シンポジウム　Symposium

第 1 日目（9 月 19 日（火））／Day 1（Sep. 19 Tue.）

9:00～11:30　A 会場（全学教育棟 1 階 E107）／Room A (Room E107, General Education Bldg. 1F)

1SAA　「流れ」から解き明かす生き物の時空間パターン：タンパク質から集団運動まで
Ta Panta rhei: Spatiotemporal dynamics of flow-related biological patterns

オーガナイザー：鹿毛 あずさ（東北大学），鳥澤 嵩征（情報通信研究機構）
Organizers: Azusa Kage (Tohoku University), Takayuki Torisawa (NICT)

"Everything flows": this statement by an ancient Greek philosopher now sheds light on a new direction of biophysical studies. In recent years, a wide variety of studies have emerged focusing on the diverse flow-related phenomena in biological systems, the components of which were cytoskeletal proteins, cilia, or cells. In this session, we would like to discuss the growing and interdisciplinary field of flow-related spatiotemporal dynamics ranging from a theory on a single element to an experiment on collective behavior of real cells with the promising young investigators with diverse backgrounds.

1SAA-1　Spatiotemporal dynamics of flow-related biological patterns: Overview
Takayuki Torisawa (*Advanced ICT Inst., NICT*)

1SAA-2　Multiscale dynamics of red blood cells in flow
Stephanie Nix, Yukitaka Ishimoto (*Akita Pref. U.*)

1SAA-3　細胞表層シートを用いた繊毛虫ゾウリムシ繊毛運動の解析
Analysis on the ciliary movements in *Paramecium* using the ciliated cortical sheet
○久冨 理[1,2], 堀 学[3]（[1]富山大・院・理工, [2]山梨大・院・医, [3]山口大・理）
Osamu Kutomi[1,2], Manabu Hori[3] ([1]*Grad. Sch. Sci. and Eng., Univ. Toyama*, [2]*Grad. Sch. Med., Univ. Yamanashi*, [3]*Fac. Sci., Yamaguchi Univ*)

1SAA-4　Emergent collective motion of the unicellular green alga *Chlamydomonas*: 2-body swimming and beyond
Azusa Kage[1], Takayuki Torisawa[2], Ken H. Nagai[3] ([1]*Sch. Eng., Tohoku Univ.*, [2]*Advanced ICT Inst., NICT*, [3]*Sch. Materials Sci., JAIST*)

1SAA-5　遊泳バクテリアで捉える自己駆動粒子の集団運動における普遍性
Universality in collective motion of self-propelled elements captured through swimming bacteria
○西口 大貴[1,2,3], 永井 健[4], Chaté Hugues[1,5], 佐野 雅己[1]（[1]CEA-Saclay, [2]東大理, [3]パスツール研究所, [4]北陸先端大, [5]北京計算科学中心）
Daiki Nishiguchi[1,2,3], Ken H. Nagai[4], Hugues Chate[1,5], Masaki Sano[1] ([1]*CEA-Saclay*, [2]*Dept. of Phys., The Univ. of Tokyo*, [3]*Pasteur Institute*, [4]*JAIST*, [5]*Beijin CSRC*)

1SAA-6　The impact of flow and environmental sensing on bacterial biofilm degradation
Knut Drescher[1, 2] ([1]*Max Planck Institute for Terrestrial Microbiology, 35043 Marburg, Germany*, [2]*Department of Physics, Philipps University Marburg, 35032 Marburg, Germany*)

9:00～11:30　B 会場（全学教育棟 2 階 B201）／Room B (Room B201, General Education Bldg. 2F)

1SBA　金属酵素の反応機構を理解するための多様な生物無機化学的アプローチ
Bioinorganic Approaches for Understanding Reaction Mechanisms of Metalloproteins

オーガナイザー：舩橋 靖博（大阪大学），柳澤 幸子（兵庫県立大学）
Organizers: Yasuhiro Funahashi (Osaka University), Sachiko Yanagisawa (University of Hyogo)

Elucidation of enzymatic reaction mechanisms is one of the most important subjects in biophysics. For understanding the essential mechanistic points, we should find correlation between structures and dynamics in the active site and protein environments, and furthermore, we should know chemical properties of the catalytic center. In this symposium, we focus on iron-containing proteins to understand enzymatic reactions using methods of structural biology, spectroscopy, coordination chemistry, and theoretical calculation. These bioinorganic approaches must lead us to get to the bottom of the biophysical phenomena.

はじめに
Opening Remarks

1SBA-1 ヘムタンパク質の電子論
Electronic Theory of Hemoprotein Chemistry
○山本 泰彦（筑波大・数理物質系化学域）
Yasuhiko Yamamoto (*Department of Chemistry, University of Tsukuba*)

1SBA-2 核共鳴非弾性散乱分光により解き明かす鉄蛋白質活性点の構造化学とダイナミックス
Nuclear resonance vibrational spectroscopic studies of the geometric structure and dynamics of iron-containing biomolecules
○太田 雄大（兵県大・院生命理学）
Takehiro Ohta (*Grad. Sch. Sci., Univ. Hyogo*)

1SBA-3 Mononuclear Nonheme Iron(IV)-Oxo Complexes with Tripodal Ligands in Oxidation Reactions
Mi Sook Seo, Wonwoo Nam (*Ewha Womans University*)

1SBA-4 X 線自由電子レーザーを用いた時間分解結晶構造解析：酵素反応への応用
Time-resolved crystallography using X-ray free electron laser: application to enzymatic reaction
○當舎 武彦（理研SPring-8）
Takehiko Tosha (*RIKEN, SPring-8*)

1SBA-5 QM/MM 計算で解明した鉄含有酵素の反応機構
Reaction mechanisms of iron-containing proteins elucidated using QM/MM calculations
○庄司 光男[1], 山崎 笙太郎[2], 栢沼 愛[1], 重田 育照[1]（[1]筑波大学計算科学研究センター, [2]筑波大学数理物質科学研究科）
Mitsuo Shoji[1], Sotaro Yamasaki[2], Megumi Kayanuma[1], Yasuteru Shigeta[1] ([1]*CCS, Univ. Tsukuba*, [2]*Grad. Sch. Of Pure & App. Sci., Univ. Tsukuba*)

おわりに
Closing Remarks

9:00〜11:30　C 会場（全学教育棟 2 階 B202）／Room C (Room B202, General Education Bldg. 2F)

1SCA　原生生物の行動
Protista behaviors

オーガナイザー：園部 誠司（兵庫県立大学），市川 正敏（京都大学）
Organizers: Seiji Sonobe (University of Hyogo), Masatoshi Ichikawa (Kyoto University)

The organisms belong to Protista have survived through their evolutions in various environments, and their fast growth and diversities make them win the cruel struggle for existence. Furthermore, recent progress has discovered unique behaviors of single cell organisms deeply connected to their life strategy. In this symposium, we will present some interesting topics on the behaviors of protists to discuss on their strange but clever responses to survive.

はじめに
Opening Remarks

1SCA-1 細胞運動における自発的シグナル生成の仕組み
A mechanism of spontaneous signal generation in cell migration
○松岡 里実[1,2], 福島 誠也[1,2], 上田 昌宏[1,2]（[1]理化学研究所生命システム研究センター, [2]大阪大学大学院生命機能研究科）
Satomi Matsuoka[1,2], Seiya Fukushima[1,2], Masahiro Ueda[1,2] ([1]*RIKEN, Quantitative Biology Center (QBiC)*, [2]*Osaka University, Graduate School of Frontier Biosciences*)

1SCA-2 連続光照射時のオオアメーバの運動
Behavior of *Amoeba proteus* on constant photo-irradiation
○西上 幸範（京都大学大学院理学研究科物理学）
Yukinori Nishigami (*Department of Physics, Graduate School of Science, Kyoto University*)

1SCA-3 繊毛虫の学習能力の再考
Rethinking the learning capacity of ciliates
○國田 樹（琉球大学工学部）
Itsuki Kunita (*University of The Ryukyus*)

1SCA-4 ロクロクビムシのプロボーシスの伸縮運動
Extension and Contraction of the Proboscis of a Ciliate, *Lacrymaria olor*
○梁瀬 隆二（兵県大・院生命理学）
Ryuji Yanase (*Grad. Sch. Sci., Univ. Hyogo*)

1SCA-5 壁面付近における繊毛虫の遊泳運動
Swimming behavior of a ciliate near a wall
○大村 拓也, 市川 正敏（京都大学大学院理学研究科）
Takuya Ohmura, Masatoshi Ichikawa (*Grad. Sch. of Sci, Kyoto Univ.*)

1SCA-6 ラビリンチュラ類の外質ネットによる栄養摂取
Nutrition of thraustochytrids (Labyrinthulea) by their ectoplasmic nets
○本多 大輔[1], 浜本 洋子[2], 岩田 いづみ[2]（[1]甲南大学　理工学部, [2]甲南大学　自然科学研究科）
Daiske Honda[1], Yoko Hamamoto[2], Izumi Iwata[2] ([1]*Faculty of Science and Engineering, Konan University*, [2]*Graduate School of Natural Science, Konan University*)

おわりに
Closing Remarks

9:00～11:30　D 会場（全学教育棟 2 階 E201）／Room D (Room E201, General Education Bldg. 2F)

1SDA　溶液中における蛋白質ダイナミクス解析
Analysis of Protein Dynamics in Solution

オーガナイザー：小川 覚之（東京大学），有坂 文雄（東京工業大学）
Organizers: Tadayuki Ogawa (The University of Tokyo), Fumio Arisaka (Tokyo Institute of Technology)

Accurate description of protein behavior in solution is required in various fields such as biophysics, structural biology, and antibody drugs. This symposium focuses on the protein analysis in solution by using multiple independent methods; liquid chromatography, dynamic light scattering, small angle X-ray scattering, analytical ultracentrifuge, calorimetry, and atomic force microscope. Fusion and integration of multiple methods will foster our deeper understanding of the protein dynamics in solution.

1SDA-1 高速原子間力顕微鏡を用いた回転軸の無い腸内連鎖球菌由来 V_1-ATPase の回転運動の解析
Analysis of Rotational Dynamics of Rotorless *Enterococcus hirae* V_1-ATPase using High-Speed Atomic Force Microscopy
○今村 元紀[1], 中本 和哉[2], 丸山 慎太郎[2], 河合 文啓[3], 飯野 亮太[3], 内橋 貴之[4], 村田 武士[2], 安藤 敏夫[1]（[1]金沢大・バイオ AFM FRC, [2]千葉大・院理, [3]岡崎統合バイオ/分子研, [4]名古屋大・院理）
Motonori Imamura[1], Kazuya Nakamoto[2], Shintaro Maruyama[2], Fumihiro Kawai[3], Ryota Iino[3], Takayuki Uchihashi[4], Takeshi Murata[2], Toshio Ando[1] ([1]*Bio-AFM FRC, Kanazawa Univ.*, [2]*Grad. Sch. Sci., Chiba Univ.*, [3]*Okazaki Inst. Integ. Biosci., IMS, NINS*, [4]*Grad Sch. Sci., Nagoya Univ.*)

1SDA-2 超遠心分析によるバイオおよびナノ粒子の溶液挙動の解析
Solution behavior of bio- and nano-particles as analyzed by analytical ultracentrifugation
○有坂 文雄（東京工業大学）
Fumio Arisaka (*Tokyo Institute of Technolgy*)

1SDA-3 Elucidation of structural dynamics of protein with binding to drugs based on kinetic and thermodynamic analysis
Satoru Nagatoishi[1,2], Kouhei Tsumoto[1,2] ([1]*The Institute of Medical Science, The University of Tokyo*, [2]*School of Engineering, The University of Tokyo*)

1SDA-4 SEC-SAXS によるタンパク質複合体の溶液構造解析
Solution structure analysis of the protein complex using SEC-SAXS
○清水 伸隆（高エネ機構・物構研・放射光）
Nobutaka Shimizu (*PF, IMSS, KEK*)

1SDA-5 高温における可逆的かつ迅速な蛋白質非天然状態の会合体形成
Reversible and rapid oligomerization of non-native proteins at high temperature
○城所 俊一（長岡技科大・生物機能）
Shun-ichi Kidokoro (*Dept. Bioeng., Nagaoka Univ. Tech.*)

1SDA-6 ピロリ菌 CagA がんタンパク質の構造多型が極性制御因子 PAR1 b 結合に及ぼす影響
Impact of structural polymorphism of the H. pylori CagA oncoprotein on binding to polarity regulating kinase PAR1b
○西川 裕子[1], 林 剛留[1], 有坂 文雄[2], 千田 俊哉[3], 畠山 昌則[1]（[1]東大・院医, [2]日大・生物, [3]物構研・高エネ研）
Hiroko Nishikawa[1], Takeru Hayashi[1], Fumio Arisaka[2], Toshiya Senda[3], Masanori Hatakeyama[1] ([1]*Grad. Sch. Med., Univ. Tokyo*, [2]*Coll. Biores. Sci., Nihon Univ.*, [3]*Inst. of Mater. Struct. Sci., KEK*)

1SDA-7 Solution-based Analyses on Microtubule Depolymerization via Depolymerizing Machine
Tadayuki Ogawa[1], Shinya Saijo[2], Nobutaka Shimizu[2], Xuguang Jiang[1], Nobutaka Hirokawa[1] ([1]*Univ. Tokyo*, [2]*KEK-PF*)

9:00～11:30　F 会場（全学教育棟 2 階 E205）／Room F (Room E205, General Education Bldg. 2F)

1SFA　いろんなスケールで働く膜タンパク質の作動原理：実験と理論の新展開
Operating principles of membrane proteins at multiscale resolutions

オーガナイザー：岡崎 圭一（分子科学研究所），渡邉 力也（東京大学）
Organizers: Kei-ichi Okazaki (IMS), Rikiya Watanabe (The University of Tokyo)

Recent developments of both experiment and theory enable us to clarify operating principles of membrane proteins such as channel, transporter and motor. These membrane proteins show diverse functions and work at multiscale resolutions. In this symposium, we cover state-of-the-art experimental and theoretical techniques from time resolved, single-molecule experiments to quantum chemical calculation, coarse-grained and atomistic MD simulations. We aim to clarify mechanisms from a complementary approach of experiment and theory.

1SFA-1 脂質二重膜がカリウムチャネル開閉に及ぼす多様な影響
Specific and non-specific actions of membrane lipids on the gating of the potassium channel
○岩本 真幸, 老木 成稔（福井・医・分子生理）
Masayuki Iwamoto, Shigetoshi Oiki (*Dept. Mol. Physiol. & Biophys., Univ. Fukui Facult. Med. Sci.*)

1SFA-2 遷移パスシミュレーションによる Na^+/H^+ antiporter の輸送メカニズム
Transport mechanism of Na^+/H^+ antiporter from transition-path simulations
○岡崎 圭一[1], Hummer Gerhard[2]（[1]分子研, [2]MPI of Biophysics）
Kei-ichi Okazaki[1], Gerhard Hummer[2] ([1]*IMS*, [2]*MPI of Biophysics*)

1SFA-3 高速原子間力顕微鏡によるナノディスクに埋め込まれた膜タンパク質のダイナミクス観察
High-speed AFM imaging of membrane proteins in lipid nanodiscs
○柴田 幹大（金沢大・新学術創成）
Mikihiro Shibata (*InFiniti, Kanazawa Univ.*)

1SFA-4 X 線自由電子レーザーで捉えたバクテリオロドプシン構造変化の三次元動画
A three-dimensional movie of structural changes in bacteriorhodopsin captured by X-ray free electron lasers
○南後 恵理子[1,2], 岩田 想[1,2]（[1]理研 放射光セ, [2]京大医）
Eriko Nango[1,2], So Iwata[1,2] ([1]*RSC*, [2]*Kyoto Univ. Med.*)

1SFA-5 分子シミュレーションで探る膜輸送体・受容体の分子機能
Atomistically deciphering functional processes of membrane transporter and receptor with molecular simulations
○林 重彦（京都大学大学院理学研究科化学専攻）
Shigehiko Hayashi (*Dept. of Chem., Grad. Sch. of Science, Kyoto Univ.*)

1SFA-6 バナナ状たんぱく質の集合による膜チューブ形成
Membrane tubulation induced by assembly of banana-shaped protein rods
○野口 博司（東大物性研）
Hiroshi Noguchi (*ISSP, Univ. Tokyo*)

9:00〜11:30　G 会場（全学教育棟 3 階 C301）／Room G (Room C301, General Education Bldg. 3F)

1SGA　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 ハイパフォーマンス・コンピューティング(HPC)による次世代創薬計算技術
Next-generation in-silico drug discovery using high-performance computing

オーガナイザー：荒木 望嗣（京都大学），池口 満徳（横浜市立大学）
Organizers: Mitsugu Araki (Kyoto University), Mitsunori Ikeguchi (Yokohama City University)

Utilization of high performance computing (HPC) in the medical field is accelerating from the K computer to post K computer. Fundamental molecular-simulation techniques previously developed in the field of biophysics are now practically applied to the drug development process. In this symposium, next-generation in-silico drug discovery involving experimental collaboration and machine learning will be discussed with young researchers in "Priority issue 1 on Post-K computer" (Building Innovative Drug Discovery Infrastructure Through Functional Control of Biomolecular Systems).

