1 日目（9 月 24 日（火））／Day 1（Sep. 24 Tue.）

8:30〜11:10　B 会場（4F 天玉）／Room B (4F Tengyoku)
1SBA　ゲノム機能発現の統合的理解に向けた多角的アプローチ
Integrative approaches towards understanding of gene expression

オーガナイザー：森 貴治（理化学研究所），関根 俊一（理化学研究所）
Organizers: Takaharu Mori (RIKEN), Shun-ichi Sekine (RIKEN)

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　真核生物における転写メディエーター複合体の構造機能解析
Structural and functional basis of the Mediator complex in the eukaryotic transcriptional system
○野澤 佳世（東京大学・定量生命科学研究所）
Kayo Nozawa (*The University of Tokyo, Institute for Quantitative Biosciences*)

1SBA-3　RNA ポリメラーゼ II によるヌクレオソーム転写のメカニズム
Structural basis of nucleosome transcription by RNA polymerase II
○関根 俊一（理研 BDR）
Shun-ichi Sekine (*RIKEN BDR*)

1SBA-4　クライオ電顕と MD 計算による RNA ポリメラーゼ II 伸長状態複合体の動態解析
Dynamic structures of the RNA polymerase II elongation complex by cryo-EM and MD approaches
○森 貴治 [1], 江原 晴彦 [2], 関根 俊一 [2], 杉田 有治 [1,3,4]（[1]理研 杉田理論分子科学, [2]理研 BDR (横浜), [3]理研 BDR (神戸), [4]理研 R-CCS）
Takaharu Mori[1], Haruhiko Ehara[2], Shun-ichi Sekine[2], Yuji Sugita[1,3,4] ([1]*RIKEN Theor. Mol. Sci. Lab.*, [2]*RIKEN BDR (Yokohama)*, [3]*RIKEN BDR (Kobe)*, [4]*RIKEN R-CCS*)

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

1SBA-6　(1Pos082) 大腸菌非六量体型 DNA ヘリカーゼ UvrD C 末端欠損変異体の 1 分子イメージング
(1Pos082) Single-molecule imaging of a non-hexameric *Escherichia coli* helicase UvrD mutant lacking C-terminal residues
○横田 浩章（光産創大・光バイオ）
Hiroaki Yokota (*Biophotonics Lab., Grad. Sch. Creation New Photon. Indust.*)

8:30〜11:10　C 会場（4F 天樹）／Room C (4F Tenjyu)

1SCA　階層を超えた柔軟な場と空間の活用：生命システムが持つ可能性を探る
Utilization of soft compartments/interfaces from nano to macroscale: Exploring the potential of living systems

オーガナイザー：佐藤 佑介（東京工業大学），森田 雅宗（産業総合技術研究所），鈴木 勇輝（東北大学）
Organizers: Yusuke Sato (Tokyo Institute of Technology), Masamune Morita (AIST), Yuki Suzuki (Tohoku University)

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 慶樹 [1], 末松 安由美 [2], 秋山 良 [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] ([1]*Kyushu University, Sci.*, [2]*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）
Yusuke Sato[1], Ken Komiya[1], Ibuki Kawamata[2], Satochi Murata[2], Shin-ichiro M. Nomura[2] ([1]*Sch. Comput. Tokyo Tech*, [2]*Grad. Sch. Eng., Tohoku Univ.*)

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], 吉延 武留 [1], 關谷 悠介 [2], 川野 竜司 [2]（[1]埼玉大学大学院 理工研, [2]東京農工大 生命工学）
Naoto Nemoto[1], Toshiki Miyajima[1], Takeru Yoshinobu[1], Yusuke Sekiya[2], Ryuji Kawano[2] ([1]*Grad. Sci. Eng., Saitama Univ.*, [2]*Dept. Biotech. Life. Sci., Tokyo Univ. Agr. Tech*)

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], ○車 兪澈 [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] ([1]*JAMSTEC*, [2]*ELSI, Titech*, [3]*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] ([1]*Fac. Sci., Japan Women's Univ.*, [2]*ExCELLS*)

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.

はじめに
Opening Remarks
中川 敦史（大阪大）
Atsushi Nakagawa (*Osaka Univ.*)

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] ([1]*IQB, Univ. of Tokyo*, [2]*RIKEN 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] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*)

1SDA-3　クライオ電子顕微鏡解析によって明らか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 慎 [4], 吉川 雅英 [2], 遠藤 斗志也 [4]（[1]金沢大・保健, [2]東大・医, [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 Sakaue[4], Takuya Shiota[5], Kaori Yunoki[4], Junko Suzuki[4], Shin Kawano[4], Masahide Kikkawa[2], Toshiya Endo[4] ([1]*Grad. Sch. of Med. Sci., Kanazawa Univ.*, [2]*Grad. Sch. of Med., Univ. of Tokyo*, [3]*AIST*, [4]*Fac. of Life Sci., Kyoto Sangyo Univ.*, [5]*OPTT, 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 Akita[1,2], Ryo Nagao[1], Koji Kato[1], Naoyuki Miyazaki[3], Jian-Ren Shen[1] ([1]*RIIS, Okayama Univ.*, [2]*PRESTO, JST*, [3]*TARA, Univ. Tsukuba*)

1SDA-6　**光合成型複合体 I がフェレドキシン依存性を示す構造基盤**
Structural Basis for the Ferredoxin-dependency of Photosynthetic Complex I
○栗栖 源嗣 [1], 田中 秀明 [1], シューラー ヤン [2], 小沼 剛 [3], 池上 貴久 [3], ノバクチック マーク [4]（[1]阪大蛋白研, [2]マックスプランク生化学研究所, [3]横市大・院生命医科学, [4]ルール大学ボーフム）
Genji Kurisu[1], Hideaki Tanaka[1], Jan M. Schuller[2], Tsuyoshi Konuma[3], Takahisa Ikegami[3], Marc M. Nowaczyk[4] ([1]*Inst. Prot. Res., Osaka Univ.*, [2]*Max Planck Institute of Biochemistry*, [3]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [4]*Ruhr University Bochum*)

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　**1 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
○伊藤 由馬, 徳永 万喜洋（東工大・生命理工学院）
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
○日比野 佳代 [1,2], 前島 一博 [1,2], 境 祐二 [3]（[1]遺伝研, [2]総研大, [3]東大・医）
Kayo Hibino[1,2], Kazuhiro Maeshima[1,2], Yuji Sakai[3] ([1]*National Institute of Genetics*, [2]*SOKENDAI*, [3]*Grad. Sch. Med., Univ. Tokyo*)

1SEA-3 (1Pos095) 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
(1Pos095) Marked Difference in DNA Compaction and Transcription is Caused by Amino Acid Sequence of Oligopeptide
○秋田谷 龍男 [1], 平松 裕之 [2], 山口 秀明 [3], 久保 康児 [4], 村田 静昭 [4], 神戸 俊夫 [5], 櫨本 紀夫 [6], 吉川 研一 [7], Zinchenko Anatoly[4]（[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・生命医）
Tatsuo Akitaya[1], Hiroyuki Hiramatsu[2], Hideaki Yamaguchi[3], Koji Kubo[4], Shizuaki Murata[4], Toshio Kanbe[5], Norio Hazemoto[6], Kenichi Yoshikawa[7], Anatoly Zinchenko[4] ([1]*Asahikawa Med. Univ.*, [2]*Fac. Pharm., Meijo Univ.*, [3]*Fac. Agr. Sci., Meijo Univ.*, [4]*Grad. Sch. Env. Std., Nagoya Univ.*, [5]*Grad. Sch. Med., Nagoya Univ.*, [6]*Grad. Sch. Pharm. Sci., Nggoya City Univ.*, [7]*Fac. Bio. Med. Sci., Doshisah Univ.*)

1SEA-4 クロマチンループを形成しないヌクレオソーム排他 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
○粟津 暁紀 [1], 松島 佑樹 [2], 坂本 尚昭 [1] ([1]広島大学大学院統合生命科学研究科, [2]広島大学大学院統合生命科学研究科）
Akinori Awazu[1], Yuki Matsushima[2], Naoaki Sakamoto[1] ([1]*Dept. of Math. and Life Sciences, Hiroshima Univ.*, [2]*Dept. of Math. and Life Sciences, Hiroshima Univ.*)

1SEA-5 (1Pos239) Molecular Dynamics of Nucleosome Assembly
Giovanni Brandani, Shoji Takada, Cheng Tan (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

1SEA-6 (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
(1Pos088) Discontinuous Phase Transition in a Chromatin Model with Epigenetic Modification
○足立 景亮, 川口 喬吾（理研 BDR）
Kyosuke Adachi, Kyogo Kawaguchi (*RIKEN BDR*)

1SEA-7 Transcription dynamics of DNA at interfaces
Tetsuya Yamamoto (*Nagoya Univ., Dep. of Mat. Phys.*)

1SEA-8 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 chromatins: perspective from polymer physics
○坂上 貴洋 [1,2]（[1]青山学院大学 理工学部 物理・数理学科, [2]JST さきがけ）
Takahiro Sakaue[1,2] ([1]*Department of Physics and Mathematics, Aoyama Gakuin University*, [2]*JST, PRESTO*)

8:30〜11:10　F 会場（4F マーブルルーム）／Room F (4F Marble Room)

1SFA　共催：新学術領域研究「共鳴誘導で革新するバイオイメージング」 生体機能の「ありのまま」の可視化と理解へ ～共鳴する生命現象と光技術～ Toward "Ari-No-Mama" visualization to reveal biological functions -Resonance between life science and optical technology~

