ポスター　Poster

1 日目（9 月 24 日（火））／Day 1（Sep. 24 Tue.）
4F 天瑞・ホワイエ／4F TENZUI・Foyer

蛋白質：構造／Protein: Structure

1Pos001* HDX-MS を用いた Fc 断片と IgG1 全長の Fc 領域における構造解析
Structural analysis of IgG Fc region in Fc fragment and IgG1 full-body by HDX-MS
Yuki Yamaguchi[1], Tesuo Torisu[1], Susumu Uchiyama[1,2] ([1]*Grad. Sch., Eng., Univ. Osaka*, [2]*ExCELLS*)

1Pos002* 呼吸鎖における拡張型超複合体の Cryo-EM による構造の解明
Elucidation of the structure of extended super-complex in the respiratory chain by cryo-EM
Kasumi Hirakawa, Wataru Ishibashi, Tomoichirou Kusumoto, Junshi Sakamoto, Takuo Yasunaga (*Grad. Sch Comp. Sci. and Sys. Eng, Kyushu Inst. Tech.*)

1Pos003* シゾロドプシンのプロトン輸送の構造基盤
Structural basis of proton transport in Schizorhodopsin
Akimitsu Higuchi[1], Wataru Shihoya[1], Keiichi Inoue[2,3,4,5], Masae Konno[2], Hideki Kandori[2,3], Osamu Nureki[1] ([1]*Department of Biological Sciences, Graduate School of science, University of Tokyo*, [2]*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology*, [3]*OptoBioTechnology Research Center, Nagoya Institute of Technology*, [4]*The Institute for Solid State Physics, The University of Tokyo*, [5]*PRESTO, Japan Science and Technology Agency*)

1Pos004* カチオン性抗菌ペプチド Hymenochirin-1Pa および変異体 D9K の細菌膜結合構造と膜選択性の解析
Membrane-bound structure and membrane selectivity of cationic antimicrobial peptide Hymenochirin-1Pa and its analog D9K
Akifumi Ohyama[1], Batsaikhan Mijiddorj[2,3], Kazuyoshi Ueda[2], Akira Naito[2], Izuru Kawamura[1,2] ([1]*Grad. Sch. Eng. Sci., Yokohama Natl. Univ*, [2]*Grad. Sch. Eng., Yokohama Natl. Univ*, [3]*Sch. Eng. Appl. Sci., Natl. Univ. Mongolia*)

1Pos005 (1SCP-5) The role of C-terminal carboxylation in α-conotoxin LsIA interactions with human α7 nicotinic acetylcholine receptor *in silico*
Jierong Wen, Andrew Hung (*Sch. Sci., RMIT Univ.*)

1Pos006 分子動力学法を用いた Hras-GTP/GDP 複合体の各部の構造変化と各部の水素結合との同時緩和モードの研究
Molecular dynamics study of simultaneous relaxation modes between structures and the hydrogen bonds in the Hras-GTP/GDP complexes
Takeshi Miyakawa[1], Ryota Morikawa[1], Masako Takasu[1,2], Kimikazu Sugimori[2], Kazutomo Kawaguchi[3], Hidemi Nagao[3] ([1]*Sch. of Life Sci., Tokyo Univ. of Pharm. and Life Sci.*, [2]*Inst. of Liberal Arts. & Sci., Kanazawa Univ.*, [3]*Coll. of Sci. and Eng., Kanazawa Univ.*)

1Pos007 自動デザイン：分子シミュレーションデータを用いた自動ドラッグデザイン
AutoDesign - an automated drug design by using protein-ligand simulation data
Hironori Kokubo, Naoki Miyamoto, Yoshi Nara (*Axcelead, Inc.*)

1Pos008 Simulating large-amplitude transitions in proteins with a coarse-grained model
Ai Shinobu[1], Chigusa Kobayashi[1], Yasuhiro Matsunaga[2], Yuji Sugita[1,3,4] ([1]*RIKEN Center for Computational Science*, [2]*Saitama Univ., Grad. Sch. Sci. Eng.*, [3]*RIKEN Cluster for Pioneering Research*, [4]*RIKEN Center for Biosystems Dynamics Research*)

1Pos009 Dynamics and interdomain interactions in a Drosophila adapter protein (Drk) and their correlation to the unfolding of the N-SH3 domain
Hisham Dokainish[1], Yusuke Suemoto[2], Teppei Ikeya[2], Takuma Kasai[3], Takanori Kigawa[3], Yutaka Ito[2], Yuji Sugita[1] ([1]*Riken, Theoretical Molecular Science Laboratory*, [2]*Department of Chemistry, Tokyo Metropolitan University*, [3]*RIKEN, Center for Biosystems Dynamics Research*)

1Pos010 微小管内タンパク質によるチューブリン格子構造の内側からの制御
Microtubule inner proteins regulate the tubulin lattice architecture from the inside
Muneyoshi Ichikawa[1], Ahmad Khalifa[2], Shintaroh Kubo[3], Kaustuv Basu[2], Daniel Dai[2], Amin Maghrebi[2], Javier Vargas[2], Khanh-Huy Bui[2] ([1]*Dept. of Systems Biol., NAIST*, [2]*McGill Univ.*, [3]*Dept. Biophysics, Kyoto Univ.*)

1Pos011 小角散乱によるアミロイド線維中のヒト α-シヌクレインの構造解析
Structural analysis of human α-synuclein within amyloid fibrils by small-angle scattering
Satoru Fujiwara[1], Tatsuhito Matsuo[1], Yasunobu Sugimoto[2] ([1]*Inst. Quantum Life Science, QST*, [2]*Nagoya Univ.*)

1Pos012 共溶媒の構造類似度を利用した共溶媒分子動力学法における密度マップの類似度の推定
Estimation of the probability map (Pmap) similarity of cosolvent MD (CMD) from structural similarities of cosolvents
Keisuke Yanagisawa[1], Yoshitaka Moriwaki[1], Tohru Terada[2,3], Kentaro Shimizu[1,2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*, [3]*Agr. Bioinfo. Res. Unit., Grad. Sch. Agr. Life Sci., Univ. Tokyo*)

1Pos013 単量体タンパク質の長時間シミュレーションのフォールディングパスウェイの動的解析
Dynamical analysis on the folding pathways of long simulations of a single protein
Ayori Mitsutake[1], Hiroshi Takano[2] ([1]*Meiji Univ.*, [2]*Keio Univ.*)

1Pos014 Targeting the cryptic sites: NMR-based strategy to improve the draggability of proteins by controlling the conformational equilibrium
Koh Takeuchi[1], Yumiko Mizukoshi[2], Yuji Tokunaga[1], Hitomi Matsuo[2], Ichio Shimada[3] ([1]*AIST, molprof*, [2]*JBiC*, [3]*The Univ. Tokyo, Grad Sch Pharm Sci*)

1Pos015 ヘリオロドプシンの構造と生物物理学的解析
Structure and biophysical characterization of the heliorhodopsin
Wataru Shihoya[1], Keiichi Inoue[2,3,4,5], Singh Manish[2], Masae Konno[2], Shoko Hososhima[2], Keitaro Yamashita[1], Kento Ikeda[6], Akimitsu Higuchi[1], Sae Okazaki[1], Izume Tamaki[1], Masanori Hashimoto[2], Ritsu Mizutori[2], Sahoko Tomida[2], Yumeka Yamauchi[2], Rei Abe-Yoshizumi[2], Kota Katayama[2,3], P. Satoshi Tsunoda[2], Mikihiro Shibata[7,8], Yuji Furutani[2,9,10], Alina Pushkarev[11], Oded Beja[11], Takayuki Uchihashi[12,13], Hideki Kandori[2,3], Osamu Nureki[1] ([1]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, [2]*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology*, [3]*OptoBioTechnology Research Center, Nagoya Institute of Technology*, [4]*The Institute for Solid State Physics, The University of Tokyo*, [5]*RESTO, Japan Science and Technology Agency*, [6]*School of Mathematical and Physical Sciences, Graduate School of Natural Science & Technology, Kanazawa University*, [7]*Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*, [8]*High-speed AFM for Biological Application Unit, Institute for Frontier Science Initiative, Kanazawa University*, [9]*Department of Life and Coordination-Complex Molecular Science, Institute for Molecular Science, National Institutes of Natural Sciences*, [10]*Department of Structural Molecular Science, The Graduate University for Advanced Studies (SOKENDAI)*, [11]*Israel Institute of Technology*, [12]*Department of Physics, Nagoya University*, [13]*Structural Biology Research Center, Graduate School of Science, Nagoya University*)

1Pos016 クロストリジウム属 2 成分毒素輸送チャネル Ib ポアのクライオ電子顕微鏡構造解析
Cryo-EM structure of clostridial binary toxin translocation channel Ib-pore
Tomohito Yamada[1], Toru Yoshida[1], Akira Kawamoto[2], Kaoru Mitsuoka[3], Kenji Iwasaki[4], Hideaki Tsuge[1] ([1]*Sch. Life Sci., Univ. Kyoto-sangyo*, [2]*Protein inst., Univ. Osaka*, [3]*Research Center for Ultra-High Voltage Electron Microscopy, Univ. Osaka*, [4]*Life Science Center for Survival Dynamics, Tsukuba Advanced Research Alliance, Univ. of Tsukuba*)

1Pos017 藍色細菌 *Anabaena variabilis* 由来 RNA 結合タンパク質の二次構造
Secondary structure of cyanobacterial RNA-binding protein, RbpD, from *Anabaena variabilis*
Hayato Morita[1], Toshihiko Sugiki[2], Chojiro Kojima[2,3], Hidenori Hayashi[4], Naoki Sato[5] ([1]*Fac. Sci., Josai. Univ.*, [2]*Inst. Prot. Res., Osaka Univ.*, [3]*Fac. Eng. Yokohama. Nat. Univ.*, [4]*Grad. Sch. Sci. Eng., Ehime Univ.*, [5]*Grad. Sch. Arts. Sci., Univ. Tokyo*)

1Pos018 Hydrogen bond donors and acceptors are generally depolarized in α-helices as revealed by a negative fragmentation approach
Yu Takano[1,2], Hiroko X. Kondo[1,3], Ayumi Kusaka[2], Shusuke Yamanaka[4], Nakamura Haruki[2] ([1]*Grad. Sch. Info. Sci., Hiroshima City U.*, [2]*IPR, Osaka U.*, [3]*Faculty Eng. Kitami Inst. Tech.*, [4]*Grad. Sch. Sci., Osaka U.*)

1Pos019 Full atomistic model building of EhV-ATPase using homology modeling/molecular dynamics simulation based on the low resolution cryoEM map
Yu Yamamori[1], Jun Tsunoda[2,3], Ray Burton-Smith[3], Chihong Song[3], Ryouta Iino[2,4], Kazuyoshi Murata[2,3], Kentaro Tomii[1] ([1]*AIST*, [2]*SOKENDAI*, [3]*NIPS*, [4]*IMS*)

1Pos020 2 次元テンプレートマッチング法によるクロマチン構造多型解析への挑戦
Challenging for multi-conformational analysis of chromatin using the two-dimensional template matching method
Atushi Tokuhisa[1,2,3], Ryo Kanada[1], Shuntaro Chiba[2], Kei Terayama[3,4,5], Shigeyuki Matsumoto[2], Yuta Isaka[1,6], Biao Ma[1,6], Narutoshi Kamiya[7], Yasushi Okuno[1,3,5,6] ([1]*RCH, RIKEN*, [2]*MIH,RIKEN*, [3]*R-CCS,RIKEN*, [4]*AIP,RIKEN*, [5]*Medicine,Kyoto U*, [6]*CCD,FBRI*, [7]*Simulation,U.Hyogo*)

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

1Pos022 Crystal structure of human Dishevelled1 PDZ with its inhibitor
Shotaro Yasukochi[1], Nobutaka Numoto[2], Kiminori Hori[1], Natsuko Tenno[1], Takeshi Tenno[1], Nobutoshi Ito[2], Hidekazu Hiroaki[1] ([1]*Grad. Sch. Pharm Sci., Univ. Nagoya*, [2]*Med Res Inst., TMDU*)

蛋白質：構造機能相関／Protein: Structure & Function

1Pos023* 拡張アンサンブル法によるビタミン D 受容体のアゴニスト/アンタゴニスト活性調節機構の研究
Regulation mechanism of agonistic / antagonistic activities of vitamin D receptor studied by generalized ensemble method
Takafumi Kudo[1], Toru Ekimoto[1], Tsutomu Yamane[1], Mitsunori Ikeguchi[1,2] ([1]*Grad. Sch. Med Life Sci., Yokohama City Univ.*, [2]*Med. Sci. Innov. Hub., Riken*)

1Pos024* MARTINI 力場を用いた粗視化シミュレーションによる分子シャペロニン GroEL の ATP に誘起される構造変化の解析
Analysis of the ATP-induced conformational change of the molecular chaperonin GroEL by coarse-grained simulations using the MARTINI
Yuya Yamaura, Tadaomi Furuta, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

1Pos025* A Theoretically Study of ATP Effect on Solubility of Intrinsically Disordered Protein under Crowded Environment
Hayato Aida[1], Ryuhei Harada[2], Yasuteru Shigeta[2] ([1]*Coll. Bio. Sci., Univ. Tsukuba*, [2]*CCS, Univ. Tsukuba*)

1Pos026* 脂質膜表面におけるシトクロム P450 還元酵素の誘電アロステリー
Dielectric allostery in cytochrome P450 reductase on the surface of lipid membrane
Mikuru Iijima, Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1Pos027* TypeIII 中間径フィラメントの細胞表面上への出現機構の解明
Elucidation of recruitment mechanism of type III intermediate filament proteins to cell surface
Beomju Hwang[1], Inu Song[1], Hirohiko Ise[2] ([1]*Grad. Sch. Eng., Kyushu univ.*, [2]*IMCE, Kyushu Univ.*)

1Pos028* 量子化学計算による EcoRV のシシルリン酸基ツイスト後のリン酸エステル加水分解反応の研究
DNA Hydrolysis by EcoRV Subsequent to Scissile-Phosphate Twist, Studied by QM/MM Metadynamics Simulation
Itaru Onishi[1], Norio Yoshida[2], Fumio Hirata[3,4], Masayuki Irisa[1] ([1]*Kyushu Inst. of Tech.*, [2]*Kyushu Univ.*, [3]*IMS*, [4]*Toyota Riken*)

1Pos029 Crystal structure of branched-chain polyamine synthase
Eiichi Mizohata[1,2], Masataka Toyoda[1], Ryota Hidese[3], Shinsuke Fujiwara[3] ([1]*Grad. Sch. Eng., Osaka Univ.*, [2]*JST-PRESTO*, [3]*Grad. Sch. Sci. Tech., Kwansei Gakuin Univ.*)

