9:45～12:15　B 会場／Room B : Mid-sized Hall 2/2

1SBA　新学術領域研究「理論と実験の協奏による柔らかな分子系の機能の科学」共催
柔らかさが制御する生体分子系の構造形成と機能
Regulating structure formation and function of biomolecular systems with softness

オーガナイザー：北尾 彰朗（東京大学），水谷 泰久（大阪大学）
Organizers: Akio Kitao (The University of Tokyo), Yasuhisa Mizutani (Osaka University)

Biomolecules and their assemblies create and control their functions by softly changing conformations. To investigate sophisticated mechanisms of biomolecular systems to function in condensed, heterogeneous, and highly noisy environments, it is necessary to employ various approaches in concerted fashion. In this symposium, we discuss the mechanisms of structure formation and functional control in soft biological molecular systems, which have been made clear by the cutting-edge theories, measurements, and molecular design.

1SBA-01　*In silico* で観察するタンパク質の柔らかで機能的な運動
Observing soft functional motion of proteins *in silico*
○北尾 彰朗（東京大学分子細胞生物学研究所）
Akio Kitao (*IMCB, Univ. Tokyo*)

1SBA-02　Continuous tracking of protein folding at microsecond resolution by a line confocal detection of single molecule fluorescence
Satoshi Takahashi (*IMRAM, Tohoku Univ.*)

1SBA-03　光応答性タンパク質の機能転換が明らかにする柔らかな構造機能相関
“Soft” structure-function relationship revealed by functional conversion of photoreceptive proteins
○神取 秀樹（名古屋工業大学）
Hideki Kandori (*Nagoya Institute of Technology*)

1SBA-04　酵素活性におけるタンパク質の柔軟性の役割
Crucial Role of Protein Flexibility in Enzymatic Catalysis
○林 重彦（京都大学大学院理学研究科化学専攻）
Shigehiko Hayashi (*Department of Chemistry, Graduate School of Science, Kyoto University*)

1SBA-05　タンパク質の機能を生み出す柔らかさの時間分解観測
Time-resolved Observation of Functionally-important Molecular Flexibility of Proteins
○水谷 泰久（大阪大学大学院理学研究科化学専攻）
Yasuhisa Mizutani (*Grad. Sch. Sci., Osaka Univ.*)

9:45～12:15　C 会場／Room C : Room 107

1SCA　Beyond Biophysics!: 細胞スケールにおける物理・化学・機械的な制御が生み出す新たな生物物理学
Beyond Biophysics!: Up-and-coming biophysical science achieved by physical, chemical and micromechanical control of a cell-sized space

オーガナイザー：瀧ノ上 正浩（東京工業大学），尾上 弘晃（慶應義塾大学），川野 竜司（東京農工大学）
Organizers: Masahiro Takinoue (Tokyo Institute of Technology), Hiroaki Onoe (Keio University), Ryuji Kawano (Tokyo University of Agriculture and Technology)

Living cells are micrometer-sized highly functional molecular systems that are hierarchically self-organized using nanometer-sized molecules. By cooperative characteristics of molecules, the living cells realize dynamic functions such as autonomous information processing, spontaneous motions, self-replication, etc. The recent progress of microtechnologies achieve control of cell-sized tiny space, molecular self-assembly, molecular reaction dynamics, mechanical properties of living cells, etc. The aim of this symposium is a further understanding of dynamical properties of life systems based on these state-of-the-art technologies, and we will discuss the current stage and the future perspectives of these novel biophysical studies.

1SCA-01　人工細胞回路を用いた DNA コンピューティングの実現
DNA computing through biological nanopore in droplet network system
○川野 竜司（東京農工大学）
Ryuji Kawano (*TUAT*)

1SCA-02　カンチレバーを用いて細胞分裂機構を探る
Examining the cell division machinery by using the cantilever system
○板橋 岳志[1], 石渡 信一[1,2]（[1]早大・理工, [2]WABIOS）
Takeshi Itabashi[1], Shin'ichi Ishiwata[1,2] ([1]*Fac. Sci. Eng., Waseda Univ.*, [2]*WABIOS*)

1SCA-03　上皮組織の発生と維持の機械・化学制御の統合的理解に向けて
Toward Understanding the Integration of Mechanical and Chemical Control of Epithelial Development and Maintenance
○杉村 薫[1,2], 梶田 美穂子[3], 藤田 恭之[3], 石原 秀至[4]（[1]京大, [2]JST・さきがけ, [3]北大, [4]明治大）
Kaoru Sugimura[1,2], Mihoko Kajita[3], Yasuyuki Fujita[3], Shuji Ishihara[4] ([1]*Kyoto Univ.*, [2]*JST PRESTO*, [3]*Hokkaido Univ.*, [4]*Meiji Univ.*)

1SCA-04　Mechanically-controlled tubular microenvironment for 3D cell culture
Hiroaki Onoe (*Dept. Mech. Eng., Keio Univ.*)

1SCA-05　MEMS technology meets scaling laws for biology
Ko Okumura (*Ochanomizu University*)

1SCA-06　生物物理学における非平衡研究のためのドロップレットマイクロ流体工学
Droplet-based microfluidics for nonequilibrium study in biophysics
○瀧ノ上 正浩[1,2]（[1]東工大・院総合理工, [2]JST・さきがけ）
Masahiro Takinoue[1,2] ([1]*Interdisciplinary Grad. Sch. Sci. & Eng., Tokyo Tech.*, [2]*PRESTO, JST*)

9:45～12:15　D 会場／Room D : Room 108

1SDA　神経ダイナミクスの計測と制御
Measurement and control of neurodynamics

オーガナイザー：伊東 大輔（北海道大学），細川 千絵（産業技術総合研究所）
Organizers: Daisuke Ito (Hokkaido University), Chie Hosokawa (National Institute of Advanced Industrial Science and Technology)

To understand higher functions of the brain, it is important to clarify spatiotemporal dynamics of nervous system at various hierarchy levels. For this purpose, novel approaches are required in the field of Biophysics. In this symposium, we invited young researchers who challenge to measure and control of neurodynamics using unique methods, such as bioimaging, nano fabrication, optical control, and multielectrode recordings. We hope that a fruitful discussion would lead to innovative studies in the future.

1SDA-01 培養神経回路網における同期バースト活動に関わる分子の探索
Analysis of the molecules involved in synchronized burst activity of cultured neuronal networks
○伊東 大輔[1], 郷原 一寿[2]（[1]北大・院先端生命, [2]北大・院工）
Daisuke Ito[1], Kazutoshi Gohara[2] ([1]*Fac. Advanced Life Sci., Hokkaido Univ.*, [2]*Fac. Engineering, Hokkaido Univ.*)

1SDA-02 培養神経細胞・神経回路操作のための表面マイクロ加工技術
Manipulating neurons and neuronal networks with micropatterned surfaces
○山本 英明[1,2], 谷井 孝至[3], 庭野 道夫[4], 平野 愛弓[2]（[1]東北大・学際研, [2]東北大・医工, [3]早大・基幹理工, [4]東北大・通研）
Hideaki Yamamoto[1,2], Takashi Tanii[3], Michio Niwano[4], Ayumi Hirano-Iwata[2] ([1]*FRIS, Tohoku Univ.*, [2]*Grad. Sch. Biomed. Eng., Tohoku. Univ.*, [3]*Sch. Fund. Sci. Eng., Waseda Univ.*, [4]*RIEC, Tohoku Univ.*)

1SDA-03 Noninvasive real-time measurement of dopamine, action potentials, and postsynaptic potentials using carbon nanotube electrodes chip
Ikuro Suzuki (*Department of Electronics, Tohoku Institute of Technology*)

1SDA-04 神経ダイナミクス解明のためのレーザー摂動技術の開発
Laser-induced perturbation into living neuronal networks: Toward understanding neurodynamics
○細川 千絵（産総研・健康工学）
Chie Hosokawa (*Health Res. Inst., AIST*)

1SDA-05 Revealing Neuronal Dynamics through Advanced Electrophysiology and Chemical Sensing using CMOS Technology
Urs Frey[1,2], Marie Engelene Obien[1], Florent Seichepine[1], Kosmas Deligkaris[1,2] ([1]*RIKEN Quantitative Biology Center*, [2]*Graduate School of Frontier Biosciences, Osaka University*)

1SDA-06 培養神経回路網における情報表現
Information presentation in cultured neuronal networks
○工藤 卓（関西学院大学 理工学部 人間システム工学科）
Suguru N. Kudoh (*Department of Human System Interaction, School of Science and Technology, Kwansei Gakuin University*)

1SDA-07 聴覚皮質における聴覚神経応答の解析及び神経ダイナミクス制御のためのマイクロデバイス開発
Analysis of auditory neural responses in the auditory cortex in vivo and development of microdevices to control neurodynamics
○西川 淳, 羽賀 健亮, 橘 唯至, 柳川 康貴, 舘野 高（北海道大学 情報科学研究科）
Jun Nishikawa, Takeaki Haga, Yuishi Tachibana, Yasutaka Yanagawa, Takashi Tateno (*Grad. Sch. of Inf. Sci. & Tech., Hokkaido Univ.*)

9:45～12:15　E 会場／Room E : Room 204

1SEA　脂質ラフトはどこまで分かったのか：新しい研究手法による再検証
What do we know about lipid rafts?: New landscape at the frontier

オーガナイザー：鈴木 健一（京都大学），森垣 憲一（神戸大学）
Organizers: Kenichi Suzuki (Kyoto University), Kenichi Morigaki (Kobe University)

The hypothesis of “lipid rafts” is now widely accepted as the basis for understanding cell membranes. However, their structures, properties, and biological functions still remain elusive. The present symposium intends to give an overview of the current understanding on the membrane heterogeneity and micro- or nano-domains in cells. We will be discussing on the most up-to-date views from recent studies using cellular membranes and model systems. By looking out on the landscape at the frontier, we seek to find new directions for future studies.

