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

**オーガナイザー：芝口 友隆（慶應義塾大学），井上 倫太郎（京都大学）**
**Organizers: Tomotaka Oroguchi (Keio Univ.), Rintaro Inoue (Kyoto Univ.)**

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

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

はじめに
Opening Remarks

1SAA-1　Visualization of domain motion in multi-domain protein as studied by neutron scattering and molecular dynamics simulation
**Rintaro Inoue** (*Institute for Integrated Radiation and Nuclear Science, Kyoto University*)

1SAA-2　情報幾何学による実験データと MD の統合: 蛋白質構造アンサンブル可視化への適用
Visualization of protein conformational ensembles by integrating experiments and MD via information geometry
○芝口 友隆（慶應大・理工・物理）
**Tomotaka Oroguchi** (*Dept. Phys., Keio Univ.*)

1SAA-3　高速原子間力顕微鏡データと分子シミュレーションの融合による生体分子の構造ダイナミクスのデータ同化解析
Data assimilation analysis of structural dynamics of biomolecules by combining HS-AFM data and molecular simulations
○渕上 壮太郎 [1], 新稲 亮 [2], 加藤 傑 [2], 松永 康佑 [3], 高田 彰二 [4]（[1] 静県大・薬, [2] 理研・BDR, [3] 埼大院・理工, [4] 京大院・理）
**Sotaro Fuchigami**[1], Toru Niina[2], Suguru Kato[2], Yasuhiro Matsunaga[3], Shoji Takada[4] ([1]*Sch. Pharm. Sci., Univ. Shizuoka*, [2]*RIKEN BDR*, [3]*Grad. Sch. Sci. & Eng., Saitama Univ.*, [4]*Grad. Sch. Sci., Kyoto Univ.*)

1SAA-4　クライオ電子顕微鏡単粒子画像からの 3D モデル直接推定によるタンパク質マルチコンフォメーション状態の解明
Uncovering Multiple Conformational States of Protein via Direct 3D Models Estimation from CryoEM single-particle images
○徳久 淳師（理研　計算科学研究センター）
**Atsushi Tokuhisa** (*RIKEN Center for Computational Science*)

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

おわりに
Closing Remarks

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## 1SBA AI や機械学習を活用した生物物理・シミュレーション研究の探究
Exploring Biophysics and Simulation Research Using AI and Machine Learning

オーガナイザー：宮下 尚之（近畿大学），米澤 康滋（近畿大学）
**Organizers: Naoyuki Miyashita (Kindai Univ.), Yasushige Yonezawa (Kindai Univ.)**

09:00〜11:30
B 会場（会議室 103+104）／Room B（Meeting Room 103+104）

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

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

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

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

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

1SBA-5 蛋白質 MD シミュレーションデータの動的特徴量とその時間依存性を精密に同時抽出する新規機械学習法
A novel machine learning method for the simultaneous and accurate extraction of dynamic features and time dependence from MD simulations
○米澤 康滋（近畿大学 先端技術総合研究所）
**Yasushige Yonezawa** (*Kindai University Institute of Advanced Technology*)

1SBA-6 機械学習手法を用いたヘムタンパク質における配列構造機能相関の解析
Analysis of sequence-structure-function relationships in heme proteins by using machine learning methods
○近藤 寛子（北見工大）
**Hiroko X. Kondo** (*Kitami Inst. Tech.*)

1SBA-7 大規模分子動力学計算・動的モンテカルロ法・機械学習を統合した不均一系における物質輸送の研究手法
Integration of large-scale MD calculation, dynamic MC method, and machine learning to study mass transport in heterogeneous systems
○永井 哲郎 [1], 吉川 信明 [2], 陣内 亮典 [2], 木村 将之 [3], 岡崎 進 [4]（[1] 福岡大学理学部化学科, [2] 株式会社豊田中央研究所, [3] トヨタ自動車株式会社, [4] 横浜市立大学生命ナノシステム科学研究科）
**Tetsuro Nagai[1]**, Nobuaki Kikkawa[2], Ryosuke Jinnouchi[2], Masayuki Kimura[3], Susumu Okazaki[4]
([1]*Department of Chemistry, Faculty of Science, Fukuoka University*, [2]*Toyota Central R&D Labs., Inc.*, [3]*Toyota Motor Corporation*, [4]*Graduate School of Nanobioscience, Yokohama City University*)

1SBA-8 疾患の複雑性を解読する：難病創薬のためのデータ駆動的アプローチ
Decoding Disease Complexity: Integrative Data-Driven Approaches for Rare Disease Drug Discovery
○夏目 やよい [1,2]（[1] 医薬基盤・健康・栄養研究所, [2] 徳島大学　先端酵素学研究所）
**Yayoi Natsume-Kitatani[1,2]** ([1]*National Institutes of Biomedical Innovation, Health and Nutrition*, [2]*Institute of Advanced Medical Sciences, Tokushima University*)

おわりに
Closing Remarks

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

共催 学術変革領域研究（A）「キラル光物質科学」

オーガナイザー：細川 千絵（大阪公立大学），尾松 孝茂（千葉大学）
**Organizers: Chie Hosokawa (Osaka Metro. Univ.), Takashige Omatsu (Chiba Univ.)**

09:00〜11:30
C 会場（会議室 105+106）／Room C（Meeting Room 105+106）

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

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はじめに
Opening Remarks

1SCA-1 生物物理学のための Structured Light
Structured light for biophysics
○尾松 孝茂（千葉大学）
**Takashige Omatsu** (*Chiba University*)

1SCA-2 らせんの組織工学の創製
Development of Helical Tissue Engineering
○松崎 典弥（大阪大学・大学院工学研究科）
**Michiya Matsusaki** (*The University of Osaka*)

1SCA-3 細胞内温度計測：蛍光性ナノ材料を用いた細胞機能の探索
Intracellular thermometry: Probing cell function with fluorescent nanomaterials
○原田 慶恵（大阪大学ヒューマン・メタバース疾患研究拠点）
**Yoshie Harada** (*PRIMe, The University of Osaka*)

1SCA-4 光渦/高速 AFM 複合機で光の螺旋性を可視化する
High-speed AFM combined with optical vortex visualizes optical helicity
○馬越 貴之（阪大院工）
**Takayuki Umakoshi** (*Dept. Appl. Phys., Univ. Osaka*)

1SCA-5 液滴およびアミロイド線維形成に至るタンパク質の光捕捉ダイナミクス
Optical trapping dynamics of protein assembly into condensates and amyloid fibrils
○茶谷 絵理 [1], 柚 佳祐 [1,2], Chien Yi-Sian[2], 増原 宏 [2]（[1] 神戸大・院理, [2] 台湾国立陽明交通大・理学院）
**Eri Chatani**[1], Keisuke Yuzu[1,2], Yi-Sian Chien[2], Hiroshi Masuhara[2] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Dept. Appl. Chem., National Yang Ming Chiao Tung Univ.*)

1SCA-6 紫外域における放射光キラル分光と生体分子の構造観測
Synchrotron radiation chiral spectroscopy in ultraviolet region and structural characterization of biomolecules
○松尾 光一（放射光・広島大学）
**Koichi Matsuo** (*Res. Inst. Synchrotron Rad. Sci., Hiroshima Univ.*)

1SCA-7 集光フェムト秒光渦レーザーによる単一神経細胞の刺激
Single-neuron stimulation with a focused femtosecond optical vortex laser
○細川 千絵（阪公大・院理）
**Chie Hosokawa** (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

1SCA-8 マウスノード不動繊毛は変形の向きを感知して左右軸を決定する
Immotile cilia mechanically sense the direction of fluid flow for left-right determination
○加藤 孝信（東大・院医）
**Takanobu Katoh** (*Grad. Sch. Med., The Univ. of Tokyo*)

おわりに
Closing Remarks

1SDA　動的高次構造の生物物理学: 計測から制御まで
Biophysics of dynamic supramolecular assemblies: measurement, investigation, and design

共催 JST さきがけ 「細胞の動的高次構造体」

オーガナイザー：大出 真央（大阪大学），戸田 浩史（筑波大学）
**Organizers: Mao Oide (The Univ. of Osaka), Hirofumi Toda (Univ. of Tsukuba)**

09:00〜11:30
D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

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

はじめに
Opening Remarks

1SDA-1　微細加工温度センサが導く単一細胞の独特な熱挙動
Unique thermal behaviors of single cells revealed by microfabricated thermometer
○猪股 直生（東北大学）
**Naoki Inomata** (*Tohoku University*)

1SDA-2　天然変性タンパク質の凝集を決定する配列ルールの解読
Decoding Sequence Rules for Condensation of Disordered Proteins
○足立 景亮 [1,2], 川口 喬吾 [2,3]（[1] 理研 iTHEMS, [2] 理研 PRI, [3] 東京大 理学系研究科 知の物理学研究センター）
**Kyosuke Adachi[1,2]**, Kyogo Kawaguchi[2,3] ([1]*RIKEN iTHEMS*, [2]*RIKEN PRI*, [3]*IPI, Grad. Sch. Sci., Univ. Tokyo*)

1SDA-3　The cellular basis of long-term memory: L-LTP-dependent extension of endoplasmic reticulum into spines via septin 3
**Natsumi Ageta-Ishihara** (*Fac. Sci., Toho Univ.*)

1SDA-4　How does the nucleus move within 'super crowded' plant cells?
**Hirotomo Takatsuka[1,2]**, Toshiki Amari[3] ([1]*Dept. Biol. Sci., NWU*, [2]*JST・Presto*, [3]*Div. Biol. Sci. Tech., Kanazawa Univ.*)

1SDA-5　**TIGR-Tas**(タイガー-タス): Nop ドメインタンパク質群によるモジュラーな RNA 誘導性システム
TIGR-Tas: Modular RNA-guided systems with Nop domain-containing proteins
○齋藤 諒（理研・開拓研究所　生命現象エンジニアリング理研 ECL 研究チーム）
**Makoto Saito** (*RIKEN PRI Biophenomena Engineering RIKEN ECL Research Team*)

1SDA-6　リボソーム液滴を標的とする新規抗菌ペプチド
A Novel Antimicrobial Peptide that Targets Liquid Ribosomal Condensates
○戸田 浩史（筑波大学　国際統合睡眠医科学研究機構）
**Hirofumi Toda** (*IIIS, University of Tsukuba*)

おわりに
Closing Remarks

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

共催 学術変革領域研究（A）「ゲノムモダリティ」

**オーガナイザー：前島 一博（国立遺伝学研究所），西山 朋子（京都大学）**
**Organizers: Kazuhiro Maeshima (NIG), Tomoko Nishiyama (Kyoto Univ.)**

09:00〜11:30
E 会場（会議室 201）／Room E（Meeting Room 201）

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

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はじめに
Opening Remarks

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

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

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

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

1SEA-5　Target-DNA searching process of a light-regulated transcription factor, Photozipper, observed by high-speed atomic force microscopy
**Akihiro Tsuji[1]**, Hayato Yamashita[1], Osamu Hisatomi[2], Masayuki Abe[1] ([1]*Grad. Sch. Eng. Sci., UOsaka*, [2]*Grad. Sch. Sci., UOsaka*)

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

おわりに
Closing Remarks

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## 1SFA　細胞外小胞を基軸とした生命の理解と操作ツール開発

Unveiling life by the function and modification of extracellular vesicles

共催 JST CREST 「細胞を遊ぶ」

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

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

09:00〜11:30

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

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

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はじめに
Opening Remarks

1SFA-1　細胞膜由来の細胞外小胞を介した効率的タンパク質伝達
Efficient protein transfer through the protrusion-derived extracellular vesicles
○西村 珠子, 末次 志郎（奈良先端大・バイオ）
**Tamako Nishimura**, Shiro Suetsugu (*NAIST*)

1SFA-2　1 粒子追跡と超解像顕微鏡観察による細胞外小胞の結合・取り込み機構の解明
Mechanisms of extracellular vesicle binding and internalization uncovered by single-particle tracking and super-resolution microscopy
○鈴木 健一 [1,2]（[1] 岐阜大・糖鎖生命コア研, [2] 国立がん研セ）
**Kenichi G. N. Suzuki**[1,2] ([1]*Gifu Univ.・iGCORE*, [2]*NCCRI*)

1SFA-3　大腸菌生細胞からのメンブレンベシクル創発：バイオポリマー合成が "引き金"
Controllable secretion of membrane vesicles (MVs) from viable *Escherichia coli* triggered by intracellular polymer accumulation
○高 相昊, 田口 精一（信州大・ARG 機構）
**Sangho Koh**, Seiichi Taguchi (*Inst. ARG, Shinshu Univ.*)

1SFA-4　細胞外小胞の物質送達機構の解明と薬物送達への応用
Analysis of intracellular trafficking of extracellular vesicles for drug delivery applications
○曽宮 正晴（大阪大学　産業科学研究所）
**Masaharu Somiya** (*SANKEN, The University of Osaka*)

1SFA-5　生物材料ナノマシーンによるゲノム編集送達
Genome Editing Delivery by Biomaterial Nanomachines
○堀田 秋津（京大・CiRA）
**Akitsu Hotta** (*CiRA, Kyoto University*)

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

おわりに
Closing Remarks

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

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

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

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

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

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はじめに
Opening Remarks

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

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

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

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

1SGA-5 高精度量子化学が解き明かす光生物学の分子メカニズム
Exploring Photobiology via High-Precision Quantum Chemistry
○藤本 和宏（名大・ITbM）
**Kazuhiro Fujimoto** (*ITbM, Nagoya Univ.*)

