シンポジウム　Symposium

第 1 日目（9 月 16 日（金））／ Day 1(Sep. 16, Fri.)

9:00~11:30　A 会場：7 号館 1 階 講義室 I 【7101】／ Room A: 【7101】

1SA　生命ネットワークのダイナミクスとロバストネス
Dynamics and Robustness in Biological networks

オーガナイザー：守屋 央朗（岡山大），小嶋 誠司（名大）
Organizer: Hisao Moriya (Okayama Univ.), Seiji Kojima (Nagoya Univ.)

With the advent of the post-genomic era, our knowledge about the components and their interactions consisting biological networks has been bursting. However, the components in a biological network are not simply connected, but they flexibly change their partners and the strength of interactions, in order to robustly perform the dynamic function of the network. An important aim of biologists in the next decade is to reveal the design principles of the networks to achieve their dynamics and robustness. In this symposium, we would like to introduce how “systems biology” tries to solve this issue with the talks of 6 invited speakers who have been leading this field.

1SA-01　**Theoretical and experimental approaches to analyze the mechanism of rotational switching in bacterial flagellar motor**
白　凡（Protonic NanoMachine Group, Graduate School of Frontier Biosciences, Osaka University）
Fan Bai[1], Tohru Minamino[1], Jianhua Xing[3], Richard Berry[2], Keiichi Namba[1] ([1]Protonic NanoMachine Group, Graduate School of Frontier Biosciences, Osaka University, [2]Clarendon Laboratory, Department of Physics, University of Oxford, Parks Road, Oxford OX1 3PU, UK., [3]Department of Biological Sciences, Virginia Polytechnic Institute and State University, Virginia, USA)

1SA-02　**Bacterial chemotaxis reveals complexity in cellular organisation and mechanisms for decision making**
Judith Armitage (OCISB, Department of Biochemistry, University of Oxford)

1SA-03　**The regulatory network controlling flagellar assembly dynamics**
Christopher V Rao (University of Illinois at Urbana-Champaign)

1SA-04　酵母細胞システムのロバストネス解析
Robusntess analysis of the yeast cellular system
守屋　央朗（岡山大学異分野融合先端研究コア）
Hisao Moriya (RCIS, Okayama University)

1SA-05　生体分子ネットワークの構造とダイナミクス：既知から未知を予測する
Structure of regulatory networks and dynamics of bio-molecules: Predicting unknown from known
望月　敦史（理研・基幹研, 東工大・総合理工）
Atsushi Mochizuki[1,2], Daisuke Saito[1] ([1]Advanced Science Inst., RIKEN, [2]Interdis. Grad. Sch. Sci. Eng., Tokyo Inst. Tech.)

1SA-06　**Feedback and feed-forward controls of cell cycle transitions**
Attila Csikasz-Nagy (The Microsoft Research-University of Trento)

9:00~11:30　B 会場：7 号館 1 階 講義室 II 【7102】／ Room B: 【7102】

1SB　生命の設計原理を問う
Exploring design principles of life

オーガナイザー：高田 彰二（京大），古賀 信康（ワシントン大）
Organizer: Shoji Takada(Kyoto Univ.), Nobuyasu Koga(Washington Univ.)

Cell is a hierarchical molecular system that has been elaborately designed during evolution. Understanding design principles of the system at each hierarchy - structure and function of protein, interaction network among proteins, modulation of gene expression, genome structure, and etc ? is one of the ultimate goal of biophysics. With the deep understanding of them, it should not be a dream to control life phenomenon by hacking gene networks with tailored proteins. In this symposium, we discuss design principles of life at different levels of the hierarchy from various perspectives of physical chemistry, biochemistry and system biology.

1SB-01　計算機によるタンパク質立体構造のデノボデザイン
Computational De Novo Design of Protein Structures

古賀　信康（ワシントン大・生化）
Nobuyasu Koga[1], Rie Koga (Tatsumi)[1], Gaohua Liu[2], Rong Xiao[2], Gaetano T. Montelione[2], David Baker[1] ([1]Univ. Washington, Dept. Biochem., [2]Mol. Biol. and Biochem., NESG, Rutgers, The State of Univ. NJ)

1SB-02 **Identification of an allosteric site from the analysis of protein fluctuation using NMR**
原田　英里砂（サントリー生科財・生有研）
Erisa Harada[1], Masakazu Sugishima[2,3], Jiro Harada[2], Masato Noguchi[2], Keiichi Fukuyama[4], Kenji Sugase[1] ([1]Bioorg. Res. Inst., Suntory Found. for Life Sci., [2]Dept. of Med. Biochem., Kurume Univ. Sch. of Med., [3]Dept. of Biochem. and Mol. Biol., Univ. of Chicago, [4]Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)

1SB-03 シアノバクテリア概日時計の出力系
Output systems of cyanobacterial circadian clock
小山　時隆（京都大学・理学・植物）
Tokitaka Oyama (Grad. Sch. Sci., Kyoto Univ)

1SB-04 ネットワーク生物学：スイッチ動力学における不均一性
Network Biology: multiple scales and heterogeneities in switching dynamics
笹井　理生（名大・計算理工, 岡崎統合バイオサイエンスセンター）
Masaki Sasai[1,2] ([1]Dept. Comp. Sci. Eng., Nagoya U., [2]Okazaki Inst. Integr. Biosci.)

1SB-05 ミニマム細胞の設計原理：比較ゲノムからのアプローチ
An evaluation of minimal cellular functions to sustain a bacterial cell
太田　元規（名大 院 情科）
Motonori Ota (Nagoya Univ.)

9:00~11:30　C 会場：5 号館 1 階 AV 教室【5101】／Room C: 【5101】
1SC　生体エネルギー代謝酵素の構造と機能　～蛋白質の構造から分子進化・機能変換の履歴をたどることは可能か？～
Structural Features and Molecular Evolution of Bioenergetic Enzymes

オーガナイザー：永野 真吾（鳥取大），日野 智也（鳥取大）
Organizer: Shingo Nagano(Tottori Univ.), Tomoya Hino(Tottori Univ.)

The first living cells on Earth are thought to have arisen more than three billion years ago, and these organisms likely utilize anaerobic respiration which is an ancestral system of aerobic respiration. This symposium seeks to integrate aspects of structure-function relationship with molecular evolution of bioenergetic enzymes. Although hypothesis of molecular evolution of biomolecules is difficult to test, crystal structures of heme copper oxidase superfamily including bacterila nitric oxide reductase (NOR), which is suggested as the urenzyme (ancestral enzyme) of cytochrome oxidases, can provide clues to elucidate the functional conversion of respiratory enzymes. Topics regarding gene regulation of aerobic and anaerobic enzymes and structure of protochlorophyllide reductase that shares common features with nitrogenase are also discussed in this symposium.

1SC-01 硝化細菌の呼吸鎖電子伝達系
The respiratory chains of nitrifying bacteria
福森　義宏（金沢大・理工・自然, 金沢大・バイオ AFM センター）
Yoshihiro Fukumori[1,2] ([1]College Sci. Eng., Kanazawa Univ., [2]Bio-AFM Frontier Research Center, Kanazawa Univ.)

1SC-02 緑膿菌における好気および嫌気呼吸酵素の特徴と遺伝子発現制御
Characterization and regulation of aerobic and anaerobic respiratory enzymes of Pseudomonas aeruginosa
新井　博之（東大院・農生科・応生工）
Hiroyuki Arai (Dept. Biotech., Univ. Tokyo)

1SC-03 一酸化窒素還元酵素の立体構造から探る呼吸酵素の分子進化
Crystal structure of nitric oxide reductase, a key enzyme in the molecular evolution of respiratory complex
日野　智也（鳥取大院・工・化学生物応用, 理研・播磨, JST ERATO, 京大院・医・分子細胞情報学）
Tomoya Hino[1,2,3,4], Yushi Matsumoto[2], Shingo Nagano[1, 2], Hiroshi Sugimoto[2], Yoshihiro Fukumori[5], Takeshi Murata[3, 4], So Iwata[3, 4], Yoshitsugu Shiro[2] ([1]Dept. of Chem. and Biotech., Grad. Sch. Eng., Tottori Univ., [2]RIKEN SPring-8 Center, [3]JST ERATO, [4]Dept. Cell Biol., Grad. Sch. Med., Kyoto Univ., [5]Grad. Sch. Nat. Sci. Tech., Kanazawa Univ.)

1SC-04 末端酸化酵素のプロトンポンプ機構の多様性
Diversity in proton pumping mechanisms of the terminal oxidases
吉川　信也（兵庫県立大学）
Hideo Shimada, **Shinya Yoshikawa** (University of Hyogo)

1SC-05 暗所作動型プロトクロロフィリド還元酵素の結晶構造－蛋白質の構造と分子進化－

X-ray crystal structure of the dark-operative protochlorophyllide oxidoreductase -Evolutionary implications-
栗栖　源嗣（阪大・蛋白研）
Genji Kurisu[1], Yuichi Fujita[2] ([1]Inst. Prot. Res., Osaka Univ., [2]Grad. Sch. Bioarg. Sci., Nagoya Univ.)

9:00~11:30　D 会場：5 号館 1 階 講義室【5103】／ Room D: 【5103】

1SD　タンパク質立体構造の揺らぎと生物機能の関連に NMR 法は何処まで迫れるか？ Dynamical aspects of proteins by NMR

オーガナイザー：嶋田 一夫（東大），甲斐荘 正恒（名大），稲垣 冬彦（北大）
Organizer: Ichio Shimada(Univ. of Tokyo), Masatsune Kainosho(Nagoya Univ.), Fuyuhiko Inagaki(Hokkaidou Univ.)

Biological NMR spectroscopy has become a highly sensitive method for examining the basic structure-function relationships of individual biological macromolecules, as well as probing the supramolecular structures of protein complexes and their inter- and intra-molecular dynamics and catalysis, due to advances in measurement techniques and stable isotope labeling. In this symposium, we will discuss the technological and methodological advances that have facilitated these latest utilizations of NMR, in terms of future applications, techniques, and next-generation methodologies.