オーガナイザー：宮脇 敦史（理化学研究所），根本 知己（北海道大学）
Organizers: Atsushi Miyawaki (RIKEN), Tomomi Nemoto (Hookaido University)

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

○勢力 馨 [1,2], 橋本 均 [1,3,4,5]（[1]大阪大・薬・神経薬理, [2]大阪大・国際共創大学院, [3]大阪大・子どものこころ, [4]大阪大・データビリティフロンティア機構, [5]大阪大・先導的学際研究機構）
Kaoru Seiriki[1,2], Hitoshi Hashimoto[1,3,4,5] ([1]*Lab. Mol. Neuropharmacol., Grad. Sch. Pharmaceutical Sci., Osaka Univ.*, [2]*Interdisciplinary Program for Biomedical Sci., Inst. Transdisciplinary Graduate Degree Programs, Osaka Univ.*, [3]*Mol. Res. Cent. Children's Mental Development, United Grad. Sch. Child Development, Osaka Univ.*, [4]*Div. Biosci., Inst. Datability Sci., Osaka Univ.*, [5]*Transdimensional Life Imaging Div., Inst. Open and Transdisciplinary Res. Initiatives, Osaka Univ.*)

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（東北大多元所）
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*)

1SFA-5 線虫の全脳機能的イメージングのための要素技術と全神経活動の解析
Bio-image informatics for whole brain activity imaging and analysis of neural activity of C. elegans
○豊島 有[1], Wu Stephen[3], 金森 真奈美[1], 佐藤 博文[1], 張 文瑄[1], 村上 悠子[2], 大江 紗[2], 徳永 旭将[4], 広瀬 修[5], 久下 小百合[2], 寺本 孝行[2], 岩崎 唯史[6], 吉田 亮[3], 石原 健[2], 飯野 雄一[1]（[1]東大・院理・生物科学, [2]九大・院理・生物科学, [3]統計数理研究所, [4]九工大・大学院情報工学研究院, [5]金沢大・生命理工学系, [6]茨城大・工・知能システム）
Yu Toyoshima[1], Stephen Wu[3], Manami Kanamori[1], Hirofumi Sato[1], Moon Sun Jang[1], Yuko Murakami[2], Suzu Oe[2], Terumasa Tokunaga[4], Osamu Hirose[5], Sayuri Kuge[2], Takayuki Teramoto[2], Yuishi Iwasaki[6], Ryo Yoshida[3], Takeshi Ishihara[2], Yuichi Iino[1] ([1]*Dept of Biological Sciences, Grad Sch of Science, Univ of Tokyo*, [2]*Dept of Biology, Facl of Sciences, Kyushu Univ*, [3]*Inst of Statistical Mathematics, Research Organization of Information and Systems*, [4]*Dept of Systems Design and Informatics, Facl of Computer Science and Systems Engineering, Kyushu Inst of Technology*, [5]*Facl of Electrical and Computer Engineering, Inst of Science and Engineering, Kanazawa Univ*, [6]*Dept. of Mec. Eng., Grad. Sch. of Sci. and Eng., Ibaraki Univ.*)

1SFA-6 Bilateral Domain 画像処理
Bilateral Domain Image Processing
○吉澤 信（理化学研究所 光量子工学研究センター 画像情報処理研究チーム）
Shin Yoshizawa (*IPRT, RAP, RIKEN*)

8:30〜11:10　G 会場（4F アイボリールーム）／Room G (4F Ivory Room)
1SGA　筋・血管系のマルチスケールメカノバイオロジーの最前線
Frontiers in multi-scale mechanobiology of muscle and vascular system

オーガナイザー：岩城 光宏（理化学研究所），原 雄二（京都大学）
Organizers: Mitsuhiro Iwaki (RIKEN), Yuji Hara (Kyoto University)

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.

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

1SGA-2 (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
(1Pos108) Elucidation of molecular mechanism of contraction rhythm homeostasis in cardiac myocytes
○新谷 正嶺[1], 鷲尾 巧[2]（[1]中部大 生命健康科学部 生命医科学科, [2]東京大学 新領域創成科学研究科）
Seine Shintani[1], Takumi Washio[2] ([1]*Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University*, [2]*Graduate School of Frontier Sciences, the University of Tokyo*)

1SGA-3 DNA ナノデバイスと高解像 1 分子イメージング技術を活用した心臓のメカノバイオロジー
Mechanobiology of Heart Revealed with DNA Nano-device and Nanometer-precision Single-molecule Imaging
○岩城 光宏 [1,2]（[1]理研・生命機能科学センター, [2]阪大・院生命機能）
Mitsuhiro Iwaki[1,2] ([1]*RIKEN, BDR*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*)

1SGA-4 Myosin filament regulation by mechanosensing in skeletal and cardiac muscle
Vincenzo Lombardi (*PhysioLab*)

1SGA-5 骨格筋再生における機械受容イオンチャネル PIEZO1 の役割
Role of a mechanosensitive cation channel PIEZO1 in skeletal muscle regeneration
○原 雄二 [1,2], 平野 航太郎 [1], 高林 征史 [1], 土谷 正樹 [1], 梅田 眞郷 [1]（[1]京都大学大学院工学研究科 合成・生物化学専攻 生体認識化学分野, [2]AMED PRIME）
Yuji Hara[1,2], Kotaro Hirano[1], Seiji Takabayashi[1], Masaki Tsuchiya[1], Masato Umeda[1] ([1]*Graduate School of Engineering, Kyoto University*, [2]*AMED PRIME*)

1SGA-6 Mechano-protective roles of sugar chain in skeletal muscle
Motoi Kanagawa (*Kobe Univ. Grad. Sch. Med.*)

1SGA-7 Lipid bilayer membrane mediated mechanotransduction in vascular endothelial cells
Kimiko Yamamoto[1], Joji Ando[2] ([1]*System Physiology, Graduate School of Medicine, The University of Tokyo*, [2]*Laboratory of Biomedical Engineering, School of Medicine, Dokkyo Medical University*)

1SGA-8 (1Pos268) 細胞内動態をサブセルレベルで制御する温和な NanoHeating 技術
(1Pos268) A Thermodynamic Tool for Mechanobiology Research: Mild Nanoheating Technology to Alter Subcellular Dynamics
○新井 敏 [1], ファーディ ナンデス [2]（[1]早大・理工研, [2]早稲田シンガポール研）
Satoshi Arai[1], Nandus Ferdi[2] ([1]*Res. Inst. Sci. Eng., Waseda Univ.*, [2]*WABIOS*)

8:30〜11:10　H 会場（4F アンバールーム）／Room H (4F Amber Room)

1SHA　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.

1SHA-1 高圧力による生きた細胞内の分子機械の活性化
Activation of molecular machinery in living cells using high-pressure techniques
○西山 雅祥（近大・理工）
Masayoshi Nishiyama (*Kindai Univ.*)

1SHA-2 (1Pos147) RhoA activation induces cell cycle exit and differentiation of skin cancer cells
Oleg Dobrokhotov, Masahiro Sokabe, Hiroaki Hirata (*Nagoya Univ., Grad. Sch. Med.*)

1SHA-3 (1Pos146) Direct observation of cell mechanics under high hydrostatic pressure
Masatoshi Morimatsu, Keiji Naruse (*Grad. Sch. of Med., Dent. and Pharma. Sci., Okayama Univ.*)

1SHA-4 (1Pos253) 高圧力下で早くなるシアノバクテリアの概日周期
(1Pos253) Pressure accelerates the circadian clock of cyanobacteria
○北原 亮 [1], 大山 克明 [2], 川村 宇宙 [2], 三橋 景汰 [2], 北沢 創一郎 [1], 安永 和寛 [1], 相良 夏乃 [1], 藤本 恵 [2], 寺内 一姫 [2]（[1]立命館大・薬, [2]立命館大・生命）
Ryo Kitahara[1], Katsuaki Oyama[2], Takahiro Kawamura[2], Keita Mitsuhashi[2], Soichiro Kitazawa[1], Kazuhiro Yasunaga[1], Natsuno Sagara[1], Megumi Fujimoto[2], Kazuki Terauchi[2] ([1]*Pharm. Sci., Ritsumeikan Univ.*, [2]*Life Sci., Ritsumeikan Univ.*)

1SHA-5 細菌べん毛モーター回転に及ぼす高静水圧の影響
Effects of high hydrostatic pressure on the rotation of the bacterial flagellar motor
○川岸 郁朗 [1,2]（[1]法政大・生命・生命機能, [2]法政大・ナノテクセンター）
Ikuro Kawagishi[1,2] ([1]*Dept. Frontier Biosci., Hosei Univ.*, [2]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

1SHA-6 圧力感受性変異 YFP の圧力応答の構造基盤
Structural basis of pressure response of a pressure sensitive YFP variant protein
○今田 勝巳 [1], 辻井 美香 [1], 永江 峰幸 [2], 畑 宏明 [3], 渡邉 朋信 [4], 西山 雅祥 [5], 北尾 彰朗 [3], 渡邉 信久 [2]（[1]阪大・院・理, [2]名大・院・工, [3]東工大・生命, [4]理研・BDR, [5]近大・理工）
Katsumi Imada[1], Mika Tsujii[1], Takayuki Nagae[2], Hiroaki Hata[3], Tomonobu Watanabe[4], Masayoshi Nishiyama[5], Akio Kitao[3], Nobuhisa Watanabe[2] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Eng., Nagoya Univ.*, [3]*Sch. LifeSci and Tech,. Tokyo Inst. Tech.*, [4]*BDR, Riken*, [5]*Sch.Sci. and Eng., Kindai Univ.*)

1SHA-7 Pressure effects on protein-protein interactions studied by molecular dynamics simulations
Hiroaki Hata[1], Yasutaka Nishihara[2], Masayoshi Nishiyama[3], Ikuro Kawagishi[4], Akio Kitao[1] ([1]*Dept. of Life Sci. and Tech., Tokyo Tech*, [2]*IMCB, UTokyo*, [3]*Grad Sch. of Sci. and Eng., Kindai Univ.*, [4]*Dept. of Frontier Biosci., Hosei Univ.*)

13:40〜16:20　B 会場（4F 天玉）／Room B (4F Tengyoku)
1SBP　オーストラリアー日本 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.

