Recent advances in experimental and theoretical techniques have enabled us to understand detailed mechanisms of gene expression. Since conventional approaches in vitro are usually not enough to fully understand them, integrative approaches combining various techniques are essential to reveal dynamic structures of proteins and DNA in the cell at the molecular level. In this symposium, we discuss how hybrid approaches using the X-ray crystallography, cryo-electron microscopy, single-molecule imaging, and molecular simulations can contribute to the integrative understandings of genome functions.

1SBA-1 Chromatin dynamics and transcription
Kazuhiro Maeshima, Kayo Hibino, Ryosuke Nagashima (Genome Dynamics Laboratory, National Institute of Genetics)

1SBA-2 Structural and functional basis of the Mediator complex in the eukaryotic transcriptional system
Kayo Nozawa (The University of Tokyo, Institute for Quantitative Biosciences)

1SBA-3 Structural basis of nucleosome transcription by RNA polymerase II
Shun-ichi Sekine (RIKEN BDR)

1SBA-4 Dynamic structures of the RNA polymerase II elongation complex by cryo-EM and MD approaches
Takaharu Mori, Haruhiko Ehara, Shun-ichi Sekine, Yuji Sugita (RIKEN Theor. Mol. Sci. Lab., RIKEN BDR (Yokohama), RIKEN BDR (Kobe), RIKEN R-CCS)

1SBA-5 Allostery of Nucleosomal DNA for Transcription Factor Binding
Cheng Tan, Shoji Takada (Kyoto University)

1SBA-6 Single-molecule imaging of a non-hexameric *Escherichia coli* UvrD mutant lacking C-terminal residues
Hiroaki Yokota (Biophotonics Lab., Grad. Sch. Creation New Photon. Indust.)
Fundamental reactions of life occur mainly in a space surrounded by a biological membrane or on its interface. Unraveling phenomena that are specific to such a ‘soft’ compartment/interface not only leads to understanding the living systems but also gives us clues in designing artificial biosystems more rationally. In this symposium, we will discuss the potential and perspectives of the use of soft compartments/interfaces at several hierarchical levels, from nano to macroscale.

1SCA-1 DNA origami lattices self-assembled on lipid bilayer membranes
Yuki Suzuki (FRIS, Tohoku Univ.)

1SCA-2 (1Pos074) 脂質分子の混み合い効果による膜貫通タンパク質結晶化の検討
(1Pos074) Crystallization of transmembrane protein driven by molecular crowding effect of lipids: Theoretical estimation by using a simple model
○須田 庆樹 1, 安田 由美 2, 秋山 丈 1 (1九州大学理学府, 2九州産業大学)
Keiju Suda 1, Ayumi Suematsu 2, Ryo Akiyama 1 (Kyushu University, Sci., Kyushu Sangyo University, Science and Engineering)

1SCA-3 生理学的等温条件下における細胞サイズリポソーム内での特定配列を持つ DNA 分子の増幅
Amplification of specific DNA molecules inside giant unilamellar vesicles at isothermal and physiological temperature
○佐藤 佑介 1, 小宮 健 1, 川又 生吹 2, 村田 智 2, 野村 M. 慎一郎 2 (1東工大・情報理工, 2東北大・院工)

1SCA-4 (1Pos078) cDNA ディスプレイとセルソーターの利用による新規リポソームポア形成ペプチドの創製
(1Pos078) Novel pore-forming peptides assembling in liposome membranes selected by combining cDNA display method with cell sorter system
○根本 直人 1, 宮嶋 俊樹 1, 吉序 武良 1, 關谷 慎介 2, 川野 竜司 2 (1埼玉大学大学院 理工研, 2東京農工大学 生命工学)

1SCA-5 (1Pos287) 光からエネルギーを合成しタンパク質合成をする人工光合成細胞の構築
(1Pos287) Artificial photosynthetic cell producing energy for protein synthesis
ベルハヌ サミュエル 2, 上田 卓也 3, 〇床 俞澄 1 (1海洋研究開発機構, 2東工大・地球生命研究所, 3東大院・新領域)
Samuel Berhanu 2, Takuya Ueda 3, Yutetsu Kuruma 1 (JAMSTEC, ELSI, Titech, Grad. Sch. of Front. Sci., Univ. of Tokyo)
1SCA-6 ベシクル型細胞モデルにおけるこみあい効果
A study of crowding effect in a cell model using a statistical mechanics approach
○夏目 ゆうの 1,2 (1日女大・理, 2生命創成セ)
Yuno Natsume 1,2 (Fac. Sci., Japan Women's Univ., 2ExCELLS)

1SCA-7 Construction of cell-containing synthetic vesicles for bottom-up synthetic biology
Masamune Morita (Biomed. Res. Inst. (BMRI), AIST)

1SCA-8 計算折り紙による3次元細胞立体構造
3D Cell Structure Optimized by Computational Origami
○繁富 香織（北海道大学）
Kaori Kuribayashi-Shigetomi (Hokkaido University)

8:30〜11:10 Ｄ会場（4F 天葉）／Room D (4F Tenyo)
1SDA クライオ電子顕微鏡でできること、できないこと—構造生命科学の最先端—
What can or cannot do by cryo-EM? The forefront of Structural Life Science
オーガナイザー：吉川 雅英（東京大学）、中川 敦史（大阪大学）
Organizers: Masahide Kikkawa (The University of Tokyo), Atsushi Nakagawa (Osaka University)
“Resolution revolution” of cryo-electron microscopy (cryo-EM) dramatically proceeded the field of structural life science. Cryo-EM is one of the best tools for structure determination of biological macromolecules, however, it is not a perfect tool to understand living system at atomic resolution. We are organizing this symposium to discuss direction of structural life science using combination of various advanced techniques including cutting-edge cryo-EM.

1SDA-1 Structural transition of nucleosome during RNA polymerase II transcription revealed by cryo-EM
Tomoya Kujirai 1,2, Haruhiko Ehara 2, Mikako Shirouzu 2, Shun-ichi Sekine 2, Hitoshi Kurumizaka 1,2 (1IQB, Univ. of Tokyo, 2RIKEN BDR)

1SDA-2 タンパク質の柔軟な構造を高速原子間力顕微鏡で可視化する
Visualizing flexibility in protein structures by high-speed atomic force microscopy
○柴田 幹大 1,2 (1金沢大・WPI-NanoLSI, 2金沢大・新学術創成)
Mikihiro Shibata 1,2 (WPI-NanoLSI, Kanazawa Univ., 2InFiniti, Kanazawa Univ.)

1SDA-3 クライオ電子顕微鏡解析によって明らかなになったミトコンドリア膜透過装置の構造と機能
Near-atomic resolution structure of the mitochondrial protein import gate
○荒磯 裕平 1, 包 明久 2, 今井 賢一郎 3, 阪上 春花 4, 塩田 拓也 5, 柚木 芳 4, 鈴木 純子 4, 河野 優 4, 吉川 雅英 2, 遠藤 忠也 4 (1金沢大・WPI-NanoLSI, 2金沢大・新学術創成, 3産総研, 4京産大・生命科, 5宮崎大)
Yuhei Araiso 1, Akihisa Tsutsumi 2, Kenichiro Imai 3, Haruka Sakae 4, Takuya Shiota 5, Kaori Yunoki 4, Junko Suzuki 4, Shin Kawano 4, Masahide Kikkawa 2, Toshiya Endo 4 (1Grad. Sch. of Med. Sci., Kanazawa Univ., 2Grad. Sch. of Med., Univ. of Tokyo, 3AIST, 4Fac. of Life Sci., Kyoto Sangyo Univ., 5OPTT, Univ. of Miyazaki)

1SDA-4 Microsystem for single molecule analysis of membrane proteins
Rikiya Watanabe (CPR, RIKEN)
1SDA-5 Cryo-EM structures of photosystem II-antenna supercomplexes
Fusamichi Akita¹², Ryo Nagao¹, Koji Kato¹, Naoyuki Miyazaki³, Jian-Ren Shen¹ (*RIIS, Okayama Univ., ²PRESTO, JST, ³TARA, Univ. Tsukuba)

1SDA-6 Structural Basis for the Ferredoxin-dependency of Photosynthetic Complex I

おわりに
Closing Remarks
中川 敦史 (大阪大)
Atsushi Nakagawa (Osaka Univ.)

8:30〜11:10　E 会場（4F クリスタルルーム）／Room E (4F Crystal Room)
1SEA 共催: 新学術領域研究「遺伝子制御の基盤となるクロマチンポテンシャル」
遺伝子制御の原理に迫るクロマチン動態の物理学
Physics of chromatin dynamics – towards understanding the regulation of gene expression

オーガナイザー：伊藤 由馬 (東京工業大学)，木村 暁 (国立遺伝学研究所)
Organizers: Yuma Ito (Tokyo Institute of Technology), Akatsuki Kimura (National Institute of Genetics)

In eukaryotic cells, genomic DNA is packed into the nucleus with a highly organized chromatin structure. Recent studies have revealed that the physical property of chromatin structure and its dynamics is important for the regulation of gene expression. In this symposium, we focus on the physics of chromatin dynamics: how can the structure and dynamics of chromatin be described in terms of physics, and how can the methods and viewpoints of physics contribute to understand the regulation of gene expression. The speakers will introduce their recent studies using various methodology including experimental and theoretical approaches that captures the essential physics of chromatin dynamics.

1SEA-1 単分子超解像局在顕微鏡法による転写装置とクロマチン構造の相互作用解析
A single-molecule localization approach to quantify the interaction between transcriptional machinery and chromatin structure
Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech)

1SEA-2 単一ヌクレオソームイメージングで迫る分裂期染色体の構築原理
Single nucleosome imaging reveals the physical aspect of the mitotic chromosome condensation
Kayo Hibino¹², Kazuhiro Maeshima¹², Yuji Sakai³ (*National Institute of Genetics, ²SOKENDAI, ³Grad. Sch. Med., Univ. Tokyo)
オリゴペプチドのアミノ酸配列はDNA compactionと転写活性に著しい違いを引き起こす
Marked Difference in DNA Compaction and Transcription is Caused by Amino Acid Sequence of Oligopeptide

Tatsuo Akitaya1, Hiroyuki Hiramatsu2, Hideaki Yamaguchi3, Koji Kubo4, Shizuaki Murata4, Toshio Kanbe5, Norio Hazemoto6, Anatoly Zinchenko4 (1旭川医大・医, 2名城大・薬, 3名城大・農, 4名大・院環境, 5名大・院医, 6名市大・院薬, 7同志社大・生命)

クロマチンループを形成しないヌクレオソーム排除DNA配列によるインスレーター活性
Insulator Activities of Nucleosome-Excluding DNA Sequences Without Chromatin Loop Formations

Akinori Awazu1, Yuki Matsushima2, Naoaki Sakamoto1 (Dept of Math. and Life Sciences, Hiroshima Univ., 2Dept. of Math. and Life Sciences, Hiroshima Univ.)

