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  
連続的観察による多分子の折り畳み過程  
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.)
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、石渡信一（早大・理工、２WABIOS）
Takeshi Itabashi¹, Shin’ichi Ishiwata¹² (¹Fac. Sci. Eng., Waseda Univ., ²WABIOS)

1SCA-03 上皮組織の発生と維持の機械・化学制御の統合的解釈に向けて
Toward Understanding the Integration of Mechanical and Chemical Control of Epithelial Development and Maintenance
○杉村薰、藤田信一、石原秀至（京大、JST・さきがけ、北大、明治大）
Kaoru Sugimura¹², Mihoko Kajita¹, Yasuyuki Fujita¹, Shuji Ishihara⁴ (¹Kyoto Univ., ²JST PRESTO, ³Hokkaido Univ., ⁴Meiji 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（東工大・院総合理工、JST・さきがけ）
Masahiro Takinoue¹² (¹Interdisciplinary Grad. Sch. Sci. & Eng., Tokyo Tech., ²PRESTO, JST)
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 Ito1, Kazutoshi Gohara2 (*Fac. Advanced Life Sci., Hokkaido Univ., *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1, 郷原 一寿2, 宇野 達夫3, 平野 愛弓1 (1: 北東大・学際研, 2: 北東大・医工, 3: 早大・基幹理工)

1SDA-03 非侵襲的リアルタイム測定を目的としたパルス波高を用いた主神経細胞電位を用いたカーボンナノチューブ電極チップの開発
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 神経ダイナミックス解明のためのレーザー操動技術の開発
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 非侵襲的神経活動の解析を通じた先端電気生理学と化学センシングを用いたCMOS技術
Revealing Neuronal Dynamics through Advanced Electrophysiology and Chemical Sensing using CMOS Technology
Urs Frey1,2, Marie Engelene Obien1, Florent Seichepine1, Kosmas Deligkaris1,2 (*RIKEN Quantitative Biology Center, 2Graduate 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, 柳川 康貴, 鶴野 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)
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 リボ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（東京農工大学工・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, □宮本 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
Supramolecular 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 University), 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 嘉治1,2, □宮崎 直幸1,2, □伊藤 新生1, □長谷川 浩司2, □成田 哲博1, □松永 茂1, □亀部 慎治1, □渡辺 正勝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）

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研究科 微生物薬品化学）
Chikara Kaito, Kazuhisa Sekimizu (Grad. Sch. Phar., Univ. Tokyo)
Swimming dynamics and energetics of the spirochete *Leptospira*

Shuichi Nakamura (Grad. Sch. Eng., Tohoku Univ.)

**Mechanical basis for the bacterial swimming and gliding**

Hirofumi Wada (Dep. Phys. Ritsumeikan Univ.)

**The development of new crystallization methods for bio-macromolecular crystallography**

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.

**Growth and characterization of protein crystals using high-strength hydrogels**

Shigeru Sugiyama¹,² (Grad. Sch. Sci., Osaka Univ., JST, ERATO, Lipid Active Structure Project)

**Protein crystallization under microgravity conditions**


**Crystalline Sponge Method: X-ray Analysis without Crystallization on the Microgram Scale**

Makoto Fujita (The University of Tokyo)

**Crystallization methods of membrane proteins**

Takeshi Murata¹,² (Science/Chiba-U, PRESTO/JST)

**Crystallization of membrane proteins using antibody fragments**

So Ivata¹,² (Kyoto Univ. Grad. Sch. Med., RIKEN Spring8 Center)

**Use of symmetric tag to increase the probability of protein crystallization**

Min Yao (Fac. of Adv. Life Sci., Hokkaido Univ.)
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 systems, and finally hope to show a new direction of the researches.