1SGA-6 チャネルロドプシンの光感度に対する電気生理学的アプローチ
A new model of light sensitivity in Channelrhodopsins
○細島 頌子 [1,2]（[1] 名古屋工業大学大学院 工学研究科, [2] オプトバイオテクノロジー研究センター）
**Shoko Hososhima[1,2]** ([1]*Graduate School of Engineering, Nagoya Institute of Technology*, [2]*Opto Bio Technology Research Center, Nagoya Institute of Technology*)

1SGA-7 タンパク質の古典的機能動態を高速 AFM でとらえる
Visualizing Classical Functional Dynamics of Proteins by High-Speed AFM
○内橋 貴之（名古屋大学）
**Takayuki Uchihashi** (*Nagoya University*)

おわりに
Closing Remarks

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

共催 細胞膜研究フォーラム

オーガナイザー：楠見 明弘（沖縄科学技術大学院大学），山城 佐和子（京都大学）
**Organizers: Akihiro Kusumi (OIST), Sawako Yamashiro (Kyoto Univ.)**

09:00〜11:30
H 会場（会議室 204）／Room H（Meeting Room 204）

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

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1SHA-1 Force Transmission and Mechanical Memory at Integrin-Based Adhesions Revealed by Live-Cell Single-Molecule Imaging
**Sawako Yamashiro[1,2]**, Ying Liu[1], David Rutkowski[3], Dimitrios Vavylonis[3], Naoki Watanabe[1,2] ([1]*Grad. Sch. Biostudies, Kyoto Univ.*, [2]*Grad. Sch. Medicine, Kyoto Univ.*, [3]*Dept. Physics, Lehigh Univ.*)

1SHA-2 Kindlin converts the talin•integrin slip bond under mechanical load to an ideal bond
**Reinhard Faessler** (*Max Planck Institute, Martinsried, Germany*)

1SHA-3 Deciphering the mechano-sensitive properties of the membrane periodic skeleton in neurons
**Gregory Giannone[1]**, Zhou Xuesi[1], Théo Dudon[1], Jean-Baptiste Trebbia[2], Anna Brachet[1], Brahim Lounis[2] ([1]*University Bordeaux, CNRS, Interdisciplinary Institute for Neuroscience, UMR 5297, Bordeaux, France*, [2]*Laboratoire Photonique Numerique et Nanosciences (LP2N), Institut d'Optique Graduate School and CNRS, UMR 5298, Talence, France*)

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

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

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## 1SIA 発生，老化，病態における細胞骨格のダイナミクス
Cytoskeletal dynamics in development, aging and disease

オーガナイザー：島本 勇太（国立遺伝学研究所），宮﨑 牧人（理化学研究所）
**Organizers: Yuta Shimamoto (NIG), Makito Miyazaki (RIKEN)**

09:00〜11:30
I 会場（会議室 205）／Room I（Meeting Room 205）

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

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はじめに
Opening Remarks

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

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

1SIA-3 微小管によるメカノケミカルクロストークが細胞移動の方向性を制御する
Mechano-chemical crosstalk induced by microtubules in directed cell migration
○西村 有香子 [1], 近藤 龍樹 [1], 折井 良太 [2], 神原 丈敏 [3], 繁富（栗林） 香織 [4], 岡田 康志 [3,5,6], 谷本 博一 [2], 茂木 文夫 [1]（[1] 北大・遺制研, [2] 横浜市立大・理, [3] 理研・BDR, [4] 北大・大機構, [5] 東大・理, [6] 東大・医）
**Yukako Nishimura[1]**, Tatsuki Kondo[1], Ryota Orii[2], Taketoshi Kambara[3], Kaori Kuribayashi-Shigetomi[4], Yasushi Okada[3,5,6], Hirokazu Tanimoto[2], Fumio Motegi[1] ([1]*Inst. Gen. Med., Hokkaido Univ.*, [2]*Dept. Sci., Yokohama City Univ.*, [3]*BDR, Riken*, [4]*Inst. Adv. Grad. Edu., Hokkaido Univ.*,, [5]*Grad. Sch. Sci., Tokyo Univ.*, [6]*Grad. Sch. Med., Tokyo Univ.*)

1SIA-4 加齢にともなう卵子の染色体数異常の細胞生物学的な原因
Cell biological mechanisms of age-associated egg aneuploidy
○北島 智也（理化学研究所生命機能科学研究センター）
**Tomoya Kitajima** (*RIKEN Biosystems Dynamics Research*)

1SIA-5 マウス Metaphase II 卵の紡錘体局在を細胞質流動から守るアクチン構造
Cytoplasmic Flow–Resistant Spindle Positioning by Actin Structures in Mouse Metaphase II Oocytes
○大杉 美穂, 寺井 康徳（東大・理・生物科学専攻）
**Miho Ohsugi**, Kotoku Terai (*Dept. Biol. Sci., Grad. Sch. Sci., Univ. of Tokyo*)

1SIA-6 細胞骨格のエネルギー動態：アクチン線維構造から細胞分裂へ
Energetics of the Cytoskeleton: From F-actin Architecture to Cell Division
○坂本 遼太 [1,2], マレル マイケル [2,3]（[1] 中央研究院・物理研, [2] イェール大・生体医工, [3] イェール大・物理）
**Ryota Sakamoto[1,2]**, Michael Murrell[2,3] ([1]*Inst. Phys., Academia Sinica*, [2]*Dept. Biomed. Engr., Yale Univ.*, [3]*Dept. Phys., Yale Univ.*)

1SIA-7 アクチン重合の光操作で探る密度依存的な細胞骨格の機能制御
Optogenetic control of actin network assembly reveals density-dependent functions of actin binding proteins
○宮﨑 牧人 [1,2,3]（[1] 理研・IMS, [2] 理研・BDR, [3] 信州大・院総合医理工学）
**Makito Miyazaki[1,2,3]** ([1]*RIKEN IMS*, [2]*RIKEN BDR*, [3]*Grad. Sch. Med., Sci., & Tech., Shinshu Univ.*)

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## 1SJA タンパク質凝集体の構造，病理，計算をつなぐ研究の新展開
New frontiers in research linking structure, pathology, and computation of protein aggregates

**オーガナイザー：田中 元雅（理化学研究所），中山 隆宏（金沢大学）**
**Organizers: Motomasa Tanaka (RIKEN), Takahiro Nakayama (Kanazawa Univ.)**

09:00〜11:30
J 会場（会議室 206）／Room J（Meeting Room 206）

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

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はじめに
Opening Remarks

1SJA-1 小胞体関連分解におけるタンパク質の逆行輸送を促進する膜上ナノクラスター構造
A nanocluster mesh on ER membranes facilitates protein retrotranslocation in ERAD
○持田 啓佑 [1,2], 梅田 健一 [3], 中戸川 仁 [1], 古寺 哲幸 [3], 田中 元雅 [2]（[1] 東京科学大・総合研究院, [2] 理研・脳神経科学, [3] 金沢大・ナノ生命科学）
**Keisuke Mochida[1,2]**, Kenichi Umeda[3], Hitoshi Nakatogawa[1], Noriyuki Kodera[3], Motomasa Tanaka[2] ([1]*IIR, Science Tokyo*, [2]*CBS, Riken*, [3]*NanoLSI, Kanazawa Univ.*)

1SJA-2 高速 AFM によるアミロイドタンパク質の構造動態と凝集機構の解明
High-speed AFM visualization of structural dynamics and aggregation mechanisms in amyloidogenic proteins
○中山 隆宏（金沢大学ナノ生命科学研究所）
**Takahiro Watanabe-Nakayama** (*WPI-Nano Life Science Institute, Kanazawa University*)

1SJA-3 α シヌクレイノパチーの病理とバイオマーカー（seed amplification assay）
Pathology and Biomarkers of Alpha-Synucleinopathies: Focus on Seed Amplification Assays
○奥住 文美（順天堂大学神経学講座）
**Ayami Okuzumi** (*Juntendo University, Department of Neurology*)

1SJA-4 アミロイド繊維形成とアミノ酸残基レベルの自由エネルギーとの相関
Amyloid Fibril Formation Correlates with Residue-Level Free Energy Profiles
○藤浪 大輔 [1], 林 成一郎 [2], 伊藤 杏 [1], 伊藤 創平 [1], 神田 大輔 [3]（[1] 静岡県大・薬食生命, [2] 分子研, [3] 九大・生医研）
**Daisuke Fujinami[1]**, Seiichiro Hayashi[2], An Ito[1], Sohei Ito[1], Daisuke Kohda[3] ([1]*Grad. Sch. Integr. Pharm. Nutr. Sci., Univ. of Shizuoka*, [2]*NINS, Institute for Molecular Science*, [3]*MIB, Kyushu Univ.*)

1SJA-5 Unveiling Protein Dynamics through Data Integration Simulations
**Osamu Miyashita** (*RIKEN Center for Computational Science*)

1SJA-6 プリオン株多様性の構造および分子基盤の解明
Structural and mechanistic basis for prion strain diversity
○田中 元雅（国立研究開発法人理化学研究所　脳神経科学研究センター）
**Motomasa Tanaka** (*RKEN Center for Brain Science*)

2 日目（9 月 25 日（木））／Day 2（Sep. 25 Thu.）

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

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

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

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

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

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はじめに
Opening Remarks

2SAA-1 Integrative Structure Modeling of Protein Complexes Using Experimental Data with Errors and Noise
**Takaharu Mori** (*Tokyo University of Science*)

2SAA-2 ゲノム分子モデリングにおける統合的多階層手法
An Integrative Multi-Scale Approach to Genome Molecular Modeling
**Giovanni Bruno Brandani** (*Department of Biophysics, Graduate School of Science, Kyoto University*)

2SAA-3 Investigation of conformational landscape from single-particle cryoEM data via reference based approach
**Mao Oide**[1], Yuji Sugita[2,3] ([1]*IPR, Osaka Univ*, [2]*CPR, RIKEN*, [3]*R-CCS, RIKEN*)

2SAA-4 生体分子の機能推定のための高速原子間力顕微鏡動画に基づく理論的考察
Theoretical considerations based on high-speed atomic force microscopy movies to estimate biomolecular functions
○炭竈 享司 [1,2]（[1] 京大・生命科学研究科, [2] 金沢大・ナノ生命科学研究所）
**Takashi Sumikama**[1,2] ([1]*Grad. Sch. Biostudies, Kyoto Univ.*, [2]*Nano Life Sci. Inst., Kanazawa Univ.*)

2SAA-5 AFM 画像セグメンテーション誘導フレキシブルフィッティングによるオートファジー関連天然変性蛋白質構造の推論
Inferring autophagy-related intrinsically disordered protein structures using AFM image segmentation guided flexible fitting
○唐澤 直之 [1], 石曽根 毅 [2], 本間 さくら [1], 前島 遼太 [3], 古寺 哲幸 [4], 中村 和幸 [5], 松永 康佑 [1,6]（[1] 埼大・院理工, [2] 明大・研究知財, [3] 明大・院先端数理, [4] 金大・WPI-NanoLSI, [5] 明大・総合数理, [6] 理研・R-CCS）
**Naoyuki Karasawa**[1], Tsuyoshi Ishizone[2], Sakura Homma[1], Ryota Maejima[3], Noriyuki Kodera[4], Kazuyuki Nakamura[5], Yasuhiro Matsunaga[1,6] ([1]*Grad. Sch. Sci. Eng., Saitama Univ.*, [2]*Organ. Strateg. Coord. Res. Intellect. Prop., Meiji Univ.*, [3]*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, [4]*WPI-NanoLSI, Kanazawa Univ.*, [5]*Sch. Interdiscip. Math. Sci., Meiji Univ.*, [6]*R-CCS, RIKEN*)

2SAA-6 Development of high performance coarse-grained molecular dynamics for large-scale biomolecular simulations
**Jaewoon Jung**[1,2], Cheng Tan[1], Yuji Sugita[1,2] ([1]*RIKEN R-CCS*, [2]*RIKEN PRI*)

2SAA-7 Integrative modeling approaches to characterize the dynamics of biomolecules
**Florence Tama**[1,2] ([1]*Grad. Sch. Sci., Nagoya University*, [2]*RIKEN Center for Computational Science*)

おわりに
Closing Remarks

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

オーガナイザー：Tran Duy Phuoc（東京科学大学），堂浦 智裕（名古屋大学）
**Organizers: Duy Phuoc Tran (Science Tokyo), Tomohiro Doura (Nagoya Univ.)**

09:00〜11:30
B 会場（会議室 103+104）／Room B（Meeting Room 103+104）

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

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はじめに
Opening Remarks

2SBA-1　Understanding Activation Mechanisms in GPCRs - 1) Biophysical studies 2) Computational Validation, and 3) Drug discovery strategies
**Robert Scott Prosser**[1], Akio Kitao[2], Duy Phuoc Tran Tran[2], Adnan Sljoka[3], David Young[4] ([1]*Chemistry & Biochemistry Departments, University of Toronto, Toronto, Ontario, Canada*, [2]*School of Life Science and Technology, Tokyo Institute of Technology, Tokyo, Japan*, [3]*RIKEN Center for Advanced Intelligence Project, Tokyo, Japan*, [4]*KisoJi Biotechnology, Canada*)

2SBA-2　プロテアーゼ活性化受容体の活性化機構と G タンパク質結合の構造的基盤
Structural Basis of Activation Mechanism and G Protein Coupling in Protease-Activated Receptors
○浅田 秀基, 林 到炫, 足立 誠（京都大学　大学院医学研究科）
**Hidetsugu Asada**, Dohyun Im, Makoto Adachi (*Kyoto University Graduate school of Medicine*)