1Pos030 Analysis of the complex molecular system composed of GGA, MPR and Ub by using titration SAXS measurement

Yugo Hayashi[1], Natsumi Endo[1], Youichi Yamazaki[1], Sachiko F. Toma[1], Hironari Kamikubo[1,2] ([1]*Div. Mat. Sci., NAIST*, [2]*IMSS KEK*)

1Pos031 Structural analysis of firefly luciferase with MM and QM/MM molecular simulations to clarify the origin of emission color-change factors

Kota Nosaka, Naohisa Wada (*Grad. Sch. Life Sci., Univ.Toyo*)

1Pos032 シアノバクテリア概日時計における KaiC 六量体の構造多様性
Structural Diversity of KaiC Hexamer in Cyanobacterial Circadian Clock

Yoshihiko Furuike[1,2], Atsushi Mukaiyama[1,2], Eiki Yamashita[3], Takao Kondo[4], Shuji Akiyama[1,2] ([1]*Research Center of Integrative Molecular Systems (CIMoS), Institute for Molecular Science (IMS)*, [2]*Department of Functional Molecular Science, SOKENDAI (The Graduate University for Advanced Studies)*, [3]*Institute for Protein Research, Osaka University*, [4]*Graduate School of Science, Nagoya University*)

1Pos033 NMR analysis of metal ion-induced conformational changes of α-helical peptides

Ikuko Iizumi[1], Yohei Miyanoiri[2], Toshiki Tanaka[3], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*Inst. Protein Res., Osaka Univ.*, [3]*Nagoya Inst. Technol.*)

1Pos034 シクロスポリン A の CHARMM 力場の開発と膜―水系の分子動力学シミュレーションへの応用
Development of the CHARMM force field for Cyclosporine A and application to molecular dynamics simulations using a membrane-water system

Tsutomu Yamane[1], Ryo Takahashi[1], Toru Ekimoto[1], Mitsunori Ikeguchi[1,2] ([1]*Grad. Sch. Med. Life Sci, Yokohama City Univ.*, [2]*RIKEN Med. Sci. Innov. Hub*)

1Pos035 ヒト成人ヘモグロビンの酸素親和性制御に関連した GHz, THz 領域振動の研究
Study on Giga- and Terahertz-frequency Motions Involved with Oxygen Affinity of Human Adult Hemoglobin

Shigenori Nagatomo[1], Kohji Yamamoto[2], Masako Nagai[3], Teizo Kitagawa[4] ([1]*Dept. Chem., Univ. Tsukuba*, [2]*Res. Center Develop. Far-IR Region, Univ. Fukui*, [3]*Res. Center Micro-Nano Tech., Hosei Univ.*, [4]*Grad. Sch.Life Sci., Univ. Hyogo*)

1Pos036 Structural basis for the intramolecular signal transduction of oxygen sensor protein FixL from Bradyrhizobium japonicum

Misaki Kamaya[1], Hiroyasu Koteishi[1], Takehiko Tosha[1,2], Seiki Baba[3], Hiroshi Sugimoto[1,2], Yoshitsugu Shiro[1], Hitomi Sawai[1,2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*RIKEN SPring-8*, [3]*SPring-8 / JASRI*)

1Pos037 心筋ナトリウムチャネル Nav1.5 と薬剤間の結合自由エネルギー計算
Calculation of the binding free energies between the Nav1.5 sodium channel and drug molecules

Tatsuki Negami[1], Tohru Terada[2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

1Pos038 DNA 修復にかかわる Hef の天然変性領域の構造と機能
The structure and function of intrinsically disordered region of Hef that is associated with a DNA repair

Takashi Oda[1], Ayako Sekino[1], Ayaka Murakami[1], Rika Oi[1], Maki Yoneyama[1], Noriyuki Kodera[2], Toshio Ando[2], Tsuyoshi Konuma[3], Kenji Sugase[3], Tomotaka Oroguchi[4], Sonoko Ishino[5], Yoshizumi Ishino[5], Mamoru Sato[1] ([1]*Grad. Sch. of Med. Life Sci., Yokohama City Unv.*, [2]*WPI NanoLSI, Kanazawa Univ.*, [3]*Grad.Sch. of Eng., Kyoto Univ.*, [4]*Faclt. Sci. Tech., Keio Univ.*, [5]*Grad. Sch. of Bioresource & Bioenviron. Sci., Kyushu Univ.*)

1Pos039 T2-like ファージ宿主認識蛋白質と宿主 OmpC の相互作用解析
Structural and functional analysis of phage receptor binding protein and OmpC

Shuji Kanamaru (*Dep. of Life Sci. & Tech., Tokyo Inst. of Tech.*)

1Pos040 ヤナギマツタケ（Agrocybe cylindracea）の Pri3 遺伝子のクローニングと特性解析
Cloning and characterization of the Pri3 gene of the edible mushroom, Agrocybe cylindracea

Chika Abematsu[1], Yamato Kuratani[1], Masashi Shin[1], Makoto Iwata[2], Toshihiko Matsumoto[1], Shoji Ando[1] ([1]*Fac. Biotech. Life Sci., Sojo Univ.*, [2]*IMB*)

1Pos041 ヒトヘアケラチン K85 の遺伝子導入細胞における機能特性と外胚葉形成不全症の原因となる変異の影響
Functional characteristics of human hair keratin K85 in transfected cells and the effects of mutations causative of ectodermal dysplasia
Masaki Yamamoto[1], Yasuko Sakamoto[1], Yuko Honda[2], Kenzo Koike[3], Hideaki Nakamura[4], Toshihiko Matsumoto[1], Shoji Ando[1] ([1]*Fac. Biotech. Life Sci., Sojo Univ.*, [2]*Fac. Med., Saga Univ.*, [3]*Kao corp.*, [4]*Fac. Phar., Sojo Univ.*)

1Pos042 巨大ヘモグロビンのアロステリック中間体の時分割構造解析
Time-resolved structure analysis of allosteric intermediate of the giant hemoglobin
Nobutaka Numoto[1], Yoshihiro Fukumori[2], Kunio Miki[3], Nobutoshi Ito[1] ([1]*Med. Res. Inst., Tokyo Med. Dent. Univ. (TMDU)*, [2]*College Sci. Eng., Kanazawa Univ.*, [3]*Grad. Sch. Sci., Kyoto Univ.*)

蛋白質：物性・構造／Protein: Property & Structure

1Pos043* 分子動力学法による RvSAHS1 の構造安定性
Structural stability of RvSAHS1 by MD simulations
Kazuhisa Miyazawa[1,2,3], Satoru Itoh[1,2,3], Hisashi Okumura[1,2,3] ([1]*SOKENDAI*, [2]*IMS*, [3]*ExCELLS*)

1Pos044* Rheo-NMR 法によるスーパーオキシドジスムターゼ 1 の動的なアミロイド形成機構の解析
Dynamic Analysis of Amyloid Formation of Superoxide Dismutase 1 Using Rheo-NMR Spectroscopy
Naoto Iwakawa[1], Daichi Morimoto[1], Erik Walinda[2], Masahiro Shirakawa[1], Kenji Sugase[1] ([1]*Grad. Sch. Eng., Kyoto Univ.*, [2]*Grad. Sch. Med., Kyoto Univ.*)

1Pos045* 統計力学モデルの拡張によるタンパク質のフォールディング反応機構の予測
Prediction of protein folding mechanisms by an extended statistical mechanical model
Koji Ooka[1], Munehito Arai[1,2] ([1]*Dept. Phys., Univ. Tokyo*, [2]*Dept. Life Sci., Univ. Tokyo*)

1Pos046 低波数基準振動で特徴づけられた多量体蛋白質の動的性質
Dynamic properties of oligomeric proteins characterized by low-frequency normal modes
Hiroshi Wako[2], **Shigeru Endo**[1] ([1]*Dept. of Phys., Sch. of Sci., Kitasato Univ.*, [2]*Sch. of Social Sci., Waseda Univ.*)

1Pos047 粗視化 Go モデルを用いた GA・GB ドメイン関連タンパク質のフォールディング機構の相違・共通性の予測
Prediction of differences and commonality in folding mechanisms of GA / GB domain related proteins using coarse-grained Go model
Shoya Hamaue (*Dept. of Bioinfo., Col. of Life sci., Ritsumeikan Univ.*)

1Pos048 Mechanism of the spontaneous elongation of the fibroin nanofiber involved in spider silk
Takuya Sawai[1], Kiichi Hayashi[1], Yugo Hayashi[1], Takehiro Sato[2], Yoichi Yamazaki[1], Sachiko Toma-Fukai[1], Hironari Kamikubo[1,3] ([1]*Div. Mat. Sci., NAIST*, [2]*Spiber Inc.*, [3]*IMSS KEK*)

1Pos049 天然様階層構造を有する人工クモ糸材料の再構成
Reconstitution of artificial materials of spider silk accompanied by native-like hierarchical structure
Satoru Onishi[1], Yuki Nakatani[1], Yugo Hayashi[1], Takehiro Sato[2], Yoichi Yamazaki[1], Sachiko Toma-Fukai[1], Hironari Kamikubo[1,3] ([1]*Div. Mat. Sci., NAIST*, [2]*Spiber Inc.*, [3]*IMSS KEK*)

蛋白質：機能／Protein: Function

1Pos050* ヒト SOD1 と Zn 欠損 SOD との比較による亜鉛と静電ポテンシャルループの役割に関する研究
Investigation on role of zinc atom and electrostatic loop by comparing human SOD1 with Zn-deficient SOD
Natsumi Koyama[1], Masami Lintuluoto[1], Juha Lintuluoto[2] ([1]*Grad. Sch. Life and Environ. sci., Kyoto pref. univ.*, [2]*Grad. sch. eng., Kyoto univ.*)

1Pos051 点変異導入による CD44 のヒアルロン酸結合のアロステリック制御
Allosteric regulation of hyaluronan binding on CD44 by point mutation
Masami Lintuluoto[1], Youta Horioka[1], Katsuhisa Matsumoto[1], Saki Hongo[1], Juha Lintuluoto[2] ([1]*Grad. Sch. Life and Environ. Sci., Kyoto pref. univ.*, [2]*Grad. sch. eng., Kyoto Univ.*)

1Pos052 アミロイド β42 を用いた天然変性タンパク質の分子シールド効果の評価
The evaluation of molecular shield effect of intrinsically disordered proteins using amyloid beta 1-42
Koki Ikeda, Yoshiki Shigemitsu, Natsuko Tenno, Takeshi Tenno, Hidekazu Hiroaki (*Grad. Sch. Pharm Sci., Univ. Nagoya*)

1Pos053 X 線小角散乱を用いた大腸菌フェリチンの鉄コアの形成に関する研究
The iron core formation of E. coli ferritin studied by small angle X-ray scattering
Takumi Kuwata, Daisuke Sato, Kazuo Fujiwara, Masamichi Ikeguchi (*Department of Bioinformatics, Soka University*)

1Pos054 柔らかいドライブシャフトを持つ F_1-ATPase のトルク伝達/発生
Torque transmission/generation of F_1-ATPase with a soft driveshaft
Shou Furuike[1], Naoki Soga[2], Yasushi Maki[1], Hideji Yoshida[1] ([1]*Phys., Osaka Med. Coll.*, [2]*Grad. Sch. Eng., Univ. Tokyo*)

蛋白質：計測・解析／Protein: Measurement & Analysis

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

1Pos056* タンパク質内部の構造変化をプローブするためのアスパラギン酸マッピングと赤外分光解析
Mapping of aspartic acids to probe protein structural changes by FTIR spectroscopy
Masanori Hashimoto, Kota Katayama, Manish Singh, Yuji Furutani, Hideki Kandori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

1Pos057* バイオ医薬品中の蛋白質凝集体の定量手法の確立
Establishment of quantification methods for protein aggregates in biopharmaceuticals
Saki Yoneda[1], Bertram Niederleitner[2], Michael Wiggenhorn[2], Hiroki Koga[1], Shinichiro Totoki[3], Elena Krayukhina[1], Wolfgang Friess[4], Susumu Uchiyama[1,5] ([1]*Dept. biotech. grad. sch. eng., Osaka. univ*, [2]*Coriolis Pharma*, [3]*Shimadzu Corporation*, [4]*LMU, Dept.Phaemacy*, [5]*ExCELLS*)

1Pos058 (1SDP-6) 新規に開発した高濃度タンパク質のためのネガティブ染色電子顕微鏡法
(1SDP-6) A newly developed negative stain EM method for protein complexes at high protein concentration
Hiroshi Imai[1], Takayuki Kato[2], Gerle Christoph[3], Etsuko Muto[4], Kaoru Mitsuoka[5], Genji Kurisu[3], Keiichi Namba[2], Takahide Kon[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*IPR, Osaka Univ.*, [4]*CBS, RIKEN*, [5]*Res. Ctr. UVHEM, Osaka Univ.*)

1Pos059 模倣細胞内分子混雑環境及び糖ガラス中の特定のタンパク質及び脂質膜の構造の中性子散乱による研究
Study of protein or membrane structure in mimicking intra-cell molecular-crowding environment and in sugar-glass using neutron scattering
Mitsuhiro Hirai[1], Satoshi Ajito[1], Shigeki Arai[2], Shinichi Takata[3], Hiroki Iwase[4] ([1]*Graduate School of Science and Technology, Gunma University*, [2]*National Institute for Quantum and Radiological Science and Technology*, [3]*J-PARC Center, Japan Atomic Energy Agency*, [4]*Comprehensive Research Organization for Science and Society*)

1Pos060 TRPV1 分子内部の回転動態の決定
Agonist- and antagonist-induced rotational motion of TRPV1 channel
Shoko Fujimura[1], Kazuhiro Mio[1], Masahiro Kuramochi[2], Sekiguchi Hiroshi[3], Muneyo Mio[1], Tai Kubo[1], Yuji Sasaki[1,2,3] ([1]*Operand OIL, National Institute of Advanced Industrial Science and Technology, Tokyo, Japan*, [2]*Graduate School of Frontier Sciences, The Univ. Tokyo, Chiba, Japan*, [3]*Japan Synchrotron Radiation Research Institute, Hyogo, Japan*)

1Pos061 レプリカ部分置換法の開発とタンパク質への応用
Development of replica sub-permutation method and its application to mini-protein
Masataka Yamauchi[1,2,3], Hisashi Okumura[1,2,3] ([1]*SOKENDAI*, [2]*ExCELLS*, [3]*IMS*)

