9:00〜11:30　Ch02
1S1　Japan-US symposium on cytoskeletal motor proteins and their associated proteins

オーガナイザー：Hayashi Kumiko（Tohoku Univ.），Niwa Shinsuke（Tohoku Univ.）
**Organizers: Kumiko Hayashi (Tohoku Univ.), Shinsuke Niwa (Tohoku Univ.)**

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Speakers in this symposium are recognized internationally as experts in the field of cytoskeletal motor proteins such as kinesin and dynein, and their associated proteins. We are planning to prepare enough time to have a deep and detailed discussion among the speakers and audience on these subjects. The symposium topics cover multidisciplinary applications of genetics, bio-engineering, bio-chemistry, medical science, and physics, which will give us new insights into the intracellular transport and motor proteins, as well as interesting applications of existing single-molecule techniques.

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Opening Remarks

1S1-1　(1-07-1418) Dissociation mechanism of $IF_1$ from mitochondrial ATP synthase revealed by single-molecule analysis and manipulation
**Ryohei Kobayashi**, Hiroshi Ueno, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

1S1-2　Engineering biomolecular motors
**Zev Bryant** (*Department of Bioengineering, Stanford University*)

1S1-3　(3-07-1342) Engineering of hybrid kinesin-1 dimer with synthetic linker by tuning the neck linker length
**Jakia Jannat Keya[1]**, Akasit Visootsat[1], Akihiro Otomo[1], Sanghun Han[2], Kazushi Kinbara[2], Ryota Iino[1] ([1]*Institute for Molecular Science, National Institutes of Natural Sciences*, [2]*School of Life Science and Technology, Tokyo Institute of Technology*)

1S1-4　Deciphering the function of activating adaptors in the motor-driven transport of mitochondria and autophagosomes
**Erika Holzbaur** (*University of Pennsylvania Perelman School of Medicine*)

1S1-5　A rogue kinesin that destroys microtubules in cells
**Kristen Verhey[1,2]**, Yang Yue[1], Lynne Blasius[1], Breane Budaitis[1] ([1]*Department of Cell & Developmental Biology, University of Michigan Medical School*, [2]*Department of Biophysics, University of Michigan*)

1S1-6　Analyses of KIF1A-associated neuronal disorder by genetics and single molecule assays
**Shinsuke Niwa** (*FRIS, Tohoku Univ.*)

1S1-7　In Vitro Reconstitution of Kinesin-1 Activation
**Kyoko Chiba** (*FRIS, Tohoku Univ.*)

9:00〜11:30　Ch03

## 1S2　共催：学術変革領域研究(A)「分子サイバネティクス」<br>ケミカル AI を創る分子システム工学の黎明<br>Dawn of Molecular System Engineering for Chemical AI

**オーガナイザー：豊田 太郎（東京大学），浜田 省吾（東北大学）**
**Organizers: Taro Toyota (The Univ. of Tokyo), Shogo Hamada (Tohoku Univ.)**

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C. Elegance has a brain consisting of 302 cells, which controls all the behaviors of the organism. The neurons in its brain are classified into three levels, and they are connected by about 6000 synapses. On what principle do these "wet" information processing systems operate? At least, such systems must be constructed by the power of chemistry. A new methodology of "how to assemble individual molecules and molecular devices into complex functional systems" is attracting attention as "molecular systems engineering". In Grant-in-Aids for transformational research "Molecular Cybernetics" (2020-2024), we will investigate principles of the molecular systems engineering. Specifically, designed molecules that function as sensors, processors, and actuators will be assembled in a micrometer-sized compartment (artificial cell) such as a liposome. The resulting artificial cells can then be further combined with each other to construct higher-order functional systems. In this symposium, we will discuss the design principles and practice of such artificial cells and other issues related to the construction of chemical artificial intelligence (AI).

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1S2-1　Molecular pattern recognition in DNA-based artificial neural networks
**Lulu Qian** (*Caltech*)

1S2-2　Computer designed organisms
**Josh Bongard** (*Dept. Computer Sci., Univ. of Vermont*)

1S2-3　**化学反応ネットワークと連携したベシクルの再生産**
Reproduction of vesicle coupled with chemical reaction network
○今井 正幸 [1], 栗栖 実 [1], わるで ぴーたー [2]（[1] 東北大・物理, [2] チューリッヒ工科大・物質）
**Masayuki Imai[1]**, Minoru Kurisu[1], Peter Walde[2] ([1]*Dep. Phys., Tohoku Univ.*, [2]*Dep. Materials, ETH Zurich*)

1S2-4　Mesoscale DNA-based machines powered by artificial metabolism
**Shogo Hamada** (*Dept. of Robotics, Tohoku Univ.*)

1S2-5　**ケミカル AI 構築に向けた修飾アデニンの光環化付加反応による人工核酸の光制御**
Photoregulation of Artificial Nucleic Acid via Photo-Cycloaddition of Modified Adenine Residues for Chemical AI
○村山 恵司 [1], 山野 雄平 [2], 浅沼 浩之 [1]（[1] 名大・院工学, [2] 東北大・多元研）
**Keiji Murayama[1]**, Yuuhei Yamano[2], Hiroyuki Asanuma[1] ([1]*Grad. Sch. Eng., Nagoya Univ.*, [2]*IMRAM, Tohoku Univ.*)

**おわりに**
Closing Remarks

9:00〜11:30　Ch04

## 1S3　共催：新学術領域「生命金属科学」<br>実験と理論の共同による生命金属動態研究の最前線<br>Recent progress in biometal sciences: synergy between theory and experiments

**オーガナイザー：重田 育照（筑波大学），當舎 武彦（理化学研究所）**
**Organizers: Yasuteru Shigeta (Univ. of Tsukuba), Takehiko Tosha (RIKEN)**

Various metallic and semi-metallic elements, which are present in very small amounts in living organisms (defined as biometals), are essential for all living organisms. Their functions range from signal transduction and electron transfer to enzymatic reactions for the production and metabolism of substances. It is mystery that these trace amounts of biometals are programmed into life besides the central dogma. In this symposium, the latest researches on biological reactions and structures involving biometals and their kinetic analysis will be presented from both theoretical and experimental approaches.

1S3-1　銅・亜鉛スーパーオキシドディスムターゼの成熟化におけるシステイン残基の役割
A dual role of cysteine residues in the maturation of prokaryotic Cu/Zn-superoxide dismutase
○古川 良明（慶應・理工）
**Yoshiaki Furukawa** (*Dept. Chem., Keio Univ.*)

1S3-2　時間分解分光法を用いたヘム ABC トランスポーター BhuUV-T における輸送過程の速度論的解析
Kinetic analysis of the transport in heme ABC transporter; BhuUV-T, by time-resolved spectroscopy
○木村 哲就（神戸大・院理）
**Tetsunari Kimura** (*Grad. Sch. Sci., Kobe Univ.*)

1S3-3　Computational study of the structural–function relationship of heme proteins
**Yu Takano[1]**, Hiroko X. Kondo[2], Yusuke Kanematsu[3] ([1]*Grad. Sch. Info. Sci., Hiroshima City Univ.*, [2]*Fac. Eng., Kitami Inst. Tech.*, [3]*Grad. Sch. Adv. Sci. Eng., Hiroshima Univ.*)

1S3-4　SR-$Ca^{2+}$-ATPase における E1/E2 転移の反応座標の解析
Analysis of reaction pathway in E1/E2 transition of SR-$Ca^{2+}$-ATPase
○小林 千草 [1], 松永 康佑 [2], Jung Jaewoon[1,3], 杉田 有治 [1,3,4]（[1] 理研・R-CCS, [2] 埼玉大・院理工, [3] 理研・CPR, [4] 理研・BDR）
**Chigusa Kobaysahi[1]**, Yasuhiro Matsunaga[2], Jaewoon Jung[1,3], Yuji Sugita[1,3,4] ([1]*RIKEN, R-CCS*, [2]*Grad. Sch. Sci. Eng., Saitama Univ.*, [3]*RIKEN, CPR*, [4]*RIKEN, BDR*)

1S3-5　Design of staphylococcal two-component pore forming toxin to change pore formation property
Nouran Ghanem[1,2], Takashi Matsui[1,3], Jun Kaneko[4], Tomomi Uchikubo-Kamo[2], Mikako Shirouzu[2], Tsubasa Hashimoto[1], Tomohisa Ogawa[1,4], Tomoaki Matsuura[5], Po-Ssu Huang[6], Takeshi Yokoyama[1,2], **Yoshikazu Tanaka[1]** ([1]*Graduate School of Life Sciences, Tohoku University*, [2]*Laboratory for Protein Functional and Structural Biology, RIKEN Center for Biosystems Dynamics Research*, [3]*School of Science, Kitasato University*, [4]*Graduate School of Agricultural Science, Tohoku University*, [5]*Earth-Life Science Institute, Tokyo Institute of Technology*, [6]*Department of Bioengineering, Stanford University*)

1S3-6　放射光顕微システムによる細胞内小分子イメージングと医学応用の試み
Visualization of intracellular small molecules using synchrotron radiation and its trials for medical application
○志村 まり（国立国際医療研究センター）
**Mari Shimura** (*Nat. Cent. for Global Health and Med.*)

9:00〜11:30　Ch05

## 1S4　共催：新学術領域「発動分子科学」<br>生体分子の構造的・機能的ダイナミクス：1 分子計測と分子シミュレーションの交流<br>Structural and Functional Dynamics of Biomolecules: Interplay between Single Molecule Measurement and Molecular Simulation

**オーガナイザー：古田 忠臣（東京工業大学），鎌形 清人（東北大学）**
**Organizers: Tadaomi Furuta (Tokyo Tech), Kiyoto Kamagata (Tohoku Univ.)**

Currently, the qualitative and quantitative developments of experimental and computational methods have made it possible to directly observe important structural and functional dynamics of various biomolecules. Recently, there have been many reports that lead to further understandings of biological phenomena by integrating information obtained from these experiments and simulations. In view of this situation, the theme of this symposium is at the stage where it should be promoted further. Therefore, in this symposium, several researchers on the experimental side, simulation side, and integrated researches will present the latest research results and general remarks, which would be clues leading to profound understandings of biological phenomena.

