09:00〜11:30　A 会場（函館アリーナ 武道館 A）／Room A（Hakodate Arena Budokan A）

1SAA　動的溶液環境が駆動するタンパク質凝集
Protein aggregation driven by dynamic solution environments

オーガナイザー：吉田 紀生（九州大学），菅瀬 謙治（京都大学）
Organizers: Norio Yoshida (Kyusyu Univ.), Kenji Sugase (Kyoto Univ.)

In cells, the solution environment is constantly changing due to varying concentrations of chemicals, mechanical stimuli, and electric fields. In recent years, it has become evident that intrinsically disordered proteins, which do not have specific conformations, undergo liquid-liquid phase separation and amyloid fibrillization in response to the 'dynamic' solution environment. This series of self-condensation processes is controlled by the protein-protein and protein-solvent interactions of intrinsically disordered proteins, which have dynamic conformations and solvation states. In this workshop, we will discuss the latest research on the self-condensation process of intrinsically disordered proteins and their future development.

はじめに
Opening Remarks

1SAA-1　TIA-1 プリオン様ドメインの ALS 変異は高度に凝縮した病原性構造体を形成する
ALS mutations in the TIA-1 prion-like domain trigger highly condensed pathogenic structures
○関山 直孝 [1], 高場 圭章 [2], 眞木 さおり [2], 赤木 謙一 [3], 大谷 寧子 [1], 今村 香代 [1], 寺川 剛 [1], 山下 恵太郎 [4], 米倉 功治 [2], 児玉 高志 [1], 杤尾 豪人 [1]（[1] 京大・理・生物物理, [2] 理研・放射光科学研究センター, [3] 医薬基盤・健康・栄養研究所, [4]MRC 分子生物学研究所）
Naotaka Sekiyama[1], Kiyofumi Takaba[2], Saori Maki-Yonekura[2], Ken-ichi Akagi[3], Yasuko Ohtani[1], Kayo Imamura[1], Tsuyoshi Terakawa[1], Keitaro Yamashita[4], Koji Yonekura[2], Takashi Kodama[1], Hidehito Tochio[1] ([1]*Dept. of Biophysics, Grad Sch. of Science, Kyoto Univ.*, [2]*RIKEN SPring-8 Center*, [3]*NIBIO*, [4]*MRC Laboratory of Molecular Biology*)

1SAA-2　流れが駆動するタンパク質のアミロイド線維化機構
Mechanism of amyloid fibrillation of a protein driven by a flow
○菅瀬 謙治 [1], 森本 大智 [2], Erik Walinda[3]（[1] 京都大学大学院農学研究科 応用生命科学専攻, [2] 京都大学大学院工学研究科分子工学専攻, [3] 京都大学大学院医学研究科細胞機能制御学）
Kenji Sugase[1], Daichi Morimoto[2], Erik Walinda[3] ([1]*Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University*, [2]*Department of Molecular Engineering, Graduate School of Engineering, Kyoto University*, [3]*Department of Molecular and Cellular Physiology, Graduate School of Medicine, Kyoto University*)

1SAA-3　生体分子のための動的溶媒和理論の開発
Development of Dynamic Solvation Theory for Biomolecules
○吉田 紀生（名古屋大・院情報）
Norio Yoshida (*Grad. Sch. Info., Nagoya Univ.*)

1SAA-4 リン酸化による HP1α の液-液相分離機構の解明
Phase separation mechanism of HP1α by phosphorylation
○古川 亜矢子 [1], 米澤 健人 [2,3], 根上 樹 [4], 吉村 ゆり子 [5], 林 亜紀 [5], 中山 潤一 [5,6], 安達 成彦 [2], 千田 俊哉 [2], 清水 謙多郎 [4], 寺田 透 [4], 清水 伸隆 [2], 西村 善文 [1,7]（[1] 横市大・生命医科学, [2] 高エネ機構・物構研, [3] 奈良先端大・CDG, [4] 東大・院農, [5] 基生研, [6] 総研大・生命科学研究科, [7] 広島大・統合生命）
Ayako Furukawa[1], Kento Yonezawa[2,3], Tatsuki Negami[4], Yuriko Yoshimura[5], Aki Hayashi[5], Jun-ichi Nakayama[5,6], Naruhiko Adachi[2], Toshiya Senda[2], Kentaro Shimizu[4], Tohru Terada[4], Nobutaka Shimizu[2], Yoshifumi Nishimura[1,7] ([1]*Grad. Sch. Med. Life Sci., Univ. Yokohama City*, [2]*IMSS, KEK,*, [3]*NAIST, CDG*, [4]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [5]*NIBB*, [6]*SOKENDAI*, [7]*Grad. Sch. Integ. Sci. Life, Univ. Hiroshima*)

1SAA-5 タンパク質の変性状態における構造ダイナミクスと溶媒環境依存性の理論的解析
Theoretical study on the conformational dynamics of proteins in disordered states under different solvent environments
○森 俊文（九大・先導研）
Toshifumi Mori (*Inst. Mat. Chem. Eng., Kyushu Univ.*)

1SAA-6 ポリマーコートされたダイヤモンドナノ粒子によるバイオセンシング
Biosensing Using Diamond Nanoparticles Coated with Polymers
○外間 進悟, 原田 慶恵（阪大・蛋白研）
Shingo Sotoma, Yoshie Harada (*IPR, Osaka Univ.*)

1SAA-7 (2Pos051) 蝶々型金ナノデバイスが可能にするタンパク質液液相分離過程の制御
(2Pos051) Control of protein condensation by butterfly-shaped gold nanodevices
○延山 知弘 [1], 高田 耕児 [2], 村上 達也 [2], 白木 賢太郎 [1,2]（[1] 筑波大・応用理工, [2] 富山県立大・院工）
Tomohiro Nobeyama[1], Koji Takata[2], Tatsuya Murakami[2], Kentaro Shiraki[1,2] ([1]*Pure and Appli.Sci., Univ.Tsukuba*, [2]*Grad. Sch. Sci. Toyama Pref. Univ*)

1SAA-8 (1Pos054) GGGGCC-RNA は、TDP43 およびそのカルボキシ断片の凝集を抑制する
(1Pos054) GGGGCC-RNA prevents aggregation of TDP43 and its carboxy terminal fragments
○藤本 愛 [1], 金城 政孝 [2], 北村 朗 [2]（[1] 北大・院・生命, [2] 北大・先端生命）
Ai Fujimoto[1], Masataka Kinjo[2], Akira Kitamura[2] ([1]*Grad. Sch. of Life Sci., Hokkaido. Univ*, [2]*Fac. Adv. Life Sci., Hokkaido. Univ*)

おわりに
Closing Remarks

09:00〜11:30　B 会場（函館アリーナ 武道館 B）／Room B（Hakodate Arena Budokan B）

1SBA　量子ビームでひも解くタンパク質の大きな構造変化 –タンパク質ダイナミクス理解の新潮流
Protein large-scale motions revealed by quantum beams -a new era in understanding protein dynamics

オーガナイザー：山本 直樹（自治医科大学），関口 博史（高輝度光科学研究センター）
Organizers: Naoki Yamamoto (Jichi Med. Univ.), Hiroshi Sekiguchi (JASRI)

Biological systems function by constantly changing their hierarchical and inter-hierarchical interactions among molecules, cells, and individuals. In order to visualize these dynamics, it is effective to approach them using penetrating quantum beams such as X-rays and neutron beams. This symposium will introduce recent advances in quantum beam techniques for biophysical research, mainly focusing on large structural changes within and between protein molecules. Furthermore, molecular dynamics simulation studies combined with the experimental researches, which deepen the knowledge on molecular mechanisms of the complexed protein systems, will also be shown.

はじめに
Opening Remarks

1SBA-1　X 線 1 分子追跡法によるヘモグロビン・アロステリーの再検討
Allosteric Transition Dynamics in Hemoglobin Reconsidered by Diffracted X-ray Tracking
○関口 博史 [1], 山本 直樹 [2], 柴山 修哉 [2], 佐々木 裕次 [1,3]（[1] 高輝度光科学研究センター, [2] 自治医科大・医, [3] 東大・新領域）
Hiroshi Sekiguchi[1], Naoki Yamamoto[2], Naoya Shibayama[2], Yuji Sasaki[1,3] ([1]*JASRI/SPring-8*, [2]*Dept. Physiology, Jichi Med. Univ.*, [3]*Grad. Sch. Front. Sci., Univ. Tokyo*)

1SBA-2　Internal dynamics of intrinscially disordered protein as studied by neutron scattering
Rintaro Inoue (*Institute for Integrated Radiation and Nuclear Science, Kyoto University*)

1SBA-3　(2Pos050) タンパク質ケージ内における芳香環相互作用ネットワークの熱力学・分子動力学的解析
(2Pos050) Thermodynamic and Molecular Dynamic Analysis of Aromatic Interaction Networks in Protein Cages
○菱川 湧輝 [1], 野谷 大樹 [1], 浅沼 明日香 [1], Maity Basudev[1], 長門石 曉 [2], 津本 浩平 [2,3], 安部 聡 [1], 上野 隆史 [1]（[1] 東工大・生命理工, [2] 東大・医科研, [3] 東大・院工）
Yuki Hishikawa[1], Noya Hiroki[1], Asuka Asanuma[1], Basudev Maity[1], Satoru Nagatoishi[2], Kouhei Tsumoto[2,3], Satoshi Abe[1], Takafumi Ueno[1] ([1]*Sch. Life Sci. Technol., Tokyo Inst. Technol.*, [2]*Inst. Med. Sci., Univ. Tokyo*, [3]*Sch. Eng., Univ. Tokyo*)

1SBA-4　(1Pos076) 3D structural determination of proteins from fluctuation X-ray scattering data
Wenyang Zhao[1], Osamu Miyashita[1], Florence Tama[1,2] ([1]*Center for Computational Science, RIKEN*, [2]*Grad. Sch. Sci., Univ. Nagoya*)

1SBA-5　Microscopic Mechanisms of Stable Amyloid β (1-42) Oligomer Formation
Ikuo Kurisaki, Shigenori Tanaka (*Graduate School of System Informatics, Kobe University*)

1SBA-6 **非干渉性中性子散乱で観測するアミロイド構造多形体及びリン脂質分子のサブナノ秒ダイナミクス**
Sub-nanosecond dynamics of amyloid polymorphs and phospholipid molecules observed by incoherent neutron scattering
○松尾 龍人 [1,2,3], Francesco Alessio De[2], Cissé Aline[2,3], Bicout Dominique[2,3], Peters Judith[2,3,4] ([1] 量研・量子生命科学研究所, [2]Institut Laue-Langevin, France, [3]Université Grenoble Alpes, France, [4]Institut Universitaire de France)
Tatsuhito Matsuo[1,2,3], Alessio De Francesco[2], Aline Cissé[2,3], Dominique Bicout[2,3], Judith Peters[2,3,4] ([1]*iQLS, QST*, [2]*Institut Laue-Langevin, France*, [3]*Université Grenoble Alpes, France*, [4]*Institut Universitaire de France*)

1SBA-7 **アミロイド線維前駆中間体の構造発達とその阻害**
Structural development of amyloid prefibrillar intermediates and its inhibition
○山本 直樹（自治医大・医）
Naoki Yamamoto (*Sch. Med. Jichi Med. Univ.*)

おわりに
Closing Remarks

09:00〜11:30　C 会場（函館アリーナ 武道館 C）／Room C（Hakodate Arena Budokan C）
1SCA　**【共催：新学術研究領域「生命金属科学」】**

生命金属のライブセルイメージング
Live-cell imaging of bio-metal species

オーガナイザー：石森 浩一郎（北海道大学），平山 祐（岐阜薬科大学）
Organizers: Koichiro Ishimori (Hokkaido Univ.), Tasuku Hirayama (Gifu Pharm. Univ.)

The inorganic ions are essential for life despite their small amounts, in addition to organic macromolecules such as proteins, DNA, carbohydrates, and lipids. The dysfunction of the homeostasis of these inorganic ion species is involved in various pathologies. To understand the dynamics and functions of the inorganic species in living things, the observation of their existence and fluctuation in living cells is necessary. In this symposium, up-and-coming researchers will give talks on innovative methods for imaging inorganic species in living cells. This symposium is a collaborative symposium with Integrated Metal-bioscience.

1SCA-1 **遊離鉄およびヘム蛍光プローブのライブセルイメージングへの応用**
Fluorescence probes for labile iron and heme and their applications to live-cell imaging
○平山 祐（岐阜薬科大学薬化学研究室）
Tasuku Hirayama (*Lab. Pharm. Med. Chem., Gifu Pharm. Univ.*)

1SCA-2 **細胞内遊離亜鉛イオンの定量解析を可能とする小分子蛍光プローブの開発**
Development of small-molecule fluorescent probes for the quantitative analysis of labile Zn^{2+} in cells
○小和田 俊行（東北大学多元物質科学研究所）
Toshiyuki Kowada (*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*)

1SCA-3 **コンディショナルプロテオミクスによる金属関連タンパク質のイメージングとプロファイリング**
Imaging and profiling of metal-related proteins by conditional proteomics strategies
○田村 朋則（京大院工）
Tomonori Tamura (*Grad. Sch. Eng., Univ. Kyoto*)

1SCA-4 量子ビームによる生命金属シングルセルイメージング
Single cell imaging by quantum beam elemental analyses for dynamics of cellular distribution of bio-metals
○武田 志乃（国立研究開発法人量子科学技術研究開発機構　放射線医学研究所）
Shino Takeda (*National institute of Radiological Sciences, National Institutes for Quantum Science and Technology*)

1SCA-5 蛍光イメージングで解き明かす細胞内マグネシウムイオンの役割
The roles of intracellular magnesium ion revealed by fluorescence imaging
○新藤 豊（慶大・理工・生命情報）
Yutaka Shindo (*Dept. Biosci. Info., Keio Univ.*)

1SCA-6 H_2S 検出蛍光プローブの開発とそれを用いた活性イオウ分子産生酵素の阻害剤スクリーニングへの応用
Development of a fluorescence probe for H_2S and its application to the inhibitor screening of reactive sulfur species-producing enzymes
○花岡 健二郎（慶應大・院薬）
Kenjiro Hanaoka (*Grad. Sch. Pharm. Sci., Keio Univ.*)

09:00〜11:30　D 会場（函館アリーナ 多目的室 A）／Room D（Hakodate Arena Multipurpose Room A）
1SDA　糖鎖の動的構造から機能へ – 実験・理論解析の最先端
Unveil glycans' function from their dynamical structures. – Cutting-edge challenges

オーガナイザー：李 秀栄（医薬基盤・健康・栄養研究所），山口 芳樹（東北医科薬科大学）
Organizers: Suyong Re (NIBIOHN), Yoshiki Yamaguchi (Tohoku Med. and Pharm.l Univ.)

Glycosylation of proteins is a ubiquitous biomolecular process. It adds extra functions or modulates existing functions of proteins, thereby affecting a range of cellular processes and diseases. Despite of the complex and dynamical nature of glycan structures, the recent advances both in experiment and computation enable us to investigate their functions based on the dynamical structures at atomic resolution, as exemplified in the "glycan-shield" of SARS-CoV-2 spike protein. In this symposium, we would like to share the cutting-edge challenges in determining functional structures and dynamics of glycans and discuss the potential future collaborations.

はじめに
Opening Remarks

1SDA-1 Viral glycosylation: HIV-1 to SARS-CoV-2
Max Crispin (*School of Biological Sciences, University of Southampton, UK*)

1SDA-2 Integrative methods in structural glycobiology
Jon Agirre (*University of York*)

1SDA-3 GLYCO: a tool to quantify glycan shielding of glycosylated proteins
Myungjin Lee (*National Institutes of Health*)

1SDA-4 Psme3 の部位特異的な *O*-GlcNAc 修飾は、P-body の恒常性の阻害を介してマウス ES 細胞の多能性維持に関与する
Site-specific *O*-GlcNAcylation of Psme3 maintains mouse embryonic stem cell pluripotency by impairing P-body homeostasis
○西原 祥子（創価大学・糖鎖生命システム融合研究所）
Shoko Nishihara (*Glycan & Life System Integration Center (GaLSIC), Soka University*)

1SDA-5 Description of the dynamic conformation of oligosaccharides by combining NMR spectroscopy and molecular simulation

Takumi Yamaguchi[1,2] ([1]*School of Materials Science, Japan Advanced Institute of Science and Technology*, [2]*Graduate School of Pharmaceutical Sciences, Nagoya City University*)

1SDA-6 病原性細菌における付着因子の糖鎖認識機構

Analyses of recognition mechanism and structure of bacteria FimH adhesin

○能登 香（北里大学・一般教育）

Kaori Ueno-Noto (*Coll. Lib. Arts Sci., Kitasato Univ.*)

09:00〜11:30　E 会場（函館アリーナ 多目的室 B）／Room E（Hakodate Arena Multipurpose Room B）

1SEA 【共催：CREST 「新たな光機能や光物性の発現・利活用を基軸とする次世代フォトニクスの基盤技術」】

先端赤外光の利用による生物物理学研究

Utilization of Advanced Infrared Sources for Biophysical Studies

オーガナイザー：古谷 祐詞（名古屋工業大学），村越 秀治（生理学研究所）

Organizers: Yuji Furutani (NITech), Hideji Murakoshi (NIPS)

Infrared (IR) light has been widely utilized for analyzing molecular structure and interaction in biological and organic materials. Nowadays, new infrared light sources have been developed, such as ultrafast pulsed IR lasers, quantum cascade lasers, and fiber lasers. These lasers are applicable not only to vibrational spectroscopy on biological molecules but also to microscopic imaging of biological systems such as tissues and cells. Multi-photon microscopy is one of the most important applications, which can shed light on deep inside brains. In this symposium, we would like to discuss the possibility of new infrared light sources in biophysical studies.