2SBA-3　活性化時の構造変化に基づく GPCR の化学遺伝学的制御
Chemogenetic regulation of GPCRs based on structural changes upon activation
○堂浦 智裕（名大・院工）
**Tomohiro Doura** (*Grad. Sch. Eng., Nagoya Uni.*)

2SBA-4　G タンパク質バイアスリガンドによるヒト GPR84 のシグナル伝達機構
Mechanism of human GPR84 signaling by G-protein biased ligands
**Shota Suzuki**[1], Duy Phuoc Tran[2], Koki Nishikawa[3], Akio Kitao[2], Yoshinori Fujiyoshi[1] ([1]*Adv. Res. Init., Science Tokyo*, [2]*Sch. of Life Sci. and Tech., Science Tokyo*, [3]*Joint Res. Crs. Adv. Biomol. Character., TUAC*)

2SBA-5　G タンパク質共役型受容体活性化・不活性化メカニズムのインシリコ研究
In silico investigation of the activation and inactivation mechanisms of G protein-coupled receptors
○北尾 彰朗（東京科学大生命理工）
**Akio Kitao** (*Sch. Life Sci. Tech, Science Tokyo*)

2SBA-6　Probing Allosteric and biased signaling with rigidity theory, NMR, and geometric Monte-Carlo simulations in GPCRs
**Adnan Sljoka** (*RIKEN*)

2SCA　予知生合成科学：実験と計算を融合する生合成研究の新たな展開
Forecasting Biosynthesis: A New Frontier in Biosynthesis Research that Integrates Experiment and Computation

共催 学術変革領域研究（A）「予知生合成科学」

オーガナイザー：森脇 由隆（東京科学大学），佐藤 玄（東京大学）
**Organizers: Yoshitaka Moriwaki (Science Tokyo), Hajime Sato (The Univ. of Tokyo)**

09:00〜11:30
C 会場（会議室 105+106）／Room C（Meeting Room 105+106）

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

はじめに
Opening Remarks

2SCA-1　3 次元立体構造を用いた酵素機能の予測：FUJISAN の開発と応用
Predicting enzyme functions using 3D Structures: Development and application of FUJISAN
○藤田 卓, 寺田 透（東大・院農）
**Suguru Fujita**, Tohru Terada (*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

2SCA-2　非生物学的化学反応を指向した酵素データベースの探索
Database Mining-driven Enzyme Discovery for Abiotic Chemical Transformations
○加藤 俊介（阪大・院工）
**Shunsuke Kato** (*Grad. Sch. Eng., UOsaka*)

2SCA-3　機械学習モデルによる新規酸素反応性 PLP 依存性酵素の発見
Machine learning-guided discovery of novel oxygen and PLP-dependent enzymes
○野口 智弘 [1,2], 淡川 孝義 [1], 齋藤 裕 [2]（[1] 北里大院・未来工学, [2] 理研・環境資源科学研究センター）
**Tomohiro Noguchi**[1,2], Takayoshi Awakawa[1], Yutaka Saito[2] ([1]*Graduate School of Frontier Engineering, Kitasato Univ*, [2]*CSRS, RIKEN*)

2SCA-4　Transformer 言語モデルを用いた天然化合物生合成遺伝子クラスターの予測と設計に向けて
A transformer-based platform for the prediction and design of biosynthetic gene clusters
○梅村 舞子（京工繊大・院）
**Maiko Umemura** (*Appl. Biol., Kyoto Inst. Tech.*)

2SCA-5　人工設計タンパク質を利用した新規酵素機能改変戦略
Engineering by Proxy: A Novel Strategy for Enzyme Function Redesign Using Synthetic Designer Proteins
○田中 俊一（京都府立大学・院生命環境科学）
**Shun-ichi Tanaka** (*Grad. Sch. Life and Environ. Sci., Kyoto Pref. Univ.*)

2SCA-6 酵素反応の理論的予測と改良
Computational prediction and improvement of enzymatic reactions
○新井 宗仁 [1,2]（[1] 東大・総合文化・生命環境, [2] 東大・理・物理）
**Munehito Arai[1,2]** ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

おわりに
Closing Remarks

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## 2SDA 化学による細胞と異世界のマリアージュ～界面の概念拡張による生命世界の拡大
A marriage of cells with “another world” produced by chemistry – Augmentation of the world of life through the innovative concept of interface

**オーガナイザー：岸村 顕広（九州大学），金原 数（東京科学大学）**
**Organizers: Akihiro Kishimura (Kyushu Univ.), Kazushi Kinbara (Science Tokyo)**

09:00～11:30
D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

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

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はじめに
Opening Remarks

2SDA-1 液体足場：細胞の未知との遭遇
Fluid Scaffolds: An Encounter with the Unknown for Cells
○中西 淳（物質・材料研究機構）
**Jun Nakanishi** (*NIMS*)

2SDA-2 Design of non-sticking microdroplets toward single cell analysis
**Mizuki Tenjimbayashi** (*National Institute for Materials Science*)

2SDA-3 生体分子集合体の階層構造が導く非球形凝縮体の創生
Supramolecular Hierarchical Assembly Involving Peptides and Oligonucleotides Forming Non-Spherical Biomolecular Condensates
○菅井 祥加（東京科学大・総合研究院）
**Hiroka Sugai** (*IIR, Science Tokyo*)

2SDA-4 低分子コアセルベートの形成と内部環境や機能化に対する化学構造の影響
Impact of Molecular Structure on Low-Molecular-Weight Coacervates: Formation, Internal Environments, and Functionalization
○東 小百合 [1,2,3], 藤本 竜太郎 [4], 廣澤 幸一朗 [5,6], 金丸 恒大 [7,8], 吉田 紀生 [7], 鈴木 健一 [5,6], 池田 将 [2,3,4,5]（[1] 岐阜大・高等研究院, [2] 岐阜大・院連創薬, [3] 岐阜大・COMIT, [4] 岐阜大・院自然科学技術, [5] 岐阜大・iGCORE, [6] 国立がん研・バイオイメージング, [7] 名古屋大・院情報学, [8] 京大・福井セ）
**Sayuri Higashi[1,2,3]**, Ryutaro Fujimoto[4], Koichiro Hirosawa[5,6], Kodai Kanemaru[7,8], Norio Yoshida[7], Kenichi Suzuki[5,6], Masato Ikeda[2,3,4,5] ([1]*Inst. Adv. Study, Gifu Univ.*, [2]*Grad. Sch. Drug Disc. & Med. Info. Sci., Gifu Univ.*, [3]*COMIT, Gifu Univ.*, [4]*Dept. Life Sci. & Chem., Grad. Sch. Nat. Sci. & Technol., Gifu Univ.*, [5]*iGCORE, Gifu Univ.*, [6]*Div. Adv. Bioimaging, NCCRI*, [7]*Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.*, [8]*FIFC, Kyoto Univ.*)

2SDA-5 コアセルベートによる革新的生体高分子送達
Innovative Delivery of Biomacromolecules via Coacervates
○川口 祥正（京大化研）
**Yoshimasa Kawaguchi** (*Inst. Chem. Res*)

おわりに
Closing Remarks

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## 2SEA 区画・領域依存的生命現象とその可視化
Compartment- and Region-Dependent Biological Phenomena and Visualization

オーガナイザー：田上 俊輔（理化学研究所），大友 康平（順天堂大学）
**Organizers: Shunsuke Tagami (RIKEN), Kohei Otomo (Juntendo Ujniv.)**

09:00〜11:30
E 会場（会議室 201）／Room E（Meeting Room 201）

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

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はじめに
Opening Remarks

2SEA-1 生命の起源：ペプチド集合体・区画による RNA 合成の活性化
The origin of life: Enhancement of RNA synthesis by peptide aggregates and compartments
○田上 俊輔（理化学研究所 IMS）
**Shunsuke Tagami** (*RIKEN IMS*)

2SEA-2 RNA が導く膜のない細胞内区画の形成：その機構と分子論的理解
RNA-Guided Formation of Membraneless Intracellular Compartments: Mechanisms and Molecular Insights
○山崎 智弘（阪大・院生命機能）
**Tomohiro Yamazaki** (*Front. Biosci., The University of Osaka*)

2SEA-3 人工細胞回路による多細胞パターンのデザイン
Programming multicellular patterns with synthetic cell-cell communication
○戸田 聡（大阪大・蛋白研）
**Satoshi Toda** (*IPR, Univ. Osaka*)

2SEA-4 植物に寄生するシストセンチュウは破壊者か？建築家か？
Cyst nematodes: Destroyers or Architects? ~Insights from the 3D structure of host plant tissues~
○大津 美奈（奈良先端大・バイオ）
**Mina Ohtsu** (*NAIST, Bio.*)

2SEA-5 ライブイメージングのための透明化試薬の開発
Minimally invasive optical clearing media for live cell imaging ex vivo and in vivo
○稲垣 成矩（九州大学　医学研究院）
**Shigenori Inagaki** (*Grad. Sch. Med. Sci., Kyushu Univ*)

2SEA-6 区画・領域依存的生命現象を可視化する 3D 蛍光顕微鏡法の開発
Novel 3D Fluorescence Microscopy to Visualize Compartment- and Region-Dependent Biological Phenomena
○大友 康平 [1,2,3]（[1] 順天堂大・医, [2] 自然科学研究機構・生理研, [3] 自然科学研究機構・ExCELLS）
**Kohei Otomo[1,2,3]** ([1]*Sch. Med., Juntendo Univ.*, [2]*NIPS, NINS*, [3]*ExCELLS, NINS*)

おわりに
Closing Remarks

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## 2SFA 力学が生みだす生体秩序
Self-transformation of living systems induced by mechanical forces

共催 学術変革領域研究（A）「生体秩序力学」

オーガナイザー：吉村 成弘（京都大学），柴田 達夫（理化学研究所）
**Organizers: Shige H. Yoshimura (Kyoto Univ.), Tatsuo Shibata (RIKEN)**

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

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

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はじめに
Opening Remarks

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

2SFA-2 CD44 を介した細胞集団内の力学ネットワーク感知と集団運動
CD44-Mediated Mechanical Network Sensing within Cell Populations and Collective Cell Migration
○柴田 桂太朗 [1], 浅野 千帆莉 [1], 石田 紘基 [2], 堀井 拓登 [2], 米村 重信 [1]（[1] 徳島大・院医歯薬学, [2] 徳島大・医学部）
**Keitaro Shibata[1]**, Chihori Asano[1], Koki Ishida[2], Takuto Horii[2], Shigenobu Yonemura[1] ([1]*Grad. Sch. Biomed. Sci., Tokushima Univ.*, [2]*Med. Faculty, Tokushima Univ.*)

2SFA-3 カルマンフィルタで上皮組織の力の時間変化を推定する
Kalman force inference for epithelial deformation: a force inference method for time-lapse movies
○荻田 豪士 [1], 三好 建正 [2], 柴田 達夫 [1]（[1] 理研・BDR, [2] 理研・R-CCS）
**Goshi Ogita[1]**, Takemasa Miyoshi[2], Tatsuo Shibata[1] ([1]*BDR, RIKEN*, [2]*R-CCS, RIKEN*)

2SFA-4 Mechanical Instability Induces Transition in Epithelial Layer Structure via Nucleation and Growth
**Shuya Fukamachi[1]**, Datta Razib[1], Makiko Arai[1], Rei Yagasaki[2], Shuhei Horiguchi[2], Satoru Okuda[2] ([1]*Grad. Sch. NanoLS., Kanazawa Univ*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

2SFA-5 変形可能細胞の数理モデルから迫る，高密度細胞集団動態
Modeling Collective Dynamics in Densely Packed Deformable Cells
○斉藤 稔（広島大・統合生命）
**Nen Saito** (*Grad. Sch. Integr. Sci. Life, Hiroshima Univ.*)

2SFA-6 メカノ勾配による Wnt モルフォゲンノイズ除去システムは組織パターン形成の頑強性を支える
“Mechano-gradients” drive morphogen-noise correction to ensure robust patterning
○青木 佳南, 石谷 太（大阪大・微研・生体統御）
**Kana Aoki**, Tohru Ishitani (*Dept. of Homeostatic regulation, RIMD, Univ. Osaka*)

2SFA-7 軟骨細胞のカラム形成を介して骨形態形成を制御する力学場
Mechanical stress field regulating bone morphogenesis through chondrocyte column formation
○横山 優花 [1], 亀尾 佳貴 [2], 須長 純子 [3], 牧 功一郎 [3,4], 安達 泰治 [3,4]（[1] 東京科学大・難治研, [2] 芝浦工大・工学, [3] 京大・医生研, [4] 京大・工学）
**Yuka Yokoyama[1]**, Yoshitaka Kameo[2], Junko Sunaga[3], Koichiro Maki[3,4], Taiji Adachi[3,4] ([1]*Med. Res. Lab., Science Tokyo*, [2]*Col. Eng., Shibaura Inst. Tech.*, [3]*Inst. Life Med. Sci., Kyoto Univ.*, [4]*Grad. Sch. Eng., Kyoto Univ.*)

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

共催 学術変革領域研究（A）「クラスター細胞学」

オーガナイザー：北村 朗（北海道大学），立川 正志（横浜市立大学）
**Organizers: Akira Kitamura (Hokkaido Univ.), Masashi Tachikawa (Yokohama City Univ.)**