1S4-1　高速 AFM による一分子動態イメージングデータと分子シミュレーション
High-speed-AFM imaging of single-molecule dynamics and molecular simulation
○内橋 貴之[1,2]（[1] 名古屋大学大学院理学研究科, [2] 自然科学研究機構 生命創成探究センター）
**Takayuki Uchihashi[1,2]** ([1]*Graduate School of Science, Nagoya University*, [2]*ExCELLS, NINS*)

1S4-2　高速原子間力顕微鏡データと分子シミュレーションのデータ同化による動的構造解析
Dynamic structure analysis by data assimilation combining high-speed atomic force microscopy data and molecular simulations
○渕上 壮太郎[1], 松永 康佑[2], 高田 彰二[1]（[1] 京大院・理, [2] 埼玉大・工）
**Sotaro Fuchigami[1]**, Yasuhiro Matsunaga[2], Shoji Takada[1] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*Fac. of Engin., Saitama Univ.*)

1S4-3　分子モーターの化学力学共役モデルのベイズ推定
Bayesian inference of the chemomechanical coupling model of molecular motors
○岡崎 圭一（分子研）
**Kei-ichi Okazaki** (*Inst. for Mol. Sci.*)

1S4-4　DNA 上や相分離複合体内でのタンパク質ダイナミクスの単分子計測と分子動力学解析
Single molecule and molecular dynamics characterization of protein action along DNA and in liquid droplets
○鎌形 清人（東北大・多元研）
**Kiyoto Kamagata** (*IMRAM, Tohoku Univ.*)

1S4-5　光子相関計測で解き明かす生体分子のマイクロ秒構造・機能ダイナミクス
Microsecond Structural and Functional Dynamics of Biomolecules Revealed by Photon Correlation Measurements
○石井 邦彦（理研・田原分子分光）
**Kunihiko Ishii** (*Mol. Spectrosc. Lab., RIKEN*)

1S4-6　生物分子モーターの再デザインと計測
Re-designing and measuring biomolecular motors
○古田 健也（情報通研、未来 ICT）
**Ken'ya Furuta** (*Advanced ICT, NICT*)

1S4-7 一分子計測からたんぱく質のエネルギー地形の階層性を抽出する
Capturing hierarchical features in protein energy landscape from single molecule time series
○小松崎 民樹 [1,2]（[1] 北大・電子研, [2] 北大・化学反応創成研究拠点）
**Tamiki Komatsuzaki[1,2]** ([1]*RIES, Hokkaido Univ.*, [2]*WPI-ICReDD, Hokkaido Univ.*)

9:00〜11:30 Ch06
1S5 1 細胞解析が切り開く新しい細胞観
New perspectives on cells provided by single cell analyses

**オーガナイザー：谷口 雄一（京都大学），黒田 真也（東京大学）**
**Organizers: Yuichi Taniguchi (Kyoto Univ.), Shinya Kuroda (The Univ. of Tokyo)**

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Single cell biology is a growing field to quantitatively understand the nature of individual cells that inherently have large heterogeneity. This growth is supported by progresses in a variety of single-cell approaches such as DNA/RNA sequencing, optical imaging, mass spectroscopy, high-throughput measurement, theory and informatics. In this symposium, we invite several single-cell biology scientists who conduct cutting-edge research using different approaches, aiming at discussing what single cell biology will bring towards understanding of life phenomena.

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はじめに
Opening Remarks

1S5-1 Large-scale transcriptome analysis at single cell level
**Piero Carninci** (*RIKEN Center for Integrative Medical Sciences*)

1S5-2 機械学習によるシングルセル・ダイナミクスからの生物学的原理の解読
Deciphering Biological Principles from Single-cell Dynamics by Machine Learning
○小林 徹也（東大・生産研）
**J. Tetsuya Kobayashi** (*IIS, UTokyo*)

1S5-3 ネットワーク化計測によるプール型細胞解析
Networked measurement for pooled cell analysis
○太田 禎生 [1,2]（[1] 東大・先端研, [2] シンクサイト株式会社）
**Sadao Ota[1,2]** ([1]*RCAST, Univ. Tokyo*, [2]*Thinkcyte Inc*)

1S5-4 情報理論解析による細胞間のばらつきを活かした正確な応答制御機構の解明
Information analysis reveals that cell-to-cell variability can improve the accuracy of the control of biological responses
○和田 卓巳 [1], 廣中 謙一 [2], 黒田 真也 [2,3]（[1] 京都大・iPS 細胞研究所, [2] 東京大・理学系, [3] 東京大・新領域創成科学）
**Takumi Wada[1]**, Ken-ichi Hironaka[2], Shinya Kuroda[2,3] ([1]*Center for iPS Research and Application, Kyoto Univ.*, [2]*Grad. Sch. Sci., Univ. Tokyo*, [3]*Grad. Sch. Front. Sci., Univ. Tokyo*)

1S5-5 一細胞プロテオーム解析を目指した三次元一分子イメージングによるバイオ分析法の開発
3D single-molecule imaging-based bioanalyses towards single-cell proteomics
○金 水縁 [1,2], Kamarulzaman Latiefa[1,3], 谷口 雄一 [1,2,3]（[1] 理研・BDR, [2] 京大・iCeMS, [3] 阪大・院生命機能研）
**Sooyeon Kim[1,2]**, Latiefa Kamarulzaman[1,3], Yuichi Taniguchi[1,2,3] ([1]*RIKEN, BDR*, [2]*iCeMS, Kyoto Univ.*, [3]*Grad. Sch. Front. Biosci., Osaka Univ.*)

おわりに
Closing Remarks

9:00〜11:30　Ch07

## 1S6　GPCR 研究における新たなコンセプトと創薬への示唆
New concepts in GPCR research and implications for drug discovery

**オーガナイザー：片山 耕大（名古屋工業大学），寿野 良二（関西医科大学）**
**Organizers: Kota Katayama (Nagoya Inst. of Tech.), Ryoji Suno (Kansai Medical Univ.)**

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The recent trend in the field of structural studies of G-protein-coupled receptors (GPCRs) using cryo-electron microscopy (Cryo-EM) and 3D reconstruction techniques supported by biophysical, computational and advanced biochemistry have facilitated GPCRs research towards drug discovery. These techniques contributed significantly to our understanding about GPCRs functions, ligand recognition, pharmacological targets in biomedicine. This symposium will highlight the latest developments in GPCR structure/function, ligand discovery and design, intracellular signalling pathways and their impact on modern drug discovery.

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はじめに
Opening Remarks

1S6-1　**ヒトプロスタグランジン受容体 EP3-G タンパク質複合体の構造解析**
Structural insights into the human Prostaglandin E2 receptor EP3- Gi signaling complex
○寿野 良二（関西医大・医）
**Ryoji Suno** (*Dept. Med., Kansai Med. Univ.*)

1S6-2　Back and forth between purified and cellular systems for GPCR biology
**Asuka Inoue** (*Grad. Sch. Pharm., Tohoku Univ.*)

1S6-3　Spatiotemporal Determinants and Allosteric Communication Modulate the Ligand Bias in GPCRs
**Nagarajan Vaidehi** (*Chair, Department of Computational & Quantitative Medicine, Beckman Research Institute of the City of Hope, Duarte, CA*)

1S6-4*　(2-06-1515) **分子シミュレーションによるオレキシン 2 受容体ーG タンパク質複合体の動的性質の研究**
(2-06-1515) Dynamics of Orexin2 Receptor and G-protein Complex with Molecular Dynamics Simulations
○横井 駿, 光武 亜代理（明治大学 理工学研究科 物理学専攻）
**Shun Yokoi**, Ayori Mitsutake (*Department of Physics, School of Science and Technology, Meiji University*)

1S6-5　**配位ケモジェネティクスによる GPCR 型グルタミン酸受容体の活性制御**
Coordination chemogenetics for direct activation of GPCR-type glutamate receptors in brain tissue
○清中 茂樹（名大・院工）
**Shigeki Kiyonaka** (*Grad. Sch. Eng., Nagoya Univ.*)

1S6-6* (2-01-1451) アデノシン $A_{2A}$ 受容体の不活性型構造を安定化するための all-α 融合パートナータンパク質のゼロからの合理デザイン
(2-01-1451) De novo design of an alpha-helical fusion partner protein to stabilize adenosine $A_{2A}$ receptor in the inactive state
○三本 斉也 [1,2], 菅谷 幹奈 [3], 風間 一輝 [3], 中野 僚介 [3], 小杉 貴洋 [1,2,4], 村田 武士 [3], 古賀 信康 [1,2,4]
([1] 総研大・物理科学, [2] 分子研, [3] 千葉大・理, [4] 自然科学・生命創成)
**Masaya Mitsumoto[1,2]**, Kanna Sugaya[3], Kazuki Kazama[3], Ryosuke Nakano[3], Takahiro Kosugi[1,2,4], Takeshi Murata[3], Nobuyasu Koga[1,2,4] ([1]*SOKENDAI*, [2]*IMS, NINS*, [3]*Grad. Sch. of Sci. and Eng., Chiba Univ.*, [4]*ExCELLS, NINS*)

1S6-7 Conformational dynamics upon ligand binding in muscarinic acetylcholine receptor revealed by FTIR spectroscopy
**Kota Katayama[1,2]** ([1]*Grad. Sch. Eng., Nagoya Inst. Tech*, [2]*PRESTO, JST*)

おわりに
Closing Remarks

16:00〜18:30 Ch01
## 1S7 インドー日本交流シンポジウム：生物物理の多彩な挑戦
India-Japan joint symposium: Various challenges on biophysical research

**オーガナイザー：坂口 美幸（埼玉大学），永井 健（北陸先端科学技術大学院大学）**
**Organizers: Miyuki Sakaguchi (Saitama Univ.), Ken H. Nagai (JAIST)**

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To promote the exchange between the Indian Biophysical Society (IBS) and the Biophysical Society of Japan (BSJ), this joint symposium focusing on energetic young scientists was planned. Four up-and-coming researchers are nominated by IBS, and they will give talks in a wide range of fields like protein function during embryogenesis, super-resolution imaging with DNA, morphogenesis in an active-polar gel, and the physical basis on self-reproducing catalytic RNAs. From BSJ, three leading researchers in related fields will also give talks. In the symposium, we will share the problems at the forefront, and exchange cutting-edge technologies and knowledge.

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はじめに
Opening Remarks

1S7-1 Secondary-probe based DNA-PAINT super-resolution imaging for unlimited multiplexing
**Mahipal Ganji** (*Department of Biochemistry, Indian Institute of Science, Bangalore, India*)

1S7-2 1 分子イメージングで迫るヒト染色体の動的組織化
Single molecule imaging unveils the dynamic organization of the human chromosomes
○日比野 佳代 [1], 境 祐二 [2], 鐘巻 将人 [1], 前島 一博 [1] ([1] 遺伝研・総研大, [2] 東京大学)
**Kayo Hibino[1]**, Yuji Sakai[2], Masato Kanemaki[1], Kazuhiro Maeshima[1] ([1]*Natl. Inst. Genet. & SOKENDAI*, [2]*Univ. Tokyo*)

1S7-3 BAR domain protein function in plasma membrane remodeling during embryogenesis
**Richa Rikhy** (*Biology, IISER, Pune, India*)

1S7-4 上皮集団遊走におけるメカノケミカルフィードバック
Mechanochemical feedbacks in collective cell migration of epithelial cells
○平島 剛志 [1,2], 日野 直也 [2,4], Boocock Daniel[4], 松田 道行 [2,3], Hannezo Edouard[4]（[1] 京大・白眉, [2] 京大・生命, [3] 京大・医, [4]IST Austria）
**Tsuyoshi Hirashima[1,2]**, Naoya Hino[2,4], Daniel Boocock[4], Michiyuki Matsuda[2,3], Edouard Hannezo[4] ([1]*The Hakubi Center, Kyoto Univ*, [2]*Grad Sch Biostudies, Kyoto Univ*, [3]*Grad Sch Med, Kyoto Univ*, [4]*IST Austria*)

1S7-5 Dynamics of active-polar gels on curved surfaces
**Vijay Kumar Krishnamurthy[1]**, Siddharth Jha[2], Swapnil Kole[2], Sriram Ramaswamy[2] ([1]*International Centre for Theoretical Sciences, Bengaluru*, [2]*Indian Institute of Science, Bengaluru*)

