventional single molecule measurements. In the meeting, we will discuss our novel experimental design for single molecule measurement and newly discovered dimensions of these two classical problems.

2Pos418 ゆらぎを利用した非侵襲力測定の軸索輸送動画解析への応用
Fluctuation-based non-invasive force measurement for dynamic image analysis of axonal transport

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Fluctuation is a typical property of protein and cell movement. Based on the fluctuation theorem, force acting on a molecule can be estimated non-invasively by analyzing fluorescent images. We have developed appropriate software for this measurement. The force involved in transporting APP (amyloid precursor protein) vesicles, by motor protein kinesin in the axon, was estimated using this software. Several kinesins were found to cooperatively produce force and transport an APP vesicles, and this cooperativity was shown to stabilize the axonal transport. In future, neuronal disorders, such as Alzheimer`s disease, may be investigated from the viewpoint of such a cooperative transport using this software.

2Pos419 生細胞核内における転写因子 MafG の２量体化に依存した１分子動態
Dimerization dependent single-molecule dynamics of MafG transcription factor in living cell

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MafG is a small Maf family transcription factor that plays a regulatory role in gene expression including hypoxic response. MafG forms repressive homodimers and activative or repressive heterodimers depending on the binding partner. However, the dynamics of dimerization in living cell is still elusive. Here, we quantified the single-molecule dynamics of MafG and its DNA-binding (N61G) and dimerization (L93D) mutants. Moving subtrajectory analysis revealed that both wild-type and mutants are composed of fast diffusive molecules and less mobile (confined) molecules. The confinement radius of the dimerization mutant is larger than that of the wilde-type and DNA-binding mutant, suggesting that dimerization contributes to the way in which MafG interact with chromatin.

2Pos420 遺伝子コード型抗体プローブを用いた翻訳後修飾の 1 分子イメージング
Single-molecule imaging of post-translational modification using genetically encoded antibody probe

Shuntaro Sato[1], Yuma Ito[1], Yuko Sato[2], Hiroshi Kimura[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*IIR, Tokyo Inst. Tech.*)

Post-translational modification of histones plays an important role in epigenetic gene expression regulation. Modification-specific intracellular antibody (mintbody) probes can be expressed in vivo and it is possible to follow histone post-translational modifications. In this study, we co-expressed H4K20me1-mintbody which specifically recognizes mono-methylated histone H4 at lysine 20 with EGFP tagged H4 in HeLa cell. Single-molecule imaging showed the immobile mintbody in the high intensity region of EGFP-H4, suggesting the specific binding of mintbody with modified histone. We will discuss nano-scale distribution of histone modification in cell nucleus by localization analysis of the mintbody molecules.

2Pos421 ヘテロクロマチンタンパク HP1α 動態の生細胞 1 分子イメージング
Dynamics of Heterochromatin protein 1α in living cells using single-molecule imaging

Takahiro Maeda[1], Yuma Ito[1], Shin-Ya Isobe[2], Chikashi Obuse[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Biosci. Grad Sch Sci., Osaka Univ*)

Heterochromatin protein 1α (HP1α) regulates gene expression by causing chromatin compaction and associating with a variety of proteins. The N-terminal chromodomain of HP1α binds with trimethylated histone H3 lysine 9, which causes the compaction. The C-terminal chromoshadow domain has two sites: a site for dimerization and a binding site for other proteins. We quantified the dynamics and interactions of the wild-type HP1α and two mutants, a protein-binding mutant and a dimerization mutant, using single-molecule tracking analysis. The wild-type and the two mutants showed two motility, fixed and mobile states. This analysis provides a tool for understanding the spatiotemporal switching of HP1α multifunctions via dimerization and association with other proteins.

2Pos422 悪性高熱症関連変異を有する骨格筋型リアノジン受容体の構造と機能変化
Structure and function change of skeletal muscle-type ryanodine receptor

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We investigated properties of the type 1 ryanodine receptor (RyR1) channels carrying disease-associated mutations at the N-terminal region. Malignant hyperthermia (MH) is a disorder of Ca^{2+}-induced Ca^{2+} release in skeletal muscles. HEK293 cells expressing the mutant RyR1 channels exhibited alterations in Ca^{2+} homeostasis, i.e., enhanced caffeine sensitivity, decrease of ER Ca^{2+} contents, increases in resting cytoplasmic Ca^{2+} concentration. Molecular dynamics analysis revealed that changes in pattern of electrostatic interaction were correlated with the alteration in Ca^{2+} homeostasis. This result suggests that exploration of the functional mutations of RyR1 is effective in preventive diagnosis of patients associated with MH disease.

2Pos423 ゼロモード導波路(ZMW)を用いた生体分子複合体の定量分析
Quantitative analysis of biomolecular complexes using Zero-Mode Waveguides (ZMW)

Kimiko Nakao[1], Hisashi Tadakuma[1], Yong-Woon Han[2], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*IMS., RIKEN*)

Analysis of fluorescence signal at single-molecule level provides stoichiometric information of biomolecular complexes. To perform precise analysis, background fluorescence noise should be reduced. Zero mode waveguides (ZMWs), in which biomolecules of interest are immobilized within nanoscale holes, are powerful devices to reduce the background noise and improve the signal-to-noise ratio of the observation. In this study, we measured several biomolecular complexes (e.g. holiday junction) to evaluate the performance of our home made ZMWs.

2Pos424 線形ゼロモード導波路を用いたアクチン重合の 1 分子解析
Single-molecule analysis of actin polymerization using linear zero-mode waveguides

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Actin polymerization occurs through nucleation, elongation, and the steady-state phase. A previous study showed that ends of actin filaments grow and shorten faster than expected from the measured rate constants of monomer association and dissociation. However, the reason of the discrepancy has not been clarified. We observed actin polymerization using single-molecule fluorescence imaging with linear zero-mode waveguides to investigate the oligomeric state of actin incorporated into the filament ends. We found that the monomers were associated with the filament ends in elongation phase, but small oligomers (dimer to trimer) were also associated with filaments in the steady-state phase. Furthermore, cooperative binding of actin at the filament ends was not observed.

3Pos001 ヒト成人ヘモグロビンの四量体構造の安定性に対する β サブユニットの Fe-His 結合の寄与
Contribution of the Fe-His Bond of the β Subunit to Stability of Tetramer of α2β2 in Human Adult Hemoglobin

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Stability of tetramer, $\alpha_2\beta_2$, of human adult hemoglobin (Hb A) is examined through ion-exchanged chromatography of rHb A, cavity mutant Hbs, both rHb(αH87G) and rHb(βH92G). There are no covalent bonds between F-helix and heme-imidazole in cavity mutant Hbs. Ion-exchange chromatography of Hb A and rHb(αH87G) show one component of tetramer, but rHb(βH92G) shows two or three components. One of the components in rHb(βH92G) showed dimer. This seems that detachment between F-helix and heme-imidazole of the β subunit in rHb(βH92G) promotes to shift tetramer-dimer equilibrium to dimer. We examined contribution of Fe-His bond to the stability of tetramer in Hb A by comparing resonance Raman results of Fe-His frequencies of rHb(βH92G) between tetramer and dimer.

3Pos002 ヘムタンパク質におけるヘム周囲のタンパク質環境の網羅解析
Global analysis of the protein environment around heme in hemeproteins

Hiroko X. Kondo[1], Masanori Fujii[1], Yusuke Kanematsu[2], Yasuhiro Imada[3], Yu Takano[2] ([1]*Fac. Eng., Kitami Inst. Tech.*, [2]*Grad. Sch. Info. Sci., Hiroshima City Univ.*, [3]*IPR, Osaka Univ.*)

Hemeprotein is a group of proteins containing heme as a cofactor. Hemeproteins play a wide range of vital roles in biological systems such as electron transfer, transportation and storage of oxygen, and signal transduction. Though the structure-function relationships have been clarified for individual hemeproteins, the origin of functional diversity is still unclear. The recent study of Imada et al. showed a relationship between the ruffled and saddled distortions of heme and their redox potentials by using density functional theory. In this study, we hypothesize that proteins regulate heme distortion, leading to changes in functions, and analyze the protein environment around heme for approximately 4,500 PDB entries of heme proteins.

3Pos003 鉄還元酵素ヒト Steap3 の分子機能解明
Analyses on the molecular function of human Steap3 as a ferric reductase

Akito Nakata[1], Mika Fujimura[1], Fusako Takeuchi[2], Motonari Tsubaki[1] ([1]*Dept. of Chem., Grad. Sch. Sci., Kobe Univ.*, [2]*IPHE, Kobe Univ.*)

Steap3 is known as a major ferric reductase in developing erythrocytes participating an important role in cellular iron uptake and, as a p53-targeted gene, it may act as a tumor suppressor by an unknown mechanism. Steap3 is predicted to receive electrons from cytoplasmic NADPH via flavin and heme to transfer them to the extracellular surface where they are used to reduce Fe3+ to Fe2+. However, little work has been done to describe its detailed functions. To clarify the details about the ferric reductase activity, we attempted and succeeded in expressing Steap3 by using Picia pastoris system. Analysis of the purified protein showed characteristic peaks in UV-visible spectra and NADPH-dependent ferric reductase activities.

3Pos004 呼吸鎖 A タイプ酸素還元酵素のカルシウムイオン結合構造
Calcium ion-binding structure of respiratory A-type oxygen reductase

Kazumasa Muramoto, Kyoko Shinzawa-Itoh (*Grad. Sch. Life Sci., Univ. Hyogo*)

Respiratory chain generates proton motive force coupled to electron transfer at high energy efficiency. Respiratory O_2 reductases are broadly classified into A, B and C-types based on their molecular structures.
A-type O_2 reductase isolated from bovine mitochondrial membrane contain sodium ion at the hydrophilic surface. It has been suggested that sodium ion was replaced by calcium ion, and the calcium-binding inhibited the enzymatic activity under limited conditions. In this study, to understand the effect of calcium-binding, we performed X-ray crystallographic analysis of the calcium-treated enzyme at 1.9 Å resolution, and determined structural change of the calcium-binding site.

3Pos005 金属タンパク質の酸化還元電位の第一原理計算
Ab initio evaluation of redox potential of metalloprotein

Cheng Cheng, Shigehiko Hayashi (*Kyoto Univ*)

Redox reactions take place in various fields, such as fuel cells, photosynthesis, energy storage and biological systems. Such reactions always occur in real and complicated bio-systems, contain flexible protein, mobile solvent water molecules and lipids. Electron transfer reactions are coupled to these fluctuations, show different properties rather than in water solutions. In this study, we evaluated the redox potential of cytochrome c by calculating the free energy difference. The calculated redox potential is 111.6 kcal/mol with an error bar of 0.6 kcal/mol, about only 4 kcal/mol overestimated rather than experimental value of 108.1 kcal/mol.We recommend it might be a rough but fast estimation of redox potentials in such metallic ligands combined proteins.

3Pos006 レーザーフラッシュフォトリシスによるリン脂質二分子膜へ再構成した proteorhodopsin の光サイクルに関する研究
A study on photocycle of proteorhodopsin reconstituted in phospholipid bilayer by laser flash photolysis

Airi Yamamoto[1], Fumio Hayashi[2], Toshinori Motegi[1], Takashi Kikukawa[3,4], Masashi Sonoyama[1] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Ctr. Inst. Anl., Gunma Univ.*, [3]*Fac. Adv. Life Sci., Hokkaido Univ.*, [4]*GI-CoRE, Hokkaido Univ.*)

Proteorhodopsin (PR), which was discovered through genomic analyses of naturally occuring marine bacterioplankton, is a light-driven proton pump with seven transmembrane helices like a well-studied membrane protein, bacteriorhodopsin. Previous biophysical studies of PR were mostly conducted in E. coli membrane and detergent micelles, therefore, effects of protein-lipid interactions on structural and functional properties of PR remain unknown. In this study, photocycle of PR in phospholipid bilayer membrane was investigated by laser flash photolysis, to reveal how photointermediates are modulated by phospholipid composition. It was shown that M intermediate is significantly affected by not only unsaturated bond in the acyl chain but also phase behaviors of lipid bilayer.

3Pos007 カロテノイド末端基のアシル化が及ぼすハロロドプシン-バクテリオルベリン複合体形成への影響
Effect of acylation of carotenoid terminal group on halorhodopsin-bacterioruberin complex formation

Fumiya Hattori, Takanori Sasaki (*Grad.Sch.Adv.Math.Sci.,Meiji Univ*)

A light driven anion pump halorhodopsin from ***N.pharaonis*** (NpHR) forms trimer on the membrane, and specifically binds a carotenoid of bacterioruberin (BR) at the crevice between the NpHRs. In this study, we compared the binding ability of the NpHR obtained from E.coli over-expression system against to the intact BR and the modified BR by acylation at the terminal OH group using gel filtration chromatography. When the NpHR and BR were mixed at the concentration ratio of 1:1.5, almost 100% of the NpHR-BR complex was formed. Contrary to this, only about 70% of the NpHR was calculated to form complex with the modified BR. These results suggest that the NpHR recognizes not only the hydrophobic backbone but also the terminal OH group of the BR for complex formation.

3Pos008 古細菌膜上におけるハロロドプシンのレチナール再結合能力
Retinal rebinding ability of halorhodopsin on archaeal membrane

Shun Yano, Takanori Sasaki (*Graduate School of Advanced Mathematical Sciences, Meiji University*)

Halorhodopsin (NpHR) from N.pharaonis is a retinal protein and forms a trimer on the archaeal membrane. Trimer NpHR also binds tightly with a carotenoid of bacterioruberin (BR) at the crevice between the NpHRs. To date, the retinal rebinding ability of NpHR on membranes has not been investigated in detail. In this study, we examined the retinal rebinding rate of the apoprotein haloopsin (NpHO) after bleached by hydroxylamine. About 10% of the NpHO has bound retinal when 0.25 μM of retinal was added to the apomembrane. In addition, retinal binding rate for NpHO was further increased by 15% when the apomembrane which removed the BR by Tween 20 was used. These results suggest the lipophilic molecules on the membrane affect to the retinal rebinding ability of the NpHO.

3Pos009 古細菌 *N.Pharaonis* 由来の膜タンパク質ハロロドプシンの複素環式化合物存在下における安定化
Thermal stability of halorhodopsin from *N.Pharaonis* in the presence of heterocyclic compound

Shinichiro Hayashi, Takanori Sasaki (*Grad. Sch. Adv. Math. Sci., Meiji Univ.*)

A light driven anion pump halorhodopsin (NpHR) binds Cl^- specifically in the ground state with dissociation constant about 2 mM, and its thermal stability is increased by binding Cl^-. In this study, we investigated whether a heterocyclic compound of 5-Chloro-2-methyl-4-isothiazolin-3-one (CMIT), which has 4.2 times more weight than Cl^-, contributes to the thermal stability of NpHR. NpHR under desalted condition and in the presence of 20 mM-NaCl were bleached about 73 and 41% by incubation at 55℃ for 30 min, respectively. In contrast, in the presence of 20 mM-CMIT, the bleaching ratio was only about 16%. These results suggest that CMIT binds to NpHR specifically and contributes significantly to its stabilization.

3Pos010 RxR の極めて高い熱安定性に対する統計熱力学
Statistical thermodynamics for the extremely high thermostability of a microbial rhodopsin from the eubacterium *Rubrobacter* (RxR)

Tomohiko Hayashi[1], Satoshi Yasuda[1,2,3], Kano Suzuki[2], Tomoki Akiyama[2], Kanae Kanehara[4], Yuki Sudo[4], Takeshi Murata[2,3,5], Masahiro Kinoshita[1] ([1]*Inst. Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Sci., Chiba Univ.*, [3]*MCRC, Chiba Univ.*, [4]*Fal. Pharm. Sci., Okayama Univ.*, [5]*PREST, JST*)

The denaturation temperature of RxR is by far the highest among the seven-transmembrane proteins. We determine its structure by X-ray crystallography and analyze the mechanism of the achievement of high thermostability. The theoretical tool is our free-energy function accounting for the solvent-entropy gain, formation of protein intramolecular hydrogen bonds (HBs), break of protein-water HBs, and recovery of water-water HBs upon the folding. The solvent is formed by hydrocarbon groups within the lipid bilayer and water molecules. The thermostability of RxR is compared with that of bacteriorhodopsin. We show that RxR is entropically and energetically more stabilized not only within the transmembrane region but also for its water-accessible portions.

3Pos011 サーモフィリックロドプシンの非常に高い熱安定性の物理起源
Physical origin of exceptionally high thermostability of thermophilic rhodopsin

Satoshi Yasuda[1,2,3], Tomohiko Hayashi[3], Yuta Kajiwara[4], Takeshi Murata[1,2,5], Masahiro Kinoshita[3] ([1]*Chiba Univ., Grad. Sch. Sci.*, [2]*Chiba Univ., MCRC*, [3]*Kyoto Univ., IAE*, [4]*Kyoto Univ., Grad. Sch. Ene. Sci.*, [5]*PRESTO*)

Thermophilic rhodopsin (TR) and xanthorhodopsin (XR) are photoreceptor proteins possessing seven helices. Although TR and XR share high similarity in the amino-acid sequence and almost the same structure, TR is much more thermostable. Here we compare the stabilities of TR and XR using our free-energy function (FEF) improved so that both of the water-accessible and transmembrane regions can be considered. We find that TR is more stabilized through a much larger decrease in energy relevant to protein-protein, protein-water, and water-water hydrogen bonds and through a closer packing of the backbone and side chains followed by a larger gain of solvent entropy upon the folding. The solvent is formed by hydrocarbon groups within the lipid bilayer and water molecules.

3Pos012 アルカリ条件下におけるバクテリオルベリンと古細菌脂質の結合に伴うハロロドプシンの熱安定化
Thermal stabilization of halorhodopsin by binding of bacterioruberin and archaeal lipids under alkaline condition

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Halorhodopsin from ***N.pharaonis*** (NpHR) binds archaeal lipids and bacterioruberin (BR) on the membrane. In this study, we researched the effect of binding of the BR and lipids to NpHR on its thermal stability. In particular, thermal bleaching ratios for NpHR obtained from ***E.coli*** expression system (eNpHR), artificial eNpHR-BR complex, and NpHR-BR-lipid complex from ***N.pharaonis*** were compared in Cl^- free, pH8.5 condition. Although eNpHR and eNpHR-BR were bleached about 52% and 20% at 40 ℃ for 1h, NpHR-BR-lipid was not bleached until 45 ℃. In addition, about 50% of bleached NpHR-BR-lipid recovered its active state immediately by addition of NaCl. These results suggest that the BR and lipids contribute to stabilization of NpHR and appearance of stable intermediate.

3Pos013 脂質二重膜中の AMPA 受容体の高速 AFM 観察
High-speed atomic force microscopy imaging of AMPA receptors in lipids

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AMPA-subtype ionotropic glutamate receptors play an important role in fast excitatory neurotransmission throughout the central nervous system. Recently, three-dimensional structures of AMPA receptors were solved by X-ray crystallography and cryo-electron microscopy with atomic resolution. However, dynamics of AMPA receptors caused by the binding of ligands was never observed yet. In this study, we applied high-speed atomic force microscopy (HS-AFM) to directly observe conformational changes of AMPA receptors at work in the lipid membrane. HS-AFM movies of AMPA receptor showed two fluctuated domains which correspond to the amino-terminal domains in the extracellular side. We would like to discuss an ion-transport mechanism of AMPA receptors based on our HS-AFM results.

3Pos014 High-speed AFM imaging of membrane protein embedded in Nanodisc

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High-speed atomic force microscopy (HS-AFM) permits direct observation of membrane proteins at high spatiotemporal resolution. The detergent-solubilized membrane proteins after purification are often reconstituted into liposomes or supported lipid bilayers. However, these methods sometimes cause problematic imaging of the small membrane proteins due to randomly distribution and orientation in a lipid bilayer, and the poor stability and the loss of activity of membrane proteins during preparation. Here, we applied Nanodiscs to HS-AFM observation of membrane proteins. In addition, Nanodiscs can keep membrane proteins stable and active at the single molecule level, which enables us to detect microscopic fluctuations of soluble domains of membrane proteins by HS-AFM.

3Pos015 構造生物学的解析に向けた TRPV3 のナノディスク化について
Reconstitution of TRPV3 into Nanodiscs for structural study

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TRPV3 is a member of TRPV ion channel family that responds to heat and chemical stimuli. Recent advances in cryo-EM technology enables to elucidate how the chemical ligands activate TRPV channels, however the mechanism of temperature induced channel opening is unclear. In this study, to determine the atomic structure of TRPV3 using cryo-EM, we tried to reconstitute human TRPV3 into proteinaceous nanodisc which was used for cryo-EM observations of several TRP channels. As a result of investigating the mixing ratio of TRPV3 with nanodsic and lipid, we found that the amount of added lipids was essential for proper reconstitution. In the meeting, we will also report the result for the purification of TRPV3 using styrene-maleic acid based nanodisc.

3Pos016 X 線 1 分子追跡法による TRPV1 チャネルの 3 次元運動
3D motion of TRPV1 cation channel depicted by diffracted X-ray tracking method

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The TRPV1 is a nonselective cation channel that responds to various signals including capsaicin, heat, and low pH condition. The Cryo-EM structures of TRPV1 have revealed some conformations. However, gating mechanisms of TRPV1 is not clearly understood. To understand the dynamics of TRPV1, we adopted the Diffracted X-ray Tracking (DXT) technique, in which individual protein was labeled with gold nanocrystals and the motion of X-ray diffraction spots from the gold crystals were investigated as the intramolecular movement of TRPV1 in real time. Here we observed molecular fluctuations of the TRPV1 proteins enhancement of twisting motions with capsaicin. This movement was further compared to the high temperature evoked TRPV1 activation together with mutational studies.

3Pos017 分子シミュレーションによるヘムインポーターの化学-力学共役機構の解明
Deciphering chemomechanical coupling mechanism of a heme importer with molecular simulations

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Heme importers belong to the large family of the type-II ATP-binding cassette (ABC) transporter. Recently, crystal structures of a bacterial type II heme importer in the nucleotide-free inward-facing form have been solved. Based on the structures and biochemical experiments, a molecular mechanism for the heme transport cycle was proposed. However, in the lack of atomic structures with bound nucleotides, the chemomechanical coupling mechanism underlying the transport cycle is not yet understood. In this study, computational modeling approach is adopted to predict the outward-facing form and the occluded intermediate of the heme importer with bound nucleotides. Based on these models, we propose a chemomechanical coupling mechanism of the heme importer.

3Pos018 Nanodisc を用いたリン脂質二重膜環境中におけるヒトセロトニン受容体の機能解析
Functional analyses of human serotonin receptor in phospholipid membrane environments using Nanodisc

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Nanodisc technology is a powerful tool for physicochemical analysis of membrane proteins *in vitro*. Additionally, it allows us to investigate the effects of lipid composition on the activity of membrane proteins. Here, we showed that membrane flexibility affected the functional activity of human serotonin receptor (5HTR) using Nanodisc. SPR and MST measurements clarified that 5HTR lost its activity in the phospholipid which had high-transition-temperature. Moreover, MD simulations demonstrated that the transition-temperature influenced the dynamics of 5HTR in the lipid bilayer. Our study indicated the necessity of lipid-GPCR interaction and proposed that appropriate choice of the lipid is important in the physicochemical characterization for the GPCR using Nanodisc.

3Pos019 ATR-FTIR を用いた細菌べん毛固定子のイオン透過経路の解析
Analysis of Na+-conducting pathway in the stator complex of the bacterial flagellar motor by ATR-FTIR spectroscopy

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Bacterial flagellum is a rotary motor like screw. Force for rotation is generated by stator-rotor interaction coupled with Na+ influx through the stator PomA/B complex. Sodium ions go through channel pore formed by transmembrane segments of the stator complex. However, it is still obscure what residues contributed in ion channel pathway except essential Asp residue in PomB. Here, we tried to measure Na+-induced structural changes by ATR-FTIR, then assign signals in a difference ATR-FTIR spectrum of NaCl- minus KCl-condition. We showed that positive signal at 1115 cm-1 is the C-O stretch mode of PomA-T158 and -T186 because Ser substitutions caused split of the 1115 cm-1 signal. Furthermore, we will discuss about Na+ influx mechanism through essential Asp residue.

3Pos020 マグネシウムイオンチャネル MgtE のイオン―タンパク質間相互作用の振動解析
Vibrational analysis for studying ion-protein interactions of a magnesium ion channel, MgtE

Tetsunari Kimura[1,2,7], Victor Lorenz-Fonfria[3,4], Shintaro Doki[5], Hideyoshi Motoki[6], Ryuichiro Ishitani[5], Osamu Nureki[5], Masahiro Higashi[6], **Yuji Furutani**[1,2] ([1]*Inst. Mol. Sci.*, [2]*SOKENDAI*, [3]*ICMol, Univ. Valencia*, [4]*Dep. Biochem. Mol. Biol., Univ. Valencia*, [5]*Grad. Sch. Sci., Univ. Tokyo*, [6]*Grad. Sch. Eng. Sci., Univ. Ryukyus*, [7]*Grad. Sch. Sci., Kobe Univ.*)

Magnesium ions are vital for living systems and utilized for various biological processes. MgtE is an ion channel highly selective to Mg^{2+}. Here, the molecular mechanisms of the ion selectivity for Mg^{2+} has been studied by ion-exchange induced difference FTIR spectroscopy with an aid of computational methods. Stretching vibrations of the carboxylate group of Asp432 in the central cavity were identified and their difference in interactions with Mg^{2+} and Ca^{2+} were investigated. We also elucidated that dissociation constant for Mg^{2+} in the cavity is much smaller than that for Ca^{2+}. Molecular dynamics showed that the difference would be explained by much higher stability in hydration of Mg^{2+} in the cavity.

3Pos021 A Multiscale Model for Flavivirus Dynamics & Host Interactions

Jan K. Marzinek, Roland G. Huber, Daniel A. Holdbrook, Peter J. Bond (*Bioinformatics Institute (A*STAR), #07-01, Matrix, 138671 Singapore*)

A multiscale simulation approach has been employed here to investigate the pathways between virion conformations associated with the dengue life cycle. We generated a near-atomic resolution model of the complete viral envelope containing proteins embedded within a lipid bilayer vesicle, and validated this against cryo-electron microscopy maps. We probed viral protein conformational changes associated with host environmental triggers, such as changes in pH and temperature, and antibody interaction. Supported by diverse biophysical data, this work enables us to propose mutations capable of blocking viral infection, and to gain novel insights into the structural basis for neutralization, maturation, and enhancement of infection upon binding of different antibodies.

3Pos022 Direct reconstitution of membrane proteins from cell membrane blebs into a model biological membrane

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Studying mammalian membrane proteins in a model membrane is rather limited due to the difficulties to purify a large amount of proteins and reconstitute them into the membrane with the native structure and orientation. We reconstitute membrane proteins into a model membrane by using blebs that bud off from the cell membrane. We expressed GPCR and GPI-anchored protein (GPI-AP) in CHO cells and produced blebs by chemical induction. A planar membrane was formed on the substrate surface, and single molecules of GPCR and GPI-AP were observed in a nanometric gap structure between the substrate and a PDMS elastomer sheet. This methodology enables to evaluate the physicochemical properties and functions for a wide range of mammalian membrane proteins.

3Pos023 1 分子イメージングによる PDGF 受容体-Akt シグナル伝達の研究
Single molecule imaging study on PDGF receptor and Akt signal transduction

Hideaki Yoshimura, Takeaki Ozawa (*Department of Chemistry, School of Science, The University of Tokyo*)

Akt is a signaling hub molecule that receives various signals and transduces them to stimulate appropriate downstreams. However, the original function of Akt is just a kinase, and the mechanisms to regulate signal transduction pathways is still not understood. In this study we performed single molecule live cell imaging of Akt and platelet-derived growth factor (PDGF) receptor to reveal the mechanisms.

3Pos024 Solubilization and purification of the Rieske/cytochrome *b* complex in green sulfur bacteria

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The *b* subunit in cytochrome (cyt) *bc* complexes has two types. One is a single contiguous polypeptide in bc_1 complexes, and another is split into two separate proteins, cytochrome b_6 and subunit IV, in b_6f complexes. The former contains 8 transmembrane helices and two hemes (b_H and b_L), but the latter does 7 ones and the third heme c_n additionally. The *b* subunit in the Rieske/cyt*b* complex of green sulfur bacteria (GSB) is supposed to contain only 7 helices regardless of the presence of two hemes based on its structural modeling. This implies that the *b* subunit of GSB would be located at a branch point evolutionary from bc_1 to b_6f complexes. We are now working on solubilization and purification of the Rieske/cyt*b* complex for its X-ray crystallographic analysis.

3Pos025 線虫 Cytochromeb_{561} ホモログ Cecytb-2 のアスコルビン酸特異的電子伝達反応解析
Analyses on the ascorbate-specific electron transfer function of Cecytb-2, a cytochrome b_{561} homolog in *Caenorhabditis elegans*

Misaki Fukuzawa, Mika Fujimura, Masahiro Miura, Tetsunari Kimura, Motonari Tsubaki (*Dept. of Chem., Grad. Sch. Sci., Kobe Univ.*)

Cytochrome b_{561} is a heme-containing membrane protein residing in neuroendocrine vesicles and regenerates ascorbate. In higher animals, there are 6 homologues belonging to the b_{561} family. One of them, Dcytb is a ferric reductase localized in the duodenum and this activity is very important for the iron uptake. Cecytb-2, one of 7 members of the b_{561} family in *C. elegans*, is most similar to Dcytb and is specifically expressed in digestive organ. In this study, we attempted to clarify the ascorbate-binding site. We have introduced several mutations around the putative ascorbate-binding site and expressed the mutants using *Pichia pastoris* system. We have analyzed reactions of the purified proteins with ascorbate to clarify the molecular mechanism of the electron transfer.

3Pos026 三量体オートトランスポーターの構造形成における荷電残基の役割
Roles of charged residues on assembly of the trimeric autotransporter transmembrane domain

Eriko Aoki, Daisuke Sato, Kazuo Fujiwara, Masamichi Ikeguchi (*Fac. of Sci. and Eng., Soka Univ.*)

Haemophilus Influenzae adhesin (Hia) belongs to the trimeric autotransporter family and consists of passenger and transmembrane domains. The transmembrane domain forms a 12-stranded β-barrel in which four strands are provided by each subunit. This domain has a unique arginine cluster, in which the side chains of the three arginine residues located at position 1077 (Arg1077) protrude into the pore of the β-barrel. In this study, we investigated the assembly of 77- and 107-residues fragments encompassing transmembrane domain and of their mutant proteins, in which Arg1077 was replaced with methionine or lysin. Results showed that electrostatic repulsion between the positive charges of Arg1077 is important for preventing the formation of misassembled oligomers in vitro.

3Pos027 Ubiquitination of MHCII changes tendency of antigen presentation due to structral conversion of MHCII

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Ubiquitination of MHC II reduce the amount of surface MHC on antigen presenting cell that is required for immune attenuation. However, recent reports suggested that the ubiquitinated MHC II may have distinct function, i.e. positive selection, T-reg induction. Therefore, we tried to find a structural difference of the ubiquitinated MHC II. We used ubiquitin ligase MARCH I KO mice to find difference in antigen presentation from wild type. We then transfected B cell lines with beta K225Rmutant. The motion of MHC II on the cell was measured by Diffracted X-ray Blinking (DXB), which revealed faster motion of WT MHC II than K225R mutant that may due to ubiquitination. We suggest that ubiquitinated MHCII has discrete structure that affect T cell activity.

3Pos028 Light-induced FTIR spectroscopic studies on quinone exchange mechanism of the LH1-RC complexes from native and chimeric purple bacteria

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In purple bacteria, a light-harvesting 1 (LH1) complex surrounds a type-2 reaction center (RC) to form an LH1-RC complex. It is believed that light-induced quinone reduction results in formation of quinol, which transfers to quinone pool through the LH1-ring. The Rba. sphaeroides LH1 is a C-shaped ring with PufX, while the Tch. tepidum LH1 is a O-shaped ring without PufX-like protein. TS2, a chimeric mutant, has the Tch. tepidum LH1 and Rba. sphaeroides RC and exhibits unique properties originated from both species. In the present study, the light-induced quinol formations of these species were monitored by FTIR spectroscopy in combination with isotope labeling and quinone replacement. Based on these findings, quinone/quinol exchange mechanisms are discussed.

3Pos029 光化学系 II の水の酸化反応における D1/V185 の役割
The role of D1/V185 in the water oxidation mechanism in Photosystem II

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Water oxidation reaction is catalyzed by Mn_4CaO_5 cluster in Photosystem II (PSII), but the mechanism is not still understood well. Hydrophobic amino acid, D1/V185, locates approximately 4 Å distance from both O5 of Mn_4CaO_5 cluster and Cl^-. Among hydrophilic environments from O5 to thylakoid lumen, D1/V185 is an unique hydrophobic residue. In this work, for understanding the role of the D1/V185 in the water oxidation mechanism, we constructed site-directed mutant D1/V185T of *Thermosynechococcus elongatus*, and analyzed effects on water oxidation function by using isolated PSII complexes. Water oxidation activity of this mutant PSII was 10 times less than wild type PSII, and kinetics of S_3 to S_0 in the mutant was significantly slow down compared to that of wild type.

3Pos030 Thermodynamic Dissociation Kinetics assay to determine the binding strengths within a membrane protein complex

Eunchul Kim, Ryutaro Tokutsu, Akimasa Watanabe, Jun Minagawa (*National Institute for Basic Biology*)

While membrane proteins have important roles in cells, interactions within membrane protein complexes have been hardly studied than that within soluble proteins due to the lack of suitable methods. Here, we present an approach to determine binding strengths within a membrane protein complex by investigating the thermodynamic dissociation kinetics of an isolated membrane protein complex using time-resolved fluorescence spectroscopy. We demonstrated different bindings of light-harvesting complex II (LHCII) trimers in a photosystem II (PSII) supercomplex isolated from a green alga Chlamydomonas reinhardtii. As a result of analysis on thermodynamic dissociation kinetics, we identified three different activation energies for the dissociations of LHCII trimers.

3Pos031 Biosynthesis of Gold Nanoparticles by photosynthetic apparatus

Hiroki Matsumura[1], Rie Nagayoshi[1], Mariko Miyachi[2], Daiki Nishiori[2], Yoshinori Yamanoi[2], Hiroshi Nishihara[2], **Tatsuya Tomo**[1] ([1]*Faculty of Science, Tokyo University of Science*, [2]*School of Science, The University of Tokyo*)

Gold nanoparticles have attracted much attention in many areas of physics, chemistry and artificial photosynthesis because of their unique physicochemical properties compared to those of the bulk gold crystals. In this study, we performed to synthesis gold nanoparticles by photosynthetic apparatus (e.g. thylakoid, cell, chlorophyll) . When we mixed thylakoid, cell, chlorophyll and $HAuCl_4$ solution, the colour of suspension turned from green-yellow to purple. The purple suspension had an absorption maximum at 540 nm. The unique feature of gold nanoparticles is their optical properties due to surface plasmon resonance. We will discuss the formation mechanism and applications of gold nanoparticles for artificial photosynthesis.

3Pos032 クロロフィル d を主要色素とするシアノバクテリア光化学系 II における分光特性
Absorption and fluorescence properties of Photosystem II complex in a chlorophyll d-dominated cyanobacterium

Reona Toyofuku[1], Seiji Akimoto[2], Toshiyuki Shinoda[1], Tatsuya Tomo[1] ([1]*Grad. Sch. Sci., Tokyo Univ. Sci.*, [2]*Grad. Sch. Sci., Univ. Kobe.*)

Chlorophylls (Chls) play essential roles in energy transfer, charge separation and electron transfer in Photosystems (PSs) I and II. Acaryochloris marina is a unique cyanobacterium that differs from the majority of photosynthetic organisms by having Chl d as the major pigment (>95%). In our previous analyses, a small number of Chl a were bound in PS II complex. If the Chl a is involved in the charge separation process, our current understanding of the overall energetics of the PS II would need to be modified. In this study, we isolated the PS II core and PS II reaction center (RC) complexes from A. marina. We analyzed the spectroscopic analyses of PS II and PS II RC. We will discuss the characteristics of energy transfer in chlorophyll d-dominated cyanobacterium.

3Pos033 The orientation of menaquinone in the heliobacterial reaction center analyzed with the EPR spectroscopy

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The reaction center of heliobacteria (hRC) forms a homodimeric structure and has been supposed to be functionally and structurally related to the heterodimeric photosystem I (PSI) RC in plants and cyanobacteria. We previously identified a new electron spin-polarized (ESP) EPR signal derived from the radical pair state of $P800^{+}$ and reduced menaquinone (MQ^{-}) in the hRC from *Heliobacterium modesticaldum*. However, the recently revealed structure of the hRC contained no quinone molecule within it. Therefore, the function and location of MQ in hRC is still unclear and under debate. We measured the angular dependence of the ESP signal using oriented membranes of *Hbt. modesticaldum*. The results suggested a unique arrangement of MQ in hRC compared to that in PSI RC.

3Pos034 Role of D1-Ser169 near O4 of the Mn4CaO5 cluster in photosynthetic water oxidation

Yuichio Shimada[1], Tomomi Kitajima-Ihara[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*RIIS, Okayama Univ.*)

In photosynthetic water oxidation, the involvement of a water chain starting from O4 of the Mn4CaO5 cluster has been proposed; however, direct experimental evidence has not been obtained yet. In this study, a site-directed mutant of D1-S169, which interacts with a water molecule H-bonded with O4, was characterized by thermoluminescence (TL) and delayed luminescence (DL) measurements. The TL glow curves of D1-S169A cells were similar to those of WT, whereas the flash-number dependence of DL showed a monotonic increase without oscillation. This indicates that transitions after S2 were inhibited in S169A without changes in the redox potentials of the Mn4CaO5 cluster, suggesting the involvement of the water molecule interacting with O4 and D1-S169 in proton/water transfer.

3Pos035 光合成水分解反応の S2→S3 遷移におけるプロトン共役電子移動の時間分解赤外分光解析
Mechanism of proton-coupled electron transfer in the S2-S3 transition of photosynthetic water oxidation revealed by TRIR analysis

Hiroshi Takemoto, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

Photosynthetic water oxidation proceeds through a light-driven cycle of five intermediates called S states (S0-S4). Sakamoto et al. (JACS, 2017) recently studied the reaction process during the S2-S3 transition using time-resolved infrared spectroscopy, and assigned the 2nd phase (t2) to water transfer and the 3rd phase (t3) to proton-coupled electron transfer. In this study, we further characterized the reaction process of this transition by examining the pH dependence of these phases. The result showed that t3 significantly decreased at a lower pH, whereas no specific pH dependence was observed in t2. It was thus concluded that proton transfer takes place as a rate-limiting process of the proton-coupled electron transfer in the last phase of the S2-S3 transition.

3Pos036 Effect of replacement of Cl- with NO3- on photosynthetic water oxidation as studied by time-resolved infrared spectroscopy

Yasutada Okamoto, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

Photosynthetic water oxidation is catalyzed at the Mn cluster through a light-driven cycle of intermediates called S states. Although several proton channels from the Mn cluster have been proposed, it remains unclear which channel is used in each S-state transition. In this study, we investigated the involvement of the proton channel near Cl- in water oxidation by examining the effect of replacement of Cl- with NO3- using time-resolved infrared spectroscopy. It was shown that NO3- substitution slowed the rates of both of the S1->S2 and S2->S3 transitions. It is thus possible that NO3- substitution retards proton transfer through the channel near Cl- in the S2->S3 transition, while it may also change the redox potential of the Mn cluster affecting the S1->S2 transition.

3Pos037 FTIR-spectroelectrochemical study on the pH dependence of the redox potential of the non-heme iron in photosystem II

Hiroki Watanabe, Takumi Noguchi, Yuki Kato (*Grad. Sch. Sci., Nagoya Univ.*)

Photosystem II possesses a redox-active non-heme iron between two quinone electron acceptors, QA and QB, on the electron-acceptor side. The redox potential of the non-heme iron, Em(Fe2+/Fe3+), is known to be ~+400 mV at pH 7 with a pH dependence of -60 mV/pH. However, the mechanism of this pH dependence remains unresolved. In this study, to elucidate the mechanism of the pH dependence of Em(Fe2+/Fe3+), we measured the Em(Fe2+/Fe3+) in a wide pH range using FTIR-spectroelectrochemistry. The Em(Fe2+/Fe3+) indeed showed a pH dependence of ~-60 mV/pH at pH 6.5-7.5, whereas the Em change was much smaller at pH 5.5-6.5. Analysis of the pH dependence curve revealed that a single amino acid residue with pKa of ~6.0 is responsible for the pH-induced shift of Em(Fe2+/Fe3+).

3Pos038 QM/MM analysis of the DOD vibrations of water molecules around the Mn4CaO5 cluster in photosystem II

Masao Yamamoto, Shin Nakamura, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

Photosynthetic water oxidation is performed at the Mn4CaO5 cluster in photosystem II. Although the X-ray structure showed several water molecules around the Mn4CaO5 cluster, their roles in water oxidation remain unresolved. In this study, we calculated the DOD bending vibrations of D2O molecules near the Mn4CaO5 cluster using the QM/MM method to analyze the DOD bands observed in FTIR difference spectra. The calculated spectrum showed a fine agreement with the experimental spectrum in the DOD region (1250-1140 cm-1). Some bands were assigned to water ligands to the Ca and Mn ions, which are candidates of substrate water. This result demonstrated that FTIR detection of the DOD vibrations is useful to monitor the reactions of water molecules involved in water oxidation.

3Pos039 光合成における電子伝達体拡散のルーメン環境依存性に関する理論的研究
Theoretical studies on dependence of diffusion of electron carriers in photosynthesis on environment in lumen side

Hidemi Nagao, Isman Kurniawan, Arwansyah Saleh, Koichi Kodama, Satoshi Nakagawa, Kazutomo Kawaguchi (*Kanazawa University*)

Plastocyanin(PC) is one of type I copper proteins which have one copper ion in their active site. In photosynthesis, PC transfers one electron from cytochrome f in cytochrome b6f complex to P700 in Photosystem I by diffusing in the lumen side of the thylakoid membrane. We discuss the diffusion processes of PC with the electron transfer in the lumen side by using a simple coarse-grained model in relation to the environment of the lumen side with the concentration gradient of the electron carriers.

3Pos040 LOV を導入したファシンによるアクチン束化の制御
Regulation of actin bundles by using LOV-fused fascin

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Optogenetically controlling actin architecture is a potent approach to reveal functions of cytoskeletal structure and to regulate cell motilities. LOV2 domain is one of the optogenetic strategies to sterically open and close the binding site with and without lights. We fused LOV2 domain to fascin, an actin bundling protein to investigate how actin bundles contribute to actin cytoskeleton and cell motility. Low speed sedimentation and TIRF assays showed that the purified LOV-fascin has a similar bundling activity with fascin only (control). The bundling efficiency is not dramatically changed with and without lights. We will genetically facilitate the LOV2 driven inhibition for actin binding site on fascin.

3Pos041 Aureo 1 における C 末端 Jα ヘリックスの役割
The role of the C-terminal Jα helix in Aureochrome-1

Hiroto Nakjima, Osamu Hisatomi, Itsuki Kobayashi (*grad.sch.sci.,Univ.Osaka*)

Photozipper (PZ) has a basic leucine zipper (bZIP) domain and a light-oxygen-voltage-sensing (LOV) domain of Aureochrome-1. Blue light-induced dimerization increased the affinity of PZ for the target sequence. Since C-terminal helix (Jα) of LOV domain was suggested to have an important role on phototropin function, we prepared mutant PZs in which site-directed mutation and deletion were introduced in the Jα helix of PZ. Upon illumination, all PZ mutants showed similar changes to wild-type PZ in absorption spectra, hydrodynamic radii and affinities to DNA. However, our data suggested that C-terminal region significantly reduced the stability of PZ.

3Pos042 Calcium concentration modulation in HeLa cells induced by mid-infrared laser irradiation

Yoshiyuki Shimizu, Toyohiko Yamauchi, Tatsuo Dougakiuchi, Gen Takebe (*Hamamatsu Photonics K.K.*)

We report that we successfully induced changes in intracellular calcium concentration in HeLa cells by mid-infrared laser irradiation. The irradiation laser was a quantum cascade laser with a wavelength of 6.1 micrometer. Live cells were cultured on specially prepared silicon bottom dishes and stained using a calcium-sensitive dye, Calcium Green-1. The cells at the irradiated area showed oscillations in their intracellular calcium concentration synchronized with the periodic mid-infrared irradiation, but had a pattern different from the temporal change of temperature. This result implies that mid-infrared light can directly change the ionic response within cells and have the ability to modulate cell functions.