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

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

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はじめに
Opening Remarks

2SGA-1 **走査型蛍光相関分光法により明らかとなったタンパク質凝集体内における低移動性 TDP-25**
Scanning fluorescence correlation spectroscopy reveals slowly mobile TDP-25 within protein aggregates
○濱田 悠太 [1], 北村 朗 [2]（[1] 北大・院生命科学, [2] 北大・院先端生命）
**Yuta Hamada[1]**, Akira Kitamura[2] ([1]*Grad. Sch. Sci. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*)

2SGA-2 **平衡および非平衡条件におけるアミロイド β 凝集の分子動力学シミュレーション**
Molecular dynamics simulation of amyloid-β aggregation under equilibrium and nonequilibrium conditions
○奥村 久士 [1,2,3]（[1] 生命創成探究センター, [2] 分子科学研究所, [3] 総合研究大学院大学）
**Hisashi Okumura[1,2,3]** ([1]*Exploratory Research Center on Life and Living Systems*, [2]*Institute for Molecular Science*, [3]*SOKENDAI*)

2SGA-3 **興奮性シナプス形成の開始誘導：ナノモラー濃度での SynGAP 液状凝縮体形成とそれが誘導する PSD95 と受容体のアセンブリー**
Initiation of excitatory synapse formation: SynGAP LLPS at nanomolar concentrations induces PSD95 and receptor oligomer recruitment
**Saahil Acharya[1]**, Taka A. Tsunoyama[1], Christian Hoffmann[2], Perez Gerard Aguilar[2], Irina Meshcheryakova[1], Aya Nakamura-Norimoto[1], Tara Mastro[3], Ward G. Walkup IV[3], Takahiro Fujiwara[4], Mary B. Kennedy[3], Dragomir Milovanovic[2], Akihiro Kusumi[1,4] ([1]*Membrane Cooperativity Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan*, [2]*Laboratory of Molecular Neuroscience, German Center for Neurodegenerative Diseases (DZNE), Berlin, Germany*, [3]*Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, California, U.S.A.*, [4]*Institute for Integrated Cell-Material Sciences (WPI-iCeMS), Kyoto University, Kyoto, Japan.*)

2SGA-4 トランスクリプトームおよび画像解析による枯草菌の遊走コロニーの時空間プロファイリング
Multimodal Spatiotemporal Profiling of *Bacillus subtilis* Swarm Development via Integrated Transcriptomics and Microscopy

○納庄 一樹 [1,2,3], Jeckel Hannah[3], Neuhaus Konstantin[3], Hastewell Alasdair[4], Skinner Dominic[4], Saha Dibya[3], Netter Niklas[3], Paczia Nicole[5], Dunkel Jörn[4], Drescher Knut[3]（[1] 東京大学 大学院農学生命科学研究科 応用生命工学専攻, [2] 東京大学 微生物科学イノベーション連携研究機構, [3] バーゼル大学 バイオセンター, [4] マサチューセッツ工科大学 数学科, [5] マックスプランク陸生微生物学研究所）

**Kazuki Nosho[1,2,3]**, Hannah Jeckel[3], Konstantin Neuhaus[3], Alasdair Hastewell[4], Dominic Skinner[4], Dibya Saha[3], Niklas Netter[3], Nicole Paczia[5], Jörn Dunkel[4], Knut Drescher[3] ([1]*Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo*, [2]*Collaborative Research Institute for Innovative Microbiology, The University of Tokyo*, [3]*Biozentrum, University of Basel*, [4]*Department of Mathematics, Massachusetts Institute of Technology*, [5]*Max Planck Institute for Terrestrial Microbiology*)

2SGA-5 上皮の細胞間接着形成過程におけるダイナミクス
Dynamic processes of cell-cell adhesion in epithelial cells

○小田 裕香子（京都大学）
**Yukako Oda** (*Kyoto University*)

2SGA-6 クライオ光電子相関顕微鏡の開発と現在の状況
Development and Current Status of Cryogenic Correlative Light and Electron Microscopy

○藤芳 暁（Science Tokyo 物理）
**Satoru Fujiyoshi** (*Dept. Phys., Science Tokyo*)

おわりに
Closing Remarks

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2SHA 鏡像生命の創成：創れるのか，創ってよいのか，創ってどうするのか？
Mirror-Life Synthesis: Its Possibility, Potential, and Problems

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

オーガナイザー：藤原 慶（慶應義塾大学），青木 航（大阪大学）
**Organizers: Kei Fujiwara (Keio Univ.), Wataru Aoki (The Univ. of Osaka)**

09:00〜11:30
H 会場（会議室 204）／Room H（Meeting Room 204）

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

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はじめに
Opening Remarks

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

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

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

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

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

おわりに
Closing Remarks

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2SIA 蛋白質液–液相分離の設計と制御
Design and control of liquid–liquid phase separation of proteins

**オーガナイザー：池田 恵介（富山大学），鎌形 清人（岐阜大学）**
**Organizers: Keisuke Ikeda (Univ. of Toyama), Kiyoto Kamagata (Gifu Univ.)**

09:00〜11:30
I 会場（会議室 205）／Room I（Meeting Room 205）

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

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

2SIA-2 ペプチドによる α-シヌクレインの液-液相分離誘導と物性制御
Peptide-Mediated Modulation of α-Synuclein Liquid–Liquid Phase Separation and Its Biophysical Properties
○池之上 達哉（大阪大・蛋白研）
**Tatsuya Ikenoue** (*IPR, Univ. Osaka*)

2SIA-3 酵母プリオン Sup35 配列由来のデザインタンパク質を用いた液-液相分離に影響を及ぼすアミノ酸の解析
Analysis of amino acids affecting liquid-liquid phase separation using a design protein based on the yeast prion Sup35 sequence
○大橋 祐美子 [1], 高畠 晴 [2], 田口 英樹 [1,2]（[1] 科学大・研究院・細胞センター, [2] 科学大・生命理工）
**Yumiko Ohhashi[1]**, Haru Takabatake[2], Hideki Taguchi[1,2] ([1]*CBC, IIR, Science Tokyo*, [2]*Sch. of Life Sci. Tech, Science Tokyo*)

2SIA-4 ALS 関連 FUS 変異体の相挙動に対する圧力・温度および低分子の影響
Effects of pressure, temperature, and small molecules on phase behavior of amyotrophic lateral sclerosis-linked FUS variants
○北原 亮 [1,2]（[1] 立命館大・薬, [2] 立命館大・院薬）
**Ryo Kitahara[1,2]** ([1]*Coll. Pharm. Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Pharm., Ritsumeikan Univ.*)

2SIA-5 タンパク質液滴を測り，操り，創る
Watching, manipulating, and creating protein droplets
○鎌形 清人（岐阜大・工・化学生命工）
**Kiyoto Kamagata** (*Fac. Eng. & Grad. Sch. Eng., Gifu Univ.*)

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## 2SJA 古くて新しいロドプシン研究最前線
Cutting Edge of Rhodopsin Research ~Where Tradition Meets Innovation~

オーガナイザー：片山 耕大（名古屋工業大学），加藤 英明（東京大学）
**Organizers: Kota Katayama (Nagoya Inst. of Tech.), Hideaki Kato (The Univ. of Tokyo)**

09:00〜11:30
J 会場（会議室 206）／Room J（Meeting Room 206）

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

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はじめに
Opening Remarks

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

2SJA-2 光駆動プロトンポンプロドプシンの新たな視点：プロトン輸送メカニズムとその方向性
New Insights into Light-Driven Proton Pump Rhodopsins: Proton Transfer Mechanism and Directionality
○潤井 泰斗（阪大院理）
**Taito Urui** (*Grad. Sch. Sci., Univ. Osaka*)

2SJA-3 ウイルスヘリオロドプシン V2HeR3 のプロトン輸送メカニズム
Mechanism of Proton Transport in the Viral Heliorhodopsin V2HeR3
○水鳥 律 [1], Nuemket Nipawan[2,3], Fangjia Luo[3], 細島 頌子 [1,5], D'Ascenzi Jacopo[4], Oliveira Leonardo[4], 大橋 沙也佳 [1], 吉住 玲 [1], Palombo Riccardo[4], 角田 聡 [1,5], 古谷 祐詞 [1,5], Béjà Oded[6], Olivucci Massimo[4,7], 南後 恵理子 [3,8], 片山 耕大 [1,5], 神取 秀樹 [1,5]（[1] 名工大・院工, [2] 高輝度光科学研究センター, [3] 理研・SPring-8, [4]Univ. Siena, [5] 名工大・オプトバイオ, [6]Technion-Israel Inst. Tech., [7]Bowling Green State Univ., [8] 東北大・多元物質科学研究所）
**Ritsu Mizutori[1]**, Nipawan Nuemket[2,3], Luo Fangjia[3], Shoko Hososhima[1,5], Jacopo D'Ascenzi[4], Leonardo Oliveira[4], Sayaka Ohashi[1], Rei Abe-Yoshizumi[1], Riccardo Palombo[4], Satoshi Tsunoda[1,5], Yuji Furutani[1,5], Oded Béjà[6], Massimo Olivucci[4,7], Eriko Nango[3,8], Kota Katayama[1,5], Hideki Kandori[1,5] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Japan Synchrotron Radiation Research. Inst.*, [3]*RIKEN SPring-8*, [4]*Univ. Siena*, [5]*OptoBioTechnology Research Cent.*, [6]*Technion-Israel Inst. Tech.*, [7]*Bowling Green State Univ.*, [8]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku Univ.*)

2SJA-4 光応答性神経による括約筋の制御と貫通型消化管の進化的起源
Light-modulated neural control of sphincter regulation in the evolution of through-gut
Junko Yaguchi[1], Kazumi Sakai[2], Atsushi Horiuchi[2], Takashi Yamamoto[3], Takahiro Yamashita[2], **Shunsuke Yaguchi[1]** ([1]*SMRC, Univ. Tsukuba*, [2]*Grad. Sch. Sci., Univ. Kyoto*, [3]*Genom. Edit. Innov. Cent., Hiroshima Univ.*)

2SJA-5 メダカでは脳下垂体に発現する光受容体が紫外線受容によって色素沈着促進ホルモンの分泌を誘導する
A Photoreceptor Expressed in Pituitary Endocrine Cells Mediates UV-Induced Hormone Release That Enhances Pigmentation in Medaka
○神田 真司 [1], 福田 彩華 [1,2], 佐藤 恵太 [3] ([1] 東京大学大気海洋研究所, [2] 基礎生物学研究所神経行動学研究部門, [3] 岡山大学医歯薬学総合研究科）
**Sinji Kanda[1]**, Ayaka Fukuda[1,2], Keita Sato[3] ([1]*Atmosphere and Ocean Research Institute, The University of Tokyo*, [2]*Division of Behavioral Neurobiology, National Institute for Basic Biology*, [3]*Faculty of Medicine, Dentistry, and Pharmaceutical Sciences, Okayama University*)

おわりに
Closing Remarks

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2SKA 日韓二国間シンポジウム： 拡大する日韓生物物理研究のフロンティア
Korea-Japan Bilateral Symposium: Expanding Frontiers of Biophysics in Two Countries

オーガナイザー：髙橋 聡（東北大学），Young-Ho Lee（Korea Basic Sci. Inst.）
**Organizers: Satoshi Takahashi (Tohoku Univ.), Young-Ho Lee (Korea Basic Sci. Inst.)**

09:00〜11:30
K 会場（天平ホール）／Room K（Tempyo Hall）

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

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はじめに
Opening Remarks

2SKA-1 Assessing druggability based on the structural features of human leucyl-tRNA synthetase 2
Seonha Park[1], Byeongmin Shin[1], Ingyo Park[1], Kyuhyeon Bang[1], Sulhee Kim[1], Ina Yoon[2], **Kwang Yeon Hwang[1]** ([1]*Departrment of Biotechnology, Korea University*, [2]*College of Pharmarcy, Yonsei University*)

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

2SKA-3 Accurate Conformational Ensembles of Intrinsically Disordered Proteins using Reweighting based on NMR Chemical Shift
Juhyeong Jeon[1], Wonjin Yang[1], Jin Hae Kim[2], Young-Ho Lee[3], **Wookyung Yu[1]** ([1]*Department of Brain Sciences, DGIST, Deagu, Republic of Korea*, [2]*Department of New Biology, DGIST, Daegu, Republic of Korea*, [3]*Research Center for Bioconvergence Analysis, Korea Basic Science Institute, Republic of Korea*)

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

2SKA-5 Cellular Mechanobiology in Phagocytosis
Min Chanhyuk[1], Cho Hyeokjin[2], Yu Jeongmin[1], Park Daeho[2], **Lee Gwangrog[1]** ([1]*Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST)*, [2]*School of Life Sciences, Gwangju Institute of Science and Technology (GIST)*)

2SKA-6 Direct Visualization of Dynamics in Prokaryotic Motility Machinery
**Takayuki Nishizaka[1]**, Masaki Mizutani[1], Daisuke Nakane[2] ([1]*Gakushuin Univ.*, [2]*Univ. Electro-Communications*)

おわりに
Closing Remarks

2SAP　エピゲノブリッジ: クロマチン構造形成におけるエピゲノムの役割とその複製機構の分子・細胞スケールに渡る理解

EpigenoBridge: Toward Understanding the Epigenome's Role in Chromatin Structure Formation and Replication Mechanisms from the Molecular to the Cellular Scale

共催 学術変革領域研究（B）「エピゲノブリッジ」

オーガナイザー：角南 智子（QST），寺川 剛（京都大学）

**Organizers: Tomoko Sunami (QST), Tsuyoshi Terakawa (Kyoto Univ.)**

16:15〜18:45

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

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

はじめに

Opening Remarks

2SAP-1　クロマチン構造の力学的解析：分子夾雑とエピゲノム継承の分子機構の理解に向けて

Mechanical Analysis of Chromatin by Optical Tweezers: Molecular Crowding and Inheritance of Epigenome