はじめに
甲斐荘　正恒（名古屋大学）
Masatsune Kainosho (Nagoya Univ.)

1SD-01　SAIL － NMR 法によるタンパク質動態構造の研究
Dynamic study of proteins by the SAIL-NMR method
武田　光広（名大院・理）
Mitsuhiro Takeda[1], Masatsune Kainosho[1, 2] ([1]Grad. Sch. Sci. Nagoya Univ., [2]Tokyo Metropolitan Univ.)

1SD-02　T 細胞レセプターはダイナミックかつ協同的な 4 次元構造変化により活性化する － NMR および光ピンセット法による解析－
A T-cell receptor quaternary structure change revealed by NMR and optical twizzer is important for T cell activation
竹内　恒（産業技術総合研究所・バイオメディシナル情報研究センター）
Koh Takeuchi (AIST, BIRC)

1SD-03　高圧力ＮＭＲから見る蛋白質の高エネルギー構造の世界
High pressure NMR discloses a rich world of high-energy structures of proteins
北原　亮（立命館大学薬学部）
Ryo Kitahara (College of Pharmaceutical Sciences, Ritsumeikan University)

1SD-04　柔軟なループへの変異で誘導される蛋白質構造ダイナミクスの変調
Protein structural dynamics modulaiton induced by a mutation to flexible loop
楯　真一（広島大学大学院理学研究科数理分子生命理学専攻）
Yuji Wada, Eiji Ohmae, Kunihiko Gekko, **Shin-ichi Tate** (Hiroshima University, MLS)

1SD-05　**Molecular recognition of the C-terminal region of SMRT by SHARP and its dynamical aspect in transcriptional regulation**
三島　正規（首都大学東京 理工学研究科）
Masaki Mishima (Grad. Sch. of Sci and Tech., Tokyo Metropolitan Univ.)

1SD-06　リアルタイムモニタリングによって示された APOBEC3G による DNA 上の極性を有したスライディングとカップルしたシトシン脱アミノ基反応
Coupling between cytidine-deamination by APOBEC3G and its sliding along DNA with polarity as revealed with real-time monitoring by NMR
片平　正人（京大・エネルギー理工学研究所）
Masato Katahira[1], Ayako Furukawa[1], Takashi Nagata[2], Hiroshi Takaku[3], Ryo Morishita[4], Akifumi Takaori[5], Akihide Ryo[6] ([1]Inst. Advanced Energy, Kyoto Univ., [2]Grad. Sch. Nanobio., Yokohama City Univ., [3]Chiba Inst. Tech., [4]CellFree Sci., [5]Grad. Sch. Med., Kyoto Univ., [6]Grad. Sch. Med., Yokohama City Univ.)

1SD-07　リン酸化により誘起されるタンパク質の構造変化と生物学的意義
Phosphorylation induced conformation change and its biological implication
稲垣　冬彦（北海道大学）
Yoshihiro Kobashigawa, Hiroyuki Kumeta, **Fuyuhiko Inagaki** (Hokkaido University)

おわりに
嶋田　一夫（東京大学）
Ichio Shimada (Univ. of Tokyo)

9:00~11:30　F会場：5号館 1階 講義室【5105】／Room F: 【5105】
1SF　細胞を構成する分子の情報ネットワーク
Progress in the understanding of intracellular signaling networks of molecules

オーガナイザー：辰巳 仁史（名大），村田 昌之（東大）
Organizer: Hitoshi Tatsumi(Nagoya Univ.), Masayuki Murata(Univ. of Tokyo)

The aim of this symposium is to introduce recent research progresses in understanding the intracellular signal networks quantitatively, and the possible application of the progresses. It is generally accepted that communication between cells is mediated by extracellular signal molecules. Some signals operate long distances and others signal from the immediate neighbors. Most cells emit and receive signals. Reception of the signal depends on receptor proteins usually on the cell surface. The binding of signaling molecules to receptors activates the receptor, which in turn activates intracellular signal networks. The relay chains of molecules, mainly intracellular signaling proteins, process the signal inside the receiving cell and distribute it to the appropriate intracellular targets, generally effecter proteins. These effectors can be gene regulatory proteins, ion channels, motor proteins and cytoskeletons. Depending on the effectors, cells may proliferate, differentiate, or immigrate, which may lead to forming complex organisms. The progress in understanding the signal networks will allow exciting future experiments in the field of biophysics. In this symposium, we will discuss the future prospects of this field of science.

1SF-01　力刺激で引き起こされる細胞内情報伝達について：力依存的な分子の集合および解離
Mechanical force-induced intracellular signaling: assembly and disassembly of adhesion-related proteins in in vitro conditions
辰巳　仁史（名古屋大学大学院・医学系研究科・細胞生物物理）
Hitoshi Tatsumi (Dept Physiol, Nagoya Univ Sch Med)

1SF-02　細胞の走化性シグナル伝達系の自己組織化による内在的極性形成と勾配認識
Inherent polarity and gradient sensing of the self-organized signaling system in chemotactic cells
柴田　達夫（理化学研究所　発生再生総合科学研究センター）
Tatsuo Shibata (RIKEN Center for Developmental Biology)

1SF-03　**Force coupling in three-dimensional epithelial morphogenesis in Drosophila**
林　茂生（理化学研究所 発生・再生科学総合研究センター）
Shigeo Hayashi (Laboratory for Morphogenetic Signaling, Riken Center for Developmental Biology)

1SF-04　組織形態形成のための３次元細胞モデル
Three-dimensional Cell Model for Tissue Morphogenesis
本多　久夫（兵庫大学健康科学部）
Hisao Honda (Hyogo University)

1SF-05　**Establishment of semi-intact cell resealing technique: Insights into intracellular logistics and signal transductions under disease state**
村田　昌之（東大・院総合文化）
Masayuki Murata, Fumi Kano (Grad. Sch. of Arts and Sci., Univ. of Tokyo)

9:00~11:30　G会場：5号館 2階 講義室【5201】／Room G: 【5201】
1SG　水と ATP がつくる非対称性
Asymmetry produced by water and ATP

オーガナイザー：鈴木 誠（東北大），松林 伸幸（京大）
Organizer: Makoto Suzuki(Tohoku Univ.), Nobuyuki Matubayasi(Kyoto Univ.)

Scope
The binding and hydrolysis of ATP are often exploited to induce uni-directional transport and/or motion. This symposium focuses upon the physical mechanism of the asymmetry brought by ATP. Several talks are presented on the observation and understanding of molecular-level asymmetry both from the experimental and theoretical/computational viewpoints. The materials treated are actomyosin, F1 molecular motor, and ABC transporter. Their chemical/biological functions are all induced with ATP/ADP and likely with water as a “hidden” player controlling the molecular mechanisms. The symposium is discussion-oriented, and is intended to clarify the current status and define the near-future perspective through discussions among the participants.

1SG-01　ＡＴＰ駆動タンパクと非対称性に関する研究のオーバービュー
Overview of studies on ATP-driven proteins and asymmetry
鈴木　誠（東北大学大学院工学研究科材料システム工学専攻）
Makoto Suzuki (Grad. Sch. Eng., Tohoku Univ.)

1SG-02　アクチンフィラメントの一方向的な構造変化：ミオシン力発生機構への関与の可能性
Unidirectional conformational changes of actin filaments: possible implications in force generation by myosin
上田　太郎（産業技術総合研究所 バイオメディカル研究部門）
Kien Xuan Ngo[1], Eisaku Katayama[2], Sosuke Iwai[3], Makoto Suzuki[4], **Taro Uyeda**[1] ([1]Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology, [2]Graduate School of Engineering, Chiba University, [3]Faculty of Education, Hirosaki University, [4]Graduate School of Engineering, Tohoku University)

1SG-03　ＡＴＰ結合とその加水分解によって駆動されるＡＢＣトランスポーターの一方向的構造変化
Unidirectional structure changes of ABC transporters driven by binding of ATP and its hydrolysis
櫻井　実（東京工業大学バイオ研究基盤支援総合センター）
Minoru Sakurai (Center for Biological Resources and Infromatics, Tokyo Institute of Technology)

1SG-04　リニアモーターの１分子計測から観た、揺らぎを制御する分子としての ATP
ATP as a fluctuation regulator of linear motor protein revealed by a single molecule measurements
岩城　光宏（大阪大学大学院医学系研究科）
Mitsuhiro Iwaki (Graduate School of Medicine, Osaka University)

1SG-05　F1 分子モーターの機能発現と非対称構造：理論的考察
Theoretical study on rotational mechanism of F1 molecular motor and asymmetric structures
池口　満徳（横浜市大・院生命ナノ）
Mitsunori Ikeguchi (Grad. Sch. Nanobiosci., Yokohama City Univ.)

1SG-06　ATP 駆動蛋白質の機能発現における水と ATP の共同効果
Cooperative Roles of Water and ATP in Functioning of ATP-Driven Proteins
木下　正弘（京都大学 エネルギー理工学研究所）
Masahiro Kinoshita (Institute of Advanced Energy, Kyoto University)

1SG-07　「水とＡＴＰがつくる非対称性」シンポジウムのまとめと展望
Summary and Near-Future Perspective of the Symposium "Asymmetry Produced by Water and ATP"
松林　伸幸（京都大学化学研究所）
Nobuyuki Matubayasi (Institute for Chemical Research, Kyoto University)

9:00~11:30　H 会場：５号館２階 講義室【5202】／ Room H: 【5202】

1SH　タンパク質の働く姿をみる！～生体分子の可視化最前線～
Visualizing proteins in action -frontiers in biomolecular imaging-

オーガナイザー：鳥羽 栞（阪市大），坂内 博子（理研）
Organizer: Shiori Toba(Osaka City Univ.), Hiroko Bannai(RIKEN, BSI)

Modern biophysics has made great studies in understanding the structure and function of proteins, which play a fundamental role in various biological phenomena. However, for further understanding mechanisms underlying the biological functions of proteins, there remains another important aspect that needs to be understood, that is, visualizing the structure and behavior of proteins “in action”.
How can we visualize proteins that are invisible, flexible and tiny? In this session, we will present frontier biomolecular imaging studies in living cells or in reconstructed cellular situations. We hope to discuss recent developments in imaging techniques and significant findings based on our observation. This symposium will encourage further applications to increase experimental throughput and general approach, and stimulate scientists in these fields.