1Pos062 凝縮系の不均一動力学(dynamical disorder)の分子論開拓: タンパク質の構造遷移・揺らぎ階層性
Theoretical investigations on microscopic heterogeneity and hierarchy in transitions and fluctuations of protein conformations
Yoshihiro Matsumura[1], Shinji Saito[1,2] ([1]*IMS*, [2]*SOKENDAI*)

1Pos063 Lytic polysaccharide monooxygenase の生化学および 1 分子解析
Biochemical and single-molecule analyses of lytic polysaccharide monooxygenase
Siti Mastura Zakaria[1,2], Akihiko Nakamura[1,3], Yasuko Okuni[1], Mayuko Yamamoto[1], Akasit Visootsat[1,3], Jun Ando[1,3], **Ryota Iino**[1,3] ([1]*IMS, NINS*, [2]*Univ. of Malaya*, [3]*SOKENDAI*)

蛋白質工学／Protein: Engineering

1Pos064 Relationship between loop geometry and register shift in parallel beta-sheet proteins
Ryuichiro Ueda, George Chikenji (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

1Pos065 2 アミノ酸同時変異戦略を用いた SBDD による超高親和性抗体の創製
Structure-based discovery of the antibodies with sub-picomolar affinity using the double amino acid mutation strategy
Shuntaro Chiba[1], Masateru Ohta[1], Aki Tanabe[2], Makoto Nakakido[2], Kouhei Tsumoto[2,3], Yasushi Okuno[1,4] ([1]*MIH, RIKEN*, [2]*Sch. Eng., Univ. Tokyo*, [3]*Inst. Med. Sci., Univ. Tokyo*, [4]*Grad. Sch. Med., Kyoto Univ.*)

1Pos066 転写コアクチベータ CBP の KIX ドメインと転写因子間の相互作用を阻害するペプチドの合理的設計
Rational design of peptides that inhibit interactions between the KIX domain of CBP and transcription factors
Nao Sato[1], Shunji Suetaka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1Pos067 分子動力学シミュレーションを用いた CDR-Grafting による合成単ドメイン抗体の構造的変化の解析
Structural effects of CDR grafting of synthetic single domain antibodies investigated by molecular dynamics simulations
Seisho Kinoshita[1], Chinatsu Mori[2], Makoto Nakakido[1,2], Daisuke Kuroda[1,2,3], Jose Caaveiro[4], Kouhei Tsumoto[1,2,3,5] ([1]*Dept. of Bioeng., Sch. of Eng., Univ. of Tokyo*, [2]*Dept. of Chem. Biotech., Sch. of Eng., Univ. of Tokyo*, [3]*Med. Dev. Dev. Reg. Res. Center, Sch. of Eng., Univ. of Tokyo*, [4]*Grad. Sch. of Pharm. Sci., Kyushu Univ.*, [5]*Inst. of Med. Sci., Univ. of Tokyo*)

1Pos068 アレルギー性喘息に関わるインターロイキン 33 の阻害剤開発に向けて
Toward the development of an inhibitor of interleukin-33 responsible for allergic asthma
Mio Sano[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1Pos069 Domain-specific monitoring of higher-order structure of therapeutic IgG on the basis of molecular recognition of artificial proteins
Hideki Watanabe[1], Naoko Hayashida[2], Shinya Honda[1,2] ([1]*BMRI, AIST*, [2]*Grad. Sci. of Fro., Univ. of Tokyo*)

1Pos070 主鎖環状化が顆粒球コロニー刺激因子に与える会合体抑制効果
An effect of resistance to self-association of backbone circularization on granulocyte-colony stimulating factor
Risa Shibuya[1], Takamitsu Miyafusa[2], Shinya Honda[1,2] ([1]*Grad. Sch. of Fro., Univ. of Tokyo*, [2]*BMRI, AIST*)

ヘム蛋白質／Heme proteins

1Pos071 Function of N-terminal acetylation of fish hemoglobin α-subunit
Satoru Unzai, Antonio Tsunesige (*Hosei University, Department of Frontier Bioscience*)

1Pos072 Functional roles of conserved residues near the active site of nitric oxide reductase based on the structural analysis
Takehiko Tosha[1], Raika Yamagiwa[2], Takuya Kurahashi[2], Hiroshi Sugimoto[1], Yoshitsugu Shiro[2] ([1]*RIKEN SPring-8*, [2]*Univ. of Hyogo*)

1Pos073 2―状態アロステリーモデルの再検討ー機能的階層の有無
INSIGHT INTO THE TWO-STATE ALLOSTERIC MODEL - ON THE EXISTENCE OF HIERARCHIES
Antonio Tsuneshige, Satoru Unzai (*Hosei Univ. Frontier Bioscience*)

膜蛋白質／Membrane proteins

1Pos074* (1SCA-2) 脂質分子の混み合い効果による膜貫通タンパク質結晶化の検討
(1SCA-2) Crystallization of transmembrane protein driven by molecular crowding effect of lipids: Theoretical estimation by using a simple model
Keiju Suda[1], Ayumi Suematsu[2], Ryo Akiyama[1] ([1]*Kyushu University, Sci.*, [2]*Kyushu Sangyo University, Science and Engineering*)

1Pos075* アミロイド前駆体タンパク質と β 切断酵素の膜貫通部位の生体膜中での相互作用
Interaction between amyloid precursor protein and beta-secretase in the bio-membrane
Kaori Yanagino, Naoyuki Miyashita (*BOST KINDAI*)

1Pos076* 多次元固体 NMR による細胞膜中のヘリオロドプシンの構造解析
Multidimensional solid-state NMR study of heliorhodopsin in a lipid environment
Shibuki Suzuki[1], Toshio Nagashima[2], Rina Kaneko[1], Takashi Okitsu[3], Akimori Wada[3], Naohiro Kobayashi[2], Toshio Yamazaki[2], Rei Abe-Yoshizumi[4], Keiichi Inoue[5], Hideki Kandori[4], Izuru Kawamura[1] ([1]*Grad. Sch. Eng. Sci., Yokohama National Univ.*, [2]*RIKEN RSC*, [3]*Kobe Pharmaceutical Univ.*, [4]*Nagoya Inst. Tech.*, [5]*Univ. Tokyo*)

1Pos077 (1SHP-6) 理論計算による熱安定化ムスカリン M2 受容体の選択的アンタゴニスト AF-DX 384 結合型構造
(1SHP-6) Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor
Ryoji Suno[1], Sangbae Lee[2], Shoji Maeda[3], Satoshi Yasuda[4], Keitaro Yamashita[9], Kunio Hirata[5,6], Takeshi Murata[7], Masahiro Kinoshita[8], Masaki Yamamoto[5], Brian Kobilka[3], Nagarajan Vaidehi[2], So Iwata[8], Takuya Kobayashi[1] ([1]*Kansai Medi. Univ.*, [2]*City Hope Med Ctr.*, [3]*Stanford Univ.*, [4]*Chiba Univ.*, [5]*RIKEN,SPring-8*, [6]*JST,PRESTO*, [7]*IAE, Kyoto Univ.*, [8]*Med,Kyoto Univ.*, [9]*Univ.Tokyo,Sci*)

1Pos078 (1SCA-4) cDNA ディスプレイとセルソーターの利用による新規リポソームポア形成ペプチドの創製
(1SCA-4) Novel pore-forming peptides assembling in liposome membranes selected by combining cDNA display method with cell sorter system
Naoto Nemoto[1], Toshiki Miyajima[1], Takeru Yoshinobu[1], Yusuke Sekiya[2], Ryuji Kawano[2] ([1]*Grad. Sci. Eng., Saitama Univ.*, [2]*Dept. Biotech. Life Sci., Tokyo Univ. Agr. Tech*)

1Pos079 特異的な残基置換が、水和水のダイナミクスにおよぼす影響を、解析するソフトを開発
Development of software to analyze the effects of specific residue substitution on hydration water dynamics
Ryoi Ashida, Nobuya Hasegawa, Takuya Azami, Kota Kasahara, Takuya Takahashi (*Graduate School of Life Science, Ritsumeikan University*)

1Pos080 A comparative study of membrane-bound structure of antimicrobial peptides L- and D-phenylseptin
Izuru Kawamura[1], Batsaikhan Mijiddorj[1], Hisako Sato[2], Yuta Matsuo[1], Akira Naito[1], Kazuyoshi Ueda[1] ([1]*Grad.Sch. Eng., Yokohama Natl. Univ.*, [2]*Grad. Sch. Sci. Eng.*)

核酸結合蛋白質／Nucleic acid binding proteins

1Pos081* Observation of Tumor Suppressor p53 Search Dynamics using Sub-millisecond Resolved Single-molecule Fluorescence Microscopy
Dwiky Rendra Graha Subekti[1,2], Agato Murata[1], Yuji Itoh[1], Satoshi Takahashi[1], Kiyoto Kamagata[1] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Sci., Tohoku Univ.*)

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

1Pos083 スピンラベル ESR によるヘテロクロマチンタンパク質 HP1 の動的構造の研究：アイソフォーム特異性とリン酸化
Structural dynamics of heterochromatin protein HP1 studied by spin labeling ESR spectroscopy: Isoform specificity and phosphorylation
Toshiaki Arata[1,5], Shigeaki Nakazawa[4], Yuichi Mishima[5], Kazunobu Sato[4], Takeji Takui[4], Toru Kawakami[5], Hironobu Hojo[5], Toshimichi Fujiwara[5], Makoto Miyata[1], Isao Suetake[2,3,5] ([1]*Dept. Biol., Grad. Sch. Sci., Osaka City Univ.*, [2]*Koshien Univ.*, [3]*Twin Research Center, Osaka Univ.*, [4]*Dept. Chem., Grad. Sch. Sci., Osaka City Univ.*, [5]*IPR, Osaka Univ.*)

1Pos084 Protein localization in DNA cruciform junction studied by molecular simulation
Mami Saito, Shoji Takada (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

1Pos085 HIV Vif–ヒト E3 ユビキチンリガーゼ複合体によるヒト抗ウイルス因子 APOBEC3G の脱アミノ化阻害の分子メカニズム
Inhibition mechanism of HIV Vif-human E3 ubiquitin ligase complex against enzymatic activity of APOBEC3G
Keisuke Kamba[1], Li Wan[1,2], Satoru Unzai[3], Ryo Morishita[4], Takashi Nagata[1,2], Masato Katahira[1,2] ([1]*Inst. of Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Energy Sci., Kyoto Univ.*, [3]*Front. Biosci., Hosei Univ.*, [4]*CellFree Sciences Co.,Ltd.*)

核酸／Nucleic acid

1Pos086* 薬剤によるリボスイッチ“SPINACH”の構造とイオンへの影響
Influence on the structure and dynamics of Riboswitch “SPINACH” and potassium ions by DFHBI
Lisa Matsukura[1], Nobutaka Onishi[1], Masaya Furue[1], Naoyuki Miyashita[1], Takuma Shiraki[1], Yasushige Yonezawa[2] ([1]*BOST, KINDAI*, [2]*IAT, KINDAI*)

1Pos087* シスプラチンは二本鎖 DNA を桁違いに硬くする：一分子揺らぎの定量的解析
Cisplatin causes DNA much stiffer: Quantitative evaluation viscoelasticity through the analysis of single molecule fluctuation
Toshifumi Kishimoto[1], Yuko Yoshikawa[1], Seiji Komeda[2], Kenichi Yoshikawa[1] ([1]*Grad.Sch.Life Med.Sci.,Univ.Doshisha*, [2]*Fac.Pharm.,Univ.Suzuka.Med.Sci*)

1Pos088 (1SEA-6) エピジェネティック修飾をもつクロマチンのモデルにおける不連続相転移
(1SEA-6) Discontinuous Phase Transition in a Chromatin Model with Epigenetic Modification
Kyosuke Adachi, Kyogo Kawaguchi (*RIKEN BDR*)

1Pos089 トリヌクレオソームから構築するポリヌクレオソーム構造の特徴
Characterization of Poly-nucleosome Structure Constructed from Tri-nucleosome
Hiroo Kenzaki[1], Shoji Takada[2] ([1]*Info. Sys. Div., ISC, RIKEN*, [2]*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)

1Pos090 局所変形下における絡まりあった DNA 溶液の緩和過程
Relaxation process of entangled DNA solution after local deformation
Akinori Miyamoto, Yoshihiro Murayama (*Department of Applied Physics,Tokyo University of Agri. and Tech.*)

1Pos091 In-cell NMR 法を用いたヒト生細胞内核酸の構造およびダイナミクスの評価
Evaluation of the structure and dynamics of nucleic acids inside the living human cells by in-cell NMR spectroscopy
Yudai Yamaoki[1], Takashi Nagata[1,2], Ayaka Kiyoishi[2], Masayuki Miyake[2], Fumi Kano[3], Masayuki Murata[3,4], Masato Katahira[1,2] ([1]*Inst. Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Energy Sci., Kyoto Univ.*, [3]*Inst. Innovative Res., Tokyo Inst. Technol.*, [4]*Grad. Sch. Arts and Sci., Univ. Tokyo*)

1Pos092 ハンマーヘッドリボザイムの酵素反応に関する理論的研究
Theoretical study on an enzymatic reaction of the hammerhead ribozyme
Ayaka Matsuyama, Masahiko Taguchi, Shigehiko Hayashi (*Kyoto University*)

1Pos093* 2 価ポリアミンが引き起こす遺伝子発現の促進と抑制：アミノ基間の炭素鎖長の重要性
Promotion and inhibition of gene expression caused by divalent polyamines: Marked effect of the distance between amino groups
Hiroko Tanaka[1], Chwen-Yang Shew[2], Yuko Yoshikawa[1], Takahiro Kenmotsu[1], Kenichi Yoshikawa[1] ([1]*Grad. Sch. Life. Med. Sci., Univ. Doshisha*, [2]*Col. Chem., City Univ. New York*)

1Pos094* Theoretical Studies on the Conformational Stability of RA-VII complex with 60S Ribosome
Arwansyah MS[1], Yoh Noguchi[2], Takeshi Miyakawa[2], Kazutomo Kawaguchi[1], Yukio Hitotsuyanagi[3], Satoshi Yokojima[3], Ryota Morikawa[2], Masako Takasu[2], Hidemi Nagao[1] ([1]*Division of Mathematical and Physical Sciences, Graduate School of Natural Science and Technology, Kanazawa University*, [2]*School of Life Science, Tokyo University of Pharmacy and Life Sciences*, [3]*School of Pharmacy, Tokyo University of Pharmacy and Life Sciences*)