はじめに
Opening Remarks
西坂 崇之（学習院大）
Takayuki Nishizaka (*Gakushuin Univ.*)

1SBP-1 Microscopic measurements of force and taxis in bacteria/archaea
Takayuki Nishizaka, Daisuke Nakane (*Dept. Phys., Gakushuin Univ.*)

1SBP-2 Biophysical models of physical rupturing of bacterial cells by nano-structured surfaces
Elena Ivanova (*RMIT University*)

1SBP-3 心筋ナノイメージング
Cardiac nano-imaging: from cells to the heart
○福田 紀男（東京慈恵会医科大学・細胞生理学講座）
Norio Fukuda (*Department of Cell Physiology, The Jikei University School of Medicine*)

1SBP-4 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*)

1SBP-5 リン脂質 flippase による細胞膜変形と細胞機能
Plasma membrane deformation by phospholipid flippase and cellular functions
○申 惠媛（京大・院・薬）
Hye-Won Shin (*Grad Sch Pharm Sci, Kyoto Univ*)

1SBP-6 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*)

おわりに
Closing Remarks
クヴァンサカル マーク（ラ・トローブ大学）
Marc Kvansakul (*La Trobe Univ.*)

13:40〜16:20　C 会場（4F 天樹）／Room C (4F Tenjyu)
1SCP　生物物理で見る脳神経回路
Cutting-edge brain research from a biophysical perspective

オーガナイザー：冨永 貴志（徳島文理大学），Bernd Kuhn（沖縄科学技術大学院大学）
Organizers: Takashi Tominaga (Tokushima Bunri University), Bernd Kuhn (OIST)

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.

1SCP-1 Simultaneous spatio-temporal dendritic voltage/calcium mapping and somatic recording from Purkinje neurons in awake mice
Bernd Kuhn, Christopher J. Roome (*OIST Graduate University*)

1SCP-2 Novel "*in vivo*" two-photon microscopy for vast and longtime neural activity
Tomomi Nemoto (*RIES, Hokkaido Univ.*)

1SCP-3 **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**
Functional optical coherence tomography with Fourier imaging reveals three-dimensional and micro-scale brain functional structure
○中道 友, 谷藤 学（理研 CBS）
Yu Nakamichi, Manabu Tanifuji (*RIKEN CBS*)

1SCP-4 **偏光で解き明かす生細胞内分子アセンブリーのナノ構造とそのダイナミクス**
Dissecting nano-scale architectures and dynamics of molecular assemblies in living cells with polarized light
○谷 知己（ウッズホール海洋生物学研究所）
Tomomi Tani (*Marine Biological Laboratory, Woods Hole*)

1SCP-5 (1Pos005) 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.*)

1SCP-6 (1Pos266) **グルタミン酸受容体を介した植物の長距離 Ca^{2+}シグナル**
(1Pos266) Long-distance Ca^{2+} transmission via glutamate receptor channels in plants
○豊田 正嗣 [1,2]（[1]埼玉大・院・理工, [2]University of Wisconsin-Madison）
Masatsugu Toyota[1,2] ([1]*Dept Biochem and Mol Biol, Saitama Univ*, [2]*University of Wisconsin-Madison*)

1SCP-7 **光信号で「見る」神経回路のはたらき–膜電位感受性色素（VSD）を中心に**
Optical view of the brain neural circuit activity: Voltage-sensitive-dye (VSD) imaging
○冨永 貴志, 冨永 洋子（徳島文理大学神経科学研究所）
Takashi Tominaga, Yoko Tominaga (*Inst. Neurosci., Tokushima Bunri Univ.*)

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)

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.

はじめに
Opening Remarks

1SDP-1 **溶液中での蛋白質間相互作用の定量的解析法**
Quantitative assessments of intermolecular protein mediated interactions in solution
○内山 進 [1,2]（[1]大阪大学大学院工学研究科先端生命工学専攻, [2]自然科学研究機構生命創成探究センター）
Susumu Uchiyama[1,2] ([1]*Department of Biotechnology, Graduate School of Engineering, Osaka University*, [2]*ExCELLS*)

1SDP-2 Native mass spectrometry of biomolecular complexes
Satoko Akashi (*Grad. Sch. Med. Life Science, Yokohama City Univ.*)

1SDP-3 (1Pos055) Biophysical analysis of alpha-synuclein oligomers by microchip electrophoresis
William E. Arter[1,2], Catherine K. Xu[1], Georg Krainer[1], Christopher M. Dobson[1], Tuomas P. J. Knowles[1,2] ([1]*Centre for Misfolding Disease, Department of Chemistry, University of Cambridge*, [2]*Cavendish Laboratory, Department of Physics, University of Cambridge*)

1SDP-4 (1Pos267) Visualization and quantification of biological samples by high-speed atomic force microscope
Hiroki Watanabe[1,2], Koichi Kato[1,2,3], Takayuki Uchihashi[1,4] ([1]*NINS, ExCELLS*, [2]*NINS, IMS*, [3]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [4]*Dept. Phys., Nagoya Univ.*)

1SDP-5 Dynamic structures and interactions of antibodies under physiologically relevant conditions
Saeko Yanaka[1,2,3], Rina Yogo[1,2,3], Hirokazu Yagi[3], Koichi Kato[1,2,3] ([1]*IMS., Natl. Inst. Nat. Sci.*, [2]*ExCELLS, Natl. Inst. Nat. Sci.*, [3]*Grad. Sch. Pharma. Sci., Nagoya City Univ.*)

1SDP-6 (1Pos058) **新規に開発した高濃度タンパク質のためのネガティブ染色電子顕微鏡法**
(1Pos058) A newly developed negative stain EM method for protein complexes at high protein concentration
○今井 洋 [1], 加藤 貴之 [2], Christoph Gerle[3], 武藤 悦子 [4], 光岡 薫 [5], 栗栖 源嗣 [3], 難波 啓一 [2], 昆 隆英 [1]（[1]阪大・院理・生物科学, [2]阪大・生命機能, [3]阪大・蛋白研, [4]理研 CBS, [5]阪大・超高圧電顕センター）
Hiroshi Imai[1], Takayuki Kato[2], Gerle Christoph[3], Etsuko Muto[4], Kaoru Mitsuoka[5], Genji Kurisu[3], Keiichi Namba[2], Takahide Kon[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*IPR, Osaka Univ.*, [4]*CBS, RIKEN*, [5]*Res. Ctr. UVHEM, Osaka Univ.*)

1SDP-7 **蛋白質相互作用の熱測定と創薬**
Thermodynamics of Protein Interaction for Therapy and Diagnosis
長門石 曉 [1,2], ○津本 浩平 [1,2]（[1]東京大学医科学研究所, [2]東京大学大学院工学系研究科）
Satoru Nagatoishi[1,2], **Kohei Tsumoto**[1,2] ([1]*Inst Med Sci, Univ Tokyo*, [2]*Sch Eng, Univ Tokyo*)

おわりに
Closing Remarks

13:40〜16:20　E 会場（4F クリスタルルーム）／Room E (4F Crystal Room)
1SEP　共催：JST さきがけ「1 細胞解析」
さきがけ「1 細胞」は何をやっている？　1 細胞研究の醍醐味と技術革新
What is “Single-cell PRESTO” doing?

オーガナイザー：城口 克之（理化学研究所），鈴木 団（大阪大学）
Organizers: Katsuyuki Shiroguchi (RIKEN), Madoka Suzuki (Osaka University)

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 Aoki[1,2], Yuji Yamauchi[1], Mitsuyoshi Ueda[1] ([1]*Graduate School of Agriculture, Kyoto University*, [2]*JST, PREST*)

1SEP-2　(1Pos196) Single-cell trajectory analysis of human iPS cell-derived neurons carrying a rare RELN deletion
Yuko Arioka[1,2,3], Emiko Shishido[1,4], Norio Ozaki[1] ([1]*Department of Psychiatry, Nagoya University Graduate School of Medicine*, [2]*Nagoya University Hospital*, [3]*Institute for Advanced Research, Nagoya University*, [4]*National 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, [2]JST さきがけ）
Satoru Okuda[1,2] ([1]*Nano LSI, Kanazawa Univ*, [2]*JST 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, [2]JST さきがけ）
Satoshi Yamaguchi[1,2] ([1]*Research Center for Advanced Science and Technology (RCAST), The University of Tokyo*, [2]*PRESTO, JST*)

13:40〜16:20　F 会場（4F マーブルルーム）／Room F (4F Marble Room)

1SFP　高感度水素検出による生体内化学反応の制御を目指して
Toward the chemical reaction control in biological environment by high-sensitive hydrogen detection

オーガナイザー：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)

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 nano-devices will discuss and overview what can be elucidated by visualizing and characterizing hydrogen atoms.