1SEA-01 GPI アンカー型タンパク質とガングリオシドの 1 分子追跡により明らかになったラフト組織化
Single-molecule tracking of GPI-anchored proteins and gangliosides revealed raft organization
○鈴木 健一（京大・iCeMS）
Kenichi G. N. Suzuki (*iCeMS, Kyoto Univ.*)

1SEA-02 細胞質分裂におけるスフィンゴミエリンラフトの役割
A role for sphingomyelin-rich lipid domains during cytokinesis
阿部 充宏, ○小林 俊秀（独立行政法人・理化学研究所）
Mitsuhiro Abe, **Toshihide Kobayashi** (*RIKEN*)

1SEA-03 Lipid Rafts and Membrane Proteins Collaborate to Organize and Shape Biological Membranes
Jeanne Stachowiak (*The University of Texas at Austin*)

1SEA-04 リポソームの膜内相分離における外場の影響
Phase separation on cell-sized liposomes in the presence of external force
○柳澤 実穂（東京農工大・工・先端物理）
Miho Yanagisawa (*Dept. Appl. Phys., Tokyo Univ. Agric. Technol.*)

1SEA-05 パターン化人工膜を用いた膜タンパク質のラフト親和性解析
Micropatterned model membrane for studying the affinity of proteins to lipid raft
○森垣 憲一, 谷本 泰士, 岡田 文子, 林 文夫（神戸大学）
Kenichi Morigaki, Yasushi Tanimoto, Fumiko Okada, Fumio Hayashi (*Kobe University*)

16:00～18:30　A 会場／Room A : Mid-sized Hall 1/2

1SAP　新学術領域研究「運動超分子マシナリーが織りなす調和と多様性」共催
マルチスケールに活躍する運動超分子マシナリー
Supramoleular motility machinery functioning in multi-scale scenes

オーガナイザー：中村 修一（東北大学），島袋 勝弥（宇部工業高等専門学校）
Organizers: Shuichi Nakamura (Tohoku Uiversity), Katsuya Shimabukuro (Ube National College of Technology)

A life system is operated by diverse supramolecular motility machineries which are finely organized functional units and allow cells intracellular material transportation and motility. In this symposium, we will invite researchers investigating the structure and operation mechanism of the motility machinery using various methodologies including structural analysis, nanophotometry, theoretical model, and molecular biological technique. We would like to present interesting and novel insights into the supramolecular motility machinery functioning in multi-scale scenes from division of genes to collective behavior.

1SAP-01 線虫精子のアメーバ運動と MSP マシナリー
Nematode sperm motility and MSP machinery
○島袋 勝弥（宇部高専・物質）
Katsuya Shimabukuro (*UNCT*)

1SAP-02 ミドリムシにおける光運動制御マシナリーの解明
Molecular machinery regulating photomovement of *Euglena*
○岩崎 憲治[1,2], 宮崎 直幸[1,2], 伊関 峰生[3], 長谷川 浩司[4], 成田 哲博[5], 松永 茂[6], 建部 益美[6], 上村 慎治[7], 渡辺 正勝[8]（[1]阪大・蛋白研, [2]生理研, [3]東邦大・薬, [4]アドバンスソフト, [5]名大・院理, [6]浜松ホトニクス（株）, [7]中大・理工, [8]光創大院）
Kenji Iwasaki[1,2], Naoyuki Miyazaki[1,2], Mineo Iseki[3], Koji Hasegawa[4], Akihiro Narita[5], Shigeru Matsunaga[6], Masumi Takebe[6], Shinji Kamimura[7], Masakatsu Watanabe[8] ([1]*Inst. for Protein Res., Osaka Univ.*, [2]*NIPS*, [3]*Pharm.Sci, Toho Univ.*, [4]*AdvanceSoft Corp.*, [5]*Struct.Biol.Res.Center, Nagoya Univ.*, [6]*Hamamatsu Photonics K.K.*, [7]*Fac.Sci.Eng., Chuo Univ.*, [8]*Grad.Sch. for the Creation of New Photonics Industry*)

1SAP-03 チューブリン様蛋白質 TubZ によるプラスミド分配の分子機構
Plasmid segregation driven by the tubulin-like GTPase TubZ
○林 郁子（横浜市立大学）
Ikuko Hayashi (*Yokohama City University*)

1SAP-04 黄色ブドウ球菌のコロニースプレッディングにおける毒素の役割
Role of toxin in *Staphylococcus aureus* colony spreading
○垣内 力, 関水 和久（東京大学 大学院薬学系研究科 微生物薬品化学）
Chikara Kaito, Kazuhisa Sekimizu (*Grad. Sch. Phar., Univ. Tokyo*)

1SAP-05 らせん細菌 *Leptospira* の遊泳力学とエネルギー論
Swimming dynamics and energetics of the spirochete *Leptospira*
○中村 修一（東北大・院工）
Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)

1SAP-06 Mechanical basis for the bacterial swimming and gliding
Hirofumi Wada (*Dep. Phys. Ritsumeikan Univ.*)

16:00～18:30　B 会場／Room B : Mid-sized Hall 2/2

1SBP　次世代タンパク質結晶化手法
The development of new crystallization methods for bio-macromolecular crystallography

オーガナイザー：田之倉 優（東京大学），姚 閔（北海道大学）
Organizers: Masaru Tanokura (The University of Tokyo), Min Yao (Hokkaido University)

Recent progress in the techniques of bio-macromolecular crystallography has made crystal structure analysis more powerful and useful method for life science. However, crystallization still remains as a major bottleneck for determining bio-macromolecular structures. Thus, further development of more advanced crystallization methods is required to increase the probability of successful crystallization. As one of the events related to International Year of Crystallography 2014, we have organized this symposium, and invited speakers who are internationally active in this field. We will discuss current hot topics and new ideas for future development.

1SBP-01 凝固したハイドロゲルを用いたタンパク質結晶の成長と特徴
Growth and characterization of protein crystals using high-strength hydrogels
○杉山 成[1,2]（[1]大阪大学大学院理学研究科化学専攻, [2]JST, ERATO脂質活性プロジェクト）
Shigeru Sugiyama[1,2] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*JST, ERATO, Lipid Active Structure Project*)

1SBP-02 微小重力下の結晶化
Protein crystallization under microgravity conditions
○田之倉 優, 中村 顕（東大・院農生科・応生化）
Masaru Tanokura, Akira Nakamura (*Dept. Appl. Biol. Chem., Grad. Sch. Agric. Life Sci., Univ. Tokyo*)

1SBP-03 結晶スポンジ法による非結晶性・極少量化合物の X 線結晶構造解析
Crystalline Sponge Method: X-ray Analysis without Crystallization on the Microgram Scale
○藤田 誠（東京大学）
Makoto Fujita (*The University of Tokyo*)

1SBP-04 膜タンパク質の結晶化法
Crystallization methods of membrane proteins
○村田 武士[1,2]（[1]千葉大・理, [2]JST・さきがけ）
Takeshi Murata[1,2] ([1]*Science/Chiba-U*, [2]*PRESTO/JST*)

1SBP-05 抗体を用いた膜蛋白質の結晶化
Crystallization of membrane proteins using antibody fragments
○岩田 想[1,2]（[1]京大院・医, [2]理研・放射光科学総合研究センター）
So Iwata[1,2] ([1]*Kyoto Univ. Grad. Sch. Med.*, [2]*RIKEN SPring8 Center*)

1SBP-06 対称性を持つタグを利用したタンパク質結晶化確率の向上
Use of symmetric tag to increase the probability of protein crystallization
○姚 閔（北海道大学大学院先端生命科学研究院）
Min Yao (*Fac. of Adv. Life Sci., Hokkaido Univ.*)

16:00～18:30　C 会場／Room C : Room 107

1SCP　あたかも生物のように動く非線形化学物理系
Nonlinear physico-chemical systems moving like living organisms

オーガナイザー：高木 清二（はこだて未来大学），住野 豊（東京理科大学），北畑 裕之（千葉大学）
Organizers: Seiji Takagi (Future University Hakodate), Yutaka Sumino (Tokyo University of Science), Hiroyuki Kitahata (Chiba University)

Recently, the motion of living organisms has been studied from the viewpoint of "active matters" in physics. To have better understanding on underlying physics, “simpler” physico-chemical systems have also been investigated rigorously. In this symposium, some examples of such “simpler” systems will be introduced, and we would like to discuss the similarities as well as differences among these physico-chemical systems and actual living systems. Through the discussion, we try to find advantages as well as critical problems in the studies on active matters based on physico-chemical systemsm, and finally hope to show a new direction of the researches.