はじめに

Opening Remarks

1SEA-1 1800 nm フェムト秒ファイバーレーザーを用いた多光子蛍光顕微鏡

Multi-photon fluorescence microscopy using a 1800 nm femtosecond fiber laser system

○藤 貴夫 [1], 村越 秀治 [2,3], 植田 大海 [2,3], 濱田 航輔 [1], 後藤 龍一郎 [4]（[1] 豊田工業大学, [2] 生理学研究所, [3] 総合研究大学院大学, [4] ファイバーラボ株式会社）

Takao Fuji[1], Hideji Murakoshi[2,3], Hiromi Ueda[2,3], Kosuke Hamada[1], Ryuichiro Goto[4] ([1]*Toyota Technological Institute*, [2]*National Institute for Physiological Sciences*, [3]*The Graduate University for Advanced Studies*, [4]*Fiberlabs Inc.*)

1SEA-2 高機能超短パルスファイバレーザーを用いた第 3 の生体の窓における生体深部イメージング

Deep tissue imaging using highly functional ultrashort pulse fiber laser in the third NIR optical tissue window

○西澤 典彦 [1], 山中 真仁 [2]（[1] 名古屋大学工学研究科電子工学専攻, [2] 大阪大学工学研究科応用物理学専攻）

Norihiko Nishizawa[1], Masahito Yamanaka[2] ([1]*Department of Electronics, Nagoya University*, [2]*Department of Applied Physics, Osaka University*)

1SEA-3 非線形光学過程を利用した 2 種類の赤外超解像顕微鏡による生体試料の観察

Selective IR super-resolution imaging of biological samples by micro-spectroscopies based on non-linear optical process

○高橋 広奈, 酒井 誠（岡山理大・理）

Hirona Takahashi, Makoto Sakai (*Faculty of Sci., Okayama Univ. of Sci.*)

1SEA-4 ロドプシンをモデルとした膜タンパク質の表面増強赤外分光計測による構造変化解析
Structural changes of rhodopsin studied by surface-enhanced infrared spectroscopy as a model system of membrane proteins
○古谷 祐詞 [1,2]（[1] 名工大・院工, [2] 名工大・オプトバイオ）
Yuji Furutani[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*OptoBio, Nagoya Inst. Tech.*)

1SEA-5 高速中赤外分光および顕微鏡
High-speed mid-infrared spectroscopy and microscopy
○井手口 拓郎（東京大学・フォトンサイエンス研究機構）
Takuro Ideguchi (*IPST, Univ. Tokyo*)

おわりに
Closing Remarks

09:00〜11:30　G 会場（函館市民会館 3F 小ホール）／Room G（Hakodate Citizen Hall 3F Small Hall）
1SGA　再構築実験によってアプローチするプロトセル研究と生命の起源への探求
Frontiers of Protocell Research: Exploring the Origin of Life through a Constructivist Approach

オーガナイザー：車 兪澈（海洋研究開発機構），Tony Z. Jia（東京工業大学）
Organizers: Yutetsu Kuruma (JAMSTEC), Tony Z. Jia (Tokyo Tech)

The search for the origin of life (OoL) is now entering a new phase, involving researchers from various fields and incorporating new scientific findings. Especially, the study of artificial cells by a constructivist approach and assembly of protocells by liquid-liquid phase separation or other non-“traditional” physical processes have been advocating a new interpretation in OoL studies. This symposium will focus on the frontiers of the construction and assembly of protocells and artificial cells with novel emergent structures and functions relevant to the origins of life.

はじめに
Opening Remarks

1SGA-1 DNA ナノテクノロジーを軸に挑む人工分子システム構築
Toward the construction of cell-like molecular systems based on DNA nanotechnology
○佐藤 佑介（九工大・院情報工）
Yusuke Sato (*Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*)

1SGA-2 (2Pos120) 人工核酸 PNA を用いた DNA の液ー液相分離制御
(2Pos120) Regulation of liquid-liquid phase separation of DNA using peptide nucleic acid (PNA)
○相馬 陸杜, 愛場 雄一郎, 柴田 将成, 有安 真也, 荘司 長三（名古屋大学大学院理学研究科）
Rikuto Soma, Yuichiro Aiba, Masanari Shibata, Shinya Ariyasu, Osami Shoji (*Graduate School of Science, Nagoya University.*)

1SGA-3 Investigating the role of membrane biophysical properties on protein folding and sorting
Neha Kamat[1,2] ([1]*Department of Biomedical Engineering, Northwestern University*, [2]*Center of Synthetic Biology, Northwestern University*)

1SGA-4 脂質を合成する人工細胞
Lipid synthesis in artificial cell
Yutetsu Kuruma[1,2], Yasuhiro Shimane[1], Rumie Matsumura[1] ([1]*JAMSTEC*, [2]*JST PRESTO*)

1SGA-5 RNA 複製と進化のための区画構造
Compartmentalization for RNA replication and evolution
○水内 良 [1,2]（[1] 東大・先進科学, [2]JST・さきがけ）
Ryo Mizuuchi[1,2] ([1]*Komaba Inst. Sci., Univ. Tokyo*, [2]*JST, PRESTO*)

1SGA-6 エクソソームが司る、がん転移の新しいストーリー
Exosomes, new players in the field of metastasis
○星野 歩子（東京工業大学）
Ayuko Hoshino (*Tokyo Institute of Technology*)

おわりに
Closing Remarks

09:00〜11:30　H 会場（函館市民会館 3F 大会議室）／Room H（Hakodate Citizen Hall 3F Conference Room）

1SHA　分子集団，細胞集団が織りなす自律特性: 生命機能の理解を目指して
Autonomous Characteristics of Molecular and Cellular Ensembles: Toward an Understanding of Biological Functions

オーガナイザー：茅 元司（東京大学），島本 勇太（国立遺伝学研究所）
Organizers: Motoshi Kaya (The Univ. of Tokyo), Yuta Shimamoto (NIG)

The autonomous characteristics of molecular and cellular assemblies are of a higher order than can be imagined from the characteristic of a single molecule or cell, and are the essence of various biological functions. In this symposium, we will invite researchers who are working on the mechanisms of cell motility, tissue formation, etc., using a variety of advanced approaches. We will discuss how understanding the autonomous characteristics of molecular and cellular ensembles can advance our understanding of biological functions.

1SHA-1 骨格筋ミオシン，心筋ミオシン分子集団の自律特性が骨格筋，心臓収縮を作り出す
Autonomous characteristics of skeletal and cardiac myosin ensembles are essential for contractile functions of skeletal muscle and heart
○茅 元司（東大・院理）
Motoshi Kaya (*Grad. Sch. Sci., Univ. Tokyo*)

1SHA-2 人工細胞による細胞動態の再構築：自発運動から波動現象の力学的理解へ向けて
Artificial cells: Reconstruction of cell-like behaviors from spontaneous migration to wave dynamics toward understanding cell mechanics
Ryota Sakamoto[1,2], Ziane Izri[3], Yuta Shimamoto[4], Makito Miyazaki[5,6,7,8], Yusuke Maeda[2] ([1]*Dept. Biomed. Engr., Yale Univ.*, [2]*Dept. Phys., Kyushu Univ.*, [3]*Dept. Phys., Minessota Univ.*, [4]*Natl. Inst. Genetics*, [5]*Hakubi Ctr., Kyoto Univ.*, [6]*Dept. Phys., Kyoto Univ.*, [7]*Institut Curie*, [8]*JST PRESTO*)

1SHA-3 紡錘体の自己組織化ダイナミクスと微小管の集団運動メカニクス
Morphological growth dynamics and active microtubule mechanics underlying spindle self-organization
○島本 勇太（国立遺伝学研究所）
Yuta Shimamoto (*National Institute of Genetics*)

1SHA-4 時計回りの組織形成を支える集団細胞移動の作動原理
Mechanical perspective of collective cell movement in epithelial morphogenesis
○倉永 英里奈（東北大・院生命科学）
Erina Kuranaga (*Grad. Sch. Life Sci., Tohoku Univ.*)

1SHA-5 魚類表皮ケラトサイト集団ではリーダー細胞とフォロワー細胞が協調的かつ強制的にフォロワーをリーダーに昇進させる
Cooperative but forcible promotion of follower cells to leaders in collective migration of fish keratocytes
○岩楯 好昭（山口大・理）
Yoshiaki Iwadate (*Dept. Biol., Yamaguchi Univ.*)

1SHA-6 Interaction rules within multicellular dynamics and biological condensates
Kawaguchi Kyogo (*RIKEN CPR/BDR*)

13:50〜16:20　A 会場（函館アリーナ 武道館 A）／Room A（Hakodate Arena Budokan A）

1SAP 【共催：文部科学省「富岳」成果創出加速プログラム「プレシジョンメディスンを加速する創薬ビッグデータ統合システムの推進」】

スーパーコンピューター「富岳」による創薬・医療の革新
Innovation of drug discovery and medical treatment using supercomputer Fugaku

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 Univ.), Mitsunori Ikeguchi (Yokohama City Univ.)

Drug discovery and medical technologies are being innovated by development of high performance computing (HPC). Large-scale molecular dynamics simulations performed on supercomputer Fugaku permit atomic-level observation of "slow" biomolecular processes such as protein conformational transition and protein-drug interaction processes, providing deeper insight into molecular mechanisms of disease and drug design to overcome it. In this symposium, we will discuss about the forefront of next-generation molecular simulation techniques for drug discovery and medical treatment.

はじめに
Opening Remarks

1SAP-1 超高周波超音波照射下での分子動力学シミュレーションによるタンパク質-医薬品結合プロセスの加速
Hypersound-perturbed molecular dynamics to accelerate slow protein-ligand binding processes
○荒木 望嗣, 奥野 恭史（京大・院医）
Mitsugu Araki, Yasushi Okuno (*Grad.Sch.Med., Kyoto Univ.*)

1SAP-2 スーパーコンピューター「富岳」による創薬へ向けた自由エネルギー摂動法の開発
Development of the free-energy perturbation method toward drug discovery on supercomputer Fugaku
○尾嶋 拓 [1], 杉田 有治 [1,2,3]（[1] 理研・BDR, [2] 理研・R-CCS, [3] 理研・CPR）
Hiraku Oshima[1], Yuji Sugita[1,2,3] ([1]*RIKEN BDR*, [2]*RIKEN R-CCS*, [3]*RIKEN CPR*)

1SAP-3 Binding Kinetics of Kinase Complexes by PaCS-MD/MSM
Kazuhiro Takemura, Akio Kitao (*SLST, TokyoTech*)

1SAP-4 MD シミュレーションで考える抗原-抗体界面：合理的な抗体医薬品設計に向けて
A molecular dynamics study on the antigen-antibody interface: Toward rational antibody drug design
○山下 雄史（東京大学）
Takefumi Yamashita (*The University of Tokyo*)

1SAP-5 大規模分子動力学シミュレーションを用いた上皮成長因子受容体キナーゼの活性化メカニズムの研究
A study of activation mechanism of epidermal growth factor receptor kinase using large-scale molecular dynamics simulations
○井上 雅郎 [1], 浴本 亨 [1], 山根 努 [2], 池口 満徳 [1,2]（[1] 横浜市大・院生命医科学, [2] 理研・計算科学研究センター）
Masao Inoue[1], Toru Ekimoto[1], Tsutomu Yamane[2], Mitsunori Ikeguchi[1,2] ([1]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [2]*RIKEN R-CCS*)

1SAP-6 Extracting protein dynamics from experimental cryo-EM maps using a machine learning technique combining with MD simulations
Shigeyuki Matsumoto[1], Shoichi Ishida[2], Kei Terayama[2], Yasushi Okuno[1,3] ([1]*Grad. Sch. Med., Kyoto Univ.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [3]*RIKEN R-CCS*)

おわりに
Closing Remarks

13:50〜16:20　B 会場（函館アリーナ 武道館 B）／Room B（Hakodate Arena Budokan B）
1SBP　【共催：学術変革領域研究（A）「クロススケール新生物学」】

細胞内メゾ複雑体の構造と機能
Structure and function of “meso-entangled bodies” in the cell

オーガナイザー：杉田 有治（理化学研究所），山本 林（東京大学）
Organizers: Yuji Sugita (RIKEN), Hayashi Yamamoto (The Univ. of Tokyo)

Proteins often assemble to form "mesoscopic" complexes – some ordered and some disordered – to exert their functions in the cell. Therefore, elucidating their architectures and physical properties is necessary to understand the molecular mechanisms underlying life phenomena and diseases. In this research area "Cross-Scale Biology", we particularly focus on mesoscopic structures in the range of 20–500 nm (including LLPS condensates), which we define as "meso-entangled bodies (MEBs)", because MEBs are thought to be key factors that determine the fate of organisms through the transition from disordered to ordered states at the mesoscale. In this symposium, researchers working on the MEBs will gather to discuss the latest technologies and findings, including In-cell AFM, cryo-EM, chemical biology, and LLPS.

1SBP-1 ナトリウムポンプのつくりかた
How to make a sodium pump
○阿部 一啓（名古屋大・細胞生理）
Kazuhiro Abe (*CeSPI, Nagoya Univ*)

1SBP-2 光可逆的蛋白質ラベル化システムによる細胞内蛋白質動態と細胞機能の光制御
Optical control of intracellular protein dynamics and cellular functions using a photoreversible protein labeling system
○水上 進（東北大・多元研）
Shin Mizukami (*IMRAM, Tohoku Univ.*)

1SBP-3 分離した RNP ミセルとしてのパラスペックル核内構造体の構築機構
Construction mechanism of nuclear paraspeckle as an isolated RNP micell
○廣瀬 哲郎 [1,2], 高桑 央 [1,3], 山本 哲也 [4], 山崎 智弘 [1]（[1] 阪大・院生命機能, [2] 阪大・先導学際機構, [3] 北大・院医, [4] 北大・化学反応拠点）
Tetsuro Hirose[1,2], Takakuwa Hiro[1,3], Yamamoto Tetsuya[4], Yamazaki Tomohiro[1] ([1]*Grad. Sch. Front. Biosci., Osaka Univ*, [2]*OTRI, Osaka Univ*, [3]*Grad. Sch. Med., Hokkaido Univ*, [4]*ICReDD, Hokkaido Univ*)

1SBP-4 細胞内における酵母プリオン伝播のクロススケール解析
Cross-scale analyais of yeast prion propagation in cells
Motomasa Tanaka (*RIKEN Center for Brain Science*)

1SBP-5 原子間力顕微鏡を用いた生きた細胞のメゾスケール表面構造体及び内部構造体観察方法の開発
Development of the method for observing mesoscale structures outside and inside living cells using atomic force microscopy
○市川 壮彦 [1], Penedo Marcos[2], 宮澤 佳甫 [1,3], 古庄 公寿 [1], Alam Mohammad Shahidul[1], 宮田 一輝 [1,3], 中村 史 [4], 福間 剛士 [1,3]（[1] 金沢大・ナノ研, [2]EPFL・生物工, [3] 金沢大・フロンティア工, [4]AIST・細胞工）
Takehiko Ichikawa[1], Marcos Penedo[2], Keisuke Miyazawa[1,3], Hirotoshi Furusho[1], Mohammad Shahidul Alam[1], Kazuki Miyata[1,3], Chikashi Nakamura[4], Takeshi Fukuma[1,3] ([1]*NanoLSI, Kanazawa Univ.*, [2]*Inst. Bioeng., EPFL*, [3]*Frontier Eng., Kanazawa Univ.*, [4]*CMB, AIST*)

1SBP-6 Structure modeling of protein complex from experimental data using molecular dynamics simulation
Takaharu Mori (*RIKEN CPR*)

1SBP-7 Ferritin phase separation driven by NCOA4 promotes two types of ferritin autophagy, macro-autophagy and endosomal micro-autophagy
Hayashi Yamamoto (*Grad. Sch. Med., Univ. Tokyo*)

13:50〜16:20　C 会場（函館アリーナ 武道館 C）／Room C（Hakodate Arena Budokan C）
1SCP　複雑システムの振る舞いの解明に向けたトポロジカルアプローチ
Topological approaches to understand behaviours of complex biological systems

オーガナイザー：望月 敦史（京都大学），岡田 崇（理化学研究所）
Organizers: Atsushi Mochizuki (Kyoto Univ.), Takashi Okada (RIKEN)

It is considered that biological functions emerge from dynamics of complex systems consisting from interactions of many biomolecules. Obtaining logical understandings for behaviors of network systems is strongly required in life sciences. To meet it, a series of mathematical methods have been developed, by which important aspects of dynamical behaviors are determined from the topology of networks alone. They have been applied to real biological systems and have made unique achievements. Recently, we see a series of technical or theoretical progresses, which broaden the scope of applications of the methods. In this symposium, we will introduce topological approaches to the network system, and discuss future perspectives of them.