はじめに
Opening Remarks

1SFP-1　**単結晶中性子回折計 iBIX の現状と将来展望**
Current status and future prospects of single-crystal neutron diffractometer iBIX at pulsed neutron source MLF, J-PARC
○日下 勝弘[1], 山田 太郎[1], 矢野 直峰[1], 細谷 孝明[1], 大原 高志[2], 田中 伊知朗[1]（[1]茨城大学，フロンティア応用原子科学研究センター, [2]日本原子力研究開発機構，J-PARC センター）
Kastuhiro Kusaka[1], Taro Yamada[1], Naomine Yano[1], Takaaki Hosoya[1], Takashi Ohhara[2], Ichiro Tanaka[1] ([1]*Frontier Researc Center for Applied Atomic Sciences, Ibaraki University*, [2]*Japan Atomic Energy Agency, J-PARC Center*)

1SFP-2　**中性子結晶構造解析で明らかになるセルラーゼの加水分解メカニズム**
Hydrolytic mechanisms of inverting cellulases clarified by neutron crystallography
○五十嵐 圭日子[1,2]（[1]東京大学, [2]VTT フィンランド技術研究センター）
Kiyohiko Igarashi[1,2] ([1]*University of Tokyo*, [2]*VTT Technical Research Centre of Finland*)

1SFP-3　**フェレドキシン依存性ビリン還元酵素の機能と基質のプロトン化状態**
Function of a ferredoxin-dependent bilin reductase and the protonation state of its substrate
○海野 昌喜[1,2]（[1]茨城大学大学院理工学研究科量子線科学専攻, [2]茨城大学フロンティア応用原子科学研究センター）
Masaki Unno[1,2] ([1]*Graduate School of Science & Engineering, Ibaraki University*, [2]*Frontier Research Center for Applied Atomic Sciences*)

1SFP-4　**(1Pos021) 創薬標的タンパク質の中性子結晶構造解析**
(1Pos021) Neutron crystallographic analysis of drug-target proteins
○横山 武司（富山大・薬）
Takeshi Yokoyama (*Fac. of Pharm. Sci., Univ. of Toyama*)

1SFP-5　Liquid properties and chemical reactions in 100 nm nanochannels
Kazuma Mawatari (*Univ. Tokyo*)

1SFP-6　**光合成水分解反応におけるプロトンおよび水分子の赤外分光検出**
Infrared detection of protons and water molecules in photosynthetic water oxidation
○野口 巧（名古屋大学大学院理学研究科物質理学専攻（物理系））
Takumi Noguchi (*Division of Material Science, Graduate School of Science, Nagoya University*)

おわりに
Closing Remarks

13:40〜16:20　G 会場（4F アイボリールーム）／Room G (4F Ivory Room)
1SGP　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　Objective and efficient procedure for inferring couplings in neuronal networks
Yu Terada[1,2], Tomoyuki Obuchi[1], Takuya Isomura[2], **Yoshiyuki Kabashima**[1] ([1]*Tokyo Tech.*, [2]*RIKEN CBS*)

1SGP-3　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, [2]JST・さきがけ, [3]東工大・情報理工, [4]京大院・情報, [5]統数研）
Takuma Kasai[1,2], Shunsuke Ono[2,3], Toshiyuki Tanaka[4], Shiro Ikeda[5], Takanori Kigawa[1,3] ([1]*RIKEN BDR*, [2]*PRESTO, JST*, [3]*Sch. Comput., Tokyo Inst. Tech.*, [4]*Grad. Sch. Inform., Kyoto Univ.*, [5]*Inst. Stat. Math.*)

1SGP-4　高速高精度一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], 櫻井 実 [3], 飯野 亮太 [1,2]（[1]自然科学研究機構 分子科学研究所, [2]総合研究大学院大学, [3]東京工業大学）
Akihiko Nakamura[1,2], Kei-ichi Okazaki[1], Tadaomi Furuta[3], Minoru Sakurai[3], Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*, [3]*Tokyo Institute of Technology*)

1SGP-5　DNA curtains: high-throughput single molecule imaging for DNA transactions
Tsuyoshi Terakawa (*Grad. School of Sci., Kyoto Univ.*)

1SGP-6　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
○福間 剛士（金沢大・ナノ生命研）
Takeshi Fukuma (*NanoLSI, Kanazawa Univ.*)

1SGP-7　細胞表面動態の高精度計測を目指した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 [1,2], 岡本 千優 [3], 今井 大達 [1], 渡辺 信嗣 [4], 安藤 敏夫 [2,4], 古寺 哲幸 [2,4]（[1]金沢大・新学術創成, [2]JST・CREST, [3]金沢大・数物, [4]金沢大・WPI-NanoLSI）
Masahiro Shimizu[1,2], Chihiro Okamoto[3], Hirotatsu Imai[1], Shinji Watanabe[4], Toshio Ando[2,4], Noriyuki Kodera[2,4] ([1]*InFiniti, Kanazawa Univ.*, [2]*CREST, JST*, [3]*Dept. Sch. Math. & Phys., Kanazawa Univ.*, [4]*WPI-NanoLSI, Kanazawa Univ.*)

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 [1,2], 新稲 亮 [1], 高田 彰二 [1,2]（[1]京大院・理, [2]JST・CREST）
Sotaro Fuchigami[1,2], Toru Niina[1], Shoji Takada[1,2] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*CREST, JST*)

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[1,3], Yan Zhang[2,3], Hongli Hu[3], Carl-Mikael Suomivuori[3], Francois Marie Ngako Kadji[4], Junken Aoki[4], Kaavya Krishna Kumar[3], Rasmus Fonseca[3], Daniel Hilger[3], Weijiao Huang[3], Naomi Latorraca[3], Asuka Inoue[4], Ron Dror[3], Brian Kobilka[3], Georgios Skiniotis[3] ([1]*The Univ. of Tokyo*, [2]*Zhejiang Univ.*, [3]*Stanford Univ.*, [4]*Tohoku Univ.*)

1SHP-4　NMR 法を用いた動的構造にもとづく GPCR のシグナル伝達機構の解明
Dynamics of G protein-coupled receptor related to various signaling revealed by NMR
○幸福 裕 [1], 白石 勇太郎 [1], 夏目 芽衣 [1], 奥出 順也 [1], 今井 駿輔 [1], 前田 正洋 [2], 辻下 英樹 [2], 倉永 健史 [1], 井上 将行 [1], 中田 國夫 [3], 水越 利巳 [3], 上田 卓見 [1], 岩井 秀夫 [4], 嶋田 一夫 [1]（[1]東大・院薬系, [2]塩野義製薬（株）, [3]味の素（株）, [4]ヘルシンキ大）
Yutaka Kofuku[1], Yutaro Shiraishi[1], Mei Natsume[1], Junya Okude[1], Shunsuke Imai[1], Masahiro Maeda[2], Hideki Tsujishita[2], Takefumi Kuranaga[1], Masayuki Inoue[1], Kunio Nakata[3], Toshimi Mizukoshi[3], Takumi Ueda[1], Hideo Iwai[4], Ichiro Shimada[1] ([1]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [2]*Shionogi Co., Ltd.*, [3]*Ajinomoto Co., Inc.*, [4]*Univ. Helsinki*)

1SHP-5　Theoretical Prediction of Thermostabilizing Mutations for GPCR: Identification of Hot-Spot Residues to be Mutated Common in Class A GPCRs
Satoshi Yasuda[1,2,3], Yuta Kajiwara[4], Yuki Takamuku[1], Nanao Suzuki[1], Yosuke Toyoda[5], Kazushi Morimoto[5], Ryoji Suno[5], So Iwata[5], Takuya Kobayashi[5], Takeshi Murata[1,2], Masahiro Kinoshita[3] ([1]*Grad. Sch. Sci., Chiba Univ.*, [2]*MCRC*, [3]*IAE*, [4]*Grad. Sch. Ener. Sci., Kyoto Univ.*, [5]*Grad. Sch. Med., Kyoto Univ.*)

1SHP-6　(1Pos077) 理論計算による熱安定化ムスカリン M2 受容体の選択的アンタゴニスト AF-DX 384 結合型構造
(1Pos077) Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor
○寿野 良二 [1], Lee Sangbae[2], 前田 将司 [3], 安田 賢司 [4], 山下 恵太郎 [9], 平田 邦生 [5,6], 村田 武士 [7], 木下 正弘 [8], 山本 雅貴 [5], Kobilka Brian[3], Vaidehi Nagarajan[2], 岩田 想 [8], 小林 拓也 [1]（[1]関西医大・医, [2]ホープ市医学センター, [3]スタンフォード大・医, [4]千葉大・理, [5]理研・SPring-8, [6]JST・さきがけ, [7]京大・エネ研, [8]京大・医, [9]東大・理）
Ryoji Suno[1], Sangbae Lee[2], Shoji Maeda[3], Satoshi Yasuda[4], Keitaro Yamashita[9], Kunio Hirata[5,6], Takeshi Murata[7], Masahiro Kinoshita[8], Masaki Yamamoto[5], Brian Kobilka[3], Nagarajan Vaidehi[2], So Iwata[8], Takuya Kobayashi[1] ([1]*Kansai Medi. Univ.*, [2]*City Hope Med. Ctr.*, [3]*Stanford Univ.*, [4]*Chiba Univ.*, [5]*RIKEN,SPring-8*, [6]*JST,PRESTO*, [7]*IAE, Kyoto Univ.*, [8]*Med,Kyoto Univ.*, [9]*Univ.Tokyo,Sci*)

2 日目（9 月 25 日（水））／Day 2（Sep. 25 Wed.）

8:30〜11:10　B 会場（4F 天玉）／Room B (4F Tengyoku)
2SBA　共催：新学術領域研究「分子夾雑の生命化学」
分子夾雑のススメ
Invitation to multimolecular crowding

オーガナイザー：田端 和仁（東京大学），三好 大輔（甲南大学）
Organizers: Kazuhito Tabata (The University of Tokyo), Daisuke Miyoshi (Konan University)

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 begining 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.