1SCP-01　はじめに
○北畑 裕之（千葉大院理）
Hiroyuki Kitahata (*Grad. Scl. of Sci., Chiba Univ.*)

1SCP-02　なぜその材料はアクティブマターになるのか？ ～Dupeyrat システムに関する考察
A Material Discussion about the Nakache and Dupeyrat System
○松下 祥子（東京工業大学）
Sachiko Matsushita (*Tokyo Institute of Technology*)

1SCP-03　拮抗剤を介した自己推進型液滴の方向感知機能
Directional sensing of self-propelled droplets mediated by antagonists
○伴 貴彦, 中田 大樹, 谷 健太郎（阪大基礎工）
Takahiko Ban, Hiroki Nakata, Kentaro Tani (*Osaka University*)

1SCP-04　Self-propelled water droplet coupled with chemical oscillatory reaction
Nobuhiko Suematsu[1,2] ([1]*Graduate School of Advanced Mathematical Sciences, Meiji University*, [2]*Meiji Institute for Advanced Study of Mathematical Sciences (MIMS), Meiji University*)

1SCP-05　界面張力勾配に駆動される自己推進液滴のモード分岐
Mode bifurcation on a self-propelled droplet driven by interfacial tension gradient
○高畠 芙弥[1], 市川 正敏[2], 吉川 研一[3]（[1]東北大院工, [2]京大院理, [3]同志社大生命医）
Fumi Takabatake[1], Masatoshi Ichikawa[2], Kenichi Yoshikawa[3] ([1]*Grad. Sch. Eng., Tohoku Univ.*, [2]*Grad. Sch. Sci., Kyoto Univ.*, [3]*Grad. Sch. Life Med. Sci., Doshisha Univ.*)

1SCP-06　水路形状およびマランゴニ流構造に依存した自律運動システム
Self-propelled system depends on the structureof Marangoni flow and the shape of water chamber
○松田 唯, 中田 聡（広大院理）
Yui Matsuda, Satoshi Nakata (*Hiroshima Univ.*)

1SCP-07　界面活性剤の会合体生成に誘起される油水界面のアメーバ状運動
Amoeba like motion of the oil-water interface induced by generation of surfactant aggregate
○住野 豊（東京理科大学理学部応用物理学科）
Yutaka Sumino (*Department of Applied Physics, Faculty of Science, Tokyo University of Science*)

1SCP-08　ある巨大アメーバ生物のアメーバ運動
Amoeboid movement of a large amoeboid organism, true slime mold
○高木 清二（はこだて未来大）
Seiji Takagi (*Future Univ. Hakodate*)

16:00〜18:30　D 会場／Room D : Room 108

1SDP　In Cell NMR と HPC が切り開く細胞内の蛋白質の動きと機能
Protein Dynamics and Function in Cells elucidated by in-cell NMR and High Performance Computing

オーガナイザー：杉田 有治（理化学研究所），伊藤 隆（首都大学東京）
Organizers: Yuji Sugita (RIKEN), Yutaka Ito (Tokyo Metropolitan University)

In living cells, a variety of soluble macromolecules exist in a very crowded environment. Recent advancements in in situ observations by NMR and in large scale simulations using K computer have been contributing to investigate the various effects perturbing proteins' structures, dynamics and folding stabilities as well as the mechanisms permitting proteins to find their binding partners efficiently under the macromolecular crowding. In this symposium, we would overview the recent progresses and discuss future perspectives of the biophysical researches under intracellular environments in the field of life science.

1SDP-01　分子間五次相互作用が細胞内でのタンパク質安定性を制御する
Intermolecular Quinary Interactions Modulate Protein Stability in Living Cells
○パイラック ガリー ジェイ（ノースカロライナ大学）
Gary J. Pielak (*University of North Carolina*)

1SDP-02　分子混雑環境における蛋白質の NMR 緩和解析
NMR relaxation analysis of the protein under macromolecular crowding environment
○岡村 英保, 木川 隆則（理研・生命システム研究センター）
Hideyasu Okamura, Takanori Kigawa (*QBiC, RIKEN*)

1SDP-03　In-cell NMR 法による細胞内タンパク質の構造多様性解析
In-cell NMR analysis for protein conformational diversity in a cell
○猪股 晃介（独立行政法人 理化学研究所 生命システム研究センター）
Kohsuke Inomata (*Quantitative Biology Center (QBiC), RIKEN*)

1SDP-04　生きた細胞中の天然変性蛋白質の動態
Dynamics of intrinsically disordered proteins in living cells
○池谷 鉄兵, 井上 仁, 伊藤 隆（首都大学東京）
Teppei Ikeya, Jin Inoue, Yutaka Ito (*Tokyo Metropolitan University*)

1SDP-05　ゲノムと立体構造を結合したシミュレーション解析
Combining Structure with Genomics
○ファイグ マイケル, アスリ イードリム（ミシガン州立大学）
Michael Feig, Yildirim Asli (*Michigan State University*)

16:00〜18:30　E 会場／Room E : Room 204

1SEP　システム協同性が操る神経細胞機能
Cooperativity in shaping the nerve cell function

オーガナイザー：村越 秀治（生理学研究所），合田 裕紀子（理化学研究所）
Organizers: Hideji Murakoshi (National Institute for Physiological Sciences), Yukiko Goda (RIKEN)

The cooperative interactions between signaling molecules/cascades, subcellular compartments, or cells are integral to the flexible and plastic cellular functions underlying biological processes. This symposium addresses how cooperativity shapes cellular responses and functions by focusing on the nervous system. The speakers will discuss cooperativity involving molecular interactions in neurons, the interplay of neuronal sub-compartments such as synapses and dendritic branches and neuronal networks in supporting the unique structural and functional features of the nervous system.

1SEP-01　CaMKII によって活性化された Rho GTPase の協同的作用によるシナプス可塑性誘起
CaMKII-induced active Rho GTPases cooperatively work for the establishment of synaptic structural plasticity
○村越 秀治[1,2]（[1]生理学研究所, [2]科学技術振興機構さきがけ）
Hideji Murakoshi[1,2] ([1]*National Institute for Physiological Sciences*, [2]*JST PREST*)

1SEP-02 The basis for regulating synaptic strength heterogeneity across the dendrite
Mathieu Letellier, **Yukiko Goda** (*RIKEN Brain Science Institute*)

1SEP-03 神経細胞軸索の細胞膜にある 2 次元拡散障壁は分子選択性フィルターである
Diffusion barrier in the neuronal axon initial-segment membrane is a molecule-selective filter in the plasma membrane
○楠見 明弘[1,2], 宮原 愛美[1], 藤原 敬弘[1]（[1]京大・iCeMS, [2]京大・再生研）
Akihiro Kusumi[1,2], Manami S.H. Miyahara[1], Takahiro K. Fujiwara[1] ([1]*iCeMS, Kyoto Univ.*, [2]*Inst. for Frontier Med. Sci., Kyoto Univ.*)

1SEP-04 Activity-dependent gene expression in learning and memory
Ryang Kim[1,2], Mio Nonaka[1], Nan Yagishita-Kyo[1,2], Takashi Kawashima[1], Masatoshi Inoue[1,2], Yuichiro Ishii[1,2], Toshihiro Endo[1], Hajime Fujii[1], Sayaka Takemoto-Kimura[1], Hiroyuki Okuno[1,3], **Haruhiko Bito**[1,2] ([1]*Department of Neurochemistry, The University of Tokyo Graduate School of Medicine*, [2]*CREST-JST*, [3]*Medical Innovation Center, Kyoto University Graduate School of Medicine*)

1SEP-05 The cooperativity of neuronal molecules analyzed with imaging mass spectrometry
Mitsutoshi Setou (*Hamamatsu University School of Medicine*)

1SEP-06 Modeling the dynamical interaction of Hebbian and homeostatic plasticity
Taro Toyoizumi[1,2], Megumi Kaneko[3], Michael P. Stryker[3], Kenneth D. Miller[2] ([1]*RIKEN Brain Sci. Inst.*, [2]*Columbia Univ.*, [3]*UCSF*)

第 2 日目（9 月 26 日（金））／Day 2（Sep. 26 Fri.）

9:00～11:30　A 会場／Room A : Mid-sized Hall 1/2
2SAA　膜動態から探るミトコンドリア・ネオバイオロジー
Mitochondrial neo-biology explored from a membrane dynamics

オーガナイザー：小柴 琢己（九州大学），遠藤 斗志也（京都産業大学）
Organizers: Takumi Koshiba (Kyushu University), Toshiya Endo (Kyoto Sangyo University)

Mitochondrion, a double-membraned organelle, is the powerhouse of eukaryotic cells and is controlling essential biological processes such as generating ATP. Recent genetic studies in many model species have demonstrated that mitochondria are not just limited to respiration and apoptosis, and establishing fundamental aspects with physiological relevance. In the symposium, we invited investigators who study a broad range of species from yeast to mammals, and they will discuss current topics regarding new aspects of mitochondrial functions.

2SAA-01 ミトコンドリアと抗 RNA ウイルス自然免疫
Mitochondria and antiviral innate immunity in mammals
○小柴 琢己（九州大・院・理・生物科学）
Takumi Koshiba (*Dep. of Biol., Faculty of Sci., Kyushu Univ.*)

2SAA-02 カルシニューリンと Notch シグナリングを介してミトコンドリアの融合は心筋細胞の分化に必須である
Mitochondrial fusion controls differentiation of ESCs into cardiac cells via a novel pathway of calcineurin and Notch signaling
○笠原 敦子[1], スコラーノ ルカ[2]（[1]ジュネーブ大学, CMU, [2]パドヴァ大学）
Atsuko Kasahara[1], Luca Scorrano[2] ([1]*University of Geneva, CMU*, [2]*University of Padua, Dep. of Biology*)

2SAA-03 ミトコンドリア呼吸鎖の多様性：寄生虫からがん細胞まで
Diversity of mitochondrial respiratory chain from parasite to cancer
○北 潔（東京大学大学院医学系研究科・生物医化学教室）
Kiyoshi Kita (*Dept of Biomedical Chemistry, Graduate School of Medicine, The University of Tokyo*)

2SAA-04 オートファジーが駆動するミトコンドリア分解の仕組み
Targeting Autophagy for Mitochondrial Clearance
○岡本 浩二（阪大・院生命機能）
Koji Okamoto (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

2SAA-05 酵母ミトコンドリアにおけるタンパク質と脂質の輸送機構
Mechanisms of protein and lipid transport in yeast mitochondria
○遠藤 斗志也（京産大・総合生命）
Toshiya Endo (*Fac. Life Sci., Kyoto Sangyo Univ.*)

9:00～11:30　B 会場／Room B : Mid-sized Hall 2/2

2SBA　日本顕微鏡学会合同シンポジウム：原子レベル分解能へ向かう生物電子顕微鏡技術
Joint Symposium with the Japanese Society of Microscopy: Recent Advancement of Electron Microscopy toward Atomic Resolution from Biological Molecules

オーガナイザー：宮澤 淳夫（兵庫県立大学），光岡 薫（次世代天然物研究組合）
Organizers: Atsuo Miyazawa (University of Hyogo), Kaoru Mitsuoka (JBIC)

Recently, several techniques for high-resolution electron microscopy, direct detectors, Cs corrector, phase plates, and so on, became commercially available and some of them are now applied to structural analysis of biological macromolecules and their complexes. As the result, atomic model of a membrane protein was determined using single particle analysis, for example. In this session, which is co-hosted by Japanese Society of Microscopy, these recent advancements and their application to biological samples toward atomic resolution will be discussed.