1Pos095 (1SEA-3) オリゴペプチドのアミノ酸配列は DNA compaction と転写活性に著しい違いを引き起こす
(1SEA-3) Marked Difference in DNA Compaction and Transcription is Caused by Amino Acid Sequence of Oligopeptide
Tatsuo Akitaya[1], Hiroyuki Hiramatsu[2], Hideaki Yamaguchi[3], Koji Kubo[4], Shizuaki Murata[4], Toshio Kanbe[5], Norio Hazemoto[6], Kenichi Yoshikawa[7], Anatoly Zinchenko[4] ([1]*Asahikawa Med. Univ.*, [2]*Fac. Pharm., Meijo Univ.*, [3]*Fac. Agr. Sci., Meijo Univ.*, [4]*Grad. Sch. Env. Std., Nagoya Univ.*, [5]*Grad. Sch. Med., Nagoya Univ.*, [6]*Grad. Sch. Pharm. Sci., Nggoya City Univ.*, [7]*Fac. Bio. Med. Sci., Doshisah Univ.*)

電子状態／Electronic state

1Pos096 Long-range Electron-Electron Interaction and Charge Transfer in Protein Complexes
David Gnandt, Thorsten Koslowski (*Institute of Physical Chemistry, University of Freiburg*)

1Pos097 —

1Pos098 拘束条件を用いた DFTB-MD シミュレーションの高速化とエネルギー保存の評価
Accelerate simulations and assessment of the energy conservation for the DFTB-MD simulations using the constraint method
Hiroaki Nishizawa, Yasuteru Shigeta (*CCS, Univ. of Tsukuba*)

1Pos099 光合成系 II の酸素発生中心の S1 状態での 12 の構造モデルの DLPNO-CCSD(T)法による計算
DLPNO-CCSD(T) calculations of twelve structural models for the S1 state of oxygen evolving complex of photosystem II
Koichi Miyagawa[1], Takashi Kawakami[2,5], Hiroshi Isobe[3], Mitsuo Shoji[4], Shusuke Yamanaka[2], Kazuhiko Nakatani[1], Mitsutaka Okumura[2], Takahito Nakajima[5], Kizashi Yamaguchi[1,5,6] ([1]*ISIR, Osaka Univ.*, [2]*Grad. Sch. of Sci., Osaka Univ.*, [3]*Grad. Sch. of Nat. Sci. and Tech., Okayama Univ.*, [4]*CCS, Univ. of Tsukuba*, [5]*R-CCS, RIKEN*, [6]*Inst. Nanosci. Design, Osaka Univ.*)

水・水和／電解質／Water & Hydration & Electrolyte

1Pos100* 生体溶液中のアニオンサイト間実効引力が発生する最大のサイトサイズ
Maximum size for attractive anionic-sites in a biological solution
Michika Takeda[1], Ayumi Suematsu[2], Ryo Akiyama[3] ([1]*Graduate of Science, Kyushu University*, [2]*Kyushu Sanyo University*, [3]*Institute of Science, Kyushu University*)

1Pos101 MD シミュレーションで、モデルタンパク質の水和水のダイナミクスを明らかにする
MD simulations reveal hydration dynamics around model proteins
Takuya Takahashi[1], Takuya Azami[2], Nobuya Hasegawa[1], Ryoi Ashida[1,2], Kota Kasahara[1] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ*)

1Pos102 All-atom molecular dynamics simulation of the reduced protein-protein interaction with metabolites in the cytoplasm
Isseki Yu[1,2], Michael Feig[3], Yuji Sugita[2] ([1]*Maebashi Institute of Technology*, [2]*RIKEN Theoretical Molecular Science Lab.*, [3]*Michigan State University*)

1Pos103 プロテインーリガンド結合における水溶媒の役割
Role of water solvent in protein-ligand binding
Yutaka Maruyama[1], Ayori Mitsutake[2], Takefumi Yamashita[3] ([1]*RIKEN R-CCS*, [2]*Dep. Phys., Meiji Univ.*, [3]*LSBM, Univ. Tokyo*)

発生・分化／Development & Differentiation

1Pos104 Mechanical symmetry breaking in *C. elegans* dorsal-ventral axis establishment
Masatoshi Nishikawa (*Dept. Frontier Bioscience, Hosei Univ.*)

1Pos105 マウスノード不動繊毛はメカノセンサーか?: 光ピンセットによる機械刺激後の Ca^{2+}応答
Are the immotile nodal cilia in mouse embryo mechanosensors?: Ca^{2+} signaling response after mechanical stimulation by optical tweezers
Takanobu A Katoh, Katsutoshi Mizuno, Hiroshi Hamada (*BDR, Riken*)

1Pos106 ライブセルイメージングが切り開くシアノバクテリアのヘテロシスト分化空間パターン維持機構
Live cell imaging sheds light on the maintenance mechanism of pattern of cyanobacterial cell differentiation
Shun-ichi Fukushima[1], Takeharu Nagai[1], Shigeki Ehira[2] ([1]*The Institute of Scientific and Industrial Research, Osaka University*, [2]*Department of Biological Sciences, Graduate School of Science, Tokyo Metropolitan University*)

1Pos107 細胞性粘菌における既知のシグナルを用いない細胞分化状態の検出
Detection of cell differentiation states without known signals in *Dictyostelium*
Yusuke V. Morimoto[1,2], Takuro Kawada[1], Masahiro Ueda[2,3] ([1]*Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*BDR, RIKEN*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*)

筋肉／Muscle

1Pos108 (1SGA-2) 心筋細胞に備わる収縮リズム恒常性の分子機構の解明
(1SGA-2) Elucidation of molecular mechanism of contraction rhythm homeostasis in cardiac myocytes
Seine Shintani[1], Takumi Washio[2] ([1]*Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University*, [2]*Graduate School of Frontier Sciences, the University of Tokyo*)

1Pos109 トロポニン T の E244D 変異による細いフィラメント構造変化の X 線小角散乱解析
Structural changes of cardiac thin filaments caused by E244D mutation of troponin T observed by small-angle X-ray scattering
Tatsuhito Matsuo, Satoru Fujiwara (*Inst. Quant. Life Sci., QST*)

1Pos110 分子動力学計算によるミオシンの第二リン酸結合部位の検証
Validation of second phosphate binding site in myosin studied by molecular dynamics simulation
Kouei Uchida, Jun Ohnuki, Takato Sato, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1Pos111 ミオシンのアクチンに対する結合親和性の低温における弱化を説明するための統計熱力学
Statistical thermodynamics on the weakening of binding affinity of myosin for actin at low temperatures
Tomohiko Hayashi, Masahiro Kinoshita (*Inst. Adv. Energy, Kyoto Univ.*)

1Pos112 1 分子・多分子実験から迫る、心機能に適した心筋ミオシンの性質
Reverse stroke of cardiac myosin revealed by single molecule microscopy is essential for heart function
Yongtae Hwang[1], Takumi Washio[2], Hideo Higuchi[1], Motoshi Kaya[1] ([1]*Department of Physics, The University of Tokyo*, [2]*Department of Human and Engineered Environmental Studies, The University of Tokyo*)

分子モーター／Molecular motor

1Pos113* 負荷に依存した細菌べん毛モーター回転速度の調節機構
Load-dependent speed regulation of the bacterial flagellar motor
Tsubasa Ishida[1], Myu Yoshida[2], Tohru Minamino[3], Yoshiyuki Sowa[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [4]*Res. Cent. Micro-Nano Tech., Hosei Univ.*)

1Pos114* F_1-ATPase の阻害状態解析
Analysis of the inhibited form of F_1-ATPase
Sougo Mori, Hiroshi Ueno, Hiroyuki Noji (*Noji laboratory, Department of Applied Chemistry, Graduate School of Engineering, University of Tokyo*)

1Pos115* Na^+の存在に依存するべん毛モーター固定子 PomAB における複合体の解離
Destabilization of the complex formation allows high Na^+ conduction in the PomAB flagellar stator complex
Tatsuro Nishikino, Hiroto Iwatsuki, Taira Mino, Seiji Kojima, Michio Homma (*Div. Biol. Sci. Grad. Sch. Sci., Nagoya Univ.*)

1Pos116* Biomolecular motor driven cargo transportation by microtubules as a mechanosensor
Syeda Rubaiya Nasrin[1], Arif Md. Rashedul Kabir[2], Kazuki Sada[1,2], Akira Kakugo[1,2] ([1]*Grad. Sch. Chem. Sci. and Engg., Hokkaido Univ.*, [2]*Fac. Sci., Hokkaido Univ.*)

1Pos117* ハイブリッド F_1-ATPase の 1 分子回転観察
Rotation observation of hybrid F_1-ATPases between bacterial and mammalian ones
Ryo Watanabe[1], Hiroshi Ueno[1], Toshiharu Suzuki[2], Ryohei Kobayashi[1], Hiroyuki Noji[1] ([1]*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*CLS., Tokyo tech.*)

1Pos118* 生体分子群ロボットによる光制御時空間貨物輸送
Photo-regulated spatiotemporal cargo transportation by biomolecular swarm robot
Mousumi Akter[1], Jakia Jannat Keya[2], Arif Md. Rashedul Kabir[2], Hiroyuki Asanuma[3], Kuzuya Akinori[4], Kazuki Sada[1,2], Akira Kakugo[1,2] ([1]*Graduate School of Chemical Science and Engineering, Hokkaido University, Sapporo 060-0810, Japan*, [2]*Faculty of Science, Hokkaido University, Sapporo 060-0810, Japan*, [3]*Department of Biomolecular Engineering, Nagoya University, Nagoya, Japan*, [4]*Department of Chemistry and Materials Engineering, Kansai University, Osaka 564-8680, Japan*)

1Pos119* べん毛モーターの分子軸受 LP リングのクライオ電子顕微鏡による構造解析
CryoEM structural analysis of the bacterial flagellar LP ring ~ a molecular bushing of the bacterial motor with almost no friction ~
Tomoko Yamaguchi[1,2], Fumiaki Makino[1,3], Tomoko Miyata[1], Takayuki Kato[1], Keiichi Namba[1,2,4] ([1]*Grad. Sch. FBS, Univ. Osaka*, [2]*BDR, Riken*, [3]*JEOL Ltd.*, [4]*Spring-8, Riken*)

1Pos120 べん毛フックの自然な構造
Structure of the native supercoiled flagellar hook
Takayuki Kato[1], Tomoko Miyata[1], Fumiaki Makino[1,2], Peter Horvath[1], Keiichi Namba[1,3] ([1]*Front. Bio., Osaka univ.*, [2]*JEOL*, [3]*BDR, Riken*)

1Pos121 細菌べん毛基部体の極低温電子顕微鏡による構造解析
Structure analysis of the bacterial flagellar basal body by electron microscopy
Tomoko Miyata[1], Takayuki Kato[1], Fumiaki Makino[1,2], Yumiko Saijo[3], Keiichi Namba[1,4] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*JEOL Ltd*, [3]*Grad. Sch. Med., Kobe Univ.*, [4]*BDR&SPring8, RIKEN*)

1Pos122 Structure of motor evolved by combination of F-ATPase and phosphoglycerate kinase for *Mycoplasma mobile* gliding
Takuma Toyonaga[1], Takayuki Kato[2], Akihiro Kawamoto[3], Tasuku Hamaguchi[4], Keiichi Namba[2,4,5], Makoto Miyata[1,6] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*IPR, Osaka Univ.*, [4]*SPring-8, RIKEN*, [5]*BDR, RIKEN*, [6]*OCARINA, Osaka City Univ.*)

1Pos123 コンデンシン分子モーターの DNA カーテン測定と構造モデリング
DNA curtain assay and structural modeling of condensin molecular motor
Hiroki Koide, Shoji Takada, Tsuyoshi Terakawa (*Dept Biophysics, Div Biology, Grad School Science, Kyoto University*)

1Pos124 nanodisc-Vo の再構成条件検討と単粒子解析
The Investigation of reconstruction and Single Particle Analysis of nanodisc-Vo
Aya Furuta[1], Jun-ichi Kishikawa[1], Takayuki Kato[2], Atsuko Nakanishi[1], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Div. Life Sci., Kyoto Sangyo Univ.*, [2]*Grad. Sch. Frontier Biosci.,Osaka Univ.*, [3]*Res. Ctr. UHVEM., Osaka Univ.*)

1Pos125 クシクラゲの櫛板はシンクロトロン放射光による繊毛軸糸の構造・機能解析に最適な試料である
Synchrotron radiation X-ray diffractionv reveals the highly ordered structure of axonemes in the comb plate of ctenophores
Hiroyuki Iwamoto[1], Kei Jokura[2], Kazuo Inaba[2] ([1]*SPring-8, JASRI*, [2]*Shimoda Marine Res. Ctr., Univ. Tsukuba*)

1Pos126 Unidirectional-rotation and helical-motion of a cargo on a microtubule indicate torque generation and biased sideward binding of kinesin
Mitsuhiro Sugawa, Yohei Maruyama, Masahiko Yamagishi, Junichiro Yajima (*Grad. Sch. Arts and Sciences, Univ. Tokyo*)

1Pos127 ウシミトコンドリア由来 F_1-ATPase の 1 分子回転解析
Single-molecule analysis of bovine mitochondrial F_1-ATPase
Ryohei Kobayashi, Hiroshi Ueno, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

1Pos128 二つの頭部のつながり方がミオシン VI の歩行運動に与える影響
Effects of interhead connection on the stepping motion of myosin VI
Tomoki P. Terada[1], Qing-Miao Nie[2], Masaki Sasai[1] ([1]*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*, [2]*Dept. Appl. Phys., Zhejiang Univ. Tech.*)

1Pos129 Allosteric Regulation of V_1-ATPase by Designing Non-catalytic Interface
Takahiro Kosugi[1,2,3], Tatsuya Iida[2], Mikio Tanabe[4], Ryota Iino[1,2], Nobuyasu Koga[1,2,3] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*, [3]*ExCELLS*, [4]*KEK*)

1Pos130 キネシン-1 人工多量体のプロセシビティと一方向運動性の評価
Evaluation of processivity and unidirectionality of artificial kinesin-1 oligomers
Kimitoshi Takeda, Akihiko Nakamura, Jun Ando, Ryota Iino (*Institute for Molecular Science*)

1Pos131 DNA ナノフィラメント上を移動する改変型ダイニンを用いた人工輸送システムの創生
Creating artificial transport systems by using engineered dynein that moves along DNA nanofilament
Ryota Ibusuki[1], Tatsuya Morishita[1], Akane Furuta[2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICR. Res. Ins., NICT. Kobe*)

1Pos132 DNA 上を動く改変ダイニンを用いて結合性と運動速度の関係を系統的に調べる
Systematic studies on the relation between binding kinetics and speed of movement using engineered DNA-based dynein motor
Tatsuya Morishita[1], Ryota Ibusuki[1], Akane Furuta[2], Kazuhiro Oiwa[1,2], Hiroaki Kojima[2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICT Res. Inst NICT*)