1SH-01　電子線トモグラフィーを用いた３次元再構成で明らかになった LIS1 による細胞質ダイニンの制御機構
Three-Dimensional Structure Reconstructed by Electron Tomography Revealed How LIS1 Regulate the Motility of the Cytoplasmic Dynein
鳥羽　栞（大阪市大・院医）
Shiori Toba (Dept. Genetic Disease Research, Osaka City Univ. Grad. Sch. of Medicine)

1SH-02　水和した細胞の電子顕微鏡観察
Electron microscopy of amorphous frozen-hydrated cells
岩崎　憲治（大阪大学・蛋白質研究所, CREST,JST）
Kenji Iwasaki[1,2] ([1]Institute for protein research, Osaka University, [2]CREST, JST)

1SH-03　機能中の生体分子の構造と動きを同時観察する高速 AFM
Simultaneous observation of structure and dynamics of functioning bio-molecules by high-speed atomic force microscopy
古寺　哲幸（金沢大学・理工・バイオ AFM 先端研究センター）
Noriyuki Kodera[1], Takayuki Uchihashi[1,2], Toshio Ando[1,2] ([1]Bio-AFM Frontier Research Center, College of Sci. & Eng., Kanazawa Univ., [2]Dept. Math. & Phys., College of Sci. & Eng., Kanazawa Univ.)

1SH-04　磁気共鳴による細胞内蛋白質と細胞の観察手法
Magnetic resonance methods for analyses of structure and dynamics of intracellular proteins and cells
白川　昌宏（京大・工）
Masahiro Shirakawa (Graduate School of Engeneering, Kyoto University)

1SH-05　脳機能を支える膜分子ダイナミクス ー生細胞１分子イメージングにより明らかになったことー
Membrane molecular dynamics supporting brain functions revealed by single molecule imaging in live cells
坂内　博子（理研・脳センター）
Hiroko Bannai[1], Misa Arizono[1,2], Fumihiro Niwa[1,3], Katsuhiko Mikoshiba[1] ([1]RIKEN BSI, [2]Univ Tokyo, Grad Sch Med, [3]Univ Tokyo, Grad Sch Frontier Sci)

9:00~11:30　I会場：5 号館 2 階 講義室【5203】／Room I: 【5203】

1SI　第４世代光源、X 線自由電子レーザーが拓く生物物理学
Biophysics to be explored using the fourth-generation light sources, x-ray free electron lasers

オーガナイザー：城地 保昌（高輝度光科学研究センター），河野 秀俊（日本原子力機構）
Organizer: Yasumasa Joti(JASRI), Hidetoshi Kono(JAEA)

X-ray free electron lasers (XFEL), one of which is under construction at SPring8, are the fourth-generation light source and will provide us short pulse x-ray beams with about one billion brightness than before. The first beam is planed to be commissioned at the beginning of the fiscal year of 2011 and user experiment will start from early 2012. In this symposium, we introduce nature of this new, bright beam and discuss its potential use in biophysical science.

1SI-01　SACLA（SPring-8 Angstrom Compact Free Electron Laser）の現状
Status of SACLA (SPring-8 Angstrom Compact Free Electron Laser)
矢橋　牧名（理化学研究所 放射光科学総合研究センター）
Makina Yabashi (RIKEN SPring-8 Center)

1SI-02　非結晶生体粒子のに対する低温コヒーレントＸ線回折顕微鏡法実験
Coherent X-ray diffraction microscopy of non-crystalline biological particles at cryogenic temperatures
中迫　雅由（慶應義塾大学・物理学科, 理化学研究所・播磨研究所）
Masayoshi Nakasako[1,2], Masaki Yamamoto[2] ([1]Department of Physics, Keio University, [2]RIKEN SPring-8 Center, RIKEN Harima Institute)

1SI-03　**SACLA in Molecular Imaging**
宋　昌容（理研播磨）
Changyong Song (RIKEN SPring-8 Center)

1SI-04　**Visualization of intracellular elements by scanning X-ray fluorescence microscopy**
志村　まり（国立国際医療研究センター・研・難治研）
Mari Shimura[1], Satoshi Matsuyama[2] ([1]Dept of Intractable Diseases, Res Inst, Nat Centr Global Health & Med, [2]Dept of Precision Sci & Tech Grad Sch of Engineering, Osaka Univ)

1SI-05　X-ray FEL を用いた膜蛋白質構造解析
X-ray FEL and membrane protein crystallography
岩田　想（京都大学大学院医学研究科分子細胞情報学）
So Iwata (Dep. Cell Biology, Grad. School of Med., Kyoto Univ.)

1SI-06　**Biophysical Imaging with Coherent X-rays**
Keith A Nugent[1,2] ([1]School of Physics, The University of Melbourne, [2]ARC Centre of Excellence for Coherent X-ray Science)

9:00~11:30　K会場：4号館 1階 講義室【4113】／Room K: 【4113】

1SK　高速計算機シミュレーションによる生体機能解析へのアプローチ
High Performance Computational Approaches to Biological Functions

オーガナイザー：中村 春木（阪大），木寺 詔紀（横浜市大），江口 至洋（理化学研究所）
Organizer: Haruki Nakamura(Osaka Univ.), Akinori Kidera(Yokohama City Univ.), Yukihiro Eguchi(RIKEN)

With rapid progress of computation technology, lots of computer simulation approaches have been developed for understanding of the complicated biological processes in integrated manner. Recent multi-scale studies will be introduced for the multi-levels from genes, molecules, cells, organs, to a body by the active researchers in many different fields. In addition, the future prospect will be discussed in this symposium.

1SK-01　マルチコピー・マルチスケール分子動力学シミュレーションプログラム開発のためのクラスライブラリ
A class library for developing multi-copy, multi-scale molecular dynamics simulation programs
寺田　透（理研 CSRP, 東大院農）
Tohru Terada[1,2], Yasuhiro Matsunaga[1,3], Kei Moritsugu[1], Akinori Kidera[1,4] ([1]CSRP, RIKEN, [2]Grad. Sch. Agri. Life Sci., Univ. Tokyo, [3]AICS, RIKEN, [4]Dept. Supramol. Biol., Yokohama City Univ)

1SK-02　タンパク質透過装置 Sec トランスロコンの分子動力学シミュレーション
Molecular dynamics simulations for the protein secretory pathway
森　貴治（理化学研究所 生命システム研究センター）
Takaharu Mori[1], Yuji Sugita[1,2,3] ([1]RIKEN QBiC, [2]RIKEN AICS, [3]RIKEN ASI)

1SK-03　創薬における結合自由エネルギー計算法
Absolute binding free energy calculation for drug development
藤谷　秀章（東大・先端研）
Hideaki Fujitani (RCAST, The University of Tokyo)

1SK-04　スパコンで焙り出すがんのシステム
Uncovering Systems in Cancer by Supercomputer
宮野　悟（東大・医科研）
Satoru Miyano (Institute of Medical Science, U. Tokyo)

1SK-05　統計的学習法を用いた神経スパイクデータからのシナプス結合推定
A statistical learning method for identifying synaptic connections from spike train data
吉本　潤一郎（沖縄科学技術研究基盤整備機構, 奈良先端科学技術大学院大学）
Junichiro Yoshimoto[1,2], Kenji Doya[1,2] ([1]Okinawa Institute of Science and Technology, [2]Nara Institute of Science and Technology)

1SK-06　ヒトとマウスの筋骨格モーフィングと筋張力解析
Musculoskeletal Morphing from Human to Mouse and Muscle Tension Analysis
池上　洋介（東京大学情報理工学研究科）
Yosuke Ikegami[1], Akihiro Yoshimatsu[1], Ko Ayusawa[1], Satoshi Oota[2], Yoshihiko Nakamura[1] ([1]Mechano-Informatics, The University of Tokyo, [2]BioResource Center, RIKEN)

9:00~11:30　L会場：4号館 2階 講義室【4211】／Room L: 【4211】

1SL　光合成研究で何が明らかにされ、これから何をできるか？ ～光合成研究の最先端とエネルギー創製研究の現状～
The leading edge of photosynthesis research and energy creation

オーガナイザー：杉浦 美羽（愛媛大），天尾 豊（大分大）
Organizer: Miwa Sugiura(Ehime Univ.), Yutaka Amao(Oita Univ.)

Recently, the photosynthesis mechanism in molecular level has been rapidly clarified. The development of the artificial photosynthesis system for the low carbon fuel production also began to look practicable as the clarification of photosynthesis mechanism. This symposium covers the elucidation of photosynthesis mechanism, the theory of artificial photosynthesis, photoreduction of carbon dioxide, and the low carbon fuel production with functional photocatalyst. In this symposium, it is a purpose that photosynthesis researcher discusses the leading edge of photosynthesis research and the low carbon energy creation.

1SL-01　光合成研究の最前線と課題
The present of photosynthesis research
杉浦　美羽（愛媛大・無細胞センター）
Miwa Sugiura (Cell-Free Sci. and Tec. Res. Cent., Ehime Univ.)