1S7-6 Compositional identity and robustness of autocatalytic RNA reaction networks in coacervate protocells
**Shashi Thutupalli[1,2]** ([1]*National Centre for Biological Sciences, Tata Institute for Fundamental Research*, [2]*International Centre for Theoretical Sciences, Tata Institute for Fundamental Research*)

1S7-7 *C. elegans* の集団運動
Collective motion of *C. elegans*
○永井 健 [1], 伊藤 浩史 [2], 杉 拓磨 [3]（[1] 北陸先端科学技術大学院大学, [2] 九州大学, [3] 広島大学）
**Ken H. Nagai[1]**, Hiroshi Ito[2], Takuma Sugi[3] ([1]*JAIST*, [2]*Kyushu University*, [3]*Hiroshima University*)

おわりに
Closing Remarks

16:00〜18:30 Ch02
## 1S8 水のダイナミクスと生物機能：再考
Water dynamics and biological functions: Revisit

**オーガナイザー：今清水 正彦（産業総合研究所），村上 洋（量子科学技術研究開発機構）**
**Organizers: Masahiko Imashimizu (AIST), Hiroshi Murakami (QST)**

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Extensive studies of hydration water dynamics show that they occur from the picosecond to nanosecond timescales. We, however, consider from recent studies that much slower dynamics of water may play critical roles in expressing biological functions. Such studies include findings of glass-like water in a model of cells and glassy behaviors of cytoplasm, and of nonthermal effects on slow biomolecular dynamics and reactions by the externally applied alternating electromagnetic field with terahertz frequency. In this symposium, we will attempt to discuss new directions that connect the physicochemical studies of hydration to biological functions through water relaxation processes in a wide temporal range.

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1S8-1 Nonthermal Excitation Effects Mediated by Sub-Terahertz Radiation on Biomolecular Hydration Dynamics and Reactions
**Masahiko Imashimizu[1]**, Yuji Tokunaga[1], Masahito Tanaka[2], Jun-ichi Sugiyama[3] ([1]*CMB, AIST*, [2]*NMRI, AIST*, [3]*NMRI, AIST*)

1S8-2 荷電フィラメント周りの協同的水分子運動 -マイクロ波誘電緩和とラマン OH 伸縮/ベンディング分光-
Collective water behavior around charged filaments by microwave dielectric relaxation and Raman OH-stretching/bending bands spectroscopy
○鈴木 誠（東北大・多元研）
**Makoto Suzuki** (*IMRAM, Tohoku Univ.*)

1S8-3* (2-02-1624) 水和水の OH 伸縮振動バンドに基づく生体保護作用を持つ小分子の水素結合強化作用の評価
(2-02-1624) Hydrogen bond strengthening effect of stabilizing osmolytes investigated by OH stretching band of hydration water
○松村 郁希 [1], 四方 俊幸 [2], 小川 雄一 [1], 鈴木 哲仁 [1], 近藤 直 [1], 白神 慧一郎 [1]（[1] 京都大・院農学研究科, [2] 東京農工大・院農学研究院）
**Fumiki Matsumura[1]**, Toshiyuki Shikata[2], Yuichi Ogawa[1], Tetsuhito Suzuki[1], Naoshi Kondo[1], Keiichiro Shiraga[1] ([1]*Grad. Sch. Agri., Kyoto Univ.*, [2]*Grad. Sch. Agri., Tokyo Univ. of Agriculture and Technology*)

1S8-4 高圧力下誘電分光測定による全濃度範囲におけるグリセロール水溶液の過冷却水のダイナミクスに関する研究
High-pressure dielectric study of dynamics of supercooled water in whole concentration range glycerol-water mixtures
○佐々木 海渡（東海大・理物）
**Kaito Sasaki** (*Dept. Phys. Sch. Sci., Tokai Univ.*)

1S8-5 The role of water for biomolecular dynamics; slaving versus plasticization
**Jan Swenson[1]**, Silvina Cerveny[1,2] ([1]*Chalmers University of Technology*, [2]*Donostia International Physics Center*)

1S8-6 Hydration shells of biomolecules: dynamics and biochemical function
**Damien Laage[1,2,3,4]** ([1]*Ecole Normale Superieure*, [2]*CNRS*, [3]*PSL Univ.*, [4]*Sorbonne Univ.*)

1S8-7 低含水率媒質中の水和水の室温ガラス状態
Glass-like state of hydration water in aqueous mediums with low water contents at room temperature
○村上 洋（量研・量子生命）
**Hiroshi Murakami** (*Inst. Quantum life Sci., QST*)

16:00〜18:30 Ch03
## 1S9 温度感覚研究の新潮流 ー温度を測る、制御する、感知機構とその意義を探るー
Trends in the research field of thermo-sensation

**オーガナイザー：内田 邦敏（静岡県大学），藤原 祐一郎（香川大学）**
**Organizers: Kunitoshi Uchida (Univ. of Shizuoka), Yuichiro Fujiwara (Kagawa Univ.)**

Since TRPV1 channel, the world's first mammalian thermo-receptor, was uncovered in 1997, several thermo-receptors have been elucidated, and the biological meaning of thermo-sensation are becoming clearer. In this symposium, we will introduce the recent works aimed to evaluate the measurement and manipulation techniques of temperature in living matter, and to elucidate the gating mechanisms of thermo-receptors by temperature changes and physiological roles of thermo-sensation. We will also discuss the biological significances and future perspectives of thermo-sensation.

1S9-1 蛍光性タンパク質温度センサーを用いた生体内温度分布の可視化とその意義の解明
Visualization and understanding of subcellular thermodynamics using fluorescent protein-based thermosensors
○坂口 怜子 [1,2]（[1] 産業医科大学・医学部, [2] 京都大・院工）
**Reiko Sakaguchi[1,2]** ([1]*Univ of Occupational and Environmental Health*, [2]*Grad Sch Engineering, Kyoto Univ.*)

1S9-2 Single-molecule dynamics of TRPV1 channel upon activation with different stimuli
**Hirofumi Shimizu** (*Div. Int. Physiol. Univ. Fukui. Fac. Med. Sci.*)

1S9-3 電位依存性 $H^+$チャネルの温度感受性ゲーティングの構造基盤
Structural Basis for Temperature-Sensitive Gating of Voltage-Gated $H^+$ Channels
○藤原 祐一郎（香川大・院医）
**Yuichiro Fujiwara** (*Grad. Sch. Med., Kagawa Univ.*)

1S9-4 温度感受性チャネル TRPM5 の温度依存的活性化及び不活性化
Temperature-dependent activation and inactivation of TRPM5 channel
○内田 邦敏（静県大・食品栄養・環境生命）
**Kunitoshi Uchida** (*Dept. Environ. Life Sci., Sch. Food Nutr. Sci., Univ. Shizuoka.*)

1S9-5 両生類の生態的な棲み分けに起因した温度感覚の進化的変化とその分子機構
The evolutionary tuning of thermal perception related to habitat selection in frogs
○齋藤 茂[1,2,3], 齋藤 くれあ[1,2], 井川 武[4], 小巻 翔平[5], 富永 真琴[1,2,3]（[1]生理研・細胞生理, [2]生命創成探究センター・温度生物, [3]総研大・生理科学, [4]広島大・両生研, [5]いわて東北メディカル・メガバンク）
**Shigeru Saito[1,2,3]**, Claire Saito[1,2], Takeshi Igawa[4], Shohei Komaki[5], Makoto Tominaga[1,2,3] ([1]*Dep. Cell Signaling, Natl. Inst. Physiol. Sci.*, [2]*Thermal Biol., ExCELLS*, [3]*Dept. Physiol. Sci., SOKENDAI.*, [4]*Amphibian Res. Center, Hiroshima Univ.*, [5]*Iwate Tohoku Med. Megabank Org.*)

1S9-6 てんかん原性域の局所発熱は TRPV4 活性化を介して病態悪化を引き起こす
Temperature elevation in epileptogenic foci exacerbates the disease through TRPV4 activation
○柴崎 貢志（長崎県立大院・人間健康科学・細胞生化学）
**Koji Shibasaki** (*Lab. Neurochem., Univ. Nagasaki*)

16:00〜18:30　Ch04
## 1S10　生命の起源とプロトセル研究における新たな進歩
Recent Advances in Origins of Life and Protocell Research

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

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One of the major questions in ancient and modern science is the question of our own creation. How did life emerge on Earth? What were the structures and functions of the first cells? Recent technological advances in biophysics, especially in Japan, are now allowing researchers in a variety of fields such as synthetic biology, evolutionary biology, and biochemistry to finally begin to answer these questions. This symposium highlights recent advances in Origins of Life and Protocell research by biophysicists from Japan and around the world. We hope to inspire other biophysicists, especially young researchers, to also consider studying these very difficult (but important) unanswered questions.

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1S10-1 Assembly of Primitive Liquid Crystal Peptide/DNA Coacervates
**Tony Z Jia[1,2]**, Tommaso P Fraccia[3] ([1]*Earth-Life Science Institute, Tokyo Institute of Technology*, [2]*Blue Marble Space Institute of Science*, [3]*Institut Pierre-Gilles de Gennes, Chimie Biologie et Innovation, ESPCI Paris*)

1S10-2 相分離を介して原始細胞モデル液滴を形成する核酸スキャフォールド
Nucleic acid scaffolds that undergo phase separation into liquid droplets serving as primitive cell models
○冨田 峻介 [1], 三村 真大 [1,2], 新海 陽一 [3], 栗田 僚二 [1,2]（[1] 産総研・健康医工, [2] 筑波大院・数理物質, [3] 産総研・バイオメディカル）
**Shunsuke Tomita[1]**, Masahiro Mimura[1,2], Yoichi Shinkai[3], Ryoji Kurita[1,2] ([1]*Health Med. Inst., AIST*, [2]*Grad. Sch. of Pure and Appl. Sci., Univ. Tsukuba*, [3]*Biomed. Res. Inst., AIST*)

1S10-3* (2-13-1427) アミノ酸配列と連携した原始生体膜の成長
(2-13-1427) Growth of Primitive Cell Membrane Coupled with Amino Acid Sequence
○馬場 晶子 [1], オルソン ウルフ [2], 今井 正幸 [1]（[1] 東北大・院理学, [2] ルンド大・院理学）
**Akiko Baba[1]**, Ulf Olsson[2], Masayuki Imai[1] ([1]*Grad. Sch. Sci., Univ. Tohoku*, [2]*Grad. Sch. Sci., Univ. Lund*)

1S10-4 高分子混雑した細胞モデル中の分子挙動決定因子としての細胞サイズ
Cell size as a key determinant of molecular behaviors in macromolecular crowding artificial cells
○渡邊 千穂 [1,2], 柳澤 実穂 [2]（[1] 広大院・統合生命科学, [2] 東大院・総合文化・先進）
**Chiho Watanabe[1,2]**, Miho Yanagisawa[2] ([1]*Hiroshima Univ.*, [2]*Univ. Tokyo*)