(1Pos239) Molecular Dynamics of Nucleosome Assembly

Giovanni Brandani, Shoji Takada, Cheng Tan (Dept Biophysics, Div Biology, Grad School Science, Kyoto University)

(1Pos088) エピジェネティック修飾をもつクロマチンのモデルにおける不連続相転移
Discontinuous Phase Transition in a Chromatin Model with Epigenetic Modification

Kyosuke Adachi, Kyogo Kawaguchi (RIKEN BDR)

Transcription dynamics of DNA at interfaces

Tetsuya Yamamoto (Nagoya Univ., Dep. of Mat. Phys.)

クロマチンの高次構造とダイナミクス～高分子物理の視点から
Structure and dynamics of chromatin: perspective from polymer physics

Takahiro Sakaue1,2 (Department of Physics and Mathematics, Aoyama Gakuin University, 2JST, PRESTO)
Visualization and quantitative analysis of in-vivo events are important for the understanding of the molecular basis and emergence of biological functions. Moreover, recent developments in optical technology such as nonlinear optics and lasers as well as new probes have led to the development of new bioimaging in life sciences. In this symposium, we will discuss young and energetic researchers about the latest achievements and future prospects about new methods developed from the resonance between life sciences and optical sciences.

1SFA-1 Genetically encoded tools for brain sciences
Atsushi Miyawaki (RIKEN)

1SFA-2 蛍光全脳イメージングのための連続断層イメージング法 FAST
Block-face serial microscopy tomography for whole-brain fluorescence imaging

1SFA-3 非回折と自己湾曲特性を用いた光ニードル顕微鏡における3次元イメージング
Three-dimensional imaging in light needle microscopy utilizing non-diffraction and self-bending characteristics
○小澤 祐市, 佐藤 俊一 (東北大学) Yuichi Kozawa, Shunichi Sato (IMRAM, Tohoku UNiv.)

1SFA-4 広視野2光子デジタル走査ライトシート顕微鏡とメダカ胚全身イメージングへの応用
Wide-field 2-photon light-sheet microscopy and its application to whole body imaging of medaka embryos
○齋藤 卓, 今村 健志 (愛媛大学) Takashi Saitou, Takeshi Imamura (Ehime University)
Bio-image informatics for whole brain activity imaging and analysis of neural activity of C. elegans

Yu Toyoshima¹, Stephen Wu³, Manami Kanamori¹, Hiroyumi Sato¹, Moon Sun Jang¹, Yuko Murakami², Suzu Oe², Terumasa Tokunaga⁴, Osamu Hirose⁵, Sayuri Kuge², Takayuki Teramoto², Yuishi Iwasaki⁶, Ryo Yoshida¹, Takeshi Ishihara³, Yuichi Iino¹ (¹Dept of Biological Sciences, Grad Sch of Science, Univ of Tokyo, ²Dept of Biology, Fac of Sciences, Kyushu Univ, ³Inst of Statistical Mathematics, Research Organization of Information and Systems, ⁴Dept of Systems Design and Informatics, Fac of Computer Science and Systems Engineering, Kyushu Inst of Technology, ⁵Fac of Electrical and Computer Engineering, Inst of Science and Engineering, Kanazawa Univ, ⁶Dept. of Mec. Eng., Grad. Sch. of Sci. and Eng., Ibaraki Univ.)

Bilateral Domain Image Processing
Shin Yoshizawa (IPRT, RAP, RIKEN)

The field of mechanobiology has grown dramatically in the past decade and diverse biological systems are currently targeted. Especially, importance of physical stimuli and the response in muscle and vascular system is well known at the phenomenological level, however, the molecular mechanism and multiscale relationships between molecules and cells, tissues or organ is still elusive. This symposium will provide an overview of the latest findings in the field, revealing the relationship between physical stimuli and activities of muscle and vascular system at each hierarchy.

Thick filament activation through a molecular-based mechanosensing, regulates forces in mathematical models of trabecula and ventricle
Lorenzo Marcucci¹,³, Takumi Washio², Toshio Yanagida³ (¹Department of Biomedical Sciences, Padova University, Italy, ²Graduate School of Frontier Sciences, The University of Tokyo, Japan, ³Center for Biosystems Dynamics Research, RIKEN, Japan)

(1Pos108) 心筋細胞に備わる収縮リズム恒常性の分子機構の解明
Seine Shintani¹, Takumi Washio² (¹Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University, ²Graduate School of Frontier Sciences, the University of Tokyo)
Mechanobiology of Heart Revealed with DNA Nano-device and Nanometer-precision Single-molecule Imaging

Mitsuhiro Iwaki\(^{1,2}\) (RIKEN, BDR, \(^{2}\)Grad. Sch. Front. Biosci., Osaka Univ.)

Myosin filament regulation by mechanosensing in skeletal and cardiac muscle

Vincenzo Lombardi (PhysioLab)

Role of a mechanosensitive cation channel PIEZO1 in skeletal muscle regeneration

Yuji Hara\(^{1,2}\), Kotaro Hirano\(^{1}\), Seiji Takabayashi\(^{1}\), Masaki Tsuchiya\(^{1}\), Masato Umeda\(^{1}\) (Graduate School of Engineering, Kyoto University, \(^{2}\)AMED PRIME)

Mechano-protective roles of sugar chain in skeletal muscle

Motoi Kanagawa (Kobe Univ. Grad. Sch. Med.)

Lipid bilayer membrane mediated mechanotransduction in vascular endothelial cells

Kimiko Yamamoto\(^{1}\), Joji Ando\(^{2}\) (System Physiology, Graduate School of Medicine, The University of Tokyo, \(^{2}\)Laboratory of Biomedical Engineering, School of Medicine, Dokkyo Medical University)

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A Thermodynamic Tool for Mechanobiology Research: Mild Nanoheating Technology to Alter Subcellular Dynamics

Satoshi Arai\(^{1}\), Nandus Ferdi\(^{2}\) (Res. Inst. Sci. Eng., Waseda Univ., \(^{2}\)WABIOS)

静水圧刺激により生命機能を操作する

Control of biological functions with hydrostatic pressure stimulation

オーガナイザー：畑 宏明（東京工業大学）、西山 雅祥（近畿大学）

Organizers: Hiroaki Hata (Tokyo Institute of Technology), Masayoshi Nishiyama (Kindai University)

Living organisms change the shape and activity as a response of external forces. The response to the force can be found in biomolecules composing life organisms. Hydrostatic pressure has been used as a tool to apply isotropic forces for investigating the force response of molecular structures and functions. However, pressures used in the previous studies were often high where the biomolecules denature. Recent studies show that much lower pressures keeping structures of biomolecules can affect cellular functions. In this symposium, we will discuss about mechanical control of cellular functions by pressure and the mechanism underlying the pressure effect.

High pressure induces cell cycle exit and differentiation of skin cancer cells

Oleg Dobrokhotov, Masahiro Sokabe, Hiroaki Hirata (Nagoya Univ., Grad. Sch. Med.)
Direct observation of cell mechanics under high hydrostatic pressure
Masatoshi Morimatsu, Keiji Naruse (Grad. Sch. of Med., Dent. and Pharma. Sci., Okayama Univ.)

Pressure accelerates the circadian clock of cyanobacteria
Ryo Kitahara1, Katsuaki Oyama2, Takahiro Kawamura2, Keita Mitsuhashi2, Soichiro Kitazawa1, Kazuhiro Yasunaga1, Natsuno Sagara1, Megumi Fujimoto2, Kazuki Terauchi2 (Pharm. Sci., Ritsumeikan Univ., 1Life Sci., Ritsumeikan Univ.)

Effects of high hydrostatic pressure on the rotation of the bacterial flagellar motor
Ikuro Kawagishi1,2 (Dept. Frontier Biosci., Hosei Univ., 2Res. Cen. Micro-Nano Tech., Hosei Univ.)

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Pression effects on protein-protein interactions studied by molecular dynamics simulations
Hiroaki Hata1, Yasutaka Nishihara2, Masayoshi Nishiyama3, Ikuro Kawagishi4, Akio Kitao1 (1Dept. of Life Sci. and Tech., Tokyo Tech, 2IMCB, UTokyo, 3Grad. Sch. of Sci. and Eng., Kindai Univ., 4Dept. of Frontier Biosci., Hosei Univ.)

13:40～16:20  B 会場（4F 天玉）/ Room B (4F Tengyoku)
1SBP オーストラリア 日本交流シンポジウム：
生体分子相互作用と介在する力にフォーカスした生物物理学の挑戦
ASB-BSJ Joint Symposium: Current challenges in biophysics centering on biomolecular interactions and the underlying forces

オーガナイザー：西坂 崇之（学習院大学）、Marc Kvansakul（La Trobe University）
Organizers: Takayuki Nishizaka (Gakushuin University), Marc Kvansakul (La Trobe University)

To promote greater engagement between the Australian Society for Biophysics and Biophysical Society of Japan we created this exciting symposium featuring presentations spanning the full breath of current challenges in biology that center on biomolecular interactions and the underlying forces driving them. Topics include determination of the forces and interactions between biomolecules including proteins, lipids as well as engineered biomolecular structures to understand the fundamental forces required to maintain or destroy life. Speakers from both societies will discuss advances in understanding the effect of direct attachment on environmental surfaces on the motility and survival of bacteria; principles governing the generation of rhythmic force in animal muscles and cardiac tissues which power life; and lastly, insights into the ability of proteins to change the architecture of lipid bilayers in order to control cellular membranes or contribute to immunity. These exciting presentations provide novel insights into the functions of proteins and their molecular mechanisms of action that control the biological processes that underpin life as we know it.
Opening Remarks

Takayuki Nishizaka (Gakushuin Univ.)