1SL-02　光合成水分解を可能にする光化学系Ⅱの原子構造
Atomic structure of photosystem II that enables photosynthetic water-splitting
沈　建仁（岡山大学大学院自然科学研究科(理)）
Jian-Ren Shen[1], Yasufumi Umena[2], Keisuke Kawakami[3], Nobuo Kamiya[3] ([1]Graduate School of Natural Science and Technology, Okayama University, [2]Institute for Protein Research, Osaka University, [3]The OCU Advanced Research Institute for Natural Science and Technology (OCARINA), Osaka City University)

1SL-03　「光化学系 II の電荷分離反応 ： P680 から D1 ブランチへ
Electron transfer in the D1 branch of Photosystem II
石北　央（京都大学 生命科学系キャリアパス形成ユニット, JST さきがけ）
Hiroshi Ishikita[1,2], Keisuke Saito[1] ([1]Kyoto University, Career-Path Promotion Unit for Young Life Scientists, [2]JST PRESTO)

1SL-04　分光電気化学計測によって得られた酸化還元電位を基にした光化学系 II のエネルギー論
Energetics within photosystem II based on redox potentials revealed by spectroelectrochemistry
加藤　祐樹（東京大学生産技術研究所）
Yuki Kato, Tadashi Watanabe (Institute of Industrial Science, the University of Tokyo)

1SL-05　**The role of Ca^{2+} and Cl^{-} in the Photosystem II water oxidation**
Alain Boussac[1], Miwa Sugiura[2], Naoko Ishida[1], Fabrice Rappaport[3] ([1]iBiTec-S, CEA Saclay/CNRS, [2]Cell-Free Science and Technology Research Center, Ehime University, [3]IBPC)

1SL-06　光化学系 II 酸素発生錯体モデルとしてのジμ-オキソ二核マンガン錯体の電子構造と不均一系触媒活性
Catalytic activities for heterogenous water oxdiatiom and electic structures of di-μ-oxo dinuclear complexes as a synthetic OEC model
八木　政行（新潟大学）
Masayuki Yagi (Niigata University)

1SL-07　**Development of bio-inspired photocatalytic water splitting systems toward solar hydrogen production**
阿部　竜（北海道大学触媒化学研究センター）
Ryu Abe (Catalysis Research Center, Hokkaido University)

1SL-08　遷移金属錯体を用いた人工光合成システム
Artificial Photosynthesis using Transition Metal Complexes
石谷　治（東京工業大学）
Osamu Ishitani (Tokyo Institute of Technology)

おわりに
天尾　豊（大分大学・工学部）
Yutaka Amao (Oita University)

8:50~11:30　M 会場：4 号館 4 階 講義室【4401】／ Room M: 【4401】

1SM　異分野融合する 1 分子研究：コンフォートゾーンを深めて超えて
Interdisciplinary research around single molecule studies; delving into and going beyond comfort zone

オーガナイザー：政池 知子（学習院大），林 久美子（東北大）
Organizer: Tomoko Masaike(Gakushuin Univ.), Kumiko Hayashi(Tohoku Univ.)

"In-depth researches and their fusion" is the theme of this symposium. The organizers T. M. and K. H. believe that both delving into and going beyond research fields are the keys to advancement of science. The encounter of the organizers itself embodies this idea; T. M. has learned biochemistry and has involved in single-molecule studies. Meanwhile, K. H. has studied theoretical physics and is applying it to single-molecule studies. The organizers are trying to combine their researches and explore a new research field. In this symposium, they wish to promote encounters of researchers in different fields by inviting people who delve into and go beyond their comfort zones. Researches around single-molecule studies are discussed from the viewpoints of biochemistry, protein biosynthesis, syntheic chemistry, statistical mechanics, protein simulation, neuroscience, and fluid mechanics.

1SM-01　F_1-ATPase と繊毛軸糸をモデルとした、酵素とその集合体の動きの可視化
F_1-ATPase and ciliary axonemes as models of imaging motions in enzymes and their assemblies
政池　知子（学習院大・理・物理）
Tomoko Masaike[1], Koji Ikegami[2], Mitsutoshi Setou[2], Takayuki Nishizaka[1] ([1]Dept. Physics, Fac. Sci., Gakushuin Univ., [2]Dept. of Cell Biology and Anatomy, Hamamatsu Univ. School of Medicine)

1SM-02　次世代１分子計測技術を用いたコドン分解能レベルのタンパク質翻訳リアルタイム可視化
Real time visualization of translation at codon resolution by next generation single molecule studies
上村　想太郎（理化学研究所横浜研究所オミックス基盤研究領域）
Sotaro Uemura (RIKEN Omics Science Center)

1SM-03　人工分子の分子内回転のリアルタイム一分子計測
Real-Time Single-Molecular Measurement of Artificial Molecular Rotor
池田　朋宏（東京大学大学院工学系研究科応用化学専攻）
Tomohiro Ikeda[1], Masayuki Takeuchi[2], Ryota Iino[1], Hiroyuki Noji[1,3] ([1]Department of Applied Chemistry, the University of Tokyo, [2]National Institute for Materials Science, [3]JST-CREST)

1SM-04　**Studying molecular motors with optical and magnetic tweezers**
Maria Manosas[1,2], Senthil Perumal[3], Steve Benkovic[3], Felix Ritort[2], Vincent Croquette[1] ([1]ENS Paris, [2]Dept. Phys., Univ. Barcelona, [3]Dept. Chem., Pennsylvania State Univ.)

1SM-05　**Functional Membrane Protein Dynamics**
Morten Jensen (D. E. Shaw Research)

1SM-06　シナプス内信号伝達、２光子励起蛍光寿命イメージング、神経生物科学 "単一シナプスにおける信号伝達の可視化"
Signaling in synapses, Neurobiology, 2-photon Fluorescence Lifetime Imaging “Signal transduction in single dendritic spines”
安田　涼平（デューク大学医療センター, ハワード・ヒューズ医学研究所）
Ryohei Yasuda[1,2] ([1]Duke University Medical Center, [2]Howard Hughes Medical Institute)

1SM-07　構造変化と流れが生み出す機能
Functions generated by the structural change and the associated flow
飯間　信（広島大学理学研究科数理分子生命理学専攻, JST CREST）
Makoto Iima[1,2] ([1]Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, [2]JST CREST)

1SM-08　揺らぎの定理による生体モーターの駆動力測定
Fluctuation theorem applied to bio-motors
林　久美子（東北大・工・応物）
Kumiko Hayashi (Sch. Eng., Appl. Phys., Tohoku Univ.)

9:00~11:30　Q 会場：書写紀念会館 1 階 会議室／ Room Q: Shosha Kinen Kaikan 1F Conference Room

1SQ　日本生物物理学会－イスラエル生物物理学会合同シンポジウム“タンパク質動力学－－分子から細胞まで”
Israel-Japan Joint Symposium on Biophysics “Protein Dynamics: From single molecules to whole cell”

オーガナイザー：Irit Sagi（Weizman Institute），片岡 幹雄（奈良先端大）
Organizer: Irit Sagi(Weizman Institute), Mikio Kataoka(NAIST)

To deepen the mutual friendship and scientific exchange between Israel and Japan Biophysical Societies, we would like to have a joint symposium. We chose protein dynamics as a main theme, because the understanding of dynamical properties of proteins is essential for the elucidation of fundamental processes in biological functions. Both countries have been contributed to the field significantly both experimentally and theoretically. The frontiers of the fields are introduced by top researchers in both countries.

1SQ-01　**Folding and Dynamics of Globular Proteins Studied by time resolved FRET Methods**
Elisha Haas (Bar Ilan University)

1SQ-02　微小管上の分子モーターの振る舞い：１分子、数分子、多分子モーターの運動特性
Behaviors of motor proteins on microtubule as single, several and many molecules
豊島　陽子（東京大学・総合文化研究科・生命）
Yoko Toyoshima[1], Ken’ya Furuta[2], Keitaro Shibata[1] ([1]Dept. of Life Sciences, The University of Tokyo, [2]Bio ICT Lab, NICT)

1SQ-03　**Structure and Intermolecular interactions of bio-molecular self-assemblies**
Uri Raviv (The Hebrew University of Jerusalem)

1SQ-04　プリオンダイナミクスと論理的創薬
Prion Dynamics and Logical Drug Design

桑田　一夫（岐阜大学）
Kazuo Kuwata (Gifu Univ.)

1SQ-05 **Anchors and Cavities in Protein Recognition**
Miriam Eisenstein (Weizmann Institute of Science)

1SQ-06 「化学的特殊性と物理的一般性を併せ持つ理論による生命現象の探求」
Exploring life phenomena with a theory featuring chemical "specificity"
平田　文男（分子科学研究所）
Fumio Hirata (Institute for Molecular Science)

第２日目（９月 17 日（土））／ Day 2(Sep. 17, Sat.)

8:50~11:30　A 会場：７号館 1 階 講義室 I 【7101】／ Room A: 【7101】
2SA　若手研究者が拓く光生物物理学
Photobiophysics promoted by young scientists

オーガナイザー：須藤 雄気（名大），増田 真二（東工大）
Organizer: Yuki Sudo(Nagoya Univ.), Shinji Masuda(Tokyo Inst. of Tech.)

Light is one of the most important energy sources and signals providing critical information to biological systems. The biological responses are regulated by respective photoreceptors. In this symposium, the molecular mechanisms of photo-signal conversion will be discussed. In addition, we will also focus on visualization and control of the biological phenomena in living cells by utilizing photoactive proteins. Six young researchers will present their own recent works based on biophysical approaches with brief introduction by a leader in photochemistry and photobiophysics.

2SA-01 **What should we learn from laser photochemistry of supramolecules? Cooperative photochemical dynamics in biological systems?**
増原　宏（奈良先端科学技術大学院大学 物質創成科学研究科）
Hiroshi Masuhara (Nara Institute of Science and Technology)

2SA-02 センサリーロドプシンから何を学ぶべきか？：光情報伝達メカニズムとその利用
What should we learn from sensory rhodopsins?: Signal transfer mechanism and its application for protein expression
須藤　雄気（名大・院理, 科学技術振興機構・さきがけ）
Yuki Sudo[1,2], Michio Homma[1] ([1]Grad. Sch. of Sci.. Nagoya Univ., [2]JST/PRESTO)

2SA-03 動物のオプシン類の多様化から何を学ぶか？：脊椎動物における新規紫外光受容システム
What should we learn from animal opsin diversification? Novel UV light-sensing system in vertebrates
山下　高廣（京大・院理・生物物理）
Takahiro Yamashita (Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.)

2SA-04 **What should we learn from BLUF proteins? Light perception and signal transduction**
増田　真二（東京工業大学 バイオ研究基盤支援総合センター）
Shinji Masuda (Center for BioRes. & Inform., Tokyo Inst. Tech.)