1SGA-1 Development of GENESIS for high performance computing of biomolecular simulations
Jaewoon Jung[1,2], Chigusa Kobayashi[1], Yuji Sugita[1,2,3] ([1]*RIKEN AICS*, [2]*RIKEN TMS*, [3]*RIKEN QBiC*)

1SGA-2 エネルギー表示溶液理論を用いた蛋白質ー蛋白質複合体構造予測
Protein-protein complex structure prediction using the solution theory in the energy representation
○竹村 和浩[1], 松林 伸幸[2], 北尾 彰朗[1]（[1]東大・分生研, [2]阪大・基礎工）
Kazuhiro Takemura[1], Nobuyuki Matubayasi[2], Akio Kitao[1] ([1]*IMCB, Univ. of Tokyo*, [2]*Grad. Sch. Eng. Sci, Osaka Univ.*)

1SGA-3 分子動力学シミュレーションと小角 X 線散乱実験を組み合わせた蛋白質の動的構造変化の解析
Protein dynamics revealed by a combination analysis of molecular dynamics simulations and small-angle x-ray scattering experiments
○浴本 亨, 池口 満徳（横浜市大）
Toru Ekimoto, Mitsunori Ikeguchi (*Yokohama City Univ.*)

1SGA-4 Molecular dynamics simulations for the study of thermodynamic properties in streptavidin mutant-biotin analog systems
Keiko Shinoda, Hideaki Fujitani (*RCAST, The Univ. Of Tokyo*)

1SGA-5 創薬ビッグデータ統合システムの開発とゲノム医療への応用
Development of Next-generation computational infrastructure for drug discovery and practical application to genomic medicine
○荒木 望嗣[1,2], 奥野 恭史[1]（[1]京都大・院医, [2]理研・AICS）
Mitsugu Araki[1,2], Yasushi Okuno[1] ([1]*Grad. Sch. Med., Kyoto Univ.*, [2]*RIKEN, AICS*)

1SGA-6 機械学習による MD 計算に基づく結合ポーズ推定の高速化
Acceleration of MD-based Binding-Pose Prediction with Ligands and Proteins by Machine Learning
○寺山 慧[1], 岩田 浩明[2], 荒木 望嗣[4], 奥野 恭史[3,4], 津田 宏治[1,5,6]（[1]東大・新領域, [2]先端医療振興財団, [3]京大・医, [4]理研・計算科学研究機構, [5]理研・革新知能統合研究センター, [6]物質・材料研究機構）
Kei Terayama[1], Hiroaki Iwata[2], Mitsugu Araki[4], Yasushi Okuno[3,4], Koji Tsuda[1,5,6] ([1]*Grad. Sch. Frontier Sci., Univ. Tokyo*, [2]*Found. for Biomedical Researcha and Innovation*, [3]*Grad. Sch. Med., Kyoto Univ.*, [4]*AICS, RIKEN*, [5]*AIP, RIKEN*, [6]*Center for Material Research By Info. Integration, NIMS*)

9:00〜11:30　I 会場（全学教育棟 3 階 E305）／Room I (Room E305, General Education Bldg. 3F)

1SIA　ナノ計測技術とバイオイメージングの融合が開く単一細胞計測の新展開
Advanced single cell analysis by fusion of nano-characterization technology and bioimaing

オーガナイザー：高橋 康史（金沢大学），樫田 啓（名古屋大学）

Organizers: Yasufumi Takahashi (Kanazawa University), Hiromu Kashida (Nagoya University)

A combination of diverse interdisciplinary approaches in nanotechnology, engineering, chemistry, optics, chemical biology starts providing a new technologies for single-cell analysis. The symposium will focus on such newly developed single-cell analysis techniques, of which recent progresses will be presented by several young scientists in this field.

1SIA-1　DNA を利用した色素間エネルギー移動の詳細な解析
Analysis of energy transfer between dyes by using DNA scaffold

○樫田 啓[1,2]（[1]名大・院工, [2]JSTさきがけ）

Hiromu Kashida[1,2] ([1]*Grad. Sch. Eng., Nagoya Univ.*, [2]*PRESTO, JST*)

1SIA-2　生きた脳で RNA の観測ができたら
in vivo RNA labelling reveals dynamic regulation of ribonucleic foci in living neurons

大本 育実[1], 梅嶋 宏樹[1], 原田 慶恵[1], 韓 Yong-Woon[1], 岡本 晃充[2], ○王 丹[1]（[1]京大iCeMS, [2]東大先端研）

Ikumi Oomoto[1], Hiroki Umeshima[1], Yoshie Harada[1], Yong-Woon Han[1], Akimitsu Okamoto[2], **Ohtan Wang**[1] ([1]*Kyoto University, iCeMS*, [2]*Research Center for Advanced Science and Technology, University of Tokyo*)

1SIA-3　CUBIC: 細胞・細胞回路の網羅的解析を目的としたセロミクスパイプライン
CUBIC: a Cell-omics pipeline for comprehensive cell and cell circuit analysis

○洲崎 悦生[1,2,3]（[1]東大医・システムズ薬理学, [2]さきがけ・JST, [3]理研・QBiC・合成生物学）

Etsuo A. Susaki[1,2,3] ([1]*Dept. Syst. Pharmacol., UTokyo Grad. Sch. Med.*, [2]*PRESTO, JST*, [3]*Lab. Synthetic Biol., RIKEN QBiC*)

1SIA-4　細胞内カルシウムシグナル解読への新しいアプローチ
A new approach to decoding of Ca^{2+} signals in a single cell

○坂内 博子[1,2], 丹羽 史尋[3], 櫻木 繁雄[4], 御子柴 克彦[2] ([1]JSTさきがけ, [2]理化学研究所 BSI, [3]パリ高等師範学校, [4]東北大・院生命科学）

Hiroko Bannai[1,2], Fumihiro Niwa[3], Shigeo Sakuragi[4], Katsuhiko Mikoshiba[2] ([1]*JST PRESTO*, [2]*RIKEN BSI*, [3]*IBENS*, [4]*Tohoku Univ, Grad. Sch. Life Sci.*)

1SIA-5　アクチン線維が負の張力センサーとして働く仕組みを分子イメージングから解明する試み
Analysis of fluctuations of a single actin filament that works as a tension sensor

○辰巳 仁史（金沢工業大学・バイオ・化学部・応用バイオ学科）

Hitoshi Tatsumi (*Department of Applied Bioscience, Kanazawa Institute of Technology (KIT)*)

1SIA-6　ゴーストサイトメトリー
Ghost Cytometry

○太田 禎生[1, 2]（[1] 東京大学大学院工学系研究科応用化学専攻, [2]科学技術振興機構さきがけ）

Sadao Ota[1, 2] ([1]*Applied Chemistry Department, University of Tokyo*, [2]*JST, PRESTO*)

9:00〜11:30　L 会場（文法学部 2 階 B1 教室）／Room L (Room B1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

1SLA　実験と理論計算で明らかになってきた細胞環境での蛋白質間相互作用
Experimental and Computational Analysis on Protein-Protein Interaction in Cellular Environments

オーガナイザー：杉田 有治（理化学研究所），津本 浩平（東京大学）
Organizers: Yuji Sugita (RIKEN), Kohei Tsumoto (The University of Tokyo)

Understanding of protein-protein interactions in cellular environments is one of the essential research issues in biophysics. To understand them, not only X-ray structures of macromolecules but also various experimental and computational methods are necessary. In particular, recent advance of computer simulations allows us to simulate multiple proteins, nucleic acids, and metabolites simultaneously. We discuss about how to combine those computational studies with experimental measurements.

1SLA-1　Specific and non-specific protein-protein interactions in cellular environments
Yuji Sugita (*RIKEN*)

1SLA-2　Atomistic modeling of protein liquid-liquid phase separation
Sanbo Qin, **Huan-Xiang Zhou** (*Florida State University*)

1SLA-3　Nonspecific protein-protein interactions in dense protein solutions and near membranes
Michael Feig[1,2] ([1]*MSU*, [2]*QBiC*)

休憩
Break

1SLA-4　網羅的変異解析による VemP 翻訳伸長停止モチーフの同定と解析
Identification and characterization of a translation arrest motif in VemP by systematic mutational analysis
○森 博幸, 坂下 宗平, 伊藤 淳, 石井 英治, 秋山 芳展（京大 ウイルス・再生研）
Hiroyuki Mori, Sohei Sakashita, Jun Ito, Eiji Ishii, Yoshinori Akiyama (*Inst. Front. Life Med. Sci., Kyoto Univ.*)

1SLA-5　細胞内での一酸化窒素の動態
NO Dynamics in Cellular System
○城 宜嗣（兵庫県立大大学院生命理学研究科）
Yoshitsugu Shiro (*Univ. Hyogo*)

9:00〜11:30　M 会場（文法学部 1 階 B2 教室）／Room M (Room B2, Faculty of Letters, Faculty of Law Main Bldg. 1F)

1SMA　CREST「構造生命」/さきがけ「構造生命科学」領域 共催
構造生命科学の新しい潮流
New trends for Structural Life Science

オーガナイザー：清水 敏之（東京大学），栗栖 源嗣（大阪大学）
Organizers: Toshiyuki Shimizu (The University of Tokyo), Genji Kurisu (Osaka University)

“Structural life science” aims to integrate cutting-edge life science areas with structural biology for innovation in life science. Structural research of proteins, which play key roles in biological events, have provided a remarkable achievement so far, and the next important step is to determine the dynamics of such proteins and to study the functional mechanisms. In this symposium, the up-and-coming researchers will give presentation using various methods targeting membrane proteins.

はじめに
Opening Remarks
Toshiyuki Shimizu

1SMA-1 Ｖ１モーターの構造形成の分子機構
Molecular mechanism of the structural formation of V1 rotary motor
○村田 武士[1,2]（[1]千葉大・理学, [2]JST・さきがけ）
Takeshi Murata[1,2] ([1]*Grad. Sch. Sci., Chiba Univ.*, [2]*PRESTO, JST*)

1SMA-2 蛋白質膜透過駆動モーター SecDF
Protein Translocation Motor SecDF
○塚崎 智也[1], 古川 新[1], 吉海江 国仁[1], 森 貴治[2], 森 博幸[3], 森本 雄祐[4], 菅野 泰功[1], 岩木 薫大[1], 南野 徹[5], 杉田 有治[2], 田中 良樹[1]（[1]奈良先端大・バイオ, [2]理研, [3]京大・ウイルス・再生医科学研, [4]九工大・情報工学, [5]阪大・生命機能）
Tomoya Tsukazaki[1], Arata Furukawa[1], Kunihito Yoshikaie[1], Takaharu Mori[2], Hiroyuki Mori[3], Yusuke V. Morimoto[4], Yasunori Sugano[1], Shigehiro Iwaki[1], Tohru Minamino[5], Yuji Sugita[2], Yoshiki Tanaka[1] ([1]*Grad. Sch. of Biol. Sci., NAIST*, [2]*RIKEN*, [3]*Inst. for Front. Life and Med. Sci., Kyoto Univ.*, [4]*Grad. Sch. of Comp. Sci. and Sys. Eng., Kyushu Inst. of Tech.*, [5]*Grad. Sch. of Front. Biosci., Osaka Univ.*)

1SMA-3 Functional dynamics of membrane proteins revealed by NMR
Takumi Ueda, Ichio Shimada (*Grad. Sch. Pharm. Sci. The Univ. of Tokyo*)

1SMA-4 Combining XFEL crystallography and single-crystal spectroscopy for studying reaction dynamics of respiratory metalloenzymes
Minoru Kubo (*RIKEN SPring-8 Center*)

1SMA-5 Structural basis of muscle force generation and regulatory mechanism by CryoEM
Takashi Fujii (*RIKEN, QBiC*)

おわりに
Closing Remarks
Genji Kurisu

9:00～11:30　N 会場（文法学部 1 階 B3 教室）／Room N (Room B3, Faculty of Letters, Faculty of Law Main Bldg. 1F)

1SNA　新学術領域研究「3D 活性サイト科学」共催
生体分子活性サイトの構造機能相関解明への新規アプローチ
Novel approaches to elucidating the structure-function relationship of the active sites in biomolecular systems

オーガナイザー：佐藤 文菜（自治医科大学），木村 哲就（神戸大学）
Organizers: Ayana Sato-Tomita (Jichi Medical University), Tetsunari Kimura (Kobe University)

Subtle changes in the active-site structures and/or the electronic states of biomolecules, such as proteins, are key dynamics to perform their functions with high-selectivity and high-efficiency, besides conformational changes in the macroscopic scale. In this symposium, we introduce a number of state-of-the-art approaches that can characterize the active-sites in bimolecular systems with high spatial and temporal resolution, namely, X-ray fluorescence holography, time-resolved or damage-free XFEL crystallography, diffracted X-ray tracking, time-resolved spectroscopy, ENDOR, and computer simulation, and discuss their structure-dynamics-function relationships.

はじめに
Opening Remarks
Ayana Sato-Tomita

1SNA-1 蛍光 X 線ホログラフィーによるヘムタンパク質の金属周辺構造観測
First X-ray fluorescence holographic imaging of iron environments in heme proteins
○佐藤 文菜[1], 柴山 修哉[1], 八方 直久[2], 林 好一[3], 佐々木 裕次[4]（[1]自治医大・生物物理, [2]広島市大・情報科学, [3]名工大・物理工学, [4]東大・新領域）
Ayana Sato-Tomita[1], Naoya Shibayama[1], Naohisa Happo[2], Kouichi Hayashi[3], Yuji Sasaki[4] ([1]*Div. Biophys., Jichi. Med. Univ.*, [2]*Grad. Sch. Info. Sci., Hiroshima City Univ.*, [3]*Dep. Phys. Sci. Eng., NITech*, [4]*Grad. Sch. Frontier Sci., Univ. Tokyo*)

1SNA-2 High resolution and time-resolved X-ray crystallographic study on enzymatic reaction of human MTH1
Teruya Nakamura[1,2], Shaimaa Waz[2], Keisuke Hirata[2], Mami Chirifu[2], Shinji Ikemizu[2], Yuriko Yamagata[2] ([1]*Priority Organization for Innovation and Excellence, Kumamoto Univ.*, [2]*Grad. Sch. of Pharmaceut. Sci., Kumamoto Univ.*)

1SNA-3 時間分解分光法による ABC トランスポーターの輸送と ATP 加水分解過程の直接観察
Direct observation of allocate-transport and ATP-hydrolysis for the ABC transport by time-resolved spectroscopy
○木村 哲就[1,2], 林 沙英[1], 城 宜嗣[3], 杉本 宏[4], 池本 夕佳[5]（[1]神戸大・院理, [2]K-CONNEX, [3]兵県大・院生命理, [4]理研・SPring-8, [5]JASRI）
Tetsunari Kimura[1,2], Sae Hayashi[1], Yoshitsugu Shiro[3], Hiroshi Sugimoto[4], Yuka Ikemoto[5] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*K-CONNEX*, [3]*Grad. Sch. Life Sci., Univ. of Hyogo*, [4]*SPring-8, RIKEN*, [5]*JASRI*)

1SNA-4 生物学的プロトントンネリング機構解明へ～新規 ENDOR 解析法によるタンパク質構造精密解析～
Substrate Positioning of Soybean Lipoxygenase For H-Atom Abstraction by ENDOR 'Crystallography'
○堀谷 正樹（佐大・農）
Masaki Horitani (*Saga Univ., Dept of Appl Biochem & Food Sci*)

1SNA-5 生自然殺害細胞内 X 線 1 分子計測
X-ray single molecular observations in living Natural killer cells
○張 宰源[1,3], 倉持 昌弘[1,3], 一柳 光平[2], 佐々木 裕次[1,3]（[1]東京大学 新領域創成科学研究科, [2]高エネルギー加速器研究機構, [3]産総研-東大 先端オペランド計測技術オープンイノベーションラボラトリ）
Jae-Won Chang[1,3], Masahiro Kuramochi[1,3], Kouhei Ichiyanagi[2], Yuji Sasaki[1,3] ([1]*Graduate School of Frontier Science, The University of Tokyo*, [2]*KEK*, [3]*OPERANDO-OIL*)

1SNA-6 SACLA と SPring-8 により可視化された亜硝酸還元酵素のレドックス依存的な構造変化
Redox-dependent structural change in nitrite reductase visualized by SPring-8 and SACLA
○溝端 栄一（大阪大・院工）
Eiichi Mizohata (*Grad. Sch. Eng., Osaka Univ.*)

1SNA-7 Energetics of proton transfer in proteins
Hiroshi Ishikita (*The University of Tokyo, RCAST*)

おわりに
Closing Remarks
Tetsunari Kimura

13:20～15:50　A 会場（全学教育棟 1 階 E107）／Room A (Room E107, General Education Bldg. 1F)

1SAP　新学術領域研究「生命分子システムにおける動的秩序形成と高次機能発現」共催
秩序が作る動きと動きが作る秩序
Dynamical ordering of biomolecular systems for creation of integrated functions: Dynamics Made of Ordering and Ordering Made from Dynamics

オーガナイザー：秋山 良（九州大学），佐藤 啓文（京都大学）
Organizers: Ryo Akiyama (Kyushu Univeristy), Hirofumi Sato (Kyoto University)

Dynamic ordering should have two aspects. First one is dynamics made of ordering. An ordered structure is constructed from molecules, and the dynamical structural change occurs due to some non-equilibrium phenomena such as chemical reactions. Second one is ordering made from dynamics. Dynamical motions cause effective attractions between units in a system and the attractions construct ordering structures. Both aspects have common frameworks like van der Waals picture on gas-liquid transition. This symposium aims for mutual development in both.