Microscopic measurements of force and taxis in bacteria/archaea

Takayuki Nishizaka, Daisuke Nakane (Dept. Phys., Gakushuin Univ.)

Biophysical models of physical rupturing of bacterial cells by nano-structured surfaces

Elena Ivanova (RMIT University)

Cardiac nano-imaging: from cells to the heart

Norio Fukuda (Department of Cell Physiology, The Jikei University School of Medicine)

How Japanese researchers can get access failing and donor tissue from the Sydney Heart Bank. A viable alternative to using animal models

Cristobal G. dos Remedios, Amy Li, Sean Lal (Bosch Institute, Discipline of Anatomy & Histology, University of Sydney)

Plasma membrane deformation by phospholipid flippase and cellular functions

Hye-Won Shin (Grad Sch Pharm Sci, Kyoto Univ)

Structural definition of phospholipid-mediated oligomerization of defensins in fungal and tumour cell lysis

Marc Kvansakul, Mark Hulett, Sofia Caria, Ivan Poon, Michael Jarva, Kha Tran Phan, Fung Lay, Amy Baxter (La Trobe University)

Closing Remarks

Marc Kvansakul (La Trobe Univ.)

The brain is an amazingly complicated and sophisticated information processing device consisting of billions of neurons and thousands of billions of connections in the mammalian brain. To understand how the brain processes information, it is essential to read out or manipulate neuronal activity on all different temporal and spatial scales. In this symposium, various state-of-the-art biophysical methods, especially optical methods, will be presented contributing towards this goal.
Simultaneous spatio-temporal dendritic voltage/calcium mapping and somatic recording from Purkinje neurons in awake mice
Bernd Kuhn, Christopher J. Roome (OIST Graduate University)

Novel "in vivo" two-photon microscopy for vast and longtime neural activity
Tomomi Nemoto (RIES, Hokkaido Univ.)

機能的光干渉断層法とフーリエイメージングによる脳機能構造の3次元マイクロ計測
Yu Nakamichi, Manabu Tanifuji (RIKEN CBS)

偏光で解き明かす生細胞内の分子アセンブリーのナノ構造とそのダイナミクス
Tomomi Tani (Marine Biological Laboratory, Woods Hole)

The role of C-terminal carboxylation in α-conotoxin LsIA interactions with human α7 nicotinic acetylcholine receptor in silico
Jierong Wen, Andrew Hung (Sch. Sci., RMIT Univ.)

グルタミン酸受容体を介した植物の長距離Ca²⁺シグナル
Masatsugu Toyota¹² (¹Dept Biochem and Mol Biol, Saitama Univ, ²University of Wisconsin-Madison)

Optical view of the brain neural circuit activity: Voltage-sensitive-dye (VSD) imaging
Takashi Tominaga, Yoko Tominaga (Inst. Neurosci., Tokushima Bunri Univ.)

The development of biophysico-chemical methods has enabled us the quantitative and systematic analysis of the behavior of biomolecules including their interactions and conformations. Due to the highly sensitive and accurate measurements, even the measurement under in situ conditions are possible. In this symposium, we will introduce solution state measurement techniques, such as analytical ultracentrifugation, thermodynamic measurements, nuclear magnetic resonance. Here we will discuss the recent applications, and future possibility of these methods.

Opening Remarks

13:40~16:20 D会場（4F天葉）/Room D (4F Tenyo)
1SDP 蛋白質の溶液物性計測の現状と課題
Current status and issues of protein solution biophysics

オーガナイザー：内山進（大阪大学）、谷中冴子（分子科学研究所）
Organizers: Sususmu Uchiyama (Osaka University), Saeko Yanaka (Institute for Molecular Science)
Quantitative assessments of intermolecular protein mediated interactions in solution

Susumu Uchiyama1,2 (*Department of Biotechnology, Graduate School of Engineering, Osaka University, 2ExCELLS)

Native mass spectrometry of biomolecular complexes

Satoko Akashi (Grad. Sch. Med. Life Science, Yokohama City Univ.)

Biophysical analysis of alpha-synuclein oligomers by microchip electrophoresis

William E. Arter1,2, Catherine K. Xu1, Georg Krainer1, Christopher M. Dobson1, Tuomas P. J. Knowles1,2 (*Centre for Misfolding Disease, Department of Chemistry, University of Cambridge, 2Cavendish Laboratory, Department of Physics, University of Cambridge)

Visualization and quantification of biological samples by high-speed atomic force microscope

Hiroki Watanabe1,2, Koichi Kato1,2,3, Takayuki Uchihashi1,4 (*NINS, ExCELLS, 2NINS, IMS, 3Grad. Sch. Pharm. Sci., Nagoya City Univ., 4Dept. Phys., Nagoya Univ.)

Dynamic structures and interactions of antibodies under physiologically relevant conditions

Saeko Yanaka1,2,3, Rina Yogo1,2,3, Hirokazu Yagi1, Koichi Kato1,2,3 (*IMS, Natl. Inst. Nat. Sci., 2ExCELLS, Natl. Inst. Nat. Sci., 3Grad. Sch. Pharma. Sci., Nagoya City Univ.)

A newly developed negative stain EM method for protein complexes at high protein concentration


Thermodynamics of Protein Interaction for Therapy and Diagnosis

Satoru Nagatoishi1,2, Kohei Tsumoto1,2 (*Inst Med Sci, Univ Tokyo, 2Sch Eng, Univ Tokyo)

Closing Remarks
We, the researchers in the “Single-cell PRESTO” project, have heterogeneous research interests. In fact, our projects are diverse; imaging, (fluorescent) probes, gene expression, omics analysis, brain/neurons, membrane, sequencing and quantification of nucleic acid molecules, development, heat-sensing/manipulation, cell-measurement/manipulation/modeling, and glycans. However, we are gathered with a keyword “single-cell studies”. Then, what is it? In this symposium, selected members will guide you to the exciting “single-cell studies” by presenting the significance and advantages of their own single-cell studies, development of new techniques, and challenges for new research fields.

1SEP-1 Cellomics approach for high-throughput functional annotation of Caenorhabditis elegans neural network
Wataru Aoki1,2, Yuji Yamauchi1, Mitsuyoshi Ueda1 (1Graduate School of Agriculture, Kyoto University, 2JST, PREST)

1SEP-2 (1Pos196) Single-cell trajectory analysis of human iPS cell-derived neurons carrying a rare RELN deletion
Yuko Arioka1,2,3, Emiko Shishido1,4, Norio Ozaki1 (1Department of Psychiatry, Nagoya University Graduate School of Medicine, 2Nagoya University Hospital, 3Institute for Advanced Research, Nagoya University, 4National Institute for Physiological Sciences)

1SEP-3 Multiphoton imaging and photostimulation techniques by spatio-temporal control of excitation pulses
Keisuke Isobe, Katsumi Midorikawa (RIKEN RAP)

1SEP-4 Chemical probes for fluorescence imaging or ablation of lacZ-positive cells with single cell resolution
Mako Kamiya (Grad. Sch. Med., Univ. Tokyo)

1SEP-5 三次元バーテックスモデル: 三次元多細胞動態の1細胞統合モデリング
3D vertex model: single cell-integrated modeling of multi-cellular dynamics in three-dimensions
○奥田覚1,2 (1金沢大・ナノ研, 2JST さきがけ)
Satoru Okuda1,2 (1Nano LSI, Kanazawa Univ, 2JST PRESTO)

1SEP-6 分子解像度での生命理解に向けて
Towards molecular-resolved biology
○谷口雄一（理研・BDR）
Yuichi Taniguchi (RIKEN BDR)

1SEP-7 1細胞操作のための光応答性細胞固定化剤の開発
Photo-responsive cell immobilization tools for single-cell manipulation
○山口哲志1,2 (1東京大学先端科学技術研究センター, 2JST さきがけ)
Satoshi Yamaguchi1,2 (1Research Center for Advanced Science and Technology (RCAST), The University of Tokyo, 2PRESTO, JST)
Hydrogen atoms play a crucial role in biological systems, including enzymatic reactions, but the presence cannot be identified in the X-ray crystal structures. Next-generation neutron sources (e.g., J-PARC) enable us to carry out neutron diffraction analysis of proteins, which provides us a lot of useful information of hydrogen atoms. In this symposium, top researchers in the fields of structural analysis, theoretical analysis, and spectroscopic analysis of proteins and nanodevices will discuss and overview what can be elucidated by visualizing and characterizing hydrogen atoms.

開催者：田中 伊知朗（茨城大学），石北 央（東京大学）
Organizers: Ichiro Tanaka (Ibaraki University), Hisroshi Ishikita (The University of Tokyo)
「高次元データ駆動科学と計測インフォマティクスによる分子観察の新展開」

New horizon in molecular observation through high-dimensional data-driven and measurement informatics approaches

オーガナイザー：木川隆則（理化学研究所）、松永康佑（埼玉大学）

Organizers: Takanori Kigawa (RIKEN), Yasuhiro Matsunaga (Saitama University)

Recent intelligent measurement/analysis methods achieved by "measurement informatics" have improved resolutions and efficiencies of measurement technologies. On the other hand, we are at a loss for analyzing the vast amount of data generated through the development of those technologies. In order to promote the "high-dimensional data-driven science", which makes full use of statistics and computational technology to acquire scientific knowledge from the high-dimensional data, it is essential to establish logical data analysis and modeling methods. In this symposium, the recent advancements in statistical science, large-scale computing, and molecular measurement will be presented in order to understand the general concept of high-dimensional data-driven and measurement informatics approaches and discuss its application to life science.

1SGP-1 ポピュレーションアニーリングによるベイズ推定
Bayesian inference with population annealing

○福島孝治（東京大学）
Koji Hukushima (The University of Tokyo)

1SGP-2 定量的安定同位体標識とテンソル分解による重複NMRシグナルの分解法
Solving signal overlap in NMR spectra using quantitative isotope labeling and tensor decomposition

○葛西卓磨1,2, 小野峻佑2,3, 田中利幸4, 池田思朗5, 木川隆則1,3 (1理研・生命機能, 2JST・さきがけ, 3東工大・情報理工, 4京大院・情報, 5統数研)

1SGP-3 高次元分子計測により明らかとなったキチン分解酵素の運動機構
Moving mechanism of chitin hydrolase was revealed by high precision and speed single molecule analysis

○中村彰彦1,2, 岡崎圭一1, 古田忠臣3, 横井英3, 賀野亮太1,2 (1自研, 2理研, 3総研, 3東工大)
Akihiko Nakamura1,2, Kei-ichi Okazaki1, Tadaomi Furuta3, Minoru Sakurai3, Ryota lino1,2 (1Institute for Molecular Science, 2SOKENDAI, 3Tokyo Institute of Technology)

1SGP-4 DNA curtains: high-throughput single molecule imaging for DNA transactions

Tsuyoshi Terakawa (Grad. School of Sci., Kyoto Univ.)