2SA-05 **The LOV/PAS-fold: what should we learn?**
人見　研一（スクリプス研究所, ローレンスバークレー国立研究所）
Kenichi Hitomi[1,2], John M. Christie[1,3], John A. Tainer[1,2], Elizabeth D Getzoff[1] ([1]The Scripps Research Institute, [2]Lawrence Berkeley National Laboratory, [3]University of Glasgow)

2SA-06 **What should we learn about concerning the color change of firefly bioluminescence?**
安東　頼子（北大院・医）
Yoriko Ando[1], Yu Wang[2], Yuhei Hayamizu[3], Miyabi Hiyama[4], Hidehiro Kubota[5], Nobuaki Koga[4], Hidefumi Akiyama[2] ([1]Grad. Sch. Med., Hokkaido Univ., [2]ISSP, Univ. of Tokyo, [3]GEMSEC, Univ. of Wasington, [4]Grad. Sch. Info. Sci., Nagoya Univ., [5]ATTO Co., Ltd.)

2SA-07 **What should we learn from light emitting organisms? Efficient energy transfer and its application for bioimaging**
永井　健治（北海道大学電子科学研究所ナノシステム生理学研究分野）
Takeharu Nagai (Research Institute for Electronic Science, Hokkaido University)

9:00~11:30　B 会場：7 号館 1 階 講義室Ⅱ【7102】／Room B: 【7102】

2SB　In-cell biophysics のための chemical biology 最前線
Frontiers in chemical biology for in-cell biophysics

オーガナイザー：松崎 勝巳（京大），菊池 和也（阪大）
Organizer: Katsumi Matsuzaki(Kyoto Univ.), Kazuya Kikuchi(Osaka Univ.)

Detection of the conformations, dynamics, and intermolecular interactions of biomolecules in living cells is a dream of biophysicists. Recent advances in instrumentation, such as the development of spectrum-imaging and lifetime-imaging fluorescence microscopy, is making this dream come true. At the same time, emerging techniques in chemical biology for this purpose cannot be overlooked. This symposium introduces novel methods in chemical biology for in-cell biophysics, such as the specific labeling of target molecules, e.g., proteins, and their delivery into cells. Furthermore, strategies for the tempo-spatial control of their intracellular localization are also presented.

2SB-01　新規膜タンパク質蛍光標識技術を用いた受容体の挙動解析
Behaviors of receptors as analyzed by novel fluorescence labeling method for membrane proteins
松崎　勝巳（京都大学大学院薬学研究科）
Katsumi Matsuzaki (Graduate School of Pharmaceutical Sciences, Kyoto University)

2SB-02　スイッチ機能を有した化学プローブのデザイン・合成によるマルチモードイメージング
DESIGN, SYNTHESIS AND BIOLOGICAL APPLICATION OF MOLECULAR IMAGING PROBES WITH TUNABLE CHEMICAL SWITCHES
菊地　和也（大阪大学大学院工学研究科, 大阪大学免疫学フロンティア研究センター）
Kazuya Kikuchi[1,2] ([1]Graduate School of Engineering, Osaka University, [2]IFReC, WPI-Osaka University)

2SB-03　細胞内送達ツールとしての膜透過ペプチド
Cell-penetrating peptides as a tool for intracellular delivery
二木　史朗（京都大学化学研究所）
Shiroh Futaki (Institute for Chemical Research, Kyoto University)

2SB-04　刺激応答型プロセッシングデバイスを利用した核－細胞質移動ペプチドの創製
Development of nucleocytoplasmic shuttle peptide using stimulus-responsive processing device
大高　章（徳島大院・ヘルスバイオサイエンス研究部）
Akira Otaka, Akira Shigenaga (Inst. Health Bio. Sci. Univ. Tokushima)

2SB-05　光応答性ヌクレオチドの設計と合成
Design and synthesis of caged nucleotides
古田　寿昭（東邦大・理）
Toshiaki Furuta (Fac. Sci., Toho Univ.)

9:00~11:30　C 会場：5 号館 1 階 AV 教室【5101】／Room C: 【5101】

2SC　一個体イメージング
Whole body imaging

オーガナイザー：中川 将司（兵庫県大），八田 公平（兵庫県大）
Organizer: Masashi Nakagawa(Univ. of Hyogo), Kohei Hatta(Univ. of Hyogo)

Life science has progressed at different levels including molecules, cells and tissues. However, our ultimate goal is to understand the mechanism of life in intact animals by revealing molecular functions and cellular dynamics at the same time. In this symposium, five presenters introduce their unique studies by using whole body imaging of small animals: ascidian, fruitfly and zebrafish that may not be familiar to most biophysicists. We hope that active discussion would lead to innovative studies in the future.

2SC-01　カタユウレイボヤ尾芽胚全体の 1 細胞レベルイメージングと 3D コンピュータ・モデリングによる形態解析
Imaging of normal tailbud-stage *Ciona intestinalis* embryo at single cell level and Analysis of anatomy by constructing 3D Virtual Embryo
堀田　耕司（慶大・理工・生命情報）
Kohji Hotta, Mitsuru Nakamura, Jun Terai, Reiko Ohkubo, Kotaro Oka (Dept. of Sci. & Tech., Keio Univ.)

2SC-02　細胞分裂と形態形成の協調：神経管閉鎖過程における伸長化した G2 期の役割
Coordination of mitosis and morphogenesis: Role of a prolonged G2 phase during chordate neural tube closure

小椋　陽介（筑波大学下田臨海実験センター）
Yosuke Ogura[1], Asako Sakaue-Sawano[2,3], Masashi Nakagawa[4], Nori Satoh[5], Atsushi Miyawaki[2,3], Yasunori Sasakura[1] ([1]Shimoda Marine Research Center, University of Tsukuba, [2]RIKEN Brain Science Institute, [3]ERATO, JST, [4]Graduate School of Life Science, University of Hyogo, [5]Marine Genomics Unit, OIST)

2SC-03　光変換型蛍光タンパク質 Kaede を用いたホヤの変態過程における中枢神経系の追跡
Tracing of the central nervous system of ascidian larva during metamorphosis with photoconvertible fluorescent protein, Kaede
堀江　健生（筑波大学・下田臨海実験センター）
Takeo Horie, Yasunori Sasakura (Shimoda Marine Research Center, University of Tsukuba)

2SC-04　器官形成を支える細胞機能の動的解析
Imaging analysis of cellular dynamics for organogenesis
倉永　英里奈（理化学研究所 CDB 組織形成ダイナミクス研究チーム）
Erina Kuranaga (Lab. Histogenetic Dynamics, RIKEN CDB)

2SC-05　単純な脊椎動物における神経構造・発生・機能のイメージング
Imaging of structure, development and function of nervous system in a simple vertebrate
八田　公平（兵庫県立大学大学院生命理学研究科）
Kohei Hatta, Shinichi Okamoto, Masashi Nakagawa, Takanori Ikenaga, Tamami Yamamoto, Yohei Nakajima, Mariko Itoh (Graduate School of Life Science, University of Hyogo)

9:00~11:30　D 会場：5 号館 1 階 講義室【5103】／ Room D: 【5103】
2SD　量子構造生物学の出発
Sail on, Quantum Structural Biology

オーガナイザー：吉川 信也（兵庫県大），三木 邦夫（京大），舘野 賢（兵庫県大）
Organizer: Shinya Yoshikawa(Univ. of Hyogo), Kunio Miki(Kyoto Univ.), Masaru Tateno(University of Hyogo)

Life phenomenon is a set of chemical reactions driven by proteins. Thus, elucidation of the mechanisms of protein functions as the chemical reaction processes is equivalent to understanding of the mechanism of Life. For investigation of these protein functions as the chemical reactions, the locations and the chemical reactivity of all the atoms comprising the reaction centers of the proteins must be determined by crystallographic and infrared analyses. For this purpose, the resolution must be better than hydrogen-atom level and a time-resolved infrared facility applicable for the protein system under physiological (aqueous) conditions. We define “Quantum Structural Biology” as a research field aiming for decribing the functions of proteins as the behavior of valence electrons for understanding what is Life. While, except for a few examples, the present resolution and sensitivity of both crystallographic and infrared analyses are far lower than “Quantum Structural Biological” levels, some groups have been challenging for many years for founding the “Quantum Structural Biology”. This symposium is for discussion on how we should let “Quantum Structural Biology” sail on!

2SD-01　タンパク質機能の量子構造生物学的理解：チトクロム酸化酵素による事例研究
Introduction: cytochrome c oxidase, a case study towards quantum structural biological understanding of protein functions
吉川　信也（兵庫県立大学）
Shinya Yoshikawa (University of Hyogo)

2SD-02　中程度の分解能で如何にしてアミノ酸側鎖のイオン化状態を決定するか
How to determine ionization states of amino acid residues by X-ray diffraction method at medium resolution
月原　冨武（兵庫県立大学大学院・生命理学研究科・ピコバイオロジー研究所, 大阪大学蛋白質研究所）
Tomitake Tsukihara[1,2] ([1]Graduate School of Life Science, University of Hyogo, [2]Institute for Protein Research, Osaka University)

2SD-03　タンパク質における外殻電子形状の観察を可能にする超高分解能結晶構造解析
Ultra-high resolution crystallography for visualizing outer-shell electrons in proteins
竹田　一旗（京都大学大学院理学研究科）
Kazuki Takeda, Yu Hirano, Kunio Miki (Graduate School of Science, Kyoto University)

2SD-04　水溶液中の蛋白質の高感度時間分解赤外分光解析
High-sensitivity time-resolved infrared analyses of proteins, functioning in aqueous solution
久保　稔（兵庫県立大学 大学院生命理学研究科 ピコバイオロジー研）
Minoru Kubo (Picobiology Inst., Grad. Sch. Life Sci., Univ. Hyogo)

2SD-05　生体高分子の機能メカニズムを解明するための量子構造生物学の創出
Theoretical and computational quantum structural biology for understanding functional mechanisms of biological macromolecular systems
舘野　賢（兵庫県立大学）
Masaru Tateno[1], Jiyoung Kang[2], Ryo Nakaki[2] ([1]University of Hyogo, [2]University of Tsukuba)