1S10-5 Multiple fusion barriers for fatty acid protocells
**Anna Wang[1]**, Tetsuya Yomo[2], Lauren Lowe[1], Daniel WK Loo[1], Yaam Deckel[1] ([1]*School of Chemistry and the Australian Centre for Astrobiology, UNSW Sydney, Australia*, [2]*Institute of Biology and Information Science, Biomedical Synthetic Biology Research Center, School of Life Sciences, East China Normal University, Shanghai, China*)

1S10-6 人工細胞における細胞内構造形成の不安定性
Understanding the instability of intracellular organization in synthetic cells
○前多 裕介（九大・物理）
**Yusuke Maeda** (*Kyushu Univ., Dept. Phys.*)

1S10-7* (2-13-1451) 多相液滴のコアを用いた人工細胞内転写反応場の構築
(2-13-1451) Development of a transcription field in the artificial cell by the core of multiphase droplets
○友原 貫志, 皆川 慶嘉, 野地 博行（東大院・工　応用化学）
**Kanji Tomohara**, Yoshihiro Minagawa, Hiroyuki Noji (*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

16:00〜18:30　Ch05

## 1S11　共催：新学術領域研究「高速分子動画」<br>原子レベルの動的構造解析が拓く生体分子機能の理解<br>Toward understanding biological functions: atomic-level characterization of structures and dynamics of biomolecules

**オーガナイザー：宮下 治（理化学研究所），南後 恵理子（東北大学）**
**Organizers: Osamu Miyashita (RIKEN), Eriko Nango (Tohoku Univ.)**

Information on the structures and dynamics of biological molecules plays a critical role in understanding their functional mechanisms and possible medicinal applications. Time-resolved serial femtosecond crystallography (TR-SFX) using X-ray free electron laser (XFEL) is a state-of-art technique that can provide 3D structures of the molecules following the time-development of reactions. Furthermore, integrative analyses combining TR-SFX data with other approaches could provide more detailed information on dynamic structures and energetics. This symposium will focus on recent updates on TR-SFX experiments and applications, as well as recent developments of other experimental techniques and computational approaches, aiming to advance our understanding of biomolecular functions through integrative research.

1S11-1　X-ray free electron lasers reveal the molecular mechanism for water oxidation in photosystem II
**Michi Suga**, Yoshiki Nakajima, Hongjie Li, Jian-Ren Shen (*Okayama Univ.*)

1S11-2　Involvement of conserved amino acids in ion transport pathways of multidrug and toxic compound extrusion (MATE) transporter
**Keiko Shinoda**[1], Hisashi Kawasaki[1], Satoshi Murakami[2], Sagar Raturi[3], Asha V. Nair[3], Himansha Singh[3], Boyan Bai[3], Hendrik W. van Veen[3] ([1]*AgTECH, GSALS, UTokyo*, [2]*Sch. of Life Sci. and Tech., Tokyo Inst. of Tech.*, [3]*Dept. of Pharmacology, Univ. of Cambridge*)

1S11-3　ギャップ結合タンパク質のナノディスクにおける構造
Structures of gap junction proteins in nanodiscs
○大嶋 篤典 [1,2]（[1] 名大・細胞セ, [2] 名大・創薬）
**Atsunori Oshima**[1,2] ([1]*CeSPI, Nagoya Univ.*, [2]*Grad. Sch. Pharm. Sci.*)

1S11-4　Molecular mechanisms involved in the regulation of the Circadian Clock
**Florence Tama**[1,2,3] ([1]*RIKEN Center for Computational Science*, [2]*Department of Physics, Nagoya University*, [3]*Institute of Transformative Bio-Molecules*)

1S11-5　XFEL analyses of molecular mechanism and structure in DNA photolyase photoreduction
**Yoshitaka Bessho**[1,2] ([1]*Academia Sinica, IBC*, [2]*RIKEN SPring-8 Center*)

1S11-6　蛋白質結合解離ダイナミクスの分子動画
Molecular movie of protein association/dissociation dynamics
○北尾 彰朗（東工大・生命理工）
**Akio Kitao** (*Sch. Life Sci. Tech., Tokyo Tech.*)

16:00〜18:30　Ch06

## 1S12　生物物理・ソフトマター物理と医学の接点を探る
Bridging biophysics/soft-matter physics and medical science

**オーガナイザー：藤崎 弘士（日本医科大学），好村 滋行（東京都立大学）**
**Organizers: Hiroshi Fujisaki (Nippon Medical School), Shigeyuki Komura (Tokyo Metro. Univ.)**

Research towards tailor-made and precision medicine is accelerating, and this requires mathematical and physical approaches in addition to empirical medical traditions. Medical physics has been established as a field that links medicine and physics, and recently, AI has been used for pathological imaging diagnosis and particle therapy. On the other hand, biological phenomena have various hierarchies, starting from the molecular level to cells, organs, individuals, and populations, and with the advancement of computers, highly precise simulations of these phenomena are now becoming possible. In this symposium, we will explore the possibility of medical applications, including therapeutic methods, from the standpoint of biophysics and soft matter physics. The main purpose of this symposium is to have a lively discussion among medical scientists, biophysicists, and physicists about the awareness of problems in the field of medicine and how to deal with them in theory and calculations.

はじめに
Opening Remarks

1S12-1　Biophysics of Infectious Diseases: How are the carriers of abnormal hemoglobin protected from severe malaria?
**Motomu Tanaka**[1,2] ([1]*Heidelberg University, Institute of Physical Chemistry*, [2]*Kyoto University, Center for Integrative Medicine and Physics*)

1S12-2　**形成外科学 とメカノバイオロジー　—物理的刺激が創傷治癒や組織再生に与える役割—**
Plastic Surgery and Mechanobiology　—The Role of Mechanical Forces on Wound Healing, Tissue Repair and Regeneration—
○小川 令（日本医科大学形成外科）
**Rei Ogawa** (*Department of Plastic, Reconstructive and Aesthetic Surgery, Nippon Medical School*)

1S12-3　**計算流体力学を用いた心血管系疾患に対する患者固有解析**
Patient-specific analyses by computational fluid dynamics for cardiovascular diseases
○水藤 寛（東北大・AIMR）
**Hiroshi Suito** (*AIMR, Tohoku Univ.*)

1S12-4　**質量分析イメージングの病理学応用**
Pathology application of mass spectrometry imaging
○鶴山 竜昭 [1,2]（[1] 京都大学医学部, [2] 放射線影響研究所）
**Tatsuaki Tsuruyama**[1,2] ([1]*Kyoto University, graduate school of medicine*, [2]*Radiation effect Reseach Foundation*)

1S12-5　**光トモグラフィーと生物物理**
Optical tomography and biophysics
○町田 学（浜松医科大学）
**Manabu Machida** (*Hamamatsu University School of Medicine*)

16:00〜18:30　Ch07

## 1S13　共催：新学術領域「シンギュラリティ生物学」
## シンギュラリティ細胞が生み出す多様な生命現象へのアプローチ
## Approaches to diverse biological phenomena produced by singularity cells

**オーガナイザー：坂内 博子（早稲田大学），若林 憲一（東京工業大学）**
**Organizers: Hiroko Bannai (Waseda Univ.), Ken-ichi Wakabayashi (Tokyo Tech)**

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In multicellular systems, there are many phenomena that result in dramatic changes in morphology and dynamics caused by a small number of cells. In this symposium, we will introduce challenging research to find rare cells, i.e. "singularity cells", which are the driving force of dramatic changes in diverse biological phenomena such as algal behavior, stem cell differentiation, organogenesis, and neurological diseases. Elucidating the mechanism by which "singularity cells" significantly change the entire system requires new perspectives and methodologies. By sharing this approach with members, we aim to spread a new methodology of biophysics and a new academic field "Singularity Biology".

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1S13-1　はじめに：「シンギュラリティ生物学」とは？
Introduction: What is "Singularity Biology"?
○坂内 博子（早大・理工学術院）
**Hiroko Bannai** (*Waseda Univ., Fac. Sci. Eng.*)

1S13-2　あまのじゃく細胞から紐解く緑藻クラミドモナス走光性の生理的意義
Significance of phototaxis in the unicellular green alga *Chlamydomonas reinhardtii* revealed by “perverse” cells
○若林 憲一 [1,2]（[1] 東工大・化生研, [2] 東工大・生命理工）
**Ken-ichi Wakabayashi[1,2]** ([1]*CLS, Tokyo Tech*, [2]*LST, Tokyo Tech*)

1S13-3　シンギュラリティ細胞の脱分化による幹細胞集団維持機構の解明
Homeostasis of stem cell populations maintained by rare de-differentiating subsets
○中西 未央（Chiba Univ.）
**Mio Nakanishi** (*Grad. Sch. Med.*)

1S13-4　Self-patterning of brain organoids
**Kent Imaizumi** (*Department of Physiology, Keio University School of Medicine*)

1S13-5　免疫応答を介したアルツハイマー病発症への寄与の解明
Involvement in the development of Alzheimer's disease through activation of systemic immune response
○伊藤 美菜子, 金子 竜晟（九大・生医研）
**Minako Ito**, Ryusei Kaneko (*Med. Inst. Bioreg., Kyusyu Univ.*)

1S13-6　社会性アメーバの時空間自己組織化過程におけるシンギュラリティ ~AMATERAS1.0 で実現した定量トランススケール解析~
Quantitative trans-scale analysis of a singularity in spatiotemporal self-organization of social amoeba by using AMATERAS1.0
○垣塚 太志 [1], 原 佑介 [2], 市村 垂生 [1], 永井 健治 [1,3], 堀川 一樹 [2]（[1] 阪大・先導, [2] 徳大・先端研究推進センター, [3] 阪大・産研）
**Taishi Kakizuka[1]**, Yusuke Hara[2], Taro Ichimura[1], Takeharu Nagai[1,3], Kazuki Horikawa[2] ([1]*OTLI, Osaka Univ.*, [2]*Adv. Res. Prom. Cen., Tokushima Univ.*, [3]*SANKEN, Osaka Univ.*)

おわりに
Closing Remarks

16:00〜18:30　Ch08

## 1S14　共催：新学術領域「情報物理学でひもとく生命の秩序と設計原理」勾配検知の情報生物物理学
## Information biophysics of gradient sensing in organisms

**オーガナイザー：石島 秋彦（大阪大学），岡田 康志（理化学研究所/東京大学）**
**Organizers: Akihiko Ishijima (Osaka Univ.), Yasushi Okada (RIKEN/The Univ. of Tokyo)**

Biological sensory systems, such as chemotaxis, phototaxis, gradient sensing and so on, are functions that are widely available in the biological world. For example, bacterial chemotaxis is one of the most well-studied areas from both theoretical and experimental perspectives. Various methods have been used in experiments, including genetics, biochemistry, and imaging. Theories have been discussed from various perspectives such as Ising model, information theory, and efficiency. In this symposium, we would like to gather theoretical and experimental researches to promote mutual integration from the viewpoint of information biophysics.