はじめに
Opening Remarks

1SCP-1 ネットワーク構造に基づく細胞運命の制御
Controlling cell fate specification system based on network structure
○望月 敦史（京都大・医生研）
Atsushi Mochizuki (*Inst. Life Med. Sci, Kyoto Univ.*)

1SCP-2 **摂動後の発現時系列データを用いた遺伝子制御ネットワーク推定法**
Estimating gene regulatory network using time-series expression data following gene perturbation
○石川 雅人[1], 永樂 元次[2], 遊佐 宏介[2], 山内 悠平[2], 木立 尚孝[1], 望月 敦史[2]（[1] 東京大・院新領域, [2] 京都大・医生研）
Masato Ishikawa[1], Mototsugu Eiraku[2], Kosuke Yusa[2], Yuhei Yamauchi[2], Hisanori Kiryu[1], Atsushi Mochizuki[2] ([1]*Grad. Sch. Front. Sci., UTokyo*, [2]*Inst. Life Med. Sci., Kyoto Univ.*)

1SCP-3 **ネットワーク構造から生化学反応の摂動応答を決める**
Network architecture determines sensitivity of biochemical reaction systems
Takashi Okada[1], Je-Chiang Tsai[2], Atsushi Mochizuki[1] ([1]*Inst. Life Med. Sci, Kyoto Univ.*, [2]*National Tsing Hua University, Taiwan*)

1SCP-4 **複雑な化学反応ネットワークを単純化する**
Simplifying complex chemical reaction networks
Yuji Hirono (*Asia Pacific Center for Theoretical Physics*)

1SCP-5 **開放系トポロジカル相**
Topological phases in open systems
○佐藤 昌利（京都大学基礎物理学研究所）
Masatoshi Sato (*Yukawa Institute for Theoretical Physics, Kyoto University*)

13:50〜16:20　D 会場（函館アリーナ 多目的室 A）／Room D（Hakodate Arena Multipurpose Room A）

1SDP　生体高分子による液液相分離: 基礎と応用
Phase Separation by Biopolymers: Basics and Applications

オーガナイザー：北原 亮（立命館大学），亀田 倫史（産業技術総合研究所）
Organizers: Ryo Kitahara (Ritsumeikan Univ.), Tomoshi Kameda (AIST)

Although cells organize many biochemical processes in membrane-less compartments via liquid-liquid phase separation (LLPS), physicochemical properties and molecular details of LLPS consisting of proteins and nucleic acids are still largely unknown. This symposium contains lectures on the physicochemical basis of biomolecular LLPS and some recent experimental and theoretical developments to elucidate its structure and dynamics. For example, pressure perturbation spectroscopy, single-molecule fluorescence microscopy, Raman microscopy, and molecular dynamics simulations for protein LLPS will be introduced.

はじめに
Opening Remarks

1SDP-1 **圧力ジャンプ法による液液相分離の速度論解析：RNA 結合タンパク質 FUS**
Pressure-jump kinetics of liquid-liquid phase separation (LLPS) : The RNA-binding protein fused in sarcoma (FUS)
○北原 亮[1,2], 李 書潔[2], 吉澤 拓也[3]（[1] 立命館大・薬, [2] 立命館大院・薬, [3] 立命館大・生命）
Ryo Kitahara[1,2], Shujie Li[2], Takuya Yoshizawa[3] ([1]*Coll. Pharm. Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Pharm. Sci., Ritsumeikan Univ.*, [3]*Coll. Life Sci., Ritsumeikan Univ.*)

1SDP-2 **アミノ酸の溶解性に基づくタンパク質の液- 液相分離**
Liquid-liquid phase separation of proteins based on the solubility of amino acids
○野本 晃, 白木 賢太郎（筑波大院・数理）
Akira Nomoto, Kentaro Shiraki (*Pure and Appl. Sci., Univ. Tsukuba*)

1SDP-3 Raman and Brillouin microscopy as a tool for quantitative study of LLPS
Shinji Kajimoto[1,2] ([1]*Grad. Sch. Pharm. Sci., Tohoku University*, [2]*JST PRESTO*)

1SDP-4 液–液相分離会合体の分子取り込みと並進拡散運動に関する分子文法解析
Molecular grammar characterization of recruitment and translational dynamics of guest proteins in liquid droplets
○鎌形 清人（東北大多元研）
Kiyoto Kamagata (*IMRAM, Tohoku Univ.*)

1SDP-5 分子動力学シミュレーションと機械学習を組み合わせたペプチド凝集予測
Prediction of peptide aggregation by combining molecular dynamics simulation and machine learning
○亀田 倫史（産総研・人工知能）
Tomoshi Kameda (*AIRC, AIST*)

おわりに
Closing Remarks

13:50〜16:20　E 会場（函館アリーナ 多目的室 B）／Room E（Hakodate Arena Multipurpose Room B）
1SEP　微細制御技術を用いたフィジコケミカルバイオロジーへの展開
Physico- and chemical biology using nanomanipulation and micromanipulation technologies

オーガナイザー：北村 朗（北海道大学），飯塚 怜（東京大学）
Organizers: Akira Kitamura (Hokkaido Univ.), Ryo Iizuka (The Univ. of Tokyo)

Various nano- and micromanipulation technologies provide novel strategies to elucidate nature in many scientific fields such as biophysics, physicobiology, and chemical biology. Here, we introduce the cutting-edge topics using nanomanipulation and micromanipulation technologies with a single molecule sensitivity, chemical biology, optogenetics, and mechanistic measurements for understanding and controlling cells and organisms. Furthermore, research topics in molecular and cellular biology from physicochemical perspectives will be discussed.

はじめに
Opening Remarks

1SEP-1 マイクロ・ナノ加工技術を用いた 3D 腫瘍組織構築と新しいがん創薬開発にむけて
Construction of 3D tumor tissue using micro/nano processing technology and toward to development of new drug discovery
○繁富（栗林） 香織（北大・高等推進）
Kaori Kuribayashi-Shigetomi (*Inst. Adv. High. Edu., Hokkaido Univ.*)

1SEP-2 Crosstalk between myosin II and formin in the regulation of force generation and actomyosin dynamics in stress fibers
Yukako Nishimura[1,2], Shidong Shi[2], Virgile Viasnoff[2,3], Alexander Bershadsky[2,4] ([1]*IGM, Hokkaido Univ.*, [2]*MBI, NUS, Singapore*, [3]*Dept.of Biol.Sci., NUS*, [4]*Dept. of Mol. Cell Biol., Weizmann Inst.*)

1SEP-3 (3Pos312) Triple-color photothermal dye-based nanoheaters to generate multiple heat spots within a single cell
Md Monir Hossain, Takeru Yamazaki, Kayoko Nomura, Satoshi Arai (*Grad. Sch. NanoLS., Kanazawa Univ.*)

1SEP-4 Evaluation of the physicochemical properties of biomolecules using microdroplets
Ryo Iizuka (*Dept. of Biol. Sci., Grad. Sch. of Sci., The Univ. of Tokyo*)

1SEP-5 (3Pos093) Control of small G-protein Ras using calmodulin-based ionochromic molecular device.
Yassine Sabek, Nobuyuki Nishibe, Kazunori Kondo, Shinsaku Maruta (*Graduate school of science and engineering , department of biosciences , soka university, Hachioji TOKYO*)

1SEP-6 (1Pos283) Centromere-kinetochore structures revealed by 12x modified expansion microscopy
Yasuhiro Hirano[1], Aussie Suzuki[2], Yasushi Hiraoka[1], Tatsuo Fukagawa[1] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*McArdle Laboratory for Cancer Research, University of Wisconsin-Madison*)

1SEP-7 ボトムアップポリマーナノテクノロジーを用いたミクロレベル・マクロレベルの液液相分離制御
Control of the microscopic and macroscopic liquid-liquid phase separation based on bottom-up polymer nanotechnology
○岸村 顕広（九州大学大学院工学研究院応用化学部門）
Akihiro Kishimura (*Department of Applied Chemistry, Faculty of Engineering, Kyushu University*)

1SEP-8 発色団補助光不活化法 (CALI) の基礎と利用
Basics and applications of chromophore-assisted light inactivation (CALI)
○北村 朗（北大・先端生命）
Akira Kitamura (*Fac. Adv. Life Sci., Hokkaido Univ.*)

おわりに
Closing Remarks

13:50～16:20　F 会場（函館市民会館 1F 大ホール）／Room F（Hakodate Citizen Hall 1F Main Hall）
1SFP　生体膜の生物物理呼応と細胞機能制御への化学的利用
Biophysical responses and biochemical/chemical controlling of membranes for cellular regulation and future therapy

オーガナイザー：中瀬 生彦（大阪公立大学），広瀬 久昭（京都大学）
Organizers: Ikuhiko Nakase (Osaka Metropolitan Univ.), Hisaaki Hirose (Kyoto Univ.)

Biological membranes participate in responses for acceptance/rejection of stimulation and environmental changes from outside/inside cells, leading to signal transduction and cellular responses including e.g., cellular uptake, migration, proliferation, and cell death. The biophysical responses/mechanisms-based membrane controlling systems are highly anticipated to be next-generation therapeutic methodologies for further achievements of disease regulation such as cancers. In this proposal symposium, advanced research technologies and achievements of visualizing and controlling membrane traffic, structures, penetration, and shape-dependent cellular signaling from the fusion viewpoints of biophysics, molecular cell biology, chemistry, and chemical biology will be presented, and membrane-based therapeutic methodology will be discussed.

はじめに
Opening Remarks

1SFP-1 Uptake mechanisms of cell-penetrating peptides
Christian Widmann (*University of Lausanne, Switzerland*)

1SFP-2 Roles of membrane lipids in the organization of cell-cell adhestion structure
Junichi Ikenouchi (*Grad. Sch. Sci., Kyushu Univ.*)

1SFP-3 (2Pos198) Mechanism study of antimicrobial peptide synergistic effects at the molecular level by combining spectroscopy and electrochemical methods
Yuge Hou, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo,*)

1SFP-4 Biofunctional peptide-modified exosomes for intracellular delivery
Ikuhiko Nakase (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

1SFP-5 Membrane shaping by the BAR domain superfamily proteins and the extracellular vesicles by the shedding of filopodia
Shiro Suetsugu[1,2,3] ([1]*Biological Science, Nara Institue of Science and Technology*, [2]*Data Science Center, Nara Institue of Science and Technology*, [3]*Digital Green-Innovation, Nara Institue of Science and Technology*)

1SFP-6 Investigating the mechano-osmotic regulation of cell membrane tension using fluorescent membrane tension probes
Aurelien Roux[1,2] ([1]*Department of Biochemistry, CH-1211, University of Geneva*, [2]*NCCR Chemical Biology, CH-1211, University of Geneva*)

おわりに
Closing Remarks

13:50〜16:20　G 会場（函館市民会館 3F 小ホール）／Room G（Hakodate Citizen Hall 3F Small Hall）

1SGP　【共催：JST さきがけ「細胞の動的高次構造体」】

高次構造体を自在に操る
Uncovering the design principles of supramolecular assemblies through manipulation of the structures, dynamics, and functions

オーガナイザー：宮﨑 牧人（京都大学），小杉 貴洋（分子科学研究所）
Organizers: Makito Miyazaki (Kyoto Univ.), Takahiro Kosugi (IMS)

Cells contains various types of supramolecular assemblies ranging from nanometer-scale structures such as protein complexes and RNA-protein complexes to micrometer-scale structures such as organelles and liquid droplets. A growing body of evidence suggests that these ordered and dynamic structures regulate various key functions of the cell which were previously unknown or unnoticed. To uncover the design principles of the supramolecular assemblies, not only identification of the molecular components and observation of the dynamics, but also manipulation of their structures, dynamics, and functions will be of crucial importance. In this symposium, we will invite talented early-career researchers in various research fields who are developing cutting-edge technologies to manipulate the supramolecular assemblies.

はじめに
Opening Remarks

1SGP-1 高次構造体の協奏的機能を合理的に制御することを目指して
Toward rational control of concerted functions by supramolecular assemblies
○小杉 貴洋 [1,2,3,4]（[1] 分子研, [2] 総研大, [3] 生命創成探究センター, [4]JST・さきがけ）
Takahiro Kosugi[1,2,3,4] ([1]*IMS*, [2]*SOKENDAI*, [3]*ExCELLS*, [4]*PRESTO, JST*)

1SGP-2　タンパク質合成を司る高次構造体を操る：リボソームの光制御
Controlling a supra-assembly dedicated to protein synthesis: optogenetic control of ribosomes in the cell
○横山 武司 [1,2,3]（[1] 東北大・生命科学, [2] 東北大・INGEM, [3]JST さきがけ）
Takeshi Yokoyama[1,2,3] ([1]*Grad. Sch. Lif. Sci., Tohoku Univ.*, [2]*INGEM, Tohoku Univ.*, [3]*JST PRESTO*)

1SGP-3　両親媒性 α ヘリックスが操るオートファジー関連分子 ATG3 の機能
Amphipathic α-helix Manipulates ATG3 Function
○西村 多喜 [1,2,3], Lazzeri Gianmarco[4], 水島 昇 [2], Covino Roberto[4], Tooze Sharon[3]（[1]JST さきがけ専任研究員, [2] 東大・医・分子生物, [3] フランシス・クリック研究所, [4] フランクフルト高等研究所）
Taki Nishimura[1,2,3], Gianmarco Lazzeri[4], Noboru Mizushima[2], Roberto Covino[4], Sharon Tooze[3] ([1]*JST PRESTO Researcher*, [2]*Dept. of Biochem & Mol. Biol., Faculty of Med., The Univ. of Tokyo*, [3]*The Francis Crick Institute*, [4]*Frankfurt Institute for Advanced Studies*)

1SGP-4　ヘテロクロマチン形成高次構造体の解明と制御
Understanding and reconstructing small RNA mediated heterochromatin formation
○岩崎 由香（慶大・医）
Yuka Iwasaki (*Keio Univ. Sch. Med.*)

1SGP-5　操ることで見えてきた細胞内相分離現象の時空間デザイン原理
Spatio-temporal design principles of intracellular phase separation
○下林 俊典（京都大学 iPS 細胞研究所）
Shunsuke Shimobayashi (*CiRA, Kyoto University*)

1SGP-6　合成生物学で生きた細胞内の動的構造体を操り、デザインし、理解する
Manipulation, design, and analysis of dynamic intracellular structures with synthetic biology tools
○中村 秀樹 [1,2]（[1] 京大・白眉センター, [2] 京大・院工学研究科）
Hideki Nakamura[1,2] ([1]*Hakubi Center, Kyoto University*, [2]*Grad. Sch. Eng., Kyoto University*)

おわりに
Closing Remarks

13:50〜16:20　H 会場（函館市民会館 3F 大会議室）／Room H（Hakodate Citizen Hall 3F Conference Room）
1SHP　【共催：学術変革領域（B）「筋肉トランススケール熱シグナリング」】

“肉”のイマとミライ
The Future of Muscle is Now

オーガナイザー：鈴木 団（大阪大学），大山 廣太郎（量子科学技術研究開発機構）
Organizers: Madoka Suzuki (Osaka Univ.), Kotaro Oyama (QST)

Muscle is one of the main subjects that have been studied extensively in the field of Biophysics. We can now explain how the force is produced and assembled at all levels of the hierarchy in muscle; single protein molecule, molecular assembly (sarcomere), myofibril, cell (fiber) and tissue. Is the end of muscle study approaching? In this symposium, we will review the current status with senior researchers, and foresee the future advances with researchers at their early- and mid-carriers who demonstrate originalities and creativities in new methods.