1SGP-5 2次元/3次元AFMによるバイオ系試料の観察と高度なAFMデータ解析の必要性
2D/3D-AFM imaging of biological systems and demands for advanced AFM data analysis

○福田剛士（金沢大・ナノ生命研）
Takeshi Fukuma (NanoLSI, Kanazawa Univ.)
1SGP-7  高速原子間力顕微鏡装置の開発
A High-speed atomic force microscope for detailed time series analysis of cell surface dynamics
○清水 将裕, 岡本 千優, 今井 大達, 渡辺 信嗣, 安藤 敏夫, 古寺 哲幸 (金沢大・新学術創成, JST・CREST, 金沢大・数物, 金沢大・WPI-NanoLSI)
Masahiro Shimizu, Chihiro Okamoto, Hirotsugu Imaizumi, Shinji Watanabe, Toshio Ando

1SGP-8  高速原子間力顕微鏡 1 分子計測と分子シミュレーションのデータ同化による生体分子 4 次元構造解析
Four-dimensional biomolecular structure analysis with data assimilation of HS-AFM single molecule measurement and molecular simulation
○渕上 壮太郎, 新稲 亮, 高田 彰二 (京大院・理, JST・CREST)
Sotaro Fuchigami, Toru Niina, Shoji Takada

13:40〜16:20  H 会場（4F アンバールーム）／Room H (4F Amber Room)
1SHP  GPCR による多様な情報伝達機構を解き明かす構造―機能相関研究の新展開
Frontier of structure-function studies to unveil diverse GPCR signaling

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 Institute of Technology), Ryoji Suno (Kansai Medical University)

GPCR signaling utilizes an allosteric coupling between the extracellular facing ligand-binding pocket and the cytoplasmic domain of the receptor selectively interacting with signal transducer. This allosteric effect enables one site of the receptor to regulate the function of another spatially distinct region. Therefore, it is important to understand the molecular mechanisms behind ligand-induced changes in receptor conformation and specific transducer-recognition for the development of GPCR-based drugs. This symposium is dedicated to discuss the latest trends on the structure-function studies to explore the molecular basis of GPCR signal transduction.

1SHP-1  Holistic Phenotyping of GPCR Signaling System by a Versatile Single-Platform Assay
Ikuo Masuho (The Scripps Research Institute FL, Department of Neuroscience)

1SHP-2  GPCR の 1 分子拡散動態から複数の薬効を読み解く
Estimation of multiple drug effects on GPCR based on the single-molecule diffusion dynamics
○柳川 正隆（理研・佐甲細胞情報研究室）
Masataka Yanagawa (Cellular Informatics Lab., Riken)

1SHP-3  Structure and conformational transitions of a neurotensin receptor 1 Gi1 protein complex
Hideaki Kato, Yan Zhang, Hongli Hu, Carl-Mikael Suomi, Francois Marie Ngako Kadji, Junken Aoki, Kaavya Krishna Kumar, Rasmus Fonseca, Daniel Hilger, Weijiao Huang, Naomi Latorraca, Asuka Inoue, Ron Dror, Brian Kobilka, Georgios Skiniotis (The Univ. of Tokyo, Zhejiang Univ., Stanford Univ., Tohoku Univ.)
The inside of the cell is occupied by a wide variety of different biomolecules, and the localization and concentration of the biomolecules change dynamically depending on the cell cycle and state. Since the beginning of life, biomolecules have evolved to express functions in multi-molecular crowding environments. However, attempts to elucidate the nature of multi-molecular crowding environment have just begun. In this symposium, we focus on liquid-liquid phase separation phenomena that are related to multi-molecular crowding, and discuss the current topics and prospects of multi-molecular crowding research.
Secondary structure of DNA for liquid-liquid phase separation
Masahiro Mimura1,2, Shunsuke Tomita2, Ryoji Kurita1,2, Kentaro Shiraki1 (1Pure and Appl. Sci., Univ. Tsukuba, 2Biomed. Res. Inst., AIST)

相分離生物学：相分離する LC ドメイン
Phasing Biology: Low-Complexity Domains Phase-Separate through Cross-β Interaction
○森 英一朗（奈良県立医科大学 医学部 未来基礎医学）

分子夾雑系における光センサー蛋白質の動的挙動―揺らぎと反応ダイナミクス―
Fluctuation and reaction dynamics of a light sensor protein in crowding environment
○中曽根 祐介, 村上 大斗, 寺嶋 正秀（京大・院理）
Yusuke Nakasone, Hiroto Murakami, Masahide Terazima (Grad. Sch. Sci., Kyoto Univ.)

細胞様構造や細胞組織体の自己創生：分子夾雑系の活用
Self-emergence of primitive cell and cellular mini-organoids under crowding environment
○吉川 研一（同志社大学 生命医科学部）
Kenichi Yoshikawa (Facul. Life Med. Sci., Doshisha Univ.)

分子構造ビッグデータの時代のバイオインフォマティクスの挑戦
Challenges of bioinformatics for the era of molecular structure big-data

The recent rapid developments in the techniques of supramolecular structure and high-throughput omics analyses enhanced the importance of the bioinformatics/data science to analyze and mining knowledge from “molecular structure big-data”. This symposium will be focused on reviewing and discussing the recent researches in this field produced from AMED-BINDS activities.

AMED-BINDS 事業におけるビッグデータ科学
Big Data Science at AMED-BINDS
○中村 春木（大阪大学蛋白質研究所）
Haruki Nakamura (Institute for Protein Research)

多層ニューラルネットワークを用いたタンパク質残基間コンタクトおよびタンパク質 - 基質相互作用の予測
Prediction of protein residue contacts and protein-ligand interactions with deep neural networks
○富井 健太郎（産業技術総合研究所）
Kentaro Tomii (National Institute of Advanced Industrial Science and Technology (AIST))

Integrated approach of experimental data and computer modeling and simulation for understanding chromatin structure and dynamics
Hidetoshi Kono, Atsushi Matsumoto, Shun Sakuraba, Hisashi Ishida (QST, Institute for Quantum Life Science (iQLS), MMS)
2SCA-4 電顕のインフォマティクス: 2D 生画像データの収集と原子モデルのフィッティング
EM informatics: archiving raw 2D images and fitting atomic models into a map
○川端 猛, 栗栖 源嗣（大阪大学 蛋白質研究所）

2SCA-5 Development of a deep-learning-based method to identify "good" regions of a cryo-EM grid

2SCA-6 クライオ電顕データ収集の効率化に資する凍結グリッド作成法やソフトウェア
Improvements in grid preparation method and software for facilitating cryoEM data collection
○難波 啓一1,2,3 (1大阪大学大学院生命機能研究科, 2理研放射光科学研究センター, 3理研生命機能科学研究センター)
Keiichi Namba1,2,3 (1Graduate School of Frontier Biosciences, Osaka University, 2RIKEN SPring-8 Center, 3RIKEN Center for Biosystems Dynamics Research)

8:30〜11:10 D 会場（4F 天葉）/ Room D (4F Tenyo)
2SDA 共催: 新学術領域研究「発動分子科学: 能量変換が拓く自律的機能の設計」
生体分子機械の非平衡エナジェティクス
Nonequilibrium Energetics of Biological Molecular Machines

オーガナイザー：Chun-Biu Li (Stockholm University), 鳥谷部 祥一 (東北大学)
Organizers: Chun-Biu Li (Stockholm University), Shoichi Toyabe (Tohoku University)

Many bio-molecular motors can operate robustly and energetic efficiently in the highly fluctuating nano-scale. How these molecules achieve such remarkable functions is an intriguing question that requires the understanding of the general principles of structure and design, enzymatic kinetics and nonequilibrium physics of biological machineries. By bringing together both experimental and theoretical experts from interdisciplinary fields, this symposium aims to explore A) Novel experimental techniques to probe the energetic efficiency in the single molecule level; B) New theoretical methods to explain the biophysical principles of molecular energetics; C) Common strategies shared among different bio-molecular machines in achieving energetic efficiency.

2SDA-1 生物系のエナジェティクス
Energetics of biological system
○鳥谷部 祥一（東北大・院工）
Shoichi Toyabe (Grad. Sch. Eng., Tohoku Univ.)

2SDA-2 歩行型モーター・キネシン1の非平衡エネルギー論
Nonequilibrium Energetics of a walking motor kinesin-1
○有賀 隆行（山口大学医学系研究科）
Takayuki Ariga (Graduate school of medicine, Yamaguchi University)

2SDA-3 FoF1-ATP 合成酵素の回転力はどのようにして発生しているのか? 構造生物・生物物理学的手法による解析
Structural and biophysical analyses of torque generation mechanism of F0F1-ATP synthase
○鈴木 俊治（東京工業大学 科学技術創成研究院 化学生命科学研究所）
Toshiharu Suzuki (Lab for Chem and Life Sci, Inst of Innov Res, Tokyo Inst of Tech)

2SDA-4 Modeling of myosin V motor dynamics to understand high-speed AFM observations
Holger Flechsig (WPI Nano Life Science Institute, Kanazawa University)
2SDA-5  Energetics and structural dynamics of a viral RNA polymerase ratcheting along DNA with fidelity control  
Jin Yu (Beijing Computational Science Research Center)

2SDA-6  Error-speed correlations in biopolymer synthesis  
Simone Pigolotti (Okinawa Institute of Science and Technology Graduate University)

2SDA-7  (2Pos121) Dynamic energy landscape of a linear motor chitinase from single-particle tracking trajectories  
Kei-ichi Okazaki, Akihiko Nakamura, Ryota Iino (Institute for Molecular Science)

8:30〜11:10  E 会場（4F クリスタルルーム）／Room E (4F Crystal Room)  
2SEA  放射光利用生物物理研究の最前線  
Frontiers of Synchrotron Radiation Biophysics

Synchrotron radiation X-rays has a wide range of applications for life sciences, including fiber diffraction and protein solution scattering, besides the most popular protein crystallography. This symposium sheds lights on synchrotron radiation techniques other than protein crystallography, and introduce the recent progress of these techniques and the results of the latest research.