1S14-1　ケモフォレシス・エンジン：ATPase 駆動型カーゴ輸送の理論
Chemophoresis Engine: Theory of ATPase-driven Cargo Transport
○菅原 武志 [1], 金子 邦彦 [1,2]（[1] 東大・生物普遍性, [2] 東大・総合文化）
**Takeshi Sugawara[1]**, Kunihiko Kaneko[1,2] ([1]*UBI, Univ. Tokyo*, [2]*Grad. Sch. Arts Sci., Univ. Tokyo*)

1S14-2　サルモネラのべん毛運動と走化性
Flagellar motility and chemotaxis in *Salmonella*
○森本 雄祐 [1,2]（[1] 九工大・院情報工, [2]JST・さきがけ）
**Yusuke V. Morimoto[1,2]** ([1]*Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*PRESTO, JST*)

1S14-3　Near-critical tuning of conformational spread revealed by single-cell FRET in bacterial chemoreceptor arrays
Johannes M. Keegstra[1], Fotios Avgidis[1], Yuval Mullah[1], John S. Parkinson[2], **Thomas Shimizu[1]** ([1]*AMOLF Institute, Amsterdam, The Netherlands*, [2]*Department of Biology, University of Utah, Salt Lake City, USA*)

1S14-4　Subpopulation of chemotactic cells with extremely high sensitivity
**Satomi Matsuoka[1,2,3]**, Masahiro Ueda[1,2] ([1]*Grad. Sch. Frontier Biosciences, Osaka Univ.*, [2]*RIKEN, BDR*, [3]*PRESTO, JST*)

1S14-5　初期胚組織はモルフォゲン勾配のノイズを感知し修復する能力を備えている
Embryonic cell community senses and eliminates the noise of morphogen gradient
○穐枝 佑紀（阪大・微研・生体統御）
**Yuki Akieda** (*Hom. Reg., RIMD, Osaka Univ.*)

1S14-6　ゼブラフィッシュ胚におけるモルフォゲン分布の制御
Spatiotemporal regulation of morphogen distribution in zebrafish embryo
○猪股 秀彦, 浜田 裕貴, 金村 節子（理研・BDR）
**Hidehiko Inomata**, Hiroki Hamada, Setsuko Kanamura (*BDR., Riken*)

9:00〜11:30　Ch01

## 2S1　共催：AMED「創薬等ライフサイエンス研究支援基盤事業(BINDS)」 高分解能クライオ電子顕微鏡の進展と共同利用
Technical Development and Sharing of High-Resolution Cryo-Electron Microscopes

**オーガナイザー：中村 春木（大阪大学），吉川 雅英（東京大学），村田 武士（千葉大学）**
**Organizers: Haruki Nakamura (Osaka Univ.), Masahide Kikkawa (The Univ. of Tokyo), Takeshi Murata (Chiba Univ.)**

Since 2017, high-end cryo-electron microscopes (EMs) have been installed with equipment grants by the BINDS (Basis for Supporting Innovative Drug Discovery and Life Science Research) project. In addition, eight more cryo-EMs are being installed in 2021 at several laboratories in Japan. These new shared cryo-EM facilities enable higher-resolution and higher-throughput structural analysis, together with the recent technological progresses, including the development of new grids and methods for online remote cryo-EM operation. In this symposium, the symposists will review the results of single particle analysis, tomography, and micro-ED by cryo-EMs. We will also review the issues to be overcome by technical development and by the next BINDS program that is expected to start in 2022.

### 2S1-1　クライオ電子顕微鏡によるクロススケール構造解析
Cross-scale structural studies by cryo-electron microscopy
○吉川 雅英（東京大学）
**Masahide Kikkawa** (*The University of Tokyo*)

### 2S1-2　高速データ収集と原子分解能を両立したクライオ電子顕微鏡撮影法と酸化修飾グラフェングリッド
High throughput atomic resolution cryoEM analysis by multi-hole imaging and epoxidized graphene grid
○難波 啓一（阪大・院生命機能）
**Keiichi Namba** (*Grad. Sch. Frontier Biosci., Osaka Uinv., RIKEN BDR & SPring-8*)

### 2S1-3　Cryo-EM ネットワークと産学連携
Industry-academia collaboration with the cryo-EM network
○千田 俊哉 [1], 村田 武士 [2], 岩崎 憲治 [3]（[1] 高エネ機構・物構研・構造生物, [2] 千葉大・院理学, [3] 筑波大・生存ダイナミクス）
**Toshiya Senda[1]**, Takeshi Murata[2], Kenji Iwasaki[3] ([1]*SBRC, IMSS, KEK*, [2]*Grad. Sch. Sci, Chiba Univ.*, [3]*TARA, Univ. Tsukuba*)

### 2S1-4　COVID-19 等の感染症に対する治療薬・ワクチン開発を目指した BSL3 クライオ電子顕微鏡を軸とする北大創薬拠点
BSL3 Cryo-EM facility of Hokkaido Univ. Drug Discovery Base for the Development of Therapeutics and Vaccines against COVID-19
○前仲 勝実（北大・院薬）
**Katsumi Maenaka** (*Facult. Pharm.Sci., Hokkaido Univ.*)

### 2S1-5　東北大学の最新クライオ電子顕微鏡の活用と共同利用について
New 300kV Cryo EM of Tohoku University: application and public utilization
○小柴 生造 [1,2,3], 木下 賢吾 [1,2,4], 山本 雅之 [1,2,3]（[1] 東北大・未来型医療創成センター, [2] 東北大・東北メディカル・メガバンク機構, [3] 東北大・院医, [4] 東北大・院情報）
**Seizo Koshiba[1,2,3]**, Kengo Kinoshita[1,2,4], Masayuki Yamamoto[1,2,3] ([1]*INGEM, Tohoku Univ.*, [2]*ToMMo, Tohoku Univ*, [3]*Grad. Sch. Med., Tohoku Univ*, [4]*Grad. Sch. Info., Tohoku Univ*)

2S1-6 **九州・西日本エリアにおける創薬支援を目指したクライオ電顕ネットワーク**
Cryo-EM network aiming to support drug discovery in the Kyushu / West Japan area
○真柳 浩太（九大・生体防御医学研究所）
**Kouta Mayanagi** (*Medical Institute of Bioregulation, Kyushu Univ.*)

**おわりに**
Closing Remarks
中村 春木（阪大）
Haruki Nakamura (*Osaka Univ.*)

9:00〜11:30　Ch02
2S2　**生物物理学的手法を駆使した細胞内プロセスにおけるタンパク質間相互作用の理解**
Biophysical basis for understanding the protein-protein interaction involved in essential cellular process

**オーガナイザー：武藤 梨沙（福岡大学），小柴 琢己（福岡大学）**
**Organizers: Risa Mutoh (Fukuoka Univ.), Takumi Koshiba (Fukuoka Univ.)**

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Protein-protein interactions are essential biological reactions occurring at inter- and intra-cellular levels. The analysis of their mechanism is generally required in order link to understand their various cellular functions. Recent biophysical methodologies provide us useful tools for investigating protein-protein interactions, especially in live cells. In this symposium, we invite domestic young investigators and discuss on new techniques (e.g. IP-MS, lipid mixing assay, bioluminescence) that explore a new study of protein-protein interaction and membrane protein complexes involved in essential cellular processes.

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**はじめに**
Opening Remarks

2S2-1 **質量分析法によるミトコンドリアタンパク質複合体の解析**
Mass spectrometry-based methods for analysing the mitochondrial interactome in mammalian cells
○小柴 琢己（福岡大・理学・化学）
**Takumi Koshiba** (*Dep. Sci., Chem., Fukuoka Univ.*)

2S2-2 **ミトコンドリア膜融合反応の試験管内再構成**
In vitro reconstitution of mitochondrial membrane fusion
○伴 匡人 [1], 石原 直忠 [2]（[1] 久留米大・分子生命科学, [2] 阪大・理・生物科学）
**Tadato Ban[1]**, Naotada Ishihara[2] ([1]*Inst. of Life Sci., Kurume Univ.*, [2]*Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.*)

2S2-3 **熱力学的解離速度分析法を用いた光化学系 I 三量体間の結合エネルギーの解析**
Investigation on the thermodynamic dissociation kinetics of Photosystem I trimer to determine the binding strengths of each protomer
○河合 寿子 [1], 金 恩哲 [2]（[1] 山形大･理学部, [2] 基生研）
**Hisako Kawai[1]**, Eunchul Kim[2] ([1]*Fac. Sci., Univ. Yamagata*, [2]*NIBB*)

2S2-4 (1-15-1330) 細胞膜中の TRPV1・TRPV4 チャネルの 1 分子動態の比較解析
(1-15-1330) Comparative analysis of single-molecule dynamics of TRPV1 and TRPV4 channels in living cells
○柳川 正隆 [1,2], 桑島 佑太朗 [1,3], 阿部 充宏 [1], 廣島 通夫 [1,4], 上田 昌宏 [4,5], 有田 誠 [3,6,7], 佐甲 靖志 [1]
([1] 理研 CPR, [2] 科学技術振興機構, [3] 慶應大・院薬, [4] 理研 BDR, [5] 阪大・院生命機能, [6] 理研 IMS, [7] 横浜市大・院生命医科学)
**Masataka Yanagawa[1,2]**, Yutaro Kuwashima[1,3], Mitsuhiro Abe[1], Michio Hiroshima[1,4], Masahiro Ueda[4,5], Makoto Arita[3,6,7], Yasushi Sako[1] ([1]*Riken CPR*, [2]*JST, PRESTO*, [3]*Faculty Pharm., Keio Univ.*, [4]*Riken BDR*, [5]*Grad. Sch. Front. Biosci., Osaka University*, [6]*Riken IMS*, [7]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

2S2-5 マルチ機能性光受容膜タンパク質・ロドプシンによる生命機能の光制御
Optical control of biological activities with multi-functional photoreactive membrane protein rhodopsin
○須藤 雄気（岡山大・院医歯薬）
**Yuki Sudo** (*Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ.*)

2S2-6 (1-02-1506) Cryo-EM analysis provides new mechanistic insight into ATP binding to $Ca^{2+}$-ATPase SERCA2b
**Yuxia Zhang[1]**, Satoshi Watanabe[1], Akihisa Tsutsumi[2], Hiroshi Kadokura[1], Masahide Kikkawa[2], Kenji Inaba[1] ([1]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*, [2]*Graduate School of Medicine, The University of Tokyo*)

2S2-7 Rhythmic ATP release from the cyanobacterial circadian clock protein KaiC revealed by real-time monitoring of bioluminescence
**Risa Mutoh[1]**, Takahiro Iida[1], Kiyoshi Onai[2] ([1]*Fac. Sci., Fukuoka Univ.*, [2]*Grad. Sch. Agr., Kyoto Univ.*)

おわりに
Closing Remarks

9:00〜11:30 Ch03
## 2S3 共催：JST さきがけ「生命機能メカニズム解明のための光操作技術」多様な光受容体とオプトジェネティクスの最前線
## A variety of photoreceptors and the frontiers of optogenetics

**オーガナイザー：徳富 哲（大阪府立大学），角田 聡（名古屋工業大学）**
**Organizers: Satoru Tokutomi (Osaka Prefect. Univ.), Satoshi P Tsunoda (Nagoya Inst. Tech.)**

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Lives have acquired a variety of photoreceptors which absorb light in the UV to far red region during the evolution, such as many different types of rhodopsin, blue-light receptors, cryptochrome and phototropin, and red-far red-light reversible phytochromes. Researchers have adapted and utilized them for photobiological studies including optogenetics. The present Symposium introduces some leading results which includes channel rhodopsin in the trendy neuroscience, a novel function of mouse cryptochrome in circadian rhythm, use of a light-inactivated rhodopsin, peropsin, for vision restoration, photoregulation of protein kinase by phototropin, application of phytochrome-PIF and cryptochrome-CIB for optogenetics, and color tuning of cyanobacteriochrome.