3Pos043 光駆動プロトンポンプ型ロドプシンのシロイヌナズナへの異種発現の試み
An attempt of heterologous expression of light-driven proton pump rhodopsins in the higher plant *Arabidopsis thaliana*

Saki Inoue[1], Yurie Nagase[2], Kyohei Harada[3], Keiichi Kojima[1,2], Shintaro Munemasa[4], Susumu Yoshizawa[5], Yoshiyuki Murata[4], Shinji Masuda[6], Yuki Sudo[1,2] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Fac. of Pharm. Sci., Okayama Univ.*, [3]*Grad. Sch. Biosci. Biotechnol., Tokyo Inst. Technol.*, [4]*Grad. Sch. Environ. Life Sci., Okayama Univ.*, [5]*AORI, UTokyo*, [6]*Cent. Biolog. Resources & Informatics, Tokyo Inst. Technol.*)

Microbial rhodopsins are used as optogenetic tools for controlling biological functions by light mainly in animals. In contrast to the typical functions of microbial rhodopsins as an “outward” proton pump, such as AR3, we recently identified a new rhodopsin named *Rm*XeR as an “inward” proton pump [Inoue et al., 2018, PCCP]. Thus, it is theoretically possible to control the pH inside the cells using AR3 and *Rm*XeR. Plants can survive under strong light stress, where changes in pH inside the thylakoid of chloroplast is considered to play an important role. To elucidate the mechanism, we tried to express AR3 and *RmXeR* in the thylakoid membranes of the higher plant *Arabidopsis thaliana*. In the meeting, we will present the progress of the challenging research.

3Pos044 緑藻クラミドモナスの葉緑体へのプロトンポンプ型ロドプシンの異所発現と葉緑体プロトン濃度勾配制御の試み
Expression of proton pump rhodopsins in the chloroplast of the alga *Chlamydomonas reinhardtii* for optical control of proton gradient

Yurie Nagase[1], Saki Inoue[2], Hiroshi Kuroda[3], Keiichi Kojima[1,2], Susumu Yoshizawa[4], Yuichiro Takahashi[3], Yuki Sudo[1,2] ([1]*Fac. of Pharm. Sci. Okayama Univ.*, [2]*Grad. Sch. of Med. Dent. Pharm. Sci. Okayama Univ.*, [3]*RIIS. Okayama Univ.*, [4]*AORI, UTokyo.*)

Microbial rhodopsins are useful optogenetics tools to control biological functions by light. In addition to the outward proton pump rhodopsins such as AR3, we recently reported an inward proton pump rhodopsin (*Rm*XeR) [Inoue et al., PCCP 2018]. It is known that proton gradient across the thylakoid membrane in the chloroplast plays essential roles in plants. Here, we introduced the genes of AR3 and *Rm*XeR in the chloroplast genomes of the alga *Chlamydomonas reinhardtii*. We cultured the algae with varying retinal concentrations (0~10μM). Western blotting analysis indicated that the algae cultured with 2μM retinal showed the effective expression without strong inhibition of the growth. We try to examine the effect of the light on the physiological aspects of the alga.

3Pos045 Development of Red-Shifted Channelrhodopsin Variants Using Long-Conjugated Retinal Analogues

Yi-Chung Shen[1], Toshikazu Sasaki[1], Takesi Matsuyama Hoyos[1], Takahiro Yamashita[1], Yoshinori Shichida[1,2], Takashi Okitsu[3], Yumiko Yamano[3], Akimori Wada[3], Toru Ishizuka[4], Hiromu Yawo[4], Yasushi Imamoto[1] ([1]*Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.*, [2]*Res. Org. for Sci. & Tech., Ritsumeikan Univ.*, [3]*Lab. of Organ. Chem. for Life Sci., Kobe Pharm. Univ.*, [4]*Dept. of Dev. Bio. & Neurosci., Grad. Sch. of Life Sci., Tohoku Univ.*)

Most channelrhodopsins effectively absorb blue-green light which is highly attenuated in the animal tissues. In this study, we red-shifted the absorption spectrum of channelrhodopsin by introducing the all-trans-retinal analogues with extra C=C at different positions. Chimeric channelrhodopsin C1C2 bearing these analogues showed the absorption spectra broadened toward the long wavelength side, with the formation of photocycle intermediate similar to the conducting state. Expansion of the chromophore binding pocket by mutation (F265A) improved the binding efficiency of analogues. Our results show that elongation of the conjugated double bond system of retinal is a promising strategy to enhance the long-wavelength light absorption of channelrhodopsin.

3Pos046 Theoretical study on molecular mechanism of a light-driven ion transport of Halorhodopsin

Ryo Oyama, Taisuke Hasegawa, Shigehiko Hayashi (*Grad. Sch. Sci., Univ. Kyoto*)

Halorhodopsin from Natronomas pharaonis functions as an inward light-driven chloride pump and is utilized to silence neurons in optogenetics technique in neuroscience. The chromophore retinal isomerizes from all-tran conformation to 13-cis one upon photoabsorption, and triggers a photocycle during which one chloride ion is transported across the membrane. In this study, we performed QM/MM RWFE-SCF calculations to examine the functional coupling of the structural change of the chromophore isomerizing from all-trans conformation to 13-cis one described at the quantum chemistry level of theory with protein large conformational changes of alternating access for the active transport of the ion described with MD simulations with a MM force field.

3Pos047 シグナル伝達分子の細胞膜上空間分布解析
Spatial distribution analysis of signaling proteins on the cell membrane

Hiroaki Takagi[1], Yukihiro Miyanaga[2], Satomi Matsuoka[3], Masahiro Ueda[2,3] ([1]*Sch. Med., Nara Med. Univ.*, [2]*Grad. Sch. Front. Bio. Sci., Osaka Univ.*, [3]*BDR, Riken*)

The positions of chemotactic receptor cAR1 (GPCR) on the cell membrane were comprehensively measured by PALM imaging in Dictyostelium cells. Spatial statistical analysis showed that cAR1 distribution is not uniformly random, and the attractive interaction among receptors is apparently suggested. Hierarchical cluster analysis showed that the cluster size follows a power-law like distribution. The effects of membrane lipid and cytoskeleton were characterized by measuring the positions of cAR1 in each inhibitor treated cells. Furthermore, the positions of PTEN, downstream molecule in signaling, were measured and the differences in distribution between cAR1 and PTEN were characterized. Possible mechanisms and functional significance of these findings will be discussed.

3Pos048 大腸菌走化性応答における CheY 極局在の役割
Role of polar localization of chemotaxis protein CheY for the intracellular signaling under non-stimulated conditions in *Escherichia coli*

Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Dept. Frontier Biosci., Osaka Univ*)

CheY localize at cell pole via histidine kinase CheA. Our resent study proposed that a transient increase and decrease in the CheYp concentration ([CheYp]) induces the switching coordination of flagellar motors. To understand the role of polar localization of CheY, we measured the switching coordination of motors on the cell with *cheA(F214A)* mutant which defects CheY binding. In the mutant, the switching of motors did not coordinate but their CW biases correlated. The localization of CheY and switching coordination were restored by the co-expression of wild-type CheA short. Thus, the polar localization of CheY may be important for the switching coordination, suggesting that the efficient phosphotransfer from CheA to CheY is responsible for the drastic change of [CheYp].

3Pos049 コレラ菌タウリン走性受容体 Mlp37 の温度依存的遺伝子発現
Temperature-dependent gene expression of the taurine sensor Mlp37 of *Vibrio cholerae*

So-ichiro Nishiyama[3], Shiori Onogi[1], Yoshiyuki Sowa[1,2], Hiroshi Urakami[3], Ikuro Kawagishi[1,2] ([1]*Dept. Frontier Biosci., Hosei Univ.*, [2]*Res. Cen. Micro-Nano Tech., Hosei Univ.*, [3]*Fac. App. Life Sci., Niigata Univ. Pharm. App. Life Sci.*)

Vibrio cholerae, the etiological agent of cholera, shows chemotaxis toward taurine, a component of bile. We previously found that the bacterium shows elevated taurine taxis when cultured at 37ºC rather than lower temperature, due to the transcriptional activation of the gene for the taurine chemoreceptor Mlp37. It has been known that *V. cholerae* controls the expression levels of its virulence factors by ToxR network in a temperature-dependent manner. We found that a *toxR* mutant showed temperature-independent taurine taxis. Experiments with *toxR* and other related mutants are underway to further understand the transcriptional regulation of the *mlp37* gene.

3Pos050 ファインバブル水を利用したタンパク質結晶化の新しいアプローチ
Novel approach for protein crystallization with ultrafine bubble water

Taichi Naruse[1], Mihoka Amano[1], Hiroaki Adachi[2], Shigeo Maeda[3], Toshihiro Fujita[3], Yusuke Mori[4], Shigeru Sugiyama[5] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*SOSHO Inc.*, [3]*IDEC Corp.*, [4]*Grad. Sch. Eng., Osaka Univ.*, [5]*Fac. Sci. & Tec., Kochi Univ.*)

Ultrafine bubbles have been favorably applied in a wide variety of areas, such as health, agriculture, food engineering, and chemical engineering. Generally, one of the important problems in protein crystallization is low reproducibility and low nucleation rate. Lately, we discovered that the rapid shrinkage of a laser-induced cavitation bubble generates a local high concentration of protein, implying that it could work as a nucleation trigger of protein crystals. Therefore, we studied the nucleation rate of protein crystals in the presence of ultrafine bubbles, finding that ultrafine bubbles accelerated the number of trypsin and lysozyme crystals. This new technology using ultrafine bubble water will present a wide variety of possibilities for protein crystallization.

3Pos051 国産無償創薬ソフトウェア myPresto の進展：ΔG 推算を中心に
Progress of free drug development software suite myPresto: focusing on ΔG estimation

Tadaaki Mashimo[1,2], Yoshifumi Fukunishi[3] ([1]*N2PC*, [2]*IMSBIO Co., Ltd.*, [3]*AIST(molprof)*)

myPresto version 5 (https://www.mypresto5.jp/) is free drug development computer software suite of Japanese origin, released at the beginning of Feb. 2018, including new features, the membrane structure modeling program "Membgene" and the GUI program "myPresto Portal". In addition, we developed docking score QSAR which is ΔG estimation method and is preparing for release. Docking score QSAR is a method of estimating binding free energy by a weighted average of docking scores for arbitrarily selected 600 probe proteins. The estimation model is calculated by descriptor-based weighted PCR with a regularization term. The compound activities of 107 kinases can be predicted with $Q^2 = 0.70$ (average error = 1.08 kcal/mol), based on a public database.

3Pos052 The binding mechanism of Hepatitis B virus X protein to Smc5/6 complex

Katsumi Omagari, Yasuhito Tanaka (*Nagoya City Univ.*)

The selective degradation of proteins in eukaryotic cells is important mechanism for maintenance of life. Hepatitis B virus hijacks the cellular DDB1 to targer Smc5/6, which does not associate with DDB1 in the cells uninfected with HBV, for uqiquitation so that enhance the transcription. HBx protein of HBV binds to the cellular DDB1 to target the Smc5/6 for degradation. To understand how HBx promotes to degrade Smc5/6, We developed the screening system for binding sites of HBx protein for DDB1 and Smc5/6. The binding sites of HBx, which is essential for DDB1 binding, were identified. And Smc5/6 could bind to DDB1 together with the HBx protein in the cells. The results suggest that those binding sites are useful for development of new antiviral drugs.

3Pos053 タンパク質–タンパク質結合の粗視化 MD シミュレーション: barnase と barstar を例として
Coarse grained molecular dynamics simulation of barnase-barstar binding

Yu Sugimoto[1,3], Yoshitaka Moriwaki[1], Tohru Terada[1,2], Kentaro Shimizu[1] ([1]*Grad. Sch. Agri. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*, [3]*JSPS*)

Protein-protein interactions (PPIs) are important in biological reactions. Understanding PPIs enables us to develop their inhibitors. In this study, we focused on barnase and barstar which show a large binding constant due to the strong electrostatic interactions between them. To investigate the effect of electrostatic interactions on the binding, we performed coarse grained molecular dynamics simulations with and without the correction term that compensates for the truncated electrostatic interactions. However, the frequency of binding to the binding site was not increased by the addition of the correction term. Therefore, the electrostatic interactions may not serve as the guide to the binding site, though they may facilitate the directional diffusion to each other.

3Pos054 アルケミカル自由エネルギー計算における遅い緩和
Slow relaxation on alchemical free energy calculations

Yoshiaki Tanida, Azuma Matsuura (*Fujitsu Laboratories Ltd.*)

Alchemical free energy calculation is widely used to compute standard free energy of a ligand binding. However, relaxation due to protein flexibility is considerably slower; as a result, it leads to incorrect binding affinity within usual simulation length. We, in this report, present a simple preconditioning way to reduce system equilibration time.

3Pos055 Rationalization of sampling space for searching fragment-binding poses

Hiroyuki Sato, Yoshiaki Tanida, Azuma Matsuura (*Fujitsu Lab. Ltd.*)

We present a novel and efficient approach to search fragment-binding poses to a protein. Firstly, our original method, non-bonding function replica-exchange method (nfREM), is carried out for searching binding-pose candidates. Then, the sampling space of molecular dynamics (MD) is restricted and rationalized using these candidates' information. Finally, metadynamics is executed to search stable and metastable binding poses in the restricted sampling space. We will discuss our approach in detail at the meeting.

3Pos056 QM/MM metadynamics シミュレーションによる trehalose-6-phosphate phosphatase の触媒機構に関する研究
QM/MM metadynamics study of the catalytic mechanism of trehalose-6-phosphate phosphatase

Toshihiro Hayashi, Tadaomi Furuta, **Minoru Sakurai** (*Tokyo Tech*)

Trehalose-6-phosphate phosphatase (T6PP) is a member of haloacid dehalogenase superfamily and catalyzes the dephosphorylation of trehalose-6-phosphate, leading to the biosynthesis of trehalose essential for the survival of pathogenic fungi. To prevent fungal infections, the development of inhibitors for T6PP is required. For this purpose, we here investigated the catalytic mechanism of T6PP using QM/MM metadynamics simulation. The simulation revealed that this dephosphorylation consists of two reaction steps via an intermediate state: in the first step, the bond ($P\text{-}O_{lg}$) connecting the phosphate group and the trehalose moiety is elongated and the proton of Asp26 is transferred to O_{lg}, in the second step, the phosphate group is transferred to the side chain of Asp24.

3Pos057 QM/MM metadynamics 計算による Chitinase A の加水分解機構の解析
Theoretical analysis of the hydrolysis mechanism in Chitinase A using QM/MM metadynamics simulation

Tsubasa Iino, Tadaomi Furuta, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

Chitinase A (ChiA) is one of the glycoside hydrolases (GHs) which catalyze the degradation of chitin, a β-(1,4)-linked polymer of N-acetylglucosamine. The catalytic reaction in ChiA is thought to proceed via a substrate-assisted mechanism, forming an oxazoline or oxazolinium ion intermediate in the first step. However, the detailed reaction mechanism remains unclear. Here, we performed QM/MM well-tempered metadynamics simulations of ChiA along several one-dimensional reaction coordinates. The results indicated that the cleavage of the β-(1,4)-glycosidic bond of chitin was a complex concerted reaction. Furthermore, the free energy profile revealed that the substrate-assisted mechanism is reasonable in ChiA.

3Pos058 Spectroscopic analysis of an electron-bifurcating [FeFe] hydrogenase

Krzysztof Pawlak[1], Nipa Chongdar[1], Olaf Rudiger[1], Edward Reijerse[1], Wolfgang Lubitz[1], James Birrell[1], **Hideaki Ogata**[1,2] ([1]*MPI CEC*, [2]*ILTS Hokkaido Univ.*)

Hydrogenases catalyze the oxidation of molecular hydrogen. [FeFe] hydrogenases are classified into three subgroups, (1) prototypical and electron-bifurcating type, (2) ancestral, and (3) sensory type. Thermotoga maritima is a hyperthermophilic bacterium, containing a sensor type and an electron-bifurcating [FeFe] hydrogenases. We have cloned the electron-bifurcating [FeFe] hydrogenase from T. maritima and heterogously overexpressed it in Escherichia coli. The active site was artificially reconstituted with the di-iron synthetic precursor. The artificially maturated enzyme showed the catalytic activity comparable to the wild type enzyme. We identified the several oxidation states of the active site of the enzyme by FT-IR spectroscopy and EPR spectroscopy.

3Pos059 鉄硫黄クラスターを利用した tRNA 硫黄修飾酵素 TtuA の反応機構の解明
Elucidation of the tRNA thiolation mechanism of TtuA involved in Fe-S cluster

Masato Ishizaka[1], Minghao Chen[1], Syun Narai[1], Masaki Horitani[2], Seiko Oka[3], Yoshikazu Tanaka[4], Min Yao[1,5] ([1]*Grad. Sch. Life Sci., Univ. Hokkaido*, [2]*Fac. Agric., Univ. Saga*, [3]*G.F.C., Univ. Hokkaido*, [4]*Grad. Sch. Life Sci., Univ. Tohoku*, [5]*Grad. Sch. Adv. Life Sci., Univ. Hokkaido*)

Thiolation is one of the post-transcriptional modifications required for biological function of transfer RNA (tRNA). TtuA catalyzes sulfur transfer from C-terminus of sulfur donor protein TtuB to substrate tRNA. Recently, we determined the structure of TtuA-TtuB complex and found that TtuA requires oxygen labile Fe-S cluster with a unique coordination Fe site. The complex structure shows that the tip of C-terminus of TtuB was trapped by the unique Fe site of Fe-S cluster. However, it is still unknown how sulfur is transferred to tRNA through Fe-S cluster. To address such question, we analyzed the intermediate state of Fe-S cluster in tRNA thiolation, and also identified key residues of TtuA for catalytic reaction. The results will be discussed in this presentation.

3Pos060 無機ポリリン酸存在下でのアクチンとミオシン間の相互作用
Interactions between actin and myosin in the presence of inorganic polyphosphates

Koji Ito, Yoshiya Miyasaka, Kuniyuki Hatori (*Grad. Sch. Sci. Eng., Yamagata Univ.*)

Force generation of myosin results from the release of terminal phosphate from adenosine triphosphate (ATP) via hydrolysis. We investigated the properties of actomyosin using inorganic polyphosphates (PPs) instead of ATP. Actomyosin could hydrolyze both tri- and tetra-polyphosphates at a maximum rate of 0.2 s^{-1}. However, actin filaments could not move on a myosin-coated glass in the presence of PPs. The Trp fluorescence of myosin decreased in the presence of PPs, indicating distinct conformations from ATP-binding myosin forms. PPs induced a higher affinity between actin and myosin than ATP. A significant difference in the affinity between PPs was not observed. The results provide insights into the role of hydrolysis for the force generation.

3Pos061 テトラヒメナ外腕ダイニンにおける致死性 P ループ変異の機能解析
Functional characterization of lethal P-loop mutations in Tetrahymena outer arm dynein (Dyh3p)

Masaki Edamatsu (*Department of Life Sciences, The University of Tokyo*)

This study demonstrates a mutation system for characterizing lethal P-loop mutations in Tetrahymena outer arm dynein (Dyh3p). The viable DYH3-knockout (vKO-DYH3) cells isolated in this study enabled the examination of lethal mutations in P-loops 1 and 2. The P1 mutant dynein localized in the oral apparatus and the proximal region of the cilia, and the P2 mutant dynein localized only in the oral apparatus. Both results are different from the localization of wild-type Dyh3p. In addition, a co-precipitation assay showed that the P1 and P2 mutant dyneins did not dissociate from microtubules in ATP plus vanadate or in no-ATP conditions, in contrast to wild-type Dyh3p. This mutation system is useful for further molecular studies of axonemal dyneins and ciliary motility.

3Pos062 ヒトジヒドロリポアミドデヒドロゲナーゼの酵素反応の制御機構における定常状態と時間分割蛍光についての研究
Steady-state and Time-resolved Fluorescence Studies on the Enzymatic Reaction Mechanism of Human Dihydrolipoamide Dehydrogenase

Yayoi Hara[1], Etsuko Nishimoto[2] ([1]*Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ.*, [2]*Fac. Agr., Kyushu Univ.*)

Dihydrolipoamide dehydrogenase (E_3) catalyzes the reactions of hydrogen abstraction and transfer from dihydrolipoamide (DHLip) to NAD^+ to initialize the pyruvate dehydrogenase (PDC) cycle. This enzymatic reaction of E_3 is mediated by FAD arranged in E_3 as the reaction center. While the fluorescence of FAD is usually observed at around 515nm, it is quenched on the abstraction of hydrogen from DHLip. Analyzing kinetically the quenching and recovering of the fluorescence of human E_3 , it was shown that NAD^+ promoted the binding of DHLip with human E_3 . In order to make clear this specific positive feed-back mechanism, binding effects of NAD^+ on the conformation near the FAD was investigated through the time-resolved fluorescence intensity and anisotropy of FAD of human E_3.

3Pos063 Optimizing the protocol for accelerating the analysis of the ATPase activity of circadian clock protein KaiC

Dongyan Ouyang[1], Atsushi Mukaiyama[1,2], Yoshihiko Furuike[1,2], Shuji Akiyama[1,2] ([1]*IMS*, [2]*SOKENDAI*)

KaiC, the core protein of the cyanobacterial circadian clock system, is a temperature-insensitiven ATPase. Although scanning-mutagenesis throughout 519 amino acid residues of KaiC can be a promising approach for identifying a structural unit responsible for this insensitivity, both production of KaiC mutants and ATPase measurements consume considerable time in the previous method. To overcome this, we first optimized expression and purification protocols of KaiC mutants, and then designed an HPLC system with a multi-channel temperature controller to simultaneously measure the ATPase activity at different temperatures. The present protocol, the efficient sample preparation followed by quick ATPase assays, is expected to save approximately 72 % of time.

3Pos064 多分子のキネシンによる協調運動の高速一分子観察
High-speed nanometer-precision tracking of the cargo transport by multiple kinesin-1 motor proteins

Tsukasa Enomoto (*Grad. Life science., Univ. Aoyama*)

Kinesin-1 is a motor protein, that is involved in cargo transport inside the cells. Motility of single kinesin-1 molecule has been extensively studied, however the mechanism of cooperative transport by multiple kinesin-1 motors using a total-internal reflection dark-field microscopy with 50 us temporal resolution. We found that gold particles mainly showed 16-nm steps, similar to that of single kinesin-1 molecule, but with a longer dwell time in the highly-fluctuating one-head-bound state before initiating forward stepping to synchronize their motions.

3Pos065 質量分析によるヌクレオソームにおけるヒストンアセチル化の解析
Characterization of histone acetylation in nucleosome core particle using mass spectrometry

Haruna Hidaka[1], Shunsuke Izumi[1], Satoko Akashi[2], Kazumi Saikusa[1,2] ([1]*Hiroshima university*, [2]*Yokohama city university*)

Post-translational modifications (PTMs) of histone tails in nucleosome core particle (NCP), such as acetylation, play crucial roles in regulating gene expression. In our previous study, it was suggested that histone acetylation reduced the structural stability of NCP against high salt concentrations. In this study, we have applied a top-down sequence analysis, MALDI-ISD experiment, to identify the acetylated sites without enzymatic digestion. The bottom-up approach is the most established method for protein characterization, but it does not always provide sufficient information on PTMs of Lys acetylation in the histone tails due to protease specificity. The present study indicates that MALDI-ISD is the useful method for characterization of PTMs of histone tails.

3Pos066 異なる pH で形成したインスリン B 鎖アミロイド核形成中間体の構造比較
Structural comparison of amyloid nucleation intermediates of insulin B chain formed at different pH values

Yuhki Yoshikawa, Naoki Yamamoto, Atsuo Tamura, Eri Chatani (*Grad.Sch.Sci.,Kobe Univ.*)

Amyloid fibrils are aggregates of proteins involved in many diseases. Although they are formed from nucleation and elongation, the nucleation mechanism has not been elucidated. We recently trapped amyloid nucleation intermediates of insulin B chain at pH 8.7. To clarify whether different intermediate structures are formed depending on reaction conditions, we have investigated aggregation of the B chain at various pH values. The result showed that the formation of intermediate could be observed in a wide pH range. At pH 5.2, peak positions and ratios of the secondary structural components of FTIR spectrum and the number of the intermediate formation steps as deduced by CD analysis seemed different from those at pH 8.7, suggesting diversity of the intermediate structure.

3Pos067 固体 NMR 常磁性緩和促進法による大腸菌細胞内生体分子の局在化解析
Localization of biomolecules in E. coli cells as studied by solid-state NMR under paramagnetic relaxation enhancement

Zhongliang Zhang, Hajime Tamaki, Kazuya Yamada, Toshimichi Fujiwara (*Institute for Protein Research, Osaka Univ.*)

We utilized paramagnetic relaxation enhancement, PRE, in solid-state NMR to localize biomolecules in E. coli cells on a submicrometer scale. This method analyzes the relaxation components obtained from the high-resolution 13C NMR detected 1H saturation recovery experiments on frozen E. coli cells with Gd-DOTA. Biomolecules closer to cell membranes are expected to have a faster relaxation rate due to the paramagnetic ions in the extracellular space. Thus the protein selectively isotope labeled in E. coli cells could be localized. The method was evaluated for E. coli cells overexpressing halorhodopsin or ubiquitin individually. Then 1H spin diffusion was simulated to obtain the cellular structural information quantitatively from PRE from the paramagnetic contrast agent.

3Pos068 High-speed single molecule tracking of allosteric transitions in hemoglobin using Diffracted X-ray Tracking (DXT)

Yuu Okamura[1], Masahiro Kuramochi[1,2], Toshiki Hiraki[3], Naoki Yamamoto[3], Naoya Shibayama[3], Hiroshi Sekiguchi[4], Yuji Sasaki[1,2,4] ([1]*The Univ. of Tokyo Grad Sch FS*, [2]*AIST-UTokyo OPELAND-OIL*, [3]*Jichi Med Univ*, [4]*SPring8/JASRI*)

Allosteric conformational changes underlie the biological function of many protein. The best studied is the tense (T) to relaxed state (R) transition in hemoglobin (Hb), which allows for efficient oxygen transport. These two end structures have been solved by crystallography, but little is known about the transition pathway and intermediates between them. Here, we use Diffracted X-ray Tracking (DXT) to monitor single molecule allosteric dynamics of trout Hb. DXT allows us to monitor the protein motions at high time resolution by tracking diffracted spots from a gold-nanocrystal attached to the protein. We elucidated the pH-dependent allosteric dynamics of trout Hb in the liganded form by statistically analyzing the interdimer rotational motions in single Hb molecules.

3Pos069 Protein Motion Analyzed by Diffracted X-ray Blinking

Hiroshi Sekiguchi[1], Masahiro Kuramochi[2], Noboru Ohta[1], Yuji Sasaki[1,2] ([1]*JASRI/SPring-8*, [2]*Frontier Sci., Univ. Tokyo*)

Diffracted X-ray Tracking (DXT) is one of techniques for investigating intra-molecule dynamics of proteins at single molecule level. A nanocrystal immobilized on the target protein is used as motion probe, and the trajectory of its diffracted spot is investigated with broad-band X-ray. The radiation damage of X-ray for the sample are thought to be problems. Here, we addressed the issue by recording diffraction intensity fluctuations with monochromatic X-ray. The transition of X-ray diffraction intensity from moving single nanocrystal were observed to cycle in and out of the Bragg condition, and the internal motions of a protein molecule labelled with nanocrystals could be extracted from the time-trajectory of this diffraction intensity. We will present its application.

3Pos070 Nanopore probe with protein: Electrical observation of small protein motility in the nanospace

Misa Yamaji, Masaki Matsushita, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

We describe a method of electrical observation in the nanospace using membrane protein α-hemolysin (αHL) and artificial small protein which is integrated into the vestibule of the nanopore. We have previously reported nanopore probe can probe behavior in a nanospace with analyzing the change in ion current when hairpin DNA (hpDNA) exists in the αHL nanopore. In this study, we have attempted to alter from hpDNA to a small protein which has the β-hairpin structure (SV28) in the nanospace. It was suggested that SV28 can maintain to stay and show the molecular motion in the vestibule. In addition, we estimated the direction of the insertion, from turn or terminus, by the signal analysis.

3Pos071 インスリンアミロイドに結合したチオフラビン T の蛍光寿命特性に対する pH の影響
Effect of pH on fluorescence lifetime behavior of Thioflavin T binding to insulin amyloid

Akinori Oda, Hiroshi Satozono, Tomoo Inubushi (*Hamamatsu Photonics K.K.*)

To reveal details of binding sites of Thioflavin T (ThT) on amyloids, we have studied fluorescence lifetime behavior of ThT. We have shown that fluorescence decays of ThT binding to $A\beta_{1\text{-}42}$ consist of four exponential decay components and that there are at least two types of binding sites from the concentration dependence of the intensities of these components. To investigate ThT binding sites of other amyloids, we measured fluorescence lifetimes of ThT binding to insulin amyloid in incubation solution (pH2.0) and weak alkaline buffer solution (pH9.0). The decay curves in the acidic and the weak alkaline solution were best modeled with four and five components, respectively. The results show that the ThT binding states to insulin amyloid were strongly affected by pH.

3Pos072 高速 AFM 画像データに対する生体分子立体構造のフレキシブルフィッティング
Flexible fitting of biomolecular structures to high-speed AFM image data

Toru Niina, Sotaro Fuchigami, Shoji Takada (*Kyoto Univ. Grad. Sch. Sci.*)

High-speed atomic force microscopy (AFM) is a powerful tool to observe large-scale structural dynamics of biomolecules without loss of their functionalities. However, the data obtained are limited to the surface shape of the molecules and there is no general tool to fit 3D structure models into an AFM image. Here, we developed novel methods to fit a structure model to an AFM image. First, we developed a method to generate a pseudo-AFM image from structure models in silico. Next, we performed Monte Carlo and molecular dynamics simulations to minimize the difference between structure-based pseudo-image and the reference AFM image. This method enables us to obtain detailed information about structural dynamics of biomolecules based on high-speed AFM measurements.

3Pos073 高転移性マウス乳癌細胞の細胞弾性におけるネスチンテールドメインの機能解析
Functional analysis of nestin tail domain in elastic modulus of highly metastatic mouse breast cancer cells

Moe Susaki[1], Mei Mizusawa[1], Ayana Yamagishi[2], Chikashi Nakamura[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Biomed. Res. Inst., AIST*)

Nestin, an intermediate filament protein, is suspected to be involved in metastasis of cancer cells. We found that nestin gene knockout (NKO) in highly metastatic mouse breast cancer cell FP10SC2 caused an increase in elastic modulus of the cell body. We predicted that nestin tail domain of 171 kDa inhibits the binding between actin and vimentin which co-polymerizes with nestin, thereby increasing flexibility of the cytoskeleton. In this study, we validated the recovery of the cell softening function of nestin by transfection of nestin expression vectors into NKO cell. As a result, the elastic modulus was significantly decreased in the nestin-expressing cells. This revealed that nestin contributes to softening of cell body.

3Pos074 タンパク質の水和／溶媒和層の定量的な評価
Quantitatively characterization of the hydration and/or solvation shell of protein

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The mechanisms of protein stabilization by uncharged solutes, such as polyols and sugars, have been intensively studied with respect to the chemical thermodynamics of molecular crowding. In particular, many experimental and theoretical studies have been conducted to explain the mechanism of the protective action on protein structures by sugars and polyols through the relationship between hydration and solvation on protein surfaces. By the complemental use of wide-angle X-ray scattering (WAXS), small-angle neutron scattering (SANS), and theoretical scattering function simulation, we have succeeded to quantitatively characterize the hydration and/or solvation shell surrounding protein. The detailed results will be given.

3Pos075 物理系と温度系の合成：カップルされた能勢ーフーバー方程式
A coupling of physical system and a temperature system: Coupled Nose-Hoover equations

Ikuo Fukuda[1], Kei Moritsugu[2] ([1]*Grad. Sch. Sim., Univ. Hyogo*, [2]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

We have created a deterministic molecular dynamics method that realizes an arbitrary distribution for both physical variables and their associated parameters simultaneously. For a temperature parameter, we built coupled Nose-Hoover equations of motion, which describe a coupling of a target physical system (PS) and a "temperature system" (TS). The TS generates a dynamically changing but predistributed temperature. The PS develops with this fluctuating temperature, allowing enhanced sampling of the physical sates. While the PS is under nonequilibrium, the equilibrium is known by reweighting. The potential of this method was validated via distributions, dynamical correlations and free energy landscapes for a normally nonergodic model and an explicitly solvated protein.

3Pos076 周期境界条件下の分子動力学シミュレーションを使った結合自由エネルギー計算で生じる有限サイズ効果を抑えるアルケミカル摂動法の開発
An effective alchemical perturbation method eliminating finite-size effect on binding free energies

Toru Ekimoto, Tsutomu Yamane, Mitsunori Ikeguchi (*Yokohama City Univ.*)

The accurate calculation of the protein-ligand binding free energies is required for computer-aided drug design. The alchemical perturbation method frequently used in the binding free energy calculations under periodic boundary conditions suffers from the finite-size effect that is the cell-size dependence of the charging free energy at different cell sizes and is not negligible in comparison with the binding free energy itself. To eliminate the finite-size effect, we propose an effective perturbation protocol, termed the warp-drive method in which a solution system consisting of a protein-ligand complex and an unbound ligand located at a distant position is used. To assess the performance, the charging free energy for systematically varied cell sizes is examined.

3Pos077 アレルギー性喘息を引き起こすインターロイキン 33 の阻害タンパク質の開発
Development of a protein that inhibits interleukin-33 responsible for allergic asthma

Mio Sano[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

Interleukin 33 (IL-33) plays a major role in biological defense and immune system. It binds to the IL-1 receptor family member ST2 on the surface of immune cells and causes allergic reactions. However, IL-33 also induces allergic diseases, especially allergic asthma. Therefore, an inhibitor of IL-33 is expected to be a therapeutic agent for allergic asthma. Here, using three extracellular domains of ST2 as a template, we attempt to rationally design the protein that inhibits IL-33 binding with ST2. We constructed *E. coli* expression systems for the ST2 extracellular domains and purified the proteins. Interactions between IL-33 and various ST2 fragments, including the wild type and rationally designed mutants of ST2, will be measured by isothermal titration calorimetry.

3Pos078 細胞内ヌクレオチド定量センサーの合理的設計
Rational design of nucleotide sensors for intracellular quantitative imaging

Yoshiki Oka[1], Shunji Suetaka[1], Hinako Ago[2], Yuna Miyachi[2], Yuuki Hayashi[1,2], Munehito Arai[1,2,3] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*College Arts Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

Intracellular concentrations of nucleotides depend on the type of cells. It is known that concentrations of nucleotides, especially UTP and CTP, are increased by 3.0 and 4.8-fold, respectively, in tumor cells than in normal cells. However, spatial and temporal changes in intracellular nucleotide concentrations remain unknown. To solve these issues, it is necessary to develop a "quantitative sensor" capable of visualizing spatial and temporal changes of intracellular nucleotide concentrations in real time using fluorescence intensity or FRET. Here, we attempt to rationally design the mutant proteins that specifically bind to CTP or UTP based on a previously reported ATP sensor. We will present our progress in the meeting.

3Pos079 抗体の親和性向上におけるフレームワーク領域へのアルギニンクラスター導入の効果
Role of Arg cluster (R5) introduced into framework region (FR3) in affinity improvement

Shingo Maeta[1], Makoto Nakakido[1,2,3], Kouhei Tsumoto[1,2,3] ([1]*Dept. of Bioeng., Univ. of Tokyo*, [2]*Dept. of Chem and Biotech., Univ. of Tokyo*, [3]*Med Proteom., Inst. of Med Sci., Univ. of Tokyo*)

Recently, it has become possible to improve affinity by introducing charged amino acids into the FR3. However, the molecular mechanism has not been described sufficiently. This research aims to analyze the influence of FR3 mutant on antigen recognition. The anti-lysozyme antibody was used as a model. WT and R5 mutant was used as a base to prepare CDR variants. The affinity was evaluated by SPR and the results showed that the association rate was improved. Although it was not possible to evaluate the kinetic parameters for the hot spot variants, the binding response increased in case of R5 mutant. According to our results, it is thought that this improvement of R5 is not caused by the change in binding of CDR, but is due to uniform enhancement of the interaction itself.

3Pos080 Characterization of the “scrap-and-build” process in the proteasome α ring formation

Taichiro Sekiguchi[1,2,4], Tadashi Satoh[3], Kentaro Ishii[1,4], Hirokazu Yagi[3], Koichi Kato[1,2,3,4] ([1]*ExCELLS*, [2]*SOKENDAI*, [3]*Nagoya City Univ*, [4]*Inst. for Mol. Sci.*)

The 20S proteasome is a huge protein complex consisting of 28 subunits, which are arranged into a four layer of heteroheptameric rings, α1-7β1-7β1-7α1-7. Formation of this structure involves conversion from an α7 homotetradecamer with a double-ring structure to the α1-7 heteroheptameric ring. We previously reported that the α7 double ring is disrupted by α6 subunit, giving rise to an α6/α7 1:7 complex. To gain deeper insights into this “scrap-and-build” mechanism, we examined whether or not the remaining α subunits act on the α7 double ring by native mass spectrometry. Our result indicated that not only α6 but also α2 and α4 can disrupt the α7 homotetradecamer, offering a unique mechanistic view on the proteasome formation.

3Pos081 状態選択的に安定化された G タンパク質共役受容体の合理デザイン
Rational Design of G-Protein Coupled Receptors Stabilized in Aimed State

Masaya Mitsumoto[1,2], Ryosuke Nakano[3], Takeshi Murata[3,4], Nobuyasu Koga[1,2] ([1]*ExCELLS, NINS*, [2]*SOKENDAI*, [3]*Fac. of Sci., Chiba Univ.*, [4]*PRESTO, JST*)

G-protein coupled receptors (GPCRs) are one of major drag targets; 34 % of FDA approved drugs target them. However, due to the innately unstable inner cellular loop 3 (ICL3), solving the structures is difficult. Furthermore, both active and inactive state structures are required for drug design, but many structures were determined in the inactive state. In contrast to GPCR, de novo designed protein structures built with naturally observed typical short loop types are extremely stable. Here, we computaionally redesigned unstable ICL3 to obtain GPCR crystal structures in aimed state using the typical short loop types.

3Pos082 ファージディスプレイ法への応用を目指した蛍光検出ファージソーターの改良
Improvement of the fluorescent detected phage sorter for the application to phage display

Hitomi Urabe[1,2], Saya Nakano[1,3], Yuki Shimizu[1,2], Naoki Mikosiba[1,3], Hiroyuki Oikawa[1,2,3], Satoshi Takahashi[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Sci., Tohoku Univ.*, [3]*Grad. Sch. Life Sci., Tohoku Univ.*)

We plan to improve the fluorescence-detected phage sorter that can be applied for the phage selection experiments to select the displayed proteins based on their structures. In the initial trials, we tried to select the fluorescent phages from a mixture of the fluorescent and non-fluorescent phages; however, the purity of the fluorescent phage after the sorting did not increase from that before the sorting. We observed the sample flow in the sorting and collection procedures, and found the unexpected backflow of the discarded phages in the collection step that caused the contamination. To prevent the contamination, we are currently conducting the simulation of flows to improve the design of the microfluidic chip.

3Pos083 Design of multi-domain protein structures for small molecule binding

Hiroko Yamada[1], Nobuyasu Koga[2] ([1]*SOKENDAI*, [2]*NINS ExCELLS*)

One of the goals for protein design is to create functional proteins from scratch. Recently, we discovered general principles for designing protein structures, which enabled the de novo design of various protein structures without function. Here, for designing functional proteins from scratch, we attempted to create protein structures with a binding pocket for small molecules by building multi-domain structures with the de novo designed proteins. Especially, we aimed to design multi domain structures with a binding pocket for ATP.

3Pos084 Designing an artificial transcription factor with a small molecular weight based on engrailed homeodomain

Tomoko Sunami, Yu Hirano, Taro Tamada, Hidetoshi Kono (*QST*)

Widely used genome editing enzymes such as TALEN and CRISPR have a high molecular weight. To develop a novel genome editing enzyme that works in a condensed environment, an enzyme with a smaller molecular weight is desired. We use the engralied homeodomain protein as such. The wild type recognizes AT-rich 6bps. To create a protein that recognizes longer DNA sequences, we connected two homeodomains with a linker of different lengths and characterized them by EMSA and B1H assay. They showed a good activity for our target sequence, however, they also bound to undesired sequences. To avoid the undesired binding, we created some mutants and confirmed their better specificity. We are now solving the crystal structure of the complex to see if the binding form is as expected.

3Pos085 立体構造に基づく配列プロファイルを利用した熱安定化 β-グルコシダーゼの設計に向けて
Toward design of thermostable β-glucosidase with structure-based sequence profile

Naoya Kobayashi[1], Shintaro Minami[1], Taku Uchiyama[2], Naoki Sunagawa[2], Kiyohiko Igarashi[2], Hiroyuki Noji[3,4], Nobuyasu Koga[1] ([1]*ExCELLS, NINS*, [2]*Dept. Biomater. Sci., Grad. Sch. Agri. Life Sci., Univ. Tokyo*, [3]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [4]*ImPACT, JST*)

Protein structure is mainly stabilized by hydrophobic interaction in the core region. To design thermostable β-glucosidase mutants, we aimed to design well-packed hydrophobic core with larger hydrophobic amino acids. We made a backbone-structure-based sequence profile that indicates favorable amino acid types at each residue position based on its mainchain dihedral angle and its 3D-structure environment around the position. Based on the profile, we predicted 20 positions (36mutants) in the core and boundary regions, which can be mutated to larger hydrophobic side-chain residues from small side-chain residues that do not form hydrogen bonds. In the presentation, we will present the prediction strategy and the results of biochemical experiments of the predicted mutants.

3Pos086 平行ベータシート蛋白質の設計図におけるデザイナビリティの評価基準
Criteria for evaluating designability of pure parallel beta sheet structures

Hayao Imakawa[1], Nobuyasu Koga[2], George Chikenji[1] ([1]*Dept. of App. Phys., Nagoya Univ.*, [2]*CIMoS, IMS*)

De novo protein design, identifying the amino acid sequences that fold into a given target structure guided by physics, has remarkable progress in the past two decades. Despite its progress, designing a protein for an arbitrary structure is still a challenging task. One of the serious problems is that there is currently no rational criteria that can quantify how designable a given blueprint is. Here we propose such criteria for pure parallel beta sheet proteins. The criteria are based on several structural rules that were found by statistical analysis of the protein structure database and confirmed by physics based folding simulation. We found a significant correlation between estimated designability and population in the database.

3Pos087 タンパク質-タンパク質結合部位の予測とエピトープマッピング
Prediction of Protein-Protein Binding Sites and Epitope Mapping

John Gunn[2], Elizabeth Sourial[2], **Kinya Toda**[1], Paul Labute[2] ([1]*MOLSIS Inc.*, [2]*Chemical Computing Group ULC*)

Computational methods for predicting protein-protein binding sites or epitopes have profound applications in many areas in the development of biologics, from understanding the mode of action to the modulation of protein properties. This work presents a novel algorithm for predicting likely antigen epitopes from protein-protein docking results using the MOE software. The approach generates an ensemble of poses which represent the most favorable interactions. Protein-protein residue contacts are then used to generate interaction fingerprints which serve to identify Boltzmann-weighted clusters of poses and extract consensus epitope residues. This method produces at least one predicted epitope with good overlap to the native structure ranked in the top five clusters.

3Pos088 理論的変異解析によるジヒドロ葉酸還元酵素の高活性化
Enhancing activity of dihydrofolate reductase by theoretical mutational analysis

Kazuhisa Ohara[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

Dihydrofolate reductase (DHFR) is a model protein for experimental and theoretical studies on the correlation between enzyme dynamics and function. In this study, we aim to rationally enhance the activity of DHFR based on previous findings and theoretical predictions. Here, using the protein design software "Rosetta", we performed theoretical mutational analysis around the substrate/product-binding site. Because product release is the rate determining step in the DHFR catalysis, we searched for mutations that weaken the interaction between the enzyme and product while maintaining the interaction with the substrate, to accelerate the product release and improve the activity. We will present the results of theoretical mutation design and its experimental verification.