はじめて
Opening Remarks  
岩本 裕之（高輝度光科学研究センター）  
Hiroyuki Iwamoto (JASRI)

2SEA-1  非結晶生体試料のシンクロトロン放射光 X 線回折実験に関する最近の進歩  
Recent progress in synchrotron radiation X-ray diffraction studies for non-crystalline biological specimens  
○岩本 裕之（SPring-8・JASRI）  
Hiroyuki Iwamoto (SPring-8, JASRI)

2SEA-2  X 線繊維回折法によって明らかとなった秒単位の微小管構造変化  
Dynamic changes of tubulin dimer configurations on a scale of sub-second revealed by high flux X-ray fiber diffraction  
○上村 慎治１，今井 洋２，八木 俊樹３，岩本 裕之４（１中大・理工・生命，２阪大・院理・生物科学，３県立広島大・生命環境，４SPring-8, JASRI）  

2SEA-3  Diffracted X-ray Tracking for protein dynamics  
Hiroshi Sekiguchi (Cent. Synchrotron Rad. Res., JASRI/SPring-8)

2SEA-4  Dynamic changes in cardiac myosin head regulation during hyperglycemic events in insulin resistant rats  
James T. Pearson¹ 2, Naoto Yagi³, Mikiyasu Shirai¹, Mark Waddingham¹, Hirotugu Tsuchimochi¹, Takashi Sonobe¹, Vijayakumar Sukumaran (¹National Cerebral and Cardiovascular Center, ²Monash University, Department of Physiology, ³JASRI)
Distribution of nucleic acids in yeast nucleus of G1 phase visualized by X-ray diffraction imaging using X-ray free electron laser

Masayoshi Nakasako, Takahiro Yamamoto, Amane Kobayashi, Mao Oide, Koji Okajima, Yuki Takayama, Tomotaka Oroguchi, Masaki Yamamoto (Keio University, RIKEN, University of Hyogo Prefecture)

Closing Remarks

Hiroyuki Iwamoto (JASRI)

Elucidation of biological functions by optical control

Organiizers: Yoshinori Shichida (Ritsumeikan University), Hisao Tsukamoto (Institute for Molecular Science)

Life science has dramatically progressed through the development of powerful biophysical techniques controlling cellular functions by light. For example, Optogenetics utilizing photoceptive proteins as an optical controlling tool has been established to analyze and manipulate various biological functions. In this symposium, active young researchers in biology and engineering will present how to elucidate biological functions by these techniques, and we and participants will discuss direction of the research in this field including necessary biophysical tools to be developed.

Opening Remarks

Yoshinori Shichida (Ritsumeikan Univ.)

Orchestrated ensemble activities constitute a hippocampal memory engram

Noriaki Ohkawa (Univ of Toyama Grad Sch of Med and Pharm Sci, PRESTO, JST)

Remote and wireless control of neuronal function using X-ray

Takayuki Yamashita (Dept. Neurosci. II, RIEM, Nagoya Univ., PRESTO, JST)

Batteryless ultra-small implantable optical stimulator

Takashi Tokuda, Thane, Nattakarn, Makito Haruta, Jun Ohta (FIRST, Tokyo Tech, Mater. Sci., NAIST)
2SFA-4 長波長レーザーによる超深部イメージングシステムの開発
Development of deep-tissue imaging system based on a long-wavelength laser
○野村 雄高（分子科学研究所）
Yutaka Nomura (Institute for Molecular Science)

2SFA-5 光操作型アデノウイルスベクターの開発と応用
Generation of photoactivatable adenovirus vector for spatiotemporally controllable gene therapy
○高山 和雄 1,2,3（大阪大薬，2医薬基盤健栄研，3さきがけ）
Kazuo Takayama1,2,3 (1Osaka University, 2NIBIOHN, 3PRESTO)

2SFA-6 (2Pos198) 微生物型ロドプシンに基づく光遺伝学ツールの探索と開発
(2Pos198) Exploration and development of microbial rhodopsin-based optogenetic tools
○小島 慧一，須藤 雄気（岡山大・院・医歯薬(薬)）
Keiichi Kojima, Yuki Sudo (Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.)

2SFA-7 「総力戦」としての光操作技術
Optical control as a fusion of neuroscience, medicine, engineering, and biophysics
○塚本 寿夫 1,2（分子科学研究所，2JST さきがけ）
Hisao Tsukamoto1,2 (1Institute for Molecular Science, 2PRESTO, JST)

8:30〜11:10 G 会場（4F アイボリールーム）／Room G (4F Ivory Room)
2SGA 電子・熱・化学エネルギーの生体内伝達と地域社会実装に向けた基盤研究
How is ‘ENERGY’ generated/transferred across the cellular systems?

オーガナイザー：和田 啓（宮崎大学），榊原 陽一（宮崎大学）
Organizers: Kei Wada (University of Miyazaki), Yoichi Sakakibara (University of Miyazaki)

The cellular systems involved in the generation/transfer of ENERGY are ‘awesome’. For instance, ATP is known in biochemistry as the "molecular currency" of intracellular energy transfer; that is, ATP is able to store and transport chemical energy within cells. The cells also possess the sophisticated systems including the utilizing the reactive sulfur species and the transfer mechanism of the electrons and the thermal energy. This symposium covers a variety of topics regarding the recent findings and advances in the biochemistry/chemistry of the energy related compounds.

2SGA-1 生体内の電子伝達金属補因子「鉄硫黄クラスター」の生合成機構
Molecular mechanism of the biosynthesis of the iron-sulfur clusters involved in the electron transport in vivo
○和田 啓（宮崎大学）
Kei Wada (Dept. of Medical Sciences, Univ. of Miyazaki)

2SGA-2 高エネルギー硫酸ヌクレオチド分子を利用した生体内代謝：硫酸転移酵素の多様な生理機能の解明
Metabolism of key endogenous molecules mediated by sulfotransferases with a hi-energy sulfonucleotide, PAPS
○黒木 勝久1, 寺本 岳大2, 角田 佳充2, Liu Ming-Cheh3, 水光 正仁1, 榊原 陽一1（1宮崎大・農・応生科, 2九大院・農・生命機能, 3トレド大・薬）
Recent studies have shown that Proteins are not static molecular machine, but play their biological role by dynamical response according to external perturbations. At present, it is believed the mechanical origin of the dynamical response involves in structure of proteins, dealing with varieties of biological systems. However, the mechanisms of the dynamic response is still debates. In this symposium, we will overlook the issue by presentations of researchers who have tackled to the problems using advanced technique or novel ideas, and discuss the future progress of this exciting scientific area.
カルシウムシグナル伝達蛋白質 Calmodulin と結合ドメインの構造変化と相互作用
Conformational changes and interactions of calcium ion signal transfer protein Calmodulin and Calmodulin-binding domain
○下山 純充（北里大学薬学部 生物分子設計学教室）
Hiromitsu Shimoyama (Kitasato-Univ.)

タンパク質中の不均一なエネルギー流と機能に関する理論的研究
Theoretical study on non-uniform energy flow and protein function
○窪田 源己, Laprevote Olivier, 倭 剛久（名古屋大学）
Genki Kubota, Olivier Laprevote, Takahisa Yamato (Nagoya University)

ダイナミン GTP アーゼはアクチン線維の束化と分散を機械的に制御する
Dynamin GTPase mechanically regulates bundling and unbundling of actin filaments
○竹居 孝二, 110 モン ラ 1, 16 田 哲也, 21 成田 哲也 3（岡山大 院医歯薬, 2 大阪市大 院理 細胞機能, 3 名大 院理 構造生物学研究センター）

Analysis of Effect of Mutation on the Response for Membrane Depolarization in the Voltage-Gated Potassium Channel Kv1.2
Hiroko X. Kondo1, Norio Yoshida2, Gen Masumoto2, Matsuyuki Shirota4,5,6, Yu Takano7,

おわりに
Closing Remarks
鷹野 優（広島市大）
Yu Takano (Hiroshima City Univ.)

The life system is maintained by dynamic tuning of metabolisms. Rewiring of the metabolic networks in bacteria, plants or human diseases is considered to be the results of the adaptation of their whole-body metabolisms to environment. The molecular mechanism underlying the metabolic adaptation can be only understood through measuring and analyzing "trans-omic" network, consisting of interactions among molecules across multi-omic layers, such as genome, transcriptome, proteome, and metabolome. Here we hold this symposium to shed light on strategies and obstacles in integrating multiple omic layers to establish trans-omic approaches, and to have discussions with cutting edge researchers in omics research fields.

オーガナイザー：岡田 真里子（大阪大学）, 馬場 健史（九州大学）
Organizers: Mariko Okada (Osaka University), Takeshi Bamba (Kyushu University)
In the field of biological science, discontinuous critical phenomena (singularities) are broadly seen, for example, the emergence of life from the primordial soup, or the evolution and outbreak of diseases. It has been indicated that only a small number of core elements are required to bring about discontinuous changes to an entire multi-component system. However, the mechanism-of-action that generates such singularity phenomena is not yet certain. For this aim, to develop an imaging platform that will achieve both wide field-of-view high-resolution imaging and high-speed long-term imaging and information analysis methods are highly desired. In this symposium, we are aimed at exploring possible biological subjects and the associated technological developments toward uncovering the underlying mechanisms for the generation of singularity cells as well as their biological functions.

Opening Remarks
永井 健治（大阪大）
Takeharu Nagai (Osaka Univ.)