はじめに
Opening Remarks

1SHP-1　筋収縮・制御機構に関する研究の現在と将来について
About the present and future of research on muscle contraction/regulation mechanism
○石渡 信一（早稲田大・理工学術院）
Shin'ichi Ishiwata (*Fac. Sci. & Engn., Waseda Univ.*)

1SHP-2　高輝度シンクロトロン放射光に照らされる筋肉研究の明るい未来
Rosy future of muscle research illuminated by bright synchrotron radiation X-rays
○岩本 裕之（高輝度光科学研究センター）
Hiroyuki Iwamoto (*SPring-8, JASRI*)

1SHP-3　局所熱パルスによる横紋筋の細いフィラメントの活性化
Microscopic heat pulses induce activation of striated muscle thin filaments
○石井 秀弥 [1], 福田 紀男 [2]（[1] 量研, [2] 慈恵医科大・細胞生理）
Shuya Ishii[1], Norio Fukuda[2] ([1]*QST*, [2]*Dept Cell Physiol, Sch Med, Jikei Univ.*)

1SHP-4　3 次元バイオプリントで作られた和牛ステーキ：未来の肉？
3D-Bioprinted Wagyu Steak: Meat of the future?
○松崎 典弥（阪大院工）
Michiya Matsusaki (*Grad. Sch. Eng., Osaka Univ.*)

1SHP-5　光熱変換を利用した局所熱パルス法による筋肉の熱暴走メカニズムの解明
Thermal runaway in muscles studied using a local heat pulse method
○鈴木 団（阪大・蛋白研）
Madoka Suzuki (*Inst. Protein Res., Osaka Univ.*)

おわりに
Closing Remarks

2 日目（9 月 29 日（木））／Day 2（Sep. 29 Thu.）

08:45〜11:15　A 会場（函館アリーナ 武道館 A）／Room A（Hakodate Arena Budokan A）
2SAA　NMR で迫る膜とペプチドの生物物理
NMR Studies in Membrane and Peptide Biophysics

オーガナイザー：川村 出（横浜国立大学），相沢 智康（北海道大学）
Organizers: Izuru Kawamura (Yokohama National Univ.), Tomoyasu Aizawa (Hokkaido Univ.)

Biomembranes and peptides have always been important research targets in the field of biophysics. In particular, their interactions and dynamic properties have not yet been fully elucidated, and many cutting-edge studies have been conducted by applying NMR techniques, which provide information at atomic resolution that is difficult to obtain by other spectroscopic methods. In this symposium, researchers in these fields are invited as speakers to discuss the results of their research using NMR methods.

はじめに
Opening Remarks

2SAA-1　Solid-State NMR spectroscopic approaches to investigate membrane-bound peptide structure
Izuru Kawamura (*Grad. Sch. Eng. Sci., Yokohama Natl. Univ.*)

2SAA-2 Mobility, location, and kinetics of membrane binding and cell entry of peptides by solution-state ^{19}F and ^{1}H NMR
Emiko Okamura (*Faculty Pharm. Sci., Himeji Dokkyo Univ.*)

2SAA-3 Sec 非依存性膜蛋白質膜挿入における大腸菌由来糖脂質 MPIase の役割解明
Role of a bacterial glycolipid MPIase in Sec-independent membrane protein integration
○野村 薫（公益財団法人サントリー生命科学財団）
Kaoru Nomura (*Suntory Foundation for Life Sciences*)

2SAA-4 Solid-state NMR measurements of amphotericin B, a natural product that interacts with lipid bilayers
Yuichi Umegawa (*Grad. Sch. Sci., Osaka Univ.*)

2SAA-5 Revealing Novel Polymorphs and Cross Propagation for 42-residue Amyloid beta by Solid-state NMR
Yoshitaka Ishii[1,2] ([1]*Tokyo Institute of Technology, School of Life Science and Technology*, [2]*RIKEN, BDR*)

08:45〜11:15　B 会場（函館アリーナ 武道館 B）／Room B（Hakodate Arena Budokan B）
2SBA　【共催：新学術領域研究「遺伝子制御の基盤となるクロマチンポテンシャル」】

先端技術と理論で迫るクロマチン機能の理解
Chromatin function as revealed by cutting-edge technique and theory

オーガナイザー：伊藤 由馬（東京工業大学），木村 宏（東京工業大学）
Organizers: Yuma Ito (Tokyo Tech), Hiroshi Kimura (Tokyo Tech)

Recent advance in genomics and imaging technologies have contributed to understanding the function of chromatin for gene regulation beyond the canonical role in genomic DNA packaging. To understand the principles of highly organized and dynamic chromatin architecture, the integrated approaches using various experimental techniques and theoretical modeling are essential. In this symposium, we aim to promote discussion by sharing the latest research on measuring and modeling the biophysical properties of chromatin and the relevance to gene regulation using state-of-the-art techniques.

2SBA-1 Chromatin mobility of X-linked loci and its epigenetic regulation
Yuko Sato[1,2], Yuma Ito[2], Satoshi Uchino[2], Makio Tokunaga[2], Hiroshi Kimura[1,2] ([1]*IIR, Tokyo Tech*, [2]*Sch. Life Sci. Tech., Tokyo Tech*)

2SBA-2 (2Pos303) ヒト生細胞の局所クロマチン動態は細胞周期を通して一定である
(2Pos303) Single-nucleosome imaging reveals steady-state motion of interphase chromatin in living human cells
○飯田 史織 [1,2], 新海 創也 [3], 伊藤 優志 [1], 田村 佐知子 [1], 鐘巻 将人 [2,4], 大浪 修一 [3], 前島 一博 [1,2]
([1] 遺伝研・ゲノムダイナミクス研究室, [2] 総研大・生命・遺伝, [3] 理研 BDR, [4] 遺伝研・分子細胞工学研究室)
Shiori Iida[1,2], Soya Shinkai[3], Yuji Itoh[1], Sachiko Tamura[1], Masato Kanemaki[2,4], Shuichi Onami[3], Kazuhiro Maeshima[1,2] ([1]*Genome Dynamics Lab., Natl. Inst. of Genet.*, [2]*Dept. of Genet., Sch. of Life Sci., SOKENDAI*, [3]*RIKEN BDR*, [4]*Mol. Cell Eng. Lab., Natl. Inst. of Genet.*)

2SBA-3 DNA の量とクロマチン構造による核のサイズ制御機構
DNA quantity and chromatin structure contribute to nuclear size control in *Xenopus laevis*
○原 裕貴（山口大・理）
Yuki Hara (*Fac. Sci., Yamaguchi Univ.*)

2SBA-4 (2Pos116) 細胞核内における underwound DNA の蛍光イメージング
(2Pos116) Fluorescence imaging of underwound DNA in the cell nucleus
○福手 淳平[1,2], 牧 功一郎[1,3], 安達 泰治[1,2,3]（[1] 京大・医生研, [2] 京大・院生命科学, [3] 京大・院工学）
Jumpei Fukute[1,2], Koichiro Maki[1,3], Taiji Adachi[1,2,3] ([1]*Inst. Life & Med. Sci., Kyoto Univ.*, [2]*Grad. Sch. Biostudies, Kyoto Univ.*, [3]*Grad. Sch. Eng., Kyoto Univ.*)

2SBA-5 (3Pos305) High-resolution mapping of chromatin compaction and dynamics in live cells by label-free interference microscopy
Yi-Teng Hsiao, Chia-Ni Tsai, Fasih Bintang Ilhami, Chia-Lung Hsieh (*Institute of Atomic and Molecular Sciences (IAMS), Academia Sinica / Taiwan*)

2SBA-6 (3Pos301) 細胞内の一分子を三次元でナノレベルの分解能で観察できる「クライオ三次元ナノスコピー」の開発
(3Pos301) Cryo-3D Nanoscopy to localize three-dimensional position of individual fluorophore with nanometer precision in the cell
○成瀬 寛太[1], 松田 剛[1], 溝内 雄太[1], 志見 剛[2], 木村 宏[2], 中田 栄司[3], 森井 孝[3], 松下 道雄[1], 藤芳 暁[1]（[1] 東京工業大学理学院物理学系物理学コース, [2] 東京工業大学科学技術創成研究院細胞制御工学研究センター, [3] 京都大学エネルギー理工学研究所）
Kanta Naruse[1], Tsuyoshi Matsuda[1], Yuta Mizouchi[1], Takeshi Shimi[2], Hiroshi Kimura[2], Eiji Nakata[3], Takashi Morii[3], Michio Matsushita[1], Satoru Fujiyoshi[1] ([1]*Department of physics, Tokyo institute of technology*, [2]*Cell Biology Center, Institute of Innovative Research, Tokyo institute of technology*, [3]*Institute of Advanced Energy, Kyoto University*)

2SBA-7 新しいクロマチン基盤ユニットである H3-H4 オクタソームのクライオ電子顕微鏡解析
Cryo-electron microscopic analysis reveal a novel structural unit of chromatin
○野澤 佳世[1], 滝沢 由政[2], 七種 和美[3], 明石 知子[4], 胡桃坂 仁志[2]（[1] 東京工業大学・生命理工学院, [2] 東京大学・定量生命科学研究所, [3] 産業技術総合研究所, [4] 横浜市立大学・生命医科学研究科）
Kayo Nozawa[1], Yoshimasa Takizawa[2], Kazumi Saikusa[3], Satoko Akashi[4], Hitoshi Kurumizaka[2] ([1]*Tokyo Institute of Technology, School of Life Science and Technology*, [2]*The University of Tokyo, Institute for Quantitative Biosciences*, [3]*National Institute of Advanced Industrial Science and Technology*, [4]*Yokohama City University, Graduate School of Medical Life Science*)

2SBA-8 斥力相互作用する溶質混合系における相分離：クロマチン高次構造の視点から
Phase separation in soft-repulsive mixtures: implication for chromatin organization
Takahiro Sakaue, Naoki Iso, Yuki Norizoe (*Dep. Phys. Aoyama Gakuin Univ.*)

2SBA-9 1 細胞全ゲノム DNA 複製解析からゲノム三次元構造動態を探る
Unraveling the dynamic 3D genome architecture through single-cell DNA replication profiling
○平谷 伊智朗（理化学研究所　生命機能科学研究センター　発生エピジェネティクス研究チーム）
Ichiro Hiratani (*Laboratory for Developmental Epigenetics, RIKEN Center for Biosystems Dynamics Research (RIKEN BDR)*)

08:45〜11:15　C 会場（函館アリーナ 武道館 C）／Room C（Hakodate Arena Budokan C）
2SCA　【共催：新学術領域研究 「発動分子科学」】

発動分子科学への若手研究者による挑戦
Tackle “Molecular Engine” by Early-career Researchers

オーガナイザー：小杉 貴洋（分子科学研究所），大友 章裕（分子科学研究所）
Organizers: Takahiro Kosugi (IMS), Akihiro Otomo (IMS)

“Molecular Engine”, design of autonomous functions through energy conversion, has bud by the orchestration of chemists, biologists, and physicists in the last five years. This scientific concept should be passed down to the next generations for further development. To this end, early-career researchers in various research fields are trying to elucidate the energy conversion mechanism of molecular machines and to design novel ones. In this symposium, budding researchers who will lead this field related to biophysics in the future will give a talk about their latest exciting research results by developing cutting-edge technologies and future prospects.

はじめに
Opening Remarks

2SCA-1　アクティブマターが示す秩序形成の幾何的設計原理
Geometric design principle for active ordering
Kazusa Beppu[1], Yusuke T. Maeda[2] ([1]*Appl. Phys., Aalto Univ. Sch. of Sci.*, [2]*Phys., Kyushu Univ.*)

2SCA-2　(1Pos217) Conversion of light-driven outward proton pump rhodopsin into inward proton pump
Maria Del Carmen Marin Perez[1], Masae Konno[1,2], Himoru Yawo[1], Keiichi Inoue[1] ([1]*ISSP, Univ. Tokyo*, [2]*PRESTO, Japan Science and Technology Agency*)

2SCA-3　フッ素化人工チャネルによる膜間物質輸送
Transmembrane material transport by fluorinated channels
○佐藤 浩平（東工大・生命理工）
Kohei Sato (*Sch. Life Sci. Tech., Tokyo Tech.*)

2SCA-4　(3Pos128) 1 分子回転操作実験によって解明されたミトコンドリア由来 ATP 合成酵素における阻害因子 IF_1 の一方向制御機構
(3Pos128) Unidirectional regulation of ATPase factor 1 in mitochondrial ATP synthase studied by single-molecule manipulation experiments
○小林 稜平 [1,2], 上野 博史 [1], 岡崎 圭一 [2], 野地 博行 [1]（[1] 東大・院工・応化, [2] 分子研）
Ryohei Kobayashi[1,2], Hiroshi Ueno[1], Kei-ichi Okazaki[2], Hiroyuki Noji[1] ([1]*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Inst. for Mol. Sci.*)

2SCA-5　1 分子計測・活性測定・タンパク質工学による回転型 V-ATPase の統合的研究
Integrated research on rotary V-ATPase approached by single-molecule observation, biochemical assay, and protein engineering
○大友 章裕 [1,2], 飯野 亮太 [1,2]（[1] 分子科学研究所, [2] 総合研究大学院大学）
Akihiro Otomo[1,2], Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*The Graduate University for Advanced Studies*)

2SCA-6 ミトコンドリア呼吸鎖における熱産生の物理化学的メカニズム
Physicochemical mechanism of heat generation in mitochondrial respiratory chain
○武安 光太郎 [1,2,3], Namari Nuning[4], 中村 潤児 [2,5]（[1] 筑波大・数理物質系, [2] 筑波大・TREMS, [3] 筑波大・ゼロ CO2, [4] 筑波大・院理工情報生命, [5] 九州大・I2CNER）
Kotaro Takeyasu[1,2,3], Nuning Namari[4], Junji Nakamura[2,5] ([1]*Fac. Pure and Appl. Sci., Unive. Tsukuba*, [2]*TREMS, Univ. Tsukuba*, [3]*Zero-CO2, Univ. Tsukuba*, [4]*Grad. Sch. Sci. Technol., Univ. Tsukuba*, [5]*I2CNER, Kyushu Univ.*)

2SCA-7 キラル液晶の自己組織化ナノ構造を利用した力学センシングと応答速度設計
Mechanical sensor using chiral liquid crystals with self-organized nanostructures and tuning of molecular recovery response
○久野 恭平 [1,2], 宍戸 厚 [2], 堤 治 [1]（[1] 立命館大・生命科学, [2] 東工大・化生研）
Kyohei Hisano[1,2], Atsushi Shishido[2], Osamu Tsutsumi[1] ([1]*Col. of Life Sci., Ritsumeikan Univ.*, [2]*Lab. for Chem. & Life Sci., Tokyo Tech*)

2SCA-8 Structural stability and dynamics of de novo designed transmembrane peptide barrels
Ai Niitsu[1], Jaewoon Jung[2], Yuji Sugita[1,2] ([1]*Wako Inst., Riken*, [2]*Kobe Inst., Riken*)

おわりに
Closing Remarks

08:45〜11:15　D 会場（函館アリーナ 多目的室 A）／Room D（Hakodate Arena Multipurpose Room A）
2SDA　先端的ラベルフリーナノポア計測による生物物理学への展開と応用
Innovative label-free nanopore sensing toward biophysical studies and applications

オーガナイザー：山崎 洋人（東京大学），庄司 観（長岡技術科学大学）
Organizers: Hirohito Yamazaki (The Univ. of Tokyo), Kan Shoji (Nagaoka Univ. of Tech.)

The understanding of the biomolecule structural and dynamic properties has provided a plethora of information about the roles of various molecules, and leads to the development of innovative industrial enzymes and pharmaceuticals. Among technologies uncovering biological molecules, nanopore sensing has become attractive since it can study single molecule properties, such as surface charge, molecular size, shape, chain length, chemical structures and so on. In this symposium, we will organize the session to present the latest nanopore research for biophysics studies and applications.

2SDA-1 Toward broadly accessible, highly scalable solid-state nanopore research
Kyle Briggs (*University of Ottawa, Department of Physics*)

2SDA-2 プローブ型人工細胞システムの応用展開
Application of Probe-Type Artificial Cell Membrane Systems
○庄司 観（長岡技大）
Kan Shoji (*Nagaoka Univ. Tech.*)

2SDA-3 ナノポアシーケンサと nanoDoc を用いた DNA/RNA 修飾解析
Detection of DNA/RNA modification using nanopore sequencer and nanoDoc
○上田 宏生（東京大・先端研・生命データサイエンス）
Ueda Hiroki (*Biological Data Science, RCAST, Univ. of Tokyo*)

2SDA-4 (2Pos290) Nanopore direct determination of DNA methylation and demethylation intermediates
Ping Liu[1], Masayuki Honda[1], Ryuji Kawano[2] ([1]*Department of Food and Energy Systems Science, Tokyo University of Agriculture and Technology*, [2]*Institute of Engineering, Tokyo University of Agriculture and Technology*)

2SDA-5 (2Pos315) ATP を検出可能な DNA ナノポアセンサの開発
(2Pos315) ATP-detectable DNA nanopore sensor
○赤井 大夢, 庄司 観（長岡技術科学大学）
Hiromu Akai, Kan Shoji (*Nagaoka University of Technology*)

2SDA-6 Integrating nanopore sensing and artificial intelligence for multiplex single-virus identification
Akihide Arima (*IIFS, Nagoya Univ.*)

2SDA-7 Probing the Effect of Ubiquitinated Histone on Mononucleosomes through solid-state nanopores
Hu Rui, Wei Guanghao, Wang Zhan, **Qing Zhao** (*Peking University, School of Physics*)

2SDA-8 Light Enhanced Solid-state Nanopore for Single Molecule Sensing
Yamazaki Hirohito (*The University of Tokyo, Department of Biological Science*)

08:45〜11:15　E 会場（函館アリーナ 多目的室 B）／Room E（Hakodate Arena Multipurpose Room B）

2SEA　100nm サイズの分子集団で顕在化する非凡な時空アロステリー
Unique Spatiotemporal Allostery Emerges in 100nm-Sized Molecular Systems

オーガナイザー：成田 哲博（名古屋大学），秋山 修志（分子科学研究所）
Organizers: Akihiro Narita (Nagoya Univ.), Shuji Akiyama (IMS)

Is it possible to explain biological phenomena occurring at the cellular level on the basis of the physicochemical properties of molecules? Observations focused on the cellular scale provide little information about molecules, while investigations of molecular structure and dynamics with high spatiotemporal resolution require handling isolated and purified samples in vitro. However, how and what kind of connections do we need in order to understand biological phenomena? In modern life science research, the initial selection of the most suitable model organism has a great impact on the success or failure of later research. In the same way, the selection of an appropriate spatiotemporal scale is important for cutting into the logic of "cross-scale causality". From this perspective, we realize that the smallest unit of the molecular system that shows some correlation with physiological properties at the tissue or cellular level is exclusively concentrated in the 100 nm scale (or several hundred molecules). In this symposium, we will examine the spatiotemporal hierarchy of the 100 nm scale from multiple perspectives of biophysics, structural biology, and computational science, and discuss strategies for the evolution of correlation into causation.