はじめに
Opening Remarks

1SAP-1 時間発展する超分子集合体
Time-dependent evolution of a metastable supramolecular assembly
○杉安 和憲（物材機構）
Kazunori Sugiyasu (*NIMS*)

1SAP-2 分子の集合・離脱が駆動する神経軸索ガイダンスの分子メカニクス
Molecular Mechanics for Axon Navigation in the Brain
○稲垣 直之（奈良先端大・バイオ）
Naoyuki Inagaki (*Nara Inst Sci Technol*)

1SAP-3 How can we control swarming of self-propeled biomolecular motors
Akira Kakugo[1,2], Jakia Jannat Keya[1], Arif Md. Rashedul Kabir[2] ([1]*Graduate School of Chemical Sciences and Engineering, Hokkaido University*, [2]*Faculty of Science, Hokkaido University*)

1SAP-4 アクトミオシン細胞骨格におけるモーター誘起応力の理論
Theory on motor-induced stress in an isotropic actin-myosin network
○平岩 徹也（東京大学理学系研究科）
Tetsuya Hiraiwa (*Department of Physics, The University of Tokyo*)

1SAP-5 ロタキサン連結高分子系超分子における組織化制御
Dynamical Ordering of Supramolecular Architecture Comprising Rotaxane-Linked Polymers
○高田 十志和（東工大・物質理工）
Toshikazu Takata (*Dept. of Chem. Sci. and Eng., Tokyo Inst. of Tech.*)

1SAP-6 基板上で自発的に運動・増殖する細胞のためのミニマル粒子モデル
A particle-based minimal model for crawling and proliferating cells on substrate
○山本 量一[1], シュニーダー サイモン[2], モリーナ ジョン[1] ([1]京都大学大学院工学研究科 化学工学専攻, [2]京都大学 福井謙一記念研究センター）
Ryoichi Yamamoto[1], Simon Schnyder[2], John J. Molina[1] ([1]*Department of Chemical Engineering, Kyoto University*, [2]*Fukui Institute for Fundamental Chemistry, Kyoto University*)

13:20～15:50　K 会場（文法学部 2 階 A1 教室）／Room K (Room A1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

1SKP　Membrane Molecular Bioenergetics の新地平：光子から超複合体まで
Frontiers in Membrane Molecular Bioenergetics: from photon to supercomplex

オーガナイザー：ゲーレ クリストフ（大阪大学），阿部 一啓（名古屋大学）
Organizers: Christoph Gerle (Osaka University), Kazuhiro Abe (Nagoya University)

Recent methodological breakthroughs in single particle cryo-EM, free electron X-ray laser crystallography, in vitro mimetic membrane syststems and theoretical approaches are rapidly reshaping our view of molecular bioenergetics. In this symposium young researchers at the very forefront of structural, functional and theoretical investigation of membrane bioenergetics will present their latest discoveries. Various fields of bioenergetics will be covered ranging from the photosynthetics light reactions over electron transport chain mediated proton motive force generation and up to the synthesis of ATP by rotary ATP synthases.

1SKP-1 光化学系 I-フェレドキシン電子伝達複合体の X 線構造および NMR 解析
X-ray structure and NMR analysis of the electron transfer complex between Photosystem I and Ferredoxin
○田中 秀明[1,2], 河合 寿子[1], 武藤 梨沙[1], ピエール セティフ[3], ノヴァチク マーク[4], レグナー マティアス[4], 池上 貴久[5], 栗栖 源嗣[1,2]（[1]大阪大学蛋白質研究所, [2]JST-CREST, [3]CEA Saclay, [4]Ruhr-University Bochum, [5]横市大・生命医科学）
Hideaki Tanaka[1,2], Hisako Kawai[1], Risa Mutton[1], Setif Pierre[3], Marc Nowaczyk[4], Matthias Rogner[4], Takahisa Ikegami[5], Genji Kurisu[1,2] ([1]*IPR, Osaka Univ.*, [2]*JST-CREST*, [3]*CEA Saclay*, [4]*Ruhr-University Bochum*, [5]*Grad. Sch. of Medical Life Science, Yokohama City Univ.*)

1SKP-2 分子構造に基づく理論解析による光合成膜蛋白質における反応機構の解明
Theoretical investigation based on molecular structures reveals reaction mechanisms in photosynthetic membrane proteins
○斉藤 圭亮（東京大学 先端科学技術研究センター）
Keisuke Saito (*RCAST, The University of Tokyo*)

1SKP-3 The Regulatory Functions and movements of quinones: It's Insane in the Membrane!
Duncan McMillan[1], Yoshio Nakatani[2], Lars Jeuken[3], Julia Butt[4], Gregory Cook[2], Hiroyuki Noji[5] ([1]*Department of Biotechnology, Delft University of Technology*, [2]*Department of Microbiology and Immunology, University of Otago*, [3]*School of Biomedical Sciences, University of Leeds*, [4]*School of Chemistry, and School of Biological Sciences, University of East Anglia*, [5]*Department of Applied Chemistry, Graduate School of Engineering, The University of Tokyo*)

1SKP-4 X 線自由電子レーザーを用いた、チトクロム酸化酵素からの一酸化炭素解離に伴う構造変化の時分割結晶構造解析
A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from 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], 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 ピコ研）
Atsuhiro Shimada[1], Minoru Kubo[2], Seiki Baba[3], Hideo Ago[2], Tomitake Tsukihara[4], Shinya Yoshikawa[5] ([1]*Fac. Appl. Biol. Sci., Gifu Univ.*, [2]*RIKEN, SPring-8 Center*, [3]*JASRI*, [4]*Inst. for Protein Res., Osaka Univ.*, [5]*Picobiol. Inst., Univ. Hyogo*)

1SKP-5 好熱菌由来 V 型 ATP 合成酵素の単粒子解析
Single-particle analysis of V-type ATPase/synthase from *Thermus thermophilus* by cryo-EM
○中西 温子[1], 岸川 淳一[1], 光岡 薫[2], 横山 謙[1]（[1]京産大・総生・生命システム, [2]阪大・超高圧電顕センター）
Atsuko Nakanishi[1], Jun-ichi Kishikawa[1], Kaoru Mitsuoka[2], Ken Yokoyama[1] ([1]*Dept. of Life Sci. Kyoto Sangyo Univ.*, [2]*Res. Ctr. UVHEM. Univ. Osaka*)

1SKP-6 Cryo-EM structures of the autoinhibited E. coli ATP synthase in three rotational states
Meghna Sobti[1], Callum Smits[1], Andrew Wong[2], Robert Ishmukhametov[3], Daniela Stock[1,4], Sara Sandin[2], **Alastair Stewart**[1,4] ([1]*VCCRI, Sydney, Australia*, [2]*SBS, NTU, Singapore*, [3]*Physics, University of Oxford, UK*, [4]*Medicine, UNSW, Australia*)

13:20〜15:50　L 会場（文法学部 2 階 B1 教室）／Room L (Room B1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

1SLP　環境効果の分子レベル解析に基づくタンパク質の構造・機能チューニング
Molecular-Level Analysis of Environment Effect toward Tuning of Protein Structure and Function

オーガナイザー：松林 伸幸（大阪大学），吉村 成弘（京都大学）
Organizers: Nobuyuki Matubayasi (Osaka University), Shige H. Yoshimura (Kyoto University)

In a living cell, proteins are folded, interact, and function in a multi-component environment. This implies that the structure and function of protein could be modulated by changing its surroundings. The present symposium focuses on understanding how protein structure and function are affected by its environments, with recent topics from solution chemistry, structural biology, protein engineering, and cell biology. The technical application of such environment-based protein tuning, which is distinct from genetic engineering, will also be discussed.

1SLP-1 タンパク質構造・配置に対する混合溶媒効果の全原子自由エネルギー計算による解析
Mixed-solvent effect on protein configuration studied by all-atom computation of free energy
○松林 伸幸（大阪大学 大学院基礎工学研究科 化学工学領域）
Nobuyuki Matubayasi (*Division of Chemical Engineering, Grad Sch Eng Sci, Osaka Univ*)

1SLP-2 好アルカリ性細菌の高アルカリ性環境適応に関与するメゾレベルでの場としての細胞表層酸性高分子役割の解明
Elucidation of the role of cell surface acidic polymers as a place at meso level from alkaliphilic bacteria
○伊藤 政博（東洋大 生命科）
Masahiro Ito (*Faculty of Life Sciences, Toyo Univ.*)

1SLP-3 リン脂質二重膜の構造変化に伴う水和状態の変化：テラヘルツ分光法による研究から
Changes in the hydration states of phospholipid bilayers accompanying bilayer structural changes: From the studies by THz spectroscopy
○菱田 真史（筑波大・数物）
Mafumi Hishida (*Dept. Chem., Univ. Tsukuba*)

1SLP-4 蛋白質―脂質相互作用と小孔形成毒素
Protein-lipid interactions in a pore-forming toxin
○津本 浩平[1], カアベイロ ホセ[2]（[1]東大・院工，医科研, [2]九大・薬学）
Kouhei Tsumoto[1], Jose Caaveiro[2] ([1]*Grad. Sch. Eng. and Inst. Med. Sci., Univ. Tokyo*, [2]*Grad. Sch. Pharm., Kyushu Univ.*)

1SLP-5 タンパク質構造への分子環境の効果：抗原抗体界面の分子動力学計算による研究
Molecular environment effects on the protein structure: Molecular dynamics studies on the antigen-antibody interface
○山下 雄史（東大先端研）
Takefumi Yamashita (*RCAST, Univ. Tokyo*)

1SLP-6 NMR analysis of proteins in living cells
Hidehito Tochio (*Dept. Biophys., Grad. Schl. Sci., Kyoto Univ.*)

13:20～15:50　M 会場（文法学部 1 階 B2 教室）／Room M (Room B2, Faculty of Letters, Faculty of Law Main Bldg. 1F)

1SMP　刺激に応答するタンパク質の構造生物学
Structural biology of proteins mediating stimulus-response

オーガナイザー：中川 敦史（大阪大学），神取 秀樹（名古屋工業大学）
Organizers: Atsushi Nakagawa (Osaka University), Hideki Kandori (Nagoya Institute of Technology)

Living organisms receive and response to stimuli from their environment. These processes are essential for living systems and many proteins work in this process. In this symposium, we will discuss the stimulus-response mechanism of living systems based on the molecular mechanisms of the proteins that function in gas-sensing, photo-sensing, mechano-sensing, voltage-sensing, and redox-sensing.

1SMP-1 Structural basis for the heme-dependent transcriptional regulation
Shigetoshi Aono[1,2] ([1]*Okazaki Int. Integ. Biosci.*, [2]*Inst. Mol. Sci.*)

1SMP-2 光活性化アデニル酸シクラーゼの構造と機能
Structure and function of photoactivated adenylyl cyclase
大木 規央[2], 朴 三用[2], ○伊関 峰生[1]（[1]東邦大・薬, [2]横浜市大・院生命医科学）
Mio Ohki[2], Sam-Yong Park[2], **Mineo Iseki**[1] ([1]*Facul. Pharm. Sci., Toho Univ.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

1SMP-3 細菌機械受容チャネル MscL のメカノゲーティングに対する計算科学的アプローチ
Computational Approach to Mechano-Gating of the Bacterial Mechanosensitive Channel MscL
○澤田 康之[1], 曽我部 正博[2]（[1]名古屋経済大学人間生活科学部管理栄養学科, [2]名大院・医・メカノバイオロジーラボ）
Yasuyuki Sawada[1], Masahiro Sokabe[2] ([1]*Dept Nutrition Fac Human Life Science Nagoya Univ Economics*, [2]*Mechanobiology Lab Nagoya Univ Grad Sch Med*)

1SMP-4 電位依存性ホスファターゼ VSP のカップリング機構に関する構造生物学的研究
Structural analysis of voltage-sensing phosphatase (VSP) on the electrochemical coupling
○成田 宏隆[1,3], 神田 直樹[1], 岡村 康司[2], 中川 敦史[1,3]（[1]阪大・蛋白研, [2]阪大・院医, [3]CREST, JST）
Hirotaka Narita[1,3], Naoki Kanda[1], Yasushi Okamura[2], Atsushi Nakagawa[1,3] ([1]*Inst. Protein Res., Osaka Univ.*, [2]*Grad. Sch. of Med., Osaka Univ.*, [3]*CREST, JST*)

1SMP-5 電位依存性プロトンチャネル VSOP/Hv1 の電場中での動態の解析
Molecular dynamics study of kinetics of the voltage-gated proton channel VSOP/Hv1 under electric fields
○近藤 寛子[1], 米澤 康滋[2], 宮下 尚之[3], 岩城 雅代[4], 竹下 浩平[5], 藤原 祐一郎[6], 城田 松之[7,8,9], 木下 賢吾[8,9,10], 岡村 康司[6], 中川 敦史[5], 神取 秀樹[4], 鷹野 優[1]（[1]広市大・院・情報, [2]近畿大・先端研, [3]近畿大・生物理工, [4]名工大・院・工, [5]阪大・蛋白研, [6]阪大・院・医, [7]東北大・院・医, [8]東北大・メガバンク, [9]東北大・院・情報, [10]東北大・加齢研）
Hiroko X. Kondo[1], Yasushige Yonezawa[2], Naoyuki Miyashita[3], Masayo Iwaki[4], Kohei Takeshita[5], Yuichiro Fujiwara[6], Matsuyuki Shirota[7,8,9], Kengo Kinoshita[8,9,10], Yasushi Okamura[6], Atsushi Nakagawa[5], Hideki Kandori[4], Yu Takano[1] ([1]*GSIS, Hiroshima City Univ*, [2]*Iat, Kindai Univ*, [3]*Bost, Kindai Univ*, [4]*Grad Sch Eng, Nagoya Inst Tech*, [5]*IPR, Osaka Univ*, [6]*Grad Sch Med, Osaka Univ*, [7]*Grad Sch Med, Tohoku Univ*, [8]*ToMMo, Tohoku Univ*, [9]*GSIS, Tohoku Univ*, [10]*IDAC, Tohoku Univ*)

1SMP-6 Structural basis of redox-dependent regulation of SERCA2b
Michio Inoue[1], Nanami Sakuta[1], Satoshi Watanabe[1], Ryou Ushioda[2], Yoshiki Tanaka[3], Tomoya Tsukazaki[3], Kazuhiro Nagata[2], **Kenji Inaba**[1] ([1]*Tohoku Univ*, [2]*Kyoto Sangyo Univ*, [3]*NAIST*)

13:20～15:50　N 会場（文法学部 1 階 B3 教室）／Room N (Room B3, Faculty of Letters, Faculty of Law Main Bldg. 1F)

1SNP　協賛　AMED 革新的先端研究開発支援事業（AMED－CREST/PRIME）
「メカノバイオロジー機構の解明による革新的医療機器及び医療技術の創出」

メカノバイオロジー研究の最先端と多様性
International symposium on mechanobiology with its cutting edge and diversity

オーガナイザー：新井 敏（早稲田大学），林 久美子（東北大学）
Organizers: Satoshi Arai (Waseda University), Kumiko Hayashi (Tohoku University)

The main-stream of mechanobiology unveils the mechanism of how cells sense and respond to the mechanical stimulus at molecular level. Furthermore, recent studies on mechanobiology spread to the broaden area by researchers who interpret the concept of “mechano” differently. This symposium proposed here will focus on the current topics in the main-stream and also covers topics regarding the mechanobiology with diversity. In particular, speakers include those who are less familiar with biophysical meeting.

1SNP-1　オルガネラサイズの熱源を作り細胞機能を温熱制御する試み
Thermal Control of Cellular Functions Using Organelle-sized Heat Spots
○新井 敏（早大・理工研）
Satoshi Arai (*Res. Inst. Sci. Eng., Waseda Univ.*)

1SNP-2　Nanostructured Smart Materials for the Remote Manipulation of Cell Behavior
Attilio Marino[1], Gianni Ciofani[1,2] ([1]*Smart Bio-Int., IIT, Italy*, [2]*Dept. Mech. Aero. Eng., Politec. Torino, Italy*)

1SNP-3　A molecular mechanism of gene regulation by matrix mechanics -A moving story of FHL2 and Force-
Naotaka Nakazawa[1], Aneesh Sathe[2], G.V. Shivashankar[2,3,4], Michael Sheetz[2,3,5] ([1]*iCeMS, Kyoto Univ.*, [2]*Mechanobiology Institute, National Univ. of Singapore*, [3]*Dept. of Biol. Sci., National Univ. of Singapore*, [4]*iFOM, Italy*, [5]*Dept. of Biol. Sci., Columbia Univ.*)

1SNP-4　Curvature-propagated mechanochemical waves in subcellular pattern formation
Min Wu, Maohan Su, Cheesan Tong, Shengping Xiao (*National Univ. Singapore*)

1SNP-5　メカノトランスダクションと心筋リプログラミング、心臓再生
Mechano-transduction and Direct Cardiac Reprogramming for Heart Regeneration
○家田 真樹（慶應義塾大学医学部循環器内科）
Masaki Ieda (*Department of Cardiology, Keio University School of Medicine*)

1SNP-6　臓器内部における末梢神経のメカノセンシング動態
Mechanosensing dynamics of peripheral nerves inside organs
○神谷 厚範（国循センター・研究所）
Atsunori Kamiya (*NCVC*)

1SNP-7　ゆらぎを利用した低侵襲な力測定による神経細胞オルガネラ輸送の解明
Non-invasive force measurement using fluctuation for organelle transport in neurons
○林 久美子（東北大工）
Kumiko Hayashi (*Sch. Eng., Tohoku Univ.*)

8:45〜11:15　A 会場（全学教育棟 1 階 E107）／Room A (Room E107, General Education Bldg. 1F)

2SAA　少数性の生命科学：Minor 要素の振る舞いがシステム全体に影響を及ぼす思わぬ仕掛け
Introduction about “Minority in life science”

オーガナイザー：永井 健治（大阪大学），上田 泰己（東京大学/理化学研究所）
Organizers: Takeharu Nagai (Osaka University), Hiroki Ueda (The Univ. of Tokyo/RIKEN)

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 minority cells would sometimes significantly alter the behavior of the whole cell population. In this symposium, we would like to discuss not only analytical methods for sensitive detection or visualization of such minority cells, but also the theories regarding principle or mechanism how the minority cells are generated and exert biological roles.