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

**Tomoko Sunami[1]**, Amarjeet Kumar[1], Kohji Hizume[2], Hidetoshi Kono[1,3] ([1]*iQLS, QST*, [2]*BRC, Med, Saitama Med U*, [3]*cQUEST, Chiba U*)

2SAP-2　Structure and dynamics of reconstituted chromatin with defined histone modification patterns

Yohsuke T Fukai[1], **Kyogo Kawaguchi[1,2]** ([1]*RIKEN PRI*, [2]*Institute for Physics of Intelligence, Department of Physics, The University of Tokyo*)

2SAP-3　Cryo-EM analysis of basic chromatin architectures isolated from cells

**Yoshimasa Takizawa[1,2]**, Haotong Zhuang[1,2], Takuro Shioi[1,3], Suguru Hatazawa[1], Yuki Kobayashi[1], Mitsuo Ogasawara[1], Yasuyuki Ohkawa[4], Hitoshi Kurumizaka[1,3,4] ([1]*IQB, Univ.Tokyo*, [2]*Grad. Sch. Fro. Sci., Univ.Tokyo*, [3]*Grad. Sch. Sci., Univ. Tokyo*, [4]*MIB, Kyushu Univ.*)

2SAP-4　化学触媒によるエピゲノム改変技術の開発

Development of epigenome modification technology by chemical catalysis

○川島 茂裕（東京大学大学院薬学系研究科）

**Shigehiro Kawashima** (*Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

2SAP-5 **複製依存的ヒストン標識（Repli-Histo 標識）を用いて明らかにする，ヒト生細胞内のユークロマチン・ヘテロクロマチンのふるまい**
Replication-dependent histone (Repli-Histo) labeling dissects the physical properties of euchromatin/heterochromatin in living human cells
○南 克彦 [1,2], 仲里 佳子 [1,2], 井手 聖 [1,2], 海津 一成 [3,4], 東 光一 [2,5], 田村 佐知子 [1], 豊田 敦 [6], 高橋 恒一 [3], 黒川 顕 [2,5], 前島 一博 [1,2]（[1] 遺伝研・ゲノムダイナミクス研究室, [2] 総研大・先端学術院, [3] 理研 BDR・バイオコンピューティング研究チーム, [4] 生命創成研究センター・細胞シミュレーション研究グループ, [5] 遺伝研・ゲノム進化研究室, [6] 遺伝研・先端ゲノミクス支援センター）
**Katsuhiko Minami[1,2]**, Kako Nakazato[1,2], Satoru Ide[1,2], Kazunari Kaizu[3,4], Koichi Higashi[2,5], Sachiko Tamura[1], Atsushi Toyoda[6], Koichi Takahashi[3], Ken Kurokawa[2,5], Kazuhiro Maeshima[1,2] ([1]*Genome Dynamics Laboratory, NIG*, [2]*SOKENDAI*, [3]*Laboratory for Biologically Inspired Computing, RIKEN BDR*, [4]*Cell Modeling and Simulation Group, ExCELLS*, [5]*Genome Evolution Laboratory, NIG*, [6]*Comparative Genomics Laboratory, NIG*)

**おわりに**
Closing Remarks

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## 2SBP 動的溶液環境の観点から紐解く生体分子凝縮体
Understanding Biomolecular Condensation from the Perspective of Dynamic Solution Environments

**オーガナイザー：関山 直孝（京都大学），中村 秀樹（京都大学）**
**Organizers: Naotaka Sekiyama (Kyoto Univ.), Hideki Nakamura (Kyoto Univ.)**

16:15〜18:45
B 会場（会議室 103+104）／Room B（Meeting Room 103+104）

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

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2SBP-1 **シナプス後肥厚タンパク質のリン酸化による凝縮体および受容体集合への影響：分子シミュレーションによる検討**
Effects of phosphorylation of postsynaptic density proteins on condensates and receptor assembly studied by molecular simulations
○山田 莉彩, 高田 彰二（京大・理・生物物理）
**Risa Yamada**, Shoji Takada (*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)

2SBP-2 Single-Molecule Studies of how Mug20-Rec25-Rec27 (MRR) Complex Mediates DNA Conformational Change and Biomolecular Condensates Formation
**Hung-Wen Li[1]**, Chieh-Yu Tsai[1], Feng-Yu Wang[2], Ya-Ching Yang[2], Ya-Chen Gong[3], Shyh-Chyang Luo[3], Peter Chi[2] ([1]*Dept. Chemistry, National Taiwan Univ.*, [2]*Inst. Biochem. Sci., National Taiwan Univ.*, [3]*Dept. Materials Sci. Eng., National Taiwan Univ.*)

2SBP-3 **液体の積分方程式理論を用いた 4 残基ペプチドデータベースの構築**
A Comprehensive Tetrapeptide Database Using Integral Equation Theory of Liquid
○金丸 恒大 [1,2], 吉田 紀生 [2]（[1] 京大・福井セ, [2] 名大・院情報）
**Kodai Kanemaru[1,2]**, Norio Yoshida[2] ([1]*FIFC, Kyoto Univ.*, [2]*Dept. Complex Syst. Sci., Grad. Sch. Informatics, Nagoya Univ.*)

2SBP-4 アミロイド多型とその形成メカニズム
Amyloid polymorphism and formation mechanisms
○宗 正智, 菅瀬 謙治（京大・院農）
**Masatomo So**, Kenji Sugase (*Grad. Sch. Agric., Kyoto Univ.*)

2SBP-5 動的溶液環境におけるアミロイドβタンパク質の分子集合
Molecular assembly of amyloid-β proteins in dynamic solution environments
○矢木 真穂 [1,2]（[1] 名市大・院薬, [2] 自然科学研究機構・生命創成探究セ）
**Maho Yagi-Utsumi**[1,2] ([1]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [2]*ExCELLS, Natl. Inst. Nat. Sci.*)

2SBP-6 動的細胞内環境における機能性アミロイド線維の可能性の探索
Investigating Neuronal Amyloid Fibrils with Potential Functional Roles in a Dynamic Intracellular Environment
○杉江 淳 [1], 小坂 二郎 [2]（[1] 京都工芸繊維大学, [2] 東京科学大学）
**Atsushi Sugie**[1], Jiro Osaka[2] ([1]*Kyoto Institute of Technology*, [2]*Institute of Science Tokyo*)

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## 2SCP 重力場における生命の適応進化戦略「細胞骨格ダイナミクス」「ホメオスタシス」から超高齢社会のQOLを考える～自己組織化・分子シャペロン・Hippo経路・可視化と意識的活動

Adaptive Evolutionary Strategy of Life in a Gravitational Field "Cytoskeletal Dynamics" ,"Mechanical Homeostasis" for Quality of Life in a Super-aging Society - Self-organization, Molecular Chaperones, Hippo Pathway, Visualization and Conscious Activity

**オーガナイザー：跡見 順子（帝京大学），井上 大介（九州大学）**
**Organizers: Yoriko Atomi (Teikyo Univ.), Daisuke Inoue (Kyushu Univ.)**

16:15～18:45
C 会場（会議室 105+106）／Room C（Meeting Room 105+106）

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

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はじめに
Opening Remarks

2SCP-1 微小管ダイナミックインスタビリティ 3.1：高精度多次元解析がもたらした意外な高次機能の発見
Microtubule Dynamic Instability 3.1: From Imaging to Insight into Hidden Functions
○清末 優子（関西医科大学 附属生命医学研究所 分子遺伝学部門）
**Yuko Mimori-Kiyosue** (*Department of Molecular Genetics, Institute of Biomedical Science, Kansai Medical University*)

2SCP-2 The Timing of the Acquisition of Eukaryotic Traits during Eukaryogenesis
**Robert Charles Robinson** (*Vidyasirimedhi Institute of Science and Technology (VISTEC) Thailand*)

2SCP-3 αB-クリスタリン，チューブリン/微小管のメカノシャペロン：階層的自己組織化とヒト特異性を活用した QOL 戦略
αB-Crystallin, mechanochaperon for tubulin/microtubule: A QOL strategy that utilizes hierarchical self-organization and human specificity
○跡見 順子（帝京大学先端総合研究機構）
**Yoriko Atomi** (*Teikyo University, ACRO*)

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

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

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

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

おわりに
Closing Remarks

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

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

16:15〜18:45
D 会場（会議室 107+108）／Room D（Meeting Room 107+108）

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

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はじめに
Opening Remarks

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

2SDP-2 線虫の全脳活動計測と遺伝子発現解析
Whole brain activity measurement and gene expression analysis of neurons in *Caenorhabditis elegans*
○豊島 有 [1,2], 飯野 雄一 [1], 楊 暁雄 [2]（[1] 東大・院理・生物科学, [2] 東大・新領域・メディカル情報生命）
**Yu Toyoshima[1,2]**, Yuichi Iino[1], Xiaoxiong Yang[2] ([1]*Grad. Sch. of Sci., Univ. of Tokyo*, [2]*Grad. Sch. of Front. Sci., Univ. of Tokyo*)

2SDP-3 Unraveling the Mechanisms of Collective Cell Migration in Epithelial Morphogenesis
**Erina Kuranaga[1,2]** ([1]*Grad Sch Pharmaceu Sci, Kyoto Univ*, [2]*Grad Sch Life Sci, Tohoku Univ*)

2SDP-4 生きた動物内で標的 GPCR を細胞種選択的に制御する化学遺伝学的アプローチ
Chemogenetic strategy for controlling target GPCRs in a cell-type-specific manner in vivo
○清中 茂樹（名大・院工）
**Shigeki Kiyonaka** (*Grad. Sch. Eng., Nagoya Univ.*)

2SDP-5 Functional Raman probes for multiplexed vibrational imaging
**Mako Kamiya** (*CLS, Science Tokyo*)

おわりに
Closing Remarks

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## 2SEP 生物物理からのアクティブマターへのアプローチ
Approaching Active Matter from Biophysics Perspective

オーガナイザー：川又 生吹（京都大学），早川 雅之（京都工芸繊維大学）
**Organizers: Ibuki Kawamata (Kyoto Univ.), Masayuki Hayakawa (Kyoto Institute of Technology)**

16:15〜18:45
E 会場（会議室 201）／Room E（Meeting Room 201）

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

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2SEP-1 アクティブに推進する生体分子エージェントとプログラムされた DNA 化学反応ネットワークの統合
Actively Gliding Biomolecular Agents Integrated with Programmed DNA Chemical Reaction Network
○川又 生吹（京都大学）
**Ibuki Kawamata** (*Kyoto University*)

2SEP-2 光照射で駆動される DNA 流体による生命的な動き
Life-like motion of active DNA fluid driven by photo-irradiation
○鵜殿 寛岳 [1], 野村 M. 慎一郎 [2], 瀧ノ上 正浩 [1]（[1] 東京科学大学 情報理工学院, [2] 東北大学大学院工学研究科 ロボティクス専攻）
**Hirotake Udono[1]**, M. Shin-ichiro Nomura[2], Takinoue Masahiro[1] ([1]*Dept. Comp. Sci., Institute of Science Tokyo*, [2]*Dept. Robotics, Sch. Eng., Tohoku University*)

2SEP-3 **完全な運動一方向性のための DNA 人工分子モーターの構造改変**
Geometry engineering of DNA artificial molecular motor for perfect unidirectionality
○原島 崇徳 [1,2], 飯野 亮太 [1,2]（[1] 分子科学研究所, [2] 総合研究大学院大学）
**Takanori Harashima[1,2]**, Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*Graduate Institute for Advanced Studies, SOKENDAI*)

2SEP-4 **非生物由来分子システムの自律的回帰性が駆動する生命性**
"Life" Actuated by Autonoumous Recursion of Non-Biological Molecular Systems
○松尾 宗征 [1,2]（[1] 広島大学, [2] 東京大学）
**Muneyuki Matsuo[1,2]** ([1]*Hiroshima University*, [2]*The University of Tokyo*)

2SEP-5 **アクティブマター研究としての単細胞の重力生物学**
Gravitational biology of unicellular organisms as active matter research
○鹿毛 あずさ（室蘭工業大学）
**Azusa Kage** (*Muroran Institute of Technology*)

2SEP-6 **磁場による遊泳バクテリア集団の秩序形成制御**
Magnetically controlled self-organization of swimming bacteria
**Kazusa Beppu[1]**, Joakim Stenhammar[2], Jaakko V. I. Timonen[3] ([1]*Dept. of Chem. Eng., Kyoto Univ.*, [2]*Div. of Phys. Chem., Lund Univ.*, [3]*Dept. of Appl. Phys., Aalto Univ. Sch. of Sci.*)

2SEP-7 **走化性を示さない細胞性粘菌にみられる集団運動**
Self-organized collective dynamics in *Dictyostelium* cells lacking chemotaxis
○早川 雅之 [1,2], Bhattacherjee Biplab[2], 桑山 秀一 [3], 柴田 達夫 [2]（[1] 京都工芸繊維大学・機械工学系, [2] 理研・生命機能科学研究センター, [3] 筑波大学・生命環境系）
**Masayuki Hayakawa[1,2]**, Biplab Bhattacherjee[2], Hidekazu Kuwayama[3], Tatsuo Shibata[2] ([1]*Dept. of Mech. Eng., Kyoto Institute of Technology*, [2]*RIKEN BDR*, [3]*Life Environ. Sci., Univ. Tsukuba*)