3Pos089 Mathematical Modeling for Morphallactic Segment Formation Using a Size-Dependent Multi-Loop Negative Feedback System

Yusuke Shibasaki[1], Chikako Yoshida-Noro[2], Minoru Saito[1] ([1]*Graduate School of Integrated Basic Sciences, Nihon University*, [2]*College of Industrial Technology, Nihon University*)

We propose a mathematical model of morphallactic segment formation based on the clock and wavefront hypothesis suggested in 1970s. We chose an invertebrate, Enchytraeus japonensis, as a model animal and applied a multiple-loop negative feedback system based on its physiological features. One of the distinctive features of the present model is that the system size (segment number) is controlled by a parameter which depends on the system size itself. The present model might provide not only a physical mechanism underlying the unique development of this model animal but also a new explanation for segmentation in vertebrate presomitic mesoderm (PSM).

3Pos090 Maximizing Local Information Transfer in Boolean Networks

Taichi Haruna[1], Kohei Nakajima[2,3] ([1]*Tokyo Woman's Christian University*, [2]*The University of Tokyo*, [3]*PRESTO, JST*)

The relationship between information and dynamics is one of the central topics in complex systems science. In contrast to most of previous work investigating how information-theoretic measures behave as parameters of state dynamics are varied, we here study emergence of rules from local information transfer maximization at each agent in a Boolean network, which is a simple model of gene regulatory networks. We mathematically derive the class of emergent rules. In particular, under the presence of small noise, they are such that their output depends only on a single input. These rules have important properties in real-world gene regulatory networks: they are both critical and highly canalized.

3Pos091 局所情報流最大化に駆動される時空間ダイナミクス
Spatiotemporal dynamics driven by maximization of local information transfer

Kohei Nakajima[1,3], Taichi Haruna[2] ([1]*The University of Tokyo*, [2]*Tokyo Woman's Christian University*, [3]*JST PRESTO*)

We consider a generic type of interacting system and investigate the relevance of maximizing information transfer among elements. As an expression of the information transfer, we focus on transfer entropy, and propose one-dimensional cellular system whose state transition is governed to maximize the local information transfer from interacting cells. As a result, we show that the maximization of local information transfer essentially degenerates the system into a certain class of cellular automata rules with memory. We also investigate the spatiotemporal dynamics of the system and characterize the statistics of spatiotemporal patterns of states and resulting information dynamics in detail suggesting the diverse nature of the system.

3Pos092 Spatial Cooperation between DNA and Actin in Micro-Confinement Generated through Spontaneous Phase Segregation

Hiroki Sakuta[1], Naoki Nakatani[1], Masahito Hayashi[2], Kingo Takiguchi[3], Kanta Tsumoto[4], Kenichi Yoshikawa[1] ([1]*Grad. Sch. Life Med. Sci., Doshisha Univ.*, [2]*Center of Brain Sci., RIKEN*, [3]*Grad. Sch. Sci., Nagoya Univ.*, [4]*Grad. Sch. Eng., Mie Univ.*)

Cells maintain their lives through generation of various microcompartments under crowding conditions of biomacromolecules. Simple binary polymer system, polyethylene glycol (PEG) and dextran (DEX), caused micro-segregation to form cell-sized aqueous/aqueous microdroplets (CAMDs). We found that CAMDs rich in DEX captured polymerized actin (F-actin) in a spontaneous manner, while monomeric actin (G-actin) is distributed evenly. When the F-actin forms bundle, it is adhered to surfaces of CAMDs. It is also shown that double-stranded DNA (>kbp) is entrapped inside CAMDs. Interestingly, in the coexistence of double-stranded DNA and F-actin in CAMDs, F-actin could create specific domains accompanied with alignment by depleting DNA molecules for both poles in a microdroplet.

3Pos093 Theoretical model of dynamics of epithelial tissue with cellular chirality

Takaki Yamamoto[1], Tetsuya Hiraiwa[2], Tatsuo Shibata[1] ([1]*Riken, Lab. Phys. Biol.*, [2]*Univ. Tokyo, Sci. Phys.*)

Morphologies of organisms, organs and tissues often break chiral symmetry. Understanding multicellular dynamics is essential to elucidate the mechanism. In contrast to such multicellular chirality, single-cell chiral behavior has been recently reported as the unidirectional rotation of isolated cells. From the mechanistic point of view, the observations imply that single cells can cell-autonomously generate torques. Here, we ask a question how torques generated by individual cells affect the multicellular dynamics, and if they can induce chiral morphogenesis. To address this problem, we propose a theoretical model for multicellular dynamics with such cellular torque. We report the results from our model on roles of cellular torque for multicellular dynamics.

3Pos094 Analysis of soliton-like collective migration of non-chemotactic *dictyostelium* cells

Masayuki Hayakawa[1], Hidekazu Kuwayama[2], Yuko Wada[1], Tatsuo Shibata[1] ([1]*BDR, Riken*, [2]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

Collective cell migration is fundamental process that occurs during morphogenesis, and has been studied in the field of biology and physics. Although various migrations have been reported, recently a migrating wave-structure which has characteristics of a soliton formed by non-chemotactic *dictyostelium* cells is attracting great attention. Because this wave-structure memorizes and keeps its structure, it is expected that insights will be obtained in the mechanism of morphogenesis. However, detailed findings about how the individual cells contribute to form the wave-structure are still unclear. Here, we argue a mechanism of wave-structure formation from the aspect of quantitative analyses. We believe that our study will contribute to develop morphogenesis studies.

3Pos095 多電極システムによる心筋細胞ネットワークにおける拍動伝導の計測技術の開発
Development of a method to track conductions in cardiomyocyte network with a multi-electrode system

Kazufumi Sakamoto[1], Natsuki Seki[1], Shota Aoki[2], Naoki Takahashi[2], Masao Odaka[3,4], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We examined characteristics of propagation of conductions in heart using ultra-high speed multi electrode array system. We tracked a series of extracellular potentials of linearly lined-up cardiomyocytes of human-induced pluripotent stem cell with two MHz sampling intervals of multi-electrodes signal acquisitions and an agarose microfabrication technology to localize the cardiomyocyte geometries. We observed beat conductions from pacemaker filed to whole the cell networks and tracked and found that local conduction speed and fluctuation were varied. The results indicated that components of cardiomyocytes in the network were not homogeneous, and the existence of plurality of conduction pathways may form the fluctuation of conductions by their random selection.

3Pos201 タンパク質複合体構造モデリングの評価のためのベンチマークデータセット
A large decoy dataset for protein-protein docking model quality assessment

Takanori Hayashi[1], Masahito Ohue[1], Juliette Martin[2], Guillaume Launay[2], Yuri Matsuzaki[3], Nobuyuki Uchikoga[3], Yutaka Akiyama[1,3] ([1]*Sch Computing, Tokyo Tech*, [2]*MMSB, CNRS, Univ Lyon*, [3]*ACLS, Tokyo Tech*)

Structural information of protein complex, which is related with protein-protein interaction, is important for understanding structural basis of its biological function and pharmaceutical research. Protein-protein docking (PPD) is a method to predict complex structure from unbound states. Model quality assessment (MQA) of predicted complex is needed to select near-native complex structures from decoys. In this study, we construct a large PPD decoy dataset for MQA using MEGADOCK and ZLAB benchmark 5.0. We also provided all MQA data (iRMS, etc.) using DockQ. MEGADOCK success to sample acceptable model in 211 unbound cases out of 240 and medium quality model in 40. We also show the distribution patterns of decoys in their conformation space.

3Pos202 Sequence profile for protein design based on database analysis of backbone environment

Shintaro Minami, Rie Koga, Nobuyasu Koga (*NINS, ExCELLS*)

De novo computational protein design has greatly developed recently. However, various manual adjustments for each individual target by human experts are still indispensable. Here, we propose a method for generating sequence profiles indicating favored amino-acid types for each residue site, which can be applied for protein design. Given a target structure, backbone environment at each site is represented by various features, and then the similar environments were searched in structure database and integrated to predict the profile. Based on the profile, our design protocol was improved: when designing amino acid sequence, rarely observed amino acid types at each site were eliminated. We present the algorithm together with test results by the new design protocol.

3Pos203 Development of a method for predicting pathogenicity of missense variants incorporating supramolecular structural information

Atsushi Hijikata, Masafumi Shionyu, Tsuyoshi Shirai (*Nagahama Inst. Bio-Sci. Tech.*)

Although recent advances in genome sequencing technologies enabled us to identify genetic variants in patients suffered from inherited diseases, it is still challenging to evaluate the effect of the variants on a given disease. We previously reported a clear relationship between molecular mechanisms of diseases caused by missense variants and the mutated residue positions in supramolecular structures. The results indicated that it was possible to infer the molecular mechanism of missense variants from the 3D structures, and thus we attempted to develop a method to predict the variant effects by machine learning approaches by incorporating supramolecular structural data as features. We will discuss the performance of the method and its biological/medical implications.

3Pos204 Performance improvement of the method for large-scale structural comparison of protein pockets

Tsukasa Nakamura[1,2], Kentaro Tomii[1,2] ([1]*CBMS, GSFS, Univ. Tokyo*, [2]*AIRC, AIST*)

Analyzing interactions between proteins and small molecules is important to predict the ligands which bind to parts of putative ligand binding pockets. Such analysis demands a fast and efficient method. Methods have been developed for representing a binding pocket with a reduced vector. However, some possible caveats must be associated with existing methods. Previously, to overcome them, we defined the similarity among all triangle patterns which are producible under our labeling method, and developed a method to represent a binding pocket with a reduced vector. Recently, we changed the definition of the similarity between triangle patterns and made the similarity matrix sparse. We confirmed this change brought higher sensitivity and made efficient calculation possible.

3Pos205 ヒト機能未知スプライシングアイソフォームの特徴解析
Analysis of characteristics of function-unknown splicing isoforms in human

Masafumi Shionyu, Atsushi Hijikata (*Fac. Biosci., Nagahama Inst. Bio-Sci. Tech.*)

Splicing isoforms produced by alternative splicing are thought to contribute to increasing the complexity of proteomes, and more than 100,000 of amino acid sequences of splicing isoforms in human are identified. However, most of them are just sequenced and not experimentally examined for their functions. Moreover, it is debated whether many known splicing isoforms are products of splicing noise. To estimate functionality of function-unknown splicing isoforms, we applied our machine learning-based approach trained on several features of function-known splicing isoforms. We will discuss the characteristics, such as structural properties, expression patterns and functional categories, of splicing isoforms estimated to be functional.

3Pos206 Characterizing SLC transporters by sequence and functional networks

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SLC (solute carrier) transporter family mediates various physiological processes by importing and exporting essential chemicals across membrane. While some members of SLC, which are recognized as therapeutic targets, have been intensively studied, little is known about the rest and majority of SLC. Here we performed network analysis on SLC transporters to elucidate the characteristics of each subfamily as well as the relationships between individual transporters. Sequence identity network revealed diversity within the same subfamilies and similarity between different subfamilies. Functional relations between SLC transporters were also investigated using coexpression, protein-protein interaction, and literature networks.

3Pos207 肺癌細胞の発現変動遺伝子を対象としたクラスタセントロイド間の相関ネットワーク
Correlated network by cluster centroids for differentially expressed genes in lung cancer cell

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Understanding the functional organization in cell by using gene expression profiles is very useful to predict the behavior of the diseased cell. For the purpose of understanding the specific biological network of lung cancer, we have calculated the correlation coefficient between the cluster centroids by k-means clustering for the differentially expressed genes. Of the 15 clusters, three centroids from clusters contained high percentage of gene ontology of cell cycle, vasculature development and cilium organization respectively, had high correlation coefficient each other. In addition, the sign reversal of the correlation efficient between the cases in normal and diseased cell was also observed, suggesting the existence of the specific network for the lung cancer.

3Pos208 機能に関する選択シミュレーションにおける P-loop 蛋白質構造の多様化
Diversification of P-loop protein structure simulated by imposing the functional requirement as a selection pressure

Kohei Inukai, Masaki Sasai, George Chikenji (*Department of Engineering, Nagoya University*)

In many cases, protein fold is highly conserved in the course of evolution. However, a great variety of protein folds are observed in the phosphate binding loop (P-loop) protein family. The reason that the P-loop family has diversified protein folds while conserving the function in its evolution has not to be revealed. To understand the course of the P-loop protein evolution, we applied a course-grained protein model (Sasaki et al., BBRC 2005) and carried out evolutionary simulations by imposing a constraint on the active-site configuration as a functional selection pressure. We focused the difference of the course of the simulated evolution according to the functional pressure.

3Pos209 脳の階差成長による皺形成シミュレーション
Winkling simulation of differential growth of brain

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Winkles of human brain is considered to serve as a function of signal processing. As the development mechanism of these winkles, two different mechanism have been proposed. One is based on the radial growth, where the growth rate of the cortical part is larger than that of the interior part. The other is based on the tangential growth, which is induced by prepattern growth along the cortical surface. To get insights into difference between these growth mechanism of winkles, we consider simple 1-dimensional circular growth model. By simulate elastic deformation of this model, we find that winkling in the tangential growth occurs more easily than the radial growth. We report this result and discuss the origin of this difference.

3Pos210 機械学習を利用した集団内細胞行動解析
System analysis of cellular behavior with machine learning during collective cell migration

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We have achieved to develop a mathematical model of cellular behavior considering mechanical and chemical interactions during collective cell migration. In-vitro experiments using normal human branch epithelial cells were conducted under the control of initial conditions by photolithography, which enabled to obtain a large amount of reliable data for cellular behavior. Then, machine learning was used for feature extraction and classification for the individual cellular dynamics, and optimization for the mathematical parameters was conducted in order to validate the hypothesis used in our proposed model. The methodology developed here can be adopted to any of the mathematical model for cellular dynamics to improve their reliability.

3Pos211 多細胞の協調的な運動時における細胞の複雑な変形のフェーズフィールドモデル
Phase-field modeling of complex cell deformation and multi-cellular motion

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The exact relationship between collective cell motion, cell positioning and the cell guidance rule remains elusive. Here, we numerically studied the behavior of a phase-field model that describes membrane deformation driven by reaction modules of excitable and bistable nature. We demonstrate that balance between these two properties give rise to typical shapes and movements resembling those observed in motile cells. We will then show the relationship between the single cell deformation and properties of multi-cellular behavior with special emphasis on anisotropic cell-cell contact-mediated interaction.

3Pos212 不正確な素子から正確な情報伝達をおこなうためのネットワーク構造と協同性
Cooperative reliable response from sloppy gene expression dynamics

Masayo Inoue[1], Kunihiko Kaneko[2] ([1]*IMS, Meiji Univ.*, [2]*Univ. of Tokyo*)

Gene expression dynamics satisfying given input-output relationships were investigated by evolving the networks. We found three types of networks depending on the sensitivity of gene expression dynamics: direct response with straight paths, amplified response by a feed-forward network, and cooperative response with a complex network. When each gene's response sensitivity is low, the last type is selected, in which many genes respond collectively, with local-excitation and global-inhibition structures. The result provides an insight into how a reliable response is achieved with unreliable units, and on why complex networks with many genes are adopted in cells.

3Pos213 A data-driven model for collective cell motion in Dictyostelium discoideum

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A variety of complex behaviours remains unexplained. In this work, we focus on a nonlinear dynamics of collective cell motion of Dictyostelium discoideum, and investigate the movement of individual cells and interactions between cells. Generally, making a mathematical model of a collective cell motion is involved, because of complicated collisions and deformations of cells. As a solution to this problem, we utilise data-driven modelling from experimental data by considering attractive and repulsive forces between cells. We demonstrate that a mathematical model derived by the data-driven modelling can explain long-term behaviour with sufficient accuracy in long-term, while a naive linear regression model suffers from a significant error in long-term.

3Pos214 ATPase activity of individual KaiC molecules decisively influences the ensemble-level oscillation of cyanobacterial KaiABC clock

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Cyanobacterial protein KaiC forms hexamer and retains extremely weak but stable ATPase activity. To understand dynamics of the KaiABC circadian clock, we proposed two theoretical models and analyzed how microscopic reactions within individual KaiC molecules affect synchronization of a large number of molecules. Simulation results suggest that ATPase activity is a driving force of phosphorylation oscillation, synchronization and temperature compensation phenomena and that ATPase activity is correlated to the oscillation frequency at single-molecule level, which should be the origin of the observed ensemble-level correlation between the ATPase activity and phosphorylation oscillation frequency.

3Pos215 Effects of the binding domain of Pin1 interacting with proteins of variable conformations

Romain Amyot, **Yuichi Togashi** (*Grad. Sch. Sci., Univ. Hiroshima*)

The peptidyl-prolyl cis-trans isomerase Pin1 is an enzyme consisting of two domains: one binds to specific motifs in proteins and the other catalyses their cis/trans isomerisation altering the shape of proteins. Pin1 has been studied experimentally highlighting its role in many biological processes such as cell cycles but little is known about its reactivity. Particularly, the conformation of Pin1 and its substrate as well as the distribution of reactive and binding motifs within the substrate should have key roles since the binding domain tethers Pin1 to its substrate, affecting the reactivity. Using Brownian dynamics simulations, we study the effects of the binding domain coupled to substrate conformational changes with different motif configurations.

3Pos216 Experimental Validation of a Mathematical Model of ErbB Receptor Signaling to Cell Cycle

Kyoichi Ebata, Hiroaki Imoto, Kazunari Iwamoto, Shigeyuki Magi, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

Activation of ErbB receptor signaling pathway induces various cellular phenotypes such as growth, proliferation and differentiation, and its impaired functions often lead to oncogenesis. Therefore, many researches targeting this pathway have been conducted for efficient cancer therapy. We perform computational analyses of a mathematical model of ErbB signaling and subsequent cell cycle progression to unveil characteristic network dynamics and molecular regulations in the system. The simulation results obtained from the model are validated based on the quantitative experimental time-series data. An integrated model consisting of ErbBs signaling and cell cycle is also constructed and examined, then it is being improved with the experimental data.

3Pos217 蟻の死骸の山の形成プロセスにおける一考察
Ant Cemeteries Grow via the Ambiguous Local Environment

Tomoko Sakiyama (*Grad. Sch. Nat. Sci. Tech., Univ. Okayama*)

Ant workers carry a corpse and drop it, which lead to the cluster pattern of ant cemeteries. Several experimental studies have revealed the corpse pile dynamics of ants. However, little is known regarding how these typical behaviours emerge from individual decision-making. In this study, I developed an agent-based model where artificial ants carry or drop a corpse competitively, thereby resulting in the corpse pile growth. In my proposed model, the agents tuned the probability of drop of corpses according to their local environment. As a result, it was revealed that the corpse pile dynamics of my proposed model partly matched the time series of corpse piles of real ants.

3Pos218 Reduction of a Markov operator representing the dynamics of stochastic neuronal model by sparse discrete cosine transform

Takanobu Yamanobe (*Hokkaido University School of Medicine*)

We reduce a Markov operator, which represents the dynamics of stochastic neuronal model, to a matrix based on the sparsity of the stochastic kernel. For the reduction, we introduce a discrete cosine transform with a deterministic sparse Fast Fourier Transform (sparse DCT-II). We show that the sparse DCT-II is superior to the standard one concerning the reduction of the number of non-zero elements of the approximated matrix. We show that the number of non-zero elements can be reduced until 6-7% using the deterministic sparse DCT-II compared to the standard one. The advantage of the sparse DCT-II is that it can determine the number of non-zero elements deterministically. It is not possible when one uses a stochastic sparse Fast Fourier Transform.

3Pos219 アルツハイマー病とシロスタゾール ー傾向スコアを用いた医療費の検討ー
Alzheimer's disease and cilostazol -medical cost through propensity score-

Izumi Kuboyama, Susumu Ito, Toshiaki Kaminaka, Katsuhiko Hata (*Kokushikan University*)

Alzheimer's disease is a chronic progressive neurodegenerative disease, which loads a severe socioeconomic burden. Cilostazol was recently reported to prevent pathological changes of Alzheimer's disease in an experimental animal model.The aim of this study was to elucidate that cilostazol saved medical cost in Alzheimer's disease patients. 22,190 patients with Alzheimer's disease were extracted from claim database of National Health Insurance. The annual medical costs of cilostazol-prescribed group and non-cilostazol prescribed group were calculated through propensity score method (ipw). The medical cost of the cilostazol-prescribed group was not lower than that of non-cilostazol-prescribed group.

3Pos220 Coupled epigenetic and genetic network gives rise to a probability landscape with eddy currents

Bhaswati Bhattacharyya, Masaki Sasai (*Department of Computational Science and Engineering, Nagoya University*)

Epigenetic modifications of histones coupled with genetic network of transcription play an important role in gene expression of eukaryotes. To understand the resultant coupled dynamics, our model considers coupled stochastic change of transcription and histone states in a self-activating gene network. We represent the dynamics with a joint probability of order parameters representing protein copy number, histone states, and transcription states. We find multiple basins of attraction in the probability landscape whose positions depends on the parameters. The probability flux derived from the Fokker-Planck equation takes the form of an eddy current. Based on these findings, we discuss effects of time-scale separation in gene expression dynamics.

3Pos301 SPI-2 感染装置先端蛋白質 SseB の集合体形成
Assembly characteristics of SseB, a putative tip protein of the SPI-2 injectisome

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Many pathogenic bacteria infect their host cells using type III secretion system (T3SS), which directly deriver virulence proteins into the host cells. *Salmonella* has two types of T3SS, SPI-1, which is required for the initial infection stage, and SPI-2, which is essential for survival of *Salmonella* in the host cells. SseB is a SPI-2 component located at the tip of the T3SS to form a translocon complex in the host cell membrane. To elucidate the mechanism of the translocon formation, we expressed and purified SseB and analyzed its assembly characteristics. The purified SseB is a pentamer and forms higher order assembly depending on pH. Since the SseB expression is induced by acidic pH, this property would be related to the function of SseB.

3Pos302 GPCR ダイマーを構成する一部の分子は、リガンド刺激前に自発的に活性化している
Spontaneous activation in a transient GPCR dimer before ligation as revealed by dual-channel single fluorescent molecule imaging

Rinshi Kasai (*Inst. Front. Life. Med. Sci., Kyoto Univ.*)

Recent studies have shown that G-protein coupled receptors (GPCRs) are in dynamic equilibrium between monomers and dimers, with dimer lifetimes of ~100-ms, in the plasma membrane. As one of the functions of such transient dimers, we previously reported that the transient dimer produces the basal activity, or so-called constitutive activity before ligation. However, the structural feature of each receptor molecule in a transient dimer was not directly examined. For this purpose, we performed the dual-channel single fluorescent molecule imaging of a GPCR dimer and the nanobody, a tiny antibody-like protein, that recognizes the activated GPCR. As a result, we found that at least one receptor molecule in a transient dimer is in the active conformation even before ligation.

3Pos303 MCF 細胞内における p52Shc の Grb2 シグナル伝達制御
Regulation of Grb2 signaling dynamics by p52Shc scaffold protein in MCF7 cells

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p52Shc (SHC) and Grb2 play an important role in breast cancer progression. Here, to examine the possibility that SHC regulates Grb2 signaling, we measured translocation dynamics of SHC and Grb2 after heregulin stimulation in living MCF7 cells. TIRF microscopy revealed that the membrane localization of SHC was sustained for at least 60 min after cell stimulation. In contrast, Grb2 was transiently translocated to the membrane in spite of the fact that tyr-313 residue of SHC, one of the Grb2 binding sites was still phosphorylated. FCCS analysis revealed that the interaction between SHC and Grb2 in the cytoplasm increased after the cell stimulation. Thus, we speculate that SHC in the cytoplasm acts as an inhibitor for membrane translocation of Grb2.

3Pos304 RhoA activation inhibits proliferation of skin cancer cells

Oleg Dobrokhotov[1,2], Atsushi Enomoto[3], Masaki Sunagawa[3], Masahide Takahashi[3], Mikhail Samsonov[4], Masahiro Sokabe[2], Hiroaki Hirata[1,2] ([1]*R-Pharm Japan*, [2]*Mechanobiology Lab., Grad. Sch. Med., Nagoya Univ.*, [3]*Dept. Pathology, Grad. Sch. Med., Nagoya Univ.*, [4]*R-Pharm*)

Contact inhibition of proliferation (CIP) is crucial for tissue homeostasis, while loss of CIP is a typical hallmark of cancer. Previously we have shown that actomyosin contractility is required for CIP in human HaCaT keratinocytes. Hence, we hypothesized that actomyosin contractility is compromised in cancer and induction of myosin activity could restore CIP. Indeed, the skin cancer tissue showed reduced actomyosin activity, while pharmacological activation of the RhoA-ROCK-myosin II axis in A431 skin cancer cells caused inhibition of their proliferation. Interestingly, the effect of RhoA activation was YAP-independent. Although further studies are required, induction of actomyosin contractility via RhoA activation might be a potent strategy for cancer therapy.

3Pos305 Size-dependent beating rate changes of cardiomyocyte clusters by environmental thermal changes

Wei Wang, Tomoyuki Kaneko (*LaRC, FB, Grad.Sch., Hosei Univ.*)

Heart rate is known to slow down or speed up depending on the environmental temperature. To clarify the size dependency of cardiomyocyte clusters, we made different-sized populations of cardiomyocytes and measured their beating rates at two environmental temperatures (room temperature and living body temperature). Our finding shows regardless of the size of cluster, the changes of beating rate tend to be the same. Heart rate slowed down at room temperature, and returned to the original pace at living body temperature. However, fluctuations compared to original pace in small clusters were also observed during temperature recovery. The results of this study demonstrate that cardiomycytes clusters can sense and respond to temperature changes regardless of the size.

3Pos306 心筋細胞メカニクスに NADPH オキシダーゼ 4 が及ぼす影響
Single cell mechanics effects of NADPH oxidase (NOX) 4 in mouse ventricular cardiomyocytes

Keiko Kaihara, Gentaro Iribe, Hiroaki Kai, Keiji Naruse (*Dept Cardio Physiol, Grad Sch med, Okayama Univ*)

Although, myocardial stretch-induced reactive oxygen species (ROS) production via NADPH oxidase (NOX) 2 modulates Ca2+ handling and cellular contractility, behavior of NOX4 during stretch is unknown. In the present study, we investigated the stretch-induced effects of NOX4. Ventricular cells isolated from wild type (WT), NOX2 knock out (KO) and NOX4 KO mouse were subjected to 5-10% axial stretch to assess stretch-induced increase in ROS production, Ca2+ spark rate and cellular contractility. Cellular contractility and ROS production were significantly suppressed in NOX2 KO and NOX4 KO group, but Ca2+ spark rate was suppressed only in NOX2 KO group. The results suggest that role of NOX4 during stretch is different from that of NOX2.

3Pos307 1 細胞レベルの電気信号伝導速度計測に向けた心筋細胞ネットワーク再構築
Reconstruction of cardiomyocyte network for measuring the signal conduction velocity at single cell level

Koki Fujii, Tomoyuki Kaneko (*LaRC, FB, Hosei univ*)

Dispersed culture of cardiomyocytes tended to make their signal conduction velocity slower than actual heart. Hence, it is important to construct cellular array like actual tissue. In our previous study, we constructed cell networks at single cell level on culture dishes and investigated dependences on stimulation voltage and frequency. Thus, we applied the method and constructed them on multi-electrode array (MEA) chip. To construct the structure that only cardiomyocytes are lined up in a row, cells were picked up and placed individually using cell-handling pipette in agarose microchambers on MEA chip. To measure the conduction velocity, we attempted to detect cellular potential of cell networks using MEA system. The potential of different two areas are focused.

3Pos308 間葉系幹細胞の温度依存形態振動に伴うメカノシグナル転写因子の核ー細胞質シャトリング
Nucleocytoplasmic shuttling of the mechanotransducing proteins in temperature-dependent shape-oscillating mesenchymal stem cells

Sayaka Masaike[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

Stemness of mesenchymel stem cells (MSCs) are easily affected and often lost depending on the shaping history: e.g., well-spread; osteogenic, round; adipogenic lineages. To avoid the deterioration of stemness of MSCs, elimination of accumulation of shape memory in the cells is expected to be effective. In this study, we tried to eliminate the shape memory in MSCs by switching the shape between spread and round ones in a period of several hours using the thermoresponsive photografted polymer substrate. We could find the optimal grafting condition of the polymer, and induce shape oscillation of MSCs as well as nucleocytoplasmic shuttling of the mechanotransducers such as YAP. We will discuss the relationship between those shuttling and maintenance of stemness in MSCs.

3Pos309 iPS 細胞は最適弾性率を持つハイドロゲル表面に移動し増殖する
iPS cells move toward and efficiently proliferate on the hydrogel surface with optimal elasticity

Mengfan Wang[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

Feeder-free dispersion culture of iPS cells has been conducted mostly on a plastic dish, while the elastic hydrogel substrates to manipulate them are not sufficiently established. The medical application needs seamless culture of iPS cells on the same hydogel materials through whole processes of cell manipulation, thus the biomechanical condition of hyrogel should be determined to assure high-qualified culture of them. For this issue, we have investigated the effect of hyrogel elasticity on iPS cells culture using microelastically-patterned gelatin gel modifed with laminin. We found that iPS cells with higher expression of Oct3 preferentially proliferate on the region of middle range of elasticity toward where they tend to gather.

3Pos310 ハイドロゲル上でのマスト細胞の刺激応答
Inhibition of degranulation in mast cells cultured on hydrogel

Atsushi Shiki, Yoshikazu Inoh, Satoru Yokawa, Tadahide Furuno (*Sch. Pharm., Univ. Aichi Gakuin*)

Mast cells are important effectors of immediate allergic responses and adhere to extracellular matrix (ECM) in various tissues and organs. To investigate the effect of ECM on mast cell activation, we analyzed cellular response on the hydrogel-coated dish. In cells on the hydrogel, the antigen-induced Ca^{2+} increase was slightly suppressed, while the degranulation was greatly inhibited. Accumulation of vinculin to focal adhesions was impaired, and acetylation of microtubule and transport of secretory granules after antigen stimulation was reduced. These results suggested that adhesion to hydrogel affected the traffic of granules along microtubule according to antigen stimulation, thereby inhibiting the degranulation in mast cells.

3Pos311 三次元細胞構造体の構築：高分子混雑環境下におけるレーザーピンセットの活用
Constructing 3D Cellular Assembly: Laser Tweezering under Depletion Effect on Albumin Solution

Ritsuki Ito, Kakehiro Yamazaki, Satoshi Kishimoto, Takahiro Kenmotsu, Koichiro Sadakane, Kenichi Yoshikawa (*Faculty of Biological and Medical Sciences, Doshisha University*)

In cell biology as well as in regenerative medicine, fabrication of 3D cellular assembly is getting important. To achieve this end, artificial scaffolds such as gel and solid substrate have been usually applied. However, these scaffold are possibly xenobiotics and definitely different from natural cellular adhesion in organisms. Recently, we have found that stable 3D cellular assemblies can be constructed in the absence of any artificial scaffold by using the laser tweezers in a crowding environment with solvable polymers such as PEG and dextran. In the present paper, we will report the successful formation of 3D cellular assembly by adapting albumin as the coexisting polymer. We will argue the merit of our novel methodology toward the construction of mini-organoids.

3Pos312 Investigation for the crosstalk mechanism of two damping oscillators, p38 MAP kinase and NF-κB

Hiroki Michida, Minami Ando, Shigeyuki Magi, Kazunari Iwamoto, Mariko Okada (*IPR Osaka Univ.*)

In a cell, there are several proteins whose activities show damping oscillation in time course. The biological function of constant oscillation is known such as circadian rhythm and cell cycle. However, the biological function of damping oscillation is yet unknown. This is a very curious problem because in order to perform such a dynamic behavior, the cell may have to take signal noises and cost a lot of energy. There must be some advantages of damping oscillation for the cell. In this study, we focus on two oscillating proteins, nuclear factor-κB (NF-κB) and p38 MAP kinase. These two proteins have been reported to have a crosstalk in their pathways and co-regulate gene expression. We investigate the crosstalk mechanism and biological functions of their oscillations.

3Pos313 多繊毛上皮細胞の基底小体の配列・配向秩序化の数理モデル
Mathematical model for alignment and orientation order of basal bodies in a multi-ciliated cell

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Hundreds of cilia on the apical membrane of a multi-ciliated cell beat in the same direction so as to transport dust and virus for exclusion in the mammalian trachea. For the synchronous beating of cilia, basal-bodies (BBs; root of the cilia) need to be well aligned and point to the same direction, however, establishment of such ordered structure of BBs yet remains unclear. We propose a mathematical model for explaining how alignment and orientation order of the BBs develop, based on interaction of the BBs with cytoskeletal (microtubule) network in the apical membrane. Our model suggests that the polarity of the cytoskeleton is indispensable for BBs to points the same direction.

3Pos314 隣接させた心臓組織片の同期化プロセスの解明
Synchronization processes of cardiac tissue fragment pair and the regional differences in the heart

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The dissected tissue fragments from the fetal heart of a chicken exhibits “beat”, spontaneous contraction rhythmically. The mechanoelectrical properties such as interbeat interval (IBI) of the fragments are different between atrium(A) and ventricle(V). For example, the IBI’s of A are faster than V’s. We have investigated the beat synchronization between two fragments, A-A, A-V and V-V, placed next to each other. Initially, each fragment beats independently and then two fragments became synchronized the beat. Interestingly, the unstable IBIs were observed before 2:1 and 1:1 synchronization. We present the various synchronization processes between A-A, A-V and V-V. We also discuss the numerical simulations of such synchronization processes including the unstable IBIs.

3Pos315 長期的機械刺激による心筋細胞集合体への影響
Long-term influence of external mechanical stimulus on cardiomyocyte aggregations

Takashi Miyazawa, Shin Arai, Takahiro Uehara, Shogo Yahagi, Toshiyuki Mitsui (*Grad. Sch. of Sci. & Eng., Aoyama Gakuin Univ.*)

Two cell types, myocytes and fibroblasts, mainly constitute the heart. The heart beats induced by anisotropic propagation of an action potential, which relies on the proper distributions of gap junction and ion channels through the heart. The heart with the distributions forms during embryonic development. However, the details of the formation process are not clear, especially mechanical contraction vs. channel and gap junction. In order to exam how the contract motion affects on the formation of the heart, we have applied mechanical stimulus imitating the motion on myocyte aggregations reassembled from embryonic myocytes in vitro over 24 hours under culture conditions. The cell types, morphology and gap junctions of the stimulated cell aggregations were investigated.

3Pos316 Exploring the basic law that determines the shape of fast moving cells

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Morphology of fast moving cells is largely dictated by the size and the number of dendritic actin networks. How is it that monopolar cells of Dictyostelium, neutrophils and keratocytes, the three most well-studied, all have distinct shape? Here, we show that, depending on the adhesive conditions, the overall morphology of polarized Dictyostelium cells is drastically altered from the archetypal shape elongated in the front-back axis to a more laterally extended fan-like morphology. The fan-like morphology was characterized by a thin and large protrusion enriched in dendritic F-actin, resembling lamellipodia in animal cells. Based on quantitative imaging analysis, we will discuss the underlying global constraints on actin assemblies.

3Pos317 AFM を用いた腫瘍微小環境を構成する細胞間の接着剥離力と細胞接触時間の関係評価
Relationship between detachment force and contact time for cells making up tumor microenvironments measured by AFM

Kenta Ishibashi[1], Tomoko Okada[2], Chikashi Nakamura[1,2], **Hyonchol Kim**[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Biomed. Res. Inst., AIST*)

Tumor microenvironments are composed of various cells, and adhesion strengths of these cells strongly related with cancer progressions, especially metastasis. In this study, detachment forces of two cancer cells were measured with various cell contact times by using cup-attached AFM chip. The force to detach two cancer cells rapidly increased as 3 and 5 times for 5-s and 30-s contacts, respectively, in comparison with that in immediate detachment (less than 1 s), and gradually saturated. The force evenly increased by the acceptance of macrophage secretions throughout measured contact time. These results suggest cell adhesion in this time scale dominated by common physics, such like receptor diffusion, and the AFM is a useful tool to discuss such mechanical processes.

3Pos318 生物発光イメージング法を用いた ECM と接着したマスト細胞の脱顆粒の可視化解析
Video-Rate Bioluminescence Imaging of Degranulation of Mast Cells Attached to the Extracellular Matrix

Satoru Yokawa[1], Takahiro Suzuki[2], Ayumi Hayashi[1], Satoshi Inouye[3], Yoshikazu Inoh[1], Tadahide Furuno[1] ([1]*Sch. Pharm., Aichi Gakuin Univ.*, [2]*Sch. Dent., Aichi Gakuin Univ.*, [3]*JNC Co., Yokohama.*)

Degranulation refers to the secretion of inflammatory mediators within mast cell granules and that trigger allergic reactions. To investigate degranulation in living cells, we used a method of video-rate bioluminescence imaging to directly detect degranulation from a single mast cell by measuring luminescence activity. The neuropeptide Y (NPY), which was colocalized with serotonin in the secretory granules, fused to GLase (NPY-GLase) was efficiently expressed in a mast-cell line RBL-2H3 cells. RBL-2H3 cells expressing NPY-GLase showed that the luminescence signals of the secreted NPY-GLase were repeatedly detected after the addition of an antigen. This imaging method was applicable for observing degranulation in RBL-2H3 cells that adhered to the extracellular matrix.

3Pos319 FERT 法による走化性受容体クラスター活性とべん毛モーター回転の 1 細胞同時計測
Simultaneous measurement of chemoreceptor array's activity and the flagellar motor rotation utilizing single cell FRET

Hajime Fukuoka, Tatsuya Yamakoshi, Sarina Nishimura, Yong-Suk Che, Akihiko Ishijima (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

Rotational switching of two motors on a same *E. coli* cell is highly coordinated, suggesting the high cooperative activation of receptor array. To validate our suggestion, we are trying to detect the activity of receptor array by performing a single cell FRET with rotation of flagellar motors. In this study, we constructed CheA-mTurquoise2 (Tq) and -mVenus (Vn) fusions, and the cell producing these fusions conferred the switching coordination of motors even in the presence of the excitation laser. Furthermore, in this condition, we also succeeded in detecting FRET from receptor array including CheA-Tq and -Vn. We are now trying to simultaneously measure the change in FRET from receptor array and the switching of motors, and will discuss our data at annual meeting.

3Pos320 大腸菌におけるべん毛の回転方向と CheY の細胞内動態の同時計測
Simultaneous measurement of flagellar motor rotation and dynamics of CheY in a single *E.coli* cell

Tatsuya Yamakoshi, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad.Sch.Frontier.Osaka Univ.*)

Recently, we proposed that the dynamic change in CheY-P concentration triggers the coordinated switching of motors without extracellular stimuli. To validate this proposal, we measured the rotational direction of motors and the polar localization of CheY-GFP as CheY bind to receptor array at the cell pole in the process of signaling. We found CheY localization change dependent on the rotational direction of the motors, suggesting the receptor's activity changes every switching event. Furthermore, we developed the measuring system to monitor the CheY-P concentration more detail via FRET between CheY and CheZ, and we succeeded in detecting FRET in a single cell. We are now trying to simultaneously measure FRET and the motor-rotation, and will discuss our result.

3Pos321 T 細胞シグナルの超解像イメージング法の開発
Development of the superresolutional imaging in T cell signaling

Hiroaki Machiyama, Ei Wakamatsu, Tadashi Yokosuka (*Dept. Immunol., Tokyo Med. Univ.*)

T cells activate when encountering specific-antigen on antigen presenting cells. Although many of signaling molecules on antigen recognition in T cells have been identified, spatio-temporal regulation of T cell signaling is poorly understood. Using supported membrane system, we previously showed that clustering of antigen receptor in T cell, named TCR microcluster, worked as a signalsome in antigen recognition. We examined the dynamics of signaling molecules localized at TCR microcluster. Halotag-tagged signaling molecules, including TCR, kinases and adaptors were expressed in T cells by retroviral infection. We demonstrated that the majority of signaling molecules slowed down their movement within TCR microclusters.

3Pos322 磁性細菌の走磁性運動におけるべん毛回転運動の生細胞イメージング
Live-cell imaging of flagellar rotation in magnetotactic bacterial cell during magneto-aerotaxis

Yuta Takaoka[1], Azuma Taoka[1], Yoshihiro Fukumori[2] ([1]*Grad. Sch. of Nat. Sci. and Tech., Kanazawa Univ.*, [2]*Vice President, Kanazawa Univ.*)

Magnetotactic bacteria (MTB) synthesize prokaryotic organelle called magnetosome to swim along the geomagnetic field for facilitating their search for microaerobic environment. The detailed flagellar rotation of MTB during magneto-aerotaxis is not revealed. Magnetospirillum magneticum AMB-1 is an amphitrichous flagellated bacterium which has a single flagellum on each end of the cell. In this study, we imaged individual polar flagellar rotations of swimming AMB-1 cells in microaerobic environment. For fluorescence imaging of flagellar rotation, we labeled both flagellum using Alexa488 or Qdot nano beads. We placed the cells in a chamber slide, and observed flagellar motility by HILO fluorescence microscopy to clarify the mechanism of magneto-aerotaxis motility.

3Pos323 高速 AFM による細胞表面の分子イメージング
Molecular imaging of dynamic process on bacterial cell surface by high speed AFM

Hayato Yamashita[1,2], Azuma Taoka[3,4], Masayuki Abe[1] ([1]*Grad. Sch. of Eng. Sci., Osaka Univ.*, [2]*PRESTO, JST*, [3]*Grad. Sch. of Nat. Sci. & Tech., Kanazawa Univ.*, [4]*Bio-AFM Frontier Research Center, Kanazawa Univ.*)

High speed atomic force microscopy (HS-AFM) is powerful tool which visualize the dynamic molecular process in physiological condition. This technique has been applied for not only imaging of purified protein but also that of living cell surface [1, 2]. Recently, we developed HS-AFM scanner for molecular imaging on cell surface at high resolution. In this study, we applied it for observing bacterial cell surface. AFM images showed molecular arrangement of porin trimers and the dynamic processes on cell outer membrane. Furthermore, we observed the reaction processes for antimicrobial agent. This technique will be useful to investigate dynamic molecular process on various bacterial cell surface. [1]Yamashita et. al,(2012) J. Mol. Biol. [2]Oestreicher et. al,(2015)Micron

3Pos324 魚類ケラトサイトの遊走メカニズムに微小管は必要ない
Microtubules are not required for crawling migration of keratocytes

Hitomi Nakashima, Chika Okimura, **Yoshiaki Iwadate** (*Fac. Sci., Yamaguchi Univ.*)

Cell-crawling migration plays an essential role in complex biological phenomena. Many processes essential to such migration are regulated by microtubules in many cell types. However, fish epidermal keratocytes treated with nocodazole, which is an inhibitor of microtubule polymerization, migrate like as normal keratocytes. Here, we discovered that not only these migration properties, but also the molecular dynamics that regulate such properties, such as the retrograde flow rate of actin filaments, distributions of vinculin and myosin II, and traction forces, are also the same in nocodazole-treated keratocytes as those in untreated keratocytes. These results suggest that microtubules are not in fact required for crawling migration of keratocytes.

3Pos325 神経突起との接着による膵島 α 細胞の細胞内顆粒動態とグルカゴン分泌の抑制
Decreased intracellular granule movement and glucagon secretion in pancreatic α cells attached to superior cervical ganglion neurites

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Autonomic neurons innervate pancreatic islets of Langerhans and participate in the maintenance of blood glucose concentrations. Here we studied the effect of superior cervical ganglia neurite adhesion on intracellular secretory granule movement and glucagon secretion in α cells. The mean velocity of granules was significantly lower in α cells attached to neurites than that in those without neurites. Stimulation by a low glucose concentration significantly increased glucagon secretion in α cells lacking neurites but not in those bound to neurites. These results suggest that adhesion to neurites decreases low glucose-induced glucagon secretion in pancreatic α cells by attenuating intracellular granule movement activity.