2SBA-1　Chemical control of protein localization in the multimolecular cellular space
Shinya Tsukiji (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

2SBA-2 Secondary structure of DNA for liquid-liquid phase separation
Masahiro Mimura[1,2], Shunsuke Tomita[2], Ryoji Kurita[1,2], Kentaro Shiraki[1] ([1]*Pure and Appl. Sci., Univ. Tsukuba*, [2]*Biomed. Res. Inst., AIST.*)

2SBA-3 **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）
Eiichiro Mori (*Dept. Future Basic Med., Sch. Med., Nara Med. Univ.*)

2SBA-4 **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.*)

2SBA-5 **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.*)

8:30～11:10　C 会場（4F 天樹）／Room C (4F Tenjyu)
2SCA　**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

オーガナイザー：白井 剛（長浜バイオ大学），寺田 透（東京大学）
Organizers: Tsuyoshi Shirai (Nagahama Institute of Bioscience and Technology), Tohru Terada (The University of Tokyo)

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.

2SCA-1 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*)

2SCA-2 **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)*)

2SCA-3 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）
Takeshi Kawabata, Genji Kurisu (*Inst.Prot.Res., Osaka Univ.*)

2SCA-5　Development of a deep-learning-based method to identify "good" regions of a cryo-EM grid
Tohru Terada[1,3], Yuichi Yokoyama[2], Kentaro Shimizu[1,3], Kouki Nishikawa[4], Yoshinori Fujiyoshi[4], Kazutoshi Tani[5] ([1]*III, Univ. Tokyo*, [2]*GSII, Univ. Tokyo*, [3]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [4]*Adv. Res. Inst., Tokyo Med. Dent. Univ.*, [5]*Grad. Sch. Med., Mie Univ.*)

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 Namba[1,2,3] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*RIKEN SPring-8 Center*, [3]*RIKEN 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：エネルギー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 F_oF_1-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

オーガナイザー：岩本 裕之（高輝度光科学研究センター），関口 博史（高輝度光科学研究センター）
Organizers: Hiroyuki Iwamoto (JASRI), Hiroshi Sekiguchi (JASRI)

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.

はじめに
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, [4]SPring-8, JASRI）
Shinji Kamimura[1], Hiroshi Imai[2], Toshiki Yagi[3], Hiroyuki Iwamoto[4] ([1]*Dept. Biol. Sci., Chuo Univ.*, [2]*Grad. Sch. Sci., Osaka Univ.*, [3]*Dept. Life Sci., Prefect. Univ. Hiroshima*, [4]*SPring-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. Pearson[1,2], Naoto Yagi[3], Mikiyasu Shirai[1], Mark Waddingham[1], Hirotsugu Tsuchimochi[1], Takashi Sonobe[1], Vijayakumar Sukumaran[1] ([1]*National Cerebral and Cardiovascular Center*, [2]*Monash University, Department of Physiology*, [3]*JASRI*)

2SEA-5 (2Pos269) G1 期酵母細胞核内における核酸分布の XFELX 線回折イメージング
(2Pos269) Distribution of nucleic acids in yeast nucleus of G1 phase visualized by X-ray diffraction imaging using X-ray free electron laser
○中迫 雅由[1,2], 山本 隆寛[1,2], 小林 周[1,2], 大出 真央[1,2], 岡島 公司[1,2], 高山 裕貴[1,2,3], 芝口 友隆[1,2], 山本 雅貴[2]（[1]慶應義塾大学, [2]理化学研究所, [3]兵庫県立大）
Masayoshi Nakasako[1,2], Takahiro Yamamoto[1,2], Amane Kobayashi[1,2], Mao Oide[1,2], Koji Okajima[1,2], Yuki Takayama[1,2,3], Tomotaka Oroguchi[1,2], Masaki Yamamoto[2] ([1]*Keio University*, [2]*RIKEN*, [3]*University of Hyogo Prefecture*)

おわりに
Closing Remarks
岩本 裕之（高輝度光科学研究センター）
Hiroyuki Iwamoto (*JASRI*)

8:30〜11:10　F 会場（4F マーブルルーム）／Room F (4F Marble Room)
2SFA　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」
光操作による生命機能解析
Elucidation of biological functions by optical control

オーガナイザー：七田 芳則（立命館大学），塚本 寿夫（分子科学研究所）
Organizers: 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 photoreceptive 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.

はじめに
Opening Remarks
七田 芳則（立命大）
Yoshinori Shichida (*Ritsumeikan Univ.*)

2SFA-1 記憶痕跡サブ・アンサンブルの協奏的活動によるエピソード記憶の脳内表現
Orchestrated ensemble activities constitute a hippocampal memory engram
○大川 宜昭[1,2]（[1]富山大学・院医薬, [2]JST・さきがけ）
Noriaki Ohkawa[1,2] ([1]*Univ of Toyama Grad Sch of Med and Pharm Sci*, [2]*PRESTO, JST*)

2SFA-2 X 線を用いた神経機能の遠隔無線操作
Remote and wireless control of neuronal function using X-ray
○山下 貴之[1]（[1]名古屋大学 環境医学研究所 神経系分野２, [2]科学技術振興機構 さきがけ）
Takayuki Yamashita[1] ([1]*Dept. Neurosci. II, RIEM, Nagoya Univ.*, [2]*PRESTO, JST*)

2SFA-3 バッテリレス超小型光刺激デバイス
Batteryless ultra-small implantable optical stimulator
○德田 崇[1], Pakpuwadon Thanet[2], Wuthibenjaphonchai Nattakarn[2], 春田 牧人[2], 笹川 清隆[2], 太田 淳[2]（[1]東工大 未来研, [2]奈良先端大 物質創成）
Takashi Tokuda[1], Thanet Pakpuwadon[2], Nattakarn Wuthibenjaphonchai[2], Makito Haruta[2], Kiyotaka Sasagawa[2], Jun Ohta[2] ([1]*FIRST, Tokyo Tech*, [2]*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]（[1]阪大院薬, [2]医薬基盤健栄研, [3]さきがけ）
Kazuo Takayama[1,2,3] ([1]*Osaka University*, [2]*NIBIOHN*, [3]*PRESTO*)

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]（[1]分子科学研究所, [2]JST さきがけ）
Hisao Tsukamoto[1,2] ([1]*Institute for Molecular Science*, [2]*PRESTO, 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 医）
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-Cheh[3], 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）
Katsuhisa Kurogi[1], Takamasa Teramoto[2], Yoshimitsu Kakuta[2], Ming-Cheh Liu[3], Masahito Suiko[1], Yoichi Sakakibara[1] ([1]*Dept. Biochem. Appl. Biosci., Fac. Agric., Univ. Miyazaki*, [2]*Dept. Biosci. Biotechnol., Grad. Sch. Agric., Kyushu Univ.*, [3]*Dept. Pharmacol., Coll. Pharm., Univ. Toledo*)

2SGA-3 **発熱植物の生体エネルギー論：シアン耐性呼吸からミトコンドリアの構造まで**
Towards understanding the roles of mitochondrial energy bypasses in heat-producing plants
○稲葉 靖子（宮崎大・農）
Yasuko Ito-Inaba (*Agric, Univ. Miyazaki*)

2SGA-4 The role of Fhod family formin proteins in mouse heart
Fumiyuki Sanematsu[1], Hideki Sumimoto[2], Ryu Takeya[1] ([1]*Dept. of Pharmacol., Fac. of Med., Univ. of Miyazaki*, [2]*Dept. of Biochem., Kyushu Univ. Grad. Sch. of Med. Sci.*)

2SGA-5 In-cell ^{19}F NMR: Chemical method for investigating nucleic acid structure in living cells
Takumi Ishizuka, Yan Xu (*Fac. Med., Univ. of Miyazaki*)

2SGA-6 **微生物電池における c 型シトクロムを介した細胞外電子伝達**
Extracellular electron transfer via c-type cytochromes in microbial fuel cells
○井上 謙吾（宮崎大・農）
Kengo Inoue (*Department of Biochemistry and Applied Biosciences, Faculty of Agriculture*)

8:30～11:10　H 会場（4F アンバールーム）／Room H (4F Amber Room)
2SHA　**タンパク質のダイナミックレスポンスに関わる未解決問題への挑戦**
Challenges to get insight into unsolved problems of dynamic response in proteins

オーガナイザー：鷹野 優（広島市立大学），米澤 康滋（近畿大学）
Organizers: Yu Takano (Hiroshima City University), Yasushige Yonezawa (Kindai University)

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.