1Pos133 Fo 回転モーターにおける固定子ー回転子間相互作用の自由エネルギー地形
Free energy landscape for stator-rotor interaction in Fo rotary motor
Dan Parkin, Daiki Yamakoshi, Genya Nakagawa, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

1Pos134 ミオシン頭部の自由エネルギーランドスケープのスイッチングを考慮した筋収縮の三状態モデル
Three-state model of muscle contraction with switched free energy landscapes for myosin heads
Kaima Matsuda, Masaki Sasai, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

1Pos135 DNA オリガミを用いたミオシンフィラメントでのミオシン II モーターの高速原子間力顕微鏡による同時観察
Simultaneous observation of individual myosin II motors in DNA origami-based thick filaments by high-speed AFM
Masashi Ohmachi[1], Hiroaki Takagi[2], Keigo Ikezaki[3], Toshio Yanagida[1,4], Mitsuhiro Iwaki[1,4] ([1]*BDR, RIKEN*, [2]*Nara Med. Univ.*, [3]*Univ. Tokyo*, [4]*Grad. Sch. Front. Biosci., Osaka Univ.*)

1Pos136 アクトミオシン運動に対するリゾチームの阻害作用
Inhibitory effect of lysozyme on the motility of actomyosin
Masaki Okami, Kuniyuki Hatori (*Grad.Sch.Sci.Eng., Yamagata Univ.*)

1Pos137 ダイナクチンサイドアームのコンフォメーション変化
Multiple conformational changes of dynactin sidearm revealed by single molecule observation
Kei Saito[1], Takuya Kobayashi[2], Takashi Murayama[2], Mitsuhiro Sugawa[1], Christian Ganser[3], Takayuki Uchihashi[3,4], Junichiro Yajima[1], Yoko Y. Toyoshima[1] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*Dept. of Pharmacology, Juntendo Univ. Sch. of Med.*, [3]*NINS, ExCELLS*, [4]*Dept. of Phys., Nagoya Univ.*)

1Pos138 The contribution of microtubule-binding ability of dynactin in dynein behaviors on microtubules
Takuya Kobayashi[1], Kei Saito[2], Takuya Miyashita[2], Yoko Y Toyoshima[2], Takashi Murayama[1] ([1]*Dept. Pharmacology, Juntendo Univ.*, [2]*Grad. sch. Arts and Sci. Univ. Tokyo*)

細胞生物的課題／Cell biology

1Pos139* (3SDA-6) 集団細胞遊走における機械的なシグナルを介した ERK 活性伝播
(3SDA-6) ERK activation waves mediated by intercellular mechanical signals during collective cell migration
Naoya Hino[1], Xavier Trepat[2], Michiyuki Matsuda[1,3], Tsuyoshi Hirashima[3] ([1]*Grad. Sch. of Biostudies, Kyoto Univ.*, [2]*IBEC, Spain*, [3]*Grad. Sch. of Med., Kyoto Univ.*)

1Pos140* スピロプラズマの螺旋交換遊泳を駆動する内部リボン構造
Internal ribbon structure driving helicity-switching swimming of *Spiroplasma*
Yuya Sasajima[1], Takayuki Kato[2], Tomoko Miyata[2], Keiishi Namba[2,3], Makoto Miyata[1,4] ([1]*Grad. Sch. Sci., Osaka City Univ., Japan*, [2]*Grad. Sch. Front. Biosci., Osaka Univ., Japan*, [3]*BDR & SPring-8 Center, Riken, Japan*, [4]*OCARINA, Osaka City Univ., Japan*)

1Pos141* 液-液相分離における荷電性残基の影響に関する分子動力学シミュレーション
Molecular dynamics simulations to dissect effects of charged residues on liquid-liquid phase separation
Hiroki Terazawa[1], Kota Kasahara[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

1Pos142* *Spiroplasma eriocheiris* の遊泳運動にかかわる細菌のアクチン MreB の重合
Polymerization of bacterial actin MreB involved in swimming motility of *Spiroplasma eriocheiris*
Daichi Takahashi[1], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci, Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*)

1Pos143* クラミドモナス細胞の鞭毛打頻度を用いた細胞内 ATP 濃度の推定
Estimation of intracellular ATP concentration from the flagellar beat frequency in *Chlamydomonas*
Wakako Takano[1,2], Toru Hisabori[1,2], Ken-ichi Wakabayashi[1,2] ([1]*CLS, Tokyo Tech*, [2]*LST, Tokyo Tech*)

1Pos144* 細菌バイオフィムの高次秩序構造
High structural order in bacteria biofilms
Kohei Takahashi[1], Kana Morinaga[1,2], Masanonri Toyofuku[3,4], Utada Andrew[3,4] ([1]*Graduate school of Life and Environment Science, University of Tsukuba*, [2]*Bioproduction Research Institute, Advanced Industrial Science and Technology*, [3]*Faculty Life Environment Science, University of Tsukuba*, [4]*Microbiology Research Center for Sustainability (MiCS), University of Tsukuba*)

1Pos145* 合成細菌における *Spiroplasma eriocheiris* 遊泳運動の再現
Reconstitution of *Spiroplasma eriocheiris* swimming motility in a synthetic bacterium
Hana Kiyama[1], Shigeyuki Kakizawa[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*AIST,Bioprocess*, [3]*OCARINA, Osaka City Univ.*)

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

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

1Pos148 ゼブラフィッシュ胚上皮組織に内在する力が創傷治癒を制御する
Residual Stress-mediated wound healing in zebrafish epithelia
Sohei Yamada[1], Yasumasa Bessho[2], Yoichiroh Hosokawa[1], Takaaki Matsui[2] ([1]*Division of Materials Science, Nara Institute of Science and Technology*, [2]*Division of Biological Science, Nara Institute of Science and Technology*)

1Pos149 TIRF 観察によるアクチン重合・脱重合における蛍光標識の影響
Effects of Dye Labels on Actin Assembly and Disassembly
Ikuko Fujiwara[1], Shuichi Takeda[2], Toshiro Oda[5], Thomas Pollard[3], Naomi Courtemanche[4], Akihiro Narita[2], Yuichiro Maeda[2] ([1]*Grad.Sch.Sci., Osaka City Univ.*, [2]*Structural Biol. Res. Cent. Gad. Sch.Sci., Nagoya Univ.*, [3]*MCDB, Yale Univ., USA*, [4]*Univ. Minnesota, USA*, [5]*Tokaigakuin Univ.*)

1Pos150 変異リアノジン受容体の分子動力学シミュレーション
Molecular dynamics simulation of mutant ryanodine receptors
Toshiko Yamazawa[1], Haruo Ogawa[2], Maki Yamaguchi[1], Takashi Murayama[3], Hideto Oyamada[4], Nagomi Kurebayashi[3], Junji Suzuki[5], Kazunori Kanemaru[6], Katsuji Oguchi[4], Takashi Sakurai[3], Masamitsu Iino[6] ([1]*Dept Mol. Physiol., Jikei Univ. Sch. Med.*, [2]*Institute Quantitative Biosci., The Univ.Tokyo*, [3]*Dept. Pharmacol., Juntendo Univ. Sch. Med.*, [4]*Dept. Pharmacol., Sch. Med., Showa Univ*, [5]*Dept. Physiol., Univ. California San Francisco*, [6]*Dept. Cell. Mol. Pharmacol., Nihon Univ. Sch. Med.*)

1Pos151 脱重合が引き起こす接着斑周囲におけるアクチン細胞骨格の向きの変化
The change of the direction of F-actin caused by the filament disassembly around focal adhesions
Kiyoshi Tohyama[1], Sawako Yamashiro[2], Naoki Watanabe[1,2] ([1]*Department of Pharmacology, Kyoto University Faculty of Medicine*, [2]*Laboratory of Single-Molecule Cell Biology, Kyoto University Graduate School of Biostudies*)

1Pos152 クラミドモナス鞭毛の根元に局在するマイナータイプダイニンの機能解析
Functional analysis of minor-type axonemal dyneins located to the basal region of *Chlamydomonas* flagella
Tomohiro Komatsu, Yusuke Kondoh, **Toshiki Yagi** (*Dept. Life Sci., Pref. Univ. Hiroshima*)

1Pos153 共焦点レーザー走査型顕微鏡で捉えた軸索タンパクのブラウン運動
Brownian motions of axonal proteins captured by a confocal laser scanning microscopy
Kazunari Mouri[1], Yasushi Okada[1,2] ([1]*RIKEN, BDR*, [2]*Univ. Tokyo, Grad. Sch. Sci., Dept. Phys.*)

1Pos154 生体内光架橋によるべん毛回転子タンパク質 FliG と固定子タンパク質 PomA 間相互作用の検出
Interaction between the flagellar rotor protein FliG and the stator protein PomA in cells detected by *in vivo* photo-crosslink
Seiji Kojima, Hiroyuki Terashima, Michio Homma (*Div. Biol. Sci., Grad. Sch. Sci., Nagoya University*)

1Pos155 ケラトサイトの回転するストレスファイバ車輪の内側の核と外側の細胞膜の動き
Movement of inner nucleus and outer cell membrane of a rotating stress fiber-wheel in a migrating keratocyte
Chika Okimura, Yoshiaki Iwadate (*Fac. Sci., Yamaguchi Univ.*)

1Pos156 バクテリアべん毛タンパク質輸送装置のゲート機構
Gating mechanism of the bacterial flagellar protein export apparatus
Miki Kinoshita[1], Keiichi Namba[1,2,3], Tohru Minamino[1] ([1]*Grad. Sch. Frontier Biosci, Osaka Univ.*, [2]*RIKEN, Spring-8*, [3]*RIKEN, BDR*)

1Pos157 スピロヘータの遊泳におけるべん毛回転と細胞形状の関係
Relationship between the flagellar rotation and cell shape in a swimming spirochete
Toshiki Kuribayashi, Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)

1Pos158 正のべん毛本数制御因子 FlhF は MS リング構成因子 FliF の極局在を促進する
The polar localization of FliF, composing MS-ring, is promoted by FlhF in Vibrio alginolyticus
Yuna Inoue, Seiji Kojima, Keiichi Hirano, Hiroyuki Terashima, Michio Homma (*Division of Biological Science, Graduate School of Science, Nagoya University*)

1Pos159 超解像顕微鏡法と単粒子追跡法による標的細胞へのエクソソーム取り込み機構の解明
Uptake mechanism of exosomes by target cells as revealed by super-resolution microscopy and single-particle tracking
Koichiro M. Hirosawa[1], Taka A. Tsunoyama[2], Yasunari Yokota[3], Kenichi G. N. Suzuki[1,4] ([1]*G-CHAIN, Gifu Univ.*, [2]*OIST*, [3]*Information Science, Gifu University*, [4]*JST-CREST*)

1Pos160 ミトコンドリアの形態と活性の間に相関はあるか？
Are there any correlations between the morphology and the activity of mitochondria?
Arima Okutani (*Tokyo University of Agriculture and Technology*)

1Pos161 酸素への電子伝達阻害時のミトコンドリアの分極機構
Mitochondrial polarization upon inhibition of electron transfer to oxygen
Hinako Tanaka[1], Emika Shida[1], Ikuroh Ohsawa[2], Yoshihiro Ohta[1] ([1]*Grad. Sch. Biotech., TUAT*, [2]*Bioregulatory function., TMGH*)

1Pos162 Single-molecule imaging of PI3K in eukaryotic motile cell
Satomi Matsuoka[1,2,3], Seiya Fukushima[1], Masahiro Ueda[1,2] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*Center for Biosystems Dynamics Research, RIKEN*, [3]*PRESTO, JST*)

1Pos163 温度条件に依存して変化する、大腸菌走化性適応過程の定量解析
Quantitative analysis of E. coli chemotaxis adaptation process that changes depending on temperature conditions
Hiroto Tanaka, Yasuaki Kazuta, Hiroaki Kojima (*Adv ICT Res Inst, NICT*)

1Pos164 細胞辺縁での Aβ の凝集は細胞運動を抑制した
Aggregation of Aβ at the cell periphery suppressed cell motility
Yusaku Chikai, Ryota Yamashita, Masahiro Kuragano, Kiyotaka Tokuraku (*Grad. Sch. Eng., Muroran Inst. Tech.*)

1Pos165 Mechanisms of negative gravitaxis in free-swimming *Chlamydomonas reinhardtii*
Azusa Kage[1], Toshihiro Omori[2] ([1]*Dept. Mech. Eng., Toyohashi U. Tech.*, [2]*Dept. Finemechanics, Tohoku U.*)

1Pos166 孤立した MDCK 細胞における形態および運動の多様性
Diversity in morphological and motile patterns of isolated MDCK epithelial cells
Shimon Shibagaki[1], Shota Mise[1], Seiya Nishikawa[1], Hiroko Nakamura[2], Hiroshi Kimura[2], Atsuko Takamatsu[1] ([1]*Dept. of Elec., Eng. & Biosci., Waseda Univ.*, [2]*Dept. of Mecha., Tokai Univ.*)

生体膜・人工膜／Biological & Artificial membrane: Structure & Property

1Pos167* リン脂質スクランブラーゼ XKR による昆虫細胞膜の高粘弾性変形能
Enhanced viscoelastic deformation of insect cell membrane by phospholipid scramblase XKR
Akifumi Shiomi[1], Kohjiro Nagao[1], Akihisa Yamamoto[2], Ryo Suzuki[2], Motomu Tanaka[2], Masato Umeda[1] ([1]*Grad. Sch. Eng., Kyoto Univ.*, [2]*Inst. Adv. Stud., Kyoto Univ.*)

1Pos168* ピコ秒時間分解けい光分光法で評価した膜標的薬物の人工脂質二重膜への影響
Effect of membrane-targeted drugs on artificial lipid bilayer membranes evaluated by picosecond time-resolved fluorescence spectroscopy
Natsumi Okada[1], Masayuki Iwamoto[2], Haruna Hayashi[1], Akira Takakado[1], Shigetoshi Oiki[3], Koichi Iwata[1] ([1]*Faculty of Science, Gakushuin University*, [2]*Faculty of Medical Sciences, University of Fukui*, [3]*Biomedical Imaging Research Center, University of Fukui*)

1Pos169* ボトムアップ配列設計による α-ヘリックスペプチドナノポアの構築
De novo design for pore-forming peptides with α-helical structure
Masataka Usami, Keisuke Shimizu, Yusuke Sekiya, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