2SAA-1　Development of techniques for imaging physiological functions toward visualization of singularity caused by minority elements
○永井 健治（阪大 産研）
Takeharu Nagai (*The Institute of Scientific and Industrial Research, Osaka University*)

2SAA-2　細胞集団に螺旋信号波をもたらす臨界現象
Critical transition controls the self-organized spiral nuclearion
○堀川 一樹（徳島大 医歯薬）
Kazuki Horikawa (*Tokushima Univ. Biomedical Sci.*)

2SAA-3　Minor 要素の人為的な活性制御を可能とする受容体の配位ケミカルジェネティクス
Coordination chemical genetics of receptors for artificially regulating minority events
○清中 茂樹（京大工）
Shigeki Kiyonaka (*Grad. Sch. Eng., Kyoto Univ.*)

2SAA-4　Small cells bur large impacts, revealed by extensive 2P / 8K-CMOS singularity imaging
○西村 智（自治医大）
Satoshi Nishimura (*Jichi Med Univ*)

2SAA-5　High speed Raman imaging for chemical profiling of cells and tissues
○藤田 克昌（阪大）
Katsumasa Fujita (*Osaka Univ*)

2SAA-6　How can one quantify singularity in cells from Single Cell Raman Imaging?
○小松崎 民樹[1,2]（[1]北大電子研, [2]北大 生命科学院）
Tamiki Komatsuzaki[1,2] ([1]*Hokkaido Univ., RIES, MSC*, [2]*Hokkaido Univ., Grad. School of Life Science*)

2SAA-7　マイノリティ細胞による自己免疫疾患発症制御機構の解明
Regulation of autoimmunity by minority cells
○岡崎 拓（徳島大学先端酵素学研究所）
Taku Okazaki (*Institute of Advanced Medical Sciences, Tokushima University*)

2SAA-8　点描画解析プラットフォームを用いた確率的全脳マッピング
Probabilistic Mapping of Mouse Brains with Scalable and Pointillistic Analytical Platform
○村上 達哉[1], 真野 智之[2,3], 犀川 周[3], 堀口 修平[4], 馬場 孝輔[5], 望月 秀樹[5], 田井中 一貴[6], 上田 泰己[1]（[1]東大・医, [2]プリンストン大, [3]東大・新領域, [4]阪大・基礎工, [5]阪大・医, [6]新潟大・脳研）
Tatsuya Murakami[1], Tomoyuki Mano[2,3], Shu Saikawa[3], Shuhei Horiguchi[4], Kousuke Baba[5], Mochizuki Hideki[5], Kazuki Tainaka[6], Hiroki Ueda[1] ([1]*Med., Univ. Tokyo*, [2]*Dept. Chem., Princeton Univ.*, [3]*Univ. Tokyo*, [4]*Osaka Univ.*, [5]*Med., Osaka Univ.*, [6]*Niigata Univ.*)

8:45～11:15　B 会場（全学教育棟 2 階 B201）／Room B (Room B201, General Education Bldg. 2F)

2SBA　糖および脂質の生物物理―医薬への展開―
Biophysics on saccharides and lipids toward medicine

オーガナイザー：松本 陽子（崇城大学），相田 美砂子（広島大学）
Organizers: Yoko Matsumoto (Sojo University), Misako Aida (Hiroshima University)

Saccharides play important roles in adhering to cells, transmitting information, and recognizing molecules in the cell membranes composed of lipids through receptors. Recently, lipid vesicles including saccharides have been generated and effective for inhibiting the growth of tumor cells. Therefore, saccharides and lipids are good targets to create a novel therapeutic system. In this symposium, we introduce biophysical and therapeutic studies related to characteristics of saccharides and lipids and discuss the development for medicine.

2SBA-1　トレハロースリポソームによるがん治療効果とアポトーシス
Therapeutic effects of trehalose liposomes against carcinoma along with apoptosis
○松本 陽子（崇城大院・応用生命）
Yoko Matsumoto (*Grad. Life, Univ. Sojo*)

2SBA-2　天然糖トレハロースによる空間認知記憶の改善とオートファジーの関与
Trehalose intake improves spatial memory through autophagy activation in the brain of mice
○丹治 邦和, 三木 康生, 森 文秋, 若林 孝一（弘前大院・医・脳神経病理）
Kunikazu Tanji, Yasuo Miki, Fumiaki Mori, Koichi Wakabayashi (*Dept. of Neuropathol., Inst. of Brain Sci., Hirosaki Univ. Graduate Sch. of Med.*)

2SBA-3　肺がん転移促進タンパク質 CERS6 およびそれを分子標的とした薬剤戦略
Targeting ceramide synthase 6-dependent metastasis-prone phenotype in lung cancer cells
○鈴木 元（名大院・医・分子腫瘍）
Motoshi Suzuki (*Nagoya Univ Grad Sch Med, Mol Carcinog*)

2SBA-4　脂質代謝酵素 PLA2 ファミリーによるリポクオリティ制御の新機軸
Novel insights into the lipoquality control by the PLA2 family
○村上 誠[1,2,3]（[1]東京大学大学院医学系研究科 疾患生命工学センター 健康環境医工学部門, [2]公益財団法人東京都医学総合研究所, [3]日本医療研究開発機構CREST）
Makoto Murakami[1,2,3] ([1]*Center for Disease Biology and Integrative Medicine, Faculty of Medicine, The University of Tokyo*, [2]*Tokyo Metropolitan Institute of Medical Science*, [3]*AMED-CREST*)

2SBA-5　実在形質膜をモデル化した脂質二重層膜の分子動力学計算
Molecular dynamics study of lipid bilayers modeling real plasma membranes
安藤 嘉倫, ○岡崎 進（名大院・工）
Yoshimichi Andoh, **Susumu Okazaki** (*Nagoya University*)

2SBA-6　広帯域分光を用いた二糖周辺の水の水素結合ネットワーク評価
Characterization of the hydrogen-bond network of water around sucrose and trehalose investigated with broadband spectroscopy
○白神 慧一郎[1], 小川 雄一[2], 中村 昌人[3], 味戸 克裕[3], 田島 卓郎[3]（[1]理研・IMS, [2]京大・農, [3]NTT・先端集積デバイス研）
Keiichiro Shiraga[1], Yuichi Ogawa[2], Masahito Nakamura[3], Katsuhiro Ajito[3], Takuro Tajima[3] ([1]*RIKEN Center for IMS*, [2]*Grad. Sch. Agri., Kyoto Univ.*, [3]*Device Technology Labs., NTT*)

2SBA-7　グルコースとトレハロースの水溶液中における構造と水和に関する ab initio QM/MM-MD 法による研究
Ab initio QM/MM-MD study on conformation and hydration of glucose and trehalose in aqueous solution
○相田 美砂子（広島大院・理）
Misako Aida (*Grad. Sch. Sci., Hiroshima Univ*)

8:45～11:15　C 会場（全学教育棟 2 階 B202）／Room C (Room B202, General Education Bldg. 2F)

2SCA　生体高分子の広い時空間での動的相関構造解析を目指した実験的手法と計算科学の新展開
New approaches of integrated use of experimental and simulation methods for dynamic correlative structural analysis of biomolecules in the wide spatiotemporal scale

オーガナイザー：杉山 正明（京都大学），中川 洋（日本原子力研究開発機構）
Organizers: Masaaki Sugiyama (Kyoto University), Hiroshi Nakagawa (Japan Atomic Energy Agency)

Biomacromolecules are functionalized by modulating their structure and assemble state in a physiological solution. This functional dynamics is subjected to the wide space-time from 10-12 m to 10-6 m and 10-12 sec to 10-6 sec and therefore it is crucially important to have analysis methods crossover this wide space-time range. In this symposium, we would like to approach to the structure and dynamics related to wide hierarchy with marriage of experimental methods, represented by quantum beam scattering techniques and NMR, and computational science.

2SCA-1　このシンポジウムの狙いについて
Introduction of hybrid/integrative structural biology
○杉山 正明（京大原子炉）
Masaaki Sugiyama (*KURRI*)

2SCA-2　モデル膜の熱揺らぎと機械的性質に及ぼすペプチドの効果
Effects of incorporating small peptide on collective thermal fluctuations and elastic and viscous properties in model lipid bilayers
○長尾 道弘[1,2], Kelley Elizabeth[1], Butler Paul[1]（[1]米国標準技術研究所, [2]インディアナ大）
Michihiro Nagao[1,2], Elizabeth Kelley[1], Paul Butler[1] ([1]*NIST*, [2]*Indiana U.*)

2SCA-3　Protein dynamics as studied by neutron spin echo and MD simulation
Rintaro Inoue[1], Takashi Oda[2], Tomotaka Oroguchi[3], Mitsunori Ikeguchi[2], Masaaki Sugiyama[1], Mamoru Sato[2] ([1]*Research Reactor Institute, Kyoto University*, [2]*Yokohama City University*, [3]*Keio University*)

2SCA-4　Protein Structural Fluctuations Investigated by X-ray Solution Scattering and Molecular Dynamics Simulation
Tomotaka Oroguchi[1,2] ([1]*Faclt. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 Center*)

2SCA-5　統合的な構造物学アプローチによるに糖タンパク質および糖鎖の構造ダイナミクスの解析
Integrative structural biology approaches for understanding conformational dynamics of oligosaccharides and glycoproteins
○矢木 宏和[1], 谷中 冴子[2], 與語 理那[1,2], 鈴木 達哉[2], 山口 拓実[3], 杉山 正明[4], 加藤 晃一[1,2]（[1]名市大・院薬, [2]自然科学研究機構・岡崎統合バイオ、分子研, [3]北陸先端・マテリアル, [4]京大・原子炉実験所）
Hirokazu Yagi[1], Saeko Yanaka[2], Rina Yogo[1,2], Tatsuya Suzuki[2], Takumi Yamaguchi[3], Masaaki Sugiyama[4], Koichi Kato[1,2] ([1]*Grad. Sch. of Pharm. Sci., Nagoya City Univ.*, [2]*Okazaki Inst. for Integra. Biosci. and Inst. for Mol. Sci., Nat. Inst. of Nat. Sci.*, [3]*Sch. Of Materials Sci., JAIST*, [4]*Research Reactor Institute, Kyoto University*)

2SCA-6　分子シミュレーションの動的解析手法によるタンパク質のダイナミクスの研究
Investigating protein dynamics by using dynamical analysis methods of molecular simulations
○光武 亜代理（慶應義塾大学理工学部物理学科）
Ayori Mitsutake (*Dept. Phys, Keio Univ.*)

2SCA-7　中性子散乱と計算機科学の融合による蛋白質のドメインダイナミクスの解析
Analysis of protein domain dynamics by integrating of neutron scattering and computer science
○中川 洋[1,2]（[1]日本原子力研究開発機構・原子力科学研究部門・物質科学研究センター・階層構造研究グループ, [2]JST, さきがけ）
Hiroshi Nakagawa[1,2] ([1]*Japan Atomic Energy Agency, Materials Science Research Center*, [2]*JST, PRESTO*)

8:45〜11:15　D 会場（全学教育棟 2 階 E201）／Room D (Room E201, General Education Bldg. 2F)

2SDA　自己複製系の新展開：創発と合成の邂逅
Frontiers in self-replicating systems: Emergence and synthesis

オーガナイザー：前多 裕介（九州大学），下林 俊典（海洋研究開発機構）
Organizers: Yusuke Maeda T. (Kyushu Univeristy), Shunsuke Shimobayashi F. (JAMSTEC)

Living cells produce themselves so that a major conceptual question in biology is self-reproduction. One may understand it for self-replication of biopolymers following von Neumann logic, which implies a memory. But, how does self-reproduction operate without apparent memory? In this symposium, recent developments of mechanical aspects for self-reproduction will be shown from physics, mathematics, and synthetic biology. Self-replication and functional expression of information coding polymers of DNA and RNA are particularly focused in both experiment and theory.

2SDA-1　Emergence of genetic information in information-polymer soup
Shoichi Toyabe (*Grad. Sch. Eng., Tohoku Univ.*)

2SDA-2　自己複製する鋳型高分子系において複雑な配列が選択される条件
Conditions for selecting complex sequences in mathematical model of self-replicating template polymer system
○松原 嘉哉, 金子 邦彦（東大・総文）
Yoshiya Matsubara, Kunihiko Kaneko (*Grad. Sch. Arts and Sci., The Univ. of Tokyo*)

2SDA-3　染色体複製サイクルの繰り返しによる環状 DNA の試験管内自律増殖
Autonomous propagation of circular DNA molecules in vitro through a continuous repetition of a chromosome replication cycle
○末次 正幸, 高田 啓（立教大・理・生命理）
Masayuki Su'etsugu, Hiraku Takada (*Col. of Sci., Rikkyo Univ.*)

2SDA-4　Emergence of DNA-encapsulating liposomes from a DNA− Lipid blend film
Shunsuke Shimobayashi (*Department of Mathematical Science and Advanced Technology, Japan Agency for Marine-Earth Science and Technology*)

2SDA-5　オンチップ人工細胞：無細胞系の遺伝子発現と幾何形状による制御
Artificial-cells-on-a-chip: cell-free gene expression in microwells with various geometries
○イズリ ジャン[1], 坂本 遼太[1], ノワロー ヴィンセント[2], 前多 裕介[1]（[1]九州大学理学研究院物理学部門, [2]ミネソタ大・物理）
Ziane Izri[1], Ryota Sakamoto[1], Vincent Noireaux[2], Yusuke Maeda[1] ([1]*Dept. Phys., Kyushu Univ.*, [2]*Dept. Phys., Univ. Minnesota*)

2SDA-6　細胞内外で機能する合成 RNA-タンパク質複合体の設計と構築
Synthetic RNA-protein nanostructured devices that function in vitro and in cells
○齊藤 博英, 大野 博久（京都大学）
Hirohide Saito, Hirohisa Ohno (*Kyoto Univ.*)

8:45〜11:15　E 会場（全学教育棟 2 階 E203）／Room E (Room E203, General Education Bldg. 2F)

2SEA　生物時計の 24 時間リズム創出原理に関するマジ（めな）議論
Molecular, Structural, and Dynamic Origins of 24-hour Period in Circadian Clock Systems

オーガナイザー：秋山 修志（分子科学研究所），八木田 和弘（京都府立医科大学）
Organizers: Shuji Akiyama (IMS), Kazuhiro Yagita (Kyoto Prefectural University of Medicine)

Circadian clocks reveal a self-sustained oscillation with an approximately 24 h period. In these days, there is a growing number of researches approaching origins of slow yet ordered dynamics from the viewpoints of biophysics, chemical biology, structural biology, and bioinformatics. The accumulated evidence offers an ideal opportunity to revisit a fundamental question in chronobiology: what determines the temperature-compensated 24 h period? In this symposium, we will present the current understanding of the clock systems in prokaryotes and eukaryotes and discuss emerging ideas.

はじめに
Opening Remarks

2SEA-1 シアノバクテリアのタンパク質時計が教えてくれること
Lessons from Cyanobacterial Circadian Clock System
○秋山 修志[1,2,3]（[1]分子研 協奏分子システム研究センター, [2]総研大, [3]理研・放射光科学総合研究センター）
Shuji Akiyama[1,2,3] ([1]*CIMoS, IMS, NINS*, [2]*SOKENDAI*, [3]*RIKEN SPring-8 Center*)

2SEA-2 天然変性タンパク質とリン酸化
Protein intrinsic disorder and phosphorylation
○太田 元規（名大・情報）
Motonori Ota (*Sch. Info. Nagoya U.*)

2SEA-3 Chemical and structural biology approaches to understand molecular mechanism underlying 24-hour period of mammalian circadian clock
Tsuyoshi Hirota (*Institute of Transformative Bio-molecules, Nagoya University*)

2SEA-4 Flexible time: turning of circadian period through the loop region of CRYPTOCHROME protein
Koji Ode[1,2], Hiroki Ueda[1,2] ([1]*Dept. Sys. Pharm., Grad. Sch. Med., The Univ. Tokyo*, [2]*Lab. Syn. Biol., QBiC, RIKEN*)

2SEA-5 哺乳類の発生過程における 24 時間周期の形成機構
Appearance of 24 hour rhythms during the developmental process in mammals
○八木田 和弘（京都府立医科大学 統合生理学）
Kazuhiro Yagita (*Kyoto Prefectural University of Medicine*)

おわりに
Closing Remarks

8:45〜11:15　F 会場（全学教育棟 2 階 E205）／Room F (Room E205, General Education Bldg. 2F)

2SFA　新学術領域研究「理論と実験の協奏による柔らかな分子系の機能の科学」共催
さまざまな環境下で発現される生体分子の柔らかさと機能
Softness and functions of biological molecules under various environments

オーガナイザー：高橋 聡（東北大学），飯野 亮太（自然科学研究機構）
Organizers: Satoshi Takahashi (Tohoku University), Ryota Iino (NINS)

Biological systems express their functions through the coordinated dynamics of soft biological macromolecules in various environments. In this symposium, we ask young investigators to present their recent investigations based on molecular dynamics simulations, in cell NMR, high speed AFM and advanced optical microscopies and to discuss the current understanding and future perspectives of their target biological systems.