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はじめに
Opening Remarks
徳富 哲 [1,2,3]（[1]JST さきがけ, [2] 大阪府大, [3] 東北大・植物園）
Satoru Tokutomi[1,2,3] ([1]*PRESTO, JST*, [2]*Osaka Pref. Univ.*, [3]*Bot. Garden, Tohoku Univ.*)

2S3-1 **海馬台からの経路選択的な情報送出：投射先を光同定した大規模活動計測による解析**
Projection-identified large-scale recording reveals pathway-specific information outflow from the subiculum
○北西 卓磨 [1,2]（[1] 大阪市立大・院医, [2] 科学技術振興機構・さきがけ）
**Takuma Kitanishi[1,2]** ([1]*Grad. Sch. Med., Osaka City Univ.*, [2]*PRESTO, JST*)

2S3-2 **概日光受容の新規メカニズムと光遺伝学への応用**
Mechanism of circadian photoreception and its application for optogenetics.
○平野 有沙, 高橋 徹, 櫻井 武（筑波大・医学医療系）
**Arisa Hirano**, Tohru Takahashi, Takeshi Sakurai (*Faculty of Medicine, University of Tsukuba*)

2S3-3 **視覚再生に向けた暗活性・光不活性化 GPCR 型光遺伝学ツールの開発**
Development of a dark-active, light-inactivated GPCR-based optogenetic tool for vision restoration
○永田 崇 [1,2]（[1] 東大・物性研究所, [2]JST・さきがけ）
**Takashi Nagata[1,2]** ([1]*Inst. Solid State Phys., Univ. Tokyo*, [2]*JST, PRESTO*)

2S3-4 Development of photoinactivatable protein kinases to manipulate plant cell growth
**Hiromasa Shikata[1,2]** ([1]*Dev. Plant Environmental Responses, NIBB*, [2]*PRESTO, JST*)

2S3-5 **培養細胞、分裂酵母、線虫における細胞内シグナル伝達系の光操作**
Optical control of cell signaling in cultured cells, fission yeast, and worms
○青木 一洋 [1,2]（[1] 自然科学研究機構・基生研, [2] 自然科学研究機構・生命創成探究センター）
**Kazuhiro Aoki[1,2]** ([1]*NIBB, NINS*, [2]*ExCELLS, NINS*)

2S3-6 **多様なシアノバクテリオクロム光受容体の発見と改変**
Discovery and engineering of diverse cyanobacteriochrome photoreceptors
○成川 礼（都立大・院理学）
**Rei Narikawa** (*Grad. Scho. Biol. Sci., Tokyo Metro. Univ.*)

9:00〜11:30　Ch04
## 2S4　共催：学術変革領域(A)「DNA の物性から理解するゲノムモダリティ」ゲノム DNA の生物物理学〜ゲノムモダリティの理解へ向けて〜
Biophysics on Genome DNA - Toward Understanding of Genome Modality -

**オーガナイザー：瀧ノ上 正浩（東京工業大学），高田 彰二（京都大学），前島 一博（国立遺伝学研究所）**
**Organizers: Masahiro Takinoue (Tokyo Tech), Shoji Takada (Kyoto Univ.), Kazuhiro Maeshima (NIG)**

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The current trends in genome research, from genome sequencing to enome editing, have revolved based on the understanding of the informational aspects of genome, such as the replication and recombination of base sequences, and epigenetic regulation by histone modifications. However, the physical properties of genomic DNA as a polymer have not been fully elucidated yet, although it is an important property underlying all the phenomena caused on the genome. In this symposium, we will introduce a research area “Genome Modalities”, which aims to reveal the true nature of genomes through understanding the physical properties of DNA, and discuss this issue with researchers inside and outside this area.

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はじめに
Opening Remarks

2S4-1 コヒーシンのリング構造とゲノム機能
Opening cohesin's ring structure is essential for genome functions
○西山 朋子（名古屋大学・院理・生命理学）
**Tomoko Nishiyama** (*Grad. Sch. Sci., Nagoya Univ.*)

2S4-2 ゲノムフォールディングを制御する SMC タンパク質の構造・機能のシミュレーション研究
Computational approach to structures and dynamic functions of SMC proteins that organize genome folding
○高田 彰二（京大・理）
**Shoji Takada** (*Kyoto Univ. Grad. Sch. Sci.*)

2S4-3 一分子ヌクレオソームイメージングによって明らかにする生細胞のクロマチン環境とその外的影響
Chromatin behavior in living cells revealed by single-nucleosome imaging
○前島 一博 [1,2]（[1] 国立遺伝学研究所, [2] 総合研究大学院大学）
**Kazuhiro Maeshima[1,2]** ([1]*National Institute of Genetics*, [2]*SOKENDAI*)

2S4-4 DNA 液滴の液-液相分離：ナノ～メソスケールの DNA 物性のゲノムモダリティ
Liquid-liquid phase separation of DNA liquid: Genome modality of DNA physics in nano-mesoscopic scale
○瀧ノ上 正浩 [1,2]（[1] 東工大・情報工学系, [2] 東工大・生命理工学系）
**Masahiro Takinoue[1,2]** ([1]*Dept. Computer Sci., Tokyo Tech*, [2]*Dept. Life Sci. Tech., Tokyo Tech*)

2S4-5 精子クロマチンの操作と測定
Manipulation and measurement of sperm chromatin
○岡田 由紀（東大・定量研）
**Yuki Okada** (*IQB, Univ. Tokyo*)

おわりに
Closing Remarks

9:00～11:30　Ch05

## 2S5　統合的多階層アプローチによるシアノバクテリア生物時計システムの新展開
An Integrated Multi-scale Approach for Studying Cyanobacterial Circadian Clock System

**オーガナイザー：秋山 修志（分子科学研究所），上久保 裕生（奈良先端科学技術大院大学）**
**Organizers: Shuji Akiyama (CIMoS), Hironari Kamikubo (NAIST)**

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Circadian rhythms are self-sustained oscillations with a period of approximately 24 h, enabling organisms to adapt to daily alterations in the environment. So far, many studies have investigated the time-measuring mechanism in the circadian clocks from bacteria to mammals. However, it remains unknown how the period is implemented in clock oscillators and kept unaffected against temperature changes (temperature compensation). In this symposium, we will focus especially on cyanobacterial circadian clock as a model system and address these questions using a multidisciplinary approach including, biophysics, structural biology, chronobiology, molecular biology, and protein engineering.

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はじめに
Opening Remarks

2S5-1 シアノバクテリアの時計タンパク質 KaiC の 2 つの ATPase ドメインによる概日時計の機械式時計モデル
Mechanical clock model for cyanobacterial circadian clock, based on the activities of two ATPase domains in KaiC
○三輪（伊藤） 久美子, 近藤 孝男（名古屋大・院理）
**Kumiko Ito-Miwa**, Takao Kondo (*Grad. Sch. Sci., Univ. Nagoya*)

2S5-2 KaiABC 振動子における温度補償性と 1 分子レベルのフィードバックループ
Temperature compensation and single-molecular feedback loops in the KaiABC oscillator
○笹井 理生（名古屋大学）
**Masaki Sasai** (*Nagoya University*)

2S5-3 連続滴定小角 X 線散乱測定を用いたリン酸化/脱リン酸化 KaiC アンサンブルに対する KaiA の滴定挙動解析
Binding behavior of KaiA for phosphorylated/dephosphorylated KaiC ensemble using continuous titration small-angle X-ray scattering
○上久保 裕生 [1,2,3], 山﨑 洋一 [2]（[1] 奈良先端大・デジタルグリーンイノベーションセンター, [2] 奈良先端大・物質創成, [3] 物構研・高エネ機構）
**Hironari Kamikubo[1,2,3]**, Yoichi Yamazaki[2] ([1]*CDG, NAIST*, [2]*MS, NAIST*, [3]*IMSS, KEK*)

2S5-4 Exploring ancient origin of circadian oscillation through KaiC evolution
**Atsushi Mukaiyama[1,2]**, Yoshihiko Furuike[1,2], Shuji Akiyama[1,2] ([1]*IMS, CIMoS*, [2]*SOKENDAI*)

2S5-5 シアノバクテリア時計タンパク質 KaiC の根幹を成すアロステリック制御
Core Allosteric Regulation in Cyanobacterial Circadian Clock Protein KaiC
○古池 美彦 [1,2], 向山 厚 [1,2], 欧陽 東彦 [1], 三輪 久美子 [3], シモン ダミアン [1,2], 山下 栄樹 [4], 近藤 孝男 [3]（[1] 分子科学研究所・協奏分子システム研究センター, [2] 総合研究大学院大学, [3] 名古屋大学大学院・理学研究科, [4] 大阪大学・蛋白質研究所）
**Yoshihiko Furuike[1,2]**, Atsushi Mukaiyama[1,2], Dongyan Ouyang[1], Kumiko Ito-Miwa[3], Simon Damien[1,2], Eiki Yamashita[4], Takao Kondo[3] ([1]*Research Center of Integrative Molecular Systems (CIMoS), Institute for Molecular Science*, [2]*SOKENDAI (The Graduate University for Advanced Studies)*, [3]*Graduate School of Science, Nagoya University*, [4]*Institute for Protein Research, Osaka University*)

9:00〜11:30　Ch06

## 2S6　蛋白質系の分子シミュレーションのサンプリング手法の発展
Advances in enhanced sampling methods for molecular simulations of protein systems

**オーガナイザー：光武 亜代理（明治大学），奥村 久士（生命創成探究センター）**
**Organizers: Ayori Mitsutake (Meiji Univ.), Hisashi Okumura (ExCELLS)**

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In recent years, it has become possible to perform molecular simulations on time scales of the order of milliseconds using special-purpose system and massive parallel computers. However, sampling methods that is about 10 to 100 times more efficient than ordinary molecular simulations are still important to investigate binding simulations and longer simulations. Since about 25 years ago, various sampling methods have been energetically introduced and developed into protein systems in Japan. Currently, many enhanced sampling methods are widely introduced in protein softwares such as AMBER, CHARMM, GENESIS, GEMB, GROMACS, NAMD, and myPresto. In this symposium, researchers who have originally developed sampling methods and applied to protein systems will give their talks.