2SBA-01 電子顕微鏡法により示された線虫イネキシン 6 ギャップ結合チャネルの特徴的なサブユニット構成
Electron microscopy of C. elegans innexin-6 gap junction channels indicates a characteristic subunit organization
○大嶋 篤典[1], 松澤 朋寛[2], 村田 和義[3], 西川 幸希[1], 藤吉 好則[1]（[1]名大・CeSPI, [2]京大・院理・生物物理, [3]生理研）
Atsunori Oshima[1], Tomohiro Matsuzawa[2], Kazuyoshi Murata[3], Kouki Nishikawa[1], Yoshinori Fujiyoshi[1] ([1]*CeSPI, Nagoya Univ.*, [2]*Dept. of Biophys., Grad. Sch. Sci., Kyoto Univ.*, [3]*NIPS*)

2SBA-02 再構成系および細胞内でのアクチンフィラメント構造解析
Structural analysis of the actin filament in vitro and in vivo
○成田 哲博[1,2]（[1]名古屋大学, [2]科学技術振興機構さきがけ）
Akihiro Narita[1,2] ([1]*Nagoya Univ.*, [2]*PRESTO*)

2SBA-03 Single particle analysis of the model post-termination complex gives insights into prokaryotic ribosome recycling process
Takeshi Yokoyama (*RIKEN, CLST*)

2SBA-04 単粒子クライオ電子顕微鏡法による 8 Å 分解能サポウイルスキャプシド構造とホモロジーモデリング
Sapovirus capsid structure at 8 Å resolution by single particle cryo-electron microscopy, and homology modeling
宮崎 直幸[1], テーラー デービッド[1], ハウスマン グラント[2], 村上 耕介[2], 片山 和彦[2], ○村田 和義[1]（[1]生理学研究所, [2]国立感染症研究所）
Naoyuki Miyazaki[1], David Taylor[1], Grant Houseman[2], Kousuke Murakami[2], Kazuhiko Katayama[2], **Kazuyoshi Murata**[1] ([1]*National Institute for Physiological Sciences*, [2]*National Institute of Infectious Diseases*)

2SBA-05 Single molecular imaging and single atom spectroscopy by electron microscopy
Kazutomo Suenaga (*AIST*)

2SBA-06 低温電子顕微鏡を用いた単粒子解析による膜たんぱく質の研究
Studying integral membrane protein by single particle cryo-EM
○Cheng Yifan（カルフォルニア大学サンフランシスコ校）
Yifan Cheng (*Dep. Biochem. Biophys., UCSF*)

9:00～11:30　C 会場／Room C : Room 107

2SCA　日本-中国-台湾　若手合同シンポジウム～超分子協同性～
Japan-China-Taiwan joint sympoium on cooperativity in supramolcular machine

オーガナイザー：林 久美子（東北大学），福岡 創（東北大学）
Organizers: Kumiko Hayashi (Tohoku University), Hajime Fukuoka (Tohoku University)

Compositional units of a biological supramolecular machine such as flagellar motor and F1-ATPase exhibit the cooperative property to enhance the efficiency of their motion. We discuss the property in terms of the results obtained by using fluorescent observation, AFM observation, electron microscopic observation and MD simulation. In the symposium, young scientists from China and Taiwan also give talks as well as Japanese researchers. We believe scientific communication among young Asian scientists keep Biophysical Society of Japan more alive.

2SCA-01　Regulation of the rotational switching of bacterial flagellar motor by binding of an intracellular signaling protein CheY
Hajime Fukuoka[1], Takashi Sagawa[2], Yuichi Inoue[1], Hiroto Takahashi[1], Akihiko Ishijima[1] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*)

2SCA-02　Visualizing stator-protein distributions of bacterial flagellar motors
Chien-Jung Lo[1,2], Tsaishun Lin[1,2] ([1]*Dept. of Phys., National Central Univ.*, [2]*Inst. Biophys., National Central Univ.*)

2SCA-03　細菌べん毛モーターの回転方向変換制御に関わる構造
Structure of the bacterial flagellar motor involved in the directional switching mechanism
○宮田 知子[1], 加藤 貴之[1], 森本 雄輔[1,2,3], 中村 修一[4], 松波 秀行[5], 難波 啓一[1,2]（[1]大阪大学大学院 生命機能研究科, [2]理研・生命システム, [3]阪大院・理, [4]東北大・工, [5]沖縄科技大・細胞膜通過輸送研究ユニット）
Tomoko Miyata[1], Takayuki Kato[1], Yusuke V. Morimoto[1,2,3], Syuichi Nakamura[4], Hideyuki Matsunami[5], Keiichi Namba[1,2] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*QBiC, RIKEN*, [3]*Grad. Sch. Sci., Osaka Univ.*, [4]*School of Engineering, Tohoku Univ.*, [5]*Trans-Membrane Trafficking Unit, OIST*)

2SCA-04　Conformational Spread as a Mechanism for Cooperativity in the Bacterial Flagellar Switch
Fan Bai (*Sch. Life Sci., Peking Univ.*)

2SCA-05　Coordination and control in the ring-shaped molecular motors
Jin Yu (*Beijing Computational Science Research Center*)

2SCA-06　高速原子間力顕微鏡によるリング状 ATPase の協同的構造変化の観察
Cooperative Conformational Change of Ring-Shape ATPase Observed by High-Speed AFM
○内橋 貴之[1,2], 飯野 亮太[3], 渡辺 洋平[4], 野地 博行[5], 安藤 敏夫[1,2]（[1]金沢大・理工, [2]金大・理工・バイオAFMセンター, [3]岡崎統合バイオ, [4]甲南大・生物, [5]東大院・工）
Takayuki Uchihashi[1,2], Ryota Iino[3], Yo-hei Watanabe[4], Hiroyuki Noji[5], Toshio Ando[1,2] ([1]*Coll.Sci. & Eng., Kanazawa Univ.*, [2]*Bio-AFM FRC, Coll.Sci. & Eng., Kanazawa Univ.*, [3]*Okazaki Inst. Integr. Biosci., NINS*, [4]*Dept. Biol., Konan Univ.*, [5]*Sch. Eng., Univ. Tokyo*)

9:00～11:30　D 会場／Room D : Room 108

2SDA　新学術領域研究「動的クロマチン構造と機能」共催

生命現象の基本に迫る動的クロマチン構造・機能研究の最前線

Studies of dynamic chromatin structure and function to understand fundamentals of life

オーガナイザー：原口 徳子（(独）情報通信研究機構 未来 ICT 研究所），徳永 万喜洋（東京工業大学）

Organizers: Tokuko Haraguchi (National Institute of Information and Communications Technology), Makio Tokunaga (Tokyo Institute of Technology)

Chromatin, which consists of DNA and proteins, plays a vital role in not only genetic activities but also biological functions. Its structure is not invariable but spatio-temporally varying in response to functions. This dynamic structural change of the chromatin is the very thing that is the basis of the biological functions and activities. Current cutting-edge researches will be presented in wide research fields, structural biology, biophysics, imaging, cell biology and so on. We discuss the basis and meaning of chromatin dynamics.

はじめに

2SDA-01　クロマチン動構造とヒストンバリアント

Structural basis of chromatin dynamics regulated by histone variants

○胡桃坂 仁志（早稲田大学理工学術院 先進理工学部）

Hitoshi Kurumizaka (*Waseda University, Faculty of Science and Engineering*)

2SDA-02　統合的イメージングアプローチによる動的クロマチン構造・機能研究

Integrated imaging approach to the study of dynamics of chromatin

○十川 久美子[1,2], 伊藤 由馬[1,2], 深川 暁弘[1], 原田 昌彦[3], 木村 宏[4], 徳永 万喜洋[1,2]（[1]東工大・院生命理工, [2]理研・統合生命医セ, [3]東北大・院農学, [4]阪大院・生命機能）

Kumiko Sakata-Sogawa[1,2], Yuma Ito[1,2], Akihiro Fukagawa[1], Masahiko Harata[3], Hiroshi Kimura[4], Makio Tokunaga[1,2] ([1]*Grad. Sch. Biosci. Biotech., Tokyo Inst. Tech.*, [2]*IMS, RIKEN*, [3]*Grad. Sch. Agr. Sci., Tohoku Univ.*, [4]*Grad. Sch. Front. Biosci. Osaka Univ.*)

2SDA-03　塩濃度変化に対する天然クロマチンファイバーの高次構造変化の直接観察

Direct observation of the higher-order structural changes of native chromatin fibers for the change of the salt concentration

○小穴 英廣[1], 西川 香里[1], 松原 央達[2], 山本 歩[2,3], 山本 孝治[4], 原口 徳子[4,5], 平岡 泰[4,5], 鷲津 正夫[1]（[1]東大院・工・機械, [2]静大院・創造科学, [3]静大・理・化学, [4]情報通信研究機構 未来ICT研, [5]阪大院・理・生物科学）

Hidehiro Oana[1], Kaori Nishikawa[1], Hirotada Matsuhara[2], Ayumu Yamamoto[2,3], Takaharu G. Yamamoto[4], Tokuko Haraguchi[4,5], Yasushi Hiraoka[4,5], Masao Washizu[1] ([1]*Dept. of Mech. Eng., The Univ. of Tokyo*, [2]*Grad. Sch. of Sci. and Tech., Shizuoka Univ.*, [3]*Dept. of Chem., Shizuoka Univ.*, [4]*Adv. ICT Res. Inst., NICT*, [5]*Dept. of Biol. Sci., Osaka Univ.*)