3Pos326 赤外線レーザー照射刺激による心筋細胞拍動変化の物理的要因
Physical effect on beating rate change of cardiomyocytes induced by infrared laser irradiation

Yukino Motohashi, Kento Nozawa, Maki Ishii, Tomoyuki Kaneko (*LaRC, FB, Hosei univ.*)

The heart rate of cardiomyocytes was known to be increased by irradiation of infrared laser (λ=1480nm). This phenomenon was predicted to be caused by thermal and/or physical effects generated by laser irradiation. To investigate the physical effects on beating rate change of cardiomyocytes, we replaced the low fluidity medium applied with polyethylene glycol or arranged cardiomyocytes in agarose micro chambers. In low fluidity condition, the longer distance between a cell and irradiation point induced the smaller increasing of heart rate. In conclusion, physical effect generated by laser irradiation is an important factor of heart rate increasing. In the future, this technology will be able to control the heart rate of real heart.

3Pos327 100 分子ほどの膜貫通足場タンパク LAT がマスト細胞の免疫反応を担っている
Only ~100 copies of a transmembrane scaffolding protein LAT are responsible in the immune response in mast cells

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Linker for activation of T cells (LAT) is a critical transmembrane adaptor molecule in immune cell responses. Using single-molecule imaging and gene editing, we found that only ~100 copies of LAT (1.1% of LAT in the cell) exist in the cytoplasmic vesicles tethered to the cytoplasmic surface of the plasma membrane (PM) by way of exocyst complexes, and that these LAT molecules, and not those in the PM (~10% of LAT), are responsible for mediating the signal from the engaged receptors to the downstream responses. PLCγ2 recruitment to LAT vesicles (leading to the critical function of mast cells, degranulation) and the existence of the metabolic system to produce the PLC γ2 substrate $PI(4,5)P_2$ in LAT vesicles suggest that the LAT vesicle serves as a key signaling platform.

3Pos401 Stiffness measurement of cell by using micro-hand systems with plate shape end effector

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Micro robotics technologies are applied to life-science field and advanced these researches. In particular, the researches about force measurement of the tissues or single cell have much attention. Many researches have reported that the mechanical stimulus is important factor of the histogenesis and cellular differentiation. Therefore, establishment of methodology for stiffness measurement is important for understanding cell differentiation mechanisms. Furthermore, evaluation of stiffness of organelle is also important for understanding disease (ex. Nuclear membrane disease). In here, we focus on cell and cell nucleus, and reported these stiffness measurement methods and evaluated result.

3Pos402 油中水滴界面を利用した DNA ハイドロゲルマイクロカプセルの構築
Construction of DNA hydrogel microcapsules using water-in-oil droplet interface

Yuji Nakashima, Yusuke Sato, Yu Kasahara, Masahiro Takinoue (*Dept. of com. sci., TITech*)

Sequence-designed DNAs are used as materials to construct various-shaped nanostructures, including DNA origamis or DNA tiles. Furthermore, the DNA nanostructures can be assembled into a large structure such as hydrogels. These techniques would be applicable for the creation of molecular robots, artificial cells, and so on. In this study, we construct micro-sized hollow gel spheres at a water-in-oil droplet interface using Y-shaped DNA nanostructures. We will discuss methods for a release of encapsulated molecules from the DNA microspheres via an external stimulation. We believe that this study will be applied to biomedical research such as drug delivery systems.

3Pos403 DNA でつくるシグナル伝達機構の実現に向けた DNA 生成反応回路の構築
Construction of a DNA Generation Circuit toward Engineering of DNA-based Signal Transduction Systems

Ken Komiya, Chizuru Noda, Masayuki Yamamura (*Sch. Comp., Tokyo Tech.*)

We developed a reaction system that generates multiple single-stranded DNA species as signals at a constant “low” temperature by taking advantage of polymerization and strand displacement activity of a DNA polymerase in combination with hydrolysis activity of a nicking endonuclease. Its modular architecture allows programming of cascading DNA generation by permutation and altering the combinations of template DNA sequences. In the present study, we experimentally investigated the feasibility of temporal control of DNA generation toward construction of DNA-based signal transduction systems that are applicable for coordination of DNA-directed motors and DNA nanomachines.

3Pos404 iPS 細胞の心筋分化誘導における血管内皮細胞の影響
Effect of vascular endothelial cells on cardiac differentiation of iPS cells

Chika Tada, Ken Takahashi, Masatoshi Morimatsu, Keiji Naruse (*Grad. Sch Med Dent Pharm Sci., Okayama Univ.*)

Research of cardiac regenerative medicine is actively studied. We investigated the effect of endothelial cells on the myocardial differentiation induction efficiency of iPS cells. Specifically, we cultured iPS cells with endothelial cells and human gingival fibroblast cells. We observed cellular morphology behavior and analyzed the expression level of differentiation marker protein. As a result, expression of troponin T (TNNT2), a cardiac differentiation marker, was evident in the cell aggregate. Furthermore, under the presence of endothelial cells, strong expression of TNNT2 was observed while size of the aggregate that caused undifferentiations was small. These results suggested that endothelial cells stimulates cardiac differentiation of iPS cells.

3Pos405 Evaluation of membrane shape deformation of giant vesicles prepared by droplet transfer method

Masamune Morita, Naohiro Noda (*Biomed. Res. Inst., AIST*)

Membrane shape deformation is closely related to important various cellular functions, such as exocytosis, endocytosis, autophagy, and cell division. Giant vesicles (GVs) as model of cell membranes have been actively employed to study for understanding of membrane shape deformation, and challenging the synthesis of membrane shape deformation. In recently, droplet transfer method is widely used to prepare the GVs. In the obtained GVs with this method, the presence of oil between the outer and inner leaflet of the membrane was reported. However, it is unclear how residual oil effects on the membrane shape deformation. Here, we evaluated that the membrane shape deformation of GVs prepared by droplet transfer method against several external stimuli.

3Pos406 細胞外電位測定による心筋細胞集団と心臓組織片の拍動同期過程の解析
Analysis of signal synchronization process between dispersed cardiomyocyte and cardiac tissue piece by measuring extracellular potential

Toru Nakamura, Chiho Nihei, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell biology, Department of Frontier Bioscience, Hosei University*)

In cardiac diseases, cardiac failure has the most number of deaths in Japan. Although research to transplant the myocardium sheet to the affected area is progressing, the mechanism of the signal synchronization process of dispersed cardiomyocyte has not been elucidated. In this study, we analyzed the signal synchronization process between dispersed cardiomyocyte and cardiac tissue piece by measuring extracellular potential. As a result, the more stable signal became a pacemaker regardless of dispersed cardiomyocyte and cardiac tissue piece. Therefore, it was found that the stability is a more important factor in signal synchronization.

3Pos407 新規心毒性検査技術を目指した心臓組織片の細胞外電位計測
Measurement of Extracellular Potential on Heart Tissue for Novel Cardiotoxicity Test

Ryohei Kobayashi, Koji Emura, Tomoyuki Kaneko (*LaRC,FB,Hosei Univ.*)

Arrhythmia is one of the lethal diseases to the living body. For safety assessment at an early stage of drug development, Multi Electrode Array (MEA) system is expected to detect the index of arrhythmia. In this study, we measured the extracellular potential of chick embryo-derived cardiac tissue pieces on MEA electrode, and calculated Field Potential Duration (FPD) and Short Term Variability (STV). As a result, applying E-4031, potassium channel blocker, FPD was prolonged and STV was increased at lower concentration than hES-cell-derived cardiomyocyte cluster. Thus, it was suggested that cardiotoxicity test using chick-embryo-derived cardiac tissue pieces could be performed with higher sensitivity than one using hES- cell-derived cardiomyocyte clusters.

3Pos408 細胞外電位計測による心臓組織片の拍動同期解析
Analysis of beating synchronization of cardiac tissue pieces by field potential measurement

Yousuke Kamei[1], Toshiyuki Mitsui[2], **Tomoyuki Kaneko**[1] ([1]*LaRC, FB, Hosei Univ.*, [2]*Dept. Math. Phys., Col. Sci. Eng., Aoyama Univ.*)

To clarify the synchronization mechanism between artificial cardiac tissue sheet and original cardiac tissue in cardiac regenerative medicine, the synchronization process between chick embryo-derived cardiac tissue pieces was investigated. In the heart, there are various parts such as the ventricle, the atrium, the sinoatrial node, etc., and the process of synchronization may be different at each parts. Two cardiac tissue pieces were placed on the Multi Electrode Array and the synchronization process of the ventricular pair, the atrial pair or the ventricle and the atrial pair was compared. In conclusion, the synchronization process was different between the ventricular pair and the atrial pair, and the ventricular and the atrial pair didn't synchronize completely.

3Pos409 血中循環腫瘍細胞をサイズ分画するための流路チップデザインの加工工程における形状の転写の加工精度の定量的評価
Quantitative evaluation of preciseness in design copy in microfabrication procedures of circulating tumor cell cluster size-filtration

Ayako Kawai[1], Moe Iwamura[2], Kenji Matsuura[3,4], Akihiro Hattori[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

We have been developing an on-chip imaging cell sorter using a microfluidics chip equipped with microstructures for size filtration of circulating tumor cell clusters. However, we found the apparent size differences between our design and the final microfabricated product of chips. Hence, we evaluated origin of size changes in three processes of microfabrication, i.e., photo-mask development, SU-8 molding, and poly-dimethylpolysiloxane (PDMS) chip fabrication. We found that the differences occurred in the process of molding by shrinkage of microstructures in a certain ratio; e.g., computer data to photo-mask 93%, photo-mask to SU-8 90%, SU-8 to PDMS 99%, and total 80%. This result shows that we need to take this shrinkage ratio into the procedure of designing of chips.

3Pos410 血中循環腫瘍細胞を選択回収するサイズ分画機能を備えた画像認識型セルソーターの開発
Development of size filtration-imaging cell sorter for real time selective collection of circulating tumor cells (CTCs) in blood

Moe Iwamura[1], Kenji Matsuura[3,4], Ayako Kawai[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

We have developed an on-chip imaging cell sorting assay equipped with cell size filtration module for identifying CTCs with their morphological characteristics. In our cell size filtration module, particles were sorted by their sizes by passing through the micro pillars aligned to the flow direction with intervals of desired filtration sizes, and an alternative current electric field perpendicular to the flow direction was applied for separation, and is settled prior to the image acquisition module. We evaluated the efficiency of filtration of this system and also evaluated the correlation of zeta potentials to determine an optimal electric field. The results showed that this imaging cell sorter can classify and identify CTCs efficiently.

3Pos411 単一細胞分析のための Ba2 + / Ca2 +アルギン酸微小滴からの選択的な細胞回収方法の検討
Selective digestion of Ba2+/Ca2+ alginate microdroplets for single-cell-analysis

Masao Odaka[1,2], Moe Iwamura[3], Ayako Kawai[4], Akihiro Hattori[1,2], Kenji Matsuura[1,2], Kenji Yasuda[1,2,3,4] ([1]*Org. Univ. Res. Initiatives, Waseda Univ.*, [2]*WASEDA Biosci. Res. Ins. in Singapore*, [3]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [4]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

Cells encapsuled by microdroplets are an effective platform for the identification and separation of individual cells for single-cell-analysis. We developed a spray method of encapsulating cells in alginate microdroplets with two divalent cations (Ba2+ and Ca2+), respectively. In addition, we examined the capability of the alginate gel to exchange linkage-divalent cations to evaluate their digestion characteristics with a chelating buffer. The result showed that the microdroplets were digested according to the difference in chelating efficiency of linkage-divalent cations and exchangeable. These results indicate that the potential applications of a mixture of alginate microdroplets with different divalent cations control the selective digestion of microdroplets.

3Pos412 Environment-dependent self-assembly of DNA nanostructures on phase-separated lipid bilayer membranes

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Self-assembly of biomolecules on lipid bilayer membranes plays a key role in many fundamental biological processes. Here, we report environment-dependent self-assembly of DNA origami structures on phase-separated lipid bilayer membranes which consist of liquid-disordered (Ld) and solid-ordered (So) phases. Experimental results showed that blunt-ended DNA origamis self-assembled into lattices on the Ld phase, whereas those on the So phase packed into aggregates. When the ionic condition was changed by the addition of NaCl, the lattices on the Ld phase desorbed from the surface while the aggregates on the So phase reorganized into the lattices. Our results would lead to the development of functional membrane domain that can be applicable for artificial molecular systems.

3Pos413 血管新生の遺伝子発現解析のためのマトリゲル構造を用いた発芽的血管内皮細胞の回収方法の開発
Development of sprouting vascular endothelial cell collection method using flexible design of Matrigel for expression analysis

Yuki Yamanaka[1], Kento Iida[1], Ryuji Takano[2], Hiromichi Hashimoto[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Matsuura[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore*)

For clarifying the mechanism of angiogenesis, single cell expression vs.cell dynamics analysis is important. We have developed a method to collect vascular endothelial cells (ECs) during angiogenesis for Chromatin immunoprecipitation (ChIP) assay to identify expressing gene sets which control sprouting angiogenesis. We applied a variety of designs of Matrigel droplets containing a gradient of VEGF concentration, on a glass base dish and cultured pancreatic islet-derived MILE SVEN 1 endothelial cells (MS-1) around the droplets. We first evaluated the size and shape dependence of Matrigels for sprouting, and found that the curvature of boundary may not influence to sprouting. The results suggest that the potential of flexible design of Matrigel for collecting cells.

3Pos414 交流磁場によるフェリチン内合成マグネタイトナノ粒子の加熱
Heating effect of magnetite nanoparticles synthesized in the ferritin cavity by alternating magnetic field

Daisuke Katayama[1], Hideyuki Yoshimura[2] ([1]*Grad. Sch. Sci Eng. Phys, Univ. Meiji*, [2]*Sci Eng. Phys, Univ. Meiji*)

Hyperthermia therapy has attracted attention in recent years as minimally invasive treatment for cancer. Magnetic particles are known to generate heat in alternating magnetic field, and sometimes utilized as a heat source for hyperthermia. Ferritin is known to produce magnetite nano-particles in the cavity in anaerobic condition and is called magnetoferritin. We succeeded to synthesize single crystal magnetite nanoparticles with homogenous diameter of 8nm in the ferritin cavity. Frequency of the applied magnetic field, solenoid inductance, concentration of nanoparticles are altered to optimize the heating conditions. Ferritin with specific binding ability for cancer cells (see Takashima et. al. Meiji Univ.) can be used for hyperthermia therapy.

3Pos415 Insertion of cancer cell specific binding peptide into ferritin

Naoki Takashima[1], Hideyuki Yhoshimura[2], Tomoko Kanamaru[2] ([1]*Grad. Sch. Sci/Eng Phy. Univ. Meiji*, [2]*Sci/Eng Phy. Univ. Meiji*)

Apoferritin is known as an iron storage protein and is distributed in various living species. This protein is consisted in 24 subunits which form spherical shell of 13 nm with cavity of 7nm. The N-terminus of the subunits exposed external surface of the molecule, and thus additional peptide which bind to some specific molecule can be extended by artificially. Here we focused on the RGD-4C peptide which is known to bind integrin αvβ3 expressed on the tumor vessels. We added the peptide to N-terminal site of horse spleen L ferritin and succeeded to form ferritin molecules. To evaluate affinity of the peptide, we are going to check the interaction between HeLa cell which express integrin αvβ3 and ferritin with iron core or rare earth nanoparticles as a molecular marker.

3Pos416 蛍光・発光タンパク質に基づくマイクロディスプレイ
Micro-display devices based on fluorescence and bioluminescence proteins

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Fluorescence and bioluminescence proteins have been used in many essential applications by enabling us to investigate spatiotemporal progressions of biological process in real time. In contrast, their applications in the field of engineering have not been fully explored. Aiming to expand the utilities of those proteins, we here report simple fabrication of electro-optic micro-display devices. Our approach relies on the two fundamental properties of gold surface: its amenability to immobilizing a variety of organic molecules, and its abounding interactions with the molecules at the surface. We show robust modulations in the emission from fluorescence or bioluminescence proteins on the bias voltage. Potential biophysical mechanisms are then discussed.

3Pos417 Photo-regulation of Small GTPase Ras using Photochromic SOS-Peptide

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Small GTPase Ras is known as a central regulator of cellular signaling. The switching of Ras activity was regulated by GEF and GAP. In this study, we focused on the interface between Ras and αH Helix of SOS (GEF) to photo-regulate Ras activity. We designed and synthesized several αH Helix mimetic peptides containing two cysteine residues at cross-linkable position with bifunctional azobenzene derivative ABDM. ABDM was stoichiometrically incorporated into the peptides. Cis-Trans isomerization of ABDM incorporated into the peptide is induced by UV and VIS light irradiations. Secondary structure of ABDM-peptide was also partially changed by Cis-Trans isomerization. One of the peptide cross-linked with ABDM showed photo reversible inhibition of GDP-GTP exchange of Ras.

3Pos418 High-throughput in vitro selection method for obtaining peptide agonists of G protein-coupled receptors

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G protein-coupled receptors (GPCRs) are one of the most important drug-targets in the pharmaceutical industry. We have developed a method for obtaining peptide agonists for GPCRs, which is a combination of in vitro selection using in vitro compartmentalization and a yeast-based fluorescence reporter assay for GPCR signaling. Here, we present a strategy for screening large-scale DNA library, which combines microfluidic flow cytometry and image-based clone selection. In in vitro selection using a DNA library with a hit rate of ~0.1%, the approach increased throughput up to 15-folds compared to the image-based manual approach, and greatly accelerated clone screening. This approach will be effective in identifying novel peptide agonists for human GPCRs.

3Pos419 Droplet-based microfluidic screening for obtaining microbes producing macromolecule-degrading enzymes

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Environmental microbes secrete enzymes capable of degrading macromolecules into smaller molecules that can be used as nutrients for growth. The enzymes have potential benefit for effective utilization of terrestrial resources such as biomass. We then devised a droplet-based microfluidic screening method for obtaining microbes producing macromolecule-degrading enzymes. Microbes are encapsulated in water-in-oil (W/O) droplets at the single-cell level. The W/O droplet where the macromolecule is progressively degraded into smaller molecules increases the deformability. The screening is achieved by using a microfluidic device that enables passive sorting of deformable W/O droplets. Employing this method, we have demonstrated agarose-degrading microbes can be obtained.

3Pos420 統合情報理論に基づく意識を持つ DNA ネットワークの設計と解析
Design and analysis of DNA network with consciousness based on integrated information theory

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Integrated information theory (IIT) has recently received attention in terms of the evaluating “consciousness”. This theory has been verified in the field of computer science and brain science, but it remains to be elucidated whether consciousness can be constructed based on biomolecular systems. In this study, we propose a simple DNA logic circuit that can be regarded as ’’conscious” from the criteria of IIT. Then, we simulate the behavior of the designed DNA network and get some parameters necessary for the experiment. I will discuss calculation of amount of integrated information as an indicator of the amount of consciousness. We believe this system could be applied to biomedical technologies.

3Pos421 The way to the perfect observation!! ~Research of drone that mimics the birds~

Ayumu Kuroda (*Tokyo Metropolitan high sch .,F-pro*)

Presently, nature observation mainly done. Drone is an artifact. So, wild animals are wary and it can’t observe the nature state. As a method to solve this problem, we aimed to develop a drone that mimics a birds. Also, for long-term use as an observer, aimed to develop aircraft capable of low-energy flight. To develop an aircraft capable of low-energy flight, We focused on migratory birds moving over long distance. The reason why migratory birds can moving long distance are many theory. So, we thought that migratory birds can do low-energy flight. Therefore, we thought that mimicking migratory birds will enable low-energy flight. So, we aimed at the development of the drone that mimics the migratory birds.

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。

Abdellatef, Shimaa A. (Abdellatef Shimaa A.) 2N1500
Abe, Jun (阿部 淳) 1Pos201
Abe, Keigo (阿部 圭吾) **2Pos314**
Abe, Koichi (阿部 紘一) **1Pos046**
Abe, Masanobu (阿部 匡伸) **1SBP-6**
Abe, Masayuki (阿部 真之) 2Pos070
3Pos323
Abe, Satoshi (安部 聡) **2SKA-2**
Abe, Takaya (阿部 拓哉) 3SEA-5
Abe-Yoshizumi, Rei (吉住 玲) 1H1406
2Pos088
Abematsu, Chika (椙松 知香) **1Pos055**
Adachi, Hiroaki (安達 宏昭) 3Pos050
Afrin, Rehana (Afrin Rehana) 2Q1606
Agata, Kazuya (縣 和哉) **2F1412**
Ago, Hideo (吾郷 日出夫) 1M1448
Ago, Hinako (吾郷 日向子) 3Pos078
Aizawa, Tomoyasu (相沢 智康) 2H1500
2H1554
Aizawa, Yasunori (相澤 康則) **1SIP-4**
Ajito, S. (味戸 聡志) 3Pos074
Ajito, Satoshi (味戸 聡志) **1K1524**
Akagi, Jin (赤城 仁) 3Pos418
Akai, Taiki (赤井 大気) 2L1412
Akama, Kenji (赤間 健司) **1O1548**
Akashi, Satoko (明石 知子) 3Pos065
Akiba, Keiichirou (秋葉 圭一郎) 2Pos107
Akihiro, N (Akihiro N) 2Pos110
Akil, Caner (Akil Caner) **2Pos109**
Akimoto, Seiji (秋本 誠志) 3Pos032
Akimoto, Takuma (秋元 琢磨) 2Pos023
Akita, Fusamichi (秋田 総理) **1F1330**
1F1342
Akiyama, Masakazu (秋山 正和) **1SAA-4**
Akiyama, Shuji (秋山 修志) 1K1500
1M1342
1Pos047
1Pos073
3Pos063
Akiyama, Tomoki (秋山 友希) **2Pos024**
2Pos056
3Pos010
Akiyama, Yoshinori (秋山 芳展) 2Pos306
Akiyama, Yutaka (秋山 泰) 1C1448
3Pos201
Alam, Md Jahangir (アラム ジャハンギル エムディ)
1Pos086
Albers, Sonja-Verena (Albers Sonja-Verena) 2E1530
Ali, Samson (Ali Samson) **2Pos110**
Amagai, Yuta (天貝 佑太) 1SGA-3
Amano, Mihoka (天野 妙法華) **2Pos020**
3Pos050
Amano, Shinji (天野 真治) **1Pos402**
Amyot, Romain (AMYOT Romain) 3Pos215
Ando, Jun (安藤 潤) **2Pos206**
2Pos405
Ando, Minami (安藤 美波) **1Q1406**
3Pos312
Ando, Shoji (安藤 祥司) 1Pos054
1Pos055
Ando, Tadashi (安藤 格士) **1Q1500**
Ando, Toshio (安藤 敏夫) 1SKA-2
1D1512
1E1448
1G1342
2D1530
2D1542
1Pos031
1Pos212
2Pos205
3Pos014
Anzai, Itsuki (安齋 樹) **1K1500**
Anzai, Kosuke (安齋 幸祐) **2Pos075**
Anzai, Naohiko (安西 尚彦) **1SOA-4**
Aoki, Eriko (青木 英莉子) 2Pos019
3Pos026
Aoki, Kazuhiro (青木 一洋) 1Pos420
Aoki, Kouji (青木 晃次) 1M1418
Aoki, Shota (青木 肖太) 1Pos311
1Pos315
1Pos319
3Pos095
Aono, Shigetoshi (青野 重利) **3SMA-1**
Aoshima, Yu (青島 佑) 2M1400
Arai, Fumihito (新井 史人) 1A1548
Arai, Munehito (新井 宗仁) 1K1354
1K1418
1K1448
1K1512
1L1448

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3Pos078
3Pos088
Arai, Ryoichi (新井 亮一) **2SIP-7**
Arai, Ryusuke (新井 隆介) 1M1418
Arai, S. (新井 栄揮) 3Pos074
Arai, Shin (新井 晋) **3Pos314**
3Pos315
Arai, Tatsuo (新井 健生) 3Pos401
Arai, Yoshiyuki (新井 由之) 1D1500
Arakawa, Takatoshi (荒川 孝俊) 1J1512
1Pos041
1Pos046
Araki, Osamu (荒木 修) 1Pos309
Aramini, James M (Aramini James M) 2Q1606
Arata, Toshiaki (荒田 敏昭) 1SDA-3
1Pos201
1Pos205
2Pos027
Arata, Yukinobu (荒田 幸信) 1O1512
2O1530
Arif Md. Rashedul, Kabir (Arif Md. Rashedul Kabir)
2Pos321
Arikawa, Keisuke (有川 敬輔) **1Pos045**
Arimoto, Mutsuko (有本 睦子) **1A1500**
Arimura, Yasuhiro (有村 泰宏) 2Pos038
Arisaka, Katsushi (Arisaka Katsushi) 1Pos306
Ariyama, Hirotaka (有山 弘高) **2Pos205**
Arulmozhiraja, Sundaram (ラジャ サンダラム)
1M1354
Asano, Yuka (浅野 友香) 2A1530
Ashida, Ryoi (芦田 凌惟) 2Pos058
Ashida, Takeshi (芦田 剛士) 1Pos023
Ashida, Yuto (蘆田 祐人) 2D1500
Ataka, Kenichi (安宅 憲一) **2G1436**
Awazu, Akinori (粟津 暁紀) 1SIA-6
1Pos104
1Pos106
1Pos108
1Pos109
2Pos051
2Pos052
2Pos102
2Pos318
Azai, Chihiro (浅井 智広) 1SRA-4
1SRA-6
3Pos024
3Pos033
Azuma, Takachika (東 隆親) 2K1518
Azuma, Toshiki (吾妻 利紀) 1Pos412
1Pos414
1Pos418
Azuma, Toshki (吾妻 利紀) **1Pos413**
Azuma, Yusuke (東 裕介) **1Pos325**
Baba, Seiki (馬場 清喜) 1M1448
2E1412
Baba, Shoji A. (馬場 昭次) 2A1542
Baba, Shunsuke (馬場 俊輔) 1Q1524
Bajpai, Archana (Bajpai Archana) **1D1330**
Ban, Nenad (バン ネナド) 2M1618
Bannai, Hiroko (坂内 博子) **3SFA-1**
Bassi, Roberto (Bassi Roberto) 1F1418
Basu, Kaustuv (Basu Kaustuv) 2M1554
Bavi, Navid (Bavi Navid) 2G1530
Beeby, Morgan (Beeby Morgan) 3SKA-4
Beja, Oded (Beja Oded) 1F1512
2H1436
2Pos092
Bekker, Gert-Jan (ベッカー ゲルトヤン) **2J1530**
Beppu, Kazusa (別府 航早) 1SFA-6
2O1542
Bershadsky, Alexander D. (Bershadsky Alexander D.)
2SBP-3
1A1430
Bessho, Yoshitaka (別所 義隆) **2SKA-1**
3SGA-4
Bhattacharyya, Bhaswati (Bhattacharyya Bhaswati)
3Pos220
Birrell, James (Birrell James) 3Pos058
Bisht, Shveta (Bisht Shveta) 1E1548
Biskup, Till (Biskup Till) 2Pos097
Bito, Haruhiko (尾藤 晴彦) 1F1536
Blanchoin, Laurent (Blanchoin Laurent) **1SMA-5**
2Pos319
Bodner, Justin (Bodner Justin) 1E1430
Boehringer, Daniel (ボーリンガー ダニエル) 2M1618
Bond, Peter J. (Bond Peter J.) **1C1342**
1Q1430
3Pos021
Bond, Peter John (Bond Peter John) 2Pos018
Boorla, Veda (Boorla Veda) 2E1554
Booth, Paula (Booth Paula) 2G1436
Boussac, Alain (Alain Boussac) 3Pos029
Brandani, Giovanni (Brandani Giovanni) **2Q1400**
Bui, Khanh Huy (Bui Khanh Huy) 2M1554
C. Robinson, Robert (C. Robinson Robert) 2Pos109
2Pos110
Cahalan, Stuart (Cahalan Stuart) 1SEA-7
Cahyadi, Harsono (Cahyadi Harsono) 1D1548
Cai, Cuiyuan (蔡 翠媛) **2Pos406**
Caner, Akil (Caner Akil) 1SMA-6
Chaen, Shigeru (茶圓 茂) 2Pos218
Chandrasekar, Sowmya (チャンドラセカー ソウミャ)
2M1618
Chandru, Kuhan (Chandru Kuhan) 2Q1606
Chang, Cheng-Hung (張 正宏) **1O1418**

Chang, Jae-won (張 宰源) 3Pos027
Chang, Jen-Chien (Chang Jen-Chien) **2Pos415**
Chang, Minhyeok (Chang Minhyeok) 3SIA-3
Chang, Wen-Hsuan (Chang Wen-Hsuan) 2Pos034
Chang, Yen Chan (張 晏展) **2Pos044**
Chatani, Eri (茶谷 絵理) **2L1412**
3Pos066
Che, Yong-Suk (蔡 栄叔) 2SAA-4
Che, Yong-Suk (蔡 栄淑) 2Pos309
2Pos310
2Pos311
2Pos312
3Pos048
3Pos319
3Pos320
Chen, Gang (Chen Gang) **3SIA-6**
Chen, Minghao (陳 明皓) 3Pos059
Chen, Ping (Chen Ping) 3SIA-7
Cheng, Cheng (成 せい) **3Pos005**
Cheng, Cheng (成 鍼) 2F1400
Chi, Peter (Chi Peter) 2Pos034
Chi, Peter HY (冀 宏源) 2SAA-3
Chiba, Hitoshi (千葉 仁志) 1J1524
Chiba, Kyoko (千葉 杏子) 2Pos418
Chiba, Shuntaro (千葉 峻太朗) 1Pos026
Chikai, Yusaku (近井 優作) **1Pos302**
Chikenji, George (千見寺 浄慈) 1Pos029
1Pos030
3Pos086
Chikenji, George (知見寺 浄慈) 3Pos208
Chirifu, Mami (池鯉鮒 麻美) 1Pos056
Choi, Samuel (崔 森悦) 1SEA-8
Chongdar, Nipa (Chongdar Nipa) 3Pos058
Chow, Sih-Yao (周 嗣堯) 2K1424
Cleaves, Henderson J (Cleaves Henderson J) 2Q1606
Cohen, Eli J. (Cohen Eli J.) **3SKA-4**
Cryershinozuka, Kazuho (クライヤー篠塚 一穂)
1Pos032
Dall'Osto, Luca (Dall'Osto Luca) 1F1418
Dam, Heui Chi (ダム ヒョウチ) 2Pos060
Dao, Hoang Anh (Dao Hoang Anh) **1Pos024**
Das, Sumita (Das Sumita) **3Pos214**
Dasgupta, Bhaskar (Dasgupta Bhaskar) **1Pos012**
Dekker, Cees (Dekker Cees) 1E1548
Demura, Makoto (出村 誠) 2H1500
2H1554
3Pos012
Dewa, Takehisa (出羽 毅久) **1F1430**
Dobrokhotov, Oleg (Dobrokhotov Oleg) **3Pos304**
Dohi, Taiki (土肥 大輝) 2Pos039
Dohmae, Naoshi (堂前 直) 2Pos306
Dohra, Hideo (道羅 英夫) 1Pos086
1Pos090
1Pos096
Doi, Motomichi (戸井 基道) 2K1530
Doi, Satoko (土井 聡子) 2H1518
Dokainish, Hisham (Dokainish Hisham) **3SAA-2**
Doki, Chihiro (土岐 知央) **2Pos316**
Doki, Shintaro (道喜 慎太郎) 3Pos020
Dougakiuchi, Tatsuo (道垣内 龍男) 3Pos042
Dunn, Alexander (Dunn Alexander) **2SEA-2**
Ebata, Kyoichi (江端 恭一) **3Pos216**
Ebata, Ryusei G (江幡 瑠星) 1Pos202
Edamatsu, Masaki (枝松 正樹) **3Pos061**
Eeftens, Jorine M. (Eeftens Jorine M.) 1E1548
Ehara, Haruhiko (江原 晴彦) 2Q1518
Eiraku, Mototsugu (永樂 元次) **2SBP-6**
Ejima, Yoshimichi (江島 義道) 1SBP-4
Eki, Toshihiko (浴 俊彦) 2F1424
Ekimoto, Toru (浴本 亨) 1Pos034
1Pos049
3Pos076
Emura, Koji (江村 光司) 3Pos407
Endo, Masayuki (遠藤 政幸) 3Pos412
Endo, Natsumi (圓東 那津実) 1Pos064
Endo, Shigeru (猿渡 茂) 1Pos035
2Pos037
Endo, Toshiya (遠藤 斗志也) 2E1412
Enomoto, Atsushi (Enomoto Atsushi) 3Pos304
Enomoto, Tsukasa (榎本 司) **3Pos064**
Etchuya, Kenji (越中谷 賢治) 1Pos008
1Pos039
Fan, Hsiu-Fang (范 秀芳) **2K1424**
Farha, Trisha.D (Farha Trisha.D) 3Pos416
Farhana, Tamanna Ishrat (Farhana Tamanna Ishrat)
2Pos222
Farina, Francesca (Farina Francesca) 2Pos319
Feig, Michael (ファイグ マイケル) 2Pos059
Fuchigami, Sotaro (渕上 壮太郎) **1J1536**
3Pos072
Fuda, Hirotoshi (布田 博俊) 1J1524
Fujie, Hiromichi (藤江 裕道) 1A1406
Fujihara, Michiko (藤原 美智子) 1M1354
Fujii, Koichi (藤井 宏一) **2Pos017**
Fujii, Koki (藤井 洸希) 1C1600
3Pos307
Fujii, Masanori (藤井 理則) 3Pos002
Fujii, Masashi (藤井 雅史) 1O1500
Fujii, Ritsuko (藤井 律子) 1F1500
Fujii, Shuji (藤井 修治) 2C1412
Fujii, Soichiro (藤井 聡一郎) **2Pos424**
Fujii, Takashi (藤井 貴志) **2Pos011**
Fujii, Yuki (藤井 裕紀) 1A1524
Fujimiya, Kana (藤宮 佳菜) 1Pos056
Fujimori, Taihei (藤森 大平) 1SAA-1
2A1400

Fujimori, Toshihiko (藤森 俊彦) 1SEA-7
Fujimoto, Akira (藤本 陽) 2Pos404
Fujimoto, Kohei (藤本 康平) 2Pos208
Fujimoto, Koichi (藤本 仰一) 3Pos209
Fujimoto, Takeshi (藤本 健史) 1Pos406
Fujimura, Mika (藤村 美香) 3Pos003
3Pos025
Fujimura, Shoko (藤村 章子) **3Pos016**
Fujimura, Yuu (藤村 祐) 3Pos418
Fujioka, Yuji (藤岡 祐次) **1C1548**
Fujisaki, Hiroshi (藤崎 弘士) **1SOA-5**
1Pos053
Fujisawa, Miho (藤澤 美穂) **2D1400**
Fujisawa, Tomotsumi (藤澤 知績) 2H1542
Fujisawa, Tomtotsumi (藤澤 知績) **2H1400**
Fujise, Kenshiro (藤瀬 賢志郎) 2A1412
Fujishiro, Shin (藤城 新) 2Pos050
Fujita, Ayano (藤田 彩乃) **1A1448**
2A1530
Fujita, Haruya (藤田 遥也) 1Pos307
Fujita, Hideaki (Fujita Hideaki) 2O1400
Fujita, Keisuke (藤田 恵介) 1Pos226
2Pos417
Fujita, Suguru (藤田 卓) **1O1500**
Fujita, Toshihiro (藤田 俊弘) 3Pos050
Fujita, Tsugumi (藤田 亜美) 1Pos305
Fujiwara, Eiji (藤原 英史) 2A1542
Fujiwara, Ikuko (藤原 郁子) **3Pos040**
Fujiwara, Kazuo (藤原 和夫) 2Pos011
2Pos012
2Pos016
2Pos019
3Pos026
Fujiwara, Kimi (藤原 希規) 2Pos106
Fujiwara, Satoru (藤原 悟) 1SDA-3
1M1430
Fujiwara, Satsuki (藤原 沙都姫) 2D1436
Fujiwara, Takahiro K. (藤原 敬宏) 2D1412
3Pos327
Fujiwara, Takashi (藤原 貴史) **2Pos210**
Fujiwara, Toshimichi (藤原 敏道) 1K1548
2Pos027
3Pos067
Fujiyama, Fumino (藤山 文乃) 1Pos320
Fujiyama, Keisuke (藤山 敬介) 1Pos066
Fujiyoshi, Yoshinori (藤吉 好則) 2G1542
Fukada, Kazuhiro (深田 和宏) **2Pos106**
Fukagawa, Tatsuo (深川 竜郎) 2M1518
Fukai, Shuya (深井 周也) 3SDA-3
Fukasawa, Atsuhito (深澤 宏仁) **1Pos403**
Fukata, Masaki (深田 正紀) 3SDA-3
Fukata, Yuko (深田 優子) 3SDA-3
Fukuda, Ikuo (福田 育夫) **3Pos075**
Fukuda, Koki (福田 孝貴) **1Pos029**
Fukuda, Masahiro (福田 昌弘) **1M1406**
Fukuda, Norio (福田 紀男) 2N1424
Fukumori, Yoshihiro (福森 義宏) 1G1342
3Pos322
Fukumoto, Kodai (福本 紘大) **2Pos105**
Fukunaga, Akira (福永 晃) **2N1518**
Fukunaga, Hiroki (福永 裕樹) **1Pos226**
Fukunishi, Yoshifumi (福西 快文) 3Pos051
Fukuoka, Hajime (福岡 創) **2SAA-5**
2Pos309
2Pos311
2Pos312
3Pos048
3Pos319
3Pos320
Fukushima, Ryosuke (福島 綾介) **2Pos409**
Fukushima, Seiya (福島 誠也) 2A1424
2A1436
Fukuyama, Tatsuya (福山 達也) 1SFA-6
Fukuzawa, Misaki (福澤 美咲) **3Pos025**
Funahashi, Yoshiki (舟橋 欣生) 1Pos307
Funatsu, Takashi (船津 高志) 1A1354
1D1406
1K1330
1O1524
2C1518
2D1424
2K1500
2Pos406
2Pos424
3Pos418
3Pos419
Furue, Masaya (古江 祐也) **1Pos027**
Furuhashi, Hiroki (古橋 弘貴) **2Pos403**
Furuike, Shou (古池 晶) **2Pos014**
Furuike, Yoshihiko (古池 美彦) 1M1342
1Pos047
1Pos073
3Pos063
Furukawa, Masayuki (古川 眞之) **2Pos217**
Furukawa, Yoshiaki (古川 良明) **3SMA-4**
1K1500
Furumoto, Yuya (古本 悠也) **1Pos412**
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1Pos414
1Pos418
Furuno, Tadahide (古野 忠秀) 3Pos310
3Pos318
3Pos325
Furusawa, Chikara (Furusawa Chikara) 2O1400
Furusawa, Chikara (古澤 力) 2O1436
1Pos080

Furuta, Akane (古田 茜) 2SMA-2
2Pos204
2Pos214
Furuta, Aya (古田 綾) **1Pos017**
Furuta, Ken'ya (古田 健也) **2SMA-2**
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2Pos204
Furuta, Ken'ya (古田 健也) 1E1536
2Pos214
Furuta, Tadaomi (古田 忠臣) **1SOA-3**
1Pos032
3Pos056
3Pos057
Furuta, Toshiaki (古田 寿昭) 2A1542
Furutani, Yuji (古谷 祐詞) 2F1530
2Pos071
3Pos020
Furuzawa, Shunta (古沢 駿太) **2Pos001**
Fushimi, Keiji (伏見 圭司) 2Pos096
Fushimi, Kokoro (伏見 こころ) 1SRA-4
Fushinobu, Shinya (伏信 進矢) 1J1512
1Pos041
1Pos046
Gaillard, Jeremie (Gaillard Jeremie) 2Pos319
Ganser, Christian (Ganser Christian) **2D1518**
Gao, Ning (高 宁) **2SBA-3**
Gao, Wenlong (Gao Wenlong) 3Pos013
Garcia-Trejo, Jose J. (Garcia-Trejo Jose J.) 2E1448
Gekko, Kunihiko (月向 邦彦) 1M1330
Germond, Arno (Germond Arno) **2O1400**
2Pos064
Giacometti, Achille (Giacometti Achille) 2Pos062
Gordon, Jesse B. (Gordon Jesse B.) 1F1418
Goto, Akane (後藤 朱音) 1D1448
Goto, Akari (後東 あかり) 1F1430
Goto, Masaki (後藤 優樹) 1Pos091
Goto, Takashi (後藤 孝) 1Pos401
Gotoh, Hitoshi (後藤 人志) 1H1548
Greene, Eric C. (Greene Eric C.) 1E1548
Guerin, Christophe (Guerin Christophe) 2Pos319
Gunn, John (Gunn John) 3Pos087
Guo, Qiyong (郭 启勇) 1SBP-4
Guo, Shiwen (Guo Shiwen) 3SIA-8
Gusain, Pooja (Gusain Pooja) **2C1542**
Haering, Christian H. (Haering Christian H.) 1E1548
Haga, Kei (芳賀 慧) 2Pos404
Haga, Yukari (芳賀 ゆかり) 2G1542
Hagihara, Chika (萩原 睦) **1L1512**
Hagiwara, Masaya (萩原 将也) **1A1548**
1C1536
3Pos210
Hama, Kosuke (濱 宏丞) **3Pos416**
Hamada, Misato (濱田 実里) 2Pos097
Hamaguchi, Tasuku (濵口 祐) 1K1512
Hamamoto, Tatsuki (濱元 樹) **2Pos311**
Hamano, Masataka (浜野 将孝) **1Pos019**
Hamaue, Shoya (浜上 翔矢) **2J1542**
Han, Yong-Woon (韓 龍雲) 2Pos423
Hanaizumi, Yuta (花泉 裕大) **1Pos215**
Hanazono, Yuya (花園 祐矢) 3Pos206
Hansen, Jeffrey C. (Hansen Jeffrey C.) 1SKA-2
Hara, Keisuke (原 圭佑) **1Pos310**
Hara, Mayu (原 舞雪) 2E1424
Hara, Rintaro (原 倫太朗) 2Pos040
Hara, Sunao (原 直) 1SBP-6
Hara, Yayoi (原 弥生) **3Pos062**
Hara, Yuji (原 雄二) **1SEA-1**
Hara, Yuki (原 裕貴) **1SFA-3**
Hara, Yuya (原 侑也) 3Pos029
Harada, Kyohei (原田 喬平) 3Pos043
Harada, Ryuhei (原田 隆平) 2F1500
Harada, Yoshie (原田 慶恵) 2Pos105
2Pos423
Harada, Yoshinori (Harada Yoshinori) 1D1548
Haraguchi, Takeshi (原口 武士) 2N1400
Harris, Nicola (Harris Nicola) 2G1436
Haruna, Taichi (春名 太一) **3Pos090**
3Pos091
Haruyama, Takamitsu (春山 隆充) 3Pos014
Hasan, Moynul (ハーサン モイヌル) **1G1418**
1Pos087
1Pos090
Hasegawa, Masashi (長谷川 将司) 3SHA-4
Hasegawa, Nagayuki (長谷川 修之) 1Pos024
Hasegawa, Nobuya (長谷川 信哉) 2Pos058
Hasegawa, Shin (長谷川 慎) 2SAA-1
Hasegawa, So (長谷川 爽) 2E1518
Hasegawa, Sumitaka (長谷川 純崇) 1Pos078
Hasegawa, Taisuke (長谷川 太祐) 3Pos046
Hashimoto, Hiromichi (橋本 広道) **1Pos415**
1Pos419
3Pos413
Hashimoto, Hitoshi (橋本 均) **3SFA-5**
Hashimoto, Kanako (橋本 佳奈子) 3Pos028
Hashimoto, Ken'ichi (橋本 賢一) 2G1518
Hashimoto, Ken-ichi (橋本 賢一) 2G1530
Hashimoto, Misa (橋本 美沙) 1H1330
Hashimoto, Mitsuki (橋本 みつき) 1Pos055
Hashimoto, Shinji (橋本 慎二) 1K1406
Hata, Katsuhiko (羽田 克彦) **1Pos309**
1Pos314
1Pos316
3Pos219
Hata, Kazuki (畑 和樹) **1Pos083**
Hatada, Yuji (秦田 勇二) 3Pos419
Hatori, Kuniyuki (羽鳥 晋由) 1A1512