はじめに
Opening Remarks
米澤 康滋（近畿大）
Yasushige Yonezawa (*Kindai Univ.*)

2SHA-1 **生物学的ネットワークの確率論的変動**
Stochastic usage of biological network
○白木 琢磨（近畿大学・生物理工学部）
Takuma Shiraki (*Kindai Univ. BOST*)

2SHA-2 Autoencoder-based analyses of dynamic allostery on proteins by regulator binding
Yuko Tsuchiya[1], Kei Taneishi[2], Yasushige Yonezawa[3] ([1]*AIRC, AIST*, [2]*RIKEN*, [3]*KINDAI University*)

2SHA-3 **大規模量子分子動力学シミュレーションを用いた光受容タンパク質におけるプロトン移動反応の解明**
Clarification of proton transfer reactions in photoreceptive proteins using large-scale quantum molecular dynamics simulations
○小野 純一 [1], 岡田 千果 [2], 西村 好史 [1], 中井 浩巳 [1,2,3]（[1]早大理工総研, [2]早大先進理工, [3]京大 ESICB）
Junichi Ono[1], Chika Okada[2], Yoshifumi Nishimura[1], Hiromi Nakai[1,2,3] ([1]*WISE, Waseda Univ.*, [2]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [3]*ESICB, Kyoto Univ.*)

2SHA-4　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 紘充（北里大学薬学部 生物分子設計学教室）
Hiromitsu Shimoyama (*Kitasato-Univ.*)

2SHA-5　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*)

2SHA-6　(2Pos057) 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
(2Pos057) Dynamin GTPase mechanically regulates bundling and unbundling of actin filaments
○竹居 孝二 [1], テ モン ラ [1], 阿部 匡 [1], 竹田 哲也 [1], 藤原 郁子 [2], 成田 哲博 [3]（[1]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）
Kohji Takei[1], La The Mon[1], Tadashi Abe[1], Tetsuya Takeda[1], Ikuko Fujiwara[2], Akihiro Narita[3] ([1]*Grad.Sch. Med.Dent. Pharm.Sci., Okayama Univ.*, [2]*Dept. Biol.Facul.Sci., Osaka City Univ.*, [3]*Struct. Biol. Res. Ctr and Divi. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

2SHA-7　Analysis of Effect of Mutation on the Response for Membrane Depolarization in the Voltage-Gated Potassium Channel Kv1.2
Hiroko X. Kondo[1], Norio Yoshida[2], Gen Masumoto[3], Matsuyuki Shirota[4,5,6], Yu Takano[7], Kengo Kinoshita[5,6] ([1]*Fac. Eng., Kitami Inst. Tech.*, [2]*Grad. Sch. Sci., Kyushu Univ*, [3]*RIKEN ISC*, [4]*Grad. Sch. Med., Tohoku Univ.*, [5]*GSIS, Tohoku Univ.*, [6]*ToMMo, Tohoku Univ.*, [7]*Grad. Sch. Info. Sci., Hiroshima City Univ.*)

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

14:10〜16:50　B 会場（4F 天玉）／Room B (4F Tengyoku)
2SBP　共催：新学術領域研究「代謝統合オミクス」
読む×解く、代謝のアダプテーション
Measure x Analyze Metabolic Adaptation of Biological Systems

オーガナイザー：岡田 眞里子（大阪大学），馬場 健史（九州大学）
Organizers: Mariko Okada (Osaka University), Takeshi Bamba (Kyushu University)

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.

2SBP-1　トランスオミクスに資する次世代メタボローム分析技術の開発
Development of next generation metabolome analytical technologies for trans-omics
○馬場 健史（九大・生医研）
Takeshi Bamba (*Med. Inst. Bioreg., Kyushu Univ.*)

2SBP-2 Novel sequencing methods to read the epigenome
Takashi Ito (*Kyushu Univ. Grad. Sch. Med. Sci.*)

2SBP-3 Sulfur Metabolism Rewiring in NRF2-Addicted Cancer Cells
Hozumi Motohashi (*Institute of Development, Aging and Cancer, Tohoku University*)

2SBP-4 **条件付き独立性を用いたネットワーク構造推定**
Network structure inference by conditional independence
○宇田 新介（九州大学）
Shinsuke Uda (*Kyushu university*)

2SBP-5 **一細胞遺伝子発現プロファイルからの細胞集団および細胞間コミュニケーションの動態モデリング**
Modeling dynamics of cell population and cell-to-cell communication from single-cell gene expression profiles
○島村 徹平（名古屋大学）
Teppei Shimamura (*Nagoya University*)

2SBP-6 **オミクスを数理モデルでつなぐ**
Analyze Omics data using kinetic model
○岡田 眞里子[1]（[1]大阪大学蛋白質研究所細胞システム研究室, [2]理化学研究所 IMS）
Mariko Okada[1] ([1]*Institute for Protein Research, Osaka University*, [2]*RIKEN IMS*)

14:10〜16:50　C 会場（4F 天樹）／Room C (4F Tenjyu)
2SCP　**共催：新学術領域研究「シンギュラリティ生物学」**
シンギュラリティ生物学：少数の要素が全体の機能を変革する
Singularity Biology: Small elements change the function of the whole systems

オーガナイザー：小松崎 民樹（北海道大学），堀川 一樹（徳島大学）
Organizers: Tamiki Komatsuzaki (Hokkaido University), Kazuki Horikawa (Tokushima 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.

はじめに
Opening Remarks
永井 健治（大阪大）
Takeharu Nagai (*Osaka Univ.*)

2SCP-1 **アルツハイマー病の解明のためにシンギュラリティ生物学ができること**
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, [2]JST ERATO, [3]理研・BDR, [4]学習院大・理）
Hiroko Bannai[1,2], Michio Hiroshima[3], Yoshiyuki Soeda[4], Akihiko Takashima[4] ([1]*Keio Univ. Sch. Med.*, [2]*JST ERATO*, [3]*RIKEN BDR*, [4]*Gakushuin Univ, Faculty. Sci.*)

2SCP-2 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*)

2SCP-3 **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・先導的学際研究機構・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 Hashimoto[1,2,3,4], Takanobu Nakazawa[1,5], Kaoru Seiriki[1,6], Atsushi Kasai[1] ([1]*Lab. of Mol. Neuropharmacol., Grad. Sch. of Pharmaceut. Sci., Osaka Univ.*, [2]*Center for Child Mental Dev, United Grad. Sch. of Child Dev., Osaka Univ.*, [3]*Div. of Biosci., Inst. for Datability Sci., Osaka Univ.*, [4]*Transdimensional Life Imaging Div., Inst. for Open and Transdisciplinary Res. Initiatives, Osaka Univ.*, [5]*Dep. of Pharmacol., Grad. Sch. of Dentistry, Osaka Univ.*, [6]*Institute for Transdisciplinary Grad. Degree Programs, Osaka Univ.*)

2SCP-4 **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]（[1]理研・BDR, [2]理研・IMS）
Taisaku Ogawa[1], Katsuyuki Shiroguchi[1,2] ([1]*RIKEN BDR*, [2]*RIKEN IMS*)

2SCP-5 (2Pos147) Morphodynamic feature space of migrating cells
Daisuke Imoto[1], Nen Saito[2], **Satoshi Sawai**[1,3] ([1]*Graduate School of Arts and Sciences, University of Tokyo*, [2]*Universal Biology Institute, Graduate School of Science, University of Tokyo*, [3]*Research Center for Complex Systems Biology, University of Tokyo*)

2SCP-6 (2Pos243) **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 Asakura[1], Yohei Kondo[2], Kazuhiro Aoki[2], Naoki Honda[1] ([1]*Grad. Sch. Biostudies, Univ. Kyoto*, [2]*Div. Quantitative Biol. ExCELLS, NIBB.*)

14:10〜16:50　D 会場（4F 天葉）／Room D (4F Tenyo)
2SDP　**台湾ー日本　二国間シンポジウム：X 線結晶構造解析とクライオ電顕**
Taiwan-Japan joint symposium on structural biology using X-ray crystallography and cryo-EM

オーガナイザー：村田 武士（千葉大学），横山 謙（京都産業大学）
Organizers: Takeshi Murata (Chiba University), Ken Yokoyama (Kyoto Sangyo University)

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.

はじめに
Opening Remarks

2SDP-1 クライオ電子顕微鏡による繊毛と微小管モーターの解析
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 Yang[1,2], Yen-Chen Chang[1,3], Tzu-Ping Ko[1], Piotr Draczkowski[1], Yu-Chun Chien[1,2], Yuan-Chih Chang[4], Kuen-Phon Wu[1], Kay-Hooi Khoo[1,2], Hui-Wen Chang[3], **Shang-Te Danny Hsu**[1,2] ([1]*Institute of Biological Chemistry, Academia Sinica*, [2]*Institute of Biochemical Sciences, National Taiwan University*, [3]*School of Veterinary Medicine, National Taiwan University*, [4]*Institute 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 V_o の単粒子解析
Single particle analysis of membrane embedded domain V_o of V-type ATP synthase
○岸川 淳一 [1], 加藤 貴之 [2], 古田 綾 [1], 中西 温子 [1], 光岡 薫 [3], 横山 謙 [1]（[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 Kishikawa[1], Takayuki Kato[2], Aya Furuta[1], Atsuko Nakanishi[1], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Dept. Mol. Biosci., Kyoto Sangyo Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*Res. 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 [1,2]（[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 Abe[1,2] ([1]*Cellular and Structural Physiology Institute, Nagoya Univ.*, [2]*Grad. Sch. Pharm. Sci., Nagoya Univ.*)

2SDP-6 PAD4 regulates p53 function through protein citrullination
Chien-Yun Lee[1], Guang-Yaw Liu[2], **Hui-Chih Hung**[1] ([1]*National Chung-Hsing University*, [2]*Chung Shan Medical University*)

おわりに
Closing Remarks

14:10〜16:50　E 会場（4F クリスタルルーム）／Room E (4F Crystal Room)
2SEP　共催：JST さきがけ「量子技術を適用した生命科学基盤の創出」
量子科学で捉える生命現象
Understanding biological systems with quantum science and technology

オーガナイザー：市村 垂生（大阪大学），塗谷 睦生（慶應義塾大学）
Organizers: Taro Ichimura (Osaka University), Mutsuo Nuriya (Keio University)

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.