2SDA-04　ヒストンとＲＮＡポリメラーゼの翻訳後修飾の生細胞・生体内計測

Monitoring histone and RNA polymerase modification dynamics in living cells and organisms

○木村 宏（阪大・生命機能）

Hiroshi Kimura (*Grad Sch Frontier Biosci, Osaka Univ.*)

2SDA-05　HP1 をとおして見えてきたヘテロクロマチンの構造と機能

Elucidation of construction and function of heterochromatin through HP1 binding proteins

○小布施 力史（北海道大学 大学院先端生命科学研究院）

Chikashi Obuse (*Grad. Sch. Life, Hokudai*)

2SDA-06　相同組換え修復における損傷クロマチン動態

Nuclear topography of homologous recombinational repair

○田代 聡（広大・原医研）

Satoshi Tashiro (*RIRBM, Hiroshima Univ.*)

2SDA-07 核膜形成における核膜タンパク質とクロマチンの動的相互作用の役割
A Role of Dynamic Interaction of Nuclear Membrane Proteins with Chromatin on the Nuclear Envelope Assembly
○原口 徳子[1,2,3], 小林 昇平[1], 荒神 尚子[1], 小坂田 裕子[1], 糀谷 知子[1,4], 森 知栄[1], 平岡 泰[1,2,3]（[1]情報通信研・未来ICT研, [2]阪大・院生命機能, [3]阪大・院理学, [4]日本女子大）
Tokuko Haraguchi[1,2,3], Shouhei Kobayashi[1], Takako Koujin[1], Hiroko Osakada[1], Tomoko Kojidani[1,4], Chie Mori[1], Yasushi Hiraoka[1,2,3] ([1]*Advanced ICT Res. Inst. Kobe, NICT*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*Grad. Sch. Sci., Osaka Univ.*, [4]*Japan Women's Univ.*)

9:00～11:30　E 会場／Room E : Room 204

2SEA　ポンプとチャネルはどちらが偉いのか
Which is important for biophysicists, pump or channel?

オーガナイザー：飯野 亮太（自然科学研究機構岡崎統合バイオサイエンスセンター），須藤 雄気（岡山大学）
Organizers: Ryota Iino (Okazaki Inst. Integ. Biosci., NINS), Yuki Sudo (Okayama University)

Membrane transporters such as pumps and channels are splendid molecular machines, and have fascinated many biophysicists for a long time because of their importance for the general understanding of the energy conversion. In this symposium, speakers will discuss the operative mechanisms of the transporters based on the results of structural analysis, single-molecule measurements, molecular simulations, creation of chimeric molecules, and cellular regulation. Particularly, each speaker will focus on their biophysical significance to gain support from the audience, and the common and individual principles of membrane transporters will be discussed together.

2SEA-01 Importance of membrane pumps and channels: an introduction
Ryota Iino[1,2,3] ([1]*Okazaki Inst. Integ. Biosci., NINS*, [2]*IMS, NINS*, [3]*Dept. of Functional Molecular Science, SOKENDAI*)

2SEA-02 VoV1 の中心回転軸における巧妙なトルク伝達機構
The ingenious structure of central rotor apparatus in VoV1; torque transmission mechanism in the central rotor of VoV1
○横山 謙（京都産業大学）
Ken Yokoyama (*Kyoto Sangyo University*)

2SEA-03 イオンポンプとの比較による、塩化物イオンチャネル CFTR の作動機構研究
Studies on the mechanism of a chloride channel CFTR in comparison with ion pumps
○政池 知子[1,2], 相馬 義郎[3]（[1]東京理科大・応用生物科学, [2]科学技術振興機構・さきがけ, [3]慶應義塾大・医学部薬理学）
Tomoko Masaike[1,2], Yoshiro Sohma[3] ([1]*Dept. Applied Biol. Science, Tokyo Univ. Science*, [2]*PRESTO, JST*, [3]*Dept. Pharmacology, School of Medicine, Keio Univ.*)

2SEA-04 多剤排出トランスポーターの薬剤取込経路の粗視化シミュレーション研究
Drug uptake pathways in multi-drug transporter studied by coarse-grained simulations
○高田 彰二（京大理 生物物理）
Shoji Takada (*Grad. Sch Sci, Kyoto Univ.*)

2SEA-05 脂質はイオンチャネルのゲート開閉をどの様に制御するのか？：新奇脂質センサーによる制御機構
How do lipids regulate the gating activity of the channel protein? : Mechanism of a novel type of the lipid sensor
○岩本 真幸, 老木 成稔（福井大・医・分子生理）
Masayuki Iwamoto, Shigetoshi Oiki (*Dept. Mol. Physiol. Biophys., Univ. Fukui Facult. Med. Sci.*)

2SEA-06 細菌多剤排出トランスポーターの制御と生理機能
Regulation and physiological function of bacterial multidrug transporters
○西野 邦彦（大阪大学産業科学研究所 感染制御学研究分野）
Kunihiko Nishino (*ISIR, Osaka Univ.*)

2SEA-07 光駆動イオンポンプから光開閉性イオンチャネルへの機能変換
Converting a light-driven ion pump into a light-gated ion channel
○須藤 雄気（岡大・院医歯薬(薬)）
Yuki Sudo (*Div. of Parm. Sci., Okayama Univ.*)

16:15〜18:45　A 会場／Room A : Mid-sized Hall 1/2

2SAP　新学術領域研究「少数性生物学―個と多数の狭間が織りなす生命現象の探求―」共催
少数性、数揺らぎが創出する機能のシナリオ
Scenario of functions from minority and number fluctuations

オーガナイザー：小松崎 民樹（北海道大学），永井 健治（大阪大学）
Organizers: Tamiki Komatsuzaki (Hokkaido University), Takeharu Nagai (Osaka University)

In intracellular environment, the number of proteins in each species is from just only a few to several thousands, which often takes a positively-skewed asymmetric distribution over single cells. Some proteins may not be described by the concept of concentration, in which discreteness in their numbers may matter, yielding individuality in molecules. Cellular individuality also exists with diverse, different numbers of proteins in each cell with same kinds of proteins. We will discuss possible roles of minorities and discreteness of numbers and, molecular and cellular individuality.

2SAP-01 分子個性と少数性
Molecular Individuality and Minority in Biology
○小松崎 民樹（北海道大学 電子科学研究所 分子生命数理研究分野）
Tamiki Komatsuzaki (*Hokkaido Univ., Res. Inst. Electronic Sci.*)

2SAP-02 触媒反応ネットワーク系における少数分子と競合
Minority molecules and competitions in a catalytic reaction network
○上村 淳, 金子 邦彦（東大総合文化）
Atsushi Kamimura, Kunihiko Kaneko (*Dept. of Basic Science, The Univ. of Tokyo*)

2SAP-03 スパインにおける確率的な Ca^{2+}の上昇はロバストでセンシティブな情報コーディングを可能にする
Stochasticity in Ca^{2+} increase in spines enables robust and sensitive information coding
○藤井 雅史[1], 上村 卓也[2], 浦久保 秀俊[1], 大橋 郁[1], 黒田 真也[1,2]（[1]東京大学大学院理学系研究科生物科学専攻, [2]東京大学理学部生物情報科学科）
Masashi Fujii[1], Takuya Koumura[2], Hidetoshi Urakubo[1], Kaoru Ohashi[1], Shinya Kuroda[1,2] ([1]*Dept. Biol. Sci., Grad. Sch. Sci, Univ. Tokyo*, [2]*Undergrad. Dept. Bioinfo. Syst, Univ. Tokyo*)

2SAP-04 定量 ATP イメージングによる単一細胞内 ATP 濃度の多様性の測定
Heterogeneity in ATP Concentrations in a Single Bacterial Cell Population Revealed by Quantitative Single-cell Imaging
○柳沼 秀幸[1,2,3], 河合 信之輔[4,5], 田端 和仁[2,6], 冨山 佳祐[3], 垣塚 彰[7], 小松崎 民樹[5], 岡田 康志[1], 野地 博行[2,3], 今村 博臣[7,8]（[1]理研・QBiC, [2]東大院・工, [3]阪大院・生命機能, [4]静大・理, [5]北大・電子研, [6]JST・さきがけ, [7]京大院・生命科学, [8]京大・白眉センター）
Hideyuki Yaginuma[1,2,3], Shinnosuke Kawai[4,5], Kazuhito Tabata[2,6], Keisuke Tomiyama[3], Akira Kakizuka[7], Tamiki Komatsuzaki[5], Yasushi Okada[1], Hiroyuki Noji[2,3], Hiromi Imamura[7,8] ([1]*QBiC, RIKEN*, [2]*Grad. Schl. Eng., Univ. Tokyo*, [3]*Grad. Schl. Frontier Biosci*, [4]*Schl. Sci, Shizuoka Univ.*, [5]*RIES, Hokkaido Univ.*, [6]*PRESTO, JST*, [7]*Grad. Schl. Biostud., Kyoto Univ.*, [8]*Hakubi Project, Kyoto Univ.*)

2SAP-05 １細胞系譜統計解析により明らかになる細胞表現型の適応度と選択圧の強さ
Single-cell lineage statistics reveals fitness and selection strength for heterogeneous phenotypic states
野添 嵩, ○若本 祐一（東大・院・総合文化）
Takashi Nozoe, **Yuichi Wakamoto** (*Univ. of Tokyo*)

2SAP-06 少数性生物学の展望
Prospect of minority biology
○永井 健治（阪大・産研）
Takeharu Nagai (*ISIR, Osaka Univ.*)

16:15～18:45　B 会場／Room B : Mid-sized Hall 2/2

2SBP　新学術領域研究「細胞シグナリング複合体によるシグナル検知・伝達・応答の構造的基礎」共催
シグナル伝達機構における構造細胞生物学的新展開
New Development of Structural Cell Biology in Signal Transduction

オーガナイザー：前仲 勝実（北海道大学），石森 浩一郎（北海道大学）
Organizers: Katsumi Maenaka (Hokkaido University), Koichiro Ishimori (Hokkaido University)

While recent progress in structural biology has revealed fine structures of biomolecules, we have not yet understood the molecular mechanism for their functions due to lack of information on the space and time dependent interactions in the biological systems. Particularly, signal transduction processes are crucial to maintain essential biological systems, and the specific and dynamic interactions leads to the integrated regulation. In this symposium, up-and-coming young researchers will present their cutting-edge researches to discuss the contribution of structural cell biology to regulation mechanisms for signal transduction systems.