2SFA-1 細胞内クラウディング環境下の蛋白質のフォールディング・ダイナミクスを NMR で観測する
NMR approaches to investigate protein folding and dynamics in the crowded intracellular environment
○伊藤 隆（首都大・理工・分子物質化学）
Yutaka Ito (*Dept. Chemistry, Tokyo Metropolitan Univ.*)

2SFA-2 長時間分子シミュレーショントラジェクトリの解析から探るタンパク質の不均一なダイナミクス
Deciphering the heterogeneous dynamics of proteins from the analysis of millisecond-long molecular dynamics simulations
○森 俊文[1,2], 斉藤 真司[1,2]（[1]分子研, [2]総研大）
Toshifumi Mori[1,2], Shinji Saito[1,2] ([1]*IMS*, [2]*SOKENDAI*)

2SFA-3 Ultrahigh-speed single-particle tracking by interferometric scattering (iSCAT) microscopy
Chia-Lung Hsieh (*Institute of Atomic and Molecular Sciences, Academia Sinica*)

2SFA-4 ラマン散乱顕微鏡とアルキン標識による生物活性小分子のイメージングとスクリーニング
Raman scattering microscopy and alkyne-tag for imaging and screening of bio-active small molecules
○安藤 潤[1,2,3,4], 藤田 克昌[1,2], 袖岡 幹子[2,3]（[1]大阪大学・応用物理学専攻, [2]AMED-CREST, AMED, [3]理研, [4]分子科学研究所）
Jun Ando[1,2,3,4], Katsumasa Fujita[1,2], Mikiko Sodeoka[2,3] ([1]*Dept. of Applied Physics, Osaka Univ.*, [2]*AMED-CREST, AMED*, [3]*RIKEN*, [4]*Institute for Molecular Science*)

2SFA-5 High-Speed AFM Observation of Domain Flexibility Related to Enzymatic Function of CRISPR-Cas9
Takayuki Uchihashi[1], Mikihiro Shibata[2,3], Hiroshi Nishimasu[4,5], Noriyuki Kodera[3,5], Seiichi Hirano[4], Toshio Ando[3,6], Osamu Nureki[4] ([1]*Dept. Phys., Nagoya Univ.*, [2]*ISFS, Kanazawa Univ.*, [3]*Bio-AFM FRC, Kanazawa Univ.*, [4]*Dept. Biol., Univ. Tokyo*, [5]*JST-PRESTO*, [6]*JST-CREST*)

2SFA-6 高速 1 分子イメージング解析で明らかとなったリニア分子モーター、回転分子モーターの化学力学共役機構
Chemo-mechanical coupling mechanisms of linear and rotary molecular motors revealed by high-speed single-molecule imaging analysis
○飯野 亮太[1,2,3]（[1]自然科学研究機構 岡崎統合バイオサイエンスセンター, [2]自然科学研究機構 分子科学研究所, [3]総合研究大学院大学）
Ryota Iino[1,2,3] ([1]*OIIB, NINS*, [2]*IMS, NINS*, [3]*SOKENDAI*)

8:45〜11:15　G 会場（全学教育棟 3 階 C301）／Room G (Room C301, General Education Bldg. 3F)

2SGA　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」共催
生体膜模倣環境としての新しい界面活性剤，リポソーム，ナノディスクの利用
New detergents, liposomes, and nanodiscs as membrane-mimetic environments

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

The solubilization with detergents and reconstitution into lipid bilayers is a critical process in membrane protein studies. Intensive talks on the basics and the applications of new detergents, liposomes, and nanodiscs for proper treatment of membrane proteins will be given to view a present and future status of the membrane-memetic technology.

2SGA-1 リポソーム・ナノディスクの膜環境と脂質ダイナミクス
Structure and Dynamics of Lipids in Liposomes and Nanodiscs
○中野 実（富山大学大学院 医学薬学研究部）
Minoru Nakano (*Graduate School of Medicine and Pharmaceutical Sciences, University of Toyama*)

2SGA-2 脂質ナノディスク形成のための膜活性ポリマーのデザイン
Molecular design of membrane-active polymers for lipid nanodisc formation
○安原 主馬, 井上 雅也, 荒木田 臣, 菊池 純一（奈良先端科学技術大学院大学 物質創成科学研究科）
Kazuma Yasuhara, Masaya Inoue, Jin Arakida, Jun-ichi Kikuchi (*Graduate School of Materials Science, Nara Institute of Science and Technology*)

2SGA-3 脂質ータンパク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
Lipid-protein cooperativity in the regulation of juxtamembrane domain dimer formation in epidermal growth factor receptor
○前田 亮[1], 佐藤 毅[2], 岡本 憲二[1], 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], Kenji Okamoto[1], Yasushi Sako[1] ([1]*Cellular Informatics Lab., RIKEN*, [2]*Kyoto Pharmaceutical Univ.*)

2SGA-4 High-speed AFM observation of membrane protein embedded in Nanodisc
Takamitsu Haruyama[1], Yasunori Sugano[1], Yoshiki Tanaka[1], Hiroki Konno[2], Tomoya Tsukazaki[1] ([1]*Grad. Sch. of Biol. Sci., NAIST*, [2]*Bio-AFM FRC, Inst. of Sci. & Eng., Kanazawa Univ.*)

2SGA-5 GraDeR: 遊離界面活性剤無膜タンパク質の調整方法
GraDeR: micelle free membrane protein preparation
○Gerle Christoph（阪大・タンパク研）
Christoph Gerle (*IPR, Osaka Univ.*)

2SGA-6 リポソーム中の膜タンパク質機能構造を捉えるクライオ電子顕微鏡単粒子解析法
CryoEM single particle analysis for functional structure of membrane proteins in liposomes
○重松 秀樹（理研ライフサイエンス技術基盤研究センター）
Hideki Shigematsu (*RIKEN CLST*)

8:45〜11:15　I 会場（全学教育棟 3 階 E305）／Room I (Room E305, General Education Bldg. 3F)
2SIA　協賛　AMED 革新的先端研究開発支援事業（AMED－CREST/PRIME）
「メカノバイオロジー機構の解明による革新的医療機器及び医療技術の創出」
メカノバイオロジーを開拓するメソドロジーの新展開
Development of methodology to explore the mechanobiology

オーガナイザー：木戸秋 悟（九州大学），曽我部 正博（名古屋大学）
Organizers: Satoru Kidoaki (Kyushu University), Masahiro Sokabe (Nagoya University)

For the development of mechanobiology, an integrated approach from multifaceted technical fields has been essential. The frontier of mechanobiology has been developed by combining various methodologies such as molecular biological techniques, sophisticated imaging probe and microscope technology, mechanical loading device, microfluidics, design of surface chemistry and viscoelasticity of materials, computational technique, etc. This session is dedicated to discuss the latest trends on the methodology to explore the mechanobioly, and not only on the methodologies but also on the basic mechanobioligic findings based on the methodlogies.

2SIA-1 メカノバイオロジー: これまでの成果とこれからの課題
Mechanobiology: Past achievements and future issues
○曽我部 正博（名大院・ 医・ メカノバイオロジー・ラボ）
Masahiro Sokabe (*Mechanobiology Lab, Nagoya Univ Grad Sch Med*)

2SIA-2 Mechanobio-materials manipulating motility and functions of stem cells
Satoru Kidoaki (*IMCE, Kyushu Univ.*)

2SIA-3 メカノバイオロジーのための形状記憶型動的培養基盤
Shape Memory-based Dynamic Culture Platforms for Mechanobiology
○宇都 甲一郎（若手国際セ・物材研）
Koichiro Uto (*ICYS, NIMS*)

2SIA-4 遺伝子発現制御に対するアクチンの役割を理解するための微細構造化細胞培養基材の開発
Microtopographical cell culture substrate to understand the role of actin cytoskeleton for regulation of gene expression
山崎 雅史[1], ○三好 洋美[1,2]（[1]首都大院・システムデザイン, [2]AMED・PRIME）
Masashi Yamazaki[1], **Hiromi Miyoshi**[1,2] ([1]*Grad. Sch. System Design, Tokyo Metropolitan Univ.*, [2]*PRIME, AMED*)

2SIA-5 Live-cell imaging of actin dynamics in cortex and lamellipodium by high-speed atomic force microscopy
Yoshitsuna Itagaki[1], Yanshu Zhan[1], Aiko Yoshida[1], Nobuaki Sakai[2], Yoshitsugu Uekusa[2], Masahiro Kumeta[1], **Shige H. Yoshimura**[1] ([1]*Grad. Schl. Biostudies, Kyoto U.*, [2]*R&D Group, Olympus Corp.*)

2SIA-6 細胞の力学：単一細胞から多細胞へ
Cell Mechanics: from single cell to multi-cellular dynamics
谷本 博一[1,2], 川口 喬吾[1,3], 上道 雅仁[1], ○佐野 雅己[1]（[1]東大院理・物理, [2]ジャックモノー研, [3]ハーバード大、システム生物）
Hirokazu Tanimoto[1,2], Kyogo Kawaguchi[1,3], Masahito Uwamichi[1], **Masaki Sano**[1] ([1]*Dept. Phys. Univ. Tokyo*, [2]*Inst. Jacques Monod*, [3]*Sys. Bio. Harvard Univ.*)

8:45〜11:15　K 会場（文法学部 2 階 A1 教室）／Room K (Room A1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

2SKA　Joint Symposium between Indian Biophysics Society and BSJ: Protein Biophysics: From Folding to Drug Discovery

オーガナイザー：金城 玲（大阪大学），バスー ゴータム（Bose Institute）

Organizers: Akira R. Kinjo (Osaka University), Gautam Basu (Bose Institute)

Computational approaches such as modeling, simulation and statistical analysis are becoming ever more crucial not only to make sense of the massive amount of biological data but to predict systems' behaviors and thereby to generate hypotheses that may drive further experimental studies. In this symposium, focusing on molecular aspects of biophysical systems, speakers from India and Japan will present some of their recent studies ranging from protein structure and folding to evolution and drug discovery using computational methods.

2SKA-1　配列空間における蛋白質フォールディング
Protein folding in the sequence space
○金城 玲（大阪大学蛋白質研究所）
Akira R. Kinjo (*Inst. Protein Res., Osaka Univ.*)

2SKA-2　Toward a Quantitative Description of Microscopic Pathway Heterogeneity in Protein Folding
Athi N. Naganathan (*IIT Madras*)

2SKA-3　Structural features of the urea denatured apomyoglobin using molecular modeling and experimental data
Yasutaka Seki (*Molecular Biophysics, Kochi Medical School, Kochi University*)

2SKA-4　Structural Proteome to Targetability Estimation: Novel Concepts in Drug Discovery
Nagasuma Chandra (*Indian Inst. Sci.*)

2SKA-5　Data integration and statistical/*ab initio* modelling towards rational drug discovery
Kenji Mizuguchi (*NIBIOHN*)

2SKA-6　Cis proline-specific protein structure and dynamics
Gautam Basu (*Bose Inst.*)

8:45〜11:15　L 会場（文法学部 2 階 B1 教室）／Room L (Room B1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

2SLA　若手研究者が考えるバイオイメージングとその応用
Happy Hacking imaging for biology by early carriers

オーガナイザー：鳥羽 栞（弘前医療福祉大学），新井 由之（大阪大学）

Organizers: Shiori Toba (Hirosaki University of Health and Welfare), Yoshiyuki Arai (Osaka University)

Optical microscopy enables us to visualize the dynamic behavior of living samples. In this session, we will present the recent imaging technologies, including superresolution, adaptive optics, digital holography, and image processing. We hope to discuss recent developments and the significant findings based on our observation. We believe this symposium will encourage the further applications to increase the experimental output and stimulating the scientist in your field.

2SLA-1　超解像光学顕微鏡法 PALM によって明らかになった軸索輸送における非定型微小管
Opening talk: visualizing unconventional biological component using super-resolution photo-activated localization microscopy
○鳥羽 栞[1,2]（[1]大阪市立大・医, [2]現所属：弘前医療福祉大）
Shiori Toba[1,2] ([1]*Osaka City Univ. Grad. Sch. of Medicine*, [2]*Present Address: Hirosaki Univ. of Health and Welfare*)

2SLA-2　新規光技術を用いた二光子励起顕微鏡の機能向上
Improvements of two-photon excitation microscopy by utilizing novel optical technologies
○大友 康平[1,2]（[1]北大・電子研, [2]北大・院・情報）
Kohei Otomo[1,2] ([1]*RIES, Hokkaido Univ.*, [2]*Grad. Sch. IST, Hokkaido Univ.*)

2SLA-3 補償光学：光の乱れの補正による深部生細胞イメージング
Adaptive optics: Towards deep imaging of living cells by active correction of optical disturbance
○玉田 洋介（基生研・生物進化）
Yosuke Tamada (*Div. Evol. Biol., Natl. Inst. Basic Biol.*)

2SLA-4 SIM/STORM イメージングの使命と将来の展望
Missions and the future of SIM/STORM super-resolution microscopy
○友杉 亘（株式会社ニコン）
Wataru Tomosugi (*Nikon Corporation*)

2SLA-5 能動学習を用いた生物画像の効率的自動分類
Efficient Automatic Classification of Biomedical Images Using Active Learning Algorithm
○朽名 夏麿[1,2], 島原 佑基[1,2], 馳澤 盛一郎[1,2]（[1]エルピクセル(株), [2]東大・院新領）
Natsumaro Kutsuna[1,2], Yuki Shimahara[1,2], Seiichiro Hasezawa[1,2] ([1]*Lpixel Inc.*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

2SLA-6 ディジタルホログラフィとバイオイメージングへの応用可能性
Digital holography and its applicability to biology
○田原 樹[1,2]（[1]関西大・システム理工, [2]JST さきがけ）
Tatsuki Tahara[1,2] ([1]*Kansai University*, [2]*PRESTO, JST*)

2SLA-7 Closing remarks: Advanced bioimaging techniques for biophysics
Yoshiyuki Arai (*ISIR, Osaka Univ*)

8:45～11:15　M 会場（文法学部 1 階 B2 教室）／Room M (Room B2, Faculty of Letters, Faculty of Law Main Bldg. 1F)

2SMA　文部科学省 光・量子融合連携研究開発プログラム「中性子と放射光の連携利用によるタンパク質反応プロセスの解明」共催
X 線と中性子の連携利用による高分解能／高精度タンパク質結晶学
High-resolution and High-precision Protein Crystallography by Combined Use of X-ray and Neutron Diffraction

オーガナイザー：玉田 太郎（量子科学技術研究開発機構），三木 邦夫（京都大学）
Organizers: Taro Tamada (National Institutes for Quantum and Radiological Science and Technology), Kunio Miki (Kyoto University)

Recent development of synchrotron facility enables us to perform protein crystal structure analyses at ultra-high resolution. As a consequence of charge-density analysis based on ultra-high resolution structures we can obtain information of outer-electron distribution of protein molecules. On the other hand, we can now discuss detailed reaction mechanism from exact hydrogen positions visualized by neutron crystallography. It is time now to utilize X-ray and neutron diffraction jointly to obtain deep information on protein structures. In this symposium, we show most recent results in this field and discuss its current methodological problems and its future view.

2SMA-1 はじめに
Introduction
○三木 邦夫（京都大学大学院理学研究科）
Kunio Miki (*Graduate School of Science, Kyoto University*)

2SMA-2 緑色蛍光タンパク質の X 線および中性子線解析
X-ray and neutron diffraction analyses of green fluorescent protein
○竹田 一旗（京都大学大学院理学研究科生物構造化学研究室）
Kazuki Takeda (*Grad. Sch. Sci., Kyoto Univ.*)

2SMA-3 Experimental environments for high-resolution diffraction data collection at SPring-8
Takashi Kumasaka, Kazuya Hasegawa (*Protein Crystal Analysis Division, Japan Synchrotron Radiation Research Institute (JASRI)*)

2SMA-4 電子伝達タンパク質の高分解能中性子結晶構造解析
High-resolution neutron crystal structural studies of electron transfer proteins
○玉田 太郎（量研・量子ビーム）
Taro Tamada (*QuBS, QST*)

2SMA-5 Challenging to visualize ammonia transposition in a channel of amidotransferase GatCAB using neutron macromolecular crystallography

Min Yao[1,2], Long Li[2] ([1]*Faculty of Advanced Life Science, Hokkaido University*, [2]*Graduate School of Life Science, Hokkaido University*)

2SMA-6 Neutron protein crystallography with single-crystal neutron diffractometer iBIX at pulsed neutron source MLF, J-PARC

Katsuhiro Kusaka[1], Taro Yamada[1], Naomine Yano[1], Takaaki Hosoya[1], Takashi Ohhara[2], Ichiro Tanaka[1], Masaki Katagiri[1] ([1]*Frontier Research Center of Applied Atomic Sciences, Ibaraki University*, [2]*J-PARC Center, JAEA*)

8:45～11:15　N 会場（文法学部 1 階 B3 教室）／Room N (Room B3, Faculty of Letters, Faculty of Law Main Bldg. 1F)

2SNA　動的不均一性がもたらす多細胞社会の秩序形成
Order from dynamic heterogeneity in multicellular systems

オーガナイザー：柴田 達夫（理化学研究所），松崎 文雄（理化学研究所）
Organizers: Tatsuo Shibata (RIKEN), Fumio Matsuzaki (RIKEN)

Recent technological advances in single cell transcriptome analysis and imaging of living tissues and organs have started to provide the view that apparently homogeneous cell populations contain in fact remarkable heterogeneities. From this finding, the question naturally arises as to how the ordered form and function of tissues and organs is created and maintained from a population of cells with disordered and stochastic characteristics. In this symposium, we will discuss the underlying principles that bridge this gap, based on the recent analysis of state transitions and linage tracing of cells in populations in vivo and in vitro.

2SNA-1 形態形成における確率過程
Stochastic process in multicellular morphogenesis

○柴田 達夫（理研QBiC）
Tatsuo Shibata (*RIKEN QBiC*)

2SNA-2 Molecular mechanism to generate heterogeneous gene expression in mouse ES cell population

Hitoshi Niwa (*IMEG, Kumamoto University*)

2SNA-3 マウス着床前発生において細胞はどのように分化するか？
How do cells differentiate during preimplantation mouse development ?