1Pos170* 脂質膜中にナノポアを構築する β シートペプチドの De novo 配列設計
De novo design of nanopore-forming β-sheet peptide in bilayer lipid membrane
Keisuke Shimizu[1], Shungo Sakashita[2], Yoshio Hamada[2], Kenji Usui[2], Batsaikhan Mijiddorj[3], Izuru Kawamura[1], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, [2]*Faculty of Frontiers of Innovative Research in Science and Technology, Konan University*, [3]*Department of Materials Science and Engineering, Yokohama National University*)

1Pos171* Investigation of local anesthetic and membrane interactions using model cell membranes
Wanjae Choi[1], Hyunil Ryu[1], Seulmini Goh[1], Chaoge Zhou[1], Soonjo Kwon[1], Sun Min Kim[2], Tae-Joon Jeon[1] ([1]*Department of Biological Engineering, Inha University, Incheon*, [2]*Department of Mechanical Engineering, Inha University, Incheon*)

1Pos172 環状ジペプチドの安定構造における系統的な傾向と特徴
Systematic trends and features in the stable structure of cyclic dipeptides
Koki Yanagi[1,2], Hiroaki Nishizawa[2], Ryunosuke Yoshino[2], Ryuhei Harada[2], Yasuteru Shigeta[2] ([1]*Phys., Pure and Applied Sci., Grad. Sch. Univ. Tsukuba*, [2]*CCS, Univ. Tsukuba*)

1Pos173 Ca2+-dependent high-conductance channel activity of F-ATP synthase matches the permeability transition pore
Andrea Urbani[1,2,5,6], Valentina Giorgio[2], Andrea Carrer[2], Cinzia Franchin[2], Giorgio Arrigoni[2], Chimari Jiko[3], Kazuhiro Abe[7], Janna F.M. Bogers[4], Shintaro Maeda[6], Kyoko Shinzawa[5], **Christoph Gerle**[1], Ildiko Szabo[2], Paolo Bernardi[2] ([1]*IPR*, [2]*Univ. Padova*, [3]*Kyoto Univ.*, [4]*TU Delft*, [5]*Univ. Hyogo*, [6]*Scripps*, [7]*Nagoya Univ.*)

1Pos174 P-SPICA: A coarse-grained force field for biological systems with a polar coarse-grained water model
Yusuke Miyazaki, Susumu Okazaki, Wataru Shinoda (*Grad. Sch. Eng., Nagoya Univ.*)

1Pos175 光照射によるリポソーム内への配列選択的 DNA 輸送
Sequence selective DNA transport into liposome by photoirradiation
Shigetaka Nakamura, Nobuharu Uehara, Takashi Hasegawa, Kenzo Fujimoto (*JAIST*)

1Pos176 生細胞膜上における相分離の誘発と可逆的制御
Induction and reversible control of phase separation on living cell membranes
Kenichi Kawano[1], Yasufumi Takahashi[2], Ryo Ohtani[3], Masanao Kinoshita[4], Shiroh Futaki[1] ([1]*Institute for Chemical Research, Kyoto University*, [2]*WPI-NanoLSI, Kanazawa University*, [3]*Department of Chemistry, Faculty of Science, Kyushu University*, [4]*Graduate School of Science, Kyushu University*)

1Pos177 気液界面における人工肺サーファクタント膜への微粒子の影響
Effect of sub-micron particles on a model lung surfactant monolayer at the air-water interface
Masahiro Hibino[1], Toshiki Kamata[2] ([1]*Div. Sust. Enviro. Eng., Muroran Inst. Tech.*, [2]*Dept. Appl. Sci., Muroran Inst. Tech.*)

1Pos178 On the condensing effects of 7β-hydroxycholesterol, 25-hydroxycholesterol, and cholesterol on DPPC bilayers
Hiroshi Takahashi, Tatsuya Hoshino (*Biophys. Lab., Grad. Sch. Sci.&Tech., Gunma Univ.*)

1Pos179 蛍光寿命測定を用いた脂質二重膜におけるセラミド-1-リン酸の動的挙動解析
Dynamic behavior of ceramide-1-phosphate in lipid bilayers examined by fluorescence lifetime measurement
Tomokazu Yasuda[1,2], J. Peter Slotte[3] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Research Foundation Itsuu Laboratory*, [3]*Åbo Akademi Univ.*)

1Pos180 Molecular dynamics simulation of the mechanical properties of lipid membranes in the presence of proteins
Diego Ugarte, Shoji Takada (*Takada Lab., Dept. Biophysics, Div. Biology, Grad. Sch. of Sci., Kyoto Univ.*)

1Pos181 EGFR 膜近傍領域のリン酸化が EGFR TM-JM 二量体構造に及ぼす影響
The impact of phosphorylation in the EGFR JM region on the dimer structure of EGFR TM-JM region
Daisuke Matsuoka[1], Yuji Sugita[1,2,3] ([1]*RIKEN Theoretical Molecular Science*, [2]*RIKEN R-CCS*, [3]*RIKEN BDR*)

1Pos182 The dipole potential probed by hydrophobic ions using the contact bubble bilayer method
Yuka Matsuki[1], Masayuki Iwamoto[2], Mariko Yamatake[2], Shigetoshi Oiki[3] ([1]*Dept. Anesth & Reanmat., Univ. Fukui Facult. Med. Sci.*, [2]*Dept. Mol. Neurosci., Univ. Fukui Facult. Med. Sci.*, [3]*Biomed. Imaging Res. Center, Univ. Fukui*)

1Pos183 膜活性な両親媒性ランダムコポリマーによる脂質ナノディスクの自発形成
Spontaneous formation of lipid nanodisc by membrane active amphiphilic random copolymer
Kazuma Yasuhara, Mitsuyoshi Yuma, Jinyu Hao, Jin Arakida, Rapenne Gwenael, Jun-ichi Kikuchi (*Div. Mater. Sci., Nara Inst. Sci. Tech.*)

1Pos184 動的および静的光散乱法によるリン脂質ベシクルの構造評価 2
Structural evaluation of phospholipid vesicles by dynamic and static light scattering techniques 2
Nobutake Tamai[1], Takeshi Nobuoka[2], Ryo Takechi[2], Masaki Goto[1], Hitoshi Matsuki[1] ([1]*Grad. Sch. Tech. Indus. Soc. Sci., Tokushima Univ.*, [2]*Dept. Biol. Tech. Sci., Col. Eng., Tokushima Univ.*)

1Pos185 脂質膜外葉のみに形成したラフト様秩序領域の物性とそれが内葉に及ぼす影響
Physicochemical properties of raft-like ordered domains formed in outer leaflet and its influence on the inner leaflet
Takuya Koga, Masanao Kinoshita, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ.*)

1Pos186 三種のリン脂質/コレステロール・リポソームにおけるクロルゾキサゾン捕捉量とコレステロール濃度との相関
Correlation between the amount of trap of chlorzoxazone by various phospholipid/cholesterol liposomes and their cholesterol concentrations
Shosei Kano, Hiroshi Takahashi (*Biophys. Lab., Grad. Sch. Sci.&Tech., Gunma Univ.*)

1Pos187 ジミリストイルホスファチジルコリン 2 重膜に形成された脂質様錯体ドメインの物理化学的特性
Physico-chemical properties of lipophilic complex-rich domains formed in dimyistoylphosphatidylcholine (DMPC) bilayers
Hikaru Watanabe, Yoshinao Kinoshita, Ryo Ohtani, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ.*)

1Pos188 低流量電子線散乱法を用いた局所的な脂質充填構造の解析
Low-flux election-diffraction discloses the local structure of lipid membrane
Shimpei Yamaguchi, Masanao Kinoshita, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ.*)

化学受容／Chemoreception

1Pos189* 全反射赤外分光法によるムスカリン性アセチルコリン M2 受容体のリガンド認識、活性化機構研究
Ligand recognition and activation mechanism in muscarinic acetylcholine receptor M2 (M2R) study by ATR-FTIR spectroscopy
Kohei Suzuki[1], Kodai Katayama[1], Ryoji Suno[2], Hideki Kandori[1] ([1]*Nagoya Institute of Technology*, [2]*Kansai Medical University*)

1Pos190 コレラ菌タウリン走性受容体 Mlp37 の制御ネットワーク
The regulatory network controls expression of the taurine chemoreceptor Mlp37 in *Vibrio cholerae*
So-ichiro Nishiyama[1], Hirotaka Tajima[2,3], Shiori Onogi[2], Hiroshi Urakami[1], Ikuro Kawagishi[2,3] ([1]*Fac. App. Life Sci., Niigata Univ. Pharm. App. Life Sci.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

1Pos191 大腸菌グローバル転写因子 PdhR による走化性受容体遺伝子発現調節
Expression of the major chemoreceptor genes is regulated by a global transcription factor PdhR in *Escherichia coli*
Ayano Inoue[1], Nana Ito[1], Yumeno Kawasaki[1], Eri Shiokawa[1], Hirotaka Tajima[2,3], Ikuro Kawagishi[1,2,3] ([1]*Grad. Sch.Sci.&Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

1Pos192 大腸菌細胞側面膜領域における走化性受容体クラスター形成
Chemoreceptor clustering of *Escherichia coli* in lateral regions of the cytoplasmic membrane
Nana Ito[1], Masatoshi Nishikawa[2], Yoshiyuki Sowa[1,2,3], Ikuro Kawagishi[1,2,3] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

1Pos193 細菌の可溶性走化性受容体と細胞膜貫通型走化性トランスデューサー相互作用解析
Probing interaction between a soluble receptor and a transmembrane transducer in bacterial chemotaxis
Hisashi Kubota[1], Kana Murakami[2], Hirotaka Tajima[2,3], Ikuro Kawagishi[1,2,3] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Res. Cen. Micro-Nano Tech., Hosei Univ.*)

神経・感覚／Neuroscience & Sensory systems

1Pos194* 脳脊髄液流動を想定した非平衡空間におけるアミロイド β 凝集
Amyloid β Aggregation in Non-equilibrium Space Mimicking Cerebrospinal Fluidic Flow
Akane Iida[1], Kei Unoura[2], Hideki Nabika[2] ([1]*Graduate School of Sci. and Eng., Yamagata Univ.*, [2]*Faculty of Sci., Yamagata Univ.*)

1Pos195* 光ピンセットを用いた AMPA 型グルタミン酸受容体分子操作における神経電気活動変化
Neuronal electrical activity induced by optical trapping of AMPA-type glutamate receptors on neurons
Tatsunori Kishimoto[1,2], Suguru Kudoh[2], Takahisa Taguchi[3], Chie Hosokawa[1,2,4] ([1]*Grad. Sch. Sci., Univ. Osaka City*, [2]*Grad. Sch. Sci. Tech., Univ. Kwansei Gakuin*, [3]*NICT,CiNet*, [4]*PhotoBIO-OIL, AIST-Osaka Univ.*)

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

1Pos197 ミミズの短期記憶メカニズム
Molecular mechanism of short-term memory formation in earthworms
Yoshiichiro Kitamura, Akira Sakane, Hikaru Tsumita (*Department of Mathematical Sciences and Physics, College of Science and Engineering, Kanto Gakuin University*)

神経回路・脳の情報処理／Neuronal circuit & Information processing

1Pos198* 時間依存性の環境変化認識のモデリング：光結合する矩形波発振子のネットワークがもたらす幾何学的フラストレーション
Perception of time-dependent environmental change: A toy model with photo-coupled electronic oscillators composing frustrated network
Hiroshi Ueno, Masatomo Matsushima (*Dep. Med. Info., Grad. Sch. Life Med. Sci., Doshisha Univ.*)

1Pos199 大脳皮質神経細胞の単一配置による神経回路の構築
Construction of neural network with arrangement of single cerebral cortical neuron
Hayato Toriumi, Tomoyuki Kaneko (*LaRC,FB,Hosei Univ*)

1Pos200 緑茶由来カテキンはナメクジの匂い嫌悪条件付け学習による記憶形成を強化する
Green tea-derived catechins enhance the long-term memory formation for an odor-aversive conditioning in the land slug
Yoshimasa Komatsuzaki[1], Keisuke Matsui[2], Kyouka Ishizuka[1], Kouki Tezuka[1], Ken Lukowiak[3], Minoru Saito[4] ([1]*CST, Nihon Univ.*, [2]*Grad. Sch. of Sci. and Tech., Nihon Univ.*, [3]*Hotchkiss Brain Inst., Fac. Med., Univ. Calgary*, [4]*Dept. Biosci., Coll. Hum. Sci., Nihon Univ.*)

1Pos201 Sites for formation and storage of associative motor memory revealed by reversible expression of metabotropic glutamate receptor 1
Yasushi Kishimoto[1], Harumi Nakao[2], Kouichi Hashimoto[3], Kazuo Kitamura[4], Miwako Yamasaki[5], Kazuki Nakao[2], Masahiko Watanabe[5], Masanobu Kano[6], Atsu Aiba[2], Yutaka Kirino[1] ([1]*Kagawa. Sch. Pharm. Sci., Tokushima Bunri Univ.*, [2]*Cent. Dis. Biol. Integr. Med., Univ. Tokyo*, [3]*Sch. Med., Hiroshima Univ.*, [4]*Sch. Med., Univ. Yamanashi*, [5]*Sch. Med., Hokkaido Univ.*, [6]*Sch. Med., Univ. Tokyo*)

光生物学：視覚・光受容／Photobiology: Vision & Photoreception

1Pos202* 光センサー LOV2 ドメインの光反応中間体の構造揺らぎ検出
Time-resolved study on structural fluctuations of transient intermediates of the light sensor LOV2 domain
Shunrou Tokonami, Yusuke Nakasone, Masahide Terazima (*Dep. Chem., Sch. Sci., Kyoto Univ.*)

1Pos203* LOV ドメイン型光活性化アデニル酸シクラーゼ mPAC の光反応ダイナミクス
Photoreaction dynamics of LOV-domain-regulated photoactivated adenylate cyclase mPAC
Misato Ikoma, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

1Pos204* 光センサータンパク質 PYP と下流分子 PBP による励起波長依存的な会合・解離反応ダイナミクス
Excitation wavelength-dependent association and dissociation dynamics between light sensor protein PYP and its downstream protein PBP
Suhyang Kim[1], Yusuke Nakasone[1], Akira Takakado[2], Yoichi Yamazaki[3], Hironari Kamikubo[3], Masahide Terazima[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Grad. Sch. Sci., Univ. Gakushuin*, [3]*Div. Mat. Sci., NAIST*)

1Pos205* TG 法を用いた OCP と FRP の時間分解相互作用ダイナミクスの検出
Detection of time-resolved interaction between OCP and FRP by using transient grating method
Takatoshi Ohata, Yusuke Nakasone, Masahide Terazima (*Grad. Sch. Sci., Univ. Kyoto*)