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趣旨説明
Opening Remarks

2S6-1 (2-01-1712) Extensive Sampling of Spike protein down, one-up, one-open, and two-up-like Conformations and Transitions in SARS-Cov-2

**Hisham Dokainish**[1], Suyong Re[4], Chigusa Kobayashi[2], Takaharu Mori[1], Jaewoon Jung[1,2], Yuji Sugita[1,2,3] ([1]*Theoretical Molecular Science Laboratory, Riken*, [2]*Computational Biophysics Research Team, RIKEN*, [3]*Laboratory for Biomolecular Function Simulation, RIKEN*, [4]*Center for Drug Design Research, National Institutes of Biomedical Innovation*)

2S6-2* (2-03-1327) An estimation method for the diffusion coefficient using MD simulations with the basic cell containing only one protein as solute

**Tomoya Iwashita**[1], Masaaki Nagao[1], Akira Yoshimori[2], Masahide Terazima[3], Ryo Akiyama[1] ([1]*Department of Chemistry, Graduate School of Science, Kyushu University*, [2]*Department of Physics, Niigata University*, [3]*Department of Chemistry, Graduate School of Science, Kyoto University*)

2S6-3 Oligomer formation of proteins studied by generalized-ensemble algorithms

**Satoru G. Itoh**[1,2,3] ([1]*IMS*, [2]*ExCELLS*, [3]*SOKENDAI*)

2S6-4 **大規模タンパク質系への適用を目指した構造サンプリング法の開発**
Enhanced sampling methods targeting at large proteins

○森次 圭（横浜市大院・生命医科学）
**Kei Moritsugu** (*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

2S6-5 **マルチドメインタンパク質のリガンド結合による構造変化の分子機構**
Moelcular mechanisms underlying ligand-induced conformational changes in multi-domain proteins

○杉田 有治 [1,2,3]（[1] 理研・開拓研究本部, [2] 理研・計算科学研究センター, [3] 理研・生命機能科学研究センター）
**Yuji Sugita**[1,2,3] ([1]*RIKEN CPR*, [2]*RIKEN R-CCS*, [3]*RIKEN BDR*)

2S6-6 **膜に埋もれたヒトエンドセリン受容体に結合するボセンタンの結合メカニズム：スライドするフライ・キャストィングと配向選択メカニズム**
Sliding fly-casting and directional-selection mechanisms of bosentan binding to human endothelin receptor embedded in membrane

○肥後 順一（兵庫県立大学情報科学研究科）
**Junichi Higo** (*Graduate School of Information Science, University of Hyogo*)

2S6-7 **生体分子シミュレーションのための拡張アンサンブル法**
Generalized-ensemble algorithms for biomolecular simulations

○岡本 祐幸（名大・院理）
**Yuko Okamoto** (*Graduate School of Science, Nagoya Univ.*)

9:00〜11:30　Ch07

## 2S7　生体膜機能の人工制御化に有用な新アプローチと生物物理呼応
New artificial approaches and biophysical communications to control function of biological membranes

**オーガナイザー：中瀬 生彦（大阪府立大学），矢野 義明（武庫川女子大学）**
**Organizers: Ikuhiko Nakase (Osaka Prefect. Univ.), Yoshiaki Yano (Mukogawa Women's Univ.)**

Biological membranes have a complex supermolecular bilayer structure composed of diverse biomolecules such as lipids, proteins, and sugars. It is well known that biomembranes contain receptor proteins to detect changes in external environments, and their ligand molecules are available for controlling cell functions. Moreover, alternative approaches are possible to artificially perturb function of biomembranes by e.g., changing their shape, permeability, and domain structures following molecular interactions with lipids. New approaches using hybrid/designed molecules, model membranes, ultrafast spectroscopy, and chemistry on/in cells, will be introduced to discuss complex membrane functions with biophysical communications and their usefulness for molecular sensing and controlling cell functions.

はじめに
Opening Remarks

2S7-1　(1-10-1442) Local membrane curvature influences lipid signaling
**Marcel Hoerning**[1], Torsten Bullmann[2], Tatsuo Shibata[3] ([1]*Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, 70569 Stuttgart, Germany*, [2]*Carl-Ludwig-Institute for Physiology, University of Leipzig, 04103 Leipzig, Germany*, [3]*Laboratory for Physical Biology, RIKEN Center for Biosystems Dynamics Research, Kobe 650-0047, Japan*)

2S7-2　Chemical tools for manipulating signaling proteins and lipids on organelle membranes
**Shinya Tsukiji** (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

2S7-3　A common oligomer identified using 2D IR spectroscoy in mammals that contract type 2 diabetes
**Martin Zanni** (*University of Wisconsin-Madison*)

2S7-4　膜貫通ペプチドを用いたナノポアの新規設計
De novo design of nanopore using transmembrane peptides
○川野 竜司（東京農工大学・院生命工学）
**Ryuji Kawano** (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

2S7-5　生体膜機能の理解に向けた脂質ー膜タンパク質相互作用解析
Interaction analysis between membrane proteins and lipids to understand biological membranes
○松森 信明（九大・院理）
**Nobuaki Matsumori** (*Grad. Sch. Sci., Kyushu Univ.*)

2S7-6　スマートシャペロン高分子による脂質膜の刺激応答性小胞・シート転移
Stimuli-responsive vesicle/sheet transformation of lipid membranes mediated by smart chaperone polymers
○丸山 厚（東工大・生命理工）
**Atsushi Maruyama** (*School of Life Sci. & Tech., Tokyo Inst. of Tech.*)

2S7-7 弱毒化カチオン性両親媒性ペプチド存在下の IgG による液滴形成と効率的細胞内移行
Liquid droplet formation and facile cytosolic translocation of IgG in the presence of attenuated cationic amphiphilic lytic peptides
○二木 史朗（京大・化研）
**Shiroh Futaki** (*Inst. Chem. Res., Kyoto Univ.*)

おわりに
Closing Remarks

3 日目（11 月 27 日（土））／Day 3（Nov. 27 Sat.）

9:00〜11:30　Ch02
3S1　オーストラリア—日本交流シンポジウム
ASB-BSJ Joint Symposium

**オーガナイザー：片山 耕大（名古屋工業大学），Matthew AB Baker（Univ. of New South Wales）**
**Organizers: Kota Katayama (Nagoya Inst. of Tech.), Matthew AB Baker (Univ. of New South Wales)**

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This symposium aims at highlighting the current main stream topics in protein science and biophysics and also searching for the collaboration and development in research filed of biophysics in the Japan-Australia region. The symposium includes three up-and-coming young researchers related to biophysics from the ASB and BSJ sides. With the rapid progress of science and technology in recent years, through this constructive discussion, we wish to keep the scientific activity, and to give a large impact to the community.

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はじめに
Opening Remarks

3S1-1 Cyclodextrins increase membrane tension and are universal activators of mechanosensitive channels
**Charles David Cox** (*Victor Chang Cardiac Research Institute, Sydney*)

3S1-2 Understanding the interaction of phenolic acids with phospholipid bilayers
Sheik Imamul Hossain[1], **Evelyne Deplazes[1,2]** ([1]*School of Life Sciences, University of Technology Sydney, Australia*, [2]*School of Chemistry and Molecular Biosciences, University of Queensland, Australia*)

3S1-3 Structural analyses on pathogenic RNA viruses
**Yukihiko Sugita[1,2]** ([1]*InFront, Kyoto Univ.*, [2]*Hakubi Center, Kyoto Univ.*)

3S1-4 酵母複製とプリオン伝送の多スケール運動・空間モデル
A multi-scale kinetic and spatial model of yeast replication and prion transmission
○Hall Damien（金沢大学　WPI-NANO-LSI）
**Damien Hall** (*Kanazawa University WPI-NANO-LSI*)

3S1-5 合成小分子を利用した細胞内タンパク質の光操作
Chemo-optogenetic manipulation of protein functions in living cells using synthetic small molecules
○吉井 達之（京都大学 iPS 細胞研究所）
**Tatsuyuki Yoshii** (*CiRA, Kyoto Univ.*)

おわりに
Closing Remarks

9:00〜11:30　Ch02

## 3S2　共催：学術変革領域研究(B)「パラメトリク翻訳」<br>パラメトリックな翻訳調節機構<br>Parametric biology based on translation rate regulatory mechanism

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

Translation is not just a linear bridge between mRNA and protein, but is highly variable and characterized by a wide dynamic range (1,000 times that of transcription), local control within the cell, and reactions that consume up to 50% of the energy in the cell. This raises the possibility that translation is not controlled by 0 or 1 on/off control, but is subtly controlled by "rate variation" within a continuous reaction. Currently, we are beginning to create a translation parametric biology that focuses on the concept of "variable translation rate. This will elucidate its role in the flexible functional control of life.

3S2-1　A specific eIF4A paralog facilitates LARP1-mediated translation repression during mTORC1 inhibition
**Shintaro Iwasaki** (*RIKEN Cluster for Pioneering Research*)

3S2-2　**人工神経回路組織における神経回路とタンパク質合成制御**
Organoids-on-a-chip models for understanding neuronal circuits and underlying protein synthesis regulations
○池内 与志穂 [1,2,3]（[1] 東大・生産研, [2] 東大・院工・化生, [3] 東大・Beyond AI 研究機構）
**Yoshiho Ikeuchi[1,2,3]** ([1]*IIS, Univ. Tokyo*, [2]*Chem. Bio., Eng., Univ. Tokyo*, [3]*Inst. AI and Beyond, Univ. Tokyo*)

3S2-3　**生理的体温変化による体内時計のパラメトリック制御**
Parametric entrainment of the circadian clock by body temperature change
○三宅 崇仁, 井ノ上 雄一, 土居 雅夫（京都大学・院薬）
**Takahito Miyake**, Yuich Inoue, Masao Doi (*Grad. Sch. Pharm. Sci., Kyoto Univ.*)

3S2-4　Fluorescent nanodiamonds for thermal biology
**Shingo Sotoma[1]**, Yoshie Harada[1,2] ([1]*IPR, Osaka Univ.*, [2]*QIQB, Osaka Univ.*)

3S2-5　**細胞内温度シグナリングによる翻訳調節機構**
Intracellular thermal signaling facilitates translation control
○岡部 弘基 [1,2]（[1] 東京大学大学院薬学系研究科, [2]JST さきがけ）
**Kohki Okabe[1,2]** ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*PRESTO, JST*)

9:00〜11:30　Ch03

## 3S3　タンパク質の水和とその凍結現象 -細胞凍結や食品冷凍保存への応用-
Protein hydration and its freezing phenomena -toward the application for cell freezing and frozen food storage-

**オーガナイザー：山本 直樹（自治医科大学），中川 洋（日本原子力研究開発機構）**
**Organizers: Naoki Yamamoto (Jichi Medical Univ.), Hiroshi Nakagawa (J-PARC)**

Protein hydration water is crucial for the activation of the dynamics related to the protein functional expression. We introduce recent progress on the understanding of the interplay between hydration water and protein in terms of the freezing of hydration water. Recent experimental results obtained by broadband dielectric spectroscopy and neutron scattering on proteins and tissues will be reported. Furthermore, present recent progress in the understanding the cell-freezing and food frozen storage will be represented. Especially, polymeric cryoprotectants, which have low toxicity and high protection capability, will be introduced and its physicochemical property will be discussed.