2SBP-01　構造細胞生物学とは
Structural cell biology
○箱嶋 敏雄（奈良先端科学技術大学院大学バイオサイエンス研究科）
Toshio Hakoshima (*Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol.*)

2SBP-02　C 型レクチン受容体 Mincle の糖脂質認識機構
Structural basis for glycolipid recognition mechanism by C-type lectin like receptor, Mincle
○古川 敦[1], 上敷領 淳[2], 尾瀬 農之[1], 山崎 晶[3], 前仲 勝実[1]（[1]北大・院薬, [2]福山大・薬, [3]九大・生医研）
Atsushi Furukawa[1], Jun Kamishikiryo[2], Toyoyuki Ose[1], Sho Yamasaki[3], Katsumi Maenaka[1] ([1]*Grad. Sch. of Pharm., Univ. of Hokkaido*, [2]*Sch. of Pharm., Univ. of Fukuyama*, [3]*Med. Inst. of Bioreg., Univ. of Kyushu*)

2SBP-03　コレラ菌の鉄獲得機構
Heme-iron uptake proteins from *Vibrio cholerae*
○内田 毅（北大院理）
Takeshi Uchida (*Grad. Sch. Sci., Hokkaido Univ.*)

2SBP-04　糖タンパク質品質管理システムにおける糖鎖修飾メカニズムの構造基盤
Structural basis for the glycan-processing mechanisms in glycoprotein quality control system
○佐藤 匡史[1,2], 加藤 晃一[1,3]（[1]名市大・院薬, [2]科学技術振興機構・さきがけ, [3]岡崎統合バイオ）
Tadashi Satoh[1,2], Koichi Kato[1,3] ([1]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [2]*JST, PRESTO*, [3]*Okazaki Inst. Integ. Biosci.*)

2SBP-05　G タンパク質共役型内向き整流性カリウムイオンチャネル 1(GIRK1)の G タンパク質による機能調節の構造基盤
Structural Basis for Regulation of G Protein-activated Inwardly Rectifying Potassium Channel 1 (GIRK1) by G Proteins
○大澤 匡範[1], 間瀬 瑤子[1], 横川 真梨子[1,2], 竹内 恒[3], 嶋田 一夫[1]（[1]東大・院薬系, [2]バイオ産業情報化コンソ, [3]産総研、創薬分子プロファイリング研究セ）
Masanori Osawa[1], Yoko Mase[1], Mariko Yokoagawa[1,2], Koh Takeuchi[3], Ichio Shimada[1] ([1]*Grad. Sch. Pharm. Sci, The Univ. of Tokyo*, [2]*JBic*, [3]*Molprof, AIST*)

2SBP-06　超遠心分析と質量分析による溶液中での蛋白質間相互作用解析
In solution characterizations of protein-protein interactions by analytical ultracentrifugation and mass spectrometry
○内山 進[1,2]（[1]阪大 工 先端生命, [2]岡崎統合バイオ）
Susumu Uchiyama[1,2] ([1]*Dept.Biotech., Grad. Sch. Eng., Osaka Univ.*, [2]*Okazaki Inst. Integ. Biosci.*)

2SBP-07　毛上皮形成における S100A3-PAD3 亜鉛シグナル伝達機構の構造生物学的解明
Structural Biology for the Zinc Signal Transduction Mechanism by S100A3-PAD3 in Hair Cuticular Cells
○海野 昌喜[1,2], 木澤 謙司[3], 眞下 隆太朗[1,2], 西條 慎也[4], 清水 伸隆[4], 秋元 恵[1,2], 高原 英成[5]（[1]茨城大院理工, [2]茨城大フロンティア, [3]カネボウ化・価値創成研, [4]高エネ研・PF, [5]茨城大・農）
Masaki Unno[1,2], Kenji Kizawa[3], Ryutaro Mashimo[1,2], Shinya Saijo[4], Nobutaka Shimizu[4], Megumi Akimoto[1,2], Hidenari Takahara[5] ([1]*Grad. Sch. Sci. Eng., Ibaraki Univ.*, [2]*iFRC, Ibaraki Univ.*, [3]*Kanebo, Cosme. Inc*, [4]*KEK, PF*, [5]*Dep. Appl. Biol. Res. Sci., Ibaraki Univ.*)

16:15〜18:45　C 会場／Room C : Room 107

2SCP　構造バイオインフォマティクスによる蛋白質機能予測・解析
Prediction and analysis of protein functions from structural bioinformatics

オーガナイザー：中村 春木（大阪大学），清水 謙多郎（東京大学）
Organizers: Haruki Nakamura (Osaka University), Kentaro Shimizu (The University of Tokyo)

By interpreting genome information to structural information of proteins and their interactions, estimation and deep understanding of their functions are now available with the bioinformatics techniques. In this symposium, recent methods in structural bioinformatics and their applications to clinical studies like effects by SNPs based on structures will be introduced and discussed.

2SCP-01　Toward a Computational Assessment of the Effect of Amino Acid Variation to Protein Structure and Function - Case Study on a Few Enzymes
Kei Yura[1,2] ([1]*Grad. Schl. Hum. Sci., Ochanomizu Univ.*, [2]*NIG*)

2SCP-02　From Personal Genome to Personal Proteins: Connection between the Reference sequences of genomic DNA and Proteins
Kengo Kinoshita[1,2,3] ([1]*Grad Sch Info Sci, Tohoku Univ.*, [2]*Tohoku Medical Megabank, Tohoku Univ.*, [3]*IDAC, Tohoku Univ.*)

2SCP-03　蛋白質の構造モチーフの際に着目した機能アノテーション
Composite structural motifs of binding sites for annotating functional differences
○金城 玲（阪大・蛋白研）
Akira Kinjo (*Institute for Protein Research, Osaka University*)

2SCP-04　アミノ酸残基間距離予測に基づくタンパク質立体構造モデルの評価
Model quality assessment method based on a residue-residue distance matrix prediction
○竹田ー志鷹 真由子（北里大学薬学部）
Mayuko Takeda-Shitaka (*Pharm., Kitasato Univ.*)

2SCP-05　粗視化分子動力学シミュレーションで探るタンパク質・リガンド結合過程
Protein–ligand binding processes studied by coarse-grained molecular dynamics simulations
○寺田 透, 根上 樹, 清水 謙多郎（東大・院農）
Tohru Terada, Tatsuki Negami, Kentaro Shimizu (*Grad. Sch. Agr. Life Sci., Univ. Tokyo*)

2SCP-06　超分子モデリングパイプラインの構築による相関構造解析•理論創薬支援
Supramolecular modeling pipeline for correlative structural analysis and rational drug-design
○白井 剛（長浜バイオ大学）
Tsuyoshi Shirai (*Nagahama Inst BioSci Tech*)

2SCP-07　Intrinsic disorder mediates cooperative signal transduction in STIM1
Daron M. Standley (*iFReC, Osaka University*)

16:15〜18:45　D 会場／Room D : Room 108

2SDP　生体分子機械の動作機構を周りの水から眺めてみる
Biomolecular machinery driven by surrounding water

オーガナイザー：原野 雄一（姫路獨協大学），西山 雅祥（京都大学）
Organizers: Yuichi Harano (Himeji Dokkyo University), Masayoshi Nishiyama (Kyoto University)

The thermodynamic aspect of the water should be essential because the dynamical behavior of biomolecules is mostly observed at large time scales. The hydration theories are revealing the role of water in terms of the thermodynamics. At the same time, recent development of experimental technique to detect the biomolecular dynamics is quite remarkable. This session will allow theoreticians and experimentalists to get together and discuss the achievements and future directions associated with dynamical behavior of biomolecules under the influence of surrounding water.