○藤森 俊彦（基生研・初期発生）
Toshihiko Fujimori (*Div. of Embryology, NIBB*)

2SNA-4 組織恒常性を支える幹細胞の動的不均一性をマウス精子形成に学ぶ
Dynamical heterogeneity of the stem cell pool underlying the homeostatic sperm production in mice

○吉田 松生（基礎生物学研究所）
Shosei Yoshida (*National Institute for Basic Biology*)

2SNA-5 機械学習によるデータ駆動型サイエンス：現状と展望
Machine learning for data-driven scientific discovery: state-of-the-art and future perspective

○吉田 亮（統数研）
Ryo Yoshida (*Inst. Stat. Math.*)

2SNA-6 脳発生過程における神経幹細胞の動的多様性
Dynamic heterogeneity of neural stem cells in brain development

○松崎 文雄（理化学研究所　多細胞システム形成研究センター）
Fumio Matsuzaki (*RIKEN Center for Developmental Biology*)

13:55～16:25　A 会場（全学教育棟 1 階 E107）／Room A (Room E107, General Education Bldg. 1F)

2SAP　生物学における数の数理：少数の分子が如何にして機能の頑健性を産み出しているのか？
Number in biology: deciphering how small number of molecules solve robustness of biological functions

オーガナイザー：小松崎 民樹（北海道大学），黒田 真也（東京大学）

Organizers: Tamiki Komatsuzaki (Hokkaido University), Shinya Kuroda (The University of Tokyo)

All live systems are composed of a sequence of chemical reactions and quite often in systems biology people have expressed molecules by "concentration valuable", but actually molecules are discrete objects, so that the number of molecules should be expressed. Moreover, the numbers of molecules in single cells are countably very small at the order of 1 to 1000 compared to Avogadro number. Naive intuition suggests that large number fluctuation in reactions is not well desired to promote signal transduction cascades robustly. Likewise, the open question in biology is to elucidate the numbers of each actors/actresses in biology and how our live system solves biological functions under the existence of such apparent conflicts.

はじめに
Opening Remarks
Tamiki Komatsuzaki

2SAP-1　生命システムにおける状態・形・少数性の問題
State, Shape, and Small-Number Issues in Biological Systems
○冨樫 祐一（広島大・理）
Yuichi Togashi (*Grad. Sch. Sci., Hiroshima Univ.*)

2SAP-2　Collective motion switches directionality of molecular motor along filament
Nen Saito (*Grad. Sch. Sci., Univ. Tokyo*)

2SAP-3　Information thermodynamic study of biochemical clock
Sosuke Ito[1], Pieter Rein Ten Wolde[2] ([1]*Hokkaido University, RIES*, [2]*FOM Institute AMOLF*)

2SAP-4　シロイヌナズナ遺伝子発現揺らぎの新規モデル分布
Novel statistical model of fluctuating gene expression levels of Arabidopsis thaliana
○粟津 暁紀[1], 永野 惇[2]（[1]広大理, [2]龍谷大農）
Akinori Awazu[1], Atsushi Nagano[2] ([1]*Dept. of Math. and Life Sci., Hiroshima Univ.*, [2]*Faculty of Agriculture, Ryukoku Univ.*)

2SAP-5　E-Cell System: from a single molecule to a whole cell
Kazunari Kaizu, Masaki Watabe, Kouichi Takahashi (*RIKEN Quantitative Biology Center (QBiC)*)

2SAP-6　スパインにおける小体積効果：Robust, Sensitive で Efficient な情報伝達
Small-Volume Effect Enables Robust, Sensitive, and Efficient Information Transfer in the Spine
○藤井 雅史（東大・院理）
Masashi Fujii (*Grad. Sch. Sci., Univ. Tokyo*)

2SAP-7　A quantitative view of the biosphere: from the most abundant taxa to the most abundant proteins
Yinon Bar-On, Rob Phillips, Ron Milo (*Weizmann Inst. Sci.*)

おわりに
Closing Remarks
Shinya Kuroda

13:55～16:25　G 会場（全学教育棟 3 階 C301）／Room G (Room C301, General Education Bldg. 3F)

2SGP　高分子混雑が支配する細胞の世界
Macromolecular crowding shapes the world of cells

オーガナイザー：柳澤 実穂（東京農工大学），優 乙石（理化学研究所）
Organizers: Miho Yanagisawa (Tokyo University of Agriculture and Technology), Isseki Yu (RIKEN)

Biopolymers such as proteins are present in very high concentrations in cells, which greatly affect the dynamics, structure, and function of them. Although these effects, so-called "macromolecular crowding" has been attracting attention, molecular-level mechanisms are still unknown due to its complexity. At this symposium, we focus on the characteristics of the cellular environment and/or cell-mimicking conditions dominated by macromolecular crowding. Combining experimental, theoretical, and computational approaches, we discuss the influence of macromolecular crowding on diffusion, structural stability, and biological reactivity of DNA or proteins.

2SGP-1　はじめに：高分子混雑の世界
Introduction: the world of macromolecular crowding
○柳澤 実穂（東京農工大学大学院工学研究院先端物理工学部門）
Miho Yanagisawa (*Tokyo Univ. Agri. Technol.*)

2SGP-2　回転および並進拡散計測による細胞内分子クラウディング状態の評価
Evaluation of molecular crowding based on the rotational and translational diffusion measurement in living cells
○山本 条太郎（北大・院先端生命）
Johtaro Yamamoto (*Fac. Adv. Life Sci.*)

2SGP-3　混雑化で生み出される人工細胞内の Min システム反応拡散波
A localization wave of proteins reconstituted in artificial cells with crowding environments
○藤原 慶（慶應大・生命情報）
Kei Fujiwara (*Dep. Biosci. and Info., Keio University*)

2SGP-4　Brownian motion in dense DNA solutions
Yoshihiro Murayama (*Tokyo Univ. of Agri. and Tech.*)

2SGP-5　不均一な環境下での異常拡散
Anomalous diffusion in heterogeneous environments
○秋元 琢磨（東京理科大学理工学部物理学科）
Takuma Akimoto (*Tokyo University of Science*)

2SGP-6　高分子混雑環境下での蛋白質 NMR 緩和解析
NMR relaxation analysis of the protein under macromolecular crowding environment
○岡村 英保[1], 木川 隆則[1,2]（[1]理研 生命システム研究センター, [2]東工大 情報理工学院）
Hideyasu Okamura[1], Takanori Kigawa[1,2] ([1]*RIKEN QBiC*, [2]*Department of Computer Science, Tokyo Institute of Technology*)

2SGP-7　細胞混雑中の蛋白質と代謝物のダイナミクス: 全原子分子動力学法による理論的研究
Dynamics of Proteins and Metabolites in Cellular Crowding Environment: Theoretical Study with All-atom Molecular Dynamics Simulation
○優 乙石[1,2], ワン ポーホン[2], ファイグ マイケル[3], 杉田 有治[1,2]（[1]理研 iTHES, [2]理研 杉田理論分子科学研究室, [3]ミシガン州立大）
Isseki Yu[1,2], Po-Hung Wang[2], Michael Feig[3], Yuji Sugita[1,2] ([1]*RIKEN iTHES*, [2]*RIKEN Theoretical Molecular Science Lab.*, [3]*Michigan State University*)

13:55～16:25　K 会場（文法学部 2 階 A1 教室）／Room K (Room A1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

2SKP　Joint Symposium between Biophysical Society of R.O.C. and BSJ: Towards tomorrow's structural biology

オーガナイザー：山本 雅貴（理化学研究所），呂 平江（National Tsing Hua University）
Organizers: Masaki Yamamoto (RIKEN), Ping-Chiang Lyu (National Tsing Hua University)

Biological functions are realized by networks of proteins in the cell. Structural biology is developing in order to elucidate its function based on the three-dimensional structure of individual proteins and currently giving the high-impact results globally. This symposium is held for information exchange and cooperation between the biophysical society of Taiwan R.O.C. and the biophysical society of Japan with an overview of the current state of structural biology and its future.

2SKP-1　タンパク質微小結晶構造解析の将来に向けて
Towards the next generation protein micro-crystallography at SPring-8 and SACLA
○山本 雅貴（理化学研究所 放射光科学総合研究センター）
Masaki Yamamoto (*RIKEN RSC*)

2SKP-2　Structure and function of the polymyxin-resistance-associated response regulator PmrA
Chwan-Deng Hsiao (*Institute of Molecular Biology, Academia Sinica*)

2SKP-3　二重殻構造を持つイネ萎縮ウイルスの構造構築機構
Structure assembly mechanism of a double-shelled virus, Rice dwarf virus
東浦 彰史, 中道 優介, 堤 研太, 宮崎 直幸, 岩崎 憲治, ○中川 敦史（阪大・蛋白研）
Akifumi Higashiuira, Yusuke Nakamichi, Kenta Tsutsumi, Naoyuki Miyazaki, Kenji Iwasaki, **Atsushi Nakagawa** (*Inst. Protein Res., Osaka Univ.*)

2SKP-4　A structural proteomic approach to understand cobra venom actions beyond neurotoxicity of the bitten victims
Wen-Guey Wu (*Institute of Bioinformatics and Structural Biology, National Tsing Hua University, Taiwan*)

2SKP-5　統合構造生物学と生理学のための最新 NMR
Advanced NMR for Integrated Structural Biology and Physiology
○児嶋 長次郎[1,2]（[1]横浜国大・工, [2]阪大・蛋白研）
Chojiro Kojima[1,2] ([1]*Grad. Sch. Eng., Yokohama Nat. Univ.*, [2]*Inst. Protein Res., Osaka Univ.*)

2SKP-6　Circular permutation: Database, Prediction and Design
Ping-Chiang Lyu (*Institute of Bioinformatics and Structural Biology, National Tsing Hua University*)

13:55～16:25　L 会場（文法学部 2 階 B1 教室）／Room L (Room B1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

2SLP　新学術領域研究「温度を基軸とした生命現象の統合的理解（温度生物学）」共催
温度と生物の接点
The Intersection between Temperature and Life

オーガナイザー：岡部 弘基（東京大学），原田 慶恵（大阪大学）
Organizers: Kohki Okabe (The University of Tokyo), Yoshie Yarada (Osaka University)

In recent years, temperature has attracted great attention in the search for deeper understanding of cell functions. Despite the universality of temperature as a physical parameter, the fundamental principles of how temperature facilitates life activities are still a mystery. In this symposium, through the introduction of the challenges thermal biology faces when exploring the mechanisms of thermal sensation and response in various organisms, we will discuss the unaddressed issues and future prospects of this innovative multidisciplinary science.

2SLP-1　細胞における温度動態：観察と意義
Thermal dynamics in individual cells: observation and significance
○森 泰生（京都大学大学院工学研究科）
Yasuo Mori (*Kyoto Univ., Grad. Sch. Engineering*)

2SLP-2 マウス体内時計の温度応答
Temperature-responses of the circadian clock oscillation in mice
○深田 吉孝（東大院理・生物科学・深田研究室）
Yoshitaka Fukada (*Dept. Biological Sciences, School of Science, The Univ. Tokyo*)

2SLP-3 16S rRNA 遺伝子の GC 含量と原核生物の生育温度との関係
Relationship between guanine-plus-cytosine content of 16S rRNA genes and growth temperature of the prokaryotic hosts
佐藤 悠[1], ○木村 浩之[2]（[1]静岡大・創造院, [2]静岡大・グリーン研）
Yu Sato[1], **Hiroyuki Kimura**[2] ([1]*Grad. Sch. Sci. Technol., Shizuoka Univ.*, [2]*Res. Inst. Green Sci. Technol., Shizuoka Univ.*)

2SLP-4 細胞内微小空間における温度と分子の相互作用
Interaction between temperature and molecules in intracellular microenvironments
○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]JST さきがけ）
Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Graduate School of Pharmaceutical Sciences, The University of Tokyo*, [2]*JST, PRESTO*)

2SLP-5 温度応答性超分子を用いたがん集積システムの開発
Development of a tumor-accumulation system using temperature-responsive supramolecule
○唐澤 悟[1,2,3], 荒木 健[3], 臼井 一晃[3], 村山 周平[4], 青木 伊知男[4]（[1]昭和薬大, [2]JSTさきがけ, [3]九大院薬, [4]量子研）
Satoru Karasawa[1,2,3], Takeru Araki[3], Kazuteru Usui[3], Shuhei Murayama[4], Ichio Aoki[4] ([1]*Univ. Showa*, [2]*JST PRESTO*, [3]*Grad. Sch. Pharm. Univ. Kyushu*, [4]*Ins. QST*)

13:55～16:25　M 会場（文法学部 1 階 B2 教室）／Room M (Room B2, Faculty of Letters, Faculty of Law Main Bldg. 1F)

2SMP　分子集合と生体膜の生物物理学
Biophysics of molecular assembly and biological membrane

オーガナイザー：末次 志郎（奈良先端科学技術大学院大学），嶋田 睦（九州大学）
Organizers: Shiro Suetsugu (NAIST), Atsushi Shimada (Kyushu University)

Biological membranes mediate the assemblies of proteins and other biomolecules to assist their physiological functions. Conversely, the membrane-associated assemblies of biomolecules could affect the three-dimensional configuration of the membrane and assist its function. In this symposium, we will discuss recent discoveries on these membrane-associated molecular assemblies involved in various cellular mechanisms. We will also discuss how biophysical techniques could contribute to these discoveries and provide an opportunity to consider the future of the expanding interdisciplinary field between biophysics and cell biology.

2SMP-1 エンドサイトーシス関連細胞質タンパク質の構造から迫るクラスリン重合機構
Insights into clathrin assembly from the structures of cytosolic endocytic proteins
○嶋田 睦[1,2]（[1]九大・生医研, [2]理研・播磨）
Atsushi Shimada[1,2] ([1]*Med. Inst. Bioreg., Kyushu Univ.*, [2]*RIKEN SPring-8 Center*)

2SMP-2 Dynamic remodeling of Dynamin complexes during membrane fission
Tetsuya Takeda[1], Daiki Ishikuro[2], Huiran Yang[1], Toshiya Kozai[2], Kaho Seyama[1], Yusuke Kumagai[2], Hiroshi Yamada[1], Takayuki Uchihashi[4], Toshio Ando[2,3], Kohji Takei[1] ([1]*Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ.*, [2]*Coll. Sci. Eng., Kanazawa Univ.*, [3]*Bio AFM, Kanazawa Univ.*, [4]*Dept. Phys., Nagoya Univ.*)

2SMP-3 エンドサイトーシス型受容体 ApoER2 のリガンド結合状態の結晶構造
Crystal structure of the endocytic receptor ApoER2 in the ligand-bound state
○禾 晃和（横市大・院生命医科）
Terukazu Nogi (*Grad. Sch. Med. Lif. Sci., Yokohama City Univ.*)

2SMP-4 Mechanisms of *trans*-synaptic adhesion for inducing synapse formation
Shuya Fukai (*IMCB, Univ. Tokyo*)

2SMP-5 The spatial distribution of the BAR domain proteins on the membrane
Shiro Suetsugu (*NAIST*)

2SMP-6 Molecular mechanisms involved in the reassembly of the actin cortex in membrane blebs
Junichi Ikenouchi (*Dept. Biol., Facl. Sci., Kyushu Univ.*)

2SMP-7 Role of plasma membrane tension in cell migration and invasion
Kazuya Tsujita (*Biosignal Research Center, Kobe University*)

2SMP-8 Actin polymerization in contact with the plasma membrane may be a Brownian ratchet-based information collector
Naoki Watanabe[1,2], Kazuma Koseki[2], Daisuke Taniguchi[2] ([1]*Kyoto Univ. Grad. Sch. Biostudies*, [2]*Kyoto Univ. Grad. Sch. Med.*)

13:55～16:25　N 会場（文法学部 1 階 B3 教室）／Room N (Room B3, Faculty of Letters, Faculty of Law Main Bldg. 1F)

2SNP　新学術領域研究「スパースモデリングの深化と高次元データ駆動科学の創成」共催
データ駆動科学が拓く新しい生命計測データ解析
Data-driven science opens up a new field in biological measurements

オーガナイザー：木川 隆則（理化学研究所），池谷 鉄兵（首都大学東京）
Organizers: Takanori Kigawa (RIKEN), Teppei Ikeya (Tokyo Metropolitan University)

Methods used in data-driven science, such as sparse modeling and machine learning, enable us to extract the maximum amount of information from experimental measurement data. In this symposium, the leading scientists in information science will introduce the basic theory and the state-of-the-art methods, and those in biology as well as non-biology fields will present the practical applications using these technologies. In addition, the future perspectives of biological measurement and observation methods developed by data-driven approaches will be discussed.

はじめに
Opening Remarks
○池谷 鉄兵（首都大学東京）
Teppei Ikeya (*Tokyo Metropolitan University*)

2SNP-1 スパースモデリングに基づく計測データ解析
Measurement data analysis based on sparse modeling
○田中 利幸（京都大学大学院情報学研究科）
Toshiyuki Tanaka (*Graduate School of Informatics, Kyoto University*)

2SNP-2 位相的データ解析とその応用
Topological Data Analysis and its Applications
○福水 健次（統数研）
Kenji Fukumizu (*ISM*)

2SNP-3 ディープラーニングを用いた医用 CT 画像のテクスチャ識別
Texture classification on Medical CT image using Deep Learning
○庄野 逸（電気通信大学）
Hayaru Shouno (*University of Electro Communications*)

2SNP-4 シミュレーション／データ両駆動型データ同化の創出へ
Towards a generation of the simulation-/data-driven data assimilation
○長尾 大道[1,2]（[1]東大地震研, [2]東大情報理工）
Hiromichi Nagao[1,2] ([1]*ERI, UTokyo*, [2]*IST, UTokyo*)

2SNP-5 低感度 NMR スペクトルから情報を得るための安定同位体標識法の in-cell NMR への応用
How to cope with noisy NMR spectra; application of a novel isotope labeling strategy to in-cell NMR
○葛西 卓磨[1,2], 樋口 佳恵[1], 猪股 晃介[1], 木川 隆則[1,3]（[1]理研・生命システム, [2]JST・さきがけ, [3]東工大・情報理工）
Takuma Kasai[1,2], Kae Higuchi[1], Kohsuke Inomata[1], Takanori Kigawa[1,3] ([1]*RIKEN QBiC*, [2]*PRESTO, JST*, [3]*Sch. Comput., Tokyo Inst. Tech.*)

2SNP-6 統計的画像処理による超解像顕微鏡法
Super-resolution imaging by statistical image data processing
○岡田 康志[1,2]（[1]理研・生命システム研究センター, [2]東大･理･物理）
Yasushi Okada[1,2] ([1]*Quantitative Biology Center, RIKEN*, [2]*Dept. Physics, Univ. Tokyo*)

おわりに
Closing Remarks
○木川 隆則（理化学研究所）
Takanori Kigawa (*RIKEN*)

第 3 日目（9 月 21 日（木））／Day 3（Sep. 21 Thu.）

9:00～11:30　A 会場（全学教育棟 1 階 E107）／Room A (Room E107, General Education Bldg. 1F)
3SAA　光散乱・吸収を用いた顕微鏡で探る生体情報
Biological information probed by optical microscopes using scattering and absorption

オーガナイザー：市村 垂生（理化学研究所），藤田 克昌（大阪大学）
Organizers: Taro Ichimura (RIKEN), Katsumasa Fujita (Osaka University)

Light is scattered and absorbed by molecules in various interaction processes, which includes elastic, inelastic, nonlinear, and photothermal effects, depending on molecular species and excitation schemes. By detecting and analyzing the optical responses, one can directly probe molecular structure, alignment, concentration, and surrounding environment without fluorescent labeling. In this symposium, several types of advanced microscopes using light scattering and absorption will be introduced. Biological information probed by the microscopes will be discussed to explore their biological application.