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2SFP **スーパーコンピュータ「富岳」による創薬と医療の促進**
Advancing drug discovery and healthcare through supercomputer Fugaku

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

オーガナイザー：荒木 望嗣（京都大学），寺山 慧（横浜市立大学）
**Organizers: Mitsugu Araki (Kyoto Univ.), Kei Terayama (Yokohama City Univ.)**

16:15〜18:45
F 会場（会議室 202）／Room F（Meeting Room 202）

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

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はじめに
Opening Remarks

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

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

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

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

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

2SFP-6 Enhancing Antibody Engineering with Automated Molecular Interaction Descriptors and Structure Modeling
**Shuntaro Chiba[1]**, Tsutomu Yamane[1], Yasushi Okuno[1,2], Mitsunori Ikeguchi[1,3], Masateru Ohta[1] ([1]*R-CCS, RIKEN*, [2]*Grad. Sch. Med., Kyoto Univ.*, [3]*Grad. Sch. Med. Life Sci., YCU*)

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

おわりに
Closing Remarks

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

共催 学術変革領域研究（A）「光合成ユビキティ」

オーガナイザー：斉藤 圭亮（東京大学），白井 剛（長浜バイオ大学）
**Organizers: Keisuke Saito (The Univ. of Tokyo), Tsuyoshi Shirai (Nagahama Inst. of Bio-Sci. Tech.)**

16:15〜18:45
G 会場（会議室 203）／Room G（Meeting Room 203）

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

はじめに
Opening Remarks

2SGP-1　暗所従属栄養条件でのシアノバクテリアの微小進化
Microevolution of cyanobacteria in the dark heterotrophic conditions
○藤田 祐一（名古屋大・院生命農）
**Yuichi Fujita** (*Grad. Sch. Bioagricultural Sci., Nagoya Univ.*)

2SGP-2　緑色硫黄細菌で見つかった嫌気的な非光化学的消光：その反応機構と生理的意義
Anaerobic non-photochemical quenching of photosynthetic green sulfur bacteria: Its reaction mechanism and physiological significance
○浅井 智広（中央大・理工）
**Chihiro Azai** (*Fac. Sci. & Eng., Chuo Univ.*)

2SGP-3　時間分解蛍光分光法による光合成色素–タンパク質複合体の機能解明
Functions of photosynthetic pigment-protein complexes, revealed by time-resolved fluorescence spectroscopy
○秋本 誠志（神戸大・院理）
**Seiji Akimoto** (*Grad. Sch. Sci., Kobe Univ.*)

2SGP-4　光合成タンパク質の分子構造と理論構造をつなぐ磁気構造
Linkage of the molecular and theoretical structures of photosynthetic proteins using magnetic spin configurations
○三野 広幸（名古屋大学・院理）
**Hiroyuki Mino** (*Grad. Sch. Sci., Nagoya Univ.*)

2SGP-5　光捕集複合体の構造に基づいた海洋性大型緑藻のカルボニルカロテノイドによる緑色光吸収の分子メカニズム
Mechanism of green light absorption by carbonyl carotenoids of marine macroalgae based on the structure of light-harvesting complexes
○藤井 律子 [1,2]（[1] 大阪公立大学人工光合成研究センター, [2] 大阪公立大学理学研究科化学専攻）
**Ritsuko Fujii[1,2]** ([1]*Research Center for Artificial Photosynthesis, Osaka Metropolitan University*, [2]*Department of Chemistry, Graduate School of Science, Osaka Metropolitan University*)

2SGP-6 光合成アンテナのデザインを目指して：in vitro 再構成光合成アンテナの構造解析
Toward the design of photosynthetic antennas: structural determination of in vitro reconstituted light-harvesting complex
○関 荘一郎 [1], 川本 晃大 [1,2], 宮田 知子 [3,4], 難波 啓一 [3,4], 藤井 律子 [5], 栗栖 源嗣 [1,2,4]（[1] 阪大・蛋白研, [2] 阪大・OTRI, [3] 阪大・生命機能, [4] 阪大・日本電子 YOKOGUSHI 協働研, [5] 阪公大・人工光合成研究センター）
**Soichiro Seki[1]**, Akihiro Kawamoto[1,2], Tomoko Miyata[3,4], Keiichi Namba[3,4], Ritsuko Fujii[5], Genji Kurisu[1,2,4] ([1]*IPR, Osaka Univ.*, [2]*OTRI, Osaka Univ.*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [4]*JEOL YOKOGUSHI Res. Alliance Labs., Osaka Univ.*, [5]*ReCAP, Osaka Metropol. Univ.*)

2SGP-7 光センサータンパク質 RcaE における「水素結合のアクセプター」となるリシン
Deprotonated Lysine Serving as a “H-bond acceptor” in the Photoreceptor Protein RcaE
○三島 正規（東京薬科大・薬学）
**Masaki Misima** (*Sch. Pharm., Tokyo Univ. Pharm. and Life Sci.*)

2SGP-8 AlphaFold と MD シミュレーションを活用したオートファジー駆動機構の解明
Elucidating the mechanism of autophagy utilizing AlphaFold prediction and MD simulations
○野田 展生 [1,2]（[1] 北大・遺制研, [2] 微化研）
**Nobuo N. Noda[1,2]** ([1]*IGM, Hokkaido Univ.*, [2]*Inst. Microbial Chem.*)

おわりに
Closing Remarks

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

共催 学術変革領域研究（A）「クロススケール新生物学」

オーガナイザー：西田 紀貴（千葉大学），笠原 健人（大阪大学）
**Organizers: Noritaka Nishida (Chiba Univ.), Kento Kasahara (The Univ. of Osaka)**

16:15〜18:45
H 会場（会議室 204）／Room H（Meeting Room 204）

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

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

2SHP-2 統合的時分割構造解析で捉えるシャペロンのフォールディング制御における速度論的特性
Kinetic Insights into Chaperone-Mediated Protein Folding from Integrative, Dynamic Structural Biology
○熊代 宗弘 [1], 久米田 博之 [2], 齋尾 智英 [1]（[1] 徳大・酵素研, [2] 北大・先端生命）
**Munehiro Kumashiro[1]**, Hiroyuki Kumeta[2], Tomohide Saio[1] ([1]*Inst. Adv. Med. Sci., Tokushima Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

2SHP-3 Modulation of Structure and Dynamics in Biomolecular Condensates Revealed by Large-Scale Molecular Dynamics Simulations
**Cheng Tan**, Yuji Sugita (*RIKEN Center for Computational Science*)

2SHP-4 PROTAC-induced Protein Structural Dynamics in Targeted Protein Degradation
**Chia-en Chang**, Kingsley Wu, Ta I David Tang (*University of California, Riverside*)

2SHP-5 Elucidation of the regulation of the Rac1/Cdc42 guanine nucleotide exchange factor DOCK6
**Mutsuko Kukimoto-Niino** (*RIKEN, Yokohama*)

2SHP-6 カーゴ受容体 ERGIC-53 によるカーゴ輸送のクライオ電顕構造解析
Cryo-EM analysis of cargo transport and release by a cargo receptor ERGIC-53
○渡部 聡, 本城 恵美, 稲葉 謙次（九大・生医研）
**Satoshi Watanabe**, Emi Honjo, Kenji Inaba (*MIB, Kyushu Univ*)

2SHP-7 高速 AFM と cryo-EM による，CAMSAP2 によって誘導される微小管およびアスター構造形成過程の直接観察
Direct observation of CAMSAP2-induced microtubule and aster formation processes using high-speed AFM and cryo-EM
**Tsuyoshi Imasaki[1]**, Ayhan Yurtsever[2], Ryota Kitano[1], Kien Xuan Ngo[2], Takaaki Kato[1], Hanjin Liu[1], Hideki Shigematsu[3], Takeshi Fukuma[2], Ryo Nitta[1] ([1]*Kobe University Graduate School of Medicine*, [2]*WPI-NanoLSI*, [3]*JASRI*)

おわりに
Closing Remarks

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2SIP 複雑な細胞機能を解き明かす：メカニズム解明と技術革新
Deciphering complex cellular functions: Mechanistic insights and technological innovations

オーガナイザー：出口 真次（大阪大学），木戸秋 悟（九州大学）
**Organizers: Shinji Deguchi (The Univ. of Osaka), Satoru Kidoaki (Kyushu Univ.)**

16:15〜18:45
I 会場（会議室 205）／Room I（Meeting Room 205）

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

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はじめに
Opening Remarks

2SIP-1 ミスセンス変異モータータンパク質の機能評価に向けた力計測アプローチ
Functional Assessment of Missense Mutations in Motor Proteins via Force Measurements
○林 久美子（東大・物性研）
**Kumiko Hayashi** (*ISSP, Univ. Tokyo*)

2SIP-2 Mechanisms of intracellular force transmission revealed by coiled-coil mechano-sensors
**Takumi Saito** (*Grad. Sch. of Engineering Science, The University of Osaka*)

2SIP-3 Alternative Force Transmission Mechanisms at Adherens Junctions with Potential Roles in Cancer Progression
**Cristina Bertocchi[1,2]** ([1]*Pontificia Universidad Católica de Chile*, [2]*The University of Osaka*)

2SIP-4 A molecular basis for neuronal migration in confined spaces
**Naotaka Nakazawa** (*Kindai University*)

2SIP-5 突起形成による力不均衡がもたらすグリオーマの移動極性
Migratory polarity emerges from protrusion-mediated force imbalance in glioma cells
○作村 諭一[1,2], 田川 晴奈[2], 兼松 大介[3], 勝間 亜沙子[2,3], 稲垣 直之[2], 金村 米博[3]（[1] 奈良先端大・DSC, [2] 奈良先端大・先端科学技術, [3] 大阪医療センター）
**Yuichi Sakumura[1,2]**, Haruna Tagawa[2], Daisuke Kanematsu[3], Asako Katsuma[2,3], Naoyuki Inagaki[2], Yonehiro Kanemura[3] ([1]*Data Science Center, Nara Inst. of Sci. and Tech.*, [2]*Grad. Sch. Sci. and Tech., Nara Inst. of Sci. and Tech.*, [3]*NHO Osaka National Hospital*)

2SIP-6 運動する細胞の応力ゆらぎ操作と計測
Dynamic Control and Analysis of Intracellular Stress Fluctuations during Cell Migration
○木戸秋 悟（九大・先導研）
**Satoru Kidoaki** (*IMCE, Kyushu Univ.*)

2SIP-7 細胞内の中間スケールにおけるゆらぎ駆動力の定量解析
Probing mesoscale physical forces in cells
○出口 真次[1,2], 上田 唯花[1]（[1] 阪大・基礎工, [2] 阪大・国際医工情報センター）
**Shinji Deguchi[1,2]**, Yuika Ueda[1] ([1]*Grad Sch Eng Sci, Univ Osaka*, [2]*MEI-Center, Univ Osaka*)

おわりに
Closing Remarks

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2SJP 日豪台三国間シンポジウム: 量子生命科学による最先端生体計測の新展開(国際量子科学技術年記念シンポジウム)
Japan-Australia-Taiwan Trilateral Symposium: New Frontiers in Biological Measurement Enabled by Quantum Life Science (International Quantum Science and Technology Year Commemorative Symposium)

オーガナイザー：石綿 整（QST），David Simpson（The Univ. of Melbourne）
**Organizers: Hitoshi Ishiwata (QST), David Simpson (The Univ. of Melbourne)**

16:15〜18:45
J 会場（会議室 206）／Room J（Meeting Room 206）

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

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はじめに
Opening Remarks

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

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

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

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

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

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

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## 2SKP 人工細胞そして生命ー非生命の境界
Artificial cell and boundary between living and non-living matters

共催 JST CREST「ゲノム合成」

**オーガナイザー：野地 博行（東京大学），市橋 伯一（東京大学）**
**Organizers: Hiroyuki Noji (The Univ. of Tokyo), Norikazu Ichihashi (The Univ. of Tokyo)**

16:15〜18:45
K 会場（天平ホール）／Room K（Tempyo Hall）

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

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はじめに
Opening Remarks

2SKP-1 小さいゲノムを持つ微生物から見る生命と非生命の境界
The Boundary Between Life and Non-Life Seen in Microorganisms with Small Genomes
○鈴木 志野（理研・開拓研究所）
**Shino Suzuki** (*PRI, RIKEN*)

2SKP-2 ヌクレオサイトウイルス門の巨大ウイルスによる感染細胞に対する思いもよらぬ影響について
Giant viruses of the Phylum Nucleocytoviricota induce unexpected behaviors in infected host cells
○武村 政春, ペ ジワン（東京理科大・院理）
**Masaharu Takemura**, Jiwan Bae (*Grad. Sch. Sci., Tokyo Univ. Sci.*)

2SKP-3 Artificial cells with dissipative structures
**Sakura Takada**, Kei Fujiwara (*Dept. of Biosci. and Info., Keio Univ.*)

2SKP-4 LLPS ドロプレットを用いた自律成長型人工細胞モデル
Artificial protocell models based on LLPS droplet
○野地 博行, 皆川 慶嘉（東京大学）
**Hiroyuki Noji**, Yoshihiro Minagawa (*University of Tokyo*)

2SKP-5 生物みたいに自己再生産できる人工システムを作りたい：現状と展望
Toward a self-regenerative in vitro central dogma; progress and future
○市橋 伯一（東大総合文化）
**Norikazu Ichihashi** (*Grad. Sch. Arts Sci. Univ. Tokyo*)