1Pos206* 固体 NMR による KR2 のレチナール結合ポケットと Na+結合サイト間の水素結合ネットワークの構造解析
Structural analysis of hydrogen-bond networks between retinal binding pocket and Na+ binding site on KR2 by solid-state NMR
Rina Kaneko[1], Arisu Shigeta[2], Toshio Nagashima[3], Toshio Yamazaki[3], Keiichi Inoue[4,5], Hideki Kandori[5], Izuru Kawamura[1,2] ([1]*Grad. Sch. Eng. Sci., Yokohama National Univ.*, [2]*Grad. Sch. Eng., Yokohama National Univ.*, [3]*RIKEN*, [4]*Univ. Tokyo*, [5]*Nagoya Inst. Tech.*)

1Pos207 SEC-SAXS 法によるシロイヌナズナ由来フィトクロム B の構造解析
Structural analysis of Arabidopsis phytochrome B by small-angle X-ray scattering coupled with size-exclusion chromatography
Mao Oide[1,2], Takaaki Hikima[2], Tomotaka Oroguchi[1,2], Takayuki Kato[3], Yuki Yamaguchi[1,2], Shizue Yoshihara[4], Masaki Yamamoto[2], Masayoshi Nakasako[1,2], Koji Okajima[1,2] ([1]*Grad. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 center*, [3]*Grad. Sci. of Front. Biosci., Osaka Univ.*, [4]*Dept. of Biol. Sci., Osaka Pref. Univ.*)

1Pos208 Structural basis of photo-stability of invertebrate rhodopsins
Midori Murakami (*Dept Physics, Nagoya Univ*)

1Pos209 ロドプシンの構成的活性変異体 M257Y のメカニズムに関する分子動力学シミュレーション
Molecular dynamics simulation study on the mechanism of constitutively active mutant M257Y of rhodopsin
Yuichiro Kanamori, Tadaomi Furuta, **Minoru Sakurai** (*Tokyo Tech*)

1Pos210 ラマン光学活性で観るハロロドプシン多量体形成による活性部位の構造変化
Raman optical activity observes a clear structural change of active site caused by trimer formation of halorhodopsin
Shogo Ogawa[1], Tomotsumi Fujisawa[1], Takashi Kikukawa[2,3], Masashi Unno[1] ([1]*Grad. Sch. Sci. Eng., Saga Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*, [3]*GSS, GI-CoRE, Hokkaido Univ.*)

1Pos211 ラマン光学活性による光駆動型内向きプロトンポンプの研究
Near-IR Raman optical activity spectroscopy of inward proton pump rhodopsin
Ryosuke Kuroiwa[1], Tomotsumi Fujusawa[2], Yuki Sudo[3,4], Megumi Kamimura[2], Saki Inoue[3], Masashi Unno[2] ([1]*Grad. Sch. Sci. Eng., Saga Univ.*, [2]*Fac. Sci. Eng., Saga Univ.*, [3]*Grad. Sch. of Med. Dent. & Pharm. Sci., Okayama Univ.*, [4]*Fac. of Pharm. Sci., Okayama Univ.*)

1Pos212 Actinotalea fementans 由来ヘリオロドプシンの物性解析
Molecular properties of Heliorhodopsin from Actinotalea fementans
Rei Abe-Yoshizumi, Ai Muto, Hideki Kandori (*Nagoya Inst. Tech.*)

1Pos213 (6-4)光回復酵素の光反応過程における時間分解分光研究
Time-resolved spectroscopic study on photoreaction of (6-4) photolyase
Daichi Yamada[1], Takashi Nomura[1], Yuna Nakajima[2], Minoru Kubo[1] ([1]*Grad. Sch. Life Sci.*, [2]*Dept. Life Sci., Univ. Hyogo, Japan*)

1Pos214 集光クマリン色素を有する DNA 光回復酵素による高効率光駆動 DNA 修復
Enhanced light-driven DNA repair by DNA photolyase bearing light-harvesting coumarin chromophore
Yuma Terai[1], Ryuma Sato[2], Risa Matsumura[1], Shigenori Iwai[1], **Junpei Yamamoto**[1] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*RIKEN BDR*)

1Pos215 Impact of a water molecule on photoreduction of (6-4) photolyase
Yuhei Hosokawa[1], Ryuma Sato[2], Shigenori Iwai[1], Junpei Yamamoto[1] ([1]*Grad. Sch. Eng. Sci., Univ. Osaka*, [2]*Riken*)

1Pos216 Characterization of Antarctic inward proton pumping microbial rhodopsins (AntRs)
Andrew Harris[1], Mizuho Tomita[2], Luiz Schubert[3], Michalis Lazaratos[4], Ethan Watt[1], Anh Hoang[1], Ana-Nicoleta Bondar[4], Joachim Heberle[3], Furutani Yuji[2], Hideki Kandori[2], Leonid Brown[1] ([1]*University of Guelph, Physics*, [2]*Nagoya Institute of Technology, Life Science and Applied Chemistry*, [3]*Freie Universitat Berlin, Experimental Physics*, [4]*Freie Universitat Berlin, Theoretical Physics*)

1Pos217 Inversion of Proton Transport Direction in Thermophilic Rhodopsin by Neutralizing the Secondary Counterion Asp229
Minori Kiyoshima[1], Takashi Kikukawa[2,3], Tomoyasu Aizawa[2,3], Makoto Demura[2,3], Yuki Sudo[4], Takashi Tsukamoto[2,3] ([1]*Grad. Sch. Life Sci. Hokkaido Univ.*, [2]*Fac. Adv. Life Sci. Hokkaido Univ.*, [3]*GSS, GI-CoRE*, [4]*Grad. Sch. Med. Dent. Pharm. Sci. Okayama Univ.*)

1Pos218 シゾロドプシンの内向きプロトン輸送経路の特性
Characterization of the inward proton transport pathway in Schizorhodopsin
Masae Konno[1,2], Keiichi Inoue[1,3], Rohit Ghai[4], Oded Beja[5], Hideki Kandori[1,2] ([1]*Life Sci. Appl. Chem., Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*Aquatic Microbial Ecology, Biology Centre CAS, Inst. Hydrobiol.*, [5]*Technion - Israel Inst. Tech.*)

光生物学：光合成／Photobiology: Photosynthesis

1Pos219* 紅色光合成細菌由来光捕集反応中心 1 複合体のスペクトル多様性と安定性におけるカルシウムイオンの役割
A dual role for calcium in expanding the spectral diversity and stability of LH1-RC photocomplexes of purple phototrophic bacteria
Michie Imanishi[1], Mizuki Takenouchi[2], Shinichi Takaichi[3], Shiori Nakagawa[4], Yoshitaka Saga[4], Shinji Takenaka[1], Michael Madigan. T[5], Jorg Overmann[6], Zheng-Yu Wang-Otomo[2], Yukihiro Kimura[1] ([1]*Grad. Sch. Agricultural Sci., Kobe Univ.*, [2]*Fac. of Sci., Ibaraki Univ.*, [3]*Fac. of Life Sci., Tokyo Univ. of Agriculture*, [4]*Dep. of Chem., Kindai Univ.*, [5]*Dep. of Microbiol.., Southern Illinois Univ.*, [6]*Microbiol., Braunschweig Univ. of Tech.*)

1Pos220 超分子複合体構造を構成する光合成アンテナ組成の解明
Elucidation of supramolecular components in photosynthetic antenna
Tetsuko Nakaniwa[1], Ryuichi Kano[2], Naoko Norioka[1], Soichiro Seki[2], Ritsuko Fujii[2,3], Genji Kurisu[1] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Sci., Osaka City Univ.*, [3]*OCARINA, Osaka City Univ.*)

1Pos221 Molecular mechanism of pH-dependent electron-flow regulation in photosystem II
Yuichiro Shimada[1], Seiryu Nakajima[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*RIIS, Okayama Univ.*)

1Pos222 緑藻の光捕集アンテナタンパク質 SCP の再構成
In-vitro reconstitution of light-harvesting complexes of a siphonous green alga, *Codium fragile*
Yuki Isaji[1], Nami Yamano[1,2], Masahiko Iha[3], Tetsuko Nakaniwa[4], Rei Toda[5], Naoko Norioka[4], Genji Kurisu[4,5], Ritsuko Fujii[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ*, [2]*OCARINA, Osaka City Univ.*, [3]*SouthProduct Co. Ltd.*, [4]*IPR, Osaka Univ.*, [5]*Grad. Sch. Sci., Osaka Univ.*)

1Pos223 LH2 タンパク質の B800 部位へ再構成したクロロフィル誘導体のスペクトル特性変化に対するテトラピロール環構造の影響
Structural effects of chlorophyll pigments on their spectral properties induced by reconstitution into the B800 site in LH2 protein
Yoshitaka Saga, Madoka Yamashita, Kanji Miyagi (*Faculty of Science and Engineering, Kindai University*)

1Pos224 ガラス基板表面におけるチラコイド膜の再構成と光合成機能解析
Reconstitution and functional analysis of thylakoid membrane on a glass substrate
Takuro Yoneda[1], Yasushi Tanimoto[1], Daisuke Takagi[2], Kenichi Morigaki[1,3] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Grad. Sch. Agr., Univ. Tohoku*, [3]*Biosignal., Univ. Kobe*)

1Pos225 光化学系複合体と酸化グラフェンを用いた水素発生
Hydrogen production using photosystem and graphene oxide
Shunsuke Sone[1], Mriko Miyachi[2], Shota Tanaka[1], Hisataka Ohta[1], Yoshinori Yamanoi[2], Akihide Iwase[1], Akihiko Kudo[1], Hiroshi Nishihara[2], Tatsuya Tomo[1] ([1]*Tokyo University of science*, [2]*The University of Tokyo*)

1Pos226 緑藻ミル糸状体のカロテノイド蓄積における培養時光条件の影響
The effect of different light regimes for carotenoid accumulation of a macro green algae, Codium fragile, in filamentous form
Soichiro Seki (*Osaka city university , department of Chemistry, Research institute for natural science and technology*)

1Pos227 Time-resolved infrared analysis of proton release pathways in photosynthetic water oxidation using a D1-N298A mutant and NO_3^- substitution
Yasutada Okamoto[1], Yuichiro Shimada[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*RIIS, Okayama Univ.*)

1Pos228 QM/MM analysis of the protonation structure of the S_0 state in the water-oxidizing Mn_4CaO_5 cluster
Masao Yamamoto, Shin Nakamura, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

1Pos229 Infrared microspectroscopic study on water oxidation in a single photosystem II microcrystal
Yuki Kato[1], Satoshi Haniu[1], Yoshiki Nakajima[2], Fusamichi Akita[2,3], Jian-Ren Shen[2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci, Nagoya Univ.*, [2]*Res. Inst. Interdiscip. Sci., Okayama Univ.*, [3]*JST-PRESTO*)

1Pos230 光化学系 II の表在性タンパク質による水分解 Mn_4CaO_5 クラスターの S_2 構造異性体平衡の制御機構
Equilibrium of the S_2-state isomers of the water-oxidizing Mn_4CaO_5 cluster in photosystem II regulated by extrinsic proteins
Shota Taguchi[1], Liangliang Shen[2], Guangye Han[2], Jian-Ren Shen[3], Takumi Noguchi[1], Hiroyuki Mino[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Key Lab. Photobiol., Inst. Botany, Chinese Acad. Sci., China*, [3]*Res. Inst. Interdiscip. Sci., Okayama Univ.*)

1Pos231 Dynamics of photosystem II protein complexes as observed by high speed atomic force microscopy
Takaya Tokano[1], Yuki Kato[1], Shogo Sugiyama[2], Takumi Noguchi[1], Takayuki Uchihashi[1,3] ([1]*Grad.Sch.Sci.,Nagoya Univ.*, [2]*Grad.Sch.Phys.,Kanazawa Univ*, [3]*EXCELLS*)

1Pos232* 酵素型ロドプシン（Rh—PDE）の非対称的 pH 効果
Asymmetric pH effect on the enzyme rhodopsin, Rh-PDE
Masahiro Sugiura[1], Kazuho Yoshida[1], Masahiro Hibi[3], Satoshi Tsunoda[1,2], Hideki Kandori[1] ([1]*Nagoya Institute of Technology*, [2]*JST PRESTO*, [3]*Graduate School of Science, Nagoya University*)

1Pos233* 光活性型 bZIP モジュールであるフォトジッパーにおける Gln317 の役割
The role of Gln317 in a light-activatable bZIP module, Photozipper
Itsuki Kobayashi, Osamu Hisatomi (*Grad. Sch. Sci., Univ. Osaka*)

1Pos234* プロトンポンプ型ロドプシンによる緑藻クラミドモナスの 非光化学的消光(NPQ)の人為的光制御
Optical control of non-photochemical quenching (NPQ) in the alga *Chlamydomonas reinhardtii* by light-driven proton pump rhodopsins
Yurie Nagase[1], Keiichi Kojima[1], Saki Inoue[1], Hiroshi Kuroda[2], Ryutaro Tokutsu[3], Shinji Masuda[4], Jun Minagawa[3], Yuichiro Takahashi[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent. & Pharm. Sci. Okayama Univ.*, [2]*RIIS., Okayama Univ.*, [3]*Div. of Environ. Photobiol., NIBB*, [4]*Cent. Biolog. Resources & Informatics, Tokyo Inst. Technol.*)

1Pos235* Theoretical study on molecular mechanics of natural anion channelrhodopsin GtACR1
Takafumi Shikakura, Cheng Cheng, Shigehiko Hayashi (*Kyoto Univ.*)

生命の起源・進化／Origin of life & Evolution

1Pos236 蝶のカモフラージュや擬態模様にみる多要素構造
Multi-component systems of camouflage and mimicry in butterfly wing patterns
Takao Suzuki (*NARO*)

1Pos237 巨大化大腸菌の再生過程可視化
Regeneration of Escherichia coli giant protoplasts
Kazuhito Tabata, Takao Sogo, Yoshiki Moriizumi, Hiroyuki Noji (*Department of Applied Chemistry, The University of Tokyo*)

ゲノム生物学／Genome biology

1Pos238 大腸菌を用いた実験室内進化におけるタンパク質の配列進化速度の制約
Constraint of protein evolution speed in de novo experimental evolution of *E. coli*
Saburo Tsuru[1], Atsushi Shibai[2], Chikara Furusawa[2] ([1]*Sch. of Sci, The Univ. of Tokyo*, [2]*RIKEN BDR*)

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

生命情報科学／Bioinformatics

1Pos240 全原子 Motion Tree による側鎖運動の記述とドメイン運動との連動
Full-atom Motion Tree detects side-chain motions and their coupling with domain motions
Ryotaro Koike, Motonori Ota (*Grad. Sch. Info., Nagoya Univ.*)