2SDP-01 アクチンモノマーの会合と多価カチオンが媒介する同符号コロイド粒子間実効引力
Association of Actin Monomers and Effective Attraction between Like-Charged Colloidal Particles Mediated by Multivalent Cations
○秋山 良（九大 院理 化学）
Ryo Akiyama (*Dept. of Chem., Kyushu Univ.*)

2SDP-02 合成化学的に構築した人工分子機械によって駆動される水中での非共有結合性分子集合体の巨視的運動
Macroscopic Motion of Soft Non-covalent Molecular Assembly in Water Actuated by Chemically Synthesized Molecular Machine
○景山 義之[1,2]（[1]北海道大学大学院理学研究院, [2]ＪＳＴ・さきがけ）
Yoshiyuki Kageyama[1,2] ([1]*Fac. Sci., Hokkaido Univ.*, [2]*PRESTO, JST*)

2SDP-03 生体分子機械を水和水であやつる
Controlling the molecular machinery by water molecules of the hydration
○西山 雅祥（京大・白眉セ）
Masayoshi Nishiyama (*The HAKUBI Center, Kyoto Univ.*)

2SDP-04 生体分子のダイナミクスに向けた水和熱力学
Hydration thermodynamics toward biomolecular dynamics
○原野 雄一（姫路獨協大学薬学部）
Yuichi Harano (*Himeji Dokkyo University*)

2SDP-05 タンパク質の構造ゆらぎと変化に対する相互作用成分解析
Interaction-Component Analysis on Protein Structure in Explicit Solvent
○松林 伸幸（大阪大学 大学院基礎工学研究科 化学工学領域）
Nobuyuki Matubayasi (*Division of Chemical Engineering, Graduate School of Engineering Science, Osaka University*)

2SDP-06 水の状態を感受する蛍光蛋白質の開発
Development of fluorescent protein to sense “state of water”
○渡邉 朋信[1,2,3]（[1](独)理研・QBiC, [2]阪大・生命機能, [3]阪大・免フロ）
Tomonobu Watanabe[1,2,3] ([1]*QBiC, RIKEN*, [2]*Grad. Sch. Front. Biosci., Osaka University*, [3]*iFRec, Osaka Univ.*)

16:15～18:45　E 会場／Room E : Room 204
2SEP　生物界における光とは？：動物・植物・微生物の光科学、そしてオプトジェネティクス
Light in life: photo-biology of animals, plants, microorganisms and optogenetics

オーガナイザー：井上 圭一（名古屋工業大学），中曽根 祐介（京都大学）
Organizers: Keiichi Inoue (Nagoya Institute of Technology), Yuusuke Nakasone (Kyoto University)

Light is the mother of life and it supplies huge benefits to survive. Most of organisms have evolved their unique systems to utilize light, and various photo-receptive proteins are playing central roles there. On the other hand, new techniques optically controlling living-organisms, “optogenetics”, are being rapidly developed by genetic application of those proteins. In this symposium, seven leading-researchers talk about a wide variety of photo biological- or optogenetic researches and we will discuss about future perspective of light and life from a viewpoint beyond species.

はじめに
○井上 圭一（名大・工，JSTさきがけ）
Keiichi Inoue (*Nagoya Institute of Technology*)

2SEP-01 カラフルな植物光受容体、赤、青、UV-B を見る
Colorful plant photoreceptors see red, blue and UV-B light
○徳富 哲, 吉原 静恵（阪府大院 理 生物）
Satoru Tokutomi, Shizue Yoshihara (*Osaka Prefect. Univ., Grad. School Sci., Dep. Biol. Sci.*)

2SEP-02 触覚パターンのオプトジェネティクス制御
Optogenetic patterning of touch sense
○八尾 寛[1,2,3], 横山 超一[1,2], 住吉 晃[4], 阿部 健太[1,2], 小泉 協[1,2], 江川 遼[1,2], 劉 越人[1,2], 大城 朝一[2,3], 松坂 義哉[2,3], 川島 隆太[4], 虫明 元[2,3], 石塚 徹[1,2]（[1]東北大・院生命, [2]JST-CREST, [3]東北大・院医学, [4]東北大・加齢医学研究所）
Hiromu Yawo[1,2,3], Yukiobu Yokoyama[1,2], Akira Sumiyoshi[4], Kenta Abe[1,2], Kyo Koizumi[1,2], Ryo Egawa[1,2], Yueren Liu[1,2], Tomokazu Ohshiro[2,3], Yoshiya Matsuzaka[2,3], Ryuta Kawashima[4], Hajime Mushiake[2,3], Toru Ishizuka[1,2] ([1]*Tohoku Univ. Grad. Sch. Life Sci.*, [2]*JST-CREST*, [3]*Tohoku Univ. Grad. Sch. Med.*, [4]*Tohoku Univ. IDAC*)

2SEP-03 脊椎動物クリプトクロムの多様性、機能および分子応用
Diversity, function and molecular application of vertebrate cryptochromes
○岡野 俊行（早大 先進理工 電気・情報生命）
Toshiyuki Okano (*Waseda Univ. Sch. Adv. Sci. & Eng.*)

2SEP-04 イェロープロテインを通じてみたセンサー蛋白質の作動機構
Molecular actions of the light sensor protein, Photoactive Yellow Protein, as a prototype for sensor proteins
○上久保 裕生（奈良先端大物質創成）
Hironari Kamikubo (*NAIST/MS*)

2SEP-05 BLUF タンパク質の光化学とオプトジェネティクス
Photochemistry and optogenetics with BLUF proteins
○増田 真二（東工大・バイオセンター）
Shinji Masuda (*Center for Biol. Res. & Inform., Tokyo Inst. Tech.*)

2SEP-06 脊椎動物の非視覚オプシン Opn5 の分子特性の多様性
Diversity of Molecular properties of vertebrate non-visual opsin Opn5
○山下 高廣（京大・院理・生物物理）
Takahiro Yamashita (*Grad. Sch. Sci., Kyoto Univ.*)

2SEP-07 フィトクロムは遺伝子発現の様々な段階を直接制御する
Phytochrome directly regulates various aspects of gene expression
○松下 智直[1,2]（[1]九大院・農, [2]JST さきがけ）
Tomonao Matsushita[1,2] ([1]*Fac. Agri., Kyushu Univ.*, [2]*JST PRESTO*)

おわりに
○中曽根 祐介（京大・理）
Yuusuke Nakasone (*Kyoto Univ.*)

第 3 日目（9 月 27 日（土））／Day 3（Sep. 27 Sat.）

9:45～12:15　A 会場／Room A : Mid-sized Hall 1/2

3SAA　新学術領域研究「感覚と知能を備えた分子ロボットの創成」共催
感覚と運動および知能を備えた分子ロボットの創成
Development of Molecular Robots equipped with Sensors and Intelligence

オーガナイザー：小長谷 明彦（東京工業大学），萩谷 昌己（東京大学），村田 智（東北大学），角五 彰（北海道大学）
Organizers: Akihiko Konagaya (Tokyo Institute of Technology), Masami Hagiya (The University of Tokyo), Satoshi Murata (Tohoku University), Akira Kakugo (Hokkaido University)

Recently the concept of molecular robotics, that is being motivated from the observation and understanding of highly efficient and coordinated natural biological systems, has emerged. In this symposium we are going to focus on this newly evolved field of research dealing with the molecular robotics. Comprehensive discussion will be made on various aspects of the molecular robotics that includes development and integration of robots using the combination of artificial and natural components such as synthetic polymers, poly-peptide, DNA, bio-molecular motors.

3SAA-01 分子ロボティクス―その展望と動機
Molecular Robotics — Perspectives and Motivation
○村田 智（東北大・院工学）
Satoshi Murata (*Grad. Sch. Eng., Tohoku Univ.*)

3SAA-02 Building Nanoscale Devices with DNA
Shawn Douglas (*UCSF*)

3SAA-03 核酸ナノ構造を活用した分子情報変換デバイスの設計
Designing DNA/RNA nanostructure-based information converters
○齊藤 博英[1], 遠藤 政幸[1], 瀧ノ上 正浩[2]（[1]京都大学, [2]東京工業大学）
Hirohide Saito[1], Masayuki Endo[1], Masahiro Takinoue[2] ([1]*Kyoto Univ.*, [2]*Tokyo Tech.*)

3SAA-04 分子ロボットのリアルタイムな動作を目指した試験管内での知能の実装
Implementation of *in vitro intelligence* for real-time operation of molecular robots
○小宮 健（東工大・院総理）
Ken Komiya (*Int. Grad. Sch. Sci. & Engi., Tokyo Tech.*)

3SAA-05 アメーバ型分子ロボットの課題と展望
Perspectives and objectives of amoeba-type molecular robots
○小長谷 明彦（東工大院知能システム科学）
Akihiko Konagaya (*Tokyo Institute of Technology*)

3SAA-06 ゲルに基づく分子ロボットとその計算モデル
Gel-based molecular robots and their computational models
○萩谷 昌己（東京大学）
Masami Hagiya (*The University of Tokyo*)

9:45～12:15　B 会場／Room B : Mid-sized Hall 2/2

3SBA　分子機械デザイン
Rise of molecular machines

オーガナイザー：野地 博行（東京大学），林 重彦（京都大学）
Organizers: Hiroyuki Noji (The University of Tokyo), Shigehiko Hayashi (Kyoto University)

Biomolecular machines are well investigated with respect to their conformational dynamics and reaction schemes. However, study seeking the principles of their structural design is still in its early stage. Furthermore, there are only few successful attempts of re-designing for function-gaining. To better elucidate the design principles of molecular machines, extensive redesign of natural molecular machines or de novo synthesis of completely novel molecular machines are needed. In this symposium, speakers will discuss their approaches toward synthetic re-designs.

はじめに

3SBA-01 Toward design of molecular motors
Nobuyasu Koga[1,2] ([1]*Inst. Mol. Sci. CIMoS*, [2]*JST, PRESTO*)

3SBA-02 The conformational change mechanism of the β subunit in F_1-ATPase revealed by all-atom MD simulations
Yuko Ito, Mitsunori Ikeguchi (*Grad. Sch. Med. Life Sci., Yokohama-City Univ.*)

3SBA-03 Molecular simulations of proton pumps and biomolecular motors
Qiang Cui (*Dept. of Chem., Univ. of Wisconsin, Madison*)

3SBA-04 F1 モーターの再デザインによる人工回転分子モーター開発の見通し
Prospects on artificial molecular motor by redesigning of F1-ATPase
○野地 博行（東京大学大学院工学系研究科応用化学専攻）
Hiroyuki Noji (*Applied Chem. U-Tokyo*)

3SBA-05 Is enzyme evolution reversible? Exploring fitness landscapes by laboratory evolution
Nobuhiko Tokuriki (*University of British Columbia*)

3SBA-06 Remote control of myosin and kinesin motors using light-activated gearshifting
Zev Bryant (*Stanford University*)

おわりに

9:45～12:15　C 会場／Room C : Room 107
3SCA　大容量生命情報時代の新しい生物学とは？
Next generation Biology at the big data era

オーガナイザー：諏訪 牧子（青山学院大学），有田 正規（国立遺伝学研究所）
Organizers: Makiko Suwa (Aoyama Gakuin University), Masanori Arita (National Institute of Genetics)

Biology is coming to a new turning point now. The biological "big data" of heterogeneous, many classes and dimensions is accumulated quickly every day and therefore it is just now to solve the origin questions about proncipal of biological process, which had been unsolvable before without big data. In this symposium, we would like to argue about the strategies of collecting and analyzing biological information for solving such origin questions, by exploring the point of contact of biophysics and bioinformatics.