はじめに
Opening Remarks

2SEA-1 アクチン線維において顕在化する時空アロステリー
Spaciotemporal allostery in the actin filament
○成田 哲博（名古屋大、理学）
Akihiro Narita (*Grad. Sci, Nagoya Univ.*)

2SEA-2 細菌べん毛モーター回転制御機構の理解の進展
Recent understanding of the control mechanism of the bacterial flagellar motor rotation
○今田 勝巳（阪大・院理）
Katsumi Imada (*Grad. Sch. Sci., Osaka Univ.*)

2SEA-3 膜と細胞骨格の動態制御におけるダイナミンのヘクトスケール分子集団のアロステリー変化
Allosteric changes of hecto-scale population of dynamin GTPases provide in dynamic regulation of membranes and cytoskeletons
○竹居 孝二, 阿部 匡史, 竹田 哲也, 山田 浩司（岡山大・院医歯薬）
Kohji Takei, Tadashi Abe, Tetsuya Takeda, Hiroshi Yamada (*Fac. Med. Dent. Pharma. Sci., Okayama Univ.*)

2SEA-4 夜明けに自律離散する概日時計システム
Autonomous Disassembly of Circadian Clock System at Dawn
○秋山 修志 [1,2]（[1] 協奏分子システム研究センター・分子研, [2] 総研大）
Shuji Akiyama[1,2] ([1]*CIMoS, IMS, NINS*, [2]*SOKENDAI*)

2SEA-5 高速 AFM による 100-nm サイズの分子集団の直接観察
Direct observation of 100 nm-sized molecular systems by high-speed AFM
○古寺 哲幸（金沢大・WPI-NanoLSI）
Noriyuki Kodera (*WPI-NanoLSI, Kanazawa Univ.*)

2SEA-6 長距離アロステリーの物理基盤としてのクーロン結合ネットワーク
Coulomb bond network as a physical basis for long-range allostery
○高野 光則（早大・先進理工）
Mitsunori Takano (*Grad. Sch. Sci. Eng., Waseda Univ*)

2SEA-7 (3Pos013) Optineurin の E50K 緑内障変異はオリゴマー粒径を増大させる
(3Pos013) The E50K mutation of optineurin increases the oligomer size
○河村 綸太郎 [1], 植月 聡也 [1], 丹澤 豪人 [2], 加藤 貴之 [2], 金城 政孝 [3], 北村 朗 [3]（[1] 北大・院生命科学, [2] 阪大・蛋白研, [3] 北大・院先端生命）
Rintaro Kawamura[1], Soya Uetsuki[1], Takehito Tanzawa[2], Takayuki Kato[2], Masataka Kinjo[3], Akira Kitamura[3] ([1]*Grad. Sci. Life Sci., Hokkaido Univ.*, [2]*Inst., for Proteins Res., Osaka Univ.*, [3]*Fac. Adv. Life sci., Hokkaido Univ.*)

おわりに
Closing Remarks

08:45〜11:15　Room F（Hakodate Citizen Hall 1F Main Hall）
2SFA　Japan-US symposium on motor proteins and associated single-molecule biophysics

Organizers: Kumiko Hayashi (Tohoku Univ.), Jakia Jannat Keya (NINS)

This is the second symposium between Japan and USA on motor proteins as a continuation of the first one held in 2021 BSJ meeting. Speakers in this symposium are internationally recognized as experts in the field of motor proteins, and their associated proteins. We are planning to prepare enough time to have a deep and detailed discussion among the speakers and audience on these subjects. The symposium topics cover multidisciplinary applications of genetics, bio-engineering, bio-chemistry, medical science, and physics, which will give us new insights into motor proteins, as well as interesting applications of existing single-molecule techniques.

Opening Remarks

2SFA-1 Torque Generation Mechanism of F_1-ATPase
Hiroyuki Noji, Hiroshi Ueno (*Grad. Sch. Eng., Univ. Tokyo*)

2SFA-2 Regulation of Motors by Microtubule-Associated Proteins
Ahmet Yildiz (*University of California Berkeley*)

2SFA-3 Cholesterol in the cargo membrane amplifies the inhibitory effects of tau on kinesin-1-based transport
Qiaochu Li[1], James Ferrare[2], Jonathan Silver[2], John Wilson[1], Luis Arteaga-Castaneda[1], Weihong Qiu[3], Michael Vershinin[4], Stephen King[5], Keir Neuman[2], **Jing Xu[1]** ([1]*Physics, University of California, Merced, CA, USA*, [2]*Laboratory of Single Molecule Biophysics, National Heart, Lung and Blood Institute, National Institutes of Health, Bethesda, MD, USA*, [3]*Physics, Oregon State University, Corvallis, OR, USA*, [4]*Physics and Astronomy, University of Utah, Salt Lake City, UT, USA*, [5]*Burnett School of Biomedical Sciences, University of Central Florida, Orlando, FL, USA*)

2SFA-4 Ultralong-Term, Real-Time Tracking of Single Cargoes in Living Neurons
Sam Peng (*Stanford University*)

2SFA-5 (1Pos137) Plus and minus ends of microtubules respond asymmetrically to kinesin binding by a long-range directionally driven allosteric mechanism
Huong T Vu[1], Zhechun Zhang[2], Riina Tehver[3], Dave Thirumalai[4] ([1]*University of Warwick*, [2]*Harvard University*, [3]*Denison University*, [4]*University of Texas*)

2SFA-6 (3Pos143) SLC26 ion transporters act as electricity-driven motor proteins
Tomohiro Shima (*Grad. Sch. Sci., Univ. Tokyo*)

Closing Remarks

08:45〜11:15　G 会場（函館市民会館 3F 小ホール）／Room G（Hakodate Citizen Hall 3F Small Hall）
2SGA　**【共催：新学術領域研究「シンギュラリティ生物学」】**

シンギュラリティ生物学を導くイメージング技術
Advanced Imaging Technologies Leading the Way to “Singularity Biology”

オーガナイザー：蛭田 勇樹（慶應義塾大学），渡邉 朋信（理化学研究所）
Organizers: Yuki Hiruta (Keio Unv.), Tomonobu Watanabe (RIKEN)

In order to study the processes that “singularity cells”, considered as minority entities, causing criticality to a multi-cellular system, comprehensive development of imaging technologies is essential because of its necessary for multi-layer and multi-modal observation of the dynamics and functions of the cells and the multi-cellular system. To do the end, the research project “Singularity Biology” have developed a trans-scale microscopy system, AMATERAS, as a basis for imaging. This symposium introduces the microscopy technologies, including AMATERAS, and advanced probe technologies to visualize singularity phenomena. We hope that this symposium will lead to the creation of effective collaboration projects on Singularity Biology.

はじめに
Opening Remarks

2SGA-1 シンギュラリティ現象を直接観るトランススケールスコープ AMATERAS
Trans-scale scope AMATERAS for direct observation of singularity phenomena
○市村 垂生 [1], 垣塚 太志 [2], 橋本 均 [1,3], 永井 健治 [1,2] ([1] 大阪大学・先導, [2] 大阪大学・産研, [3] 大阪大学・薬学)
Taro Ichimura[1], Taishi Kakizuka[2], Hitoshi Hashimoto[1,3], Takeharu Nagai[1,2] ([1]*OTRI, Osaka Univ.*, [2]*SANKEN, Osaka Univ.*, [3]*Grad. Sch. Pharm., Osaka Univ.*)

2SGA-2 Chemical probes for detecting enzyme activities in living cells with single cell resolution
Mako Kamiya (*Dep. Life Sci. Tech., Tokyo Tech.*)

2SGA-3 (3Pos277) Decoding single-cell transcriptomic phenotypes from cell images enabled by robotic data acquisition and deep learning
Jianshi Jin[1], Taisaku Ogawa[1], Nozomi Hojo[1], Kirill Kryukov[2], Kenji Shimizu[3], Tomokatsu Ikawa[4], Tadashi Imanishi[2], Taku Okazaki[3], Shiroguchi Katsuyuki[1] ([1]*BDR, RIKEN*, [2]*Dept. of Mol. Life Sci., Tokai Univ. Sch. of Med.*, [3]*Inst. for Quant. Biosci., Univ. of Tokyo*, [4]*Res. Inst. for Biomed. Sci., Tokyo Univ. of Sci.*)

2SGA-4 局所かつ任意のタイミングで摂動を与える光操作技術 CALI 法とその応用
A light manipulation technology by CALI that provides localized and arbitrarily timed perturbations
○竹本 研（三重大学大学院医学系研究科生化学分野）
Kiwamu Takemoto (*Mie University, Graduate School of Medicine*)

2SGA-5 最小の発光酵素「picALuc」の開発とその応用
Development of the smallest luciferase “picALuc” and its applications
○大室 有紀 [1], 金 誠培 [2], 松井 勇人 [1], 叶井 正樹 [1], 古田 忠臣 [3]（[1] 島津製作所, [2] 産総研, [3] 東工大・生命理工）
Yuki Ohmuro[1], Sung Bae Kim[2], Hayato Matsui[1], Masaki Kanai[1], Tadaomi Furuta[3] ([1]*Shimadzu Corporation*, [2]*AIST*, [3]*Sch. Life Sci. Tech., Tokyo Tech*)

2SGA-6 時空間トランススケールイメージングを可能にするケージドルシフェリンの開発
Development of caged luciferin enabling spatiotemporal trans-scale imaging
○蛭田 勇樹（慶應大・理工）
Yuki Hiruta (*Fac. Sci. Tech., Keio Univ.*)

08:45〜11:15　H 会場（函館市民会館 3F 大会議室）／Room H（Hakodate Citizen Hall 3F Conference Room）
2SHA　【共催：学術変革領域研究（B）
「生体分子工学と低物理エネルギーロジスティクスの融合による次世代非侵襲深部生体操作」】

生体分子工学と低物理エネルギーロジスティックスで切り拓く新たな生体操作学
Next-generation biological manipulation pioneered by biomolecular engineering and low-physical energy logistics

オーガナイザー：井上 圭一（東京大学），今村 博臣（京都大学）
Organizers: Keiichi Inoue (The Univ. of Tokyo), Hiromi Imamura (Kyoto Univ.)

Optogenetics enabled us precisely and noninvasively manipulate a variety of biological events in vivo such as neural firing, gene expression, cellular morphological change and so on. To expand the concept of optogenetics toward biological events in deep tissue which are difficult by using visible light, further paradigm shift of manipulation technology is required. To achieve this goal, we are focusing on using photothermal effect, ultrasound and magnetic field as novel external-field technologies to manipulate biological responses even in deep tissues by combining biomolecular engineering of new molecular systems and low-physical energy logistics. In this symposium, we will introduce cutting-edge researches for next generation biological manipulation.

はじめに
Opening Remarks

2SHA-1 **光熱変換を利用した細胞操作に向けた試み**
Toward cell manipulation through photothermal conversion
○今村 博臣（京都大学生命科学研究科）
Hiromi Imamura (*Graduate School of Biostudies, Kyoto University*)

2SHA-2 **高効率光熱変換タンパク質ヒーター創出に向けた分子内熱伝導機構の解明**
Elucidation of intramolecular heat transfer mechanism for construction of highly effective photothermal protein heaters
○水野 操（阪大・院理）
Misao Mizuno (*Grad. Sch. Sci., Osaka Univ.*)

2SHA-3 **BMI のための高密度皮質脳波電極の開発**
Development of high-density ECoG array for BMI
○鈴木 隆文 [1], 海住 太郎 [1], 平田 雅之 [1,2]（[1] 脳情報通信融合研究センター（情報通信研究機構、大阪大学）, [2] 大阪大学大学院医学系研究科）
Takafumi Suzuki[1], Taro Kaiju[1], Masayuki Hirata[1,2] ([1]*Center for Information and Neural Networks (CiNet), NICT & Osaka Univ.*, [2]*Osaka Univ. graduate school of medicine*)

2SHA-4 **深部神経活動磁場操作に向けた新規分子ツール開発**
Development of molecular tools for magnetic manipulation of neural activity in the deep tissue
○井上 圭一（東大・物性研）
Keiichi Inoue (*Inst. Solid State Phys., Univ. Tokyo*)

2SHA-5 **生体内磁性粒子を操るための磁気力場の設計と最適化**
Design and optimization of magnetic force field for manipulating magnetic particles in living bodies
○関野 正樹 [1], 吉岡 輝 [1], 中川 桂一 [1], 井上 圭一 [2]（[1] 東大・工, [2] 東大・物性研）
Masaki Sekino[1], Hikaru Yoshioka[1], Keiichi Nakagawa[1], Keiichi Inoue[2] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*ISSP, Univ. Tokyo*)

おわりに
Closing Remarks

13:50〜16:20　A 会場（函館アリーナ 武道館 A）／Room A（Hakodate Arena Budokan A）
2SAP　**【共催：新学術研究領域「情報物理学でひもとく生命の秩序と設計原理」】**

多細胞系の情報物理学
Information Physics of multi-cellular systems

オーガナイザー：小林 徹也（東京大学），川口 喬吾（理化学研究所），石島 秋彦（大阪大学）
Organizers: Tetsuya J. Kobayashi (The Univ. of Tokyo), Kyogo Kawaguchi (RIKEN), Akihiko Ishijima (Osaka Univ.)

Physical understanding of multi-cellular systems is the unexplored frontier in biophysics. Sparked by the rapid advancements in bioimaging, bioinformatics, symthetic biology and so on, multi-cellular systems are becoming a promising target of biophysics. In this symposium, we showcase the attempts to investigate the design principles of multi-cellular systems by using or integrating the methods of physics, informatics, and other disciplines.

2SAP-1 **多細胞系の情報物理学**
Information Physics of multi-cellular systems
○小林 徹也（生産研・東大）
Tetsuya J. Kobayashi (*IIS, UTokyo*)

2SAP-2 **内皮細胞集団動態と血管新生**
Collective endothelial cell migration and angiogenesis
○田久保 直子（東京大学アイソトープ総合センター）
Naoko Takubo (*Isotope Science Center, The University of Tokyo*)

2SAP-3 **細胞間コミュニケーションの操作による多細胞パターンのデザイン**
Programming multicellular pattern formation with synthetic cell-cell signaling
○戸田 聡（金沢大学・ナノ生命）
Satoshi Toda (*NanoLSI, Kanazawa Univ.*)

2SAP-4 **(3Pos118) グラフニューラルネットワークによる細胞間の時空間相互作用の推定**
(3Pos118) Graph-based machine learning reveals rules of spatiotemporal cell interactions in tissues
Takaki Yamamoto[1], Katie Cockburn[2], Valentina Greco[2,3], Kyogo Kawaguchi[1,4,5] ([1]*Nonequilibrium Physics of Living Matter RIKEN Hakubi Research Team, RIKEN BDR*, [2]*Department of Genetics, Yale School of Medicine*, [3]*Departments of Cell Biology and Dermatology, Yale Stem Cell Center, Yale Cancer Center, Yale School of Medicine*, [4]*RIKEN CPR*, [5]*Universal Biology Institute, The University of Tokyo*)

2SAP-5 **線虫の神経回路における多重情報コードの情報物理学的解析**
Analyisis of multiplexed information coding in the nervous system of C.elegans
○豊島 有, 松本 朱加, 飯野 雄一（東大・院理・生科）
Yu Toyoshima, Ayaka Matsumoto, Yuichi Iino (*Grad. Sch. Sci., Univ. of Tokyo*)

2SAP-6 **器官形態形成プロセスの種間スケーリング**
Scaling of organ morphogenetic process between species
○森下 喜弘（理化学研究所　生命機能科学研究センター）
Yoshihiro Morishita (*RIKEN Center for Biosystems Dynamics Research*)

おわりに
Closing Remarks

13:50〜16:20　B 会場（函館アリーナ 武道館 B）／Room B（Hakodate Arena Budokan B）
2SBP　【共催：「富岳」成果創出加速プログラム
「全原子・粗視化分子動力学による細胞内分子動態の解明」】

富岳を用いた高性能計算による生物物理
High-performance computational biophysics with supercomputer Fugaku

オーガナイザー：松永 康佑（埼玉大学），信夫 愛（理化学研究所）
Organizers: Yasuhiro Matsunaga (Saitama Univ), Ai Shinobu (RIKEN)

Computational approaches are becoming increasingly important in biophysics, not only for simulations but also for the detailed interpretation of various measurement data. In particular, with the recent launch of modern supercomputers such as Fugaku, enormous computational resources have become available, and new computational methods and applications that were not computationally feasible in the past are becoming possible. In this symposium, we invite researchers who conduct cutting-edge high-performance computations. We discuss current computational research using supercomputers as well as future directions of computational biophysics.