2SD-06　量子構造生物学の創成に向けて
Creation and Future Evolution of Quantum Structural Biology
三木　邦夫（京都大学大学院理学研究科化学専攻）
Kunio Miki (Department of Chemistry, Graduate School of Science, Kyoto University)

9:00~11:30　F会場：5号館 1階 講義室【5105】／Room F: 【5105】

2SF　分子ロボティクスの勃興：人工分子複合体や分子相互作用ネットワークを設計して創って動かす
Emergence of molecular robotics: designing, creating, and driving of artificial molecular complex systems and interaction networks

オーガナイザー：小宮 健（東工大），瀧ノ上 正浩（東工大），野村 慎一郎（東北大）
Organizer: Ken Komiya(Tokyo Inst. of Tech.), Masahiro Takinoue(Tokyo Inst. of Tech.), Shinichiro M Nomura(Tohoku University)

Living organisms are “soft robots” exhibiting hierarchically organized architectures built with molecules as nanometer-scale construction materials. As a consequence of self-organizing and cooperative behaviors by molecules, a number of sophisticated functions of systems are achieved; the functions are specific to living organisms such as self-replication and autonomous motion. The living systems are, thus, expected to have an unknown operation principle that is significantly different from one adopted so far in artificial hard robots or machine systems at macro-scale. However, it may not be sufficient that conventional approaches based only on measurement and description for uncovering the unknown operation principle or achieving artificial molecular systems that can operate in a biological environment.
In this symposium, we discuss synthetic approaches that utilize various materials and technologies, each at a distinct scale, to design, create and drive complex molecular systems consisting of cells and/or biomolecules. For providing a useful guideline to attain a sophisticated system’s function, the novel methodologies to construct elementary devices and integrate them are presented from the viewpoint of “molecular robotics.” Such a synthetic approach, stepping further from the limited construction of a single molecular device by modifying biomolecules, should open the door for a novel biophysical research.

2SF-01　**Building complex dynamic behaviors in a tube**
Adrian Padirac[1], Kevin Montagne[1], Raphael Plasson[2], Teruo Fujii[1], Yannick Rondelez[1] ([1]LIMMS/CNRS-IIS, Institute of Industrial Science, the University of Tokyo, [2]Department of Applied Chemistry, Faculty of Science and Technology, Keio University)

2SF-02　無細胞タンパク質合成システムの自己複製に向けた tRNA およびリボソームの再構成
Reconstitution of tRNA and the ribosome for the self-replication of a cell-free protein synthesis system
清水　義宏（理化学研究所 生命システム研究センター）
Yoshihiro Shimizu (RIKEN Quantitative Biology Center (QBiC))

2SF-03　細胞内空間ダイナミクスを理解するために細胞モデルを構築する
Constructing Cell Model, to Study the Spatial Organization of the Cell
木村　暁（国立遺伝学研究所・細胞建築研究室, 総研大・遺伝学専攻）
Yuki Hara[1], **Akatsuki Kimura**[1,2] ([1]Cell Architecture Lab, National Institute of Genetics, [2]Dept. Genetics, SOKENDAI)

2SF-04　マランゴニ効果による液滴の運動
Spontaneous motion of a droplet through Marangoni effect
北畑　裕之（千葉大院理, JST さきがけ）
Hiroyuki Kitahata[1,2], Natsuhiko Yoshinaga[3], Ken Nagai[4], Yutaka Sumino[5] ([1]Grad. Scl. of Sci., Chiba Univ., [2]PRESTO, JST, [3]Fukui Insititute, Kyoto Univ., [4]Grad. Scl. of Sci., Univ. of Tokyo, [5]Aichi Univ. of Educ.)

2SF-05　バイオ構造システム工学―生物学的解析のための複合生体組織システムの構築―
Bio-Architectural System Engineering: Fabrication of 3D Complex Tissues for Biological Analysis
松永　行子（東京大学生産技術研究所, JST, さきがけ）
Yukiko T. Matsunaga[1,2] ([1]Institute of Industrial Science, The University of Tokyo, [2]PRESTO, JST)

9:00~11:30　G 会場：5 号館 2 階 講義室【5201】／Room G: 【5201】

2SG　生命分子の揺らぎを探る新たなアプローチ
New approaches for probing biomolecular fluctuations

オーガナイザー：加藤 晃一（岡崎統合バイオ），芳坂 貴弘（北陸先端大）

Organizer: Koichi Kato(National Inst. of Natural Sci.), Takahiro Hohsaka(Japan Advanced Inst. of Sci. and Tech.)

It is being revealed that structural fluctuations of biomolecules such as proteins, nucleic acids, sugar chains, and membrane lipids play important roles in expression of various biological functions. In this symposium, we will focus on new approaches for probing the biomolecular fluctuations, which enable us to detect and control such fluctuations and also to explore the relationships between the molecular fluctuations and biological functions. The frontier researchers who are currently investigating biomolecular fluctuations using various methods including nuclear magnetic resonance (NMR), fluorescence resonance energy transfer (FRET), protein engineering, single-molecule measurement, and molecular simulation, will review current, cutting-edge knowledge on the topic and future perspectives in the fields of molecular science of fluctuations toward biological functions.

2SG-01　ユビキチン-プロテアソームシステムにおけるオリゴマータンパク質の構造揺らぎ
Conformational fluctuations of oligomeric proteins involved in the ubiquitin-proteasome system

加藤　晃一（自然科学研究機構・岡崎統合バイオサイエンスセンター, 名古屋市立大学・大学院薬学研究科）

Koichi Kato[1,2] ([1]Okazaki Institute for Integrative Bioscience, National Institutes of Natural Sciences, [2]Graduate School of Pharmaceutical Sciences, Nagoya City University)

2SG-02　ライン型共焦点顕微鏡によるタンパク質フォールディングや基質結合過程のサブミリ秒ダイナミクス
Submillisecond dynamics of protein folding and ligand binding detected by the line conforcal microscopy

高橋　聡（東北大・多元研）

Hiroyuki Oikawa[1], Kiyoto Kamagata[1], Issei Iijima[2], Takahiro Hohsaka[2], Yoshihiro Sambongi[3], **Satoshi Takahashi**[1] ([1]IMRAM, Tohoku Univ., [2]Sch. Material Sci., JAIST, [3]Grad. Sch. Biospare Sci., Hiroshima Univ.)

2SG-03　系統的アミノ酸置換によるタンパク質の揺らぎ問題への挑戦
Tackling the protein fluctuation problem by systematic amino acid substitutions

新井　宗仁（東大・院総合文化・生命環境）

Munehito Arai (Dept. Life Sci., Univ. Tokyo)

2SG-04　脂質・DNA 複合体の動的構造と細胞内核酸送達能
Polyamine-lipid/DNA complex (lipoplex) for nucleic acid delivery: Relationship between metamorphosis of lipoplex and its function

出羽　毅久（名古屋工業大学大学院未来材料創成工学専攻）

Takehisa Dewa[1], Kiyoshi Kato[1], Yusuke Kouzuma[1], Yousuke Okita[1], Yugo Urita[1], Tomohiro Asai[2], Naoto Oku[2], Mamoru Nango[1] ([1]Department of Frontier Materials, Graduate School of Engineering, Nagoya Institute of Technology, [2]University of Shizuoka Graduate School of Pharmaceutical Sciences)

2SG-05　QM/MM reweighting 自由エネルギー SCF 法による酵素反応分子機構の解析
Molecular mechanism of enzymatic reaction studied by the QM/MM reweighting free energy SCF method

林　重彦（京都大学大学院理学研究科化学専攻）

Shigehiko Hayashi, Takahiro Kosugi (Department of Chemistry, Graduate School of Science, Kyoto University)

2SG-06　天然揺らぎ構造の蛋白質折りたたみへの関与
Change of apomyoglobin folding intermediate by engineering the natively disordered F helix

西村　千秋（帝京平成大学薬学部）

Chiaki Nishimura (Fac. of Pharma. Sci., Teikyo Heisei Univ.)

2SG-07　タンパク質の揺らぎ研究への非天然アミノ酸導入技術の応用
Application of nonnatural amino acid mutagenesis to proving protein fluctuations

芳坂　貴弘（北陸先端科学技術大学院大学）

Takahiro Hohsaka (Japan Advanced Institute of Science and Technology)

9:00~11:30　H 会場：5 号館 2 階 講義室【5202】／Room H: 【5202】

2SH　膜タンパク質の構造変化を研究するための新しい実験ツール
New Experimental Tools for Structural Changes of Membrane Proteins: Beyond X-ray Structures

オーガナイザー：神取 秀樹（名工大），内橋 貴之（金沢大）

Organizer: Hideki Kandori(Nagoya Inst. of Tech.), Takayuki Uchihashi(Kanazawa Univ.)

Several decades ago, structural determination of membrane proteins was impossible, and mechanism of signal transduction and materials transportation across the membrane remained a mystery. Such a situation has dramatically changed by recent progress in structural biology. Structures of many important membrane proteins have been determined, and it's time for us biophysicists to start understanding of structure-function relationship of membrane proteins. For this aim, "structural dynamics" is a key word, and we need experimental and theoretical tools to capture molecular motions of such proteins. From the experimental point of view, higher temporal and spatial resolutions are required for better understanding of structural dynamics. Questions are; What can spectroscopy do? What can diffraction do? How strong is single-molecule detection? In this symposium, speakers present their own experimental methods to study structural changes of membrane proteins such as visual and microbial rhodopsins, KcsA pottasium channel, FoF1-ATP synthase, etc. We like to discuss the scenarios to uncover the mystery of membrane proteins.