はじめに
Opening Remarks
○藤田 克昌（大阪大学）
Katsumasa Fujita (*Osaka University*)

3SAA-1　散乱光で細胞・分子の状態を測る
Light scattering microscopes to quantify the cellular and molecular states
○市村 垂生, 金城 純一, Germond Arno, 渡邉 朋信（理研・QBiC）
Taro Ichimura, Junichi Kaneshiro, Arno Germond, Tomonobu Watanabe (*RIKEN QBiC*)

3SAA-2　光第二高調波イメージングの細胞生物学研究への応用
Application of SHG imaging to cell biology
○塗谷 睦生[1,2]（[1]慶應義塾大学医学部薬理学教室, [2]横浜国立大学環境情報研究院）
Mutsuo Nuriya[1,2] ([1]*Department of Pharmacology, Keio University School of Medicine*, [2]*Graduate School of Environment and Information Sciences, Yokohama National University*)

3SAA-3　Quantitative and multimodal phase imaging for analysis of cellular characteristics
Nicolas Pavillon, **Nicholas Smith** (*Osaka Univ, IFReC*)

3SAA-4　非ラベル分子の画像化のための位相敏感広帯域 CARS 分光
Phase-sensitive multiplex-CARS spectroscopy for label-free molecular imaging
○鈴木 隆行[1], 小原 祐樹[2], 三沢 和彦[2]（[1]明治大・院理工, [2]農工大・院工）
Takayuki Suzuki[1], Yuki Obara[2], Kazuhiko Misawa[2] ([1]*Grad. Sch. Sci., Meiji Univ.*, [2]*Grad. Sch. Eng., Tokyo Univ. of A&T*)

3SAA-5　誘導ラマン散乱顕微法による高速代謝物イメージング
High-speed imaging of metabolites with stimulated Raman scattering microscopy
○小関 泰之（東京大学大学院工学系研究科電気系工学専攻）
Yasuyuki Ozeki (*Department of Electrical Engineering and Information Systems, University of Tokyo*)

3SAA-6　光熱変換顕微法による生物組織の高感度・高分解光吸収イメージング
Photothermal microscopy for high sensitivity and high resolution absorption contrast imaging of biological tissues
○宮崎 淳（和歌山大学システム工学部）
Jun Miyazaki (*Fac. Sys. Eng., Wakayama Univ.*)

おわりに
Closing Remarks
○市村 垂生（理化学研究所）
Taro Ichimura (*RIKEN*)

9:00～11:30　B 会場（全学教育棟 2 階 B201）／Room B (Room B201, General Education Bldg. 2F)
3SBA　量子ビーム技術を活用した放射線生物物理学の最前線
Frontiers in radiation biophysics utilizing quantum beam technologies

オーガナイザー：冨田 雅典（電力中央研究所），中島 徹夫（量子科学技術研究開発機構）
Organizers: Masanori Tomita (Central Research Institute of Electric Power Industry), Tetsuo Nakajima (National Institute of Radiological Sciences)

Nowadays the quantum beam technology progresses remarkably. Energy and targeted irradiation region of quantum beams, including high-energy charged particles, synchrotron radiations and microbeams, can be controlled with high accuracy. These advances have led us to elucidate the long-term issues in radiation biophysics, i.e., distribution of DNA damage, intra- and inter-cellular communications, inter-tissue signaling, different effects due to radiation qualities etc. In this symposium, we introduce recent progresses of radiation biophysics using quantum beam technology and discuss the application of our results to studies of radiation effects and radiotherapy.

3SBA-1　高 LET 重イオン線によってヒト正常線維芽細胞に誘導されるバイスタンダーシグナル伝達と細胞死の機構解明
High-LET heavy-ion-induced bystander signalling and cell death in normal human fibroblasts
○冨田 雅典（電中研・原技研・放射線安全）
Masanori Tomita (*Radiat. Safety Res. Cent., CRIEPI*)

3SBA-2　高 LET 放射線による DNA 酸化損傷の生成とその分布観察
Observation of DNA oxidative damage induced by high LET radiation
○伊藤 敦（東海大・工）
Atsushi Ito (*Sch. Eng. Tokai Univ.*)

3SBA-3　Analysis of the modification of cell death by energy deposition to a local site in a cell
Munetoshi Maeda (*Proton Medic. Res. Gr., WERC*)

3SBA-4　Computational analysis of bystander signaling in cellular population irradiated with microbeam
Yuya Hattori[1], Akinari Yokoya[2], Daisuke Kurabayashi[1], Ritsuko Watanabe[2] ([1]*Dept. of Sys. & Ctrl. Eng., Sch. of Eng., Tokyo Tech.*, [2]*Quantum Beam Science Research Directorate, QST*)

3SBA-5　マイクロビーム照射とシミュレーションを用いた線虫の筋運動に対する放射線影響の解析
Analyses of radiation effects on muscular movements in *Caenorhabditis elegans* using microbeam irradiation and simulation-based approach
○鈴木 芳代[1], 服部 佑哉[2], 坂下 哲哉[1], 横田 裕一郎[1], 小林 泰彦[1], 舟山 知夫[1]（[1]量研 高崎研 放射線生物応用, [2]東工大 工学院 システム制御系）
Michiyo Suzuki[1], Yuya Hattori[2], Tetsuya Sakashita[1], Yuichiro Yokota[1], Yasuhiko Kobayashi[1], Tomoo Funayama[1] ([1]*Dept. of Radiat. Appl. Biol. Res., QST-Takasaki*, [2]*Dept. of Sys. & Ctrl. Eng., Sch. of Eng., Tokyo Tech*)

3SBA-6　メダカ胚で観察された重イオン局所照射によって誘発される照射野以外への影響
Abscopal activation of microglia in embryonic fish brain following targeted irradiation with heavy-ion microbeam
○保田 隆子[1], 尾田 正二[1], 舟山 知夫[2], 三谷 啓志[1]（[1]東京大 新領域, [2]量研機構 高崎量子応用研 放射線生）
Takako Yasuda[1], Shoji Oda[1], Tomoo Funayama[2], Hiroshi Mitani[1] ([1]*Grad. Sch. Frontier Sci., Univ. Tokyo*, [2]*TARRI, QuBS, QST*)

3SBA-7　生物影響からみた光子放射線と粒子放射線の違いー評価と防護ー
Differences between photon and particle radiations in terms of their biological effects: Evaluation and protection
○中島 徹夫（量研機構・放医研・放射線影響）
Tetsuo Nakajima (*Dept of Radiation Effects Research, NIRS, QST*)

9:00～11:30　C 会場（全学教育棟 2 階 B202）／Room C (Room B202, General Education Bldg. 2F)

3SCA　ATP をエネルギー源とする生物装置の構造、機能、および ATPase による動力発生機構
ATP energized biological machines: their structure, function and force generation mechanism coupled with ATPase

オーガナイザー：加藤 博章（京都大学），前田 雄一郎（名古屋大学）
Organizers: Hiroaki Kato (Kyoto University), Yuichiro Maeda (Nagoya University)

ATP is the energy source of organism and the cleavage of one of the phosphoanhydride bonds generates force that drives biologically important processes. This symposium focuses force generation mechanism of biomolecules such as a proton pump, dynein motor, ATP binding cassette transporter, circadian clock, KaiC, and filamentous actin. The speakers we invited have been studying the structure and mechanism of each machine at the research frontier. We try to find their common mechanistic behavior underlying force generation mechanism by ATP hydrolysis.

はじめに
Opening Remarks

3SCA-1　F 型結晶構造から明らかとなったアクチン重合と ATP 加水分解機構
ATPase mechanism and dynamic assembly of actin revealed by the F-form crystal structures
○武田 修一[1], 成田 哲博[1], 小田 俊朗[2], 田中 康太郎[1], 小池 亮太郎[3], 太田 元規[3], 藤原 郁子[4], 渡邉 信久[5], 前田 雄一郎[1]
([1]名大・院生命理学, [2]東海学院大, [3]名大・院情報科学, [4]名工大・材料科学フロンティア研究院, [5]名大・シンクロトロン）
Shuichi Takeda[1], Akihiro Narita[1], Toshiro Oda[2], Kotaro Tanaka[1], Ryotaro Koike[3], Motonori Ota[3], Ikuko Fujiwara[4], Nobuhisa Watanabe[5], Yuichiro Maeda[1] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Univ. Tokaigakuin*, [3]*Grad. Sch. of Info. Sci., Univ. Nagoya*, [4]*FRIMS., NITech*, [5]*SRRC., Univ. Nagoya*)

3SCA-2　Struture and mechanism of dynein motors
Takahide Kon (*Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.*)

3SCA-3　回転分子モーターの分子動力学シミュレーション
Molecular dynamics simulations of molecular rotary motors
○池口 満徳（横浜市立大学）
Mitsunori Ikeguchi (*Yokohama City Univ.*)

3SCA-4　Design of circadian clock of cyanobacteria by dual ATPases in KaiC
Takao Kondo (*Nagoya Univ*)

3SCA-5　ABC トランスポーターは ATP 結合と加水分解のエネルギーを多剤排出にどのように利用するのか
How ATP binding cassette (ABC) transporter harnesses the energy of ATP binding and hydrolysis to multidrug export
○加藤 博章[1,2]（[1]京大・院薬, [2]理研・播磨）
Hiroaki Kato[1,2] ([1]*Grad. Sch. Pharm. Sci., Kyoto Univ.*, [2]*RIKEN/SPring-8*)

おわりに
Closing Remarks
Yuichiro Maeda

9:00〜11:30　D 会場（全学教育棟 2 階 E201）／Room D (Room E201, General Education Bldg. 2F)

3SDA　ゲノム機能制御の多階層的理解 〜クロマチンの分子構造から核内動態まで〜
Understanding genomic functions in multiscale from chromatin structure to intranuclear dynamics

オーガナイザー：日比野 佳代（国立遺伝学研究所/総合研究大学院大学），落合 博（広島大学）
Organizers: Kayo Hibino (NIG / SOKENDAI), Hiroshi Ochiai (Hiroshima University)

The structure and dynamics of chromatin have been suggested to be closely related to the nuclear functions and disease. However, it is not fully understood how they regulate the function in the nucleus. Recent technologies related to live imaging, genome editing, and higher-order genomic structural analysis are clarifying how genomic DNA behaves dynamically in the nucleus. Based on these cutting-edge research results, we will discuss the relationship among the structure, dynamics of chromatin, and nuclear function from the molecule to the entire nuclear level.

3SDA-1　Structural analysis of the centromere specific nucleosome
Hiroaki Tachiwana[1,2], Midori Suzuki[3], Yoshimasa Takizawa[4], Matthias Wolf[4], Hitoshi Kurumizaka[2] ([1]*Japanese Foundation for Cancer Research, Cancer Institute*, [2]*Faculty of Science & Engineering, Waseda University*, [3]*Graduate School of Advanced Science & Engineering, Waseda University*, [4]*Okinawa Institute of Science and Technology Graduate University*)

3SDA-2　単一ヌクレオソームイメージングが明かすクロマチンダイナミクスと転写
Single nucleosome imaging reveals global chromatin stabilization upon transcription
○日比野 佳代[1,2], 永島 崚甫[2], 前島 一博[1,2]（[1]遺伝研, [2]総研大）
Kayo Hibino[1,2], Ryosuke Nagashima[2], Kazuhiro Maeshima[1,2] ([1]*NIG*, [2]*SOKENDAI*)

3SDA-3　Relationship between kinetics of higher-order genomic structure and transcriptional activity
Hiroshi Ochiai[1,2] ([1]*PRESTO, JST*, [2]*Grad. Sch. Sci., Hiroshima Univ.*)

3SDA-4　Transcription dynamics in living Drosophila embryos
Takashi Fukaya, Tyler Heist, Michael Levine (*Lewis-Sigler Institute for Integrative Genomics, Princeton University*)

3SDA-5　リボソーム RNA 遺伝子の核内動態： DNA 複製阻害タンパク質 Fob1 と DNA 損傷チェックポイントタンパク質に依存した核膜孔との結合
Fob1-dependent binding of ribosomal RNA genes to the nuclear periphery in budding yeast
○堀籠 智洋[1], 鵜之沢 英理[1,2,3], 大木 孝将[1], 小林 武彦[1,2,3]（[1]東京大学・分生研, [2]遺伝研, [3]総研大）
Chihiro Horigome[1], Eri Unozawa[1,2,3], Takamasa Ooki[1], Takehiko Kobayashi[1,2,3] ([1]*Inst. Mol. Cell. Biosci., Univ. Tokyo*, [2]*NIG*, [3]*SOKENDAI*)

3SDA-6　３次元ゲノム構造の多階層的理解〜ヌクレオソームレベルから全染色体レベルまで〜
Understanding 3D genome structure in mulitiscale from the nucleosome to whole choromosome level
○谷口 雄一（理化学研究所生命システム研究センター）
Yuichi Taniguchi (*Quantitative Biology Center, RIKEN*)

3SDA-7　キャプチャー Hi-C を用いたゲノム間相互作用解析
Genome wide interaction analysis using Capture Hi-C
○堤 修一[1], 岡部 篤史[2], 油谷 浩幸[1]（[1]ゲノムサイエンス, 東大・先端研, [2]分子腫瘍, 千葉大・院・医学研究院）
Shuichi Tsutsumi[1], Atsushi Okabe[2], Hiroyuki Aburatani[1] ([1]*Genome Sci. Div., RCAST, Univ. Tokyo*, [2]*Mol. Onc., Grad. Sch. of Med., Univ. Chiba*)

3SDA-8　Bridging the gap between the dynamics and organization of chromatin domains by mathematical modeling
Soya Shinkai[1,2], Tadasu Nozaki[3], Kazuhiro Maeshima[3], Yuichi Togashi[2] ([1]*RIKEN QBiC*, [2]*RcMcD, Hiroshima Univ.*, [3]*Natl. Inst. of Genet.*)

9:00〜11:30　F 会場（全学教育棟 2 階 E205）／Room F (Room E205, General Education Bldg. 2F)

3SFA　多角的な視点で読み解く膜デバイスの基本原理と新しい機能解析技術
Multiple aspects to understand mechanisms of membrane proteins as devices and novel approaches to dissect biomolecules

オーガナイザー：西坂 崇之（学習院大学），小嶋 誠司（名古屋大学）
Organizers: Takayuki Nishizaka (Gakushuin University), Seiji Kojima (Nagoya University)

How far is the elucidation of the basic principle of membrane proteins approaching the goal? In this symposium, we would like to address this question with the audience by introducing latest results based on various innovative methods. Topics include new developments of structural biology, computational simulation, advanced optical microscopies and microfabrications. These original researches from a multilateral perspective will reveal mechanisms of diverse membrane devices such as membrane receptors, pumps and transporters, which help us to look at the direction of biophysics ten years ahead.

はじめに
Opening Remarks
Takayuki Nishizaka

3SFA-1 Single-Molecule Detection of Biomolecules and Protein Conformational Dynamics
Takayuki Nishizaka[1], Shoko Fujimura[2], Yoshiro Sohma[2,3], Daisuke Nakane[1] ([1]*Dept. Phys., Gakushuin Univ.*, [2]*Sch. of Med, Keio Univ.*, [3]*Sch. of Pharm, IUHW*)

3SFA-2 小胞型ヌクレオチドトランスポーターのアロステリック制御
Allosteric regulation of vesicular nucleotide transporter
○表 弘志（岡山大学大学院医歯薬）
Hiorshi Omote (*Okayama University Grad. School of Med., Dent. and Pharm. Sci.*)

3SFA-3 Single molecule analysis of membrane transport proteins using artificial cell-membrane microsystems
Rikiya Watanabe (*Department of Applied Chemistry, The University of Tokyo*)

3SFA-4 ギャップ結合チャネルのクライオ電子顕微鏡単粒子解析
Single particle cryo-EM of a gap junction channel
○大嶋 篤典[1,2]（[1]名古屋大学細胞生理学研究センター, [2]名大・院・創薬）
Atsunori Oshima[1,2] ([1]*CeSPI, Nagoya Univ.*, [2]*Dept. Pha., Nagoya Univ.*)

3SFA-5 Ca^{2+}-ATPase の E1/E2 転移における大規模構造変化の分子動力学法シミュレーション
Molecular dynamics simulations for conformational changes on E1/E2 transition of Ca^{2+}-ATPase
○小林 千草[1], 松永 康佑[1,2], Jung Jaewoon[1,3], 杉田 有治[1,3,4]（[1]理研, AICS, [2]JST, さきがけ, [3]理研, 杉田理論分子科学, [4]理研, QBiC）
Chigusa Kobayashi[1], Yasuhiro Matsunaga[1,2], Jaewoon Jung[1,3], Yuji Sugita[1,3,4] ([1]*RIKEN, AICS*, [2]*JST, PRESTO*, [3]*RIKEN, TMS*, [4]*RIKEN, QBiC*)

3SFA-6 Mechanics of Single Protein Molecules
Matthias Rief (*Technischen Universität München, Physik-Department*)

9:00～11:30　G 会場（全学教育棟 3 階 C301）／Room G (Room C301, General Education Bldg. 3F)

3SGA　実験・シミュレーション・データ科学の融合による遺伝情報分子システムの生物物理
Biophysics of genetic information molecules and systems: Integrated approach of experiments, simulations, and data science

オーガナイザー：高田 彰二（京都大学），笹井 理生（名古屋大学）
Organizers: Shoji Takada (Kyoto University), Masaki Sasai (Nagoya University)

Genome contains not only gene sequence information but also information on which, when, and how genes are expressed. To understand genetic information molecules, we need to know proteins working therein, 3D chromatin structures, and transcriptions. Towards that goal, we integrate experiments with physical simulations and data science. In this symposium, we discuss biophysical challenges for genetic information molecules by experiments, simulations, data science, and their collaboration.