1SCP-01 はじめに
○北畑 裕之（千葉大学院理）
Hiroyuki Kitahata (Grad. Sci. 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？～Duperayt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 抗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 (1Graduate School of Advanced Mathematical Sciences, Meiji University, 2Meiji 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, 市川 正敏, 吉川 研一（1東北大工, 2京大理工, 3同志社大生命医）

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 structure of Marangoni flow and the shape of water chamber
○松田 唯, 中田 聡（広大理工）
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（東京理科大学理工部応用物理学科）
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)
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**

Intermolecular Quinary Interactions Modulate Protein Stability in Living Cells

Gary J. Pielak (University of North Carolina)

**1SDP-02**

NMR relaxation analysis of the protein under macromolecular crowding environment

Hideyasu Okamura, Takanori Kigawa (QBiC, RIKEN)

**1SDP-03**

In-cell NMR analysis for protein conformational diversity in a cell

Kohsuke Inomata (Quantitative Biology Center (QBiC), RIKEN)

**1SDP-04**

Dynamics of intrinsically disordered proteins in living cells

Teppei Ikeya, Jin Inoue, Yutaka Ito (Tokyo Metropolitan University)

**1SEP-01**

CaMKII-induced active Rho GTPases cooperatively work for the establishment of synaptic structural plasticity

Hideji Murakoshi, Yildirim Asli (Michigan State University)
The basis for regulating synaptic strength heterogeneity across the dendrite
Mathieu Letellier, Yukiko Goda (RIKEN Brain Science Institute)

Diffusion barrier in the neuronal axon initial-segment membrane is a molecule-selective filter in the plasma membrane
○楠見 明弘, 宮原 愛美, 藤原 敬弘 (京大・iCeMS, 京大・再生研)
Akihiro Kusumi, Manami S.H. Miyahara, Takahiro K. Fujiwara (iCeMS, Kyoto Univ., Inst. for Frontier Med. Sci., Kyoto Univ.)

Activity-dependent gene expression in learning and memory
Ryang Kim, Mio Nonaka, Nan Yagishita-Kyo, Takashi Kawashima, Masatoshi Inoue, Yuichiro Ishii, Toshihiro Endo, Hajime Fujii, Sayaka Takemoto-Kimura, Hiroyuki Okuno (iCeMS, Kyoto University Graduate School of Medicine, CREST-JST, Medical Innovation Center, Kyoto University Graduate School of Medicine)

The cooperativity of neuronal molecules analyzed with imaging mass spectrometry
Mitsutoshi Setou (Hamamatsu University School of Medicine)

Modeling the dynamical interaction of Hebbian and homeostatic plasticity
Taro Toyoizumi, Megumi Kaneko, Michael P. Stryker, Kenneth D. Miller (RIKEN Brain Sci. Inst., Columbia Univ., UCSF)

The cooperativity of neuronal molecules analyzed with imaging mass spectrometry
Mitsutoshi Setou (Hamamatsu University School of Medicine)
2SAA-04 Targeting Autophagy for Mitochondrial Clearance
Koji Okamoto (Grad. Sch. Frontier Biosci., Osaka Univ.)

2SAA-05 Mechanisms of protein and lipid transport in yeast mitochondria
Toshiya Endo (Fac. Life Sci., Kyoto Sangyo Univ.)

9:00~11:30 B 会場/Room B : Mid-sized Hall 2/2
Joint Symposium with the Japanese Society of Microscopy: Recent Advancement of Electron Microscopy toward Atomic Resolution from Biological Molecules
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 Electron microscopy of C. elegans innexin-6 gap junction channels indicates a characteristic subunit organization
Atsunori Oshima, Tomohiro Matsuzawa, Kazuyoshi Murata, Kouki Nishikawa, Yoshinori Fujiyoshi (CeSPI, Nagoya Univ., Dep. of Biophys., Grad. Sch. Sci., Kyoto Univ., NIPS)

2SBA-02 Structural analysis of the actin filament in vitro and in vivo
Akihiro Narita (Nagoya Univ., 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 Sapovirus capsid structure at 8 Å resolution by single particle cryo-electron microscopy, and homology modeling
Naoyuki Miyazaki, David Taylor, Grant Houseman, Kousuke Murakami, Kazuhiko Katayama, Kazuyoshi Murata (National Institute for Physiological Sciences, National Institute of Infectious Diseases)

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

2SBA-06 Studying integral membrane protein by single particle cryo-EM
Yifan Cheng (Dep. Biochem. Biophys., UCSF)
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 Fukuoka¹, Takashi Sagawa², Yuichi Inoue¹, Hiroto Takahashi¹, Akihiko Ishijima¹ (¹IMRAM, Tohoku Univ., ²Grad. Sch. Life Sci., Tohoku Univ.)