2SKP-6 動的な人工細胞のための核酸ベースの知的な凝集体
Nucleic Acid-based Smart Condensates for Dynamic Artificial Cells
○瀧ノ上 正浩 [1,2,3]（[1] 東京科学大・情報理工, [2] 東京科学大・生命理工, [3] 東京科学大・自律システム材料学研究センター）
**Masahiro Takinoue[1,2,3]** ([1]*Sch. Computing, Science Tokyo*, [2]*Sch. Life Sci. Tech., Science Tokyo*, [3]*ASMat, IIR, Science Tokyo*)

2SKP-7 細胞死の理論と「安定に機能する生化学システム」の珍しさ
A theory of cell death and the rarity of stably functioning biochemical systems
○姫岡 優介（東京大学大学院理学系研究科生物普遍性研究機構）
**Yusuke Himeoka** (*Universal Biology Institute, The University of Tokyo*)

おわりに
Closing Remarks

3 日目（9 月 26 日（金））／Day 3（Sep. 26 Fri.）

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3SAA ノルウェー・日本の二国間シンポジウム
Norway-Japan Bi-lateral Symposium

オーガナイザー：古池 美彦（分子科学研究所）
**Organizers: Yoshihiko Furuike (IMS)**

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

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

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

3SAA-2 Nanoscale motion tracing of spermatozoa
**Jean-Claude Tinguely**[1], Sunil Bhatt[2], Ankit Butola[1], Mona Nystadq[3,4], Dalip Singh Mehta[2], Krishna Agarwal[1] ([1]*Institute of Physics and Technology, UiT The Arctic University of Norway, Tromsø, Norway*, [2]*Department of Physics, Indian Institute of Technology Delhi, New Delhi, India*, [3]*Department of Clinical Medicine, UiT The Arctic University of Norway, Tromsø, Norway*, [4]*Department of Obstetrics and Gynecology, University Hospital of North Norway, Tromsø, Norway*)

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

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

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

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

おわりに
Closing Remarks

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3SBA 生物発光における合成・定量計測・理論計算の融合研究
Bioluminescence Interdisciplinary Collaboration between Experimental and Theoretical Approach

オーガナイザー：樋山 みやび（群馬大学），山本 典史（千葉工業大学）
**Organizers: Miyabi Hiyama (Gunma Univ.), Norifumi Yamamoto (Chiba Inst. of Tech.)**

09:00〜11:30
B 会場（会議室 103+104）／Room B（Meeting Room 103+104）

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

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はじめに
Opening Remarks

3SBA-1 **生体内深部を観察可能な近赤外 in vivo 光イメージング材料**
Innovation of NIR luciferin analogues using firefly bioluminescence for in vivo imaging
**Nobuo Kitada**[1,2,3], Genta Kamiya[1], Jumpei Hatakeyama[1], Ryohei Moriya[4], Masahiro Kiyama[5], Satoshi Iwano[5], Takashi Hirano[1], Shojiro Maki[1,2,3] ([1]*Grad. Sch. Info. Eng., UEC*, [2]*Env. Saf. San. Mgmt. Ctr., UEC*, [3]*CNBE, UEC*, [4]*Fac. Sci., Kitasato Univ.*, [5]*Tenure-Track Prom. Off., Univ. Miyazaki*)

3SBA-2 **ホタル生物発光基質類似体の理論的研究**
Theoretical study for firefly bioluminescence substrate analogs
○樋山 みやび（群馬大学）
**Miyabi Hiyama** (*Gunma University*)

3SBA-3 **発光タンパク質イクオリンの時分割シリアルフェムト秒結晶構造解析**
Time-resolved serial femtosecond crystallography of the bioluminescent protein Aequorin
○森口 舞子, 中津 亨（和医大・薬）
**Maiko Moriguchi**, Toru Nakatsu (*Fac. Pharm. Sci., Wakayama Med. Univ.*)

3SBA-4 **ハイブリッド QM/MM 自由エネルギー法によるイクオリンの生物発光過程についての理論的研究**
Theoretical study on the bioluminescent process of Aequorin by hybrid QM/MM free energy method
○安東 智大 [1], 船橋 俊也 [2], 中津 亨 [3], 林 重彦 [1]（[1] 京大院理, [2] 京大院薬, [3] 和医大薬）
**Tomohiro Ando**[1], Toshiya Funahashi[2], Toru Nakatsu[3], Shigehiko Hayashi[1] ([1]*Grad. Sch. of Sci. Kyoto Univ.*, [2]*Grad. Sch. of Pharm. Sci. Kyoto Univ.*, [3]*Sch. of Pharm. Sci. Wakayama Med. Univ.*)

3SBA-5 **古代のルシフェラーゼを復元する**
Resurrecting the ancient luciferase
○大場 裕一（中部大・応用生物）
**Yuichi Oba** (*Dept. Env. Biol., Chubu Univ.*)

3SBA-6 **分子シミュレーションで探るホタルの太古の光**
Molecular Simulations of the Ancient Glow of Fireflies
○山本 典史（千葉工業大学）
**Norifumi Yamamoto** (*Chiba Tech*)

3SBA-7 ホシホウネンエソ発光器に局在する紫色素タンパク質の生化学的解析
Biochemical analysis of the purple pigment protein localized in the light organ of the hatchetfish
○水野 雅玖 [1], 矢野 大地 [2], 今井 日奈乃 [1], パイティオ ジョゼ [1,3], 磯貝 泰弘 [4], 白井 剛 [5], 大場 裕一 [1] ([1] 中部大・応用生物, [2] 和歌山高専・生物応用化学, [3] サンパウロ大学, [4] 富山県立大・工学・医薬品工学, [5] 長浜バイオ大・バイオサイエンス)
**Gaku Mizuno[1]**, Daichi Yano[2], Hinano Imai[1], Jose Paitio[1,3], Yasuhiro Isogai[4], Tsuyoshi Shirai[5], Yuichi Oba[1] ([1]*Col. Biosci. Biotech., Chubu Univ.*, [2]*Dep. Apl. Chem. Biochem., Nat. Ins. Tech. Wakayama Col.*, [3]*Univ. Sao Paulo*, [4]*Dep. Pharm. Eng., Toyama Pref. Univ.*, [5]*Fac. Biosci.., Nagahama Ins. Biosci. Tech.*)

3SBA-8 全電子第一原理 GWΓ 法の開発
Development of all-electron first-principles GWΓ method
○野口 良史（静岡大院･工）
**Yoshifumi Noguchi** (*Grad. Sch. Eing., Shizuoka Univ.*)

3SBA-9 半導体レーザーを用いたポータブルピコ秒パルス光源と生物物理への応用
Semiconductor laser based portable picosecond pulse light source for biophysics applications
○小林 真隆 [1], 柴田 桂成 [1,2], 中前 秀一 [1], 金 昌秀 [1,3], 伊藤 隆 [3], 樋山 みやび [4,5], 秋山 英文 [1,3] ([1] 東大物性研, [2] 筑波大数理物質系, [3] ㈱ LDseed, [4] 群馬大院理工, [5] 群馬大食健康セ)
**Masataka Kobayashi[1]**, Keisei Shibata[1,2], Hidekazu Nakamae[1], Changsu Kim[1,3], Takashi Ito[3], Miyabi Hiyama[4,5], Hidefumi Akiyama[1,3] ([1]*ISSP, Univ. of Tokyo*, [2]*Grad. Sch. Pure and Appl. Sci, Univ. of Tsukuba*, [3]*LDseed Co., Ltd.*, [4]*Grad. Sch. Sci. Tech., Gunma Univ.*, [5]*Gunma Univ. Center for Food Science and Wellness*)

おわりに
Closing Remarks

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## 3SEA NMR の方法論開発と複雑な生体分子系への応用の新展開
Advances in NMR Methodologies and Applications to Complex Biological Systems/Landscapes

オーガナイザー：石井 佳誉（東京科学大学），松木 陽（大阪大学）
**Organizers: Yoshitaka Ishii (Science Tokyo), Yoh Matsuki (Univ. Osaka)**

09:00〜11:30
E 会場（会議室 201）／Room E（Meeting Room 201）

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

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はじめに
Opening Remarks

3SEA-1 Innovations in Sensitivity-Enhanced High-Dimensional Protein Solid-state NMR and Applications to Amyloid Proteins
**Yoshitaka Ishii** (*Institute of Science Tokyo*)

3SEA-2 溶解 DNP-NMR 法を用いた蛋白質の相互作用，構造動態解析法の開発
Development of protein interaction and structural dynamics studies using dissolved DNP and isotope-aided NMR
赤木 謙一, 池之上 達哉, ○宮ノ入 洋平（阪大・蛋白研）
Ken-ichi Akagi, Tatsuya Ikenoue, **Yohei Miyanoiri** (*Inst. Prot. Res., Univ. Osaka*)

3SEA-3 固体 NMR を用いた微生物型ロドプシンの残基特異的な知見
Residue-specific insights on microbial rhodopsins using solid-state NMR
○川村 出（横浜国大・院理工）
**Izuru Kawamura** (*Grad. Sch. Eng. Sci, Yokohama Natl. Univ.*)

3SEA-4 分子シャペロンを対象とした構造・キネティクス解析
Structural and kinetic insights into molecular chaperones
○齋尾 智英（徳島大・先端酵素）
**Tomohide Saio** (*IAMS, Tokushima Univ.*)

3SEA-5 大腸菌における内在性糖脂質 MPIase の機能的役割
Functional roles of the endogenous glycolipid MPIase in *Escherichia coli*
○野村 薫（サントリー生科財団）
**Kaoru Nomura** (*Suntory Foundation for Life Sciences*)

3SEA-6 Methods and Instruments for High-Field MAS DNP toward Intracellular Structural Biology
**Yoh Matsuki** (*Inst. Prot. Res., Univ. Osaka*)

おわりに
Closing Remarks

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## 3SFA 学際研究で迫る生物物理的視点からの生命の起源研究
Interdisciplinary investigations into the biophysics of the origins of life

オーガナイザー：Tony Z. Jia（広島大学），車 兪澈（海洋研究開発機構）
**Organizers: Tony Z. Jia (Hiroshima Univ.), Yutetsu Kuruma (JAMSTEC)**

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

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

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はじめに
Opening Remarks

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

3SFA-2 **生命における代謝経路選択と熱力学的制約**

Thermodynamic constraints and the choice of metabolic pathways in life

○瀬戸 繭美[1], 佐々木 里璞[1], 大岡 英史[2], 中村 龍平[2,3]（[1] 奈良女子大学, [2] 理化学研究所生体機能触媒研究チーム, [3] 東京科学大学地球生命研究所）

**Mayumi Seto[1]**, Risa Sasaki[1], Hideshi Ooka[2], Ryuhei Nakamura[2,3] ([1]*Nara Women's University*, [2]*Biofunctional Catalyst Research Team, RIKEN Center for Sustainable Resource Scienc*, [3]*Earth- Life Science Institute (ELSI), Institute of Science Tokyo*)

3SFA-3 **深海における人工細胞の生存可能性について**

The Potential of Artificial Cells Functioning under *In Situ* Deep-Sea Conditions

○車 兪澈, 野牧 秀隆, 磯部 紀之, 松岡 大佑, 嶋根 康弘（海洋研究開発機構）

**Yutetsu Kuruma**, Hidetaka Nomaki, Noriyuki Isobe, Daisuke Matsuoka, Yasuhiro Shimane (*Japan Agency for Marine-Earth Science and Technology*)

3SFA-4 **貨幣分子間のカップリングにおける熱力学的制約**

Thermodynamic constraint on the coupling of currency metabolites

○山岸 純平[1], 畠山 哲央[2]（[1] 理研・神戸 BDR, [2] 科学大・ELSI）

**Jumpei Yamagishi[1]**, Tetsuhiro S. Hatakeyama[2] ([1]*BDR, Riken*, [2]*ELSI, Science Tokyo*)

3SFA-5 **電子が導いた生命の起源と生物最古の枝分かれ**

Electrons and the origin of three divisions of life

○延 優（海洋研究開発機構・超先鋭）

**Masaru Konishi Nobu** (*JAMSTEC*)

3SFA-6 **超臨界 $CO_2$ による脱水反応を介した前生物的な核酸合成**

Supercritical $CO_2$ promotes prebiotic nucleotide synthesis via dehydration condensation

○藤島 皓介[1], 田川 翔大朗[2], 森野 航平[3]（[1] 東京科学大学 地球生命研究所, [2] 海洋研究開発機構 超先鋭研究開発プログラム, [3] 東京科学大学 生命理工学院）

**Kosuke Fujishima[1]**, Shotaro Tagawa[2], Kohei Morino[3] ([1]*Earth-Life Science Institute, Science Tokyo*, [2]*Institute for Extra-cutting-edge Science and Technology Avant-garde Research Japan Agency for Marine-Earth Science and Technology*, [3]*School of Life Science and Technology, Science Tokyo*)

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3SGA **計測科学 x 情報科学が切り開く生物学の地平線**

Integrating Measurement and Information Science: Unlocking New Frontiers in Biology

共催 JST CREST 「革新的計測解析」

**オーガナイザー：小松崎 民樹（北海道大学）**

**Organizers: Tamiki Komatsuzaki (Hokkaido Univ.)**

09:00〜11:30

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

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

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はじめに
Opening Remarks

3SGA-1 計測インフォマティクスの発展と展開 ー情報計測から革新的計測解析へー
Development and Evolution of Measurement Informatics - From Intelligent Measurement Analysis to Innovative Measurement and Analysis -
○鷲尾 隆（関西大学ビジネスデータサイエンス学部）
**Takashi Washio** (*Faculty of Business Data Science, Kansai University*)