3SGA-1　分子シミュレーションによるヌクレオソームと転写因子の動態研究
Dynamics of nucleosomes and transcription factors studied by molecular simulations
○高田 彰二（京大院理・生物物理）
Shoji Takada (*Biophys. Sci. Kyoto Univ*)

3SGA-2　methyl CpG 結合ドメインタンパク質の分子基盤研究
Structural biochemistry of methyl CpG binding domain containing proteins
○有吉 眞理子（阪大・院・生命機能）
Mariko Ariyoshi (*Grad. Sch. Frotier Bio.*)

3SGA-3　高速 AFM による天然変性タンパク質の構造動態解析
Structural dynamics analysis of intrinsically disordered proteins by high-speed AFM
○古寺 哲幸[1], 能代 大輔[1,2], Dora Sujit[1], 安藤 敏夫[1,2]（[1]金沢大・バイオAFM, [2]CREST・JST）
Noriyuki Kodera[1], Daisuke Noshiro[1,2], Sujit Dora[1], Toshio Ando[1,2] ([1]*Bio-AFM FRC, Kanazawa Univ.*, [2]*CREST, JST*)

3SGA-4　Chromosome association of noncoding RNA during homologous chromosome pairing in fission yeast meiosis
Da-Qiao Ding[2], Tokuko Haraguchi[1,2], **Yasushi Hiraoka**[1,2] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*National Institute of Information and Communications Technology*)

3SGA-5　シーケンシングと分子動力学計算の組み合わせによるクロマチン 3D 構造解析
3D chromatin structure revealed by the combination of sequencing analysis and molecular dynamics simulation
○大野 雅恵[1], 安藤 格士[2], 谷口 雄一[1]（[1]理研・QBiC, [2]東理大・基礎工・電子応用）
Masae Ohno[1], Tadashi Ando[2], Yuichi Taniguchi[1] ([1]*QBiC, RIKEN*, [2]*Dept. of Appl. Elec., Tokyo Univ. of Science*)

3SGA-6　高解像度 Hi-C データを活用した遺伝子発現制御の理解
Understanding gene regulation by using high-resolution Hi-C data
○須山 幹太（九州大学生体防御医学研究所）
Mikita Suyama (*Medical Institute of Bioregulation, Kyushu University*)

3SGA-7　The phase-separation principle of human genome architecture
Shin Fujishiro, Masaki Sasai (*Dept. Comp. Sci. & Eng., Nagoya Univ.*)

9:00～11:30　I 会場（全学教育棟 3 階 E305）／Room I (Room E305, General Education Bldg. 3F)

3SIA　新機能分子系を創出してきた地球生物進化と試験管内進化の対話
Dialogue between in vitro evolution and biological evolution, both of which have created new functional biomolecules

オーガナイザー：根本 直人（埼玉大学），赤沼 哲史（早稲田大学）
Organizers: Naoto Nemoto (Saitama University), Satoshi Akanuma (Waseda University)

Unlike biological evolution in organisms, in vitro evolutionary molecular engineering has focused on single molecules as the targets of evolution to understand the basic principle of molecular evolution. The research field has now created functional molecules so called 'NEO-biomolecules'. The next step of artificial evolution is to evolve systems involving more than one molecule, such as ribosomes. In this symposium, we will discuss the relationship between evolutions of single molecules and complex systems, to accelerate the progress of both fields.

3SIA-1　Biobit の可能世界
Possible world of Biobit
○伏見 譲（JST先端計測）
Yuzuru Husimi (*Japan Science and Technology Agency*)

3SIA-2　VHH ファージライブラリーからの有用な抗体の迅速単離と試験管内抗体進化
Rapid isolation of valuable antibodies from VHH phage display libraries and in vitro antibody evolution
○村上 明一[1], 吉田 麻衣子[1,2], 塚原 成俊[3], 東 隆親[2], 岸本 英博[1]（[1]琉球大学大学院医学研究科 寄生虫・免疫病因病態学講座, [2]株式会社抗体工学研究センター, [3]イノベックスサイエンス株式会社）
Akikazu Murakami[1], Maiko Yoshida[1,2], Narutoshi Tsukahara[3], Takachika Azuma[2], Hidehiro Kishimoto[1] ([1]*Grad. Sch of Med., U-Ryukyus*, [2]*Antibody Engineering Research Center Inc.*, [3]*Innovex Science Co., Ltd.*)

3SIA-3　網羅的配列解析による抗体ファージライブラリーからの抗原特異的抗体の効率的な選別
Efficient selection of antigen-specific antibodies from phage library using high throughput sequencing
○伊東 祐二（鹿児島大学大学院理工学研究科生命化学専攻）
Yuji Ito (*Grad. Sch. Sci. and Eng., Kagoshima Univ.*)

3SIA-4　アミノ酸の種類が制限された cDNA ディスプレイライブラリからのポリメラーゼリボザイムに対するコファクターペプチドの試験管内淘汰
In Vitro selection of cofactor peptides of polymerase ribozyme form a cDNA display library composing of limited set of amino acids
○熊地 重文（(株）Epsilon Molecular Engineering）
Shigefumi Kumachi (*Epsilon Molecular Engineering Inc.*)

3SIA-5　Evolutionary Engineering and Characterization of Membrane Proteins Using Liposome Display
Tomoaki Matsuura (*Dep. Biotechnol, Grad. Sch. Eng., Osaka Univ.*)

3SIA-6　Rapid adaptation of RNA bacteriophage to environmental changes
Akiko Kashiwagi (*Fac. Agr and LifSci, Hirosaki Univ.*)

3SIA-7　バクテリア 16S rRNA の進化中立性の実験的検証
Comparative RNA function analysis reveals primarily neutral evolvability of bacterial 16S rRNA genes
○宮崎 健太郎[1,2]（[1]産総研 生物プロセス, [2]東大院 新領域）
Kentaro Miyazaki[1,2] ([1]*AIST*, [2]*Univ Tokyo*)

3SIA-8　Evolution and function of OEC-family proteins in chloroplasts
Kentaro Ifuku (*Grad. Sch. Biostudies, Kyoto Univ.*)

3SIA-9　進化分子工学と極限環境生物
Evolutionary Engineering and Extremophiles
○大島 泰郎（共和化工(株)環境微生物学研究所）
Tairo Oshima (*Inst. Environ. Microbiol., Kyowa-Kako*)

9:00〜11:30　K 会場（文法学部 2 階 A1 教室）／Room K (Room A1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

3SKA　メカニカルコミュニケーションが生み出す生体運動の多様性
Diversity of biological motility generated by mechanical communications

オーガナイザー：宮田 真人（大阪市立大学），今田 勝巳（大阪大学）
Organizers: Makoto Miyata (Osaka City University), Katsumi Imada (Osaka University)

While living organisms commonly utilize the energy produced by hydrolysis of nucleotide or electrochemical potential across cell membrane for their motility, they have developed various power transmission mechanisms unique to each individual. In this symposium, we will discuss molecular mechanism of power transmission that produces diversity of the biological motility, namely ‘mechanical communication’, from various viewpoints including structure, theory, molecular and cellular biology, and dynamics.

はじめに
Opening Remarks
Makoto Miyata

3SKA-1　ハプト藻に存在するハプトネマの急速コイリング運動における微小管ダイナミクス
Microtubule dynamics for rapid coiling movement of haptonema in the haptophyte algae
○野村 真未[1], 阿閉 耕平[1], 広瀬 恵子[2], 柴 小菊[1], 稲葉 一男[1]（[1]筑波大学 下田臨海実験センター, [2]産業技術総合研究所 バイオメディカル研究部門）
Mami Nomura[1], Kohei Atsuji[1], Keiko Hirose[2], Kogiku Shiba[1], Kazuo Inaba[1] ([1]*Shimoda Marine Research Center, University of Tshukuba*, [2]*Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology*)

3SKA-2　螺旋形細菌レプトスピラの遊泳と滑走のメカニズム
Swimming and gliding mechanisms of the spirochete *Leptospira*
○中村 修一（東北大・院工）
Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)

3SKA-3　Structure, mechanics, and shape dynamics of Spiroplasma
Hirofumi Wada (*Department of Physical Sciences, Ritsumeikan University*)

3SKA-4　Mechano-electrical communications in actin filament
Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

3SKA-5　Hypervariation in primary and quaternary structures of ParMs, prokaryotic actin-like polymerizing motors
Robert C. Robinson[1,2] ([1]*Institute of Molecular and Cell Biology*, [2]*RIIS, Okayama Univ.*)

3SKA-6　クライオ電子顕微鏡で解き明かす細菌べん毛モーター回転子の立体構造と回転対称性
Structure and rotational symmetry of the rotor of the bacterial flagellar motor revealed by electron cryomicroscopy
○川本 晃大[1], 宮田 知子[1], 木下 実紀[1], 南野 徹[1], 加藤 貴之[1], 難波 啓一[1,2]（[1]阪大院・生命機能, [2]理研・QBiC）
Akihiro Kawamoto[1], Tomoko Miyata[1], Miki Kinoshita[1], Tohru Minamino[1], Takayuki Kato[1], Keiichi Namba[1,2] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ*, [2]*QBiC., RIKEN*)

3SKA-7　べん毛軸構造蛋白質の構造と集合体形成
Structure and assembly of bacterial flagellar axial proteins
○今田 勝巳（阪大・院理）
Katsumi Imada (*Grad. Sch. Sci., Osaka Univ.*)

9:00〜11:30　L 会場（文法学部 2 階 B1 教室）／Room L (Room B1, Faculty of Letters, Faculty of Law Main Bldg. 2F)

3SLA　疾患関連タンパク質の生物物理学とその医学・薬学への応用
Biophysical approach on disease-related proteins toward application for medical and pharmaceutical sciences

オーガナイザー：濵田 大三（神戸大学），李 映昊（大阪大学）
Organizers: Daizo Hamada (Kobe University), Young-Ho Lee (Osaka University)

Biophysical approaches have been widely applied to medical and pharmaceutical researches on disease-related proteins. Despite of extensive endeavors, much remains to be learnt about how biophysical application is effectively used to understand the underlying molecular mechanisms of disease onset and progression, and to develop the methodologies for the prevention and cure of diseases. In this symposium, we invite several qualified researchers and discuss the state-of-the-art biophysical method and perspective of the biophysics for medical and pharmaceutical researches.

3SLA-1　AL アミロイドーシスにおけるアミロイド形成の引金 - 診断と阻害戦略への展望
Triggers of amyloid formation in AL amyloidosis - perspective for development of diagnosis and inhibition strategy
○濵田 大三[1,2,3]（[1]神戸大・工, [2]神戸大 統合研究拠点 応用構造科学, [3]理研 SPring-8）
Daizo Hamada[1,2,3] ([1]*Grad Sch Eng, Kobe Univ*, [2]*CASS, Kobe Univ*, [3]*RIKEN SPring-8*)

3SLA-2　Ras がん遺伝子産物を分子標的としたがん治療薬のインシリコ創薬
In silico discovery of anti-cancer drugs targeting the Ras oncoproteins
○片岡 徹（神戸大・院医）
Tohru Kataoka (*Grad Sch Med, Kobe Univ.*)

3SLA-3　Computational approach for understanding protein-aggregation diseases
Sihyun Ham (*Dept of Chem, Sookmyung Women's Univ.*)

3SLA-4　動的構造解析による多剤耐性転写制御因子の非特異的かつ高親和性な結合メカニズムの解明
Promiscuous high-affinity recognition of a multidrug resistance transcriptional regulator revealed by structural dynamics analyses
○竹内 恒[1], 今井 美咲[1,2], 德永 裕二[1], 嶋田 一夫[3]（[1]産総研・創薬分子, [2]バイオ産業情報化コンソ, [3]東京大・院薬系）
Koh Takeuchi[1], Misaki Imai[1,2], Yuji Tokunaga[1], Ichio Shimada[3] ([1]*AIST, Molprof*, [2]*JBIC*, [3]*The Univ of Tokyo, Grad Sch Pharma Sci*)

3SLA-5　熱測定によるアミロイド疾患の診断を目指した研究
Calorimetric approach for investigating disease-related amyloidogenesis
○李 映昊（大阪大・蛋白質研究所）
Young-Ho Lee (*Inst of Protein Res, Osaka Univ.*)

9:00〜11:30　M 会場（文法学部 1 階 B2 教室）／Room M (Room B2, Faculty of Letters, Faculty of Law Main Bldg. 1F)

3SMA　構造生物学研究ツールの進展〜どう使い分けるか？
Tools in a new epoch for structural biology. ~How to use them properly?~

オーガナイザー：岩崎 憲治（大阪大学），タマ フロハンス（名古屋大学/理化学研究所）
Organizers: Kenji Iwasaki (Osaka University), Florence Tama (Nagoya University/RIKEN)

While X-ray crystallography is a longstanding, powerful tool in structural biology, cryo-electron microscopy and X-ray free electron laser have recently reported vivid results which would not be obtainable by conventional methods. Furthermore, integration of these experimental data work computational methods such as molecular dynamics, can provide information on dynamics and conformational states of biological molecules. In this symposium, studies illustrating these methods, integration of these methods to gain insights into structure and dynamics will be presented.

3SMA-1　原子分解能をめざしたクライオ電子顕微鏡の技術開発
Towards atomic resolution structural analysis by electron cryomicroscopy
○難波 啓一（阪大・生命機能）
Keiichi Namba (*Grad Schl Frontier Biosci, Osaka Univ*)

3SMA-2 近原子分解能クライオ電子顕微鏡単粒子解析に向けたデータ測定及び画像処理条件の最適化
Studies on Data Acquisition Conditions and Image Processing for Near-atomic Resolution Cryo-EM Single Particle Analysis
○横山 武司（理研CLST）
Takeshi Yokoyama (*CLST., RIKEN*)

3SMA-3 SACLA を用いたタンパク質の時間分割構造解析
Time-resolved x-ray crystallography at SACLA
○岩田 想[1,2]（[1]京大院・医, [2]理研・放射光科学総合研究センター）
So Iwata[1,2] ([1]*Grad. Sch. Med., Univ. Kyoto*, [2]*SPring-8 Center, RIKEN*)

3SMA-4 XFEL によって明らかになった光化学系 II 水分解触媒の中間体構造と反応機構
Structure of an intermediate S-state of photosystem II and the mechanism of water-splitting revealed by XFEL
○沈 建仁（岡山大学異分野基礎科学研究所）
Jian-Ren Shen (*Res. Inst. for Interdiscip. Sci., Okayama Univ.*)

3SMA-5 Computational tools to characterize structure and dynamics of biomolecular systems from single molecule experiments
Florence Tama[1,2,3] ([1]*RIKEN AICS*, [2]*Nagoya University, Physics*, [3]*ITbM-WPI*)

3SMA-6 電子顕微鏡法のための画像解析と構造決定法の紹介
Image analysis and structural reconstruction for electron microscopy
○安永 卓生（九工大・情報工・生命情報工）
Takuo Yasunaga (*Dept. of Biosci. Bioinfo., Sch. of Comp. Sci. Sys. Eng., Kyutech*)

9:00～11:30　N 会場（文法学部 1 階 B3 教室）／Room N (Room B3, Faculty of Letters, Faculty of Law Main Bldg. 1F)

3SNA　生体分子におけるケト-エノール互変異性
Keto-enol tautomerism in biomolecules

オーガナイザー：岩田 達也（東邦大学），伊藤 奨太（名古屋工業大学）
Organizers: Tatsuya Iwata (Toho University), Shota Ito (Nagoya Institute of Technology)

Keto (R–C(=O)CH–R'R'') and enol (R–C(OH)=C–R'R'') forms are tautomers of each other, and the equilibrium is called as keto-enol tautomerism. In general, the keto form is more stable than its enol tautomer in simple compounds. However, keto-enol tautomerism is utilized for the regulation of proper reactions in biomolecules. Therefore, response regulation mechanism by keto-enol tautomerism reaction on biomolecules is one of the interesting topic in biophysics. Researches on keto-enol tautomerism of biomolecules will be presented and variety and reaction mechanisms will be discussed.

はじめに
Opening Remarks

3SNA-1 Keto-enol tautomerism of Gln on BLUF domain
Shota Ito (*Nagoya Inst. Tech.*)

3SNA-2 核酸分子におけるケト-エノール互変異性
Keto-enol tautomerism in nucleic acids
○紙谷 浩之（広島大・院医歯薬保（薬））
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3SNA-3 タンパク質環境における互変異性に関する計算科学的研究
Computational Studies on tautomerism in protein environment
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3SNA-4 植物の葉の香りを決めるケトエノール互変
Keto-enol tautomerism determining plant leaf fragrance
○山内 靖雄（神戸大学大学院農学研究科）
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3SNA-5 Keto-enol tautomerism of curcumin upon binding to amyloid fibrils
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