**2SCA-02**  Visualizing stator-protein distributions of bacterial flagellar motors  
Chien-Jung Lo¹,², Tsaiushin Lin¹,² (¹Dept. of Phys., National Central Univ., ²Inst. 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  
Tomoko Miyata¹, Takayuki Kato¹, Yusuke V. Morimoto¹,², Syuichi Nakamura³, Hideyuki Matsunami³, Keiichi Namba¹,² (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²QBiC, RIKEN, ³Grad. Sch. Sci., Osaka Univ., ⁴School of Engineering, Tohoku Univ., ⁵Trans-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  
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.

### 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 智弘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, 3東北大・院農学, 4阪大・生命機能)

### 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 冨子4,5, 平岡 泰4,5, 鷹津 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研究所, 5阪大・理・生物科学)

### 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)
**Hirosi 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, 関根 智1, 小坂田 賢子1, 稲谷 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 Haraguchi1,2,3, Shohei Kobayashi1, Takako Koujin1, Hiroko Osakada1, Tomoko Kojidani1,4, Chie Mori1, Yasushi Hiraoka1,2,3 (1Advanced ICT Res. Inst. Kobe, NICT, 2Grad. Sch. Front. Biosci., Osaka Univ., 3Grad. Sch. Sci., Osaka Univ., 4Japan 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 Iino1,2,3 (1Okazaki Inst. Integ. Biosci., NINS, 2IMS, NINS, 3Dept. 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
○橫山 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 Masaike1,2, Yoshiro Sohma3 (1Dept. Applied Biol. Science, Tokyo Univ. Science, 2PRESTO, JST, 3Dept. 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)

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)
Kunihiro Nishino (JSIR, Osaka Univ.)
Converting a light-driven ion pump into a light-gated ion channel

Yuki Sudo (Div. of Parm. Sci., Okayama Univ.)

Scenario of functions from minority and number fluctuations

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.

Molecular Individuality and Minority in Biology

Tamiki Komatsuzaki (Hokkaido Univ., Res. Inst. Electronic Sci.)

Minority molecules and competitions in a catalytic reaction network

Atsushi Kamimura (Dept. of Basic Science, The Univ. of Tokyo)

Stochasticity in Ca\(^{2+}\) increase in spines enables robust and sensitive information coding

Masashi Fujii\(^1\), Takuya Koumura\(^2\), Hidetoshi Urakubo\(^1\), Shinya Kuroda\(^1,2\) (\(^1\)Dept. Biol. Sci., Grad. Sch. Sci, Univ. Tokyo, \(^2\)Undergrad. Dept. Bioinfo. Syst, Univ. Tokyo)

Heterogeneity in ATP Concentrations in a Single Bacterial Cell Population Revealed by Quantitative Single-cell Imaging

Hideyuki Yaginuma\(^1,2,3\), Shinnosuke Kawai\(^4,5\), Kazuhito Tabata\(^2,6\), Keisuke Tomiyama\(^7\), Akira Kakizuka\(^7\), Tamiki Komatsuzaki\(^7\), 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.)

Single-cell lineage statistics reveals fitness and selection strength for heterogeneous phenotypic states

Takashi Nozoe, Yuichi Wakamoto (Univ. of Tokyo)

Prospect of minority biology

Takeharu Nagai (ISIR, Osaka Univ.)
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.
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 Yura1,2 (Grad. Schl. Hum. Sci., Ochanomizu Univ., NIG)

2SCP-02 From Personal Genome to Personal Proteins: Connection between the Reference sequences of genomic DNA and Proteins
Kengo Kinoshita1,2,3 (Grad Sch Info Sci, Tohoku Univ., Tohoku Medical Megabank, Tohoku Univ., 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-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）

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)

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 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-02 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-03 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・免疫）
Tomonobu Watanabe1,2,3 (1QBIC, RIKEN, 2Grad. Sch. Front. Biosci., Osaka University, 3iFRec, Osaka Univ.)