What singularity biology can do for understanding Alzheimer’s disease
○坂内 博子 1,2, 廣島 通夫 3, 添田 義行 4, 高島 明彦 4（1慶應大・医, 2JST ERATO, 3理研・BDR, 4学習院大・理）
Hiroko Bannai1,2, Michio Hiroshima3, Yoshiyuki Soeda4, Akihiko Takashima4 (1Keio Univ. Sch. Med., 2JST ERATO, 3RIKEN BDR, 4Gakushuin Univ, Faculty. Sci.)
Delineation of the activation trajectory of autoreactive T cells

Taku Okazaki, Hikari Okamura, Il-mi Okazaki, Kenji Shimizu, Takumi Maruhashi, Daisuke Sugiura (Div Imm Reg, Inst Adv Med Sci, Tokushima Univ)

全脳イメージングシステム FAST を用いたアンバイアスで仮説に依らない脳内シンギュラリティの検出

Unbiased and hypothesis-free approach to detect singularity in the brain using whole-brain imaging system FAST

○橋本 均1,2,3,4, 中澤 敬信1,5, 勢力 薫1,6, 笠井 淳司1 (1大阪大・薬・神経薬理, 2大阪大・連合小児発達・子どものこころの発達研究センター, 3大阪大・データビリティフロンティア機構・バイオサイエンス部門, 4大阪大・先端的学際研究機構・超次元ライフイメージング研究部門, 5大阪大・歯・薬理, 6大阪大・国際共創大学院学位プログラム推進機構)

Hitoshi Hashimoto1,2,3,4, Takanobu Nakazawa1,5, Kaoru Seiriki1,6, Atsushi Kasai1 (1Lab. of Mol. Neuropharmacol., Grad. Sch. of Pharmaceut. Sci., Osaka Univ., 2Center for Child Mental Dev, United Grad. Sch. of Child Dev., Osaka Univ., 3Div. of Biosci., Inst. for Datability Sci., Osaka Univ., 4Transdimensional Life Imaging Div., Inst. for Open and Transdisciplinary Res. Initiatives, Osaka Univ., 5Dep. of Pharmacol., Grad. Sch. of Dentistry, Osaka Univ., 6Institute for Transdisciplinary Grad. Degree Programs, Osaka Univ.)

顕微鏡ライブイメージングと1細胞 RNA-seq を組み合わせた自動化システムの開発とシンギュラリティ生物学への応用

An automated system for combining single-cell RNA-seq with live cell imaging and its applications for Singularity Biology

○小川 泰策1, 城口 克之1,2 (理研・BDR, 2理研・IMS)

Taisaku Ogawa1, Katsuyuki Shiroguchi1,2 (1RIKEN BDR, 2RIKEN IMS)

Morphodynamic feature space of migrating cells

Daisuke Imoto1, Nen Saito2, Satoshi Sawai1,3 (1Graduate School of Arts and Sciences, University of Tokyo, 2Universal Biology Institute, Graduate School of Science, University of Tokyo, 3Research Center for Complex Systems Biology, University of Tokyo)

上皮メカノケミカル動態の同定

(2Pos243) System identification of mechano-chemical epithelial sheet dynamics

○浅倉 祥文1, 近藤 洋平2, 青木 一洋2, 本田 直樹1 (1京大・生命科学, 2基生研・定量生物学)

Yoshifumi Asakura1, Yohei Kondo2, Kazuhiro Aoki2, Naoki Honda1 (1Grad. Sch. Biostudies, Univ. Kyoto, 2Div. Quantitative Biol. ExCELLS, NIBB.)

Cryo-electron microscopy (cryo-EM) is rapidly becoming the main technology for studying 3D structures of proteins, while X-ray crystallography is a powerful traditional tool in structural biology. At the same time, we are facing several issues for cryo-EM such as machine-time limitation, and grid preparation difficulties. In this joint symposium, cutting-edge results using these methods are presented by researches from Taiwan and Japan, and we discuss the mutual methodological problems and future view in this field.
Opening Remarks

2SDP-1 Cryo-EM analysis of cilia and microtubule-based motor proteins
○吉川 雅英（東京大学）
Masahide Kikkawa (The Univ. of Tokyo)

2SDP-2 Cryo-EM Analysis of a Feline Coronavirus Spike Protein Reveals a Unique Structure and Camouflaging Glycans
Tzu-Jing Yang1,2, Yen-Chen Chang1,3, Tzu-Ping Ko1, Piotr Draczkowski1, Yu-Chun Chien1,2, Yuan-Chih Chang4, Kuen-Phon Wu1, Kay-Hooi Khoo1,2, Hui-Wen Chang3, Shang-Te Danny Hsu1,2
(1Institute of Biological Chemistry, Academia Sinica, 2Institute of Biochemical Sciences, National Taiwan University, 3School of Veterinary Medicine, National Taiwan University, 4Institute of Cellular and Organismic Biology, Academia Sinica)

2SDP-3 CryoEM studies of bacterial glutamine synthetase
Kuen-Phon Wu, Chia-Wei Chou (Institute of Biological Chemistry, Academia Sinica)

2SDP-4 V型ATP合成酵素の膜内在性ドメインV0の単粒子解析
Single particle analysis of membrane embedded domain V0 of V-type ATP synthase
○岸川 淳一，加藤 貴之，古田 隆，中西 温子，光岡 薫，横山 謙
(1京都産業大学 総合生命科学部 生命システム学科，2大阪大学大学院 生命機能研究科，3大阪大学 超高圧電子顕微鏡センター)
Jun-ichi Kishikawa1, Takayuki Kato2, Aya Furuta1, Atsuko Nakanishi1, Kaoru Mitsuoka3, Ken Yokoyama1 (1Dept. Mol. Biosci., Kyoto Sangyo Univ., 2Grad. Sch. Frontier Biosci., Osaka Univ., 3Res. Ctr. UHVEM., Osaka Univ.)

2SDP-5 胃プロトンポンプの輸送機構に対する構造基盤
Structural basis for the transport mechanism of the gastric proton pump
○阿部 一啓（1名古屋大学 細胞生理学研究センター，2名古屋大学大学院創薬科学研究科）
Kazuhiro Abe1,2 (1Cellular and Structural Physiology Institute, Nagoya Univ., 2Grad. Sch. Pharm. Sci., Nagoya Univ.)

2SDP-6 PAD4 regulates p53 function through protein citrullination
Chien-Yun Lee1, Guang-Yaw Liu2, Hui-Chih Hung1
(1National Chung-Hsing University, 2Chung Shan Medical University)

Closing Remarks
Recent years have witnessed remarkable progresses in quantum technologies based on quantum science, and these technologies and viewpoints are expected to bring innovations to measurement technologies and interpretations of biological phenomena. However, its application to life science is still in its early days and further leaps are expected in the future. In this symposium, researchers in the field of quantum biology aiming at such attempts will introduce their latest research achievements, and explore the future prospects of the fusion of quantum science and biophysics through discussions with the audiences.

### Opening Remarks

#### 2SEP-1
Materials chemistry of photo-excited triplet state for dynamic nuclear polarization
Nobuhiro Yanai\(^1,2\) ((Grad. Sch. Eng., Kyushu Univ., JST-PRESTO))

#### 2SEP-2
Incorporation of quantum chemical effect of solvation into molecular dynamics simulation and the applications to biomolecules
○渡邊 宙志\(^1,2\) (慶應義塾大学, JST さきがけ)
Hiroshi Watanabe\(^1,2\) (Keio Univ. KQCC, PRESTO JST)

#### 2SEP-3
Imaging dynamics of molecules inside the brain tissue by the application of multiphoton microscopy
○塗谷 睦生\(^1,2,3\) (慶應義塾大学医学部, JST さきがけ, 横浜国立大学)
Mutsuo Nuriya\(^1,2,3\) (Keio University School of Medicine, JST PRESTO, Yokohama National University)

#### 2SEP-4
Contextuality and Non-Locality in Quantum Physics and Cognitive Science
Yoshihiro Maruyama (Kyoto University)

#### 2SEP-5
Label-free molecular vibrational spectro-microscopy
Takuro Ideguchi\(^1\) (The University of Tokyo, PRESTO, JST)

#### 2SEP-6
Nanoscale thermometry and magnetometry in biology using NV center in diamond
Hitoshi Ishiwata\(^1,2\) (PRESTO, Tokyo Institute of Technology)

#### 2SEP-7
(2Pos288) グラフェン電界効果トランジスタとフェムトリットルチャンバーを用いたデバイ遮蔽を超える電気的バイオオセンサ
(2Pos288) Electrical Biosensing beyond the Debye Screening Length Using Graphene Field-Effect Transistor in Femtoliter Microchamber
○小野 克生\(^1\), 金井 康\(^1\), 井上 恒一\(^1\), 渡邊 洋平\(^2\), 中北 慎一\(^3\), 河原 敏男\(^4\), 鈴木 康夫\(^4\), 松本 和彦\(^4\)
(阪大産研, 京府医大, 香川大, 中部大)
Takao Ono\(^1\), Yasushi Kanai\(^1\), Koichi Inoue\(^1\), Yohei Watanabe\(^2\), Shin-ichi Nakakita\(^3\), Toshio Kawahara\(^4\), Yasuo Suzuki\(^4\), Kazuhiko Matsumoto\(^1\) (ISIR, Osaka Univ., Kyoto Pref. Univ of Med., Kagawa Univ., Chubu Univ.)
Living organisms do not evolve in perfectly random directions, instead, we recognize unevenness and directionalities in phenotypic variations and evolutionary changes. However, mechanisms for these directionality or evolutionary constraints remains unclear so far. In this symposium, we will show recent development in this field, in particular, analysis of evolutionary dynamics by constructive approaches to unveil constraints and directionalities in evolution, and discuss current subjects and future perspectives.

2SFP-1 共生進化生物学の最前線
Frontiers in experimental evolutionary biology of symbiosis
○深津 武馬（産業技術総合研究所 生物プロセス研究部門）
Takema Fukatsu (AIST)

2SFP-2 What makes animal embryos to follow the hourglass model?
Naoki Irie1,2, Yui Uchida1,2, Masahiro Uesaka3 (1Univ. Tokyo, Sch. of Science, 2Univ. Tokyo, Universal Biology Institute, 3RIKEN)

2SFP-3 Impact of polyploidy on the evolutionary rate
Ryudo Ohbayashi1, Tetsuhiro Hatakeyama2 (1BDR, RIKEN, 2Dept. of Basic Sci., Univ. of Tokyo)

2SFP-4 Analysis of Evolutionary Constraints and Plasticity by Microbial Laboratory Evolution
Chikara Furusawa1,2 (1BDR, RIKEN, 2UBI, Univ. Tokyo)

The drug development process is about to be innovated by launching the post-K supercomputer, which is designed to be the successor of the K computer. In recent years, various next-generation in-silico drug discovery techniques have been developed by combining fundamental molecular-simulation techniques with advanced experimental technologies or artificial intelligences (AIs). In this symposium, the forefront of the in-silico drug discovery will be discussed with young researchers in "Priority issue 1 on Post-K computer" (Building Innovative Drug Discovery Infrastructure Through Functional Control of Biomolecular Systems).