はじめに
Opening Remarks

2SBP-1　富岳と超並列分子動力学を用いたタンパク質の構造変化、会合と解離
Protein conformational change, association and dissociation observed using Fugaku and massively parallel molecular dynamics simulations
○北尾 彰朗（東工大・生命理工）
Akio Kitao (*Scl. Life Sci. Tech., Tokyo Tech*)

2SBP-2　Molecular dynamics study of multidrug efflux transporter complex embedded in lipid bilayer: Role of membrane lipids in the transporter
Keiko Shinoda, Hisashi Kawasaki (*AgTECH, GSALS, UTokyo*)

2SBP-3　(3Pos186) エンベロープ型ウイルス粒子の粗視化シミュレーション：B 型肝炎ウイルス
(3Pos186) Coarse-grained Molecular Dynamics Study of Enveloped Virus Particle: Hepatitis B Virus
○浦野 諒, 篠田 渉（岡山大学・異分野基礎研）
Ryo Urano, Wataru Shinoda (*Res. Inst. Interdiscip. Sci., Okayama Univ.*)

2SBP-4　Binding free energy landscapes of Src Kinase to its inhibitors sampled by two-dimensional replica exchange molecular dynamics simulations
Ai Shinobu[1], Suyong Re[1,2], Yuji Sugita[1] ([1]*RIKEN*, [2]*National Institutes of Biomedical Innovation, Health, and Nutrition*)

2SBP-5　REST シミュレーションによるタンパク質やペプチドリガンドの活性制御機構の解析
Applications of REST simulation to understanding regulation mechanism of protein activation and peptide ligands
○浴本 亨 [1], 山根 努 [2], 池口 満徳 [1,2]（[1] 横浜市大・生命医, [2] 理研・R-CCS）
Toru Ekimoto[1], Tsutomu Yamane[2], Mitsunori Ikeguchi[1,2] ([1]*Grad. Med. Life Sci., Yokohama City Univ.*, [2]*R-CCS, Riken*)

2SBP-6 (1Pos027) Automated Density Extraction of Isomorphous Difference map and Occupancy-estimation for Conformer Fitting
Sriram Srinivasa Raghavan[1], Florence Tama[1,2,3], Osamu Miyashita[1] ([1]*RIKEN Center for Computational Science, Kobe, Japan.*, [2]*Institute of Transformative Biomolecules (WPI-ITbM), Nagoya University, Aichi, Japan.*, [3]*Department of Physics, Graduate School of Science, Nagoya University, Aichi, Japan.*)

2SBP-7 スーパーコンピュータ「富岳」を用いたテンプレートマッチング法による生体分子のマルチコンフォメーション解析
Multi-conformational analysis of biomolecule by the template-matching method using the supercomputer Fugaku
○徳久 淳師（理研・R-CCS）
Atsushi Tokuhisa (*R-CCS, Riken*)

おわりに
Closing Remarks

13:50〜16:20　C 会場（函館アリーナ 武道館 C）／Room C（Hakodate Arena Budokan C）
2SCP　生体分子の人工設計：タンパク質、RNA、DNA
Design of biomolecules, protein, RNA, and DNA

オーガナイザー：古賀 信康（分子科学研究所），神谷 由紀子（名古屋大学）
Organizers: Nobuyasu Koga (IMS), Yukiko Kamiya (Nagoya Univ.)

The biomolecules, protein, RNA, and DNA, control cell functions. The design technologies for the biomolecules and their interactions have been greatly advanced, which made it possible to create a wide range of biomolecules not existing in nature. In this symposium, each of the biomolecular design geeks will present the basics of the design technology and latest results. We then discuss about future perspectives to create novel biomolecules.

2SCP-1 タンパク質構造の人工設計
De novo design of novel protein structures
○古賀 信康（自然・ 生命創成）
Nobuyasu Koga (*NINS, ExCELLS*)

2SCP-2 Towards the de novo design of binding proteins through beta-sheet folds
Enrique Marcos (*Molecular Biology Institute of Barcelona (IBMB-CSIC), Protein Design and Modeling Lab*)

2SCP-3 Protein engineering for biogeeks; practical examples of structural redesigns of a model protein and therapeutic antibody designs
Koki Makabe (*Grad. Sch. Sci. and Eng., Yamagata univ.*)

2SCP-4 非環状型人工核酸による天然核酸認識の設計
Understanding the design of acyclic artificial nucleic acids that recognize natural nucleic acids
○神谷 由紀子（名大・院工）
Yukiko Kamiya (*Grad. Sch. Eng., Nagoya Univ.*)

2SCP-5 Engineering RNA-protein interactions by directed evolution
Keisuke Fukunaga, Yohei Yokobayashi (*Nucleic Acid Chemistry and Engineering Unit, OIST*)

2SCP-6 DNA ナノ構造によるデザインされた人工細胞と人工オルガネラの実現へ向けて
Toward DNA nanostructure-based designed artificial cells and artificial organelles
○瀧ノ上 正浩（東工大・情報理工）
Masahiro Takinoue (*Sch. Computing, Tokyo Tech*)

13:50〜16:20　D 会場（函館アリーナ 多目的室 A）／Room D（Hakodate Arena Multipurpose Room A）
2SDP　金属イオン制御による酵素の動態
Metal-ion regulation of enzyme dynamics

オーガナイザー：織田 昌幸（京都府立大学），森川 耿右（京都大学）
Organizers: Masayuki Oda (Kyoto Prefectural Univ.), Kosuke Morikawa (Kyoto Univ.)

Enzyme function closely correlates with its structural dynamics, and is often regulated by metal-ion binding. In many cases, metal-ions bind to enzymes rather weakly, and induce protein conformations or conformational ensembles. This essential structure-function relationship is an attractive but difficult target to be analyzed. The invited speakers present challenging efforts on enzymes, such as cutinase, RNaseH, and DNAzyme, which are regulated by Ca2+ or Mg2+. We hope that discussions based on presented biophysical data could facilitate us to understand real dynamic views of metal-enzyme interactions.

はじめに
Opening Remarks

2SDP-1 酵素反応における弱い金属イオン結合の意義
Significance of weak metal-ion binding in enzymatic reactions
○織田 昌幸（京府大・院生環科）
Oda Masayuki (*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*)

2SDP-2 PET 分解酵素 Cut190 における弱く結合した Ca^{2+} イオンを介したアロステリック制御
Allosteric regulation of PET-degrading enzyme Cut190 through the weakly bound Ca^{2+} ion
○沼本 修孝（医科歯科大・難研）
Nobutaka Numoto (*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

2SDP-3 RNaseHI の触媒反応機構：必須金属は 1 個か 2 個か？
Catalytic mechanism of RNaseHI: one metal or two metals?
○森川 耿右（京大・生命科学）
Kosuke Morikawa (*Kyoto Univ.*)

2SDP-4 エレクトロスプレーイオン化質量分析法による活性型リボヌクレアーゼ HI：RNA/DNA:金属イオン複合体の検出
Active ternary complex of ribonuclease HI: RNA/DNA hybrid: metal ions probed by ESI mass spectrometry
○高尾 敏文 [1], 安東 友繁 [1], 林 潤美 [1], Jongruja Nujarin[2], 奥村 宜明 [1], 森川 耿右 [3], 金谷 茂則 [2] ([1] 大阪大・蛋白研, [2] 大阪大・院工学, [3] 京都大・院生命科学)
Toshifumi Takao[1], Tomoshige Ando[1], Hiromi Hayashi[1], Nujarin Jongruja[2], Nobuaki Okumura[1], Kosuke Morikawa[3], Shigenori Kanaya[2] ([1]*Inst. Protein Res., Osaka Univ.*, [2]*Grad. Sch. Eng., Osaka Univ.*, [3]*Grad. Sch. Biostudies, Kyoto Univ.*)

2SDP-5 (2Pos026) Structural basis of the significant metal-histidine coordination in *E. coli* RNase HI
Zengwei Liao[1], Takuji Oyama[2], Yumi Kitagawa[3], Katsuo Katayanagi[4], Kosuke Morikawa[5], Masayuki Oda[3] ([1]*Grad. Sch. Agri. and Life Sci., the Univ. of Tokyo*, [2]*Faculty of Life and Environ. Sci., Univ. of Yamanashi*, [3]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [4]*Grad. Sch. Integrated Sci. for Life, Hiroshima Univ.*, [5]*Grad. Sch. Biostudies, Kyoto Univ.*)

2SDP-6 Metal interaction and Conformational Changes in HIV-1 Reverse Transcriptase
Rieko Ishima (*University of Pittsburgh School of Medicine*)

2SDP-7 High-resolution and time-resolved insights into an RNA-cleaving DNA catalyst
Manuel Etzkorn[1,2] ([1]*Heinrich Heine University Düsseldorf*, [2]*Research Center Jülich*)

おわりに
Closing Remarks

13:50〜16:20　E 会場（函館アリーナ 多目的室 B）／Room E（Hakodate Arena Multipurpose Room B）
2SEP　ダイナミックな翻訳 その開始から終わりまで
Dynamic translation: from initiation to the end

オーガナイザー：丹澤 豪人（大阪大学），楊 倬皓（東京大学）
Organizers: Takehito Tanzawa (Osaka Unv.), Zhuohao Yang (The Univ. of Tokyo)

Translation on ribosomes is a fundamental biological phenomenon that requires strict spatiotemporal regulation and quality control. Since translation is a multi-step reaction, it is necessary to clarify the details of each step in order to understand its whole glance. Recently, with advancing and developing analytical methods such as structural analysis, single molecular imaging, and NGS, it has been uncovered that the translation cycle on ribosomes is regulated in various ways. In this symposium, we would like to have young researchers from different fields shed light on and discuss the dynamics of cis/trans-acting translational control on ribosomes from theoretical and experimental perspectives.

はじめに
Opening Remarks

2SEP-1 Novel repressive role of eIF4A1 during mTORC1 inhibition
Yuichi Shichino (*RIKEN CPR*)

2SEP-2 (1Pos121) 自由エネルギー地形から探る開始コドン認識機構
(1Pos121) Computational Analysis of the Start Codon Recognition Mechanism Based on Free Energy Landscape
○亀田 健 [1], 浅野 桂 [2,3,4], 冨樫 祐一 [1,5]（[1] 立命大 生命, [2] カンザス州立大 生物, [3] 広島大 HiHA, [4] 広島大 統合生命, [5] 理研 BDR）
Takeru Kameda[1], Katsura Asano[2,3,4], Yuichi Togashi[1,5] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Div. Biol., Kansas State Univ.*, [3]*HiHA, Hiroshima Univ.*, [4]*Grad. Sch. Integ. Sci. Life, Hiroshima Univ.*, [5]*RIKEN BDR*)

2SEP-3 (2Pos109) RNase T2 のリボソームへの結合を介した翻訳阻害機構
(2Pos109) Regulation mechanism of translation through the interaction of RNase T2 with ribosome
○南 篤 [1], 丹澤 豪人 [2], 楊 倬皓 [3], 船津 高志 [3], 加藤 貴之 [2], 葛山 智久 [1,4], 吉田 秀司 [5], 小川 哲弘 [1,4]
([1] 東大・院農生科, [2] 阪大・蛋白研, [3] 東大・院薬, [4] 東大・CRIIM, [5] 大阪医薬大・医)
Atsushi Minami[1], Takehito Tanzawa[2], Zhuohao Yang[3], Takashi Funatsu[3], Takayuki Kato[2], Tomohisa Kuzuyama[1,4], Hideji Yoshida[5], Tetsuhiro Ogawa[1,4] ([1]*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*, [2]*IPR, Osaka Univ.*, [3]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [4]*CRIIM, Univ. Tokyo*, [5]*Fac. Med., Osaka Med. Pharm. Univ.*)

2SEP-4 High-speed AFM visualizes translational GTPase factor pool formed around the ribosomal P-stalk
Hirotatsu Imai[1,2], Toshio Uchiumi[3], Noriyuki Kodera[2] ([1]*Fac. Med., Univ. Ryukyus*, [2]*Nano-LSI, Kanazawa Univ.*, [3]*Fac. Sci., Niigata Univ.*)

2SEP-5 The mechanical stability of SecM translation arrest
Zhuohao Yang[1], Ryo Iizuka[2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [2]*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

2SEP-6 Attempt to visualize the synthetic polypeptide during translational arrest
Takehito Tanzawa (*IPR., Osaka Univ.*)

2SEP-7 The final step of protein synthesis; the capture of an unfolded polypeptide by chaperonin GroEL
Kevin Mac Alister Stapleton (*Grad. Sch. Frontier BioSci., Osaka Univ.*)

2SEP-8 ER Redox shift through the ribosome translation
Ryo Ushioda[1,2] ([1]*Fac. of Life Sci., Kyoto Sangyo Univ.*, [2]*Inst. for Protein Dynamics, Kyoto Sangyo Univ.*)

おわりに
Closing Remarks

13:50〜16:20　F 会場（函館市民会館 1F 大ホール）／Room F（Hakodate Citizen Hall 1F Main Hall）
2SFP　【共催：学術変革領域研究（B）「遅延制御超分子化学」】

生物物理学による脳の理解と化学的再生
Biophysical elucidation of neural network and chemical regeneration of neural tissue

オーガナイザー：村岡 貴博（東京農工大学），齋尾 智英（徳島大学）
Organizers: Takahiro Muraoka (Tokyo Univ. of Agriculture and Tech.), Tomohide Saio (Tokushima Univ.)

In recent years, brain science has made remarkable progress. Understanding neural circuits and elucidation of signal transduction processes at the molecular level are being carried out. Not only neuroscience but also mechanistic biochemical studies on neural diseases are progressing. Neurodegenerative diseases are one representative example, and the structure and dynamics of the causative protein are being elucidated at the single-molecule level. Integrating discussions between biophysical neuroscience and chemical research of the brain should address important unexplored issues such as the precise elucidation of brain function and the development of neuronal tissue regeneration technology.

はじめに
Opening Remarks

2SFP-1 Phase separation provides a reaction chamber for autophagy progression
Yuko Fujioka (*Institute for Genetic Medicine, Hokkaido Univ.*)

2SFP-2 蛋白質ミスフォールディング病における蛋白質凝集の分子機構
The molecular mechanism of protein aggregation in protein misfolding disease
Young-Ho Lee[1,2,3] ([1]*Research Center for Bioconvergence Analysis, Korea Basic Sci. Inst., Korea*, [2]*Bio-Analytical Sci., Uni. of Sci. and Tech., Korea*, [3]*Grad. Sch. of Analytical Sci. and Tech., Chungnam National Uni., Korea*)

2SFP-3 脳神経疾患研究における 1 分子イメージング研究の現状・課題・可能性
Current status, problems, and potential of single molecule imaging studies in neurological disease research
○坂内 博子（早大・理工学術院）
Hiroko Bannai (*Fac. Sci. Eng., Waseda Univ.*)

2SFP-4 超分子ペプチドゲルを用いた損傷脳再生
Injured brain regeneration using supramolecular peptide hydrogels
○味岡 逸樹 [1,2]（[1] 東京医科歯科大学・脳統合機能研究センター, [2] 神奈川県立産業技術総合研究所）
Itsuki Ajioka[1,2] ([1]*Center for Brain Integration Research (CBIR), Tokyo Medical Dental Univ (TMDU)*, [2]*KISTEC*)

2SFP-5 相反する匂い価値の脳内表現と神経回路基盤
Representations and circuits for opposing odor values in the brain
○風間 北斗（理化学研究所脳神経科学研究センター）
Hokto Kazama (*RIKEN Center for Brain Science*)

おわりに
Closing Remarks

13:50～16:20　G 会場（函館市民会館 3F 小ホール）／Room G（Hakodate Citizen Hall 3F Small Hall）
2SGP　物理化学的解析から探るアミロイド・ゲルの構造ダイナミクス
Physicochemical analyses of structural dynamics for amyloid and gel

オーガナイザー：田中 元雅（理化学研究所），真板 宣夫（量子科学技術研究開発機構）
Organizers: Motomasa Tanaka (RIKEN), Nobuo Maita (QST)

Disease-associated proteins often form apparently rigid aggregates such as amyloids and gels. Interestingly, however, recent studies have found that amyloids and gels are not the final dead-end products of proteins, but rather undergo dynamic structural changes by cellular proteins and environmental factors, which potentially provide great impacts on cellular phenotypes. However, compared to static structures of amyloids and gels, the details of their dynamic structural changes remain poorly understood. In this symposium, we would like to share and discuss the latest findings that clarify the structural dynamics of amyloids and gels by physicochemical analyses through the development of new technologies, and contribute to further advances of the research field.