2SDP-04 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, 2JST・さきがけ）
Yoshiyuki Kageyama1,2 (1Fac. Sci., Hokkaido Univ., 2PRESTO, JST)

2SDP-05 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 理化学）
Ryo Akiyama (Dept. of Chem., Kyushu Univ.)

2SDP-06 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)

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 静惠（阪府大 理 生物）
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 朝一3, 松坂 義哉2,3, 川島 隆太4, 虫明 元5, 石堤 俊6,7,8,9 (東北大学・院生), 2JIST-CREST, 3東北大・院医学, 4東北大・加齢医学研究所)
Hiromu Yawo1,2,3, Yukiobu Yokoyama1,2, Akira Sumiyoshi1,2, Kenta Abe1,2, Kyo Koizumi1,2, Ryo Egawa1,2, Yueren Liu1,2, Tomokazu Ohshiro2,3, Yoshiya Matsuzaka2,3, Ryuta Kawashima4, Hajime Mushiake2,3, Toru Ishizuka1,2, (Tohoku Univ. Grad. Sch. Life Sci., 2JIST-CREST, 3Tohoku Univ. Grad. Sch. Med., 4Tohoku 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, 2JST さきがけ)
Tomonao Matsushita1,2, (Fac. Agri., Kyushu Univ., 2JST PRESTO)

おわりに
○中曾根 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）、薮谷 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（京都大学）、遠藤 政幸（東京工業大学）、瀧ノ上 正浩（京都大学）
Hirohide Saito¹, Masayuki Endo¹, Masahiro Takinoue² (Kyoto Univ., ²Tokyo 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 Koga¹,² (Inst. Mol. Sci. CIMoS, ²JST, PRESTO)

3SBA-02 The conformational change mechanism of the β subunit in F₁-ATPase revealed by all-atom MD simulations
Yuko Ito, Mitsunori Ikekuchi (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)
Remote control of myosin and kinesin motors using light-activated gearshifting

Zev Bryant (Stanford University)

Database for Biology: which data deserve maintaining?

Masanori Arita1,2 (1National Institute of Genetics, 2RIKEN CSRS)
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.
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 Analysis of an unusually stable kinetic refolding intermediate
Hayuki Sugimoto (Fac. Agri. Univ. NIIGATA)

3SEA-02 Kinetics of Chain Condensation during SNAse Folding studied by FRET and ultrarapid mixing methods
Takuya Mizukami1, Ming Xu1, Hong Cheng1, Heinrich Roder1,2, Kosuke Maki3 (1FCCC, 2UPenn, 3Nagoya University)

3SEA-03 Non-sequential structural similarity in the protein world
Shintaro Minami1, Motonori Ota1, George Chikenji2 (1Grad. Sch. of Inf. Sci., Nagoya Univ., 2Grad. Sch. of Eng., Nagoya Univ.)

3SEA-04 The approach to the function-stability tradeoff: A case of the design of a humanized protein mimicking the albumin-binding protein
Satoshi Oshiro1, Shinya Honda1,2 (1Dept. of Medical Genome Sci., Grad. Sch. of Frontier Sci., The Univ. of Tokyo, 2BioMed. Research Inst., AIST)

3SEA-05 The interaction between transcription factors Sp1 and TAF4 via the intrinsically disordered regions
Emi Hibino1, Rintaro Inoue2, Masaki Sugiyama2, Jun Kuhara2, Katsumi Matsuzaki1, Masaru Hoshino1 (1Grad. Pharm., Univ. Kyoto, 2KURRI, 3Fac. of Pharm., Doshisha Univ.)

3SEA-06 Intrinsic disorder under crowded environment: thermodynamic simulation of α-synuclein amyloid fibril formation
Nobuhiro C. Shirai (Grad. Sch. Sci., Kyoto Univ.)