3SGA-2 血小板生物学 x 人工知能
Intelligent platelet biology
○合田 圭介 [1,2,3,4]（[1] 東京大学大学院理学系研究科化学専攻, [2] カリフォルニア大学ロサンゼルス校工学部生体工学科, [3] 武漢大学工業科学研究院, [4] 東北大学国際放射光イノベーション・スマート研究センター）
**Keisuke Goda[1,2,3,4]** ([1]*Department of Chemistry, University of Tokyo*, [2]*Department of Bioengineering, University of California, Los Angeles*, [3]*Institute of Technological Sciences, Wuhan University*, [4]*International Center for Synchrotron Radiation Innovation Smart, Tohoku University*)

3SGA-3 Theoretical Perspectives on the Hidden Structures in Biological Systems
**Ayaka Sakata[1,2]** ([1]*Dept. Infor. Sci. Ochanomizu Univ.*, [2]*RIKEN AIP*)

3SGA-4 2 細胞計測技術を用いた免疫細胞とがん細胞の 1 細胞相互作用解析
Single-cell analysis of interactions between immune cells and cancer cells using dual-cell measurement technology
○山口 哲志（大阪大学産業科学研究所）
**Satoshi Yamaguchi** (*SANKEN, Univ. of Osaka*)

3SGA-5 電圧マトリックスを用いたナノポア測定によるタンパク質混合物の識別
Voltage-Matrix Nanopore Profiling for the Discrimination of Protein Mixtures
**Sotaro Uemura[1]**, Ryo Akita[1], Lysenko Artem[1], Keith Boroevich[1], Tatsuya Yokota[2], Daiki Kawai[1], Ryo Iizuka[1], Tatsuhiko Tsunoda[1] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Dep.Comp.Sci, Nagoya Inst.Tech*)

3SGA-6 多階層マルチオミックスデータの統合理解に向けた挑戦：ラマンスペクトルとトランスクリプトームを用いたケーススタディ
Toward a Cross-Layer Understanding through Biological Multimodal Data: A Case Study Using Raman Spectroscopy and Transcriptomes
○渡邉 朋信 [1,2]（[1] 理化学研究所生命機能科学研究センター, [2] 広島大学原爆放射線医科学研究所）
**Tomonobu M Watanabe[1,2]** ([1]*RIKEN BDR*, [2]*RIRBM, Hiroshima University*)

3SGA-7 計測介入型 AI が拓く生物学の展開
Unveiling New Frontiers in Biology with Measurement-Intervening AI
○小松崎 民樹（北大・電子研，化学反応創成拠点）
**Tamiki Komatsuzaki** (*RIES, WPI-ICReDD, Hokkaido Univ.*)

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

共催 JST CREST 「予測数学基盤」

オーガナイザー：望月 敦史（京都大学），今吉 格（京都大学）
**Organizers: Atsushi Mochizuki (Kyoto Univ.), Itaru Imayoshi (Kyoto Univ.)**

09:00〜11:30
H 会場（会議室 204）／Room H（Meeting Room 204）

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

はじめに
Opening Remarks

3SHA-1　光遺伝学的手法を用いた神経幹細胞の新規転写制御メカニズムの同定
Uncovering Novel Transcriptional Regulatory Mechanisms of Neural Stem Cells Using Optogenetic Approaches
○今吉 格[1,2]（[1] 京大・院生命科学, [2] 京大・医生研）
**Itaru Imayoshi[1,2]** ([1]*Grad. Sch. Biostudies., Univ. Kyoto*, [2]*LiMe., Univ. Kyoto*)

3SHA-2　Nano-electrokinetics が隠れた転写動態と単一細胞の確率的挙動を結びつける
Nano-Electrokinetics Links Hidden Transcriptomic Dynamics to Stochastic Single-Cell Behavior
○新宅 博文[1,2], 塩見 晃史[1,2], 金子 泰洸ポール[1,2], 峯岸 美紗[1,2], 鳥井 孝太郎[1,2], 土田 新[2]（[1] 京大・医生研, [2] 理研・開拓）
**Hirofumi Shintaku[1,2]**, Akifumi Shiomi[1,2], Taikopaul Kaneko[1,2], Misa Minegishi[1,2], Kotaro Torii[1,2], Arata Tsuchida[2] ([1]*LiMe, Kyoto University*, [2]*CPR, RIKEN*)

3SHA-3　De co de, predict, and control biological systems through single-cell omics and modelling approaches
**Kenji Kamimoto[1,2,3]** ([1]*Research Institute for Microbial Diseases, The University of Osaka*, [2]*Premium Research Institute for Human Metaverse Medicine (WPI-PRIMe), The University of Osaka*, [3]*Bioinformatics Center, The University of Osaka*)

3SHA-4　高速・広視野 $Ca^{2+}$ イメージングが明らかにする大脳皮質の機能的ネットワーク構造
High-speed, Large-FOV $Ca^{2+}$ Imaging Reveals Functional Cortical Network Architecture
○村山 正宜（理化学研究所　脳神経科学研究センター）
**Masanori Murayama** (*RIKEN Center for Brain Science*)

3SHA-5 ネットワークトポロジーに由来する生命機能と機能単位
Biological functions and functional modules originated in the topology of chemical reaction networks
○望月 敦史[1], 山内 悠平[1], 杉山 博紀[2], 後藤 祐平[3,4], 青木 一洋[3,4,5]（[1] 京都大・医生研, [2] 東京大・院工学, [3] 京都大・院生命科学, [4] 自然科学研究機構・基礎生物学研究所, [5] 自然科学研究機構・生命創成探究センター）
**Atsushi Mochizuki[1]**, Yuhei Yamauchi[1], Hironori Sugiyama[2], Yuhei Goto[3,4], Kazuhiro Aoki[3,4,5] ([1]*LiMe, Kyoto Univ.*, [2]*Sch. Eng., Univ. Tokyo*, [3]*Grad. Sch. Biostudies, Kyoto Univ.*, [4]*NIBB, NINS*, [5]*ExCELLS, NINS*)

おわりに
Closing Remarks

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## 3SIA 人工細胞膜をつくる・つかう分子テクノロジー
Molecular technologies for creating and utilizing artificial cell membranes

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

09:00〜11:30
I 会場（会議室 205）／Room I（Meeting Room 205）

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

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はじめに
Opening Remarks

3SIA-1 合成両親媒性高分子で膜活性ペプチドを真似る
Mimicking Membrane-Active Peptides with Synthetic Amphiphilic Polymers
○安原 主馬[1,2,3,4]（[1] 奈良先端大院物質, [2] 奈良先端大院デジタルグリーンイノベーションセンター, [3] 奈良先端大院データ駆動型サイエンス創造センター, [4] 奈良先端大院メディルクス研究センター）
**Kazuma Yasuhara[1,2,3,4]** ([1]*Div. Mat. Sci., Grad. Sch. Sci. Tech., Nara Inst. Sci. Tech.*, [2]*Ctr. Digital Green-innovation, Nara Inst. Sci. Tech.*, [3]*Data Sci. Ctr., Nara Inst. Sci. Tech.*, [4]*Medilux Res. Ctr., Nara Inst. Sci. Tech.*)

3SIA-2 ペプチドと脂質がもたらす膜相分離型ハイブリッド細胞膜とその応用
Peptide-Lipid Hybrid Vesicle with Phase-Separated Domains
○上田 一樹[1,2]（[1] 都立大院 環境応用化学, [2] 理研 CSRS）
**Motoki Ueda[1,2]** ([1]*Dept. Appl. Chem., Tokyo Metropolitan Univ.*, [2]*RIKEN CSRS*)

3SIA-3 次世代分子ロボティクスのための脂質膜通型 DNA デバイス
Lipid Membrane-Translocating DNA Devices for Next-Generation Molecular Robotics
○野村 慎一郎（東北大院工・ロボ）
**Shin-ichiro M. Nomura** (*Dept. Robotics, Grad. Sch. Eng., Tohoku Univ.*)

3SIA-4 **触媒システムの構築に向けた赤血球ゴースト-金属化合物ハイブリッドの設計**
Design of red blood cell ghost-metal compound hybrids for construction of catalytic systems
○越山 友美（立命館大 生命科学）
**Tomomi Koshiyama** (*Coll. Life Sci., Ritsumeikan Univ.*)

3SIA-5 **人工膜と蛍光 1 分子観察を用いた，膜分子の機能解析**
Combining an artificial membrane and a single-molecule imaging technique to investigate the function of membrane protein
○笠井 倫志（国立がん研究センター研究所）
**Rinshi Kasai** (*Natl. Cancer Ctr. Res. Inst.*)

3SIA-6 **人工生体膜分子およびドメインの光操作**
Optical Manipulation of Molecules and Domains in Biological Membranes Models
○谷本 泰士, 森山 俊哉, 増井 恭子, 細川 千絵（阪公大・院理）
**Yasushi Tanimoto**, Shunya Moriyama, Kyoko Masui, Chie Hosokawa (*Grad. Sch. Sci., Osaka Metropolitan Univ.*)

3SIA-7 **ペプチドナノディスクを用いたパターン化人工膜への膜タンパク質導入技術の開発**
Reconstitution of membrane proteins in a micro-patterned model membrane using peptide nanodisc
○森垣 憲一 [1,2], 小松 愛華 [2], 肥塚 雅人 [2], 杭田 美子 [2], 谷本 泰士 [1,4], 林 文夫 [3]（[1] 神戸大・バイオシグナル, [2] 神戸大・院農学, [3] 神戸大・院理学, [4] 大阪公立大・院理学）
**Kenichi Morigaki[1,2]**, Aika Komatsu[2], Masato Koezuka[2], Fuko Kueda[2], Yasushi Tanimoto[1,4], Fumio Hayashi[3] ([1]*Biosignal, Kobe Univ.*, [2]*Grad. Sch. Agri. Sci., Kobe Univ.*, [3]*Grad. Sch. Sci., Kobe Univ.*, [4]*Grad. Sch. Sci., Osaka Metropol. Univ.*)

**おわりに**
Closing Remarks

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

共催 学術変革領域研究（A）「時間タンパク質学」

**オーガナイザー：大出 晃士（東京大学），原田 慶恵（大阪大学）**
**Organizers: Koji Ode (The Univ. of Tokyo), Yoshie Harada (The Univ. of Osaka)**

09:00〜11:30
J 会場（会議室 206）／Room J（Meeting Room 206）

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

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はじめに
Opening Remarks

3SJA-1 開花まで 120 年：タケにおける超長周期タイマーへの挑戦
120 years for flowering: Challenge to the ultra-long timer in bamboo
○村中 智明[1], 高橋 望[2], 遠藤 求[2], 久本 洋子[3]（[1] 名古屋大・院生命農学, [2] 奈良先端大, [3] 東京大・院農学生命）
**Tomoaki Muranaka[1]**, Nozomu Takahashi[2], Motomu Endo[2], Yoko Hisamoto[3] ([1]*Grad. Sch. Bio. Agri., Naoyga Univ.*, [2]*Grad. Sch. Sci. Tech., NAIST*, [3]*Grad. Sch. Agri., Univ. of Tokyo*)

3SJA-2 緑藻における転写非依存的な概日時計
Transcription-Independent Circadian Rhythms in Green Algae
○松尾 拓哉（北里大学　理学部　生物科学科　分子生物学講座）
**Takuya Matsuo** (*Laboratory of Molecular Biology, Department of Biosciences, School of Science, Kitasato University*)

3SJA-3 Exploring the molecular origin of self-sustained circadian oscillator through clock protein evolution
**Atsushi Mukaiyama** (*Dept. of Biosci. and Biotech., Fukui Pref. Univ.*)

3SJA-4 シアノバクテリアの試験管内概日リズムに反応液の pH が与える影響
Effect of pH on the cyanobacterial circadian oscillator in vitro
○三輪（伊藤） 久美子[1,2], 尾上 靖宏[3], 近藤 孝男[1,2], 寺内 一姫[3]（[1] 名古屋大・院理, [2] 名古屋大・高等研究院, [3] 立命館大・生命科学）
**Kumiko Ito-Miwa[1,2]**, Yasuhiro Onoue[3], Takao Kondo[1,2], Kazuki Terauchi[3] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*IAR, Nagoya Univ.*, [3]*Ritsumeikan Univ.*)

3SJA-5 概日リズムの温度補償および同期化に関わる波形歪み
Waveform distortion for temperature compensation and synchronization in circadian rhythms
Shingo Gibo[1,3], Teiji Kunihiro[2], Tetsuo Hatsuda[1], **Gen Kurosawa[1]** ([1]*RIKEN iTHEMS*, [2]*Yukawa Institute for Theoretical Physics, Kyoto University*, [3]*Institute for Basic Science*)

3SJA-6 細胞内在性発熱による温度シグナリング機構
A thermal signaling mechanism driven by intracellular endogenous heat generation
中馬 俊祐[1], 原田 慶恵[2], ○岡部 弘基[1]（[1] 東大・院薬, [2] 阪大・ヒューマン・メタバース疾患研究拠点）
Shunsuke Chuma[1], Yoshie Harada[2], **Kohki Okabe[1]** ([1]*Graduate School of Pharmaceutical Sciences, The University of Tokyo*, [2]*PRIMe, The University of Osaka*)

3SJA-7 反復刺激による神経オルガノイド回路組織の再編と機能性獲得
Repetitive Input Drives Network Refinement and Stimulus-Specific Output in Connected Neural Organoids
**Yoshiho Ikeuchi[1,2]** ([1]*Institute of Industrial Science, The University of Tokyo*, [2]*Institute for AI and Beyond, The University of Tokyo*)