はじめに
神取　秀樹（名古屋工業大学）
Hideki Kandori (Nagoya Institute of Technology)

2SH-01　過渡回折格子法を用いた微生物型ロドプシンの研究と新規測定技術
Transient grating study of microbial rhodopsins and a new TG technique
井上　圭一（名古屋工業大学 大学院工学研究科 未来材料創成工学専攻）
Keiichi Inoue (Department of Frontier Materials, Graduate School of Engineering, Nagoya Institute of Technology)

2SH-02　急速溶液混合全反射赤外分光法によるイオン輸送蛋白質の構造変化ダイナミクス計測への挑戦
Development of Stopped-flow Attenuated Total Reflection FTIR Spectroscopy for Detecting Dynamic Strucutral Changes in Ion Transporters
古谷　祐詞（分子科学研究所 生命・錯体分子科学研究領域, 総合研究大学院大学 構造分子科学専攻）
Yuji Furutani[1,2], Tetsunari Kimura[1,2] ([1]Department of Life and Coordination-Complex Molecular Science, Institute for Molecular Science, [2]Department of Structural Molecular Science, The Graduate University for Advanced Studies)

2SH-03　ロドプシン活性化の一分子計測
Single Molecule Detection of Rhodopsin Activation
今元　泰（京都大学大学院理学研究科生物科学専攻生物物理学教室）
Yasushi Imamoto (Graduate School of Science, Kyoto University)

2SH-04　In vitro および生細胞での ATP 合成酵素の 1 分子リアルタイムイメージング
Single-molecule real-time imaging of ATP synthase in vitro and in living cells
飯野　亮太（東京大学大学院工学系研究科応用化学専攻）
Ryota Iino (Department of Applied Chemistry, University of Tokyo)

2SH-05　膜タンパク質研究の新しいツールとしての高速原子間力顕微鏡
High-Speed Atomic Force Microscopy: a tool for elucidating structural dynamics of membrane proteins
内橋　貴之（金沢大学）
Takayuki Uchihashi[1], Mikihiro Shibata[1], Hayato Yamashita[1], Hideki Kandori[2], Toshio Ando[1] ([1]Kanazawa University, [2]Nagoya Institute of Technology)

2SH-06　AFM によるチャネルゲートの 1 分子操作
Direct Manipulation of a Single Channel Gate with an AFM Probe
井出　徹（光産業創成大学院大学, 理化学研究所・生命システム研究センター）
Toru Ide[1,2], Minako Hirano[2], Daichi Okuno[2], Mitsunori Kitta[3] ([1]The Graduate School for the Creation of New Photonics Industries, [2]Quantitative Biology Center, RIKEN, [3]National Institute of Advanced Industrial Science and Technology)

2SH-07　X 線 1 分子計測法によるカリウムイオンチャネルの 1 分子ダイナミクス計測
Tracking the Motions of Single Potassium Channels by Time resolved X-ray Diffraction
清水　啓史（福井大学医学部分子生理学講座）
Hirofumi Shimizu[1], Masayuki Iwamoto[1], Takashi Konno[1], Antoine Royant[2,4], David von Stetten[4], Laurent Guerin[3], Michael Wulff[4], Shigetoshi Oiki[1] ([1]University of Fukui Faculty of Medical Sciences, [2]Institut de Biologie Structurale Jean-Pierre Ebel, UMR 5075 CNRS-CEA-Universite Joseph Fourier, [3]Institut de Physique de Rennes- CNRS UMR 6251 Universite de Rennes 1, [4]European Synchrotron Radiation Facility)

9:00~11:30　I会場：5 号館 2 階 講義室【5203】／Room I: 【5203】

2SI　原生動物の生存様式に人類が学ぶこと
Biomimetics focused on the life style of protozoa

オーガナイザー：園部 誠司（兵庫県大），細谷 浩史（広島大）
Organizer: Seiji Sonobe(Univ. of Hyogo), Hiroshi Hosoya(Hiroshima Univ.)

The protozoa are unicellular organisms and each cell is an individual, in which all reactions for existence occur. In this meaning, it is possible to say that the protozoa are ultimate nanomachines. During evolution, they have acquired a variety of abilities for survival as a single cell with remarkable ideas, producing numerous species of protozoa in this world and many unique devices, which are never observed in cells of multicellular organisms. Our group aims at creating new technologies for human being upon studying the protozoan wisdom, finding new principal in the protozoan devices and utilizing protozoa themselves. In this symposium, we will present three categolies of protozoan technologies:
Energy production (Hosoya and Endo), Environmental technology (Suzaki) and Nanomachine (Hirono, Ichikawa and Sonobe). We are indeed hoping to have a fruitful discussion with constructive advices and ideas from participants.

2SI-01　ミドリゾウリムシ共生藻が産生する遊離糖に関する研究
Roles of symbiotic algae in green paramecia *Paramecium bursaria*
細谷　浩史（広島大学大学院理学研究科生物科学専攻）
Hiroshi Hosoya, Kazuya Ujihiro, Eiji Hiraki, Koyo Tetsukawa, Yoshihiko Yamashin, Kozue Hamao (Department of Biological Science, Graduate School of Science, Hiroshima University)

2SI-02　太陽虫の細胞質収縮運動と水質汚染の生物モニタリングへの応用
Cytoplasmic contractility in heliozoa and its application to biomonitoring for aquatic pollution
洲崎　敏伸（神戸大学理学研究科生物学専攻）
Toshinobu Suzaki (Dept. Biol., Grad. Sch. Sci., Kobe Univ.)

2SI-03　テトラヒメナによる新規セルロース分解系構築の試み
Potentially Efficient Cellulolysis by the Protozoan Ciliate *Tetrahymena*
遠藤　浩（金沢大・院自然科学）
Hiroshi Endoh (Grad. Sch. Nat. Sci. and Technol., Kanazawa Univ.)

2SI-04　中心子の普遍的な９回対称性構造の構築機構
Mechanism for establishing the “nine-ness” of the centriole structure
廣野　雅文（東京大学大学院理学系研究科生物科学専攻）
Masafumi Hirono (Department of Biological Sciences, University of Tokyo)

2SI-05　**Unique and specific properties of the cell-sized model systems**
市川　正敏（京都大学大学院理学研究科物理学第一教室）
Masatoshi Ichikawa (Dept. Phys., Kyoto Univ.)

2SI-06　原生動物の運動; アメーバとイカダケイソウ
Motility of protozoa; Amoeba and Bacillaria
園部　誠司（兵庫県立大学大学院生命理学研究科）
Seiji Sonobe, Yukinori Nishigami, Atsushi Tniguchi, Nozomi Yamaoka (Graduate School of Life Science, University of Hyogo)

9:00~11:30　J会場：5 号館 2 階 講義室【5204】／Room J: 【5204】

2SJ　タンパク質複合体研究の新展開：分子から超分子、凝集体まで
New developments in protein complex research: From molecules to supramolecules and aggregates

オーガナイザー：廣田 俊（奈良先端大），樋口 芳樹（兵庫県大）
Organizer: Shun Hirota(NAIST), Yoshiki Higuchi(Univ. of Hyogo)

Many proteins form complexes to function *in vivo*. It is also known that proteins form aggregates in conformation diseases. Protein complexes exhibit various sizes, ranging from a bimolecular complex to a complex formed by several molecules and up to that with more than 50 subunits. The functions of these complexes are closely related with their higher-order structures. Recently, structures of supramolecular complexes have been elucidated, owing to progresses in structural analytical methods. On the other hand, proteins which react in a monomeric form have been shown to exhibit oligomeric forms. In this symposium, we will give an overview of advanced research on these diverse protein complexes.

2SJ-01　高分解能電子伝達複合体結晶構造を用いた蛋白質分子間相互作用と電子移動反応過程の解析
Analysis of Protein-Protein Interaction and Electron Transfer Processes Based on the Protein Electron-Transfer Complex Structures
野尻　正樹（阪大・院理・化学）
Masaki Nojiri (Dept. of Chem., Grad. School of Sci., Osaka Univ.)

2SJ-02　シトクロム *c* －シトクロム *c* 酸化酵素間の電子伝達複合体における相互作用
Interactions in Electron Transfer Complex between Cytochrome *c* and Cytochrome *c* Oxidase
石森　浩一郎（北大・院理）
Koichiro Ishimori (Fac. Sci., Hokkaido Univ.)

2SJ-03　ドメインスワッピングによるシトクロム *c* ポリマー化
Cytochrome *c* polymerization by domain swapping
長尾　聡（奈良先端大物質創成）
Satoshi Nagao[1], Yoko Hattori[1], Mariko Ueda[1], Midori Taketa[2], Hisao Osuka[1,2], Hirofumi Komori[2,3], Hironari Kamikubo[1], Shigeru Negi[4], Yukio Sugiura[4], Mikio Kataoka[1], Yoshiki Higuchi[2,3], Shun Hirota[1] ([1]Graduate School of Materials Science, Nara Institute of Science and Technology, [2]Graduate School of Life Science, University of Hyogo, [3]RIKEN SPring-8 Center, [4]Faculty of Pharmaceutical Sciences, Doshisha Women's University)

2SJ-04　超分子複合体のための最先端電子顕微鏡法：in vitro, in vivo, in situ そして、in silico
Advanced electron microscopy for supramolecular assemblies: in vitro, in vivo, in situ and then in silico
安永　卓生（九州工業大学大学院情報工学研究院生命情報工学研究系）
Takuo Yasunaga (Dept. of Bioscience and Bioinformatics, Faculty of Computer Science and System Engineering, Kyushu Institute of Technology)

2SJ-05　細胞質内で最大の分子量を持つ核酸-蛋白質複合体ボルトの構造
X-ray structure of the vault, the largest cytoplasmic ribonucleo protein particle
田中　秀明（阪大・蛋白所, JST さきがけ）
Hideaki Tanaka[1,2], Koji Kato[3], Eiki Yamashita[1], Tomoyuki Sumizawa[4], Yong Zhou[5], Min Yao[5], Kenji Iwasaki[1], Masato Yoshimura[6], Tomitake Tsukihara[1,3] ([1]IPR, Osaka Univ., [2]JST, PRESTO, [3]Grad. Sch. Sci., Univ. Hyogo, [4]Dept. Life Sci., Kagoshima W.J.C., [5]Grad. Sch. Life Sci., Hokkaido Univ., [6]NSRRC, Taiwan)

2SJ-06　タンパク質線維の構造に多型を生み出すメカニズム
Polymorphism of protein aggregates produced by genetic and chemical modifications
古川　良明（慶應大・理工・化学）
Yoshiaki Furukawa (Dept. of Chem., Keio Univ.)