3Pos060
Hattori, Akihiro (服部 明弘) 1Pos203
1Pos311
1Pos315
1Pos319
1Pos412
1Pos413
1Pos414
1Pos415
1Pos418
1Pos419
3Pos095
3Pos409
3Pos410
3Pos411
3Pos413
Hattori, Fumiya (服部 文哉) **3Pos007**
Hattori, Mitsuru (Hattori Mitsuru) 1D1354
Hattori, Motoyuki (服部 素之) 2G1606
3Pos013
Hawkins, Taviare L. (Hawkins Taviare L.) 1Pos050
Hayakawa, Mai (早川 舞) **1Pos089**
Hayakawa, Masayuki (早川 雅之) **3Pos094**
Hayakawa, Yuuki (早川 悠貴) **1Pos222**
Hayami, Tomonori (速水 智教) **1L1418**
2J1424
Hayano, Toshiya (早野 俊哉) 1Pos021
Hayashi, Ayumi (林 あゆみ) 3Pos318
Hayashi, Fumio (林 史夫) 3Pos006
Hayashi, Fumio (林 文夫) 1SIA-6
1G1330
2Pos070
3Pos022
Hayashi, Haruna (林 春菜) **1Pos088**
Hayashi, Humio (林 文夫) 2Pos102
Hayashi, Kumiko (林 久美子) **2SAA-1**
1Pos209
2Pos220
2Pos418
Hayashi, Masahito (林 真人) 2Pos072
Hayashi, Masahito (林 真人) **2Q1618**
3Pos092
Hayashi, Sayaka (林 紗弥香) 1Pos106
Hayashi, Shigehiko (林 重彦) **2SGA-1**
2F1400
3Pos005
3Pos046
Hayashi, Shinichiro (林 慎一郎) **3Pos009**
Hayashi, Takanori (林 孝紀) 1C1448
3Pos201
Hayashi, Tomohiko (林 智彦) 2Pos061
2Pos062
2Pos063
3Pos010
3Pos011
Hayashi, Toshihiro (林 俊洋) 3Pos056
Hayashi, Yugo (林 侑吾) 2Pos098
Hayashi, Yugo (林 有吾) 2K1412
1Pos064
1Pos402
Hayashi, Yuki (林 佑紀) 1Pos100
Hayashi, Yuuki (林 勇樹) 1K1354
1K1418
1K1448
3Pos077
3Pos078
3Pos088
Hazuki, Terajima (寺島 葉月) 1Pos089
Heberle, Joachim (Heberle Joachim) 2G1436
Helal, Khalifa Mohammad (Helal Khalifa Mohammad)
1D1548
Hibi, Masahiko (日比 正彦) 1SHA-6
Hibino, Emi (日比野 絵美) **1J1330**
Hibino, Hiroshi (日比野 浩) **1SEA-8**
Hibino, Kayo (日比野 佳代) 1D1418
2Q1412
Hibino, Masahiro (日比野 政裕) **1Pos093**
Hidaka, Haruna (日高 はる菜) **3Pos065**
Hidema, Jun (日出間 純) **3SBA-3**
Hieda, Yasuhiro (稗田 康洋) **2Pos418**
Higashi, Masahiro (東 雅大) 3Pos020
Higashi, Tsunehito (東 恒仁) 2Pos326
Higashimura, Chika (東村 智佳) 2F1400
Higashitani, Atsushi (東谷 篤志) **3SBA-4**
Higo, Junichi (肥後 順一) 1C1354
1C1430
1J1430
1L1418
2J1424
Higuchi, Hideo (樋口 秀男) 1D1342
1E1342
1E1524
2D1500
2N1500
2Pos210
2Pos213
Higuchi, Masayuki (樋口 真之) 1Pos410
Higuchi, Yoshiki (樋口 芳樹) 2SOA-2
2SOA-3
Hijikata, Atsushi (土方 敦司) **3Pos203**
3Pos205
Hikima, Takaaki (引間 孝明) 1Pos047
Hikiri, Simon (肥喜里 志門) **2Pos063**
Hilbert, Manuel (Hilbert Manuel) 2Pos301
Hino, Tomoya (日野 智也) 1Pos066
2Pos087

3Pos015
Hira, Daisuke (平 大輔) **3SMA-2**
Hirai, M. (平井 光博) **3Pos074**
Hirai, Mitsuhiro (平井 光博) 1K1524
Hiraiwa, Tetsuya (平岩 徹也) 2SBP-5
1O1342
1O1354
2O1518
3Pos093
Hirakawa, Rika (平川 利佳) 1Pos227
Hiraki, Toshiki (開 俊樹) 3Pos068
Hiramoto-Yamaki, Nao (平本ー山木 菜央) 3Pos327
Hirano, Kazumi (平野 和己) 1A1524
Hirano, Keiichi (平野 圭一) **2Pos305**
Hirano, Ken (平野 研) **2Pos039**
Hirano, Kotaro (平野 航太郎) 1SEA-1
Hirano, Makoto (平野 誠人) **1H1430**
Hirano, Minako (平野 美奈子) 1Pos403
2Pos077
2Pos078
Hirano, Yu (平野 優) 3Pos084
Hirano-Iwata, Ayumi (平野 愛弓) **2SFA-3**
Hiranyakorn, Methanee (ヒランヤコン メタニー)
2M1424
Hiraoka, Osamu (平岡 修) 2Pos022
Hiraoka, Wakako (平岡 和佳子) 1Pos076
1Pos077
Hirashima, Tsuyoshi (平島 剛志) **2C1424**
Hirata, Fumio (平田 文男) 1Pos019
1Pos020
1Pos059
Hirata, Hiroaki (Hirata Hiroaki) 3Pos304
Hirata, Hiroaki (平田 宏聡) 2SEA-4
Hirata, Keisuke (平田 啓介) 1Pos056
Hirata, Kunio (平田 邦生) 2E1412
Hiratsuka, Yuichi (平塚 祐一) 2N1400
3Pos416
Hirayama, Akiyoshi (平山 明由) 1O1500
Hirayama, Nozomi (平山 望) 3SEA-5
Hirayama, Ryoichi (平山 亮一) **1Pos078**
Hiroaki, Hidekazu (廣明 秀一) **2M1412**
Hirokawa, Nobutaka (廣川 信隆) 2SIP-1
Hirokawa, Takatsugu (広川 貴次) **2SGA-7**
1Pos061
Hironaka, Ken-ichi (廣中 謙一) 3Pos209
Hirono, Masafumi (廣野 雅文) 2Pos207
2Pos301
Hirono, Moritoshi (廣野 守俊) **1Pos320**
Hirosawa, Koichiro M. (廣澤 幸一朗) **3Pos327**
Hirose, Keiko (広瀬 恵子) **2N1500**
Hirose, Matsumi (廣瀬 松美) 3SFA-1
Hirose, Osamu (広瀬 修) 1Pos317
Hirose, Yudai (廣瀬 湧大) **1Pos108**
Hirose, Yuu (広瀬 侑) **2F1424**
Hiroshima, Michio (廣島 通夫) **1SKA-6**
2Pos417
Hirota, Shun (廣田 俊) **2SOA-3**
Hirota, Tsuyoshi (Hirota Tsuyoshi) 2J1400
Hisabori, Toru (久堀 徹) 1E1418
2A1554
2E1412
Hisada, Misaki (久田 美咲) 2M1412
Hisatomi, Osamu (久冨 修) 1H1500
2F1436
3Pos041
Hisauchi, Haruka (久内 晴加) **2C1530**
Hitotsuyanagi, Yukio (Hitotsuyanagi Yukio) 2Pos031
Hizukuri, Yohei (檜作 洋平) **2Pos306**
Hohng, Sungchul (Hohng Sungchul) **3SIA-5**
Holdbrook, Daniel A. (Holdbrook Daniel A.) 3Pos021
Homma, Kazuaki (本間 和明) 1E1430
Homma, Michio (本間 道夫) 1Q1418
2A1618
2E1500
1Pos217
1Pos218
2Pos302
2Pos303
2Pos304
2Pos305
2Pos308
3Pos019
Honda, Gen (本田 玄) **3Pos316**
Honda, Hajime (本多 元) 1Pos202
2Pos201
2Pos202
2Pos317
Honda, Naoki (本田 直樹) **1Pos321**
Honda, Yuko (本田 裕子) 1Pos054
Hongo, Yayoi (本郷 やよい) 2Q1606
Hori, Manabu (堀 学) **2Pos084**
Horibe, Kazuya (堀部 和也) 3Pos209
Horigane, Makoto (堀金 慎) 1Pos401
Horinouchi, Takaaki (Horinouchi Takaaki) 2O1400
Horinouchi, Takaaki (堀之内 貴明) 1Pos080
Horinouchi, Takahiro (堀之内 孝広) 2Pos326
Horitani, Masaki (堀谷 正樹) **2L1500**
3Pos059
Hoshi, Yutaka (星 雄高) 2C1518
Hosoe, Yuhi (細江 雄飛) **1L1500**
Hosokawa, Chie (細川 千絵) 1C1548
1Pos312
Hosokawa, Yuhei (細川 雄平) **2Pos093**
2Pos094
Hososhima, Shouko (細島 頌子) 2H1448
Hossain, Farzana (ホセイン ファーザナ) **1Pos095**

Hossain, Md Nadim (Hossain Md Nadim) **1D1354**
Housaka, Ayako (芳坂 綾子) 2D1554
Hsiao, Chwan-Deng (David) (Hsiao Chwan-Deng (David)) 2Pos036
Hsu, Kuan-Wei (許 冠偉) 2K1424
Hsu, Tzu Chin (Hsu Tzu Chin) 2M1554
Hu, Shu-Xin (Hu Shu-Xin) 1Pos421
Huber, Roland G. (Huber Roland G.) **1Q1430**
3Pos021
Hui, Shu-Ping (惠 淑萍) 1J1524
Hukuoka, Hajime (福岡 創) 2Pos310
Hwang, Beomju (ファン ボンジュ) **1Pos062**
Hwang, Yongtae (黄 勇太) **1E1342**
Ibusuki, Ryota (指宿 良太) 2SMA-2
2Pos204
Ichihashi, Norikazu (市橋 伯一) **1SIP-5**
1C1512
Ichihashi, Yuki (市橋 裕樹) 1SKA-4
Ichikawa, Muneyoshi (市川 宗厳) **2M1554**
Ichimura, Taro (Ichimura Taro) 2O1400
Ichimura, Taro (市村 垂生) **1SEA-5**
Ichinose, Takako M. (一ノ瀬 孝子) 1Pos324
Ide, Ichiro (井手 一郎) **2Pos057**
Ide, Takahiro (井手 隆広) 2A1554
Ide, Toru (井出 徹) 1Pos403
2Pos077
2Pos078
2Pos082
Ieki, Nao (家城 直) 3SEA-5
Igarashi, Kazuei (五十嵐 一衛) 2Pos020
Igarashi, Kiyohiko (五十嵐 圭日子) 1Pos046
3Pos085
Iguchi, Ayaka (井口 彩香) 3Pos418
Ihara, Kunio (井原 邦夫) **1Q1418**
Ii, Miki (Ii Miki) 1Pos306
Iida, Keita (飯田 渓太) **2O1412**
Iida, Kento (飯田 健斗) 1Pos415
1Pos419
3Pos413
Iida, Mamiko (飯田 真美子) 2L1424
Iida, Naoya (飯田 直也) 2E1412
1Pos207
Iida, Shinji (飯田 慎仁) **1C1354**
Iijima, Mikuru (飯島 美来) **1L1354**
Iijima, Yuta (飯島 悠太) **2E1518**
Iino, Masamitsu (飯野 正光) 2Pos422
Iino, Ryota (飯野 亮太) 2E1542
2E1554
1Pos009
2Pos203
2Pos206
2Pos405
Iino, Tsubasa (飯野 翼) **3Pos057**
Iino, Yuichi (飯野 雄一) 1Pos317
Iizuka, Ryo (飯塚 怜) 1K1330
2K1500
2Pos424
3Pos418
3Pos419
Iizumi, Ikuko (飯住 郁子) **2K1400**
Ikawa, Tomokatsu (伊川 友活) 1O1448
Ikeda, Kazuho (池田 一穂) **2Pos028**
Ikeda, Keisuke (池田 恵介) 1G1500
2Pos007
Ikeda, Kento (池田 健人) **3Pos013**
Ikeda, Manami (池田 麻奈美) **1Pos043**
Ikeda, Masanori (池田 真教) 1D1430
Ikeda, Masayuki (池田 将幸) 1Pos055
Ikeda, Yusaku (池田 優作) **1O1512**
2O1530
Ikegami, Takahisa (池上 貴久) 3SDA-2
Ikegaya, Yuji (池谷 裕二) 2C1518
Ikeguchi, Masamichi (池口 雅道) 2Pos011
2Pos012
2Pos016
2Pos019
3Pos026
Ikeguchi, Mitsunori (池口 満徳) 1Pos034
1Pos049
2Pos063
3Pos076
Ikemizu, Shinji (池水 信二) 1Pos056
Ikezaki, Keigo (池崎 圭吾) 1Pos226
1Pos228
Ikura, Teikichi (伊倉 貞吉) 1M1354
1Pos040
Ikuta, Tatsuya (生田 達也) 2H1424
Imada, Katsumi (今田 勝己) 1Pos057
Imada, Katsumi (今田 勝巳) 1A1330
2A1606
2A1618
2M1500
2M1542
1Pos016
3Pos301
Imada, Yasuhiro (今田 康博) 3Pos002
Imai, Hiroo (今井 啓雄) **3SEA-3**
1H1406
Imai, Hiroshi (今井 洋) 2N1518
2Pos215
Imai, Minori (今井 みの莉) 2Pos103
Imai, Shunsuke (今井 駿輔) 2G1606
Imakawa, Hayao (今川 駿) **3Pos086**
Imamoto, Yasushi (今元 泰) 1H1548
2F1530
2Pos101

3Pos045
Imamura, Hiroshi (今村 比呂志) 2Pos026
Imamura, Motonori (今村 元紀) **2D1530**
Imanishi, Michie (今西 三千絵) **1H1418**
3Pos028
Imaseki, Masamichi (今関 眞倫) **1D1406**
Imayasu, Mieko (今康 身依子) 3Pos416
Imoto, Daisuke (井元 大輔) 1SAA-1
3Pos211
Imoto, Hiroaki (井元 宏明) **2O1500**
3Pos216
Imura, Yoshino (伊村 芳野) **2Pos302**
Inaba, Kazuo (稲葉 一男) 1A1536
2A1542
2N1448
Inaba, Keita (稲葉 啓太) 1Q1418
Inaba, Kenji (稲葉 謙次) 1SGA-3
3SDA-1
Inaba, Satomi (稲葉 理美) 1L1500
2Pos045
Inaba, Takehiko (稲葉 岳彦) **2Q1554**
Inabe, Kosuke (稲辺 宏輔) **1E1418**
Inada, Masataka (稲田 壮峰) **1G1448**
Inage, Taisuke (稲毛 太亮) 1Pos410
Inaki, Mikiko (稲木 美紀子) 1SAA-4
Inamoto, Yurie (稲本 有里江) **1Pos205**
Ingrosso, Francesca (Ingrosso Francesca) 2Pos003
Inoh, Yoshikazu (伊納 義和) 3Pos310
3Pos318
3Pos325
Inoue, Daisuke (井上 大介) **2Pos319**
Inoue, Kanako (井上 加奈子) 2D1448
Inoue, Keiichi (Inoue Keiichi) 1F1512
Inoue, Keiichi (井上 圭一) **2SHA-1**
1G1430
1H1342
1H1354
2H1412
2H1436
2Pos088
2Pos091
2Pos092
Inoue, Keiya (井上 慶也) **1Pos008**
Inoue, Masao (井上 雅郎) **2Pos062**
Inoue, Masayo (井上 雅世) **3Pos212**
Inoue, Michio (井上 道雄) **3SDA-1**
Inoue, Rintaro (井上 倫太郎) 2L1412
1Pos006
1Pos052
2Pos038
Inoue, Saki (井上 紗希) **3Pos043**
3Pos044
Inoue, Yasuhiro (井上 康博) 1SAA-4
1SAA-6
1SMA-2
Inoue, Yuichi (井上 裕一) 2Pos410
Inoue, Yuna (井上 祐菜) **2Pos303**
Inouye, Satoshi (井上 敏) 3Pos318
Inubushi, Tomoo (犬伏 知生) 3Pos071
Inukai, Kohei (犬飼 耕平) **3Pos208**
Iribe, Gentaro (入部 玄太郎) **3SBA-2**
1Pos206
3Pos306
Irie, Katsumasa (入江 克雅) **2G1542**
Isaka, Yuta (井阪 悠太) 1Pos026
Ise, Hirohiko (伊勢 裕彦) 1Pos062
Ishi, Hisao (石井 久夫) 2Pos056
Ishibashi, Kenta (石橋 健太) **1Pos304**
2Pos212
3Pos317
Ishida, Hisashi (石田 恒) **2SGA-2**
Ishida, Masaki (石田 正樹) 2Pos084
Ishida, Motohiko (石田 元彦) 2A1400
Ishida, Ryuichi (Ishida Ryuichi) 1D1354
Ishida, Ryuji (石田 竜次) 2SGA-3
1Pos048
Ishida, Tsubasa (石田 翼) 2SAA-4
1E1500
Ishido, Tomoya (石堂 智也) **2Pos078**
Ishige, Masayuki (石毛 真行) 3Pos418
Ishiguro, Takashi (石黒 隆) 2Pos201
2Pos202
Ishihara, Jun-ichi (石原 潤一) **2O1448**
Ishihara, Shuji (石原 秀至) 2N1530
3Pos313
Ishihara, Takeshi (石原 健) 1Pos317
Ishii, Hisao (石井 久夫) 2Pos057
Ishii, Jun (石井 純) 3Pos418
Ishii, Kentaro (石井 健太郎) 3Pos080
Ishii, Kunihiko (石井 邦彦) 2O1606
Ishii, Maki (石井 真希) 3Pos326
Ishii, Shin (石井 信) 1Pos420
Ishii, Shoko (石井 頌子) 1K1536
Ishii, Shuya (石井 秀弥) **1E1330**
Ishii, Yoshitaka (石井 佳誉) **2L1448**
Ishijima, Akihiko (石島 秋彦) 2Pos309
2Pos310
2Pos311
2Pos312
3Pos048
3Pos319
3Pos320
Ishikawa, Ryoki (石川 良樹) 1A1524
Ishikita, Hiroshi (石北 央) 1SHA-3
1SRA-2
1F1406

2H1518
Ishikuro, Daiki (石黒 大輝) **1D1448**
Ishimori, Koichiro (石森 浩一郎) 1SGA-4
2L1530
Ishitani, Ryuichiro (石谷 隆一郎) 1M1406
2G1606
3Pos020
Ishiwata, Shin'ichi (石渡 信一) 1E1330
1O1354
2Pos323
Ishizaka, Masato (石坂 優人) **3Pos059**
Ishizaki, Akihito (石崎 章仁) **3SHA-1**
Ishizuka, Toru (石塚 徹) 3Pos045
Isiwata, Shin'ich (石渡 信一) 2N1424
Islam, Alrazi M.D. (Islam M.D. Alrazi) 2Pos225
Islam, Md Alrazi (イスラム エムディ アルラジ)
2Pos224
Islam, Md. Zahidul (イスラム エムディ ザヒドゥル)
2G1400
Isobe, Hiroshi (磯部 寛) 1SDA-7
2Pos054
Isobe, Shin-Ya (磯部 真也) 2Pos421
Isogai, Yasuhiro (磯貝 泰弘) **2Pos026**
Isomura, Akihiro (磯村 彰宏) **1SFA-4**
Isozaki, Naoto (磯崎 直人) 1Pos050
Itabashi, Takeshi (板橋 岳志) 1Pos324
2Pos323
Itaya, Hayato (板谷 颯人) **1Q1448**
Ito, Hiroaki (伊藤 寛朗) 1Pos104
Ito, Hiroaki (伊藤 弘明) **1Pos084**
Ito, Hirotaka (伊藤 洋貴) 1Pos202
Ito, Kohji (伊藤 光二) **2N1400**
Ito, Koichi (伊藤 耕一) 2G1606
Ito, Koji (伊藤 光司) 1A1512
3Pos060
Ito, Masahiro (伊藤 政博) 1Pos219
Ito, Mashiho (伊藤 真志保) **1Pos071**
2Pos006
Ito, Mei (伊藤 芽) 3Pos419
Ito, Nana (伊藤 那奈) 2C1448
Ito, Nobutoshi (伊藤 暢聡) 1M1354
1Pos040
Ito, Ritsuki (伊藤 立樹) **3Pos311**
Ito, Shota (伊藤 奨太) 1H1342
2H1412
Ito, Sohei (伊藤 創平) 1M1354
Ito, Sosuke (伊藤 創祐) **1O1406**
Ito, Susumu (伊藤 挙) 1Pos309
1Pos314
1Pos316
3Pos219
Ito, Yuki (伊藤 友基) 2Pos099
Ito, Yuma (伊藤 由馬) 2A1500
2Pos419
2Pos420
2Pos421
Itoga, Hibiki (糸賀 響) **2Pos083**
Itoh, Ayaka (伊藤 綾香) 1Pos308
Itoh, Shigeru (伊藤 繁) 1SRA-4
3Pos033
Itoh, Shinobu (伊東 忍) **2SOA-5**
Itoh, Yuji (伊藤 優志) 2Q1500
2Pos035
Itsuji, Daigo (井辻 大悟) 2Pos058
Iwadate, Yoshiaki (岩楯 好昭) 2Pos315
3Pos324
Iwahori, Tetsuya (岩堀 哲也) 1Pos308
Iwai, Shigenori (岩井 成憲) 2Pos093
2Pos094
Iwaki, Masayo (岩城 雅代) 2E1500
1Pos044
2Pos304
3Pos019
Iwaki, Mitsuhiro (岩城 光宏) **1SKA-1**
1Pos226
1Pos228
2Pos417
Iwaki, Takafumi (岩城 貴文) 2Pos041
Iwakura, Shota (岩倉 将太) 1A1406
Iwamoto, Hiroyuki (岩本 裕之) **2N1448**
2Pos209
Iwamoto, Kazunari (岩本 一成) 1Q1406
2O1500
2Q1554
3Pos216
3Pos312
Iwamoto, Masayuki (岩本 真幸) **2Pos079**
Iwamura, Moe (岩村 萌絵) 3Pos409
3Pos410
3Pos411
Iwane, Atsuko (岩根 敦子) 2D1448
Iwane, Atsuko H. (岩根 敦子) **1Pos324**
Iwasaki, Hiroshi (岩崎 博史) 2SAA-3
Iwasaki, Kenji (岩崎 憲治) **3SGA-2**
2M1530
1Pos009
2Pos404
Iwasaki, Yuishi (岩崎 唯史) **1Pos317**
Iwase, H. (岩瀬 裕希) 3Pos074
Iwata, Koichi (岩田 耕一) 1Pos088
Iwata, Makoto (岩田 眞人) 1Pos055
Iwata, Ryoko (岩田 涼子) 2Pos106
Iwata, Seiji (岩田 誠司) **1E1512**
Iwata, So (岩田 想) **2SKA-5**
Iwata, Tatsuya (岩田 達也) 2F1448
2Pos097

3Pos040
Iwata, Tatsuya (岩田 達哉) 2SFA-1
Iwatani, Miki (岩谷 三樹) 3Pos040
Iwatsuki, Hiroto (岩月 哲人) 2E1500
Iwatsuki, Hiroto (岩月 啓人) 1Pos217
2Pos304
Izri, Ziane (イズリ ジャン) 2O1542
Izumi, Shunsuke (泉 俊輔) 3Pos065
Izutsu, Minako (井筒 弥那子) 2O1436
Jain, Ankit (Jain Ankit) 2Q1606
Jang, Moon Sun (ジャン ムンソン) 1Pos317
Javkhlantugs, Namsrai (Javkhlantugs Namsrai) 1L1524
Jenal, Urs (Jenal Urs) 3SKA-5
Jeyamohan, Prashanti (Jeyamohan Prashanti) 2Pos415
Jia, Tony Z (Jia Tony Z) **2Q1606**
Jian-Ren, Shen (沈 建仁) 1SDA-6
Jin, Teturo (神 哲郎) 1H1430
Johnson, Reid (Johnson Reid) 2Q1500
Johnson, Reid C. (Johnson Reid C.) 1Q1330
Jokura, Kei (城倉 圭) **1A1536**
2N1448
Jomaa, Ahmad (ヨマア アフマド) 2M1618
Jones, Gareth E. (Jones Gareth E.) 2SBP-3
1A1430
Jonic, Slavica (ジョニック スラビカ) 1M1512
Joti, Yasumasa (城地 保昌) 3SGA-4
Jung, Jaewoon (Jung Jaewoon) 1Pos070
Jung, Jaewoon (鄭 載運) **1J1448**
Jurica, Peter (ユリツァ ペテル) 2O1530
Kadomatsu, Kyoko (門松 恭子) **2Pos099**
Kage, Azusa (鹿毛 あずさ) **2C1436**
Kai, Hiroaki (甲斐 寛彬) 1Pos206
3Pos306
Kaihara, Keiko (貝原 恵子) **3Pos306**
Kaihatsu, Shusei (開発 秀星) **2D1542**
Kajiwara, Yuta (梶原 佑太) 3Pos011
Kakiuchi, Yasutaka (垣内 康孝) **2O1554**
Kakizawa, Shigeyuki (柿澤 茂行) **3SKA-2**
Kakizuka, Taishi (垣塚 太志) **2Pos408**
Kakugo, Akira (角五 彰) 2Pos321
Kakuta, Hiroki (加来田 博貴) 1M1354
Kalashnikova, Anna (Kalashnikova Anna) 1SKA-2
Kalodimos, Charalampos G. (Kalodimos Charalampos G.) 1SGA-4
Kamagata, Kiyoto (鎌形 清人) 1Q1330
2Q1500
2Pos035
Kamamoto, Naoya (鎌本 直也) 3Pos209
Kamatari O, Yuji (鎌足 雄司) 2K1518
Kambara, Taketoshi (神原 丈敏) 2Pos213
2Pos223
Kameda, Takeru (亀田 健) **2Pos052**
Kamei, Ken-ichiro (亀井 謙一郎) 2Q1542
Kamei, Ken-ichiro F. (亀井 健一郎) **1Pos417**
Kamei, Yousuke (亀井 陽介) 3Pos408
Kameyama, Yutaro (亀山 裕太郎) **2Pos065**
Kamikubo, Hionari (上久保 裕生) 1Pos402
Kamikubo, Hironari (上久保 裕生) **2SIP-6**
2K1412
1Pos064
2Pos098
Kamimura, Kenji (上村 健二) 1Pos202
Kamimura, Yoichiro (上村 陽一郎) 2A1448
Kaminaka, Toshiaki (神中 俊明) 1Pos309
1Pos314
1Pos316
3Pos219
Kamiya, Koki (神谷 厚輝) **1Pos099**
Kamiya, Motoshi (神谷 基司) 2J1500
Kamiya, Narutoshi (神谷 成敏) 2J1530
1Pos026
Kamiya, Nobuo (神谷 信夫) 1SDA-6
1H1430
Kamiya, Ritsu (神谷 律) 2Pos207
Kamo, Naoki (加茂 直樹) 1H1536
Kamonprasertsuk, Supawich (Kamonprasertsuk Supawich) **2Pos010**
Kanada, Ryo (金田 亮) 1Pos026
Kanahara, Kanae (金原 加苗) 2Pos056
Kanahara, Yuko (金原 裕子) 1C1500
Kanamaru, Shuji (金丸 周司) **2K1448**
Kanamaru, Tomoko (金丸 朋子) 3Pos415
Kanatani, Misa (金谷 美沙) 3SFA-1
Kanayama, Naoki (金山 直樹) 1SBP-2
Kanazawa, Riko (金澤 莉香) **2Pos215**
Kanchanawong, Pakorn (Kanchanawong Pakorn) 2SBP-3
1A1430
Kandori, Hideki (Kandori Hideki) 3SAA-2
1F1512
Kandori, Hideki (神取 秀樹) 1G1430
1H1342
1H1354
1H1406
2E1500
2F1412
2F1448
2H1412
2H1424
2H1436
2H1448
2H1606
1Pos044
2Pos088
2Pos091
2Pos092

2Pos097
2Pos100
2Pos304
3Pos019
3Pos040
Kaneda, Shiho (Kaneda Shiho) 1L1524
Kanehara, Kanae (金原 加苗) 2Pos087
3Pos010
Kaneko, Akimasa (金子 明正) **2H1606**
2Pos086
Kaneko, Kota (金子 弘汰) **2Pos077**
Kaneko, Kunihiko (金子 邦彦) 2C1400
2O1424
3Pos212
Kaneko, Makoto (金子 真) 1Pos084
Kaneko, Rina (金子 莉奈) **1G1430**
2H1412
Kaneko, Taikopaul (Kaneko Taikopaul) 2Pos222
Kaneko, Taikopaul (金子 泰洸ポール) **1E1536**
2Pos217
Kaneko, Tomoyuki (金子 智行) 1C1600
1Pos089
1Pos313
1Pos416
2Pos073
3Pos305
3Pos307
3Pos314
3Pos326
3Pos406
3Pos407
3Pos408
Kanemaru, Kazunori (金丸 和典) 2Pos422
Kanematsu, Yusuke (兼松 佑典) 3Pos002
Kaneshige, Yukito (金重 先人) **2Pos102**
Kaneta, Miku (金田 実久) 1Pos401
Kanie, Akemi (蟹江 朱美) 1SEA-7
Kanno, Emiri (菅野 英美里) 2Pos207
Kano, Ayumu (加納 歩) 2C1412
Kano, Shosei (狩野 勝星) 1Pos092
Kao, Chih-Yuan (Kao Chih-Yuan) 2Pos034
Karal, Mohammad Abu Sayem (カラール モハマド アブ サエム) 1G1418
Karasawa, Yasuaki (唐沢 康暉) 1O1500
Karube, Fuyuki (苅部 冬紀) 1Pos320
Kasahara, Kota (笠原 浩太) 1C1406
1C1430
1J1430
1L1418
1Q1448
1Q1512
1Q1536
2J1424
2Pos058
Kasahara, Yu (笠原 悠) **2Pos048**
3Pos402
Kasai, Atsushi (笠井 淳司) 3SFA-5
Kasai, Rinshi (笠井 倫志) 3Pos022
3Pos302
Kasai, Rinshi S. (笠井 倫士) 2D1412
Kasai, Taishi (笠井 大司) 2SAA-4
1E1448
2E1518
Kashiwagi, Hiroko (柏木 広子) **1O1536**
Kashiwagi, Keiko (柏木 敬子) 2Pos020
Kastritis, Panagiotis L. (Kastritis Panagiotis L.) 2M1554
Kasuya, Yuzo (粕谷 有造) 1Pos207
Katagiri, Erina (片桐 絵里奈) 2Pos025
Katahira, Masato (片平 正人) 2L1424
2Pos061
Kataoka, Chihiro (片岡 千尋) **2H1436**
Kataoka, Tatsuki (片岡 樹紀) 2Pos003
Kataoka, Tohru (片岡 徹) 1L1512
Katayama, Daisuke (片山 大輔) **3Pos414**
Katayama, Kazuhiko (片山 和彦) 2Pos404
Katayama, Kota (片山 耕大) 1H1406
2Pos100
Katayama, Kouta (片山 耕大) 2H1436
Kato, Akane (加藤 茜) **2Pos005**
Kato, Hiroaki (加藤 博章) 1Pos048
Kato, Kohei (加藤 康平) 1M1418
Kato, Koichi (加藤 晃一) 2SIP-4
2M1424
3Pos080
Kato, Koji (加藤 公児) 1F1330
Kato, Minoru (加藤 稔) **2Pos009**
Kato, Misaki (加藤 岬) 1SHA-3
Kato, Suguru (加藤 傑) **2Pos004**
Kato, Takayuki (加藤 貴之) 2A1606
2M1500
2M1518
2M1606
1Pos014
1Pos036
1Pos212
1Pos214
2Pos307
Kato, Tomoya (加藤 朝也) **2H1554**
Kato, Yuki (加藤 祐樹) **1F1342**
3Pos037
Kato, Yukinari (加藤 幸成) 3SDA-1
Katoh, Kaoru (加藤 薫) 1A1524
Katsuki, Yudai (香月 佑太) 2Pos005
Katsuta, Hiroki (勝田 紘基) 1SEA-7
Kawabata, Takeshi (川端 猛) **1C1330**
Kawade, Raiji (河出 来時) **1L1342**

Kawagishi, Ikuro (川岸 郁朗) **2C1448**
2C1500
3Pos049
Kawaguchi, Atsushi (川口 敦史) 3SGA-2
Kawaguchi, Kazutomo (Kawaguchi Kazutomo) 1L1330
2Pos031
Kawaguchi, Kazutomo (川口 一朋) **2G1500**
1Pos001
1Pos094
2Pos003
3Pos039
Kawaguchi, Kyogo (川口 喬吾) 2Pos325
Kawaguchi, Tetsuya (川口 徹也) 2C1500
Kawahara, Shigenori (川原 茂敬) 1Pos320
Kawahara, Yoshinobu (河原 吉伸) 1D1500
Kawai, Ayako (川合 絢子) **3Pos409**
3Pos410
3Pos411
Kawai, Masataka (河合 正隆) 1E1330
Kawakami, Keisuke (川上 恵典) 1SDA-6
1H1430
Kawakami, Takashi (川上 貴資) 2Pos054
Kawakubo, Wataru (川久保 渉) 3Pos419
Kawamoto, Akihiro (川本 晃大) **2M1500**
1Pos212
1Pos214
2Pos307
Kawamoto, Takashi (河本 隆志) **3Pos027**
Kawamura, Izuru (Kawamura Izuru) 1L1524
Kawamura, Izuru (川村 出) 1G1430
1H1536
2H1412
Kawamura, Satoru (河村 悟) 2Pos099
Kawamura, Seiko (河村 聖子) 1SDA-3
Kawamura, Takashi (河村 高志) 1L1512
Kawano, Mutsumi (河野 睦) 2Pos084
Kawano, Ryuji (川野 竜司) 1G1406
2Pos076
3Pos070
3Pos420
Kawaoka, Yoshihiro (河岡 義裕) 2SBA-2
Kawasaki, Hisashi (川崎 寿) 2G1518
2G1530
Kawato, Suguru (川戸 佳) **1Pos318**
Kaya, Motoshi (茅 元司) 1E1342
2D1500
2Pos213
Kayanuma, Megumi (栢沼 愛) 1L1430
Kazuta, Yasuaki (數田 恭章) 2A1518
Ke, Yonggang (Ke Yonggang) **2SMA-5**
Keiichi, Namba (難波 啓一) 1Pos214
Kenmotsu, Takahiro (剣持 貴弘) 2Q1530
2Pos042
3Pos311
Kenny, Linda J (Kenny Linda J) 3Pos301
Kenzaki, Hiroo (検崎 博生) **2Q1424**
Khelashvili, George (Khelashvili George) 1SIA-3
Kida, Mamoru (木田 葵) 2A1606
Kidera, Akinori (木寺 詔紀) 2SGA-3
1Pos048
Kidoaki, Satoru (木戸秋 悟) 3Pos308
3Pos309
Kiga, Daisuke (木賀 大介) **1SIP-6**
Kikegawa, Tatsuki (亀卦川 樹) 1Pos008
Kikkawa, Masahide (吉川 雅英) 2SBA-4
2SIP-5
Kikuchi, Chihiro (菊地 ちひろ) 2H1500
Kikuchi, Hiroto (菊地 浩人) **1Pos053**
Kikuchi, Jun-ichi (菊池 純一) 2G1412
Kikuchi, Masuzu (菊池 真鈴) **2Pos086**
Kikuchi, Nobuaki (菊池 宣明) 2Pos012
Kikuchi, Takahito (菊池 隆仁) **1Pos311**
1Pos315
1Pos319
Kikuchi, Takeshi (菊地 武司) 2J1542
1Pos019
1Pos020
1Pos021
1Pos023
Kikuchi, Tatsuya (菊地 龍弥) 1SDA-3
Kikuchi, Yousuke (菊池 洋輔) **1G1342**
Kikukawa, Takashi (菊川 峰志) 1H1330
2H1400
2H1500
2H1542
2H1554
3Pos006
3Pos012
Kikusui, Takefumi (菊水 健史) 3SEA-5
Kim, Eunchul (Kim Eunchul) **3Pos030**
Kim, Hyonchol (金 賢徹) 1Pos304
3Pos317
Kim, Ju Yaen (金 宙妍) 3SDA-2
Kimura, Atsuomi (木村 敦臣) 2D1448
Kimura, Hiroshi (木村 啓志) 1O1512
2O1530
Kimura, Hiroshi (木村 宏) 2Pos415
2Pos420
Kimura, Takashi (木村 隆志) 3SGA-4
Kimura, Tetsunari (木村 哲就) 1K1536
1Pos069
2Pos017
3Pos020
3Pos025
Kimura, Yoshitaka (木村 芳孝) 2O1412
Kimura, Yukihiro (木村 行宏) 1SRA-1

1H1418
3Pos028
Kinjo, Masataka (金城 政孝) 2O1618
1Pos405
1Pos411
2Pos033
2Pos409
Kinoshita, Kengo (木下 賢吾) 1Pos072
3Pos206
Kinoshita, Makoto (木下 専) 1SMA-2
Kinoshita, Masahiro (木下 正弘) 2Pos024
2Pos061
2Pos062
2Pos063
3Pos010
3Pos011
Kinoshita, Masanao (木下 祥尚) 1G1448
Kinoshita, Miki (木下 実紀) 2A1606
2M1500
2Pos307
Kinoshita, Yoshimi (木下 慶美) **2Pos213**
Kinosita, Kazuhiko (木下 一彦) 1Pos207
Kinosita, Yoshiaki (木下 佳昭) 1E1512
2E1530
Kiribayashi, Ryo (桐林 遼) 1Pos067
Kirimoto, Atsushi (桐本 淳司) 1Pos084
Kishi, Rikako (岸 利華子) **3Pos028**
Kishikawa, Jun-chi (岸川 淳一) **1Pos004**
Kishikawa, Jun-ichi (岸川 淳一) 1SDA-5
1Pos005
Kishimoto, Hiraku (岸本 拓) **3Pos024**
Kishimoto, Satoshi (岸本 幹史) 3Pos311
Kishimoto, Toshifumi (岸本 幹史) **1Q1354**
Kitagawa, Teizo (北川 禎三) **2SOA-7**
3Pos001
Kitagawa, Tomoki (北川 智規) **2Pos042**
Kitahara, Ryo (北原 亮) **2M1400**
Kitahashi, Yuki (Kitahashi Yuki) 1L1524
Kitajima, Tomoya (北島 智也) 1SFA-2
Kitajima-Ihara, Tomomi (北島（井原） 智美) 3Pos034
Kitamura, Ayaka (北村 彩佳) 1Pos065
Kitamura, Yoshiichiro (北村 美一郎) **1Pos307**
Kitao, Akio (Kitao Akio) 3SAA-2
Kitao, Akio (北尾 彰朗) 2E1500
2J1448
Kitazawa, Satoko (北澤 怜子) **2D1554**
Kitazawa, Soichiro (北沢 創一郎) 2M1400
Kitoh-Nishioka, Hirotaka (鬼頭（西岡） 宏任) **2F1500**
Kiwa, Toshihiko (紀和 利彦) **1SBP-5**
Kiyonari, Hiroshi (清成 寛) 3SEA-5
Kobayashi, Amane (小林 周) 2Pos416
Kobayashi, Chigusa (小林 千草) 1J1448
1Pos070
Kobayashi, Huminori (小林 史典) 1Pos031
Kobayashi, Itsuki (小林 樹) **1H1500**
2F1436
3Pos041
Kobayashi, Kaito (小林 海斗) 2Pos201
Kobayashi, Kan (小林 幹) **2M1618**
Kobayashi, Kohei (小林 昂平) **1E1448**
Kobayashi, Masayuki (小林 正幸) 1H1418
3Pos028
Kobayashi, Naohiro (小林 直宏) 1K1548
2Pos061
Kobayashi, Naoto (小林 直登) 1Pos310
Kobayashi, Naoya (小林 直也) 1K1548
3Pos085
Kobayashi, Ryo (小林 凌) 1Pos323
Kobayashi, Ryohei (小林 稜平) 1E1406
2E1424
Kobayashi, Ryohei (小林 遼平) **3Pos407**
Kobayashi, Sawako (小林 佐和子) **1Pos098**
Kobayashi, Takuya (小林 琢也) 1Pos224
Kobayashi, Tetsuya (小林 徹也) 1Pos326
Kobayashi, Tetsuya J. (小林 徹也) 3Pos213
Kobayashi-Kirschvink, Koseki J. (小林 鉱石) 1Pos417
Kobirumaki-Shimozawa, Fuyu (小比類巻 生) **2N1424**
Kobori, Yasuhiro (小堀 康博) **3SHA-4**
1Pos069
2Pos097
Kobori, Yuta (小堀 雄大) 2Pos068
Kodama, Aya (児玉 彩) 1A1330
Kodama, Koichi (児玉 浩一) 3Pos039
Kodera, Noriyuki (古寺 哲幸) **1SKA-2**
1D1430
1D1448
1D1512
1D1524
1E1448
1G1342
2D1530
1Pos031
1Pos212
1Pos222
1Pos223
3Pos014
Koga, Kenichiro (甲賀 研一郎) 2Pos008
Koga, Nobuyasu (古賀 信康) 1K1548
1Pos208
1Pos209
1Pos211
3Pos081
3Pos083
3Pos085
3Pos086
3Pos202

Koga, Rie (古賀 理恵) 1K1548
1Pos208
1Pos209
1Pos211
3Pos202
Koguchi, Shin (小口 伸) **2Pos312**
Kohda, Daisuke (Kohda Daisuke) 1L1406
Kohda, Jiro (香田 次郎) 1Pos067
Koie, Nobuyoshi (鯉江 信慶) 2N1400
Koike, Kenzo (小池 謙造) 1Pos054
Koiso, Yurika (小礒 由里加) 1Pos224
Kojima, Hiroaki (小嶋 寛明) 2SMA-2
1O1342
2A1518
2N1542
2Pos204
2Pos214
Kojima, Keiichi (小島 慧一) **1SHA-1**
1F1524
1F1536
1H1330
2H1518
2H1530
2H1606
2Pos086
2Pos087
2Pos089
2Pos090
3Pos043
3Pos044
Kojima, Masaru (小嶋 勝) **3Pos401**
Kojima, Seiji (小嶋 誠司) 1Q1418
2A1618
1Pos217
1Pos218
2Pos302
2Pos303
2Pos304
2Pos308
Kokubo, Hironori (小久保 裕功) **1Pos002**
Komatsu, Hideyuki (小松 英幸) 1J1548
Komatsu, Ryota (小松 亮太) **1G1330**
1Pos098
Komatsu, Tomohiro (小松 大洋) **2Pos208**
Komatsu, Toru (小松 徹) **1SKA-4**
1Pos407
Komatsu, Yasuo (小松 康雄) 1Pos408
Komatsuzaki, Tamiki (Komatsuzaki Tamiki) 1D1548
Komatsuzaki, Tamiki (小松崎 民樹) **3SFA-2**
Komatsuzaki, Yoshimasa (小松崎 良将) **1Pos308**
Komazawa, Kosuke (駒澤 光祐) 2G1530
Komeda, Seiji (米田 誠治) 1Q1354
Komiya, Ken (小宮 健) **3Pos403**
Komori, Tomotaka (小森 智貴) 1E1430
2Pos216
Komori, Tomotka (小森 智貴) 1K1430
Komoto, Nana (河本 奈々) **2Pos104**
Kon, Takahide (昆 隆英) 2N1518
2Pos206
2Pos215
Kondo, Akihiko (近藤 明彦) 3Pos418
Kondo, Daichi (近藤 大地) **1Pos023**
Kondo, Hiroko X (近藤 寛子) 1Pos067
Kondo, Hiroko X. (近藤 寛子) **3Pos002**
Kondo, Kazuma (近藤 一馬) **1Pos020**
Kondo, Kazunori (近藤 和典) 3Pos417
Kondo, Masaharu (近藤 政晴) 1F1430
1H1430
Kondo, Ryohei (近藤 遼平) **1Q1536**
Kondo, Shigeru (近藤 滋) 1Pos324
Kondo, Takao (近藤 孝男) 1M1342
1Pos073
Kondo, Toru (近藤 徹) **1SRA-5**
1F1418
3Pos033
Kondo, Yohei (近藤 洋平) **1Pos420**
Kondo, Yuichi (近藤 雄一) **1E1524**
2N1500
Kondo, Yusuke (近藤 裕祐) **2Pos207**
2Pos208
Kondou, Suguru (近藤 傑) 2O1448
Kondow, Akiko (近藤 晶子) 2C1412
Kong, Lingbing (Kong Lingbing) **1G1524**
Konno, Hiroki (紺野 宏紀) 1Pos031
Konno, Hiroki (紺野 宏記) 2D1554
3Pos014
Konno, Masae (今野 雅恵) **1SHA-2**
2Pos091
2Pos092
Konno, Takashi (今野 卓) **1Pos033**
Kono, Fumiaki (河野 史明) 1SDA-3
1M1430
Kono, Hidetoshi (河野 秀俊) 2SGA-2
2Q1436
2Pos038
3Pos084
Koseki, Haruhiko (古関 明彦) **2SDA-4**
Kosugi, Takahiro (小杉 貴洋) **2SMA-1**
1K1548
Kotani, Susumu (小谷 享) 2Pos316
2Pos321
Koteishi, Hiroyasu (小手石 泰康) 2Pos082
Kotera, Hidetoshi (小寺 秀俊) 1E1536
2Pos217
Kouyama, Tsutomu (神山 勉) **1H1524**
Koyama, Ryuta (小山 隆太) 2C1518