はじめに
Opening Remarks

2SGP-1 Putting prions in context: towards in vivo structural biology using DNP NMR
Kendra King Frederick (*UT Southwestern*)

2SGP-2 The single-particle cryo-electron microscopic analysis of amyloid disaggregation reaction
Takashi Nomura[1], Yoshiko Nakagawa[1], Yusuke Komi[1], Shingo Tamai[1,2], Masako Yamazaki[1], Motomasa Tanaka[1] ([1]*CBS, RIKEN*, [2]*Biomed. Sci. & Eng., Grad. Sch. of Med. &Dent. Sci., TMDU*)

2SGP-3 Critical Jamming and gel rheology of droplet suspensions in living cells
Daisuke Mizuno (*Kyushu University*)

2SGP-4 レオロジー NMR 法による SOD1 アミロイド形成の多状態その場観察
Multiple-state *in situ* observation of SOD1 amyloid formation by Rheo-NMR spectroscopy
○森本 大智 [1], ヴァリンダ エリック [2], 白川 昌宏 [1], シェラー ウルリッヒ [3], 菅瀬 謙治 [4] ([1] 京大・院工学, [2] 京大・院医学, [3]IPF, [4] 京大・院農学)
Daichi Morimoto[1], Erik Walinda[2], Masahiro Shirakawa[1], Ulrich Scheler[3], Kenji Sugase[4] ([1]*Grad. Sch. Eng., Kyoto Univ.*, [2]*Grad. Sch. Med., Kyoto Univ.*, [3]*IPF*, [4]*Grad. Sch. Agr., Kyoto Univ.*)

2SGP-5 TDP43-LC ドメインの病原性変異と線維形成能の網羅的解析
Comprehensive studies of disease-related mutations on cross-β polymerization of TDP43-LC domain
Nobuo Maita[1], Yuko Kajino[1], Masato Kato[1,2] ([1]*National Institutes for Quantum Science and Technology*, [2]*UT Southwestern Medical Center*)

13:50〜16:20　H 会場（函館市民会館 3F 大会議室）／Room H（Hakodate Citizen Hall 3F Conference Room）

2SHP　【共催：学術変革領域研究（A）「マルチファセットプロテインズ」】

マルチファセット・プロテインズへの生物物理アプローチ
Biophysical approach for multifaced protein world

オーガナイザー：渡邉 力也（理化学研究所），太田 元規（名古屋大学）
Organizers: Rikiya Watanabe (RIKEN), Motonori Ota (Nagoya Univ.)

In recent years, our perception of the "protein world" has been expanding and transforming with the discovery of many aspects that were previously unseen. In this symposium, we would like to discuss the biophysical approaches to clarify the molecular mechanism and physiological significance of the expanding and changing protein world from a "multifaceted" perspective.

2SHP-1 mRNA の翻訳制御を 1 分子解像度で in situ イメージングする
Translational regulation visualized at single-molecule resolution in cells
○小林 穂高 [1,2]（[1]JST さきがけ, [2] 東京大学 定量生命科学研究所）
Hotaka Kobayashi[1,2] ([1]*JST PRESTO*, [2]*IQB, The University of Tokyo*)

2SHP-2 SARS-CoV-2 nsp1 はホスト翻訳系をどう乗っ取るのか？
SARS-CoV-2 nsp1: how do they hijack the host translation?
○桜庭 俊 [1], 謝 祺琳 [2], 笠原 浩太 [3], 岩切 淳一 [4], 河野 秀俊 [1]（[1] 量研機構, [2] 立命館大・院生命科学, [3] 立命館大・生命, [4] 東京大・院新領域）
Shun Sakuraba[1], Qilin Xie[2], Kota Kasahara[3], Junichi Iwakiri[4], Hidetoshi Kono[1] ([1]*Natl. Inst. Quantum Sci. & Tech.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [3]*Col. Life Sci., Ritsumeikan Univ.*, [4]*Grad. Sch. Frontier Sci., Univ. Tokyo*)

2SHP-3 神経変性疾患を引き起こすアミロイド線維のクライオ電顕解析
Cryo-EM analyses of the amyloid fibrils causing neurodegenerative diseases
○山形 敦史（理化学研究所・生命機能科学研究センター）
Atsushi Yamagata (*RIKEN Center for Biosystems Dynamics Research*)

2SHP-4 (2Pos260) 新規遺伝子の誕生と機能獲得の進化メカニズムに迫るゲノム計算科学：バイオインフォマティクスのその先に遺伝子の本質を探求する
(2Pos260) How do *de novo* genes evolve and acquire function?: Computational genomics to revisit the nature of genes beyond bioinformatics
○山内 駿 [1], 岩崎 渉 [1,2]（[1] 東大・院理学系, [2] 東大・院新領域）
Shun Yamanouchi[1], Wataru Iwasaki[1,2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

2SHP-5 Multifaceted view of protein diffusion
Eiji Yamamoto (*Dept. Syst. Des. Eng., Keio Univ.*)

2SHP-6 生体分子の 1 分子解析とその応用
Single-molecule analysis of bio-molecules and its applications
○渡邉 力也（理研・CPR）
Rikiya Watanabe (*CPR, RIKEN*)

3 日目（9 月 30 日（金））／Day 3（Sep. 30 Fri.）

09:00〜11:30　A 会場（函館アリーナ 武道館 A）／Room A（Hakodate Arena Budokan A）
3SAA　発光・蛍光計測と光学顕微鏡の標準化を目指して
Toward a standardization of luminescence, fluorescence measurements and light microscopy

オーガナイザー：佐々木 章（産業技術総合研究所），近江谷 克裕（産業技術総合研究所）
Organizers: Akira Sasaki (AIST), Yoshihiro Ohmiya (AIST)

The quantitative aspect of luminescence, fluorescence measurement and light microscopy is becoming significant. The challenge now lies in improving the accuracy and precision of the data obtained from such measurements. Standardization is the way to achieve precise, reproducible and inter-comparable measurement. Improving these will facilitate the comparison of results between different instruments/institutions and therefore ensure the reproducibility of results. In this symposium, recent standardization effort in the world (e.g. ISO) will be introduced in addition of leading edge researches of the related field.

はじめに
Opening Remarks

3SAA-1 定量的な蛍光顕微鏡計測に向けて - FCS を用いた顕微鏡ベンチマーク -
Toward traceable quantitative fluorescence microscopy - Benchmarking microscope using FCS technique -
○佐々木 章（産総研・バイオメディカル）
Akira Sasaki (*BMRI, AIST*)

3SAA-2 Supporting cellular analysis by quantitative imaging with standards and reference materials
Michael Halter, Ed Kwee, Alexander Peterson, John T Elliott (*National Institute of Standards and Technology (NIST), USA*)

3SAA-3 細胞を用いた分析・製造分野における細胞形態計測の信頼性向上を目指して～ISO 標準化活動の紹介
Towards improvement of the reliability of cell morphometry for analysis and manufacturing of cells - Role of ISO standardization
○能見 淑子（千代田化工建設株式会社）
Yoshiko Nomi (*Chiyoda Corporation*)

3SAA-4 (1Pos289) Morphological Analysis of Hydrogel Induced Cancer Stem Cells in Synovial Sarcoma Model Cells
Zannatul Ferdous[1], Masumi Tsuda[1,3,4], Jean-Emmanuel Clément[3], Jian Ping Gong[1,3,6], Shinya Tanaka[3,4,6], Tamiki Komatsuzaki[2,3,5], Koji Tabata[2] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Research Center of Mathematics for Social Creativity, Research Institute for Electronic Science, Hokkaido University, Sapporo, Japan*, [3]*Institute for Chemical Reaction Design and Discovery (WPI-ICReDD), Hokkaido University, Sapporo, Japan*, [4]*Department of Cancer Pathology, Hokkaido University Faculty of Medicine, Sapporo*, [5]*Graduate School of Chemical Sciences and Engineering, Hokkaido University, Sapporo, Japan*, [6]*Global Station for Soft Matter, Global Institution for Collaborative Research and Education (GI-CoRE), Hokkaido University, Sapporo, Japan*)

3SAA-5 Quantification of receptor clustering and activation at the cell surface using correlation and lifetime-based methods
Andrew Harry Albert Clayton (*Cell Biophysics, Optical Sciences Centre, Swinburne University of Technology, Hawthorn, Australia*)

3SAA-6 (1Pos288) Size determination of cytoplasmic condensates of optineurin using spatial image correlation spectroscopy (SICS)
Yuta Hamada[1], Masataka Kinjo[2], Akira Kitamura[2] ([1]*Grad. Sch. Sci. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ*)

3SAA-7 絶対発光量計測技術に基づく生物発光反応の量子収率解析とバイオ分析機器標準化
Absolute light measurement for the investigation of bioluminescence quantum yield and standardization of bioanalysis instruments
○丹羽 一樹（産業技術総合研究所物理計測標準研究部門）
Kazuki Niwa (*National Metrology Institute of Japan (NMIJ), National Institute of Advanced Industrial Science and technology (AIST)*)

3SAA-8 定量的 in vivo, ex vivo 生物発光イメージング
Quantitative bioluminescence imaging in vitro and ex vivo
○近江谷 克裕 [1,2]（[1] 産業技術総合研究所, [2] 大阪工業大学）
Yoshihiro Ohmiya[1,2] ([1]*AIST*, [2]*Osaka Institute of technology*)

おわりに
Closing Remarks

09:00〜11:30　B 会場（函館アリーナ 武道館 B）／Room B（Hakodate Arena Budokan B）
3SBA　【共催：新学術研究領域「高速分子動画」】

様々な先端的手法で挑む生体分子の構造ダイナミクスの可視化
Visualization of structural dynamics of biomolecules using a variety of advanced techniques

オーガナイザー：梅名 泰史（名古屋大学），清水 伸隆（高エネルギー加速器研究機構）
Organizers: Yasufumi Umena (Nagoya Univ.), Nobutaka Shimizu (KEK)

Time-resolved serial femtosecond crystallography (TR-SFX) using X-ray free-electron laser (XFEL) has recently been established as one of the approaches to obtain structural dynamics of biological molecules. Furthermore, various biophysical analyses are necessary to understand complicated biological dynamic events properly, and novel methods have been proposed to obtain more detailed interpretations. The integrated collaborations between these methods and TR-SFX will take us to visualize biological processes as "molecular movies" in the future. In this session, we will introduce not only the latest SFX studies but also the various novel approaches to capture dynamic biological events and advance to understand the biomolecular functions through integrative research.

はじめに
Opening Remarks

3SBA-1　ポールシェーラー研究所でのいろいろな実験手法を組み合わせた時分割シリアル結晶学への取り組み
Time resolved serial crystallography with various methods at the Paul Scherrer Institut
Takashi Tomizaki, Tsujino Soichiro (*Paul Scherrer Institut*)

3SBA-2　分子動力学シミュレーションによるタンパク質の構造ダイナミクス研究
Structural dynamics of proteins studied using molecular dynamics simulations
○池口 満徳 [1,2]（[1] 横浜市大・生命医, [2] 理研・計算科学研究セ）
Mitsunori Ikeguchi[1,2] ([1]*Grad. Sch. Med Life Sci., Yokohama City Univ.*, [2]*R-CCS, RIKEN*)

3SBA-3　生体分子の動的構造解析のためのマイクロ流体デバイスの開発
Development of microfluidic devices for structural dynamics measurement of biomolecules
○真栄城 正寿 [1,2,3]（[1] 北海道大学大学院工学研究院, [2]JST・さきがけ, [3] 高エネルギー加速器研究機構 物質構造科学研究所）
Masatoshi Maeki[1,2,3] ([1]*Faculty of Engineering, Hokkaido University*, [2]*JST PRESTO*, [3]*Institute of Materials Structure Science, High Energy Accelerator Research Organization (KEK)*)

3SBA-4　Serial Femtosecond Crystallography reveals structural intermediates during CO-dissociation process in ba3-type Cytochrome c Oxidase
Swagatha Ghosh[1,2], Cecilia Safari[1], Rebecka Andersson[1], Jonatan Johannesson[1], Peter Dahl[1], Eriko Nango[3], Rie Tanaka[3], So Iwata[3], Richard Neutze[1], Gisela Brändén[1] ([1]*Dept. Chem. and Mol. Bio, Gothenburg University, Sweden*, [2]*Dept. Appl.Physics, Nagoya University, Japan*, [3]*RIKEN Spring-8 Center, Hyogo, Japan*)

3SBA-5　光化学系 II 酸素発生中心における V185 の役割についての QM/MM-MD 解析
QM/MM-MD study of the role of valine 185 in the oxygen-evolving center of photosystem II
○庄司 光男 [1,2], 宮川 晃一 [1], 三嶋 謙二 [1], 山口 兆 [3], 重田 育照 [1]（[1] 筑波大 CCS, [2] さきがけ, [3] 大阪大学）
Mitsuo Shoji[1,2], Koichi Miyagawa[1], Kenji Mishima[1], Kizashi Yamaguchi[3], Yasuteru Shigeta[1] ([1]*CCS, U.Tsukuba*, [2]*JST-PRESTO*, [3]*Osaka Univ.*)

3SBA-6 光活性化アデニル酸シクラーゼ OaPAC の動的構造解析による反応機構の解明
Reaction mechanisms of photoactivated adenylate cyclase OaPAC using dynamic structural analysis
○石本 直偉士 [1], 梅名 泰史 [3], Trampari Sofia[2], 辻野 壮一郎 [2], 富崎 孝司 [2], 朴 三用 [1] ([1] 横浜市大・院生命医科学, [2] ポールシェラー研究所, [3] 名大・シンクロトロン光研究センター）
Naito Ishimoto[1], Yasufumi Umena[3], Sofia Trampari[2], Soichiro Tsujino[2], Takashi Tomizaki[2], Sam-Yong Park[1] ([1]*Grad. Sch. MLS, Yokohama City Univ. / Japanese*, [2]*Paul Scherrer Institute / Switzerland*, [3]*Synchrotron Radiation Research Center, Nagoya University / Japanese*)

おわりに
Closing Remarks

09:00〜11:30　C 会場（函館アリーナ 武道館 C）／Room C（Hakodate Arena Budokan C）
3SCA　自主・自発の階層と適応：冗長性を行動力(健康)につなげる分子-細胞-筋-身体-脳連携
Hierarchies of autonomy and spontaneity and adaptation: Molecular-cell-muscle-bodybrain linkage of redundancy to action (health)

オーガナイザー：跡見 順子（東京農工大学），岩城 光宏（理化学研究所）
Organizers: Yoriko Atomi (Tokyo Univ. of Agriculture & Technology), Mitsuhiro Iwaki (RIKEN)

Fumio Osawa, the founder of the Biophysical Society of Japan, saw the essence of life as "independence and spontaneity. Humans, who are at the mercy of fragmented science, technology, and concepts, have lost sight of the larger framework for creating independence and spontaneity. This symposium will explore the path to extend the hierarchy of life's autonomy and spontaneity, in which protein interactions lead to emergence and molecular chaperones lead to adaptation, from the cell to the human body and mind. This will provide the basis for the creation of new health, industry, and medical science and education.

はじめに
Opening Remarks

3SCA-1 Myosin molecular motors convert information into motion
Toshio Yanagida[1,2,3,4] ([1]*NICT*, [2]*Grad. Sch. Info. Sci. Tech., Osaka Univ.*, [3]*Grad. Sch. Front. Biosci., Osaka Univ.*, [4]*iFReC*)

3SCA-2 The network of microtubule integrates the spatial information provided by the actin network along the cell periphery
Manuel Thery (*CEA (French Atomic Energy Reserch Center)*)

3SCA-3 Molecular mechanisms of the chaperones that assist in the folding of actin and tubulin
Masafumi Yohda (*Grad. Sch. Eng., Tokyo Univ. Agr. Tech.*)

3SCA-4 多細胞動物ヒトの筋適応の素過程：ストレス因子カルシウム、微小管及び分子シャペロン αB-クリスタリン
Elementary processes of slow muscle adaptation in multicellular human: calcium, microtubules and the molecular chaperone αB-crystallin
○跡見 順子（東京農工大）
Yoriko Atomi (*Tokyo University of Agriculture and Technology*)

3SCA-5 骨格筋幹細胞の活性化・分化と筋再生のサーカディアン制御
Circadian regulation of skeletal muscle stem cell activation differentiation, and muscle regeneration
○朝倉 淳（ミネソタ大学医学部・幹細胞研究所）
Atsushi Asakura (*Stem Cell Institute, University of Minnesota Medical School*)

3SCA-6 ヒトの不安定な立位姿勢における頭部-体幹部の構造的冗長性の制御
Control of structural redundancy from head to trunk during unstable upright standing in humans
○跡見 友章（杏林大学保健学部）
Tomoaki Atomi (*Health Sci., Univ. Kyorin*)

おわりに
Closing Remarks

09:00〜11:30　D 会場（函館アリーナ 多目的室 A）／Room D（Hakodate Arena Multipurpose Room A）
3SDA　【共催：学術変革領域研究（A）「新興硫黄生物学が拓く生命原理変革」】

硫黄のタンパク質科学の最前線
New implications of sulfur in protein science

オーガナイザー：増田 真二（東京工業大学），中林 孝和（東北大学）
Organizers: Shinji Masuda (Tokyo Tech), Takakazu Nakabayashi (Tohoku Univ.)