2SGP-1 拡張アンサンブル法を用いたタンパク質-リガンド結合ポーズの自由エネルギー解析
Free-energy analysis of protein-ligand binding pose using generalized ensemble methods
○尾嶋 拓, 李 秀栄, 杉田 有治（理研 BDR）
Hiraku Oshima, Suyong Re, Yuji Sugita (RIKEN BDR)
2SGP-2 An efficient screening, an accurate evaluation, and a simple prediction of protein complex structures
Kazuhiro Takemura, Akio Kitao (Sch. Life Sci. Tech., Tokyo Tech.)

2SGP-3 (2Pos029) Determination of protonated states for native and mutant structures of HIV-1 protease with indinavir by free energy calculations
Masahiko Taguchi, Ryo Oyama, Masahiro Kaneso, Shigehiko Hayashi (Kyoto University)

2SGP-4 創薬標的タンパク質の溶液構造解析
Ligand-bound forms of drug-discovery target protein in solution studied by molecular dynamics simulations
○浴本 亨 1, 工藤 崇文 1, 山根 努 1, 池口 満徳 1,2 (1横浜市大・生命医, 2理研)
Toru Ekimoto 1, Takafumi Kudo 1, Tsutomu Yamane 1, Mitsunori Ikeguchi 1,2 (1Yokohama City Univ., 2RIKEN)

2SGP-5 アラニン置換による抗体親和性の向上のメカニズム
Mechanism of antibody-affinity enhancement through alanine-substitution
○山下 雄史 (東京大学)
Takefumi Yamashita (The University of Tokyo)

2SGP-6 タンパク質アポ構造から発展した発展的分子動力学シミュレーションによる薬剤結合モードの予測
Protein-drug binding mode prediction from the apo-protein structure using a molecular dynamics-based pocket generation approach
○荒木 望嗣 1,2, 奥野 恭史 1,2 (1京大・院医, 2理研・計算科学研究機構)
Mitsugu Araki 1,2, Yasushi Okuno 1,2 (1Grad. Sch. of Med., Kyoto Univ., 2RIKEN, AICS)

2SGP-7 Reinforcement Learning and Global Optimization Techniques in Molecular Dynamics Simulations
Kei Terayama 1,2,3, Yasushi Okuno 3, Koji Tsuda 1,4,5 (1AIP, RIKEN, 2MIH, RIKEN, 3Grad. Sch. Med., Kyoto Univ., 4Grad. Sch. Frontier Sci., Univ. Tokyo, 5NIMS)

2SGP-8 (2Pos075) 天然変性タンパク質 p53 を標的としたペプチドの人工設計—液液相分離の制御—
(2Pos075) Rational design of peptide targeting intrinsically disordered protein p53 -regulation of function and phase-phase separation-
○鎌形 清人 1, 間野 絵梨子 1, 伊藤 優志 1, 上林 さおり 1, 本多 優也 1, 北原 亮 2, 龜田 倫史 3 (1東北大・多元研, 2立命大・薬, 3産総研・創薬基盤)
Kiyoto Kamagata 1, Eriko Mano 1, Yuji Itoh 1, Saori Kanbayashi 1, Masaya Honda 1, Ryo Kitahara 2, Tomoshi Kameda 3 (1IMRAM, Tohoku Univ., 2Coll. Pharmacy Sci., Ritsumeikan Univ., 3AIRC, AIST)
Cells carry highly organized architectures. Here we introduce the frontier research findings determining the actual image of intracellular architecture such as structural change of chromatin and nucleic acids, enzymatic activity, and signal transduction process via posttranslational modification by visualization using optical imaging and microscopic control devices, or mathematical modeling. We will select more than two subjects from those for the poster presentation (female and/or young researchers are more acceptable), and also we have a comprehensive discussion.

2SHP-1 Deciphering genome organization and dynamics by mathematical modeling and simulation
Soya Shinkai (RIKEN BDR)

2SHP-2 Reading out G-quadruplex RNA structure using transient state (TRAST) of photochemical reaction of fluorophores

2SHP-3 Isolation and analysis of specific cells, organelles and supramolecular complexes using microfluidic microdroplets
Ryo Iizuka (Grad. Sch. of Pharm. Sci., The Univ. of Tokyo)

2SHP-4 Observation of unstained bone tissues and immuno-EM in liquid by ASEM and cryo-TEM
○佐藤 主税¹, 杉本 真也², 雛野 恵里¹, 佐藤 真理¹, 坂井 詠子³ (¹産総研 バイオメディカル, ²慈恵医大 細菌学, ³長崎大歯科薬理学)
Chikara Sato¹, Shinya Sugimoto², Yuri Hatano¹, Mari Sato¹, Eiko Sakai³ (¹Biomedical Res. Inst., AIST, ²Dept. Bacteriol., The Jikei Univ. Sch. Med., ³Dental Pharmacology, Nagasaki Univ.)

2SHP-5 Cellular insulin-like growth factor-I (IGF-I) signal can be oscillated
○増田 正人, 伯野 史彦, 高橋 伸一郎 (東大・院農生科・応動)

2SHP-6 Live cell imaging analyses by input control system
Kazuya Kabayama¹,²,³ (¹Department of Chemistry, Graduate School of Science, Osaka University, ²Project Research Center, Graduate School of Science, Osaka University, ³Institute for Radiation Sciences, Osaka University)
Within a thermally fluctuating protein molecule under physiological conditions, tightly packed amino acid residues are interacting with each other exchanging energies between them. Thanks to the recent developments in theoretical/computational/experimental techniques, biophysical mechanisms of protein functions have been elucidated at atomic detail. In particular, heme proteins provide an ideal research targets for biophysicists because of their natural “probe” built in a protein matrix. In this symposium, we would like to discuss recent advancement of biophysical studies on heme proteins and molecular basis of their functions.

3SBA-1 Theoretical model of the allosteric transition of oxygen sensor domain of FixL
Takahisa Yamato (Nagoya University)

3SBA-2 Molecular Mechanism of NO Reduction by Nitric Oxide Reductase in Cellular System
Yoshitsugu Shiro (Univ. of Hyogo)

3SBA-3 Direct observation of vibrational energy flow in hemepeptides
Misao Mizuno (Grad. Sch. Sci., Osaka Univ.)

3SBA-4 Observation of photolysis reaction of myoglobin and hemoglobin in crystals
○佐藤 文菜（自治医大）
Ayana Sato-Tomita (Jichi Med. Univ.)

3SBA-5 Watching energy transport in proteins: Identifying dynamic networks and thermodynamic properties
David Leitner (University of Nevada, Reno)
‘Why living things move?’: this question has attracted many people since the ancient Greek times. In addition to major types of cell motility such as swimming and crawling, recent studies have revealed that many organisms adopt unique mechanisms of cell motility. Moreover, reconstitution approach and mathematical modelling aim to reproduce cell-like movements. In this session, we would like to discuss diversity and universality of motile mechanism of living things in reference to such diverse studies.

オーガナイザー：中村 修一（東北大学），鹿毛 あずさ（豊橋技術科学大学）
Organizers: Shuichi Nakamura (Tohoku University), Azusa Kage (Toyohashi University of Technology)

3SCA-1
君主は豹変す：シアノバクテリアも心変わりする
Cyanobacteria change their mind
○中根 大介, 西坂 崇之（学習院大・理・物理）
Daisuke Nakane, Takayuki Nishizaka (Dept. Phys., Gakushuin Univ.)

3SCA-2
Visualization of bacteria motility strategies and biofilm formation in tight microfluidic environments
Andrew Utada (Univ. of Tsukuba)

3SCA-3
アーキアべん毛の生物物理学的視点による特性評価
Biophysical characterization of molecular motors in archaea
○木下 佳昭 1,2, Helen Miller1, Zhengqun Li2, 三上 渚 2, Quax E.F. Tessa2, Albers Sonja-Verena2, Berry Richard1 (1オックスフォード大学, 2フライブルク大学)
Yoshiaki Kinoshita 1,2, Miller Helen1, Li Zhengqun2, Nagisa Mikami2, E.F. Tessa Quax2, Sonja-Verena Albers2, Richard Berry1 (1Oxford University, 2University of Freiburg)

3SCA-4
バクテリア細胞質のガラス的動力学の代謝活動による流動化現象について
Glassy dynamics of a model of bacterial cytoplasm with metabolic activities
○大山 倫弘 1, 川崎 猛史 2, 水野 英如 3, 池田 昌司 3（1産業技術総合研究所, 2名古屋大学, 3東京大学）
Norihiro Oyama1, Takeshi Kawasaki2, Hideyuki Mizuno3, Atsushi Ikeda3 (1AIST, 2Nagoya University, 3University of Tokyo)

3SCA-5
ボルボックス目緑藻の光行動
Photomovements of Chlamydomonas, Volvox and Tetrabaena
○若林 憲一（東工大・化生研）
Ken-ichi Wakabayashi (CLS, Tokyo Tech)

3SCA-6
Collective swimming of living spinners
Azusa Kage1, Takayuki Torisawa2,3, Ayano A. Medo4,5, Ken H. Nagai6 (1TUT, 2NIG, 3SOKENDAI, 4U Hyogo, 5Present address: Kyoto U, 6JAIST)
Rotation of stress fiber-wheel in migrating fish keratocytes

Chika Okimura (Fac. Sci., Yamaguchi Univ.)