Koyama, Yohei (小山 洋平) 2K1542
Koyanagi, Mitsumasa (小柳 光正) 1SHA-4
Kozakai, Taro (小坂井 太郎) 2Pos106
Kozono, Haruo (小園 晴生) 3Pos027
Kozono, Yuko (小園 裕子) 3Pos027
Kozuka, Jun (小塚 淳) 1SKA-6
Krah, Alexander (Krah Alexander) **2Pos018**
Kroiss, Daniela (Kroiss Daniela) 2Q1606
Kubo, Minoru (久保 稔) 1K1536
1M1448
Kubo, Shintaroh (久保 進太朗) 2Pos047
Kubo, Shintaroh (久保 進太郎) **2Pos211**
Kubo, Tai (久保 泰) 3Pos016
Kubota, Soichiro (窪田 総一郎) 2Pos009
Kubota, Tomoya (久保田 智也) 1Pos102
Kuboyama, Izumi (窪山 泉) 1Pos309
1Pos314
1Pos316
3Pos219
Kuboyama, Masahiro (久保山 正浩) **3Pos417**
Kudo, Hisashi (工藤 恒) **1K1354**
Kudo, Takafumi (工藤 崇文) **1Pos034**
Kudoh, Suguru (工藤 卓) 1Pos312
Kudoh, Suguru N. (工藤 卓) 1C1548
2C1530
Kuge, Sayuri (久下 小百合) 1Pos317
Kugimiya, Akimitsu (釘宮 章光) 1Pos067
Kuhara, Atsushi (久原 篤) **1Pos306**
Kumamoto, Eiichi (熊本 栄一) **1Pos305**
Kumamoto, Yasuaki (Kumamoto Yasuaki) 1D1548
Kumar, Vipin (Kumar Vipin) 2O1400
Kumasaka, Takashi (Kumasaka Takashi) 1Pos068
Kumasaka, Takashi (熊坂 崇) 1L1512
2E1412
Kumayama, Akane (熊山 あかね) **1Pos410**
Kunihara, Tomoko (椚原 朋子) 1K1418
1K1448
Kunita, Itsuki (國田 樹) 2Pos317
Kura, Tomomi (久良 知実) 2Pos058
Kuragano, Masahiro (倉賀野 正弘) 1Pos302
Kuramochi, Masahiro (倉持 昌弘) **2K1530**
3Pos016
3Pos027
3Pos068
3Pos069
Kurebayashi, Nagomi (呉林 なごみ) 2Pos422
Kurihara, Kensuke (栗原 顕輔) 1Pos081
Kurihara, Marie (栗原 眞理恵) 1F1524
1H1330
2Pos089
Kurihara, Rika (栗原 里佳) **1F1536**
Kurisu, Genji (栗栖 源嗣) 1SRA-4
3SDA-2
1C1330
3Pos024
Kurniawan, Isman (Kurniawan Isman) **1L1330**
Kurniawan, Isman (クルニアワン イスマン) 3Pos039
Kurobe, Atushi (黒部 淳史) 2Pos016
Kuroda, Ayumu (黒田 歩夢) **3Pos421**
Kuroda, Daisuke (黒田 大祐) 1L1342
1Pos067
3Pos018
Kuroda, Hiroshi (黒田 洋詩) 3Pos044
Kuroda, Junpei (黒田 純平) 1Pos324
Kuroda, Shinya (黒田 真也) 1O1500
Kurumizaka, Hitoshi (胡桃坂 仁志) 2Pos038
Kusaka, Chikako (草合 千嘉子) 2O1448
Kusakizako, Tsukasa (草木迫 司) 2G1606
Kusumi, Akihiro (楠見 明弘) 2D1412
3Pos327
Kusumoto, Tomoichirou (楠本 朋一郎) 1J1548
Kuwabara, Makoto (桑原 誠) **1E1430**
1K1430
Kuwata, Takumi (桑田 巧) **2Pos016**
2Pos019
Kuwayama, Hidekazu (桑山 秀一) 2A1448
3Pos094
Kyogoku, Hirohisa (京極 博久) **1SFA-2**
Labute, Paul (Labute Paul) 3Pos087
Lajoie, Marc (Lajoie Marc) **2SMA-3**
Lan, Wei-Hsuan (Lan Wei-Hsuan) **2Pos034**
Launay, Guillaume (Launay Guillaume) 3Pos201
Le, Minh (レ ミン) 2C1412
Lee, Hyoung Jae (リ ヒョンゼ) 1Pos066
Lee, Jae Ho (リー ヤエ ホ) 2M1618
Lee, Jong-Bong (Lee Jong-Bong) **3SIA-3**
Lee, Seohyun (Lee Seohyun) **1D1342**
Lee, Youna (李 宥奈) 2SFA-1
Lennon-Dumenil, Ana-Maria (Lennon-Dumenil Ana-Maria) 2Pos319
Levadny, Victor (レバツニー ビクター) 1G1418
Levadnyy, Victor (レバツニー ビクター) 2G1400
Li, Chunlin (李 春林) 1SBP-4
Li, Guohong (Li Guohong) 3SIA-7
Li, Hung Wen (李 弘文) 2Pos044
Li, Hung-Wen (Li Hung-Wen) 2Pos034
2Pos036
Li, Hung-Wen (李 弘文) **2SAA-3**
Li, Ming (Li Ming) **3SIA-1**
3SIA-7
1Pos421
Li, Siyao (Li Siyao) 1Pos021
Li, Songling (Li Songling) 1Pos065
Li, Wei (Li Wei) **3SIA-7**
Li, Zhengqun (Li Zhengqun) 2E1530
Li, Zhenhai (李 振海) **2Q1436**

Lim, Wei Ming (林 偉銘) 2A1500
Lin, Min Guan (Lin Min Guan) 2Pos036
Lin, Sheng-Yao (Lin Sheng-Yao) 2Pos034
Lin, Tsai-Shun (Lin Tsai-Shun) **1Pos218**
Liu, Dinan (Liu Dinan) 2M1554
Liu, Ping (劉 娉) **2Pos076**
Liu, Ye (Liu Ye) 2Pos415
Liu, Zhenfeng (柳 振峰) **2SBA-1**
Lloyd, Kento (ロイド 賢人) **1Pos102**
Lo, Chien-Jung (Lo Chien-Jung) **2SAA-6**
1Pos218
1Pos220
Lo, Chien-Jung (羅 健榮) 2Pos313
Lorenz-Fonfria, Victor (Lorenz-Fonfria Victor) 3Pos020
Lori, Christian (Lori Christian) 3SKA-5
Lu, Chih-Hao (盧 致豪) 2SAA-3
Lu, Kai (魯 慨) **2D1436**
Lu, Ying (Lu Ying) **1Pos421**
Lubitz, Wolfgang (Lubitz Wolfgang) 3Pos058
Lucas, Robert (Lucas Robert) 1SHA-4
Lukacs, Viktor (Lukacs Viktor) 1SEA-7
Lukowiak, Ken (Lukowiak Ken) 1Pos308
M. Watanabe, Tomonobu (M. Watanabe Tomonobu) 2O1400
Ma, Benson (マ ベンソン) 2J1530
Ma, Biao (馬 彪) 1Pos026
Ma, Huimin (馬 慧敏) 2Pos077
Ma, Yue (馬 越) **2Pos043**
Machiyama, Hiroaki (町山 裕亮) **1SEA-4**
3Pos321
Madigan, M.T. (Madigan M. T.) 1H1418
Mae, Yasushi (前 泰志) 3Pos401
Maeda, Ryo (前田 亮) **2G1618**
Maeda, Shigeo (前田 重雄) 3Pos050
Maeda, Sumihiro (前田 純宏) 3SFA-1
Maeda, Takahiro (前田 高宏) 2Pos419
2Pos421
Maeda, Tomoki (前田 朋輝) 3Pos015
Maeda, Tomoya (前田 倫也) 1Pos094
2Pos003
Maeda, Tomoya (前田 智也) 1Pos080
Maeda, Yuichiro (前田 雄一郎) 1Pos204
Maeda, Yusuke (前多 裕介) 1O1354
Maeda, Yusuke (前田 雄介) 2Pos040
Maeda, Yusuke T. (前多 裕介) **1SFA-6**
2O1542
2Q1542
Maeshima, Kazuhiro (Maeshima Kazuhiro) 1Pos110
Maeshima, Kazuhiro (前島 一博) 1D1418
2Q1412
Maestre-Reyna, Manuel (Maestre-Reyna Manuel) **3SAA-3**
Maeta, Shingo (前田 真吾) **3Pos079**
Magari, Masaki (曲 正樹) **1SBP-2**
Magi, Shigeyuki (間木 重行) 1Q1406
2O1500
3Pos216
3Pos312
Magi, Yasuhiro (間木 靖裕) **1Pos082**
1Pos083
Magori, Nobuya (馬郡 信弥) 1Pos305
Maki, Kosuke (槇 亙介) 2Pos001
2Pos002
Maki, Misayo (真木 美紗代) 2H1530
Maki, Yasushi (牧 泰史) 2Pos014
Makino, Fumiaki (牧野 文信) 2A1606
2M1518
1Pos214
Makino, Yoshiteru (槇野 義輝) 1H1536
1L1512
Mandali, Sridhar (Mandali Sridhar) 2Q1500
Mano, Eriko (間野 絵梨子) 2Q1500
Martin, Juliette (Martin Juliette) 3Pos201
Martinac, Boris (Martinac Boris) 2G1530
Martines-Costa, Marilia (Martines-Costa Marilia) 2Pos003
Marumoto, Moegi (丸本 萌) 1A1548
3Pos210
Maruno, Takahiro (丸野 孝浩) 2K1400
Maruta, Shinsaku (丸田 晋策) 2Pos224
2Pos225
2Pos226
3Pos417
Maruyama, Hisataka (丸山 央峰) 1A1548
Maruyama, Kenshiro (丸山 兼四朗) 2C1412
1Pos323
Maruyama, Shintaro (丸山 慎太郎) 2Pos057
Maruyama, Tatsuro (丸山 達朗) 2G1606
Maruyama, Yutaka (丸山 豊) **1J1418**
Marzinek, Jan K. (Marzinek Jan K.) **3Pos021**
Masaike, Sayaka (政池 彩雅) **3Pos308**
Masaike, Tomoko (政池 知子) 2E1400
1Pos208
1Pos209
1Pos211
1Pos410
Masaki, Noritaka (正木 紀隆) **2F1554**
Mashiko, Ryota (猿子 良太) **1Pos202**
Mashima, Tsukasa (真嶋 司) **2L1424**
Mashimo, Tadaaki (真下 忠彰) **3Pos051**
Masuda, Hideki (増田 秀樹) **2SOA-6**
Masuda, Junko (増田 潤子) **1SBP-3**
Masuda, Shinji (増田 真二) 3Pos043
Masuda, Tomohiro (増田 友広) 2Pos410
Masumoto, Hiroshi (増本 博) 1Pos401
Matsubara, Hitomi (松原 瞳) **2Pos074**

Matsubayashi, Akiko (松林 亜希子) 1K1536
Matsuda, Isamu (松田 勇) 2L1448
Matsuda, Keisuke (松田 佳祐) 2Pos081
Matsuda, Koji (松田 光司) 1SHA-6
Matsuda, Kyohei (松田 恭平) **1Pos224**
Matsuda, Makoto (松田 真) 3SDA-4
Matsuda, Michiyuki (松田 道行) 2C1424
2F1518
Matsuda, Tomoki (Matsuda Tomoki) 1D1354
Matsuda, Tomoki (松田 知己) 2D1436
Matsuda, Yuka (松田 祐佳) **2Pos214**
Matsueda, Anna (松枝 杏奈) **3Pos418**
Matsui, Akito (松井 亮人) **1Pos411**
Matsui, Kazuhumi (松井 一史) 2Pos321
Matsui, Koki (松井 香樹) **2Pos107**
Matsui, Takaaki (松井 崇晃) **1Pos326**
Matsui, Toru (Matsui Toru) 1L1330
Matsuike, Daiki (松生 大輝) **1K1512**
Matsuki, Hitoshi (松木 均) 1Pos091
Matsukura, Lisa (松倉 里紗) **1Pos028**
Matsumori, Nobuaki (松森 信明) 1G1448
Matsumoto, Atsushi (松本 淳) 3SGA-2
2Pos038
Matsumoto, Ayaka (松本 朱加) 2A1400
Matsumoto, Hideyuki (松本 英之) 3SEA-5
Matsumoto, Kazuhiko (松本 和彦) **2SFA-4**
Matsumoto, Shigeyuki (松本 篤幸) 1L1512
1Pos026
Matsumoto, Shiori (松本 栞里) **2Pos220**
Matsumoto, Tomoharu (松本 友治) 3Pos040
Matsumoto, Toshihiko (松元 俊彦) 1Pos054
1Pos055
Matsumura, Hiroki (松村 洋貴) 3Pos031
Matsumura, Shigeyoshi (松村 茂祥) **1SFA-5**
Matsunaga, Yasuhiro (松永 康佑) **1SOA-2**
1Pos070
1Pos097
Matsunami, Hideyuki (松波 秀行) 2SBA-2
Matsuno, Kenji (Matsuno Kenji) 1SAA-4
Matsuo, Koichi (松尾 光一) **1M1330**
Matsuo, Muneyuki (松尾 宗征) **1Pos081**
Matsuo, Naoya (松尾 直也) 1M1354
Matsuo, Tatsuhito (松尾 龍人) **1SDA-3**
1M1430
Matsuoka, Daisuke (松岳 大輔) **1Pos097**
2Pos022
Matsuoka, Satomi (松岡 里実) **2A1424**
2A1436
2Pos074
2Pos082
3Pos047
Matsuoka, Shigeru (松岡 茂) 2Pos022
Matsuoka, Yukiko (松岡 由希子) 1SBP-2
Matsushima, Yuki (松島 佑樹) **2Pos051**
Matsushita, Katsuyoshi (松下 勝義) **3Pos209**
Matsushita, Masaki (松下 雅季) **1G1406**
3Pos070
Matsushita, Masaya (松下 将也) 1Pos106
Matsushita, Yuki (松下 優貴) **2C1400**
Matsuura, Azuma (松浦 東) 3Pos054
3Pos055
Matsuura, Kenji (松浦 賢志) 1Pos203
1Pos311
1Pos315
1Pos319
1Pos412
1Pos413
1Pos414
1Pos415
1Pos418
1Pos419
3Pos095
3Pos409
3Pos410
3Pos411
3Pos413
Matsuura, Koji (松浦 宏治) **2A1530**
Matsuura, Tetsu (松浦 哲) **1Pos094**
Matsuyama Hoyos, Takesi (松山オジョス 武) 3Pos045
Matsuzaki, Katumi (松崎 勝巳) 1Q1448
Matsuzaki, Kohei (松崎 興平) 2Pos219
2Pos221
Matsuzaki, Shigenobu (松崎 茂展) 2M1530
Matsuzaki, Yuri (松崎 由理) 1C1418
1C1448
3Pos201
Maturana, Andres D. (Maturana Andrés D.) 2G1606
Mazaki, Yuichi (真崎 雄一) **2Pos326**
McElheny, Dan (McElheny Dan) 2L1448
McMillan, Duncan G.G (McMillan Duncan G.G) 2E1448
Mekubo, Tomohiro (目久保 知宏) 2O1448
Mendoza - Hoffmann, Francisco (Mendoza - Hoffmann Francisco) 2E1448
Menon, Anant K. (Menon Anant K.) **1SIA-3**
Michida, Hiroki (道田 大貴) **3Pos312**
Mie, Yasuhiro (三重 安弘) **1Pos408**
Mijiddorj, Batsaikhan (Batsaikhan Mijiddorj) **1L1524**
Mikami, Nagisa (三上 渚) 2E1530
Mikawa, Tsutomu (美川 務) 2Pos045
Mikoshiba, Katsuhiko (御子柴 克彦) 3SFA-1
Mikosiba, Naoki (御子柴 直紀) 3Pos082
Minagawa, Jun (皆川 純) 3Pos030
Minami, Shintaro (南 慎太朗) 1Pos075
3Pos085
3Pos202

Minamino, Tohru (南野 徹) **1SMA-7**
1E1500
2A1606
2M1500
1Pos215
1Pos216
2Pos307
Minato, Seiya (港 聖也) 1Pos102
Minato, Shotaro (湊 翔太郎) 1Pos401
Mino, Hiroyuki (三野 広幸) 3SHA-4
1F1354
Mino, Taira (三野 平) 1Pos217
Minobe, Reina (見延 玲奈) 3SHA-4
Minoda, Akiko (蓑田 亜希子) 2Pos415
Minoda, Ayumi (蓑田 歩) **3SMA-5**
Minoda, Hiroki (箕田 弘喜) 2Pos107
Minoshima, Wataru (箕嶋 渉) **1Pos312**
Minoura, Takako (箕浦 高子) 2Pos207
Mio, Kazuhiro (三尾 和弘) 2K1530
3Pos016
Mio, Muneyo (三尾 宗代) 3Pos016
Mishima, Yuichi (三島 優一) 2Pos027
Misonou, Hiroaki (御園生 裕明) 1Pos320
Misu, Kohei (三須 滉平) **3Pos207**
Misumi, Yuko (三角 裕子) 3SDA-2
Mita, Kenichiro (三田 建一郎) 2G1554
Mitaku, Shigeki (美宅 成樹) **1Pos105**
Mitsui, Toshiyuki (三井 敏之) 1Pos102
3Pos314
3Pos315
3Pos408
Mitsuishi, Yachiyo (三ツ石 弥千代) 1J1330
Mitsumoto, Masaya (三本 斉也) **3Pos081**
Mitsuoka, Kaoru (光岡 薫) **1SDA-5**
1Pos004
1Pos005
1Pos015
2Pos215
Mitsutake, Ayori (光武 亜代理) 1J1418
2J1554
Mitsuyama, Toutai (光山 統泰) 1D1330
Miura, Masahiro (三浦 雅央) 3Pos025
Miura, Takashi (三浦 岳) **1SAA-5**
Miyachi, Mariko (宮地 麻里子) 3Pos031
Miyachi, Yuna (宮地 佑奈) 3Pos078
Miyagawa, Koichi (宮川 晃一) **2Pos054**
Miyakawa, Takeshi (Miyakawa Takeshi) 2Pos031
Miyakawa, Takeshi (宮川 毅) **1Pos001**
1Pos221
2Pos083
Miyake, Jun (三宅 淳) **1Q1524**
Miyake, Tomoya (三宅 智也) 1Pos404
Miyanaga, Yukihiro (宮永 之寛) 2A1424
2A1448
3Pos047
Miyanoiri, Yohei (宮ノ入 洋平) 1L1500
Miyasaka, Go (宮坂 豪) **1Pos039**
Miyasaka, Hiroshi (宮坂 博) 1F1430
Miyasaka, Yoshiya (宮坂 禎也) **1A1512**
3Pos060
Miyashita, Naoyuki (宮下 尚之) **2J1436**
1Pos027
1Pos028
2Pos029
Miyashita, Osamu (Miyashita Osamu) 1L1406
1M1500
1Pos012
Miyashita, Osamu (宮下 治) 1M1512
Miyashita, Yurina (宮下 由里奈) 1M1354
Miyata, Makoto (宮田 真人) 1A1330
1A1342
1A1418
1E1448
1K1512
1Pos212
2Pos027
Miyata, Tomoko (宮田 知子) 2A1606
2M1500
2M1606
1Pos214
2Pos307
Miyauchi, Seiji (宮内 正二) 2Pos081
Miyawaki, Atsushi (宮脇 敦史) 3Pos416
Miyazaki, Kentaro (宮崎 健太郎) 1Pos079
Miyazaki, Makito (宮﨑 牧人) **1SFA-1**
1O1354
Miyazaki, Naoyuki (宮崎 直幸) 1F1330
2M1530
1Pos009
2Pos404
Miyazaki, Shota (宮崎 翔太) 2C1412
Miyazaki, Toh (宮崎 杜夫) **1SHA-5**
Miyazaki, Yuri (宮崎 裕理) 3SDA-3
Miyazaki, Yuusuke (宮崎 裕介) **1Pos101**
Miyazawa, Takashi (宮沢 高司) **3Pos315**
Miyazono, Yuya (宮薗 侑也) 2Pos105
Miyoshi, Hiromi (三好 洋美) 1A1406
Miyoshi, Masanobu (三好 優乃生) 1Pos406
Miyoshi, Natsuki (三好 菜月) **2H1518**
Mizoguchi, Tadashi (溝口 正) 1SRA-4
Mizuhara, Yukinobu (水原 志暢) 1Pos013
Mizukami, Taku (水上 卓) **2Pos060**
Mizukami, Takuya (水上 琢也) 2Pos002
Mizuno, Akira (水野 彬) 2Pos308
Mizuno, Misao (水野 操) 1H1548
2H1606

Mizusawa, Mei (水澤 愛衣) 3Pos073
Mizushima, Ryota (水島 良太) **2D1448**
Mizuta, Kotaro (水田 恒太郎) 1Pos305
Mizutani, Masaharu (水谷 正治) 1Pos066
Mizutani, Masaki (水谷 雅希) **1A1342**
Mizutani, Yasuhisa (水谷 泰久) 1H1548
2H1606
Mizutori, Ritsu (水鳥 律) **2Pos092**
Mochizuki, Kazushi (望月 一志) 2Pos004
Mochizuki, Kazuto (望月 和人) 1Pos028
Mogami, George (最上 譲二) **2Pos066**
Moghal, Md. Mizanur (モゴール エムディ ミザヌル)
2G1400
1Pos095
Momosaki, Satoru (桃崎 哲) **1Pos405**
Moniruzzaman, Md. (モニルザマン エムディー)
2G1400
Moniruzzaman, Md. (モニルザマン エムディー、)
1Pos095
Mori, Hideki (森 英樹) 1A1548
Mori, Hikari (森 ひかり) 1Pos324
Mori, Ichiro (森 一郎) 1L1512
Mori, Kensaku (森 憲作) 3SEA-5
Mori, Ryota (森 遼太) 1Pos071
2Pos006
Mori, Takaharu (森 貴治) **2Q1518**
Mori, Yusuke (森 勇介) 3Pos050
Morigaki, Kenichi (森垣 憲一) **1SIA-6**
1F1448
1G1330
2Pos070
2Pos102
3Pos022
Morigaki, Kennichi (森垣 憲一) 1Pos098
Morii, Hisayuki (森井 尚之) 1L1500
Morikawa, Ryota (Morikawa Ryota) 2Pos031
Morikawa, Ryota (森河 良太) 1Pos001
1Pos221
2Pos083
Morimatsu, Masatoshi (森松 賢順) 1A1448
2A1530
1Pos206
3Pos404
Morimitsu, Tohru (森光 達) 1Pos091
Morimoto, Ayaka (森本 彩加) **2Pos094**
Morimoto, Yusuke V. (森本 雄祐) 1Pos215
1Pos322
Morishima, Ken (守島 健) 1Pos006
1Pos052
Morishima, Kenta (森島 健太) **2Pos309**
Morishita, Tatsuya (森下 達矢) 2Pos204
Morita, Masahiko (森田 正彦) 3SEA-5
Morita, Masahiko (横田 秀夫) 3SEA-5
Morita, Masamune (森田 雅宗) 1Pos089
2Pos049
3Pos405
3Pos412
Moritsugu, Kei (森次 圭) **2SGA-3**
1Pos048
3Pos075
Moriwaki, Yoshitaka (森脇 由隆) 1J1512
1Pos041
1Pos042
1Pos051
3Pos053
Moriya, Hisao (守屋 央朗) 2Pos090
Morizono, Nami (森園 那未) **2Pos073**
Motegi, Fumio (茂木 文夫) **2SBP-1**
Motegi, Toshinori (茂木 俊憲) 3Pos006
Motohashi, Yukino (本橋 幸乃) **3Pos326**
Motoki, Hideyoshi (根木 秀佳) 3Pos020
Motono, Chie (本野 千恵) **1Pos061**
Motoyama, Ayaka (本山 彩香) 2Pos025
Mouri, Kazunari (毛利 一成) **2Pos414**
Mukai, Hideo (向井 秀夫) 1Pos310
Mukai, Yuri (向井 有理) 1Pos008
1Pos039
Mukaiyama, Atsushi (向山 厚) 1K1500
1M1342
1Pos047
1Pos073
3Pos063
Munemasa, Shintaro (宗正 晋太郎) 3Pos043
Muneyuki, Eiro (宗行 英朗) 2E1436
1Pos210
Murabe, Keisuke (村部 圭祐) 2H1554
Murai, Masatoshi (村井 正俊) 1Pos004
Murakami, Hiroki (村上 博紀) 1SBP-6
Murakami, Hiroshi (村上 洋) **1C1500**
Murakami, Midori (村上 緑) **1H1512**
Murakami, Mitsuki (村上 美月) 2Pos106
Murakami, Ryo (村上 僚) 1K1430
Murakami, Shota (村上 祥大) 1Pos401
Murakami, Shuhei (村上 周平) **1Pos076**
Murakami, Syuhei (村上 周平) 1Pos077
Muraki, Yasushi (村木 靖) 2Pos324
Muramoto, Kazumasa (村本 和優) **3Pos004**
Murase, Kohji (村瀬 浩司) **1SGA-1**
Murata, Agato (村田 崇人) 2Pos035
Murata, Kazuyoshi (村田 和義) 2M1530
1Pos009
2Pos404
Murata, Masayuki (村田 昌之) 3Pos303
Murata, Michio (村田 道雄) 2Pos022
Murata, Satoshi (村田 智) 3Pos412
Murata, Takeshi (村田 武士) 1K1548

1Pos009
2Pos024
2Pos056
2Pos057
3Pos010
3Pos011
3Pos081
Murata, Yoshiyuki (村田 芳行) 3Pos043
Murata, Yudai (村田 雄大) **1J1548**
Murata, Yutaka (村田 隆) **1Pos074**
Muratsubaki, Naoyuki (村椿 直之) **1Pos227**
Murayama, Takashi (村山 尚) 2Pos422
Muro, Ikumi (室 郁弥) **1Pos031**
Muta, Mikihisa (牟田 幹悠) **2K1500**
Mutoh, Risa (武藤 梨沙) 1SRA-4
2Pos402
3Pos024
Mweti Mwangangi, Dennis (Mweti Mwangangi Dennis)
2Pos228
Mylemans, Bram (ミレマンス ブラム) 1J1500
Müller, Pavel (Müller Pavel) **3SAA-4**
Nada, Shigeyuki (名田 茂之) 1Pos065
Nagai, Masako (長井 雅子) 3Pos001
Nagai, Rina (永井 里奈) 2D1448
Nagai, Rurika (永井 るりか) **3Pos022**
Nagai, Takeharu (Nagai Takeharu) 1D1354
Nagai, Takeharu (永井 健治) 1D1500
2D1436
Nagamune, Hideaki (長宗 秀明) 1Pos091
Nagano, Shingo (永野 真吾) **1Pos066**
2Pos087
3Pos015
Nagano, Tetsuo (長野 哲雄) 1SKA-4
Nagao, Hidemi (Nagao Hidemi) 1L1330
2Pos031
Nagao, Hidemi (長尾 秀実) 2G1500
1Pos001
1Pos094
2Pos003
3Pos039
Nagao, Masahito (長尾 真仁) 2Pos301
Nagao, Ryo (長尾 遼) 1F1330
3Pos034
Nagao, Soichi (永雄 総一) 1Pos320
Nagasawa, Yutaka (長澤 裕) 1F1430
Nagase, Yurie (長瀬 友里恵) 3Pos043
3Pos044
Nagashima, Hiroki (長嶋 宏樹) 3SHA-4
2Pos097
Nagashima, Kenji (永島 賢治) 3Pos028
Nagashima, Ryosuke (永島 崚甫) **1D1418**
Nagashima, Toshio (長島 敏雄) 1G1430
Nagashima, Tosho (長島 敏雄) **2F1542**
Nagata, Kazuhiro (永田 和宏) 3SDA-1
Nagata, Takashi (永田 崇) **1SHA-4**
2L1424
2Pos061
Nagataki, Akinori (長瀧 瑛詔) **2Pos310**
Nagatani, Yasuko (永谷 康子) 1Pos022
Nagatoishi, Satoru (長門石 暁) 2SDA-3
Nagatomo, Shigenori (長友 重紀) **3Pos001**
Nagatosihi, Satoru (長門石 暁) 3Pos018
Nagatsuka, Hideyuki (長塚 秀幸) 1Pos093
Nagayama, Kuniaki (永山 國昭) **2D1606**
Nagayoshi, Rie (永吉 里江) 3Pos031
Naito, Akira (Naito Akira) 1L1524
Naito, Akira (内藤 晶) **1H1536**
Nakada, Shogo (仲田 正吾) 1Pos308
Nakae, Setsu (中江 摂) **1Pos018**
2Pos026
Nakagawa, Atsushi (中川 敦史) 3SDA-4
1Pos044
1Pos065
Nakagawa, Satoshi (中川 聖) **2Pos003**
3Pos039
Nakagawa, Taro (中川 太郎) 2Pos026
Nakagawa, Yuka (中川 由佳) 2SOA-2
Nakai, Hiromi (中井 浩巳) 2Pos103
2Pos104
Nakai, Hiroyuki (中井 博之) 1Pos046
Nakai, Masahiro (中井 昌弘) 1Pos065
Nakai, Tomokazu (中井 友和) 1Pos065
Nakajima, Akihiko (中島 昭彦) 1SAA-1
2A1400
Nakajima, Kazuki (中嶋 一喜) 2Pos410
Nakajima, Kenji (中島 健次) 1SDA-3
Nakajima, Kohei (中嶋 浩平) 3Pos090
3Pos091
Nakajima, Masahiro (中島 将博) 1Pos046
Nakajima, Masako (中島 昌子) 2A1554
Nakajima, Takahito (中嶋 隆人) 1SDA-7
Nakajima, Yoshiki (中島 芳樹) 1F1342
Nakajima, Yuta (中島 悠太) **1H1354**
Nakakido, Makoto (中木戸 誠) 3Pos079
Nakama, Masaki (仲間 政樹) 1F1524
2Pos089
Nakamizo, Yushi (中溝 祐志) **2H1542**
Nakamura, Akihiko (中村 彰彦) 2E1542
2E1554
2Pos203
2Pos206
2Pos405
Nakamura, Chikashi (中村 史) 1Pos304
3Pos073
3Pos317
Nakamura, Haruki (中村 春木) 1C1330

1C1354
1L1418
Nakamura, Masayuki (中邨 真之) 1Q1418
Nakamura, Shin (中村 伸) 3Pos038
Nakamura, Shuichi (中村 修一) 1Pos215
2Pos314
Nakamura, Shun (中村 駿) 2G1542
Nakamura, Teruya (中村 照也) **1Pos056**
Nakamura, Toru (中村 透) **3Pos406**
Nakamura, Tsukasa (中村 司) **3Pos204**
Nakamura, Yasuyuki (中村 泰之) 3Pos418
Nakane, Daisuke (中根 大介) **3SKA-1**
1E1512
1E1600
1Pos057
Nakanishi, Atsuko (中西 温子) 1SDA-5
1Pos004
1Pos005
Nakaniwa, Tetsuko (仲庭 哲津子) **1SRA-4**
Nakano, Gaku (中野 学) 1Pos403
Nakano, Kohei (仲野 耕平) 1Pos100
Nakano, Masaki (中野 将希) 1J1330
Nakano, Miki (中野 美紀) **1M1512**
Nakano, Minoru (中野 実) 1G1500
2Pos007
Nakano, Ryosuke (中野 僚介) 3Pos081
Nakano, Saya (中野 沙耶) **2Pos015**
3Pos082
Nakano, Shogo (中野 祥吾) 1M1354
Nakano, Yasuhisa (中野 靖久) 1Pos067
Nakao, Hiroyuki (中尾 裕之) 1G1500
Nakao, Kaori (中尾 香) **1G1512**
Nakao, Kimiko (中尾 公子) **2Pos423**
Nakasako, Masayoshi (中迫 雅由) 1J1342
1Pos014
2Pos416
Nakashima, Hitomi (中嶋 仁珠) 3Pos324
Nakashima, Ryousuke (中島 良介) 1G1512
Nakashima, Satoru (中島 聡) **2SOA-4**
Nakashima, Wataru (中島 渉) 2Pos410
Nakashima, Yuji (中島 裕司) **3Pos402**
Nakasone, Yusuke (中曽根 祐介) **2SHA-3**
1H1448
1Pos409
2Pos095
Nakata, Akito (中田 壮人) **3Pos003**
Nakata, Yoshiki (中田 吉紀) 1Pos412
1Pos413
1Pos414
1Pos418
Nakatani, Kazuhiko (中谷 和彦) 2Pos054
Nakatani, Naoki (中谷 真規) 3Pos092
Nakatsumi, Hirokazu (中津海 洋一) 1Pos065
Nakayama, Kazuhisa (中山 和久) 1Pos064
3Pos327
Nakayama, Keiichi I. (中山 敬一) 1Pos065
Nakayama, Koji (中山 浩次) 2M1542
1Pos016
1Pos057
Nakayama, Takahiro (中山 隆宏) 1Pos031
Nakayama, Yohei (中山 洋平) 2E1436
1Pos210
Nakayama, Yoshitaka (中山 義敬) **2G1530**
Nakazawa, Shigeaki (中澤 重顕) 2Pos027
Nakazawa, Takanobu (中澤 敬信) 3SFA-5
Nakazawa, Yuki (中澤 友紀) **2Pos301**
Nakjima, Hiroto (中島 碩士) **3Pos041**
Namatame, Hirofumi (生天目 博文) 1M1330
Namba, Keiichi (難波 啓一) 2A1606
2M1500
2M1518
2M1606
1Pos014
1Pos036
1Pos212
1Pos215
1Pos216
2Pos307
Namba, Toshinori (難波 利典) **3Pos313**
Nango, Eriko (南後 恵理子) 1L1512
Narai, Syun (奈良井 峻) 3Pos059
Narikawa, Rei (成川 礼) **2SHA-4**
2Pos096
Narita, Akihiro (成田 哲博) **2SBA-5**
1Pos204
3Pos040
Narita, Haruka (成田 晴香) **1K1430**
Narita, Hirotaka (成田 宏隆) **3SDA-4**
1Pos044
Narita, Tomoyuki (成田 知恕) **1D1430**
1D1524
Naruse, Keiji (成瀬 恵治) 1A1448
2A1530
1Pos206
3Pos306
3Pos404
Naruse, Taichi (成瀬 太智) 2Pos020
3Pos050
Natarajan, Meenubharathi (Natarajan Meenubharathi) 2SBP-3
1A1430
Natsume, Yuno (夏目 ゆうの) 2Pos083
Negami, Tatsuki (根上 樹) 2SGA-4
2J1518
Nemoto, Aki (根本 亜季) 2Pos088
Nemoto, Mitsutaka (根本 充貴) 1Pos027

Nemoto, Sayaka (根元 紗也加) 2Pos024
Ngo, Kien X (ンゴー キエン) 1Pos222
Ngo, Kien Xuan (んごー すあん きえん) **1Pos223**
Nguyen, Viet Cuong (グェン ヴェト クーン) 2Pos060
Nie, Qing-Miao (Nie Qing-Miao) 1Pos225
Nihei, Chiho (二瓶 千穂) 3Pos406
Niina, Toru (新稲 亮) 1J1536
1Pos074
2Pos047
3Pos072
Niioka, Hirohiko (新岡 宏彦) 1Q1524
Nikuni, Tetsuro (二国 徹郎) 1Pos309
Nin, Fumiaki (任 書晃) 1SEA-8
Ninomiya, Yuzo (二ノ宮 裕三) 3SEA-2
Nisha Bte Mohd, Rafiq (Nisha Bte Mohd Rafiq) 2SBP-3
Nishi, Hafumi (西 羽美) 1Pos072
3Pos206
Nishibe, Nobuyuki (西部 伸幸) 2Pos226
3Pos417
Nishihara, Hiroshi (西原 寛) 3Pos031
Nishihara, Yasutaka (西原 泰孝) 2E1500
Nishikawa, Kaori (西川 香里) 1O1342
2Pos213
Nishikawa, Keigo (西川 圭吾) 2Pos024
Nishikawa, Koji (西川 幸志) **2SOA-2**
Nishikawa, Masatoshi (西川 正俊) 2C1448
Nishikino, Keizaburo (錦野 敬三郎) **3Pos213**
Nishikino, Tatsuro (錦野 達郎) 1Pos217
Nishimori, Hiraku (西森 拓) 1Pos104
1Pos108
1Pos109
2Pos051
2Pos102
2Pos318
Nishimoto, Etsuko (西本 悦子) 2Pos005
3Pos062
Nishimura, Chiaki (西村 千秋) **2M1436**
Nishimura, Masaki (西村 正樹) 1J1330
Nishimura, Sarina (西村 彩莉奈) 3Pos319
Nishimura, Yoshifumi (西村 好史) 2Pos103
Nishimura, Yukako (西村 有香子) 2SBP-3
1A1430
Nishina, Saori (仁科 咲織) 2A1530
Nishino, Kunihiko (西野 邦彦) **1SGA-6**
1G1512
Nishino, Yoshinori (西野 吉則) **3SGA-4**
Nishio, Takuhiro (西尾 卓広) 1Pos103
Nishio, Tkashi (西尾 天志) 2Pos042
Nishioka, Noriko (西岡 典子) 1Q1418
Nishiori, Daiki (西織 大輝) 3Pos031
Nishiyama, Makoto (西山 真) 1Pos042
Nishiyama, Masayoshi (西山 雅祥) 2Pos072
Nishiyama, Masayoshi (西山 雅祥) **3SBA-1**
1A1448
1Pos206
Nishiyama, Nobuaki (西山 宣昭) 2O1554
Nishiyama, So-ichiro (西山 宗一郎) **3Pos049**
Nishiyama, Soichiro (西山 宗一郎) 2C1500
Nishizaka, Takayuki (西坂 崇之) 3SKA-1
1E1512
1E1600
Nishizawa, Hiroaki (西澤 宏晃) **2Pos053**
Nishizumi, Hirofumi (西住 裕文) 3SEA-5
Niwa, Shinsuke (丹羽 伸介) 2SAA-1
2Pos220
Nobata, Rina (野畑 李奈) **1C1536**
Nobunaga, Yuta (延永 裕太) 2A1412
Noda, Chizuru (野田 千鶴) 3Pos403
Noda, Naohiro (野田 尚宏) 2O1618
3Pos405
Noda, Takeshi (野田 岳志) 2SBA-2
Noga, Akira (苗加 彰) 2Pos301
Nogi, Terukazu (禾 晃和) **1SGA-2**
Noguchi, Hiroki (野口 大貴) **1J1500**
Noguchi, Hiroshi (野口 博司) **2G1424**
Noguchi, Naoto (野口 直人) **2Pos101**
Noguchi, Takumi (野口 巧) **3SHA-6**
1F1342
3Pos034
3Pos035
3Pos036
3Pos037
3Pos038
Noguchi, Yoh (Noguchi Yoh) 2Pos031
Noji, Hiroyuki (Noji Hiroyuki) 2E1448
Noji, Hiroyuki (野地 博行) 1SKA-4
1SIP-2
1C1524
1E1406
1G1354
1O1548
1Q1342
2E1412
2E1424
1Pos079
1Pos208
1Pos209
1Pos211
1Pos407
1Pos410
2Pos069
3Pos085
Noji, Tomoyasu (野地 智康) 1H1430
Nomura, Kento (野村 健人) 2Pos070
Nomura, Nobuhiko (野村 暢彦) 1G1342
Nomura, Shin-ichiro M. (野村 M. 慎一郎) 3Pos412

Nomura, Takashi (野村 高志) 1K1536
Nonomura, Keiko (野々村 恵子) **1SEA-7**
Norris, James (Norris James) 3SHA-4
Nosaka, Michiko (野坂 通子) **2J1606**
Nowaczyk, Marc (ノヴァチク マーク) 3SDA-2
Nozaki, Shohei (野崎 梢平) 3Pos327
Nozaki, Tadasu (Nozaki Tadasu) 1Pos110
Nozawa, Kento (野澤 剣人) 3Pos326
Nuemket, Nipawan (Nuemket Nipawan) **1Pos068**
Numao, Manabu (沼尾 学) 1A1406
Numoto, Nobutaka (沼本 修孝) **1M1354**
Nureki, Osamu (濡木 理) 1M1406
2G1606
2H1424
3Pos020

Oasa, Sho (大浅 翔) 2Pos033
Oba, Wato (大場 倭利) 2Pos066
Obana, Nozomu (尾花 望) 1G1342
Obata, Nobuaki (尾畑 伸明) 2O1412
Obino, Dorian (Obino Dorian) 2Pos319
Obuse, Chikashi (小布施 力史) 2Pos421
Ochiai, Hiroshi (落合 博) 1Pos106
Ochiai, Yuto (落合 悠人) **1Q1342**
Oda, Akinori (小田 明典) **3Pos071**
Oda, Masayuki (織田 昌幸) 1L1500
2K1400
2K1518
Oda, Toshiro (小田 俊郎) 1SDA-3
1Pos204
3Pos040
Oda, Toshiyuki (小田 賢幸) 2SBA-4
Odaka, Masao (尾高 正朗) 1Pos203
1Pos311
1Pos315
1Pos319
1Pos412
1Pos413
1Pos414
1Pos415
1Pos418
1Pos419
3Pos095
3Pos409
3Pos410
3Pos411
3Pos413
Odaka, Shouko (小高 祥子) 1E1600
Oe, Suzu (大江 紗) 1Pos317
Ogasawara, Naotake (小笠原 直毅) 2O1448
Ogata, Hideaki (緒方 英明) **3Pos058**
Ogawa, Akira (小川 輝) 1Pos065
Ogawa, Haruo (小川 治夫) 2Pos422
Ogawa, Sayaka (小川 紗也香) 1SBP-2