はじめに
Opening Remarks

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

2SEP-2　溶媒和の量子化学効果の分子動力学シミュレーションの開発と生体分子への応用
Incorporation of qunatum chemical effect of solvation into molecular dynamics simulation and the applications to biomolecules
○渡邉 宙志 [1,2]（[1]慶應大, [2]JST さきがけ）
Hiroshi Watanabe[1,2] ([1]*Keio Univ. KQCC*, [2]*PRESTO JST*)

2SEP-3　多光子顕微鏡の応用による脳組織内の分子動態の可視化解析
Imaging dynamics of molecules inside the brain tissue by the application of multiphoton microscopy
○塗谷 睦生 [1,2,3]（[1]慶應義塾大学医学部, [2]JST さきがけ, [3]横浜国立大学）
Mutsuo Nuriya[1,2,3] ([1]*Keio University School of Medicine*, [2]*JST PRESTO*, [3]*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] ([1]*The University of Tokyo*, [2]*PRESTO, JST*)

2SEP-6　Nanoscale thermometry and magnetometry in biology using NV center in diamond
Hitoshi Ishiwata[1,2] ([1]*PRESTO*, [2]*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センシング
(2Pos288) Electrical Biosensing beyond the Debye Screening Length Using Graphene Field-Effect Transistor in Femtoliter Microchamber
○小野 堯生 [1], 金井 康 [1], 井上 恒一 [1], 渡邊 洋平 [2], 中北 愼一 [3], 河原 敏男 [4], 鈴木 康夫 [4], 松本 和彦 [1]（[1]阪大産研, [2]京府医大, [3]香川大, [4]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] ([1]*ISIR, Osaka Univ.*, [2]*Kyoto Pref. Univ of Med.*, [3]*Kagawa Univ.*, [4]*Chubu Univ.*)

14:10〜16:50　F 会場（4F マーブルルーム）／Room F (4F Marble Room)
2SFP　共催：新学術領域研究「進化の制約と方向性」
構成的アプローチを用いた進化研究：拘束と進化可能性の理解へ向けて
Constructive Approaches for Evolution: Toward Understanding of Directionarity and Constraints

オーガナイザー：古澤 力（理化学研究所 / 東京大学），入江 直樹（東京大学）
Organizers: Chikara Furusawa (RIKEN / The University of Tokyo), Naoki Irie (The University of Tokyo)

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 Irie[1,2], Yui Uchida[1,2], Masahiro Uesaka[3] ([1]*Univ. Tokyo, Sch. of Science*, [2]*Univ. Tokyo, Universal Biology Institute*, [3]*RIKEN*)

2SFP-3　Impact of polyploidy on the evolutionary rate
Ryudo Ohbayashi[1], Tetsuhiro Hatakeyama[2] ([1]*BDR., RIKEN*, [2]*Dept. of Basic Sci., Univ. of Tokyo*)

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

14:10〜16:50　G 会場（4F アイボリールーム）／Room G (4F Ivory Room)
2SGP　ポスト「京」始動を見据えた計算創薬の新展開
New horizon of in-silico drug discovery toward launching post-K computer

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

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] ([1]*Yokohama City Univ.*, [2]*Riken*)

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出発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] ([1]*Grad. Sch. of Med., Kyoto Univ.*, [2]*RIKEN, 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] ([1]*AIP, RIKEN*, [2]*MIH, RIKEN*, [3]*Grad. Sch. Med., Kyoto Univ.*, [4]*Grad. Sch. Frontier Sci., Univ. Tokyo*, [5]*NIMS*)

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ー液液相分離の制御ー**
(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], 亀田 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] ([1]*IMRAM, Tohoku Univ.*, [2]*Coll. Pharmacy Sci., Ritsumeikan Univ.*, [3]*AIRC, AIST*)

14:10〜16:50　H 会場（4F アンバールーム）／Room H (4F Amber Room)

2SHP　可視化デバイス開発と数理モデル化を用いた細胞内アーキテクチャの解読
Decoding intracellular architecture using visualizing device development and mathematical modeling

オーガナイザー：北村 朗（北海道大学），樺山 一哉（大阪大学）
Organizers: Akira Kitamura (Hokkaido University), Kazuya Kabayama (Osaka University)

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
Akira Kitamura[1,2] ([1]*Lab. Mol. Cell Dynamics, Fac. Adv. Life Sci., Hokkaido Univ.*, [2]*JSPS Scientist for Joint International Research*)

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　(2Pos268) 大気圧走査電子顕微鏡 ASEM による骨組織再構築の水中免疫電顕法と cryo-TEM 観察
(2Pos268) 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], 簇野 悠里 [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 Sato[1], Shinya Sugimoto[2], Yuri Hatano[1], Mari Sato[1], Eiko Sakai[3] ([1]*Biomedical Res. Inst., AIST*, [2]*Dept. Bacteriol., The Jikei Univ. Sch. Med.*, [3]*Dental Pharmacology, Nagasaki Univ.*)

2SHP-5　(2Pos246) 細胞内のインスリン様成長因子-I(IGF-I)シグナルは振動する
(2Pos246) 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）
Masato Masuda, Fumihiko Hakuno, Shin-Ichiro Takahashi (*Dep. App. Ani. Sci., Grad. Sch. Agr. Lif. Sci., The Univ. Tokyo*)

2SHP-6　入力制御によるライブセルイメージング解析
Live cell imaging analyses by input control system
○樺山 一哉 [1,2,3]（[1]大阪大学大学院 理学研究科 化学専攻, [2]大阪大学大学院 理学研究科 基礎理学プロジェクト研究センター, [3]大阪大学 放射線科学基盤機構）
Kazuya Kabayama[1,2,3] ([1]*Department of Chemistry, Graduate School of Science, Osaka University*, [2]*Project Research Center, Graduate School of Science, Osaka University*, [3]*Institute for Radiation Sciences, Osaka Univeresity*)

おわりに
Closing Remarks
北村 朗（北大）
Akira Kitamura (*Hokkaido Univ.*)

3 日目（9 月 26 日（木））／Day 3（Sep. 26 Thu.）

8:30〜11:10　B 会場（4F 天玉）／Room B (4F Tengyoku)
3SBA　**ヘム蛋白質の機能を司る構造・ダイナミクスとエネルギー流：理論と実験**
Structure, Dynamics and Energy Flow that Govern Heme Protein Functions: Theory and Experiments

オーガナイザー：倭 剛久（名古屋大学），David Leitner（University of Nevada）
Organizers: Takahisa Yamato (Nagoya University), David Leitner (University of Nevada)

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” build 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 hemeproteins
Misao Mizuno (*Grad. Sch. Sci., Osaka Univ.*)

3SBA-4　**ミオグロビンとヘモグロビンの結晶内光解離反応過程の観測**
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*)

8:30〜11:10　C 会場（4F 天樹）／Room C (4F Tenjyu)

3SCA　生体運動の多様性と普遍性―細胞内ダイナミクスから集団運動まで―
Diversity and universality of motile mechanism of living things: From intracellular dynamics to collective motion

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)

'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.

はじめに
Opening Remarks
中村 修一（東北大学）
Shuichi Nakamura (*Tohoku Univ.*)

3SCA-1　**君子は豹変す: 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 Miller[1], Zhengqun Li[2], 三上 渚 [2], Quax E.F. Tessa[2], Albers Sonja-Verena[2], Berry Richard[1]（[1]オックスフォード大学, [2]フライブルク大学）
Yoshiaki Kinosita[1,2], Miller Helen[1], Li Zhengqun[2], Nagisa Mikami[2], E.F. Tessa Quax[2], Sonja-Verena Albers[2], Richard Berry[1] ([1]*Oxford University*, [2]*University 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 Oyama[1], Takeshi Kawasaki[2], Hideyuki Mizuno[3], Atsushi Ikeda[3] ([1]*AIST*, [2]*Nagoya University*, [3]*University 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 Kage[1], Takayuki Torisawa[2,3], Ayano A. Medo[4,5], Ken H. Nagai[6] ([1]*TUT*, [2]*NIG*, [3]*SOKENDAI*, [4]*U Hyogo*, [5]*Present address: Kyoto U*, [6]*JAIST*)

3SCA-7　**魚類表皮の遊走細胞ケラトサイトのストレスファイバ車輪の回転**
Rotation of stress fiber-wheel in migrating fish keratocytes
○沖村 千夏（山口大・理）
Chika Okimura (*Fac. Sci., Yamaguchi Univ.*)

8:30〜11:10　D 会場（4F 天葉）／Room D (4F Tenyo)
3SDA　**生命現象の理解を目指す光遺伝学の新展開**
Optogenetics: Applying photoreceptor for understanding biological phenomena

オーガナイザー：角田 聡（名古屋工業大学），井上 圭一（東京大学）
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-1　**オルガネラ・オプトジェネティクス - 細胞内 Ca^{2+}ダイナミクスの光操作**
Organelle optogenetics: Optical manipulation of intracellular Ca^{2+} dynamics
○八尾 寛 [1], 浅野 豪文 [2], 五十嵐 敬幸 [3], 石塚 徹 [4]（[1]東大・物性研, [2]東京医歯大・細胞生物, [3]ウェスタン大・シューリッチ医歯校, [4]東北大・生命）
Hiromu Yawo[1], Toshifumi Asano[2], Hiroyuki Igarashi[3], Toru Ishizuka[4] ([1]*ISSP, Univ. Tokyo*, [2]*Cell Biol., TMDU*, [3]*Western Univ., Schulich Sch. Med. Dent., Canada*, [4]*Tohoku Univ. Grad. Sch. Life Sci.*)