はじめに
○諏訪 牧子（青学）
Makiko Suwa (*Aoyama Gakuin Univ.*)

3SCA-01 生物システムの理解に本質的な３つの未解決問題
Three unsolved problems for essential understanding of biological systems
○美宅 成樹（豊田理研）
Shigeki Mitaku (*Toyota Phys. Chem. Res. Inst.*)

3SCA-02 リン酸化プロテオームとメタボロームデータからのインスリン作用のグローバルネットワークの再構築
Reconstruction of global network of acute insulin action from phosphor-proteome and metabolome data
○黒田 真也, 柚木 克之（東京大学理学系研究科生物科学専攻）
Shinya Kuroda, Katsuyuki Yugi (*Biological Sciences, The University of Tokyo*)

3SCA-03 全ゲノム規模の１細胞内１分子遺伝子発現情報からのデータマイニング
Mining genome-wide datasets of single-cell gene expressions at single-molecule resolution
○谷口 雄一（理化学研究所生命システム研究センター）
Yuichi Taniguchi (*Quantitative Biology Center, RIKEN*)

3SCA-04 分子バーコーディングによる一分子の分解能をもつゲノムワイド遺伝子発現絶対定量法
Absolute genome-wide quantification of gene expression with single molecule resolution using molecular barcoding
○城口 克之（理研・統合生命医科学研究セ）
Katsuyuki Shiroguchi (*IMS RIKEN*)

3SCA-05 大容量生命情報時代の生物学のボトルネック
Fundamental bottlenecks in big-data biology
○岩崎 渉（東大・院理・生物科学）
Wataru Iwasaki (*Dept Biol Sci, Grad Sch Sci, UTokyo*)

3SCA-06 Database for Biology: which data deserve maintaining?
Masanori Arita[1,2] ([1]*National Institute of Genetics*, [2]*RIKEN CSRS*)

9:45～12:15　D 会場／Room D : Room 108

3SDA　ラマン顕微分光および先端光計測が拓く生物物理の視界
Cutting-Edge Optical Imaging Approaches and Raman Micro-Spectroscopy Pioneering Bio-Physics

オーガナイザー：盛田 伸一（東北大学），坂内 博子（名古屋大学）
Organizers: Shin-ichi Morita (Tohoku University), Hiroko Bannai (Nagoya University)

Recent progress in optical measurements for live cells to small animals provides us new and unique visions in biophysics. In this symposium, we aim to introduce cutting-edge imaging techniques that will be upcoming standards in biophysical research in near future. Young leading researchers introduce their recent studies ranging from single molecule imaging to whole-animal imaging with light-sheet microscopy, new laser sources and bio-sensors, as well as the Raman microscopy, including Raman scattering (SRS) microscope, Raman-tagged live cell imaging.

はじめに
○盛田 伸一（東北大院理）
Shin-ichi Morita (*Tohoku Univ.*)

3SDA-01　「膜分子のふるまい」を見て「細胞内シグナル」を知る
Watch the “membrane protein behavior” to know the “intracellular signaling pathway”
○坂内 博子[1,2], 丹羽 史尋[2], Triller Antoine[3], 御子柴 克彦[2]（[1]名大・院生命理学, [2]理研・BSI, [3]パリ高等師範学校生物学研究所）
Hiroko Bannai[1,2], Fumihiro Niwa[2], Antoine Triller[3], Katsuhiko Mikoshiba[2] ([1]*Nagoya Univ., Grad. Sch. Biol. Sci.*, [2]*RIKEN BSI*, [3]*IBENS*)

3SDA-02　Improvement of two-photon laser scanning microscopy for live imaging utilizing laser technology
Tomomi Nemoto[1,2,3] ([1]*RIES, Hokkaido Univ.*, [2]*JST CREST*, [3]*Grd. Sch. Info., Hokkaido Univ.*)

3SDA-03　吸収増幅顕微鏡による細胞イメージング
Cavity reflection enhanced light absorption microscopy for cellular imaging
○新井 由之[1], 山本 高之[1], 南川 丈夫[2], 高松 哲郎[2], 永井 健治[1]（[1]阪大・産研, [2]京都府立医大）
Yoshiyuki Arai[1], Takayuki Yamamoto[1], Takeo Minamikawa[2], Tetsuro Takamatsu[2], Takeharu Nagai[1] ([1]*ISIR, Osaka Univ.*, [2]*Kyoto Pref. Univ. Med.*)

3SDA-04　光シート顕微鏡による生体まるごとイメージング
Live imaging of whole organisms by light-sheet microscopy
○野中 茂紀（基生研）
Shigenori Nonaka (*NIBB*)

3SDA-05　小分子から生細胞までーラマン顕微鏡にできることー
Small Molecules and Live Cells Characterized Using Raman Microscopes
○盛田 伸一（東北大院理）
Shin-ichi Morita (*Tohoku Univ.*)

3SDA-06　近赤外吸収プローブとしての Pt(II)ジラジカル錯体の機能開発
Development of a function of Pt(II)-diradical complex as a near-infrared absorbing probe
○升谷 敦子, 田村 昂作, 星野 仁, 壹岐 伸彦（東北大院環境）
Atsuko Masuya, Kosaku Tamura, Hitoshi Hoshino, Nobuhiko Iki (*Graduate School of Environmental Studies, Tohoku University*)

3SDA-07　誘導ラマンによって何が見えるのか？
What could be visualized with stimulated Raman scattering?
○小関 泰之（東大院工）
Yasuyuki Ozeki (*UTokyo*)

9:45～12:15　E 会場／Room E : Room 204

3SEA　タンパク質物性研究の最前線：若手研究者による挑戦
Frontiers in physical properties of proteins: challenges by young scientists

オーガナイザー：新井 宗仁（東京大学），濵田 大三（三重大学）
Organizers: Munehito Arai (The University of Tokyo), Daizo Hamada (Mie University)

The aim of this symposium is to encourage discussions especially between younger generations at the earlier stages of research career particularly working on physicochemical properties of proteins. The selected speakers are PhD students, postdocs or assistant professors who are actively studying the mechanism of protein folding or methodologies for de novo protein design using variety of experimental or theoretical approaches.

3SEA-01　きわめて長い半減期をもつフォールディング中間体の解析
Analysis of an unusually stable kinetic refolding intermediate
○杉本 華幸（新潟大農）
Hayuki Sugimoto (*Fac. Agri. Univ. NIIGATA*)

3SEA-02　FRET と高速溶液混合法による SNase の凝縮過程の速度論研究
Kinetics of Chain Condensation during SNase Folding studied by FRET and ultrarapid mixing methods
○水上 琢也[1], Xu Ming[1], Cheng Hong[1], Roder Heinrich[1,2], 槇 亙介[3]（[1]フォックスチェイス癌センター, [2]ペンシルベニア大学, [3]名大・理）
Takuya Mizukami[1], Ming Xu[1], Hong Cheng[1], Heinrich Roder[1,2], Kosuke Maki[3] ([1]*FCCC*, [2]*UPenn*, [3]*Nagoya University*)

3SEA-03　様々な蛋白質間で観察される配列順序非保存な構造類似性
Non-sequential structural similarity in the protein world
○南 慎太朗[1], 太田 元規[1], 千見寺 浄慈[2]（[1]名大・情報科学, [2]名大・工）
Shintaro Minami[1], Motonori Ota[1], George Chikenji[2] ([1]*Grad. Sch. of Inf. Sci., Nagoya Univ.*, [2]*Grad. Sch. of Eng., Nagoya Univ.*)

3SEA-04　機能と構造安定性のトレードオフに対するアプローチ：アルブミン結合タンパク質を模倣したヒト型タンパク質のデザインを例として
The approach to the function-stability tradeoff: A case of the design of a humanized protein mimicking the albumin-binding protein
○大城 理志[1], 本田 真也[1,2]（[1]東大・新領域・メディカルゲノム, [2]産総研・バイオメディカル）
Satoshi Oshiro[1], Shinya Honda[1,2] ([1]*Dept. of Medical Genome Sci., Grad. Sch. of Frontier Sci., The Univ. of Tokyo*, [2]*BioMed. Research Inst., AIST*)

3SEA-05　転写因子 Sp1 と TAF4 の天然変性領域を介した相互作用
The interaction between transcription factors Sp1 and TAF4 via the intrinsically disordered regions
○日比野 絵美[1], 井上 倫太郎[2], 杉山 正明[2], 桑原 淳[3], 松崎 勝巳[1], 星野 大[1]（[1]京大院薬, [2]京大原子炉, [3]同女薬）
Emi Hibino[1], Rintaro Inoue[2], Masaaki Sugiyama[2], Jun Kuwahara[3], Katsumi Matsuzaki[1], Masaru Hoshino[1] ([1]*Grad. Pharm., Univ. Kyoto*, [2]*KURRI*, [3]*Fac. of Pharm., Doshisha WUniv.*)

3SEA-06　混雑環境下での天然変性タンパク質の振る舞い: α-synuclein のアミロイド形成に関する熱力学シミュレーション
Intrinsic disorder under crowded environment: thermodynamic simulation of α-synuclein amyloid fibril formation
○白井 伸宙（京大・院理）
Nobuhiro C. Shirai (*Grad. Sch. Sci., Kyoto Univ.*)