Ogawa, Tadayuki (小川 覚之) **2SIP-1**
Ogawa, Taisaku (小川 泰策) **1O1448**
Ogawa, Tomohisa (小川 智久) 1Pos018
Ogawa, Tomoka (小川 倫加) 2Pos207
Ogino, Seiya (荻野 聖也) 1SBP-6
Ogiue-Ikeda, Mari (池田荻上 真理) 1Pos318
Ogura, Takashi (小倉 尚志) 2SOA-2
2SOA-3
Ogura, Toshihiko (小椋 利彦) 3Pos401
Oh, Jaeho (Oh Jaeho) 3SIA-3
Oh-oka, Hirozo (大岡 宏造) 1SRA-4
1H1430
3Pos024
3Pos033
Ohara, Kazuhisa (大原 和久) **3Pos088**
Ohara, Masayuki (大原 正行) 2Pos076
Ohashi, Kaoru (大橋 郁) 1O1500
Ohashi, Ryo (大橋 燎) 2J1436
2Pos029
Ohata, Takatoshi (大畑 貴聖) **2Pos095**
Ohba, Shotaro (大庭 将太郎) 1E1536
Ohba, Yasunori (大庭 裕範) 1Pos201
Ohmachi, Masashi (大町 優史) 1Pos226
1Pos228
Ohnuki, Jun (大貫 隼) 1L1354
1Pos013
2Pos013
Ohnuma, Kiyoshi (大沼 清) **2C1412**
1Pos323
Ohshiro, Takahito (大城 敬人) **1SKA-5**
Ohta, Akane (太田 茜) 1Pos306
Ohta, Noboru (太田 昇) 3Pos069
Ohta, Yasutaka (太田 安隆) 2Pos320
Ohta, Yoshihiro (太田 善浩) 1G1536
1O1536
Ohta, Yshihiro (太田 義浩) 2Pos080
Ohtani, Yoshio (大谷 芳夫) 1SBP-4
Ohto, Umeharu (大戸 梅治) **3SDA-6**
Ohtsuki, Takashi (大槻 高史) **1SBP-1**
2Pos407
Ohuchi, Hideyo (大内 淑代) 1H1548
Ohue, Masahito (大上 雅史) **1C1448**
3Pos201
Oide, Mao (大出 真央) **1Pos014**
2Pos416
Oikawa, Hiroyuki (小井川 浩之) 3SGA-1
2Pos010
2Pos015
3Pos082
Oikawa, Tsukasa (及川 司) 2Pos326
Oiki, Shigetoshi (老木 成稔) 1SDA-2
2G1554
2Pos079

Oiwa, Kazuhiro (大岩 和弘) 2SMA-2
1E1536
2A1518
2N1530
2Pos204
2Pos209
2Pos212
2Pos214
2Pos227
Oiwa, Kazuhiro (大岩 弘和) 1O1342
Ojima, Kaname (小島 要) 3Pos015
Oka, Natsuki (岡 夏輝) **2Pos098**
Oka, Seiko (岡 征子) 3Pos059
Oka, Yoshiki (岡 芳樹) 1K1418
3Pos077
3Pos078
3Pos088
Okabe, Kohki (岡部 弘基) 1A1354
1D1406
1O1524
2C1518
2D1424
2Pos406
Okada, Kodai (岡田 広大) 2M1542
1Pos016
1Pos057
Okada, Mariko (岡田 眞里子) 1Q1406
2O1500
2Q1554
3Pos216
3Pos312
Okada, Masato (岡田 雅人) 1Pos065
Okada, Tomoko (岡田 知子) 1Pos304
3Pos317
Okada, Yasushi (岡田 康志) **2SBP-2**
2Pos028
2Pos223
2Pos408
2Pos411
2Pos412
2Pos413
2Pos414
Okajima, Akira (Okajima Akira) 1D1548
Okajima, Koji (岡島 公司) 2Pos416
Okajima, Takaharu (岡嶋 孝治) 1A1524
Okamoto, Kenji (岡本 憲二) 2L1400
Okamoto, Yasutada (岡本 泰直) **3Pos036**
Okamoto, Yuko (岡本 祐幸) 1Pos007
1Pos301
Okamura, Yasushi (岡村 康司) 3SDA-4
1Pos044
Okamura, Yuu (岡村 優) **3Pos068**
Okaniwa, Tomoaki (岡庭 有明) **2E1436**
Okano, Taiji (岡野 太治) 1SIP-3
Okazaki, Kei-ichi (岡崎 圭一) **2E1542**
Okazaki, Shigetoshi (岡崎 茂俊) 2F1554
Okazaki, Susumu (岡崎 進) 1J1406
1Pos101
Okazaki, Taku (岡崎 拓) **3SFA-6**
Okimura, Chika (沖村 千夏) **2Pos315**
3Pos324
Okitsu, Takashi (沖津 貴志) 1H1536
2H1606
3Pos045
Okumura, Hisashi (奥村 久士) 1Pos003
1Pos301
2Pos053
Okumura, Mitsutaka (奥村 光隆) 2Pos054
Okuno, Daichi (奥野 大地) 2Pos082
Okuno, Yasushi (奥野 恭史) 1Pos026
Omagari, Katsumi (尾曲 克己) **3Pos052**
Omichi, Kazuki (Omichi Kazuki) 1Pos068
Omori, Satoshi (大森 聡) **1Pos072**
Onagi, Jun (小名木 淳) 1SKA-4
Onami, Shuichi (大浪 修一) **2SBP-7**
1Pos325
Onishi, Kizashi (大西 萌) **1Pos069**
Ono, Junichi (小野 純一) **2Pos103**
2Pos104
Ono, Katsuhiko (小野 勝彦) 1H1548
Ono, Kenjiro (小野 賢二郎) 2L1436
Ono, Ryota (小野 良太) **2Pos090**
Onodera, Yasuhito (小野寺 康仁) 2Pos326
Onoe, Sakura (尾上 さくら) **1Pos219**
Onogi, Shiori (小野木 汐里) 3Pos049
Onoue, Yasushiro (尾上 靖宏) 2E1500
Ooka, Koji (大岡 紘治) **1L1448**
Ookubo, Akino (大久保 明野) 1SAA-4
Oosaki, Marika (大﨑 麻里加) 1G1548
Or Rashid, Md. Mamun (オア ラシッド エムディ マムン) **1Pos090**
Orf, Gregory S. (Orf Gregory S.) **1SRA-3**
Oroguchi, Tomotaka (苳口 友隆) **1J1342**
1Pos014
2Pos416
Osaki, Toshihisa (大崎 寿久) 1Pos099
Osawa, Masanori (大澤 匡範) 1M1406
2G1606
Oshima, Hiraku (尾嶋 拓) 2J1500
1Pos038
Oshima, Taku (大島 拓) 2O1448
Ota, Kunitaka (太田 匡隆) 2J1412
Ota, Takeru (太田 岳) 1SEA-8
Otomo, Seiu (大友 征宇) **1SRA-1**
Otsuka, Yumeto (大塚 夢斗) **2Pos021**
2Pos022

Ouchi, Kana (大内 華奈) **1Q1330**
Oue, Tatsuya (大上 達也) 1Pos404
Ouyang, Dongyan (欧陽 東彦) **3Pos063**
Oyama, Kotaro (大山 廣太郎) 2N1424
Oyama, Ryo (小山 糧) **3Pos046**
Oyamada, Hideto (小山田 英人) 2Pos422
Ozaki, Shogo (尾崎 省吾) **3SKA-5**
Ozawa, Kentaro (小澤 健太郎) **2Pos317**
Ozawa, Takeaki (小澤 岳昌) 3Pos023
Pal, Ayan (Pal Ayan) 2Q1606
Panina, Yulia (Panina Yulia) **2Pos064**
Pappas, Charalampos G (Pappas Charalampos G) 2Q1606
Parkin, Dan (パーキン 暖) 1E1354 **1Pos213**
Parvez, Farliza (パーベツ、ファーリザ、) **1Pos086**
Patapoutian, Ardem (Patapoutian Ardem) 1SEA-7
Pawlak, Krzysztof (Pawlak Krzysztof) 3Pos058
Petretto, Emanuele (Petretto Emanuele) 2Pos062
Pham, Tien Lam (ファム ティエン ラム) 2Pos060
Phonexay, Vongsaksid (ボンサクシッド ポーンサイ) 2J1606
Pinnola, Alberta (Pinnola Alberta) 1F1418
Plotnikov, Sergey V. (Plotnikov Sergey V.) 2SBP-3 1A1430
Popp, D (Popp D) 2Pos110
Porter-Goff, Mary E. (Porter-Goff Mary E.) 1SKA-2
Prevost, Chantal (Prevost Chantal) 2Pos045
Pushkarev, Alina (Pushkarev Alina) 1F1512
Quax, Tessa (Quax Tessa) 2E1530
Rafiq, Nisha Bte Mohd (Rafiq Nisha Bte Mohd) 1A1430
Rajiv, Kumar (Rajiv Kumar) 2Pos094
Rak, Malgorzata (Rak Malgorzata) **1SEA-6**
Rakers, Christin (Rakers Christin) 2J1400
Re, Suyong (李 秀栄) **2J1500** 1Pos038
Reading, Eamonn (Reading Eamonn) 2G1436
Reijerse, Edward (Reijerse Edward) 3Pos058
Ri, Seirin (李 聖林) 2Pos318
Rikitake, Masato (力武 柾人) 2J1606
Robinson, Bob (Robinson Bob) **1SMA-6**
Robinson, R. (Robinson R.) 2Pos228
Robinson, Robert C. (Robinson Robert C.) 1Pos060
Roca-Cusachs, Pere (Roca-Cusachs Pere) **2SEA-1**
Ross, Jennifer L. (Ross Jennifer L.) 1Pos050
Rudiger, Olaf (Rudiger Olaf) 3Pos058
Ruiz-Lopez, Manuel F (Ruiz-Lopez Manuel F) 2Pos003
Rögner, Matthias (レグナー マティアス) 3SDA-2
Sabe, Hisataka (佐邊 壽孝) 2Pos326
Sadakane, Kei (貞包 慧) 2Pos224 **2Pos225**
Sadakane, Koichiro (貞包 浩一朗) 2Pos043 3Pos311
Sagawa, Misaki (佐川 美咲) **2Pos227**
Sagawa, Takashi (佐川 貴志) 2SAA-1 **2Pos410** 2Pos418
Saha, Samiron Kumar (サハ サミロン クマール) 1Pos087
Saiki, Masatoshi (佐伯 政俊) 1K1406
Saikusa, Kazumi (七種 和美) 3Pos065
Saio, Tomohide (斉尾 智英) **1SGA-4**
Saio, Tomohide (斎尾 智英) 2L1530
Saito, Harumi (斎藤 治美) **3SEA-5**
Saito, Hirohide (齊藤 博英) **2SMA-6**
Saito, Kai (斉藤 開) 3Pos419
Saito, Keisuke (斉藤 圭亮) **3SHA-5** 1F1406
Saito, Mami (齋藤 真美) **2Pos030**
Saito, Mineki (齊藤 峰輝) 2Pos324
Saito, Minoru (斎藤 稔) 1Pos308 3Pos089
Saito, Nen (斉藤 稔) 1SAA-1 **1SAA-3** 3Pos211
Saito, Toru (齋藤 徹) 1Pos067
Saitou, Syoma (斎藤 翔馬) 2Pos316
Saka, Tatsuya (坂 達也) 1Pos309 1Pos314
Sakaguchi, Miyuki (坂口 美幸) **2O1606**
Sakai, Karibu (酒井 加里武) **2Pos216**
Sakai, Kasumi (酒井 佳寿美) 1H1548
Sakai, Kenji (堺 健司) 1SBP-5
Sakai, Makoto (酒井 誠) 1Pos404 **1Pos406**
Sakai, Takahiro (酒井 貴弘) 1F1354
Sakai, Tatsuya (堺 立也) **2Pos324**
Sakai, Yoko (酒井 洋子) 2Pos219
Sakai, Yui (酒井 結衣) **2F1448**
Sakakibara, Hitoshi (榊原 斉) **2N1542** 2Pos227
Sakakibara, Yuki (榊原 由季) 2L1500
Sakakura, Masayoshi (坂倉 正義) 1Pos038
Sakamaki, Yusuke (酒巻 裕介) 1Pos052
Sakamoto, Hiroshi (坂本 寛) 1J1548
Sakamoto, Kazufumi (坂本 一史) **3Pos095**
Sakamoto, Kazuhumi (坂本 一史) 1Pos203
Sakamoto, Kotaro (坂本 航太郎) **1L1430**
Sakamoto, Naoaki (坂本 尚昭) 1Pos106 2Pos051
Sakamoto, Ryota (坂本 遼太) **1O1354**
Sakamoto, Shingo (坂本 眞伍) 1SKA-4 **1Pos407**
Sakamoto, Shinichi (坂本 信一) 1SOA-4
Sakamoto, Taiichi (坂本 泰一) **2Pos040**
Sakamoto, Tetsuro (阪本 哲郎) **2Pos049**

Sakamoto, Yasuko (坂本 泰子) **1Pos054**
Sakano, Hitoshi (坂野 仁) 3SEA-5
Sakano, Taichi (坂野 太一) 2A1542
Sakata-Sogawa, Kumiko (十川 久美子) 2A1500
2Pos419
Sakiyama, Tomoko (崎山 朋子) **3Pos217**
Sako, Yasushi (佐甲 靖志) 1SKA-6
1O1512
2G1618
2L1400
2O1530
2Q1554
3Pos303
Sakuma, Koya (佐久間 航也) **1K1548**
Sakuma, Mayuko (佐久間 麻由子) 2A1618
Sakuma, Morito (佐久間 守仁) 1C1524
1Pos079
Sakumura, Yuichi (作村 諭一) 2Pos315
Sakurai, Keisuke (櫻井 啓介) 1G1512
Sakurai, Minoru (櫻井 実) 1Pos032
3Pos056
3Pos057
Sakurai, Takashi (櫻井 貴志) 3Pos418
Sakurai, Takashi (櫻井 隆) 2Pos422
Sakurai, Toshihiro (櫻井 俊宏) 1J1524
Sakurazawa, Shigeru (櫻沢 繁) 2Pos317
Sakuta, Hiroki (作田 浩輝) **3Pos092**
Sakuta, Nanami (作田 菜奈美) 3SDA-1
Saleh, Arwansyah (され あるわんしゃ) 3Pos039
Saleh, Muhammad Arwansyah (Saleh Muhammad Arwansyah) **2Pos031**
Samejima, Masahiro (鮫島 正浩) 1Pos046
Samsonov, Mikhail (Samsonov Mikhail) 3Pos304
Sanematsu, Keisuke (實松 敬介) **3SEA-2**
Sanjeevi, Sivasankar (Sanjeevi Sivasankar) 2Pos401
Sano, Daisuke (佐野 大輔) **2Pos056**
2Pos057
Sano, Masaki (佐野 雅己) 2Pos325
Sano, Mio (佐野 美桜) **3Pos077**
Sasai, Masaki (Sasai Masaki) 1Pos110
3Pos214
3Pos220
Sasai, Masaki (笹井 理生) 1Pos071
1Pos225
2Pos006
2Pos050
2Pos065
3Pos208
Sasajima, Yuya (笹嶋 雄也) **1A1418**
Sasaki, Akira (佐々木 章) **2O1618**
Sasaki, Kazuo (佐々木 一夫) 1E1524
1O1330
Sasaki, Takanori (佐々木 貴規) 1Pos107
3Pos007
3Pos008
3Pos009
3Pos012
3Pos207
Sasaki, Takuma (佐々木 拓磨) **1H1406**
Sasaki, Toshikazu (佐々木 寿算) 3Pos045
Sasaki, Yuji (佐々木 裕次) 2K1530
3Pos027
3Pos068
3Pos069
Sasaki, Yuji C. (佐々木 裕次) 3Pos016
Sato, Daisuke (佐藤 大輔) 2Pos016
2Pos019
3Pos026
Sato, Fumiaki (佐藤 史彬) **1C1406**
Sato, Hirofumi (佐藤 博文) 1Pos317
Sato, Hiroyuki (佐藤 博之) **3Pos055**
Sato, Hisako (Sato Hisako) 1L1524
Sato, Kazunobu (佐藤 和信) 2Pos027
Sato, Keiko (佐藤 啓子) **1Pos057**
Sato, Keita (佐藤 恵太) **1H1548**
Sato, Kyosuke (佐藤 恭介) **1Pos063**
Sato, Nobuhiro (佐藤 信浩) 1Pos006
1Pos052
Sato, Ryuma (佐藤 竜馬) 2F1500
2Pos055
2Pos093
Sato, Shinya (佐藤 慎哉) **2F1518**
Sato, Shunsuke (佐藤 俊輔) 2Pos320
Sato, Shuntaro (佐藤 駿太郎) **2Pos420**
Sato, Takaaki (佐藤 尭彰) **1Pos051**
Sato, Takato (佐藤 昂人) 1L1354
2Pos013
Sato, Takeshi (佐藤 毅) **1SIA-2**
2G1618
Sato, Teppei (佐藤 哲平) 2F1424
Sato, Tomoyasu (佐藤 友保) **1Pos209**
Sato, Wataru (佐藤 航) **2L1530**
Sato, Yuko (佐藤 優子) 2Pos415
2Pos420
Sato, Yusuke (佐藤 佑介) 3Pos402
3Pos412
Sato, Yuta (佐藤 優太) 1J1512
Satoh, Tadashi (佐藤 匡史) 3Pos080
Satozono, Hiroshi (里園 浩) 3Pos071
Sawada, Hiroki (澤田 浩樹) **1C1524**
Sawada, Kazuaki (澤田 和明) **2SFA-1**
Sawada, Ryusuke (澤田 隆介) 1Pos105
Sawada, Yasuyuki (澤田 康之) **2G1518**
Sawai, Satoshi (澤井 哲) **1SAA-1**
1SAA-3
2A1400

3Pos211
3Pos316
Schlau-Cohen, Gabriela S. (Schlau-Cohen Gabriela S.) 1F1418
Schlesinger, Ramona (Schlesinger Ramona) 2G1436
Scipion, Clement P. M. (Scipion Clement P. M.) **1Pos060**
Sehara, Atsuko (瀬原 淳子) **3SBA-5**
Seiriki, Kaoru (勢力 薫) 3SFA-5
Seki, Natsuki (関 菜月) 3Pos095
Seki, Yasutaka (関 安孝) **2M1448**
Sekiguchi, Hiroshi (関口 博史) **1SDA-1**
2Pos045
3Pos016
3Pos068
3Pos069
Sekiguchi, Taichiro (関口 太一朗) **3Pos080**
Sekiguchi, Tetsushi (関口 哲志) 3Pos418
3Pos419
Sekine, Shun-ichi (関根 俊一) 2Q1518
Selvarajan S, Ashwin (Selvarajan S Ashwin) **1Pos110**
Senda, Hisamichi (千田 久通) 1Pos104
Seno, Keiji (妹尾 圭司) 2Pos099
Seo, Daisuke (瀬尾 悌介) **2L1518**
Seo, Sangjae (Seo Sangjae) **2G1448**
Seto, Ayaka (世戸 彩華) 2Pos084
Shan, Shu-ou (シャン シュ オウ) 2M1618
Sharmin, Sabrina (シャーミン サブリナ) 2G1400
1Pos096
Sheetz, Michael (Sheetz Michael) **2SEA-5**
Shen, Jian-Ren (沈 建仁) 3SHA-3
1F1330
1F1342
Shen, Yi-Chung (沈 宜中) 2F1530
3Pos045
Shi, Beini (時 ベイニ) **2D1424**
Shi, Shidong (Shi Shidong) 2SBP-3
1A1430
Shiba, Kogiku (柴 小菊) 1A1536
2A1542
Shibahara, Osamu (芝原 理) 1M1354
Shibai, Atsushi (芝井 厚) **2O1436**
Shibasaki, Koji (柴崎 貢志) 2C1518
Shibasaki, Yusuke (柴﨑 雄介) **3Pos089**
Shibata, Daisuke (柴田 大輔) 1A1536
Shibata, Kaoru (柴田 薫) 1SDA-3
1M1430
Shibata, Kosei (柴田 耕生) **1H1448**
Shibata, Mikihiro (柴田 幹大) **2SIP-3**
1D1448
2Pos403
3Pos013
Shibata, Satoshi (柴田 敏史) **2M1542**
1Pos016
Shibata, Takahiro (柴田 貴弘) 1G1536
Shibata, Tatsuo (柴田 達夫) **2SBP-5**
3Pos093
3Pos094
Shibata, Yutaka (柴田 穣) **3SHA-2**
Shibayama, Naoya (柴山 修哉) **1SDA-4**
3Pos068
Shibukawa, Atsushi (渋川 敦史) 2H1530
Shichida, Yoshinori (七田 芳則) 1H1548
2Pos101
3Pos045
Shida, Emika (志田 枝実香) **2Pos080**
Shigematsu, Hideki (重松 秀樹) 3SDA-3
Shigemura, Noriatsu (重村 憲徳) 3SEA-2
Shigemura, Shunta (重村 竣太) **2H1448**
Shigenobu, Shuji (重信 秀治) 1A1536
Shigeta, Arisu (重田 安里寿) 1G1430
2H1412
Shigeta, Yasuteru (Shigeta Yasuteru) 1L1330
Shigeta, Yasuteru (重田 育照) 1SDA-7
2SKA-4
1L1430
2F1500
Shigihara, Eiji (鴫原 永之) 3Pos419
Shigyo, Kazuki (執行 航希) 2D1542
Shih, Chi-Tin (施 奇廷) **1D1536**
Shihoya, Wataru (志甫谷 渉) 2H1424
Shiina, Masaaki (椎名 政昭) 2Pos419
Shiki, Atsushi (志岐 敦) **3Pos310**
Shima, Fumi (島 扶美) 1L1512
Shima, Tomohiro (島 知弘) 1E1430
1K1430
2Pos206
2Pos216
Shimabayashi, Masato (島林 真人) 1Q1524
Shimabukuro, Katsuya (島袋 勝弥) 2Pos315
Shimada, Atsuhiro (島田 敦広) **1M1448**
Shimada, Ichio (嶋田 一夫) 1SGA-5
1J1430
2G1606
1Pos037
Shimada, Naotaka (島田 尚鷹) **2Pos407**
Shimada, Satoru (島田 悟) 1G1548
Shimada, Yuichio (嶋田 友一郎) **3Pos034**
Shimamoto, Yuta (島本 勇太) **1SMA-3**
Shimanaka, Koki (嶋中 洸貴) 1Pos401
Shimato, Takuya (島戸 拓也) **1C1430**
1L1418
Shimizu, Hirofumi (清水 啓史) 1Pos015
Shimizu, Kanade (清水 奏) 1M1354
Shimizu, Keisuke (清水 啓佑) 2Pos076
Shimizu, Kentaro (清水 謙多郎) 1J1512

1Pos041
1Pos042
1Pos051
3Pos053
Shimizu, Masahiro (清水 将裕) 1D1430
1D1524
2Pos047
Shimizu, Masahiro (清水 政宏) **1Pos007**
Shimizu, Nobutaka (清水 伸隆) **2SKA-3**
1Pos022
Shimizu, Takashi (清水 貴史) **1SHA-6**
Shimizu, Toshiyuki (清水 敏之) 3SDA-6
Shimizu, Yoshiyuki (清水 良幸) **3Pos042**
Shimizu, Youske (清水 洋輔) **2Pos218**
Shimizu, Yuki (清水 悠生) 3Pos082
Shimo, Rieko (下 理恵子) 2N1518
2Pos215
Shimono, Kazumi (下野 和実) 2H1606
2Pos081
Shimoyama, Hiromitsu (下山 紘充) **1Pos010**
Shimozawa, Togo (下澤 東吾) 2N1424
Shimura, Ryo (志村 諒) **1Pos042**
Shin, Hye-Won (申 惠媛) 1Pos088
Shin, Masashi (進 正志) 1Pos055
Shinagawa, Ryota (品川 遼太) **1O1330**
Shindo, Asako (進藤 麻子) **1SMA-2**
Shindo, Yuki (新土 優樹) 2O1530
Shingyoji, Chikako (真行寺 千佳子) 2Pos210
Shino, Genki (篠 元輝) **2Pos047**
Shinobu, Ai (信夫 愛) **2E1500**
Shinoda, Toshiyuki (篠田 稔之) 3Pos032
Shinoda, Wataru (篠田 渉) **2SGA-5**
1J1406
2G1448
1Pos101
Shinohara, Ken-ichi (篠原 健一) 3Pos416
Shinohara, Yuta (篠原 雄太) **2K1542**
Shinozawa, Tomoki (篠沢 智伎) **1K1330**
Shintaku, Hirofumi (新宅 博文) 1E1536
Shintaku, Hirohumi (新宅 博文) 2Pos217
Shintani, Seine (新谷 正嶺) **2N1412**
Shinzawa-Itoh, Kyoko (伊藤･新澤 恭子) 3Pos004
Shinzawa-Itoh, Kyoko (伊藤（新澤） 恭子) **1G1548**
Shioi, Takuma (塩井 拓真) 2N1518
2Pos215
Shionyu, Masafumi (塩生 真史) 1Pos018
3Pos203
3Pos205
Shiraga, Misaki (白髪 美咲) 2Pos227
Shirai, Nobu C. (白井 伸宙) **1Pos075**
Shirai, Tsuyoshi (白井 剛) 1Pos018
2Pos026
3Pos203
Shiraki, Takaharu (白木 天晴) **2Q1542**
Shirasu, Mika (白須 未香) **3SEA-6**
Shiro, Yoshitsugu (城 宜嗣) **2SOA-1**
1K1536
3Pos017
Shiroguchi, Katsuyuki (城口 克之) **3SFA-4**
1O1448
Shirota, Matsuyuki (城田 松之) **1Q1548**
Shirouzu, Mikako (白水 美香子) 3SDA-3
Shoji, Mikio (庄子 幹郎) 2M1542
1Pos016
Shoji, Mitsuo (Shoji Mitsuo) 1L1330
Shoji, Mitsuo (庄司 光男) **1SDA-7**
2Pos054
Shoji, Shuichi (庄子 習一) 3Pos418
3Pos419
Shomura, Yasuhito (庄村 康人) **3SDA-5**
Siga, Miyuki (志賀 美由貴) 2Pos316
Singh, Manish (Singh Manish) **1F1512**
Siomi, Mikiko (塩見 美喜子) 1K1430
Sitia, Roberto (Sitia Roberto) 1SGA-3
Skamoto, Masayuki (坂本 雅行) 1F1536
Skrbic, Tatjana (Skrbic Tatjana) 2Pos062
Slevin Ohama, Hana (スレヴィン大浜 華) **1Pos303**
Smith, Adam W. (Smith Adam W.) **1SIA-5**
So, Masatomo (宗 正智) 2L1424
Soda, Kazuya (曽田 和也) 2Pos202
Soe, Tet Htut (ソー テタット) 1SBP-1
Soga, Naoki (曽我 直樹) 1C1524
1G1354
1Pos207
2Pos014
2Pos069
Soga, Tomoyoshi (曽我 朋義) 1O1500
Sokabe, Masahiro (Sokabe Masahiro) 3Pos304
Sokabe, Masahiro (曽我部 正博) **2SEA-4**
2G1518
Soma, Mika (相馬 ミカ) 1Pos318
Song, Chihong (ソン チホン) 1Pos009
2Pos404
Sonoyama, Masashi (園山 正史) 2Pos022
3Pos006
Sourial, Elizabeth (Sourial Elizabeth) 3Pos087
Sowa, Yoshiyuki (曽和 義幸) **2SAA-4**
1E1500
2C1448
2C1500
2E1518
1Pos219
3Pos049
Srikanta, Chowdhury (Srikanta Chowdhury) 1SHA-5
Srivastava, Arpita (Srivastava Arpita) **1L1406**
Srivastava, Ashutosh (Srivastava Ashutosh) **2J1400**

Standley, Daron M. (Standley Daron M.) 1Pos065
Steinmetz, Michel O. (Steinmetz Michel O.) 2Pos301
Struzik, Zbigniew (スツルジグ ズビグニェフ) 2O1530
Su, Bo-Yu (蘇 柏宇) 2K1424
Su'estugu, Masayuki (末次 正幸) 1C1524
Su'etsugu, Masayuki (末次 正幸) **1SIP-1**
1Q1342
Sudo, Yuki (須藤 雄気) 1SHA-1
1F1524
1F1536
1H1330
1H1536
2H1518
2H1530
2H1606
2Pos024
2Pos056
2Pos086
2Pos087
2Pos089
2Pos090
3Pos010
3Pos043
3Pos044
Suematsu, Yuma (末松 佑麿) 1K1448
Suetaka, Shunji (季高 駿士) **1K1418**
1K1448
3Pos078
Suetake, Isao (末武 勲) **2Pos027**
Suga, Michi (菅 倫寛) **3SHA-3**
Suga, Michihiro (菅 倫寛) 1F1342
Sugano, Yasunori (菅野 泰功) 3Pos014
Sugawa, Mitsuhiro (須河 光弘) 2E1400
1Pos224
Sugawara, Ko (菅原 皓) 1D1406
Sugi, Takuma (杉 拓磨) 1J1330
Sugihara, Takanori (杉原 崇憲) **1J1430**
Sugiki, Toshihiko (杉木 俊彦) 1K1548
Sugimori, Kimikazu (杉森 公一) 1Pos001
Sugimoto, Hayuki (杉本 華幸) **2Pos025**
Sugimoto, Hiroshi (杉本 宏) 3Pos017
Sugimoto, Masahiro (杉本 昌弘) 3Pos207
Sugimoto, Yu (杉本 悠) **3Pos053**
Sugita, Masatake (杉田 昌岳) 1J1330
1Pos020
1Pos021
1Pos059
Sugita, Masatake (杉田 昌武) 1Pos019
Sugita, Yuji (杉田 有治) 1J1448
2J1500
2Q1518
1Pos038
1Pos070
1Pos097
2Pos059
3Pos017
Sugita, Yukihiko (杉田 征彦) **2SBA-2**
Sugiura, Miwa (杉浦 美羽) 3Pos029
Sugiura, Taichi (杉浦 太一) **1G1500**
Sugiura, Yuuki (杉浦 裕樹) 2Pos007
Sugiyama, Ayaka (杉山 文香) 1Pos106
Sugiyama, Hiroshi (杉山 弘) 3Pos412
Sugiyama, Masaaki (杉山 正明) 2L1412
1Pos006
1Pos052
2Pos038
Sugiyama, Rei (杉山 玲) 1M1418
Sugiyama, Shigeru (杉山 成) 2Pos020
2Pos021
2Pos022
3Pos050
Sugiyama, Shogo (杉山 翔吾) **1Pos058**
Sui, Sen-Fang (隋 森芳) **2SBA-6**
Sumi, Tomonari (墨 智成) **2Pos008**
Sumi, Tomonari (高橋 智成) 2Pos026
Sumikama, Takashi (炭竈 享司) 1SDA-2
2G1554
Sumino, Ayumi (角野 歩) **1SDA-2**
1D1448
Sumitomo, Yohei (住友 洋平) 1O1500
Sumiyoshi, Takaaki (住吉 孝明) 1A1500
Sun, Hongzan (孫 洪贊) 1SBP-4
Sun, Yi-Jen (孫 翊仁) **2Pos313**
Sunaga, Fumiko (須永 史子) 1SIP-3
Sunagawa, Masaki (Sunagawa Masaki) 3Pos304
Sunagawa, Naoki (砂川 直樹) 3Pos085
Sunagawa, Naoki (砂川 直輝) 1Pos046
Sunami, Takeshi (角南 武志) 1C1512
Sunami, Tomoko (角南 智子) **3Pos084**
Susaki, Moe (須﨑 萌) **3Pos073**
Sushida, Takamichi (須志田 隆道) 1SAA-4
Suzuki, Akihiro (鈴木 明大) 3SGA-4
Suzuki, Hiroaki (鈴木 宏明) **1SIP-3**
Suzuki, Hiromi (鈴木 博実) **1Pos025**
Suzuki, Hiromu (鈴木 拓) 2H1500
Suzuki, Junji (鈴木 純二) 2Pos422
Suzuki, Kana (鈴木 香菜) 1E1600
Suzuki, Kano (鈴木 花野) 1K1548
3Pos010
Suzuki, Kazushi (鈴木 一史) 2Pos025
Suzuki, Ken-ichi (鈴木 賢一) 1Pos106
Suzuki, Kenichi (鈴木 健一) **1SIA-1**
3Pos022
Suzuki, Kenichi G.N. (鈴木 健一) 2D1412
3Pos327
Suzuki, Madoka (鈴木 団) 1E1330

Suzuki, Motofumi (鈴木 基史) 1Pos078
Suzuki, Satoshi (鈴木 悟) 3SEA-5
Suzuki, Shoko (鈴木 翔子) 2Pos081
Suzuki, Takahiro (鈴木 崇弘) 3Pos318
3Pos325
Suzuki, Takehiro (鈴木 健裕) 2Pos306
Suzuki, Tomohiko (鈴木 知彦) 2Pos021
Suzuki, Toshiharu (鈴木 俊治) 1E1406
2E1412
2E1424
1Pos207
Suzuki, Yuki (鈴木 勇輝) 3Pos412
Suzuki, Yurina (鈴木 柚里奈) 2Pos320
Suzuki, Yuta (鈴木 祐太) 1Pos056
Szostak, Jack W. (Szostak Jack W.) 2Q1606
Tabata, Kazuhito (田端 和仁) 1C1524
1Pos079
1Pos410
Tachi, Yuhei (多知 裕平) **1Pos301**
Tachibanaki, Shuji (橘木 修志) 2Pos099
Tachikawa, Masashi (立川 正志) **1SAA-2**
Tachikawa, Takashi (立川 貴士) 2Pos097
Tada, Chika (多田 千香) **3Pos404**
Tadakuma, Hisashi (多田隈 尚史) **2SMA-4**
2N1500
2Pos105
2Pos423
Tadokoro, Naoki (田所 直樹) **1Pos416**
Taga, Serika (多賀 芹華) **1Pos107**
Tagawa, Seiichi (田川 聖一) 1Q1524
Taguchi, Hayao (田口 速男) 1Pos046
Taguchi, Masahiko (田口 真彦) **2F1400**
Taguchi, Takahisa (田口 隆久) 1C1548
Tahara, Tahei (田原 太平) **2SKA-6**
2O1606
Tahara, Yuhei (田原 悠平) 1E1448
1K1512
Tai, Hulin (太 虎林) 2SOA-3
Tai, Yang (邰 洋) 1Pos024
Taii, Kenichi (泰井 賢一) 2Pos225
2Pos226
3Pos417
Taiji, Makoto (泰地 真弘人) 2Pos055
Taira, Junichi (平 順一) 1J1548
Tajima, Hirotaka (田島 寛隆) **2C1500**
Takaba, Kiyofumi (高場 圭章) 1Pos024
Takabe, Kyosuke (高部 響介) 2Pos314
Takachi, Itsuki (高智 五輝) **3Pos029**
Takada, Miho (高田 美帆) 1SBP-2
Takada, Naoto (高田 直人) 1Pos088
Takada, Shoji (高田 彰二) 2SGA-6
1J1536
2Q1400
2Q1424
1Pos074
1Pos303
2Pos004
2Pos030
2Pos032
2Pos047
2Pos067
2Pos211
3Pos072
Takada, Shyouzi (高田 彰二) 1Pos043
Takagi, Daisuke (高木 大輔) 1F1448
Takagi, Hiroaki (高木 拓明) 2A1424
2O1530
2Pos324
3Pos047
Takagi, Junichi (高木 淳一) 3SDA-1
1Pos009
Takagi, Seiji (高木 清二) **2Pos085**
Takagi, Shin (高木 新) 2H1530
Takahashi, Akihisa (髙橋 昭久) 3SBA-3
Takahashi, Daichi (高橋 大地) **1A1330**
Takahashi, Daiki (高橋 大輝) 1Pos008
Takahashi, Hideo (高橋 栄夫) 1Pos037
1Pos038
Takahashi, Hiroki (高橋 弘喜) 2O1448
Takahashi, Hirona (高橋 広奈) **1Pos404**
1Pos406
Takahashi, Hiroshi (高橋 浩) **1Pos092**
Takahashi, Kazuhiro (高橋 一浩) 2SFA-1
Takahashi, Ken (高橋 賢) 3Pos404
Takahashi, Ken-ichi (高橋 健一) 2Pos026
Takahashi, Masahide (Takahashi Masahide) 3Pos304
Takahashi, Masatsuyo (高橋 正剛) 1Pos022
Takahashi, Masayuki (高橋 正行) 1Pos302
2Pos045
Takahashi, Naoki (高橋 直樹) **1Pos203**
3Pos095
Takahashi, Norimi (高橋 徳実) 1Pos401
Takahashi, Ryoko (高橋 涼子) 1G1548
Takahashi, Satoe (高橋 里枝) 1E1430
Takahashi, Satoshi (高橋 聡) **3SGA-1**
1Q1330
2Pos010
2Pos015
2Pos035
3Pos082
Takahashi, Shigeko (高橋 成子) 1SBP-4
Takahashi, Takuya (高橋 卓也) 1C1406
1C1430
1Q1448
1Q1512
1Q1536

Takahashi, Takuya (高橋 卓也) 2J1424
2Pos058
Takahashi, Teruo (高橋 輝雄) 2Pos411
Takahashi, Yuichiro (高橋 裕一郎) 3Pos044
Takai, Akira (高井 啓) 2Pos408
2Pos413
Takakado, Akira (高門 輝) 1Pos088
Takamiya, Kazunori (高宮 一徳) **2Pos318**
Takamori, Shohta (高森 翔汰) **2Pos201**
Takamori, Shota (高森 翔汰) 2Pos202
Takanashi, Chiaki (高梨 千晶) 2K1530
Takano, Hiroshi (高野 宏) 2J1554
Takano, Jun (高野 純) **1D1512**
Takano, Mitsunori (高野 光則) **1SMA-4**
1E1354
1L1354
1Pos013
1Pos213
2Pos013
Takano, Ryuji (高野 隆治) 1Pos415
1Pos419
3Pos413
Takano, Yu (鷹野 優) **1SDA-8**
1Pos067
3Pos002
Takao, Kazutaka (高尾 和孝) **1Pos109**
Takaoka, Yuta (高岡 祐太) **3Pos322**
Takarada, Masaharu (寶田 雅治) **1O1524**
Takaramoto, Shunki (宝本 俊輝) **1Pos409**
Takase, Yasumichi (高瀬 安迪) **2K1412**
Takashiba, Shogo (高柴 正悟) 1A1448
Takashima, Akihiko (高島 明彦) 3SFA-1
Takashima, Naoki (高嶋 直輝) **3Pos415**
Takasu, Masako (Takasu Masako) 2Pos031
Takasu, Masako (高須 昌子) 1Pos001
1Pos221
2Pos083
Takayama, Riho (高山 理穂) 2H1606
Takayama, Yuki (高山 雄揮) **1Pos104**
Takazaki, Hiroko (髙﨑 寛子) **1Pos015**
Takebe, Gen (建部 厳) 3Pos042
Takebe, Satuki (竹部 皐月) 2Pos016
Takeda, Hanae (武田 英恵) **1K1536**
Takeda, Hiroyuki (武田 洋幸) 2SBA-4
Takeda, Kazuki (竹田 一旗) 1Pos024
Takeda, Kenichi (竹田 健一) **3Pos012**
Takeda, Seiji (武田 晴治) **1J1524**
Takeda, Shuichi (武田 修一) 1Pos204
3Pos040
Takeda, Tetsuya (竹田 哲也) **2A1412**
Takeda, Yuka (竹田 百花) **2Pos096**
Takeda, Yuki (武田 祐希) 2Pos056
Takei, Kohji (竹居 孝二) 2A1412
Takeishi, Naoki (武石 直樹) 1Pos084
Takekawa, Norihiro (竹川 宜宏) **2A1618**
Takemoto, Hiroshi (竹本 寛) **3Pos035**
Takemura, Kazuhiro (竹村 和浩) **2J1448**
Takenaka, Shinji (竹中 慎治) 1H1418
3Pos028
Takeshima, Kazuhiro (竹島 和優) 2Pos208
Takeshima, Tomochika (竹嶋 智親) 2Pos411
Takeshita, Kohei (竹下 浩平) 1Pos044
Taketomo, Yui (竹友 唯) 2J1436
Taketoshi, Makiko (Taketoshi Makiko) 2C1542
Takeuchi, Atsuko (竹内 敦子) 1H1548
Takeuchi, Fusako (武内 総子) 3Pos003
Takeuchi, Koh (竹内 恒) **1SGA-5**
1Pos037
Takeuchi, Nobuto (竹内 信人) **2O1424**
Takeuchi, Reiwat (竹内 レイワ) 2J1436
Takeuchi, Shoji (竹内 昌治) 1Pos099
Taki, Masumi (瀧 真清) 1Pos028
Takiguchi, Kingo (瀧口 金吾) 2Q1618
2Pos072
3Pos092
Takimoto-Kamimura, Midori (上村 みどり) **2SDA-2**
Takinoue, Masahiro (瀧ノ上 正浩) 2Pos048
2Pos049
3Pos402
3Pos412
3Pos420
Takui, Takeji (工位 武治) 2Pos027
Tama, Florence (Tama Florence) **3SGA-6**
1L1406
1M1500
2J1400
1Pos012
Tama, Florence (タマ フロハンス) 1M1512
Tamada, Taro (玉田 太郎) 3Pos084
Tamai, Nobutake (玉井 伸岳) **1Pos091**
Tamaki, Hajime (田巻 初) 3Pos067
Tamakoshi, Masatada (玉腰 雅忠) 1Pos005
1Pos221
Tamba, Yukihiro (丹波 之宏) 1Pos085
Tame, Jeremy (テイム ジェレミー) 1J1500
Tamiaki, Hitoshi (民秋 均) 1SRA-4
Tammana, Farhana (Tammana Farhana) 2Pos217
Tamogami, Jun (田母神 淳) 2H1400
Tamura, Atsuo (田村 厚夫) 2L1412
3Pos066
Tamura, Koichi (田村 康一) **3Pos017**
Tamura, Koji (田村 浩二) 1Q1500
Tamura, Miki (田村 水季) **2Pos321**
Tamura, Tomohiro (田村 具博) 1Pos408
Tan, Cheng (譚 丞) **2SGA-6**
2Pos032

Tanabe, Masatoshi (田邉 優敏) 1O1354
Tanabe, Naoki (田邊 直己) **1Pos067**
Tanaka, Daiki (田中 大器) 3Pos419
Tanaka, Hideaki (田中 秀明) 1SRA-4
3SDA-2
3Pos024
Tanaka, Hideo (Tanaka Hideo) 1D1548
Tanaka, Hiroko (田中 寛子) **2Q1530**
Tanaka, Hiroto (田中 裕人) **2A1518**
Tanaka, Ichiro (田中 伊知朗) **1M1418**
Tanaka, Junko (田中 潤子) 2Pos021
2Pos022
Tanaka, Kozo (田中 耕三) 1D1430
Tanaka, Minami (田中 みなみ) **1A1524**
Tanaka, Natsuki (田中 菜月) 2Pos208
Tanaka, Noriki (田中 登己) 2A1530
Tanaka, Shigenori (田中 成典) **2SDA-5**
Tanaka, Shunsuke (田中 駿介) 2Pos072
Tanaka, Shunsuke (田中 駿介) 2Q1618
Tanaka, Taisei (田中 泰誠) 3Pos401
Tanaka, Toshiki (田中 俊樹) 2K1400
Tanaka, Yasuhito (田中 靖人) 3Pos052
Tanaka, Yoshikazu (田中 良和) 3Pos059
Tanaka, Yoshiki (田中 良樹) 3SDA-1
3Pos014
Tanaka, Yuhei (田中 悠平) 1Pos311
1Pos315
1Pos319
Tanaka, Yuya (田中 有弥) 2Pos057
Tang, Bo (唐 博) 3Pos327
Tang, Qingnan (Tang Qingnan) 3SIA-8
Tani, Tomomi (谷 知己) **3SIA-4**
Tanida, Sakurako (谷田 桜子) **1O1342**
Tanida, Yoshiaki (谷田 義明) **3Pos054**
3Pos055
Tanigawa, Masato (谷川 雅人) **2Pos041**
Taniguchi, Masaki (谷口 雅樹) 1M1330
Taniguchi, Yuichi (Taniguchi Yuichi) 2O1400
Tanii, Takashi (谷井 孝至) 2Pos424
Tanimoto, Taishi (谷本 泰士) 2Pos102
Tanimoto, Yasushi (谷本 泰士) 1SIA-6
1F1448
1G1330
2Pos070
3Pos022
Taoka, Azuma (田岡 東) 1G1342
3Pos322
3Pos323
Taomori, Hirotaka (垰森 大空) 2Pos317
Taruno, Akiyuki (樽野 陽幸) **3SEA-4**
Tasaki, Sohei (田﨑 創平) 2SAA-1
Tate, Shin-ichi (楯 真一) **1SOA-6**
Tateyama, Samu (館山 佐夢) 2F1436
Tatsumi, Hitoshi (辰巳 仁史) **1SEA-2**
Tawa, Keiko (田和 圭子) 1Pos312
Taylor, J. Nicholas (Taylor J. Nicholas) **3SGA-5**
1D1548
Tenno, Takeshi (天野 剛志) 2M1412
Terada, Mika (寺田 美花) **1Pos085**
Terada, Tohru (寺田 透) 2SGA-3
2SGA-4
1J1512
2J1518
1Pos041
1Pos042
1Pos046
1Pos051
3Pos053
Terada, Tomoki P. (Terada Tomoki P.) 3Pos214
Terada, Tomoki P. (寺田 智樹) 1Pos071
1Pos225
2Pos006
Terahara, Naoya (寺原 直矢) 2M1606
1Pos036
1Pos216
Terahara, Yoko (寺原 陽子) 2Pos028
Terai, Yuma (寺井 悠馬) 2Pos094
Terakawa, Tsuyoshi (寺川 剛) **1E1548**
Terakita, Akihisa (寺北 明久) 1SHA-4
Teramoto, Takayuki (寺本 孝行) 1Pos317
Terao, Kyohei (寺尾 京平) 2Pos039
Terashima, Hiroyuki (寺島 浩行) 2E1500
2Pos304
2Pos305
3Pos019
Terayama, Kei (寺山 慧) 1Pos026
Terazawa, Hiroki (寺澤 裕樹) **1Q1512**
Terazima, Masahide (寺嶋 正秀) 1H1448
1Pos409
2Pos095
Terushima, Kosuke (照島 功祐) 2Pos306
Tezuka, Kota (手塚 晃太) 1E1354
Thery, Manuel (Thery Manuel) 2Pos319
Thiagarajan, Visalatchi (Thiagarajan Visalatchi) 2SBP-3
1A1430
Tieleman, D. Peter (Tieleman D. Peter) **1SIA-4**
Tiwari, Sandhya Premnath (Tiwari Sandhya Premnath)
1M1500
Toda, Kinya (東田 欣也) **3Pos087**
Todaka, Reiko (戸高 玲子) 2Pos404
Todoroki, Takuma (轟 拓磨) **1Pos013**
Togashi, Yuichi (冨樫 祐一) 2Pos052
3Pos215
Togawa, Toru (外川 徹) 2Pos218
Tokiwa, Hiroaki (常盤 広明) 1M1354
Tokuhisa, Atsushi (徳久 淳師) **1Pos026**