3SDA-2　**光遺伝学ツールとしての光サイクル型動物オプシンの最適化**
Engineering of photocyclic animal opsin as a potential optogenetic tool
○山下 高廣（京大・院理）
Takahiro Yamashita (*Grad. Sch. of Sci., Kyoto Univ.*)

3SDA-3　**(3Pos142) 生体組織への応用が期待される光感度の高いチャネルロドプシン**
(3Pos142) Novel optogenetics tool: A light-gated cation channel with high-reactivity to weak light
○細島 頌子 [1], 重村 竣太 [1], 神取 秀樹 [1], 角田 聡 [1,2]（[1]名古屋工業大学, [2]JST, さきがけ）
Shoko Hososhima[1], Shunta Shigemura[1], Hideki Kandori[1], Satoshi Tsunoda[1,2] ([1]*Nagoya Institute of Technology*, [2]*JST, PRESTO*)

3SDA-4　Optical Switches of Membrane Receptor Activities Using CRY2
Takeaki Ozawa (*Dept. Chem., Univ. Tokyo*)

3SDA-5　**腹側被蓋野の GABA 作動性神経がノンレム睡眠を調節する**
VTA-GABA neurons regulate NREM sleep
○山中 章弘 [1,2]（[1]名古屋大学環境医学研究所, [2]科学技術振興機構 CREST）
Akihiro Yamanaka[1,2] ([1]*RIEM, Nagoya University*, [2]*CREST, JST*)

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 Xavier[2], 松田 道行 [1,3], 平島 剛志 [3]（[1]京大・院生命科学, [2]IBEC, Spain, [3]京大・院医学）
Naoya Hino[1], Xavier Trepat[2], Michiyuki Matsuda[1,3], Tsuyoshi Hirashima[3] ([1]*Grad. Sch. of Biostudies, Kyoto Univ.*, [2]*IBEC, Spain*, [3]*Grad. 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, [2]JST さきがけ）
Kohki Okabe[1,2] ([1]*Grad. Sch. Pharma. Sci., The Univ. of Tokyo*, [2]*PRESTO, 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 Imashimizu[1], Masahito Tanaka[1], Hiromichi Hoshina[2], Koh Takeuchi[1] ([1]*AIST*, [2]*RIKEN*)

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 耕治郎, ○梅田 眞郷（京都大学）
Akira Murakami, Kohjiro Nagao, **Masato Umeda** (*Kyoto University*)

おわりに
Closing Remarks

8:30〜11:10　F 会場（4F マーブルルーム）／Room F (4F Marble Room)
3SFA　ナノ空間の生物物理
Biophysics in Nano-space

オーガナイザー：多田隈 尚史（大阪大学），北川 大樹（東京大学）
Organizers: Hisashi Tadakuma (Osaka Univ.), Daiju Kitagawa (The University of Tokyo)

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 Tsuboyama[1], Shintaro Iwasaki[2], Yukihide Tomari[1] ([1]*UTokyo IQB RNA function lab*, [2]*Riken 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して
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 Kishi[1,2,5], Sylvain W. Lapan[3,5], Brian J. Beliveau[1,2,5], Emma R. West[3,5], Allen Zhu[1,2], Hiroshi M. Sasaki[1,2], Sinem K. Saka[1,2], Yu Wang[1,2], Constance L. Cepko[3,4], Peng Yin[1,2] ([1]*Wyss Institute, Harvard Univ.*, [2]*Dept. Systems Biology, Harvard Medical School*, [3]*Dept. Genetics, Blavatnik Institute, Harvard Medical School*, [4]*Howard Hughes Medical Institute*, [5]*These authors contributed equally*)

3SFA-7 (3Pos075) 三次元構造モデルから発生過程における細胞機能の理解を試みる
(3Pos075) Attempt to understand the cellular function during developmental process from 3D structural model
黒田 純平 [1,4], 板橋 岳志 [1,2,3], 一ノ瀬 孝子 [1], 近藤 滋 [4], ○岩根 敦子 [1,2,3]（[1]理研・BDR・細胞場, [2]広大院・統合生命科学, [3]阪大院・生命機能, [4]阪大院・生命機能・パターン形成）
Junpei Kuroda[1,4], Takeshi Itabashi[1,2,3], Takako M. Ichinose[1], Shigeru Kondo[4], **Atsuko H. Iwane**[1,2,3] ([1]*Cell Field Struc., BDR, Riken*, [2]*Grad. sch. Integ. Sci. Life, Hiroshima Univ.*, [3]*Spec. Res. Promot. Group, Grad. Sch. Fronti., Biosci., Osaka Univ.*, [4]*Pattern formation, Grad. Sch. Fronti., Biosci., Osaka Univ.*)

3SFA-8 ナノスケール空間における中心小体複製メカニズム
Mechanisms of centriole duplication in nano-space
○北川 大樹, 山本 昌平, 高尾 大輔（東京大学大学院薬学系研究科 生理化学教室）
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

オーガナイザー：角山 貴昭（沖縄科学技術大学院大学），笠井 倫志（京都大学）
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. Wakefield[1], Kathleen M. Lennon[1], Steven J. Tobin[1], Matthew S. Brehove[1], Adam L. Maddox[1], Ajay Goel[3], Kendall Van Keuren-Jensen[2], Daniel Schmolze[1], **Tijana Jovanovic-Talisman**[1] ([1]*City of Hope*, [2]*TGen*, [3]*Baylor 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 (3Pos179) 転写伸長を制御するメディエーターの 1 分子超解像イメージングによる分子局在と動態の定量解析
(3Pos179) Molecular localization and dynamics of Mediator regulating transcription elongation using single-molecule and super-resolution microscopy
伊藤 由馬 [1], 國見 慎之介 [1], 高橋 秀尚 [2], ○徳永 万喜洋 [1]（[1]東工大・生命理工学院, [2]横浜市大・院医学）
Yuma Ito[1], Shinnosuke Kunimi[1], Hidehisa Takahashi[2], **Makio Tokunaga**[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

8:30〜11:10　H 会場（4F アンバールーム）／Room H (4F Amber Room)
3SHA　タンパク質の“質”を評価する
The Quality of Proteins - Multiple Approaches for Protein Evaluation -

オーガナイザー：小川 覚之（東京大学），内橋 貴之（名古屋大学）
Organizers: Tadayuki Ogawa (The University of Tokyo), Takayuki Uchihashi (Nagoya University)

Proteins undergo a variety of their qualitative changes throughout their life. The variety of their “quality” provide 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*)

3SHA-1　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
Iodine staining as a useful probe for amyloid polymorphism and its propagation
○茶谷 絵理 [1], 平松 貴人 [1], 柚 佳祐 [1], 山本 直樹 [2]（[1]神戸大院理, [2]自治医大医）
Eri Chatani[1], Takato Hiramatsu[1], Keisuke Yuzu[1], Naoki Yamamoto[2] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Fac. Med., Jichi Medical Univ.*)

3SHA-2　フィブロインタンパク質からクモ糸への人工的再構成
Artificial reconstitution of the multi-hierarchical structure in spider silk from fibroin proteins
○上久保 裕生 [1,2], 佐藤 健大 [3]（[1]奈良先端大 物質創成, [2]高エネ機構 物構研, [3]Spiber 株式会社）
Hironari Kamikubo[1,2], Takehiro Sato[3] ([1]*NAIST MS*, [2]*KEK IMSS*, [3]*Spiber Inc.*)

3SHA-3　Biophysical characterization of environment-dependent protein assemblies of physiological and pathological interest
Maho Yagi-Utsumi, Koichi Kato (*ExCELLS, NINS*)

3SHA-4　(3Pos096) 過渡的に形成される GPCR ダイマーの研究：細胞内蛍光 1 分子観察によるアプローチ
(3Pos096) Examining the transiently formed GPCR dimer: an approach by single fluorescent molecule observation in living cells
○笠井 倫志（京大 ウイ・再生研）
Rinshi Kasai (*Inst. Front. Life. Med. Sci., Kyoto Univ.*)

3SHA-5　(3Pos014) STAP-2 により Breast tumor kinase が活性化する機構の解明
(3Pos014) Molecular basis of Breast tumor kinase by an adaptor protein, STAP-2
○中迫 純希 [1], 松尾 友樹 [2], 神田 諒 [2], 田中 睦乃 [2], 姚 閔 [3], 松田 正 [2], 前仲 勝実 [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, [4]JST さきがけ）
Junki Nakasako[1], Yuki Matsuo[2], Ryo Kanda[2], Yoshino Tanaka[2], Min Yao[3], Tadashi Matsuda[2], Katsumi Maenaka[2], Toyoyuki Ose[2,3,4] ([1]*Graduate school of Life Science*, [2]*Faculty of Pharm.*, [3]*Faculty of Advanced Life Science, Hokkaido University*, [4]*JST PRESTO*)

3SHA-6　Visualization of Qualitative Change of Proteins with High-Speed Atomic Force Microscopy
Takayuki Uchihashi[1,2] ([1]*Department of Physics*, [2]*ExCELLS, NINS*)

3SHA-7 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*)