はじめに
Opening Remarks

3S3-1　誘電緩和分光法で観測する水和角質層中の水と氷
Water and ices in hydrated stratum corneum observed via dielectric relaxation spectroscopy
○中西 真大（福岡工業大・工学部）
**Masahiro Nakanishi** (*Fac. Eng., Fukuoka Inst. Tech.*)

3S3-2　中性子散乱を用いて明らかとなった水和水の熱活性がタンパク質ダイナミクスに与える影響
Effect of hydration and its thermal energy on protein dynamics monitored by neutron scattering
○山本 直樹（自治医大・医）
**Naoki Yamamoto** (*Sch. Med., Jichi Med. Univ.*)

3S3-3　生体分子と水の凍結・融解・ガラス転移
Freezing, Thawing and Glass Transition of Biomolecules and Water
○中川 洋（日本原子力研究開発機構）
**Hiroshi Nakagawa** (*Japan Atomic Energy Agency*)

3S3-4　Polyampholytes for low-temperature preservation of cells and proteins
**Robin Rajan**, Kazuaki Matsumura (*Japan Advanced Institute of Science and Technology*)

おわりに
Closing Remarks

9:00〜11:30　Ch04

## 3S4　統合的アプローチによるタンパク質の大規模ダイナミクスの探索
Probing large-scale dynamics in protein through integrative approaches

**オーガナイザー：齋尾 智英（徳島大学），井上 倫太郎（京都大学）**
**Organizers: Tomohide Saio (Tokushima Univ.), Rintaro Inoue (Kyoto Univ.)**

Large scale dynamics" (LS-dynamics) such as domain-domain correlation motion, often drives protein activity, but the scarcity of the information regarding them impedes the understanding of the mechanism. In other words, the LS-dynamics of protein is still a frontier in protein science. Everyone recognizes that, although state-of-the-art techniques provide the knowledge of various aspects of LS-dynamics, only a single method could not adequately cover the ranges of length and time scales required for the LS-dynamics. Hence, agenda are how to integrate their results and build the full picture of LS-dynamics. In this symposium, young scientists from variety of scientific fields, solution scattering, NMR, cryo-EM, and computation, will lead to discuss about the integration of their methods aiming to unveil the biologically significant LS-dynamics.

はじめに
Opening Remarks

3S4-1　KEK クライオ電顕施設の運用と現状について
Operation and recent activities of the cryo-EM facility in KEK
○安達 成彦（高エネ機構・物構研・構造生物）
**Naruhiko Adachi** (*SBRC, IMSS, KEK*)

3S4-2　X 線小角散乱データと粗視化分子動力学計算に基づく生体分子の構造ダイナミクスの解明
Modeling structural dynamics of biomolecules using small angle X-ray scattering data and coarse-grained molecular dynamics simulations
○清水 将裕, 奥田 綾, 守島 健, 柚木 康弘, 佐藤 信浩, 井上 倫太郎, 裏出 令子, 杉山 正明（京都大・複合研）
**Masahiro Shimizu**, Aya Okuda, Ken Morishima, Yasuhiro Yunoki, Nobuhiro Sato, Rintaro Inoue, Reiko Urade, Masaaki Sugiyama (*KURNS., Kyoto Univ.*)

3S4-3　NMR と EPR を組み合わせたマルチドメインタンパク質の大規模ダイナミクスの探索
Large-scale conformational distribution of a multi-domain protein enzyme investigated by NMR and EPR
○齋尾 智英（徳島大・先端酵素）
**Tomohide Saio** (*Inst. of Adv. Med. Sci.*)

3S4-4　X 線/中性子散乱と MD シミュレーションを用いた統合的アプローチによる IDP の動的構造と機能の理解
Integrated approach using X-ray/Neutron scattering and MD simulation for understanding dynamic structure and function of IDP
○小田 隆 [1,2]（[1] 立教大学理学部生命理学科, [2] 横浜市立大学大学院生命医科学研究科）
**Takashi Oda[1,2]** ([1]*Department of Life Science, Rikkyo University,*, [2]*Graduate School of Medical Life Science, Yokohama City University*)

3S4-5 ストレス刺激により誘起される ATP 枯渇および低 pH 条件における MAPK p38α の頑強な酵素活性を担う機能的構造平衡の解明
Functional equilibrium underlying the robust kinase activity of MAPK p38α under the stress-associated ATP-depleted, low pH condition
○徳永 裕二 [1], 竹内 恒 [1], 高橋 栄夫 [2], 嶋田 一夫 [3]（[1] 産総研・細胞分子工学, [2] 横市大・生命医科学, [3] 理研・鶴見）
**Yuji Tokunaga[1]**, Koh Takeuchi[1], Hideo Takahashi[2], Ichio Shimada[3] ([1]*CMB, AIST*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [3]*Tsurumi Inst., Riken*)

おわりに
Closing Remarks

9:00〜11:30 Ch05
## 3S5 ペプチド-膜生物物理学 : 膜結合抗菌ペプチドおよびアミロイドペプチドの最新生物物理研究
Peptide-Membrane Biophysics: Current Biophysical Studies of Membrane-bound Antimicrobial Peptides and Amyloid Peptides

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

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In the biophysical research field, the structure and dynamics of peptide and lipid molecules within complex biomolecular assemblies have been investigated for many years with a special focus on membrane-interaction of antimicrobial peptides (AMPs) and kinetics of amyloid fibril formation. In this symposium, current research topics on "peptide-membrane biophysics" by imaging, NMR, and computational methods will be presented. Additionally, advanced over-expression technology and deep learning for molecular design of AMPs will be presented.

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はじめに
Opening Remarks

3S5-1 遺伝子組換え抗菌ペプチド生産と NMR 解析への応用
Application of novel overexpression systems of recombinant antimicrobial peptides for NMR analysis
○相沢 智康（北大・院生命科学）
**Tomoyasu Aizawa** (*Grad. Sch. Life Sci., Hokkaido Univ.*)

3S5-2 AI で設計した膜貫通ペプチドの分子動力学計算による選択と理解
Using molecular dynamics simulations to prioritize and understand AI-generated cell penetrating peptides
○津田 宏治（東大・新領域）
**Koji Tsuda** (*Grad. Sch. Frontier Sci., Univ. Tokyo*)

3S5-3 単一巨大リポソーム法や単一細胞実験から解明された抗菌ペプチドの作用機構
Modes of Action of Antimicrobial Peptides (AMPs) revealed by the Single Giant Unilamellar Vesicle (GUV) Method and Single Cell experiments
○山崎 昌一 [1,2,3]（[1] 静大・電研, [2] 静大・創造院・統合バイオ, [3] 静大・院理）
**Masahito Yamazaki[1,2,3]** ([1]*Res. Inst. Ele., Shizuoka Univ.*, [2]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

3S5-4* (2-10-1351) 放射光円二色性・直線二色性・蛍光異方性により明確化された生体膜に誘起されたマガイニン 2β 凝集体の特徴
(2-10-1351) Membrane-Induced β-Aggregates of Magainin 2 Characterized by Circular Dichroism, Linear Dichroism, and Fluorescence Anisotropy
○熊代 宗弘 [1], 末永 翔磨 [1], 松尾 光一 [2]（[1] 広大・院理学, [2] 広大・放射光）
**Munehiro Kumashiro[1]**, Shoma Suenaga[1], Koishi Matsuo[2] ([1]*Grad. Sch. Sci., Hiroshima Univ.*, [2]*HiSOR, Hiroshima Univ.*)

3S5-5 Conformational plasticity defines cell permeabilization activity of cyclic peptides
**Koh Takeuchi[1,2]** ([1]*CMB, AIST*, [2]*Grad. Sch. Pharm. Sci., The Univ. of Tokyo*)

3S5-6 アミロイド β ペプチドの凝集と解離の分子動力学シミュレーション
Molecular Dynamics Simulations for Aggregation and Disaggregation of Amyloid-β Peptides
○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] 総研大）
**Hisashi Okumura[1,2,3]** ([1]*Exploratory Research Center on Life and Living Systems*, [2]*Institute for Molecular Science*, [3]*SOKENDAI*)

3S5-7 膜環境におけるアミロイド β の分子集合
Molecular assembly of amyloid-β in membrane environments
○矢木 真穂 [1,2]（[1] 自然科学研究機構・生命創成探究セ, [2] 自然科学研究機構・分子研）
**Maho Yagi-Utsumi[1,2]** ([1]*ExCELLS, NINS*, [2]*IMS, NINS*)

9:00〜11:30 Ch06
## 3S6 ライブセルイメージングと融合した機能的オミクス解析の新潮流
New Trends in Functional Omics Analysis Integrated with Live Cell Imaging

**オーガナイザー：白崎 善隆（東京大学），城口 克之（理化学研究所）**
**Organizers: Yoshitaka Shirasaki (The Univ. of Tokyo), Katsuyuki Shiroguchi (RIKEN)**

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Cells change their function from time to time based on the alteration of their gene expression. Live cell imaging is an excellent technique for tracking the cellular functions, though it has limited targets. On the other hand, omics analyses such as high-throughput sequencing and mass spectrometry have advantages for comprehensiveness on gene expression analysis, although they cannot obtain time-series information due to disruptive manipulations. In this symposium, we will focus on advanced single-cell technologies that bridge the gap between time-series and comprehensive information on dynamic cellular functions, and will discuss the future prospects of this field.

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はじめに
Opening Remarks

3S6-1 SCOPE-seq: Scalable Technology for Linking Live Cell Imaging and Single-Cell RNA-seq
**Peter Sims** (*Columbia University*)

3S6-2 (2-15-1736) 微小電気穿孔法を用いた細胞膜の機械特性と遺伝子発現の統合解析
(2-15-1736) A combined analysis of membrane-mechanical phenotyping and transcriptomics using nanoelectroporation
○塩見 晃史, 金子 泰洸ポール, 西川 香里, 新宅 博文（理研・開拓・白眉）
**Akifumi Shiomi**, Taikopaul Kaneko, Kaori Nishikawa, Hirofumi Shintaku (*Hakubi, CPR, RIKEN*)

3S6-3 **免疫細胞の活性化の瞬間を視て採って調べる**
Analysis of Gene Expression at the Moment of Immune Cell Activation by Live Cell Imaging & Harvesting
○白崎 善隆（東京大学・院薬）
**Yoshitaka Shirasaki** (*Grad.Sch.Pharm., Univ. Tokyo*)

3S6-4 **超高速流体制御が拓くオンチップ細胞操作・計測**
On-chip cell manipulation and analysis opened up by ultra-high-speed flow control
○佐久間 臣耶（九大・機械工学部門）
**Shinya Sakuma** (*Dept. of Mechanical Engineering, Kyushu University*)

3S6-5 **1 細胞メタボローム・プロテオーム解析への挑戦**
Challenge to single-cell metabolome and proteome analyses
○和泉 自泰 [1], 中谷 航太 [1], 秦 康祐 [1], 山村 昌平 [2], 松本 雅記 [3], 馬場 健史 [1]（[1] 九州大学生体防御医学研究所, [2] 産業技術総合研究所健康医工学研究部門, [3] 新潟大学大学院医歯学総合研究科）
**Yoshihiro Izumi[1]**, Kohta Nakatani[1], Kosuke Hata[1], Shohei Yamamura[2], Masaki Matsumoto[3], Takeshi Bamba[1] ([1]*Medical Institute of Bioregulation, Kyushu University*, [2]*Health and Medical Research Institute, National Institute of Advanced Industrial Science and Technology*, [3]*Graduate School of Medical and Dental Sciences, Niigata University*)

3S6-6 Decoding single-cell transcriptomic states from cell images enabled by robotic data acquisition and deep learning
**Jianshi Jin**, Katsuyuki Shiroguchi (*BDR, RIKEN*)

**おわりに**
Closing Remarks