Optogenetics: Applying photoreceptor for understanding biological phenomena

Organizers: Satoshi Tsunoda (Nagoya Institute of Technology), Keiichi Inoue (The University of Tokyo)

This symposium is aimed to introduce the cutting edge technology in optogenetics. Optogenetics markedly revolutionized life science. This technique allows fast and precise control of defined biological event, such as neuronal excitation, cell locomotion and gene expression, even in complex system such as freely moving animals. Optogenetics has been realized through understanding molecular properties of photoreceptors, developing new optical technique, genetics in model systems and modern brain science. In this symposium, we gather scientist with diverse expertise to discuss existing and newly emerging approaches which open new landscape for study of biology in future.
3SDA-6 (1Pos139) 集団細胞遊走における機械的なシグナルを介した ERK 活性伝播
(1Pos139) ERK activation waves mediated by intercellular mechanical signals during collective cell migration
○日野 直也 1, Trepat Xavier2, 松田 道行 1,3, 平島 剛志 3（1京大・院生命科学, 2IBEC, Spain, 3京大・院医学）
Naoya Hino1, Xavier Trepat2, Michiyuki Matsuda1,3, Tsuyoshi Hirashima3（1Grad. Sch. of Biostudies, Kyoto Univ., 2IBEC, Spain, 3Grad. Sch. of Med., Kyoto Univ.）

8:30〜11:10 E 会場（4F クリスタルルーム）/ Room E (4F Crystal Room)
3SEA 共催：新学術領域研究「温度を基軸とした生命現象の統合的理解（温度生物学）」
温度を基軸とした生物物理現象の理解
Thermal Biology

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

Temperature has attracted great attention in the search for deeper understanding of various life activities. In recent years, the emergence of thermometric methodologies for and insights into the thermal response of cellular organelles has opened a door for thermal biology at the single cell level. In this symposium, through the introduction of the challenges in single-cell thermal biology faces when exploring the mechanisms of thermal sensation and response inside a cell, we will discuss the fundamental principles of how temperature facilitates cell functions.

3SEA-1 単一細胞内温度シグナリングによるストレス顆粒形成の分子機構
The molecular mechanism of thermal signaling-dependent SG formation in single cells
○岡部 弘基 1,2（1東京大学大学院薬学系研究科, 2JSTさきがけ）
Kohki Okabe1,2（1Grad. Sch. Pharma. Sci., The Univ. of Tokyo, 2PRESTO, JST）

3SEA-2 (1Pos263) ラマンイメージングを用いた細胞内の水の可視化とラベルフリー細胞内温度測定への応用
(1Pos263) Raman imaging of water in a cell and its application to label-free evaluation of intracellular temperature
○杉村 俊紀, 梶本 真司, 中林 孝和（東北大院・薬）
Toshiki Sugimura, Shinji Kajimoto, Takakazu Nakabayashi (Grad. Sch. Pham. Sci., Tohoku Univ)

3SEA-3 (3Pos064) 温度上昇とテラヘルツ光照射は転写反応に異なる影響を及ぼす。
(3Pos064) Terahertz radiation and temperature increase differently affect transcription by RNA polymerase
○今清水 正彦 1, 田中 真人 1, 保科 宏道 2, 竹内 恒 1（1産総研, 2理研）
Masahiko Imashimizu1, Masahito Tanaka1, Hiromichi Hoshina2, Koh Takeuchi1（1AIST, 2RIKEN）

3SEA-4 小胞体-ミトコンドリア間クロストークを介した褐色脂肪細胞の機能制御
Regulation of brown adipocyte function through the crosstalk signaling between mitochondria and the endoplasmic reticulum
○西頭 英起（宮崎大・医・機能生化）
Hideki Nishitoh (Lab. of Biochem. and Mol. Biol., Dept. of Med. Sci., Univ. of Miyazaki)

3SEA-5 膜脂質を介する細胞内温度の制御機構
Membrane lipid-mediated regulation of intracellular temperature
村上 光, 長尾 賢治郎, ○梅田 眞晃（京都大学）
Akira Murakami, Kohjiro Nagao, Masato Umeda (Kyoto University)
Biomolecules such as proteins and nucleic acids are nano-meter sized materials. Therefore, it is important to understand how these biomolecules interact with each other and function in a specific environment. Recently, cutting-edge technologies and new approaches open the frontier of biophysics. Here, we will discuss the novel factors and phenomena in nano-space driving the biological activities.

3SFA-1 How nano-space affects biological phenomea
Hisashi Tadakuma (IPR, Osaka University)

3SFA-2 グアニン四重鎖とi-モチーフ構造を分子プローブとして使ったナノ空間の物性の検討
Investigation of physical properties of a confined nanospace using G-quadruplex and i-motif as a molecular probe
○遠藤 政幸（京大・院理）
Masayuki Endo (Grad. Sch. Sci. Kyoto Univ.)

3SFA-3 A widespread family of heat-resistant obscure (Hero) proteins protect against protein instability and aggregation
Kotaro Tsuboyama1, Shintaro Iwasaki2, Yukihide Tomari1 (1UTokyo IQB RNA function lab, 2Riken RNA systems biochemical lab)

3SFA-4 有限体積下で働く分子システム設計：人工細胞モデル構築を通じて
Molecular system design that works under finite volume: through artificial cell model construction
○野村 慎一郎（東北大学大学院 工学研究科 ロボティクス専攻）
Shin-ichiro Nomura (Dep. Robotics, TOHOKU Univ.)

3SFA-5 (3Pos195) Intracellular delivery of biologics using magnetically-navigated nanocarrier
Yoshihiro Sasaki, Ryosuke Mizuta, Naoya Kinoshita, Kazunari Akiyoshi (Department of Polymer Chemistry, Graduate School of Engineering, Kyoto University)

3SFA-6 Using SABER to amplify multiplexed FISH signal from RNA and DNA targets
Jocelyn Y Kishi1,2,5, Sylvain W. Lapan3,5, Brian J. Beliveau1,2,5, Emma R. West3,5, Allen Zhu1,2, Hiroshi M. Sasaki1,2, Sinem K. Saka1,2, Yu Wang1,2, Constance L. Cepko3,4, Peng Yin1,2 (1Wyss Institute, Harvard Univ., 2Dept. Systems Biology, Harvard Medical School, 3Dept. Genetics, Blavatnik Institute, Harvard Medical School, 4Howard Hughes Medical Institute, 5These authors contributed equally)
3SFA-7 (3Pos075) Attempt to understand the cellular function during developmental process from 3D structural model


3SFA-8 Mechanisms of centriole duplication in nano-space

Daiju Kitagawa, Shohei Yamamoto, Daisuke Takao (Graduate School of Pharmaceutical Sciences, The University of Tokyo)

8:30～11:10 G会場（4F アイボリールーム）／Room G (4F Ivory Room)

3SGA 超解像顕微鏡による生物物理学的生理学・病理学

Biophysical Physiology and Pathology by the Application of Superresolution Microscopy

Organizers: Taka A. Tsunoyama (OIST), Rinshi S. Kasai (Kyoto University)

Superresolution microscopy is widely used now a days, while its contributions for biophysics are still smaller than single molecule imaging. However, superresolution microscopy has the potential for solving the problems in physiology and pathology from biophysical point of view. In this symposium, the speakers are leading researchers in the field, and we expect innovative ideas and fruitful discussions.

3SGA-1 Advancing molecular medicine with quantitative single molecule localization microscopy

Devin L. Wakefield1, Kathleen M. Lennon1, Steven J. Tobin1, Matthew S. Brehove1, Adam L. Maddox1, Ajay Goel1, Kendall Van Keuren-Jensen2, Daniel Schmolze1, Tijana Jovanovic-Talisman1 (1City of Hope, 2TGen, 3Baylor Research Institute)

3SGA-2 High resolution systems approach to discover mitotic regulation of the nucleus

Paul S. Maddox (Department of Biology, University of North Carolina at Chapel Hill)

3SGA-3 Actin-induced compartments and islands in focal adhesions as revealed by simultaneous ultrafast PALM and single-molecule tracking

Takahiro Fujiwara (WPI-iCeMS, Kyoto Univ.)

3SGA-4 The axonal cytoskeleton at the nanoscale

Christophe Leterrier (INP CNRS-AMU UMR7051)

3SGA-5 Molecular localization and dynamics of Mediator regulating transcription elongation using single-molecule and super-resolution microscopy

Proteins undergo a variety of their qualitative changes throughout their life. The variety of their “quality” provides their specific function and behavior, which forms the basis of biological systems. Therefore, accurate and precise analyses of the quality of proteins will deepen our knowledge in the fundamental behavior of the protein molecules in biological systems and pathogenesis. From this perspective, this session focuses on the multiple protein analyses on the protein quality, including supra-structure in solution, post-translational modification, pathogenic stress, aging, etc., from the basic research to the medical and industrial applications, and discuss about the comprehensive usage of multiple analyses.

### はじめに
**Opening Remarks**

小川 覚之 (東京大)

Tadayuki Ogawa (Univ. of Tokyo)

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<th>3SHA-1</th>
<th>ヨウ素染色によるアミロイド線維構造多形と構造伝播の解析の試み</th>
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<td>Iodine staining as a useful probe for amyloid polymorphism and its propagation</td>
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<td>○茶谷 絵理 1, 平松 貴人 1, 袴 佳祐 1, 山本 直樹 2 (1神戸大院理, 2自治医大)</td>
</tr>
<tr>
<td></td>
<td>Eri Chatani 1, Takato Hiramatsu 1, Keisuke Yuzu 1, Naoki Yamamoto 2 (1Grad. Sch. Sci., Kobe Univ., 2Fac. Med., Jichi Medical Univ.)</td>
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<tr>
<td></td>
<td>Hironari Kamikubo 1,2, Takehiro Sato 3 (1NAIST MS, 2KEK IMSS, 3Spiber Inc.)</td>
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<th>3SHA-3</th>
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<td>Molecular basis of Breast tumor kinase by an adaptor protein, STAP-2</td>
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<td>○中迫 純希 1, 松尾 友樹 2, 神田 朋子 3, 田中 睦乃 2, 姫 譲 3, 松田 正 2, 前仲 勝美 2, 尾瀬 農之 2,3,4 (1北大院 生命科学, 2北大院 薬, 3北大院 先端生命, 4JST さきがけ)</td>
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<td>Junki Nakasako 1, Yuki Matsuo 2, Ryo Kanda 2, Yoshino Tanaka 2, Min Yao 3, Tadashi Matsuda 2, Katsumi Maenaka 2, Toyouki Ose 2,3,4 (1Graduate school of Life Science, 2Faculty of Pharm., 3Faculty of Advanced Life Science, Hokkaido University, 4JST PRESTO)</td>
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<td>Takayuki Uchihashi 1,2 (1Department of Physics, 2ExCELLS, NINS)</td>
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Aggregation and misfolding of therapeutic antibodies in bioprocessing

Masayoshi Onitsuka$^{1,2}$ ($^1$Grad. Sch. of Tech. Ind. Soc. Sci., Tokushima Univ., $^2$Manufacturing Technology Association of Biologics)