9:00~11:30　K 会場：4 号館 1 階 講義室【4113】／ Room K: 【4113】
2SK　圧力がひらくバイオサイエンス
Pressure opens new paradigm of bioscience

オーガナイザー：前野 覚大（近畿大），今井 隆志（理研），西山 雅祥（京大）
Organizer: Akihiro Maeno(Kinki Univ.), Takashi Imai(RIKEN), Masayoshi Nishiyama(Kyoto University)

Life is quite dynamic and to explore its basis we need to explore dynamics of proteins and other macromolecules. Pressure has been known to have a strong effect on biological phenomena. For example, E-coli cells stop growing above a few hundred bars. The motor protein flagella move strangely under pressure. Such high-sensitivity of biological systems to pressure on the macroscopic level is a manifestation of the high pressure sensitivity of protein and membrane structures, which has become increasingly clear by recent NMR, SAXS, fluorescence, microscope and MD calculation studies under pressure. This symposium, covering pressure sensitivity of the microscopic structural fluctuations in proteins as well as of the macroscopic phenomena on biological creatures, will illustrate the utility of pressure as a new tool to explore the origin of the dynamics of life based on the dynamic and thermodynamic characteristics of protein and membrane structures.

2SK-01　高圧力顕微鏡を用いたバクテリア遊泳運動観察
High-pressure microscopy reveals the mechanism how applied pressures affect on the bacterial motility
西山　雅祥（京大院理, JST）
Masayoshi Nishiyama[1,2] ([1]Kyoto Univ., [2]JST)

2SK-02　生体膜相挙動と膜タンパク質に与える静水圧の影響
Effect of High Hydrostatic Pressure on Membrane Phase Behaviour and Membrane Proteins
楠部　真崇（和歌山高専・物質工学）
Masataka Kusube (Dept. Mat Sci., Wakayama NCT)

2SK-03　タンパク質の高圧構造転移の分子機序：分子液体論と分子シミュレーションで明らかになったこと
Molecular Mechanism of Pressure-Induced Structural Transition of Proteins Clarified by Molecular Liquid Theory and Simulation
今井　隆志（理研 QBiC）
Takashi Imai (RIKEN QBiC)

2SK-04　**Cavity hydration and the dynamics of a protein**
前野　覚大（近大・院生物理工, 近大・高圧蛋白研センター）
Akihiro Maeno[1,4], Ryo Kitahara[2], Yuji O. Kamatari[3], Sunilkumar P.N.[1,4], Kazuyuki Akasaka[1,4] ([1]Gradate school of Bio. Sci. and Tech., Kinki Univ., [2]Colledge of Pharm. Sci., Ritsumeikan Univ., [3]Life Science Research Center, Gifu University, [4]High Pressure Protein Research Center, Kinki Univ.)

2SK-05　**High Pressure NMR - Probing Differences in Transient States of Prion Proteins**
Werner Kremer (Inst. Biophys. and Phys. Biochem., University of Regensburg)

9:00~11:30　L 会場：4 号館 2 階 講義室【4211】／Room L: 【4211】

2SL　生命システムの情報処理
Information processing of biological systems

オーガナイザー：黒田 真也（東大），小林 徹也（東大）
Organizer: Shinya Kuroda(Univ. of Tokyo), Tetsuya J. Kobayashi(Univ. of Tokyo)

Static functions and symbolic information of proteins and genes are considered to be important in biological systems; however, dynamic information encoded in temporal and spatial patterns of molecular concentrations and activities are also another important aspects of information processing in biological systems. How do molecular networks process such dynamic information? To address this issue, interdisciplinary approach by use of temporal filters, statistical inference and information theory will be needed.
In this symposium, such cutting edge approach will be introduced and discussed.

2SL-01　ERK シグナル伝達経路の情報コーディング
Information coding of ERK signaling network
黒田　真也（東京大学理学系研究科生物化学専攻）
Shinya Kuroda, Shinsuke Uda, Takeshi Saito (Dept. Biophys. Biochem., Univ. Tokyo)

2SL-02　細胞における自発的シグナル生成と柔軟な環境応答
Spontaneous signal generation and flexible responses to environmental cues in living cells
上田　昌宏（大阪大学大学院・生命機能研究科, 理化学研究所・生命システム研究センター, 科学技術振興機構）
Masahiro Ueda[1,2,3] ([1]Grad. Schl. Front. Biosci., Osaka Univ., [2]QBiC, RIKEN, [3]JST, CREST)

2SL-03　ゆらぐ細胞内情報処理の数理
Mathematical aspects of information-processing in stochastic intracellular networks
小林　徹也（東京大学生産技術研究所, JST さきがけ）
Tetsuya Kobayashi[1,2], Atsushi Kamimura[1,2] ([1]Institute of Industrial Science, the University of Tokyo, [2]JST PREST)

2SL-04　Waddington 地形上において自律的な細胞間シグナリングによって表現系を多様化する調節可能なシステムの細胞内における構築
Tunable synthetic phenotypic diversification on Waddington's landscape through autonomous signaling
木賀　大介（東工大・院総理・知能システム, JST さきがけ）
Ryoji Sekine[1], Masayuki Yamamura[1], Shotaro Ayukawa[1], Kana Ishimatsu[1], Satoru Akama[1], Masahiro Takinoue[1], Masami Hagiya[2], **Daisuke Kiga**[1,3] ([1]Dept. Computational Intelligence and Systems Science, Tokyo Tech, [2]Grad. Sch. Information Science and Technology, U. Tokyo, [3]JST PRESTO)

2SL-05　形態形成過程における位置情報最適コーディング
Optimal coding design of positional information for robust morphogenesis
森下　喜弘（九州大学）
Yoshihiro Morishita (Kyushu University)

2SL-06　走化性細胞の倍変化検出とその背後のネットワークトポロジー
Adaptive fold-change detection in chemotactic cells and its underlying network topology
澤井　哲（東大・院総合文化, 複雑系生命研究センター）
Keita Kamino[1], Yohei Kondo[1], Koichi Fujimoto[3], **Satoshi Sawai**[1,2] ([1]Grad Sch of Arts & Sci, Univ Tokyo, [2]Research Ctr for Complex Systems Biology, [3]Osaka Univ)

9:00~11:30　Q 会場：書写紀念会館 1 階 会議室／ Room Q: Shosha Kinen Kaikan 1F Conference Room

2SQ　メカノバイオロジーの展開：基礎から医学的応用へ
Developing Mechanobiology: from fundamentals to medical applications

オーガナイザー：曽我部 正博（名大），成瀬 恵治（岡山大）
Organizer: Masahiro Sokabe (Nagoya Univ.), Keiji Naruse(Okayama Univ.)

Mechanobiology is an emerging interdisciplinary field. This symposium focuses on how the mechanobiology of molecular and cellular levels could develop to that of tissues and organs, and how the mechanobiology is practically useful in medicine. The first two talks deal with biophysical mechanobiology of actomyosin complex, and the middle two organ mechanophysiology where intercellular mechanosignaling via mechanically released ATP are shown up. The last two topics concern how mechanobiology contributes to clinical medicine, including early diagnosis of atherosclerosis and infertility therapy.

2SQ-01　細胞張力ホメオスタシスのメカニズムと重要性
Nonmuscle Myosin II-Based Regulation of Cellular Tensional Homeostasis
出口　真次（東北大学）
Shinji Deguchi[1], Tsubasa Matsui[1], Roland Kaunas[2], Masaaki Sato[1] ([1]Tohoku University, [2]Texas A&M University)

2SQ-02　ミオシン 1 方向運動のためのメカノセンシングの役割
Myosin mechanical-sensing for directional motion
岩根　敦子（大阪大学大学院生命機能研究科特別研究推進講座, 大阪大学医学部分子生理学教室）
Atsuko Iwane[1,2], Toshio Yanagida[1] ([1]Special Research Promotion Group, Graduate School of Frontier Biosciences, Osaka University, [2]Department of Physiolgy and Biosignaling, Graduate School of Medicine, Osaka University)

2SQ-03　肺における機械刺激感受性ヌクレオチド放出
Mechanosensitive nucleotide release in the lung
Ryszard Grygorczyk[1], Sabina Tatur[1], Kishio Furuya[2], Masahiro Sokabe[2,3] ([1]Dept Med, Univ Montreal, [2]FIRST Res Ctr Innovative Nanobiodevices, Nagoya Univ, [3]Dept Physiol, Nagoya Univ Grad Sch Med)

2SQ-04　乳腺のミルク放出に関するメカノフィジオロジー
Mechano-physiology of milk ejection in mammary glands
曽我部　正博（名大・院医・細胞生物物理, 名大・革新ナノバイオデバイス研究センター）
Masahiro Sokabe[1,2], Kishio Furuya[2] ([1]Dept. Physiol., Nagoya Univ. Grad. Sch. Med., [2]FIRST Res Center Innovative Nanobiodevice, Nagoya Univ.)

2SQ-05　細胞の力学応答を利用した血管機能評価：動脈硬化の早期診断
Artery function evaluation using mechanical responses of cells: early diagnosis of atherosclerosis
松本　健郎（名工大・機械）
Takeo Matsumoto[1], Takahiro Kurokawa[1], Yoshihito Kato[1], Kazuaki Nagayama[1], Hiromasa Tsukahara[2], Hiroshi Masuda[2] ([1]Mech. Engng., Nagoya Inst. Tech., [2]UNEX Corp.)

2SQ-06　生殖メカノバイオロジー：不妊治療への応用
Reproductive Mechanomedicine: Applications to Infertility Treatment
成瀬　恵治（岡山大学大学院医歯薬学総合研究科）
Keiji Naruse (Okayama University Graduate School of Medicine, Dentistry and Pharmaceutical Sciences)