In recent years, attention has been focused on physiological phenomena involving sulfur, such as finding supersulfide molecules consisting of multiple sulfur atoms in mammals, including humans. In this symposium, six presenters introduce their recent results of structure-function relationships of sulfur-related proteins. We would like to discuss how biophysics can be applied to physiological phenomena involving sulfur.

はじめに
Opening Remarks

3SDA-1 Mechanism of sulfide/supersulfide sensing in bacteria
Shinji Masuda (*Grad. Sch. Life Sci. & Technol., Tokyo Inst. Tech.*)

3SDA-2 Intramolecular disulfide bond switches enzymatic activity of SOD1
Shinya Tahara[1], Kousuke Yamazaki[1], Takumi Ohyama[1], Kunisato Kuroi[2], Takakazu Nakabayashi[1]
([1]*Grad. Sch. Pharm. Sci., Tohoku Univ.*, [2]*Dept. Pharm. Sci., Kobe Gakuin Univ.*)

3SDA-3 Reaction mechanism of tRNA sulfur modifying enzyme using a cofactor iron-sulfur cluster
Min Yao (*Fac. Adv. Life Sci., Hokkaido Univ.*)

3SDA-4 2 つの異なるタイプの PLP 依存型システイン脱硫酵素と基質 L-システインおよび阻害剤との反応
Actions of two distinct types of PLP-dependent cysteine desulfurase enzymes with substrate L-cysteine and inhibitors
○藤城 貴史（埼玉大学大学院理工学研究科）
Takashi Fujishiro (*Grad. Sch. Sci. Engeneer., Saitama Univ.*)

3SDA-5 Structural and functional analyses of *E. coli* SufBCD complex involved in iron-sulfur clusters biogenesis

Kei Wada[1,2], Yoshikazu Tanaka[3], Yasuhiro Takahashi[4] ([1]*Department of Medical Sciences, University of Miyazaki*, [2]*Frontier Science Research Center, University of Miyazaki.*, [3]*Graduate School of Life Sciences, Tohoku University*, [4]*Graduate School of Science and Engineering, Saitama University*)

3SDA-6 アミノ酸とナノカーボンの相互作用：物理吸着およびシステインの化学反応
Interactions of carbon nanomaterials with amino acids: physical adsorption and chemical reaction with cysteine

○平野 篤（産総研・ナノ材料）
Atsushi Hirano (*NMRI, AIST*)

おわりに
Closing Remarks

09:00〜11:30　E 会場（函館アリーナ 多目的室 B）／Room E（Hakodate Arena Multipurpose Room B）

3SEA　【共催：NEDO ムーンショット型研究開発事業】

生物を利用したゼロエミッション・CO_2 資源化技術の可能性
Potential of zero-emission and CO_2-utilizing biotechnologies

オーガナイザー：加藤 創一郎（産業技術総合研究所），近藤 英昌（産業技術総合研究所）
Organizers: Souichiro Kato (AIST), Hidemasa Kondo (AIST)

"Zero-emission", which will reduce the emission of greenhouse-gases such as CO_2, CH_4, and N_2O to mitigate climate changes, are being tackled internationally. The technologies attracting attention in recent years are physicochemical methods such as Direct Air Capture (DAC) and CO_2 Capture and Storage (CCS). Considering the mitigation of greenhouse gases generated from agriculture and the utilization of CO_2, it is necessary to develop new technologies that utilize specific abilities of living organisms. In this symposium, research projects for innovative zero-emission and CO_2-utilizing biotechnologies conducted by Moonshot Research & Development Program are introduced.

はじめに
Opening Remarks

3SEA-1 微生物電気化学を活用した二酸化炭素資源化技術
CO_2 utilization technologies based on microbial electrochemistry

○加藤 創一郎（産総研・生物プロセス）
Souichiro Kato (*BPRI, AIST*)

3SEA-2 気相微生物反応
Microbial gas-phase reaction

○堀 克敏（名古屋大学大学院工学研究科）
Katsutoshi Hori (*Grad. Sch. Eng., Nagoya Univ.*)

3SEA-3 資源循環の最適化による農地由来の温室効果ガスの排出削減
Mitigation of greenhouse gas emissions from agricultural lands by optimizing nitrogen and carbon cycles

○南澤 究（東北大・院生命）
Kiwamu Minamisawa (*Graduate School of Life Sciences, Tohoku University*)

3SEA-4 土壌団粒構造と微生物
Soil aggregate structure and microorganisms
○和穎 朗太（農研機構・農業環境部門）
Rota Wagai (*NARO/NIAES*)

3SEA-5 ウシルーメンマイクロバイオーム制御による消化管メタンの削減をはかる新しい家畜生産システム開発に向けて
Toward a new livestock production system to reduce enteric methane through controlling bovine rumen microbiome
○小林 泰男（北海道大学大学院農学研究院）
Yasuo Kobayashi (*Research Faculty of Agriculture, Hokkaido University*)

3SEA-6 牛ルーメンからのメタン低減に向けた微生物利用の可能性
Potential microbial target for mitigating enteric methane production in the rumen of cows
○真貝 拓三（国立研究開発法人　農業・食品産業技術総合研究機構　畜産研究部門）
Takumi Shinkai (*Institute of Livestock and Grassland Science, National Agricultural and Food Research Organization*)

おわりに
Closing Remarks

09:00～11:30　F 会場（函館市民会館 1F 大ホール）／Room F（Hakodate Citizen Hall 1F Main Hall）
3SFA　クライオ電子顕微鏡が魅せる生命の未知なる動的なメカニズム
Unexpected dynamic mechanisms of life uncovered by Cryo-EM

オーガナイザー：濡木 理（東京大学），西増 弘志（東京大学）
Organizers: Osamu Nureki (The Univ. of Tokyo), Hiroshi Nishimasu (The Univ. of Tokyo)

Recent outstanding development of single particle analysis of cryo-EM allows high-resolution structure determinations of huge and flexible supramolecular complexes, which have been never available. In this symposium, we will present and discuss on current topics of unexpected dynamic molecular and cellular mechanisms of protein and nucleic acid supramolecular complexes involved in various life phenomena.

3SFA-1 Structure-function relationship of pump-like cation channelrhodopsins
Koichiro Kishi[1], Yoon Seok Kim[2], Masahiro Fukuda[1], Masatoshi Inoue[2], Tsukasa Kusakizako[3], Peter Wang[2], Toshiki Matsui[1], Keitaro Yamashita[4], Takashi Nagata[5], Masae Konno[5], Tomoko Uemura[6], Kehong Liu[6], Mikihiko Shibata[7], Norimichi Nomura[6], So Iwata[6], Osamu Nureki[3], Keiichi Inoue[4], Karl Deisseroth[2], **Hideaki Kato[1]** ([1]*Komaba Inst. Sci., Grad. Sch. Arts. Sci., Univ. Tokyo*, [2]*Stanford Univ.*, [3]*Grad. Sch. Sci., Univ. Tokyo*, [4]*MRC*, [5]*ISSP, Univ. Tokyo*, [6]*Grad. Sch. Med., Kyoto Univ.*, [7]*Kanazawa Univ.*)

3SFA-2 III-E 型 CRISPR-Cas7-11 エフェクター複合体の立体構造と分子改変
Structure and engineering of the type III-E CRISPR-Cas7-11 effector complex
○西増 弘志（東京大学）
Hiroshi Nishimasu (*The University of Tokyo*)

3SFA-3 (2Pos003) クライオ電子顕微鏡による高分解能解析によって明らかになってきた二成分毒素の膜透過機構
(2Pos003) High-resolution Cryo-EM analysis reveals the mechanism of binary toxin translocation
○山田 等仁 [1], 杉田 征彦 [2,3], 野田 岳志 [2], 津下 英明 [1]（[1] 京都産業大学 大学院生命科学研究科, [2] 京都大学 微細構造ウイルス学分野, [3] 京都大学 白眉センター）
Tomohito Yamada[1], Yukihiko Sugita[2,3], Takeshi Noda[2], Hideaki Tsuge[1] ([1]*Graduate School of Life Science, Kyoto Sangyo University*, [2]*Laboratory of Ultrastructural Virology, Institute for Life and Medical Sciences, Kyoto University*, [3]*Hakubi Center for Advanced Research, Kyoto University*)

3SFA-4 IscB–ωRNA 複合体による RNA 依存性 DNA 切断の構造基盤と Cas9 への進化的洞察
Structure of the IscB–ωRNA ribonucleoprotein complex, the likely ancestor of CRISPR-Cas9
○加藤 一希 [1], 岡崎 早恵 [1], Kannan Soumya[2], Zhang Feng[2], 西増 弘志 [1]（[1] 東大・先端研, [2]MIBR, MIT）
Kazuki Kato[1], Sae Okazaki[1], Soumya Kannan[2], Feng Zhang[2], Hiroshi Nishimasu[1] ([1]*RCAST, Univ. Tokyo*, [2]*MIBR, MIT*)

3SFA-5 ミトコンドリアのリボソームの成熟過程から翻訳開始過程に至る構造解析
Structural analysis of the late assembly states of mitochondorial ribosome to the translation initiation
Yuzuru Itoh[1,2], Anas Khawaja[3], Joanna Rorbach[3], Alexey Amunts[2] ([1]*Dept. BioSci., Grad. Sch. Sci., Univ. Tokyo*, [2]*SciLifeLab, DBB, Stockholm University*, [3]*Karolinska Institutet*)

3SFA-6 膜タンパク質と非翻訳 RNA の分子機構の構造基盤
Structural basis for molecular mechanisms of membrane proteins and non-coding RNA
○濡木 理（東京大学・院理）
Osamu Nureki (*Grad. Sch. Sci., Univ. Tokyo*)

09:00〜11:30　G 会場（函館市民会館 3F 小ホール）／Room G（Hakodate Citizen Hall 3F Small Hall）

3SGA 自己組織化で超分子生体膜を創る: 材料科学と生物物理学の接点
Creation of supramolecular biomembrane by the bottom-up self-assembly:Where material science meets biophysics

オーガナイザー：安原 主馬（奈良先端科学技術大学院大学），森垣 憲一（神戸大学）
Organizers: Kazuma Yasuhara (NAIST), Kenichi Morigaki (Kobe Univ.)

In biological systems, unique material properties of the membrane play central roles. The two-dimensional fluid and compartmentalization are essentially important in a variety of biological functions such as signal transduction and energy conversion. Bottom-up approaches based on the self-assembly of materials are promising to reproduce the unique membrane structures and functions, providing insights into the machinery of the biological membrane and enabling to exploit applications in real-life. This symposium will introduce unique studies to create novel artificial biomembranes using not only conventional phospholipids but also synthetic polymers, nanoparticles, and their hybrids to explore the interface between biophysics and material science.

はじめに
Opening Remarks

3SGA-1 ポリマー化脂質膜と天然脂質膜からなるパターン化人工膜
Micropatterned model membrane composed of polymerized and natural lipid bilayers
○森垣 憲一 [1,2]（[1] 神戸大・バイオシグナル, [2] 神戸大・院農学）
Kenichi Morigaki[1,2] ([1]*Biosignal Res. Cen., Kobe Univ.*, [2]*Grad. Sch. Agrobio., Kobe Univ.*)

3SGA-2 **メカノクロミック生体膜を用いたペプチドー脂質相互作用の検出**
Mechanochromic biomembranes for studying peptide-lipid interactions
○杉原 加織（東大・生研）
Kaori Sugihara (*IIS, Univ. Tokyo*)

3SGA-3 **多価不飽和脂質によって形成される脂質ドメイン**
Lipid domains generated by polyunsaturated lipids
ゴー メルヴィン ウェイ シェン, ○手老 龍吾（応化生命系・豊橋技科大）
Melvin Wei Shern Goh, **Ryugo Tero** (*Dept. Appl. Chem. Life Sci., Toyohashi Univ. Tech.*)

3SGA-4 **リキッドマーブル：粒子膜で安定化された液滴**
Liquid marble: Droplet covered by particulate membrane
○藤井 秀司（大阪工業大学）
Syuji Fujii (*Osaka Institute of Technology*)

3SGA-5 **(2Pos188) DNA ゲル骨格が決定する人工細胞の力学特性**
(2Pos188) Cytoskeletons of self-assembled DNA regulate the mechanical properties of artificial cells
○増田 和俊 [1], 大野 風優 [2], 柳澤 実穂 [1,2]（[1] 東京大学教養学部, [2] 東京大学大学院総合文化研究科）
Kazutoshi Masuda[1], Fuyu Ohno[2], Miho Yanagisawa[1,2] ([1]*College of Arts and Sciences, The University of Tokyo*, [2]*Graduate school of Arts and Sciences, The University of Tokyo*)

3SGA-6 **生体膜表面を模倣した高分子自己集合体**
Self-assembled polymer aggregates with mimetic cell membrane surface
○遊佐 真一（兵庫県立大学大学院工学研究科応用化学専攻）
Shin-ichi Yusa (*Department of Applied Chemistry, Graduate School of Engineering, University of Hyogo*)

3SGA-7 **合成高分子によって形成される最小モデル膜としての脂質ナノディスク**
Lipid nanodisc as a minimal model membrane formed with synthetic polymers
○安原 主馬 [1,2]（[1] 奈良先端大院・物質, [2] 奈良先端大・デジタルグリーンイノベーションセンター）
Kazuma Yasuhara[1,2] ([1]*Div. Mat. Sci, Nara Inst. Sci. Tech.*, [2]*Ctr. for Digital Green-innovation, Nara Inst. Sci. Tech.*)

おわりに
Closing Remarks

09:00～11:30　H 会場（函館市民会館 3F 大会議室）／Room H（Hakodate Citizen Hall 3F Conference Room）

3SHA　【共催：学術変革領域研究（A）「超越分子システム」 / 学術変革領域研究（B）「SPEED」】

高次機能性分子システム～創る方法の解明に向けて～
Construction of Higher-ordered Molecular Systems - How to Create Them?

オーガナイザー：松浦 友亮（東京工業大学），川野 竜司（東京農工大学），鈴木 雄太（京都大学）
Organizers: Tomoaki Matsuura (Tokyo Tech), Ryuji Kawano (Tokyo Univ. of Agriculture and Tech.), Yuta Suzuki (Kyoto Univ.)

We would like to take place a joint symposium collaborated with the “Cell-free molecular system” (Grant-in-Aid for Transformative Research Areas (A)) and the “SPEED” (Grant-in-Aid for Transformative Research Areas (B)). This symposium aims to shed light on the bottom-up construction of the cell-free system and the superior protein engineering by evolution and design.

はじめに
Opening Remarks

3SHA-1　Constructing an in vitro gene screening system for membrane proteins and its application
Tomoaki Matsuura (*ELSI, Tokyo Tech*)

3SHA-2　人工金属酵素を用いた触媒システムの構築
Artificial enzymes towards systems catalysis
○岡本 泰典（東北大・学際研）
Yasunori Okamoto (*FRIS, Tohoku Univ.*)

3SHA-3　2 次元ナノ材料界面を利用した高感度バイオセンサの開発
Development of Highly Sensitive Biosensor Using Two-Dimensional Nanomaterial Interface
○早水 裕平（東工大・物質理工）
Yuhei Hayamizu (*Sch.Mater, Tokyo Tech*)

3SHA-4　分子進化によるタンパク質集合体の構築
Directed evolution of protein assembly
○寺坂 尚紘 [1], 菅 裕明 [1], Hilvert Donald[2]（[1] 東京大・院理学, [2]Laboratory of Organic Chemistry, ETH Zurich）
Naohiro Terasaka[1], Hiroaki Suga[1], Donald Hilvert[2] ([1]*Grad. Sch. Sci., The Univ. of Tokyo*, [2]*Laboratory of Organic Chemistry, ETH Zurich*)

3SHA-5　人工細胞膜システム：デノボ設計ナノポアの構築
Artificial Cell-membrane system: the construction of *de novo* nanopores
○川野 竜司（東京農工大学 工学研究院 生命工学専攻）
Ryuji Kawano (*Dept. Biotech&Life Sci., Tokyo University of Agriculture and Technology*)

3SHA-6　合理設計による機能性タンパク質集合体の構築
Rational design of protein assembly
○鈴木 雄太（京大・白眉）
Yuta Suzuki (*Hakubi Center, Kyoto University*)