Tokumitsu, Hiroshi (德光 浩) 1SBP-2
Tokunaga, Makio (徳永 万喜洋) **2A1500**
2Pos419
2Pos420
2Pos421
Tokunaga, Terumasa (徳永 旭将) 1Pos317
Tokunaga, Yuji (徳永 裕二) **1Pos037**
Tokuraku, Kiyotaka (徳楽 清孝) 1Pos227
1Pos302
2Pos316
2Pos321
Tokutsu, Ryutaro (得津 隆太郎) 3Pos030
Toma, Shoko (當間 頌子) 1Pos036
Tomida, Sahoko (富田 紗穂子) **1H1342**
2H1412
Tomii, Kentaro (富井 健太郎) 1Pos011
3Pos204
Tominaga, Motoki (富永 基樹) 2N1400
Tominaga, Taiki (富永 大輝) 1SDA-3
Tominaga, Takashi (Tominaga Takashi) 2C1542
Tominaga, Takashi (冨永 貴志) **2C1554**
2Pos084
Tominaga, Yoko (Tominaga Yoko) 2C1542
Tominaga, Yoko (冨永 洋子) 2C1554
Tomishige, Michio (富重 道雄) 2Pos219
2Pos221
Tomita, Masahiro (冨田 昌弘) 1Pos100
Tomita, Takeo (富田 武郎) 1Pos042
Tomo, Tatsuya (鞆 達也) **3Pos031**
3Pos032
Tomonari, Sayuri (友成 さゆり) 1H1548
Torisawa, Takayuki (鳥澤 嵩征) **2N1530**
Toriumi, Hayato (鳥海 早杜) **1Pos313**
Tosha, Takehiko (當舎 武彦) **3SMA-3**
1K1536
Toshiharu, Suzuki (Toshiharu Suzuki) 2E1448
Toyabe, Shoichi (鳥谷部 祥一) 1Pos082
1Pos083
1Pos210
Toyoda, Atsushi (豊田 敦) 1Pos306
Toyoda, Takahiro (豊田 貴大) 1D1448
Toyofuku, Masanori (豊福 雅典) 1G1342
Toyofuku, Reona (豊福 玲於奈) **3Pos032**
Toyonaga, Takuma (豊永 拓真) 1E1448
1Pos212
Toyoshima, Yoko Y. (豊島 陽子) 1Pos224
Toyoshima, Yu (豊島 有) 1Pos317
Toyota, Taro (豊田 太郎) 2Pos072
Tozawa, Sho (戸澤 奨) 1Pos308
Tsubaki, Motonari (椚木 基成) 1Pos069
2Pos017
3Pos003
3Pos025
Tsubomoto, Risa (坪本 梨沙) 2A1518
Tsuchiya, Masaki (土谷 正樹) 1SEA-1
Tsuchiya, Yuko (土屋 裕子) 1Pos035
Tsuda, Sakae (津田 栄) 2K1530
Tsugane, Mamiko (津金 麻実子) 1SIP-3
Tsuhara, Shoko (津原 祥子) 2L1412
Tsuji, Gakushi (辻 岳志) **1C1512**
Tsujimoto, Takumi (辻本 拓海) **3Pos301**
Tsujiuchi, Yutaka (辻内 裕) **1Pos401**
Tsukada, Keiji (塚田 啓二) 1SBP-5
Tsukamoto, Hisao (塚本 寿夫) **2Pos071**
Tsukamoto, Takashi (塚本 卓) 1H1330
2H1500
2H1554
2H1606
Tsukazaki, Tomoya (塚崎 智也) 3SDA-1
3Pos014
Tsukihara, Tomitake (月原 冨武) 1M1448
Tsukihara, Tomitake (月原 富武) 1G1548
Tsumoto, Kanta (湊元 幹太) **1Pos100**
3Pos092
Tsumoto, Kouhei (津本 浩平) **2SDA-3**
1L1342
1Pos067
3Pos018
3Pos079
Tsuneshige, Antonio (常重 アントニオ) 2Pos026
Tsunoda, Jun (角田 潤) **1Pos009**
Tsunoda, Makoto (角田 誠) 2Pos424
Tsunoda, Satoshi (角田 聡) **2SHA-5**
2H1424
2H1448
3Pos040
Tsunoda, Satoshi P. (角田 聡) 2H1606
Tsunoyama, Taka A. (角山 貴昭) **2D1412**
3Pos327
Tsutsui, Hidekazu (筒井 秀和) 3Pos416
Tsutsumi, Akihisa (包 明久) **2SIP-5**
Tsutsumi, Koji (堤 弘次) **2Pos320**
Tulum, Isil (トゥルム イシル) 1A1418
Uchida, Takeshi (内田 毅) 2L1530
Uchihashi, Takayuki (内橋 貴之) 1SDA-2
2SIP-4
3SGA-3
2D1518
2E1554
1Pos058
2Pos401
3Pos014
Uchikoga, Nobuyuki (内古閑 伸之) **1C1418**
1C1448
1Pos107
3Pos201

Uchiyama, Jumpei (内山 淳平) 2M1530
Uchiyama, Susumu (内山 進) **2SIP-2**
Uchiyama, Taku (内山 拓) 3Pos085
Uda, Koji (宇田 幸司) 2Pos021
Uda, Shinsuke (宇田 新介) 1O1500
Ueda, Hiroki (上田 泰己) 2K1542
Ueda, Kazuyoshi (Ueda Kazuyoshi) 1L1524
Ueda, Kazuyoshi (上田 一義) 1H1536
Ueda, Keisuke (植田 啓介) 2F1542
Ueda, Masahiro (上田 昌宏) 1SKA-6
2A1424
2A1436
2A1448
1Pos322
2Pos074
2Pos082
3Pos047
Ueda, Masahito (上田 正仁) 2D1500
Ueda, Ryuichiro (上田 龍一郎) **1Pos030**
Uehara, Takahiro (上原 貴宏) 3Pos315
Ueki, Noriko (植木 紀子) 2A1554
Ueki, Shoji (植木 正二) 1Pos201
1Pos205
Uemura, Sotaro (上村 想太郎) 1E1430
1K1430
2Pos216
Uene, Shigefumi (上根 滋史) 1G1548
Ueno, Hiroshi (Ueno Hiroshi) 2E1448
Ueno, Hiroshi (上野 博史) 1E1406
1Q1342
2E1424
1Pos009
1Pos079
1Pos208
1Pos209
1Pos210
1Pos211
1Pos410
Ueno, Masaru (上野 勝) 1Pos104
Ueno, Takafumi (上野 隆史) 2SKA-2
Uesaka, Kazuma (上坂 一馬) 1Q1418
Ueta, Tetsuya (上田 哲也) **2Pos087**
Ueta, Tsuyoshi (植田 毅) 2Pos083
Ugarte, Diego (ウガルテ ディエゴ) 1Pos303
2Pos067
Ujisawa, Tomoyo (宇治澤 知代) 1Pos306
Ulijn, Rein V (Ulijn Rein V) 2Q1606
Umeda, Kenichi (梅田 健一) 2D1530
Umeda, Masato (梅田 眞郷) 1SEA-1
Umeki, Nobuhisa (梅木 伸久) 3Pos303
Umena, Yasufumi (梅名 泰史) **1SDA-6**
1F1342
Umeno, Daisuke (梅野 太輔) 2Pos024
Umeno, Keita (梅野 恵太) 3SDA-2
Umetani, Miki (梅谷 実樹) 2D1400
Umezawa, Koji (梅澤 公二) 1Pos013
Umezawa, Naoki (梅澤 直樹) 2Q1530
Unno, Masashi (海野 雅司) 2H1400
2H1542
Urabe, Hitomi (卜部 仁美) **3Pos082**
Urakami, Hiroshi (浦上 弘) 3Pos049
Urano, Ryo (浦野 諒) **1J1406**
Urano, Yasuteru (浦野 泰照) 1SKA-4
1Pos407
Ushioda, Ryo (潮田 亮) 3SDA-1
Utada, Andrew (Utada Andrew) **3SKA-6**
Uwamichi, Masahito (上道 雅仁) **2Pos325**
Uyeda, Taro (上田 太郎) **1SMA-1**
1Pos207
1Pos222
Uyeda, Taro Q.P. (上田 太郎) 1Pos223
1Pos227
2Pos013
2Pos322
Uzawa, Akiko (鵜澤 玲子) 1Pos078
Viasnoff, Virgile (Viasnoff Virgile) **2SBP-4**
1A1430
Vignon, Paul (Vignon Paul) 2Pos203
Virgile, Viasnoff (Viasnoff Virgile) 2SBP-3
Visootsat, Akasit (Visootsat Akasit) **2Pos203**
2Pos206
Voet, Arnout (ヴット アルノウト) 1J1500
Wada, Akimori (和田 昭盛) 1H1536
1H1548
2H1606
3Pos045
Wada, Takeshi (和田 猛) 2Pos040
Wada, Yuko (和田 裕子) 3Pos094
Wakabayashi, Ken-ichi (若林 憲一) 1E1418
2A1554
2Pos075
Wakai, Satoshi (若井 暁) **3SMA-6**
Wakamatsu, Ei (若松 英) 3Pos321
Wakamoto, Takuro (若本 拓朗) 2M1400
Wakamoto, Yuichi (若本 祐一) 1O1430
2D1400
1Pos417
Wakatsuki, Soichi (若槻 壮市) 1Pos064
Wako, Hiroshi (輪湖 博) **1Pos035**
2Pos037
Wallingford, John (Wallingford John) 1SMA-2
Wan, Yue (Wan Yue) 1Q1430
Wang, Mengfan (王 夢繁) **3Pos309**
Wang, Wei (王 瑋) **3Pos305**
Wang, Yao (Wang Yao) 3Pos013
Wang-Otomo, Zheng-Yu (大友 征宇) 1H1418

Wang-Otomo, Zheng-yu (大友 征宇) 3Pos028
Wasano, Koichiro (和佐野 浩一郎) 1E1430
Washio, Takashi (鷲尾 隆) 1D1500
Watabe, Kiyoto (渡部 聖人) 3Pos325
Watanabe, Akimasa (渡邉 顕正) 3Pos030
Watanabe, Bunta (渡辺 文太) 1Pos066
Watanabe, Chiho (渡邊 千穂) **2Pos068**
Watanabe, Go (渡辺 豪) 2Pos320
Watanabe, Hiroki (渡辺 大輝) 2SIP-4
2E1554
2Pos401
Watanabe, Hiroki (渡辺 紘生) 1C1448
Watanabe, Hiroki (渡邉 弘貴) **3Pos420**
Watanabe, Hiroki (渡邊 大貴) **3Pos037**
Watanabe, Hiroshi (渡邉 宙志) **1SHA-3**
Watanabe, Hiroshi (渡邊 宙志) 2H1518
Watanabe, Kazuhide (渡辺 和秀) 2Pos415
Watanabe, Kazunori (渡邉 和則) 1SBP-1
2Pos407
Watanabe, Keiichi (渡邉 啓一) 2L1500
Watanabe, Naoki (渡邊 直希) 1J1330
Watanabe, Rikiya (Watanabe Rikiya) 2E1448
Watanabe, Rikiya (渡邉 力也) **1SKA-3**
1SKA-4
1G1354
1Pos407
2Pos069
Watanabe, Ryo (渡邉 亮) **1E1406**
Watanabe, Satoshi (渡辺 恵) 1Pos320
Watanabe, Satoshi (渡部 聡) **1SGA-3**
3SDA-1
Watanabe, Shigeo (渡部 重夫) **2Pos411**
Watanabe, Shinichi (渡辺 信一) 1Pos028
Watanabe, Shinji (渡辺 信嗣) 1D1512
2D1542
2D1554
Watanabe, Takeshi (渡邉 剛志) 2Pos025
Watanabe, Tomonobu (Watanabe Tomonobu) 2Pos064
Watanabe, Tomonobu (渡邉 朋信) 1SEA-5
2Pos408
Watanabe, Tomonobu (渡邊 朋信) 2D1448
Watanabe, Tomonobu M. (渡邉 朋信) **3SFA-3**
Watanabe, Yukihaya (渡邉 行隼) **1Pos077**
Watanabe, Yukihaya (渡邊 行隼) 1Pos076
Watanabe, Yuta (渡邊 裕太) 1Pos049
Watanabe-Nakayama, Takahiro (中山 隆宏) 2D1554
2L1436
Watari, Masahito (渡 雅仁) **2H1424**
Waz, Shaimaa (Waz Shaimaa) 1Pos056
Wazawa, Tetsuichi (和沢 鉄一) **1D1500**
2D1436
Weber, Stefan (Weber Stefan) 2Pos097
Wen, Jin-Der (Wen Jin-Der) **2SAA-2**
Widyawillis, S. (Widyawillis S.) 2Pos228
Wijerathne, Nadeesha K (Wijerathne Nadeesha K) 2Q1606
Wolf, Matthias (Wolf Matthias) 2M1542
Wolf, Matthias (ウォルフ マティアス) 2SBA-2
Wouters, Staf (ウォウター スタッフ) 1J1500
Wu, Jinglong (呉 景龍) 1SBP-4
Wu, Qiong (呉 瓊) **1SBP-4**
Wu, Stephen (Wu Stephen) 1Pos317
Xiao, Yiling (Xiao Yiling) 2L1448
Xie, Hong-Qing (謝 宏慶) 1O1418
Xu, Chun-Hua (Xu Chun-Hua) 1Pos421
Yabukami, Haruka (藪上 春香) 2Pos415
Yagi, Hirokazu (矢木 宏和) 2SIP-4
3Pos080
Yagi, Toshiki (八木 俊樹) 2Pos207
Yagi-Utsumi, Maho (矢木-内海 真穂) 2M1424
Yaginuma, Hideyuki (柳沼 秀幸) **2Pos412**
Yahagi, Shogo (矢作 祥吾) 3Pos315
Yajima, Junichiro (矢島 潤一郎) 2E1400
1Pos224
Yajima, Kaho (矢嶋 香歩) 2Pos081
Yakushiji, Fabiana Lica (薬師寺 Lica Fabiana) 1Pos009
Yamada, Daichi (Yamada Daichi) 3SAA-2
Yamada, Daichi (山田 大智) **3SAA-5**
2F1412
2F1448
2H1424
Yamada, Hiroko (山田 寛子) **3Pos083**
Yamada, Hiroshi (山田 浩司) 2A1412
Yamada, Kazuya (山田 和哉) 3Pos067
Yamada, Masahito (山田 正仁) 2L1436
Yamada, Masato (山田 雅人) **1G1354**
Yamada, Masayuki (山田 真行) **1J1512**
Yamada, Taiga (山田 大雅) **2Pos219**
Yamada, Tatsuya (山田 達矢) **2Pos061**
Yamagata, Atsushi (山形 敦史) **3SDA-3**
Yamagata, Hitoshi (山形 仁) 3Pos206
Yamagata, Yuriko (山縣 ゆり子) 1Pos056
Yamagishi, Ayana (山岸 彩奈) 3Pos073
Yamaguchi, Akihito (山口 明人) 1G1512
Yamaguchi, Chiaki (山口 千晶) **1Pos021**
Yamaguchi, Hiroshi (山口 博史) **2SBA-4**
Yamaguchi, Katsushi (山口 勝司) 1A1536
Yamaguchi, Kizashi (山口 兆) 1SDA-7
2Pos054
Yamaguchi, Maki (山口 眞紀) 2Pos422
Yamaguchi, Shin (山口 真) 2Pos410
Yamaguchi, Tomohiro (山口 知洋) **2Pos029**
Yamaguchi, Tomoko (山口 智子) **1Pos036**
Yamaguchi, Yohhei (山口 陽平) 1Pos206
Yamaji, Misa (山地 未紗) **3Pos070**
Yamakoshi, Daiki (山越 大希) **1E1354**

Yamakoshi, Tatsuya (山越 達矢) 3Pos319
3Pos320
yamakoshi, Daiki (山越 大希) 1Pos213
Yamamori, Yu (山守 優) **1Pos011**
Yamamoto, Airi (山本 愛理) **3Pos006**
Yamamoto, Daisuke (山本 大輔) **2Pos402**
Yamamoto, Eiji (山本 詠士) **2Pos023**
Yamamoto, Jhotaro (山本 条太郎) 2Pos033
Yamamoto, Johtaro (山本 条太郎) 2O1618
1Pos405
1Pos411
2Pos409
Yamamoto, Junpei (山元 淳平) **3SAA-1**
2Pos093
2Pos094
Yamamoto, Kimiko (山元 季実子) 2C1500
Yamamoto, Masaki (山本 雅貴) **2SDA-1**
1Pos054
2Pos416
Yamamoto, Masamichi (山本 正道) 2Pos424
Yamamoto, Masao (山本 真生) **3Pos038**
Yamamoto, Masaya (山本 雅哉) 2Pos066
Yamamoto, Mayuko (山本 真由子) 2Pos206
2Pos405
Yamamoto, Naoki (山本 直樹) 2L1412
3Pos066
3Pos068
Yamamoto, Ryousuke (山本 遼介) 2N1518
2Pos215
Yamamoto, Sakiyo (山本 祥世) 2Pos081
Yamamoto, Shuya (山本 修也) 1Q1524
Yamamoto, Takahiro (山本 隆寛) **2Pos416**
Yamamoto, Takaki (山本 尚貴) 2SBP-5
3Pos093
Yamamoto, Takashi (山本 卓) 1Pos106
Yamamoto, Tubasa (山本 翼) 2Pos009
Yamamoto, Yuta (山本 悠太) 2C1412
Yamamura, Masayuki (山村 雅幸) 3Pos403
Yamanaka, Akihiro (山中 章弘) 1SHA-5
Yamanaka, Ryo (山中 諒) 2G1412
Yamanaka, Shin'nosuke (山中 信之介) 2D1530
Yamanaka, Shusuke (山中 秀介) 2Pos054
Yamanaka, Yuki (山中 幸) 3Pos301
Yamanaka, Yuki (山中 悠希) 1Pos415
1Pos419
3Pos413
Yamanashi, Taro (山梨 太郎) **2H1530**
2Pos090
Yamane, Tsutomu (山根 努) **1SOA-1**
1Pos049
3Pos076
Yamano, Nami (山野 奈美) **1F1500**
Yamano, Yumiko (山野 由美子) 3Pos045
Yamanobe, Takanobu (山野辺 貴信) **3Pos218**
Yamanoi, Yoshinori (山野井 慶徳) 3Pos031
Yamaoka, Takanori (山岡 敬典) **2K1518**
Yamaoki, Yudai (山置 佑大) 2L1424
Yamasaki, Seiji (山崎 聖司) 1G1512
Yamashita, Akihiro (山下 晶洸) 1Pos203
Yamashita, Atsuko (山下 敦子) **3SEA-1**
Yamashita, Daisuke (山下 大輔) **2Pos033**
Yamashita, Eiki (山下 栄樹) 1M1342
2E1412
1Pos065
1Pos073
Yamashita, Hayato (山下 隼人) 1SIA-6
2Pos070
3Pos323
Yamashita, Jiro (山下 慈郎) 2Pos411
Yamashita, Ryota (山下 涼太) 1Pos302
Yamashita, Takahiro (山下 高廣) **2SHA-6**
1H1548
2Pos101
3Pos045
Yamashita, Takayuki (山下 貴之) 1SHA-5
Yamato, Takahisa (倭 剛久) **2J1412**
Yamauchi, Akari (山内 彩加林) 2K1530
Yamauchi, Masataka (山内 仁喬) **1Pos003**
Yamauchi, Shunpei (山内 竣平) **1O1430**
Yamauchi, Toyohiko (山内 豊彦) 3Pos042
Yamauchi, Yumeka (山内 夢叶) **2Pos091**
3Pos040
Yamawaki, Yuki (山脇 裕貴) **1K1406**
Yamazaki, Kakehiro (山崎 健広) 3Pos311
Yamazaki, Masahito (山崎 昌一) 1G1418
2G1400
1Pos086
1Pos087
1Pos090
1Pos095
1Pos096
Yamazaki, Masashi (山崎 雅史) **1A1406**
Yamazaki, Tomoya (山崎 友也) 2C1448
Yamazaki, Toshio (山崎 俊夫) 1G1430
2F1542
Yamazaki, Yoichi (山崎 洋一) **2SHA-2**
2K1412
1Pos064
1Pos402
2Pos098
Yamazaki, Yosuke (山崎 陽佑) **2Pos322**
Yamazawa, Toshiko (山澤 徳志子) **2Pos422**
Yan, Jie (Yan Jie) **3SIA-8**
Yan, Kangmin (厳 康敏) 2N1500
Yanagawa, Hiroshi (柳川 弘志) 2Pos061
Yanagawa, Masataka (柳川 正隆) **3SIA-2**

	3Pos303
Yanagawa, Yuchio (柳川 右千夫)	1Pos320
Yanagi, Takashi (柳 昂志)	**1A1354**
Yanagida, Toshio (Yanagida Toshio)	2O1400
Yanagida, Toshio (柳田 敏雄)	1Pos226
	1Pos228
	2Pos417
Yanagisawa, Miho (柳澤 実穂)	2Pos068
Yanagisawa, Sachiko (柳澤 幸子)	2SOA-3
	1G1548
Yanaka, Saeko (谷中 冴子)	**2SIP-4**
	2M1424
Yang, Han Lin (Yang Han Lin)	**2Pos036**
Yang, Shunkai (Yang Shunkai)	2M1554
Yang, Zhaomin (Yang Zhaomin)	1Pos058
Yano, Daichi (矢野 大地)	2Pos021
Yano, Shun (矢野 峻)	**3Pos008**
Yano, Yoshiaki (矢野 義明)	1Q1448
Yao, Min (姚 閔)	3Pos059
Yasuda, Aya (安田 亜矢)	1SRA-4
Yasuda, Kenji (安田 賢二)	**2SFA-2**
	1Pos203
	1Pos311
	1Pos315
	1Pos319
	1Pos412
	1Pos413
	1Pos414
	1Pos415
	1Pos418
	1Pos419
	3Pos095
	3Pos409
	3Pos410
	3Pos411
	3Pos413
Yasuda, Satoshi (安田 賢司)	2Pos024
	2Pos062
	3Pos010
	3Pos011
Yasuhara, Kazuma (安原 主馬)	**2G1412**
Yasui, Masato (安井 真人)	1SKA-6
Yasukochi, Shotaro (安河内 章太郎)	2M1412
Yasunaga, Takuo (安永 卓生)	1Pos015
Yasutake, Yoshiaki (安武 義晃)	1Pos408
Yatabe, Keiko (谷田部 景子)	1Pos022
Yato, Mirai (谷頭 未來)	1Pos041
Yawo, Hiromu (八尾 寛)	1SHA-5
	3Pos045
Yhoshimura, Hideyuki (吉村 英恭)	3Pos415
Yi, Zhang (張 翼)	1Pos407
Yodogawa, Akira (淀川 良)	2Pos013
Yogo, Rina (與語 理那)	2SIP-4
Yokawa, Satoru (横川 慧)	3Pos310
	3Pos318
	3Pos325
Yokogawa, Mariko (横川 真梨子)	1M1406
Yokoi, Osamu (横井 修)	1Pos309
	1Pos314
Yokojima, Satoshi (Yokojima Satoshi)	2Pos031
Yokojima, Satoshi (横島 智)	**2Pos046**
Yokokawa, Ryuji (Yokokawa Ryuji)	2Pos222
Yokokawa, Ryuji (横川 隆司)	1E1536
	1Pos050
	2Pos217
Yokomuro, Kaho (横室 夏帆)	**2Pos202**
Yokosuka, Tadashi (横須賀 忠)	1SEA-4
	3Pos321
Yokota, Azusa (横田 あずさ)	1K1536
Yokota, Hiroaki (横田 浩章)	**2Q1448**
	1Pos403
Yokota, Ryo (横田 亮)	3Pos213
Yokota, Ryuichi (横田 龍一)	**2E1400**
Yokoyama, Ken (横山 謙)	1SDA-5
	1Pos004
	1Pos005
Yokoyama, Masaru (横山 勝)	2Pos404
Yoneda, Mayu (米田 真由)	**1G1536**
Yoneda, Takuro (米田 卓郎)	**1F1448**
Yoneda, Yusuke (米田 勇祐)	1F1430
Yonehara, Ryo (米原 涼)	**1Pos065**
Yonekawa, Chinatsu (米川 千夏)	2F1424
Yonemura, Shigenobu (米村 重信)	**2SEA-3**
Yonezawa, Kento (米澤 健人)	**1Pos022**
Yoo, Brian (Yoo Brian)	2L1448
Yoon, Dong Hyun (尹 棟鉉)	3Pos418
	3Pos419
Yoshida, Akiko (吉田 晃子)	2Pos075
Yoshida, Amane (吉田 周)	1Pos412
	1Pos413
	1Pos414
	1Pos418
Yoshida, Hideji (吉田 秀司)	2Pos014
Yoshida, Hiroshi (吉田 寛)	**2Pos108**
Yoshida, Kazuho (吉田 一帆)	2H1424
Yoshida, Kouhei (吉田 浩平)	**3Pos018**
Yoshida, Masasuke (吉田 賢右)	2E1412
	1Pos207
Yoshida, Megumi (吉田 愛美)	2Pos075
Yoshida, Myu (吉多 美祐)	1E1500
	1Pos219
Yoshida, Ryo (吉田 亮)	1Pos317
Yoshida, Shuichi (吉田 秀一)	**1Pos103**
Yoshida, Takuya (吉田 琢哉)	2C1424
Yoshida, Tetsuro (吉田 鉄郎)	**1C1600**
Yoshida, Ukyo (吉田 右京)	1G1500

Yoshida-Noro, Chikako (野呂 知加子) 3Pos089
Yoshihara, Akihide (吉原 明秀) 2Pos106
Yoshii, Noriyuki (吉井 範行) 1J1406
Yoshikawa, Kenichi (吉川 研一) 1Q1354
2Q1530
2Pos042
2Pos043
3Pos092
3Pos311
Yoshikawa, Shinya (吉川 信也) 1M1448
Yoshikawa, Takeshi (吉川 武司) 2Pos104
Yoshikawa, Yuhki (吉川 祐樹) **3Pos066**
Yoshikawa, Yuko (吉川 祐子) 1Q1354
2Q1530
2Pos043
Yoshikawa, Yuuko (吉川 裕子) 2Pos042
Yoshimura, Hideaki (吉村 英哲) **3Pos023**
Yoshimura, Hideyuki (吉村 英恭) 3Pos414
Yoshimura, Kenjiro (吉村 建二郎) 2Pos075
Yoshimura, Kohei (吉村 孝平) 2N1400
Yoshioka, Daisuke (好岡 大輔) **2Pos082**
Yoshizaki, Satoru (吉崎 慧) **1K1448**
Yoshizawa, Keiko (慶澤 景子) 2Pos408
Yoshizawa, Ryo (吉澤 亮) **3Pos303**
Yoshizawa, Susumu (吉澤 晋) **3SKA-3**
1F1524
1H1330
2Pos086
2Pos089
3Pos043
3Pos044
Yu, Cheng-han (Yu Cheng-han) **1SEA-3**
Yu, Isseki (優 乙石) **2Pos059**
Yuasa, Hideya (湯浅 英哉) 1SHA-5
Yura, Kei (由良 敬) **2SDA-6**
Zarco - Zavala, Mariel (Zarco - Zavala Mariel) **2E1448**
Zhang, Suxiang (張 素香) 2O1500
3Pos216
Zhang, Yi (張 翼) 1SKA-4
Zhang, Zhen (Zhang Zhen) 2SBP-3
1A1430
Zhang, Zhongliang (張 仲良) **3Pos067**
Zheng, Jing (Zheng Jing) 1E1430
Zhou, Hang (周 航) **1Pos050**
Zhuang, Xiang-Yu (Zhuang Xiang-Yu) **1Pos220**

第 56 回日本生物物理学会年会　ランチョンセミナー

研究者の自由な光学系構築を支援する「コアユニット顕微鏡」

発表日：9 月 15 日 (土) 11:45 – 12:35　　会場：D 会場 (A 棟 3 階 A36)

シグマ光機株式会社　開発部　井上 裕一

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- 光学顕微鏡をお使いの人は、思い通りの実験ができていますか？
- 予算不足で諦めた光学系はありませんか？
- 若手研究者や学生が MY 顕微鏡を持つことは無理なのでしょうか？

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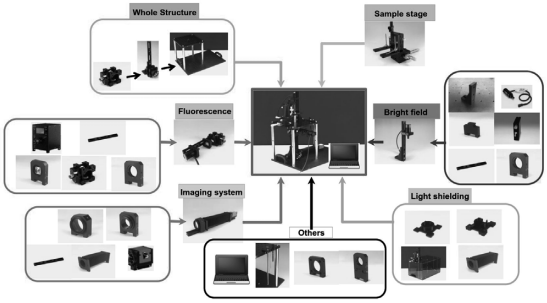
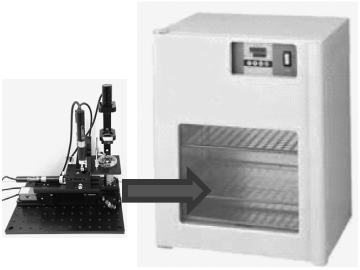
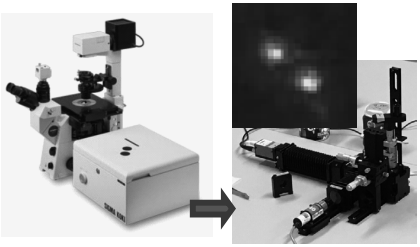


1）「コアユニット顕微鏡」とは何か



2）培養細胞の長期間観察は
いくらから始められるか



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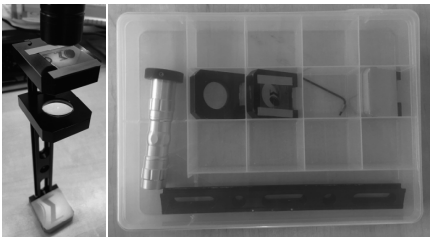

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第 56 回日本生物物理学会年会　共催ランチョンセミナー

細胞内１分子イメージングの自動化とシグナル伝達への適用

上田　昌宏　先生

（理化学研究所・生命機能科学研究センター、大阪大学大学院・生命機能研究科）

日時　2018 年 9 月 15 日（土）11:45～12:35

会場　E 会場（A 棟 3 階 A37）

講演者はこれまで佐甲靖志（理研）らと共に、シグナル伝達に関わる分子の動態を細胞内で1分子計測し定量解析するという方法論を確立してきた。最近、ニコン全反射照明蛍光顕微鏡をベースに、画像取得から解析までの1分子計測の全行程を自動化する顕微鏡システム（AiSIS）の開発に成功した（Yasui, Hiroshima et al., 2018）。機械学習を用いた自動細胞認識や自動フォーカス、自動オイル供給などの自動化の要素技術の紹介と共に、シグナル伝達解析への適用例について紹介する。

株式会社ニコン インステック

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E-mail：Nit.Biomarketing@nikon.com

電話：(03)6433-3982

第 56 回日本生物物理学会年会　ランチョンセミナープログラム No. 1LSG

ライカマイクロシステムズ㈱　ランチョンセミナー　Leica Microsystems K.K.

日時：　9 月 15 日（土）11:45 – 12:35　　会場：　G 会場（B 棟 3 階 B33）

See The Hidden/See More

未知のプロセスを可視化するイノベーション

新製品 TCS SP8 FALCON (Fast Lifetime Contrast)
蛍光寿命イメージング技術のブレークスルー

演者　**Giulia Ossato**　Leica Microsystems CMS GmbH (Language: English)

蛍光分子固有の蛍光寿命にもとづいて新たな生体情報を得ることができる蛍光寿命イメージングは、細胞内の代謝、微小環境、分子間相互作用などの機能解析、アンミキシングや無染色イメージングなど、幅広いアプリケーションに対応する、たいへん有用なイメージング技術です。一方で、画像取得に時間を要する、システムやソフトウェア取り扱いの煩雑さなどの理由から、これまでは一部の研究者のみが扱う、限られた技術でした。このたびライカが発表した TCS SP8 FALCON は、ライカ先進の光学技術、新開発のソフトウェアアルゴリズムにより、これまで困難とされていた高速の蛍光寿命イメージングを実現しました。本セミナーでは、機能解析イメージングの新たなステージを提供する FALCON の最新技術について紹介します。

新製品 DMi8S (Widefield Photo Stimulation)& LAS X Navigator
隠れた細胞プロセスを見つけ出す

演者　**柴田 加苗**　ライカマイクロシステムズ株式会社（発表言語：日本語）

細胞観察から細胞間相互作用などのハイエンドイメージングに至るまで、倒立顕微鏡ライカ DMi8 は 1 つのプラットフォームをベースに、ニーズの変化、高度化に合わせて成長します。See The Hidden では 2 本のインフィニティポートを統合し、追加光源やレーザーシステムの組み込みを可能にした結果、光刺激と画像取得を同時進行し、刺激直後の細胞プロセスを確実に画像取得します。See More では、新感覚の操作で今までにない画像タイリングを可能にします。本セミナーでは、これらの高度な研究をパワフルにサポートするライカの革新的なアップグレードツール DMi8 S & LAS X Navigator の有効性について実例を交えてお伝えします。

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PDBj Protein Data Bank Japan

Luncheon Seminar
at the 56th Annual Meeting of Biophysical Society of Japan

September 16 (Sun), 11:45 ～ 12:35, D site (Room A36, Bldg. A)

1. Making full use of the wwPDB validation reports
wwPDB 検証レポートの活用法

Masashi Yokochi
Institute for Protein Research, Osaka University

wwPDB validation reports provide an assessment of structure quality which shows that obtained structure model is consistent with experimental data and how the model agrees to the widely accepted criteria at atomic level. It is essential resource not only for structural interpretation of original publication, but also development of bioinformatics, and drug discovery. In order to improve accessibility and usability, we developed two semantic versions of the wwPDB validation reports, PDBx/mmCIF compatible XML and RDF, respectively. I will outline the basic concepts of the new archives and explain the effective way to use them through case-study.

2. Introduction to NIG Supercomputer and DDBJ
遺伝研スパコンと DDBJ の紹介

Masanori Arita
National Institute of Genetics

DDBJ is a part of International Nucleotide Sequence Database (INSD) in collaboration with NCBI and ENA/EBI since 1987. Our service includes next-generation sequence data in Sequence Read Archive, research projects in BioProject, biological sources and materials in BioSample, and personal genomes in JGA. More than half of our computing resource is open to domestic researchers (and foreign collaborators), and > 500 registered users from > 120 institutions perform their own research free of charge. Modern research requires a complicated software environment and we keep providing the up-to-date system for all scientists in Japan.

Protein Data Bank Japan
https://pdbj.org/

Institute for Protein Research, Osaka University,
3-2 Yamadaoka, Suita, Osaka 565-0871, Japan
TEL: +81-(0)6-6879-4311

9月16日(日) 11:45-12:35
E会場（A棟3階　A37）

Taylor分散法による溶液中の蛋白質のサイズ解析

マルバーン・パナリティカル事業部 （スペクトリス株式会社）
バイオサイエンス スペシャリスト アジア パシフィック地域 志波 公平

蛋白質はそれぞれユニークな構造を持ち、その構造を保つことによって機能を示すことは広く知られています。そのため、溶液中における蛋白質の情報は、機能との関連性を考える際に重要な情報となります。その中でもサイズ情報は、高次構造の変化を直接的に結びつけることが期待されます。また、溶液中の物性解析の多くは蛋白質間に生じる相互作用の情報を含んでいます。この情報を応用し、産業的、具体的には蛋白質医薬品などには、これらのパラメータを分散安定性の予測に活用したりするケースも増えています。

Taylor分散 (Taylor Dispersion) 法は1950年代にG. I. Taylorらによって提唱され、1980年代にH. Brennerらによって確立された手法で、キャピラリ内に生じる流体速度分布によって高分子の拡散係数を導く手法です。この手法の特徴はUVによる検出が可能であり、ごく微量で計測できる点にあります。再現性に優れており、1 nm以下のサイズ変化の議論も可能になります。

本発表では、Taylor分散法によるいくつかのサイズ測定のアプリケーションの紹介と、以下の表にあるDLS、GPC-LS、TDAおよびSAXSについて、それぞれからどのような情報が得られるのかについて、アプリケーション事例を通じて紹介します。

各装置の原理と特徴

	動的光散乱法（DLS）	ゲルろ過光散乱法（GPC-LS）	Taylor分散法（TDA）	X線小角散乱法（SAXS）
主な獲得パラメータ	Rh 拡散係数	絶対分子量 Rg	Rh 拡散係数	Rg, Dmax 絶対分子量
推奨対象粒子サイズ（半径）	1 – 1,000 nm	1 – 1,000 nm (使用カラムに依存)	0.2 – 50 nm	0.1 – 10 nm
特徴	広く全般が見渡せる 簡便、濃度範囲が広い、 短時間測定	分離直後の 詳細な解析ができる	サブナノ・シングルナノサ イズの分解能が高い、再現性よい短時間測定	形状がわかる
制限項目	粗大粒子 存在下の再現性	カラム依存的、 Running Bufferを多く使用	大きな粒子への対応 分布が出せない	濃度、サンプル量が必要、測定時間が長い

第56回 日本生物物理学会年会

浜松ホトニクス株式会社
ランチョンセミナー

◇ プログラムNo. 2LSG
◇ 日時:2018年9月16日(日)　11:45 ～ 12:35
◇ 会場:G会場(B棟3階　B33)

演題1

「蛍光、偏光、顕微鏡」

"Fluorescence, Polarization, Microscope"

谷　知己 先生

Associate Scientist
Marine Biological Laboratory, Woods Hole,
Massachusetts, USA

演題2

「浜松ホトニクスの最新イメージング技術」

- 焦点深度伸長デバイスと最新イメージング技術 -

"The latest imaging technology of Hamamatsu Photonics"
- Extended Focus Device and the latest imaging technologies -

伊東 克秀

浜松ホトニクス株式会社 システム事業部

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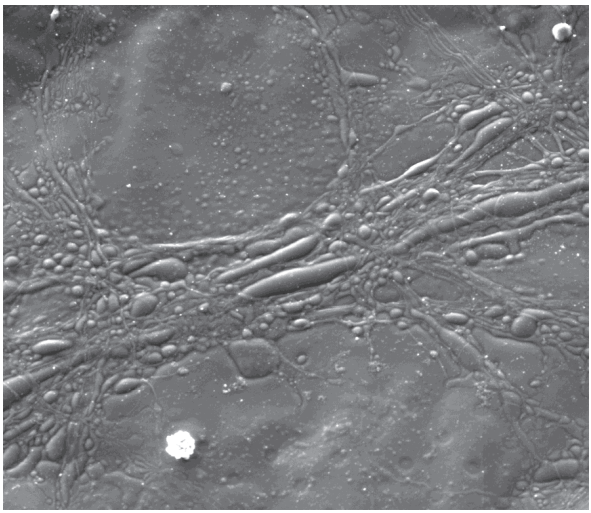
E-mail: sales@sys.hpk.co.jp

Thermo Fisher Scientific & Leica Microsystems
共催ランチョンセミナー
細胞生物学に向けたCryo Tomography Workflow



画像提供: 福田　善之　博士　（東京大学大学院医学系研究科）　初代培養神経細胞由来の神経突起

- 日時: 9月17日（月）11:45 – 12:35
- 会場: G会場（B棟3階 B33）
- 演者: 福田　善之　先生　（東京大学大学院医学系研究科）
  石原　あゆみ　（ライカマイクロシステムズ株式会社）
  葦原　雅道　（サーモフィッシャーサイエンティフィック　日本エフイー・アイ株式会社）
- 演題: 細胞生物学に向けたCryoTomography Workflow
- 要旨:

近年、クライオ電子顕微鏡法は著しく発展を遂げ、特に単粒子解析法 (Single Particle Analysis) は、これまで結晶化の難しさからX線結晶構造解析法での着手が困難であったタンパク質複合体の構造決定に大きく貢献しはじめました。そのため、単粒子解析法は構造解析手法のメインストリームの一つになりつつあります。その一方で、生命をより深く理解するためには、タンパク質が細胞の中でどのようなふるまいをするかの解明が必要となります。したがって、構造解析の次のターゲットとして、細胞やオルガネラにおける超分子複合体に関心が集まっています。そして、これら複合体を細胞から単離することなく、*In situ*（その場）での構造解析を可能とするのがクライオ電子線トモグラフィー法です。しかしながら、細胞は数-数十umの大きさをもつことから透過型電子顕微鏡での観察が困難です。細胞試料のクライオ電子線トモグラフィーを行うために、2つの技術が開発されました。1つは、凍結した細胞試料を物理的応力無く薄膜加工し ” Cryo lamella” を作製するために考案されたのがAquilosに代表されるCryo-FIBシステムです。
もう1つは、光学顕微鏡と電子顕微鏡の視野のギャップを埋め、細胞内の目的のタンパク質の位置情報を共有するために考案されたCLEM (Correlative Light and Electron Microscopy)技術です。ライカ社による最新のCLEMシステムであるEM Cryo CLEMは、電子顕微鏡との位置相関を取るために必要な光学分解能を有し、クライオ電子顕微鏡用試料のスクリーニングに最適化されています。これら全てのソリューションを実現することで、細胞内の目的タンパク質の3次元構造を電子線トモグラフィーにより解明することが可能となります。
本セミナーでは、凍結試料作製からEM Cryo CLEM による細胞の標的化、Aquilos による切削加工、クライオ電子線トモグラフィーにいたるまでの一連のワークフローをご紹介します。

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本誌記事の動物実験における実験動物の扱いは，所属機関のルールに従っています.

生物物理 SEIBUTSU BUTSURI
日本生物物理学会 THE BIOPHYSICAL SOCIETY OF JAPAN

Vol.58 Supplement 1-2　2018 年 8 月 20 日発行

編集発行　一般社団法人日本生物物理学会
制作　中西印刷株式会社
〒602-8048　京都市上京区下立売通小川東入ル
TEL 075-441-3155　FAX 075-417-2050

定価 3,500円

昭和43年2月19日 学術刊行物（第4種郵便物）指定
平成30年8月20日 増刊号