1Pos241 マルチカノニカル法を用いた蛋白質球状ドメイン外の相互作用の解析
Analysis of the protein-protein interaction between regions external to globular domains with multi-canonical molecular method
Takuya Shimato[1], Takuya Takahashi[2], Kota Kasahara[2], Junichi Higo[3] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Sim. Studies, Univ. Hyogo*)

1Pos242 並列タンパク質間相互作用予測システム MEGADOCK の高速化・仮想化
Acceleration and virtualization of parallel protein-protein interaction prediction system MEGADOCK
Masahito Ohue[1], Hiroki Watanabe[1,2], Kento Aoyama[1,2], Yutaka Akiyama[1] ([1]*Sch Computing, Tokyo Tech*, [2]*RWBC-OIL, AIST*)

1Pos243 蛋白質における Non-local 接触を持たない領域に関する統計解析
Segments without non-local contacts in protein structures
Kota Kasahara[1], Shintaro Minami[2], Yasunori Aizawa[3], Ryohei Kondo[4], Takuya Shimato[4], Takuya Takahashi[1] ([1]*Coll. Life. Sci., Ristumeikan Univ.*, [2]*EXCELLS, NINS*, [3]*Sch. Life Sci., Tech., TokyoTech*, [4]*Grad. Sch. Life Sci., Ritsumeikan Univ.*)

1Pos244 Direct coupling analysis of amino-acid sequences based on the Hopfield-Potts model
Kai Shimagaki, Martin Weigt (*Sorbonne Universite, Paris-IV*)

数理生物学／Mathematical biology

1Pos245 繊維状粒子凝集の CA タイプ解析
Attempts at CA-type formal analysis of fibrous assembly of particles
Takashi Konno (*Biomath.Med.Univ.Fukui*)

1Pos246 エピジェネティックな状態変化が細胞のがん化に及ぼす影響のランドスケープ理論による解析
Landscape analyses of epigenetic state change in cancerization
Yutaro Kameyama, Masaki Sasai (*Dept. Appl. Phys., Grad. Sch. Eng., Univ. Nagoya*)

1Pos247 筋分化過程で誘導される細胞競合は IGF シグナルを同期化する
Synchronization of IGF signal by cell competition during myogenesis
Fumihiko Hakuno, Masato Masuda, Ryosuke Okino, Shin-Ichiro Takahashi (*Dep. App. Ani. Sci., Grad. Sch. Agri. Life. Sci., The Univ. of Tokyo.*)

1Pos248 モジホコリ変形体における輸送管ネットワークの分岐則
Direct observation of branching rules in transportation network of *Physarum* plasmodium
Masahiro Shibata, Atsuko Takamatsu (*Dept. of Elec., Eng. & Biosci., Waseda Univ.*)

1Pos249 シグナル伝達分子の細胞膜上クラスター形成機構の数理研究
Mathematical study on cluster formation of signaling proteins on the cell membrane
Hiroaki Takagi (*Dep. Phys., Sch. Med., Nara Med. Univ.*)

1Pos250 線虫の graded ニューロンはどのようにして確率的な 2 状態スイッチングダイナミクスを生成するか？
How do graded neurons generate stochastic binary switching dynamics in C. elegans?
Yuishi Iwasaki (*Fac. Eng., Ibaraki Univ.*)

非平衡・発生リズム／Nonequilibrium state & Biological rhythm

1Pos251* Effects of in vivo rhythm-damping mutations to KaiA on circadian rhythm in vitro
Masahiro Wakayama[1], Risa Imada[1], Yuki Nakamoto[1], Rie Kumagai[1], Keisuke Serizawa[2], Masahiro Ishiura[3], Kousuke Maki[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Sch. Sci., Nagoya Univ.*, [3]*Nagoya Univ.*)

1Pos252* Exploring a simply phosphorylation cycle by using phosphorylation site variants of clock protein KaiC
Rie Kumagai[1], Risa Imada[1], Shun Terauchi[1], Yuki Nakamoto[1], Masahiro Ishiura[2], Kosuke Maki[1] ([1]*Grad. Sci, Nagoya Univ*, [2]*Nagoya Univ*)

1Pos253 (1SHA-4) 高圧力下で早くなるシアノバクテリアの概日周期
(1SHA-4) Pressure accelerates the circadian clock of cyanobacteria
Ryo Kitahara[1], Katsuaki Oyama[2], Takahiro Kawamura[2], Keita Mitsuhashi[2], Soichiro Kitazawa[1], Kazuhiro Yasunaga[1], Natsuno Sagara[1], Megumi Fujimoto[2], Kazuki Terauchi[2] ([1]*Pharm. Sci., Ritsumeikan Univ.*, [2]*Life Sci., Ritsumeikan Univ.*)

1Pos254 心筋細胞ネットワークにおける局所伝導ゆらぎの幾何学的理解
Geometrical understanding of the local fluctuation in propagation of excitation conduction in cardiomyocyte network
Shota Aoki[1], Kazufumi Sakamoto[1], Yoshitsune Hondo[2], Akihiro Hattori[3], Masao Odaka[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

1Pos255 Observation of direction-dependent asymmetrical propagation velocities in excitation conduction in a same cardiomyocyte networks on a chip
Kazufumi Sakamoto[1], Shota Aoki[1], Yoshitsune Hondo[2], Masao Odaka[3], Akihiro Hattori[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

計測／Measurements

1Pos256 **水素化アモルファスシリコンと紫外可視光変換で増強されたセンサのためのゲル電気化学素子と分子薄膜**
Gel electrochemical element and molecular film for sensor enhanced by hydrogenated amorphous silicon and ultra violet light conversion
Koki Shimanaka[1], Shota Murakami[1], Kairi Shimazaki[1], Kishiro Seino[1], Hikaru Hatakeyama[1], Shu Mugita[1], Hiroshi Masumoto[2], Takashi Goto[3], Yutaka Tsujiuchi[1] ([1]*Mat Sci Akita Univ*, [2]*FRIS Tohoku Univ*, [3]*IMR Tohoku Univ*)

1Pos257 On-chip differential analysis of sequential phagocytosis on identical position of single macrophages
Yuya Furumoto[1], Toshiki Azuma[1], Amane Yoshida[1], Takahiro Kitahara[2], Tomoyasu Sakaguchi[2], Masao Odaka[3], Akihiro Hattori[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

1Pos258 **水素化アモルファスシリコンに積層した脂質とバクテリオロドプシン複合膜の構造変化観察**
Observation of structural change of lipid film and lipid and bacteriorhodopsin film laminated on hydrogenated amorphous silicon film
Hikaru Hatakeyama[1], Hiroshi Masumoto[2], Takashi Goto[3], Yutaka Tsujiuchi[1] ([1]*MatSci AkitaUNIV*, [2]*FRIS TohokuUNIV*, [3]*IMR TohokuUNIV*)

1Pos259 **高速走査レーザーマイクロダイセクションシステムの開発**
Development of a high-speed scanning laser microdissection system
Masahito Hasegawa[1,2], Yasushi Kudo[2], Minako Hirano[1], Hiroaki Yokota[1] ([1]*Grad.Sch.Creation Photon Indust.*, [2]*Disc Tech*)

1Pos260 **光-電子相関顕微鏡法（CLEM）による同一試料観察に向けた相関・位置合わせ精度の評価**
Evaluation of correlation and alignment accuracy toward the same sample observation by CLEM
Yuki Gomibuchi[1], Risa Ezoe[2], Hiroko Takazaki[1], Takuo Yasunaga[1] ([1]*Dept. of Phys. Info. Tech., Kyushu Inst. Tech.*, [2]*Dept. of Biosci. Bioinfo., Kyushu Inst. Tech*)

1Pos261 **原子間力顕微鏡にひと工夫 ー*Volvox* 1 個体の推進力を「直接」測るー**
A trick to atomic force microscopy enabling direct measurement of forces generated by swimming *Volvox* spheroids
Noriyo Mitome[1,2], Kosaku Horinaga[2], Kazumo Wakabayashi[2], Hikaru Emoto[2], Airi Shintome[2], Kazutaka Fujita[3], Noriko Ueki[4], Ken-ichi Wakabayashi[5], **Katsuya Shimabukuro**[2] ([1]*NIT, Chem. Biochem., Numazu Col.*, [2]*NIT, Chem. Bio. Eng., Ube Col.*, [3]*NIT, NIT, Mech., Ube Col.*, [4]*Sci. Res. Cent., Hosei Univ.*, [5]*CLS, Tokyo Tech*)

バイオイメージング／Bioimaging

1Pos262 Intron seqFISH enables transcriptome-wide visualization of genome organization and nascent transcription in single cells
Yodai Takei[1], Sheel Shah[2], Wen Zhou[1], Eric Lubeck[3], Jina Yun[1], Chee-Huat Linus Eng[1], Noushin Koulena[1], Christopher Cronin[1], Christoph Karp[1], Eric Liaw[2], Mina Amin[4], Long Cai[1] ([1]*California Institute of Technology*, [2]*University of California, Los Angeles*, [3]*Stanford University*, [4]*University of California, Riverside*)

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

1Pos264* Elastin 様ポリペプチドに基づく分子温度センサー
Molecular Thermometer Based on Elastin-Like Polypeptide
Cong Vu, Tetsuichi Wazawa, Takeharu Nagai (*ISIR, Osaka Univ.*)

1Pos265* 新規小分子プローブによるアクチン繊維の可視化と光操作
Visualization and manipulation of actin cytoskeleton by using novel small molecular probes
Takeru Takagi[1], Tasuku Ueno[1], Yusuke Nomura[1], Daisuke Asanuma[2], Yasuteru Urano[1,2,3] ([1]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [2]*Grad. Sch. Med., The Univ. Tokyo*, [3]*AMED, CREST*)

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

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

1Pos268 (1SGA-8) 細胞内動態をサブセルレベルで制御する温和な NanoHeating 技術
(1SGA-8) A Thermodynamic Tool for Mechanobiology Research: Mild Nanoheating Technology to Alter Subcellular Dynamics
Satoshi Arai[1], Nandus Ferdi[2] ([1]*Res. Inst. Sci. Eng., Waseda Univ.*, [2]*WABIOS*)

1Pos269 クライオ電子顕微鏡により明らかになったノロウイルスの動的構造変化
Dynamic Structural Change of Norovirus Revealed by Cryo-electron Microscopy
Chihong Song[1], Reiko Todaka[2], Masaru Yokoyama[3], Naoyuki Miyazaki[4,5], Kenji Iwasaki[4,5], Kazuhiko Katayama[2], Kazuyoshi Murata[1] ([1]*NIPS*, [2]*Kitasato Univ.*, [3]*NIID*, [4]*IPR, Osaka Univ.*, [5]*Univ. Tsukuba*)

1Pos270 化学発光ビリルビンセンサーの開発
Development of bioluminescent unconjugated bilirubin indicator
Yukino Ito[1], Yoshiyuki Arai[2], Mitsuru Hattori[2], Takeharu Nagai[2] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*The Institute of Scientific and Industrial Research, Osaka University*)

1Pos271 高速原子間力顕微鏡 1 分子計測データを用いた粒子フィルタ法によるリンカー DNA 付きヌクレオソームの動的構造解析
Dynamic structure analysis of nucleosome with linker DNAs by particle filter method using single molecule measurement data by HS-AFM
Sotaro Fuchigami[1,2], Toru Niina[1], Shoji Takada[1,2] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*CREST, JST*)

1Pos272 化学発光トロンビンセンサーの開発
Development of chemiluminescent thrombin sensor toward whole body imaging of living mice
Nae Sugiura[1], Mitsuru Hattori[2], Tomoki Matsuda[2], Takeharu Nagai[2] ([1]*Graduate School of Frontier Biosciences, Osaka univ.*, [2]*Institute of Scientific and Industrial Research, Osaka univ.*)

1Pos273 ESPT 型バイオセンサーの設計
Design of fluorescent biosensors based on Excited State Proton Transfer (ESPT) in the chromophore of a fluorescent protein
Kazunori Sugiura[1,2], Toru Hisabori[2], Shoko Mihara[2], Takeharu Nagai[1] ([1]*ISIR, Univ. Osaka*, [2]*CLS, Tokyo Tech*)

1Pos274 4 次元透過型電子顕微鏡：理論とシミュレーション
4-Dimensional Transmission Electron Microscopy: Theory and Simulation
Kuniaki Nagayama (*N-EM Labos LLC*)

1Pos275 環境の温度変化に対する細胞応答の分子機構
The molecular mechanism of cell response to environmental temperature change
Hiroki Shibata[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ of Tokyo*, [2]*PRESTO, JST*)

1Pos276 相平衡状態にある核小体内領域における核小体構成タンパク質の 1 分子動態と超解像分子局在解析
Single-molecule dynamics and localization of nucleolar proteins in phase-separated compartments of nucleolus
Supanut Sirisukhodom[1], Daiki Matsumoto[1], Yuma Ito[1], Noriko Saitoh[2], Kumiko Sakata-Sogawa[3], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Tech*, [2]*Dept. of Cancer Biol., The Cancer Inst. JFCR.*, [3]*Grad. Sch. Agr. Sci., Tohoku Univ.*)

1Pos277 Development of designable RNA-binding proteins for visualization and manipulation of authentic RNAs in living cells
Akira Takai[1], Yasushi Okada[1,2] ([1]*BDR, RIKEN*, [2]*Univ. of Tokyo, Grad. Sch. of Sci., Dept. of Phys.*)

1Pos278 相分離に関わるヘテロクロマチンタンパク質 HP1α の 1 分子超解像イメージングによる分子局在と動態
Dynamics and localization of Heterochromatin protein 1α involved in phase separation using single-molecule and super-resolution imaging
Takahiro Maeda[1], Yuma Ito[1], Shin-Ya Isobe[2], Chikashi Obuse[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Tech*, [2]*Biosci. Grad Sch Sci., Osaka Univ*)

1Pos279 Imaging transcriptional dynamics of the endogenous gene with a bright fluorogenic RNA
Tetsuro Ariyoshi[1], Yasushi Okada[1,2] ([1]*RIKEN BDR, Cell Polarity Regulation*, [2]*Dept. Phys., Grad. Sch. Sci., UTokyo*)

1Pos280 ネクロプトーシスに伴う DAMPs 放出の LCI-S による可視化
Live Cell Imaging for Secretion Activity (LCI-S) of DAMPs Release Accompanying with Necroptosis
Yoshitaka Shirasaki[1,2], Mai Yamagishi[1], Sotaro Uemura[1] ([1]*Dept. of Biological Sciences, Grad School of Science, The Univ. of Tokyo*, [2]*JST PRESTO*)

バイオエンジニアリング／Bioengineering

1Pos281* 単一分子伝導計測に基づく表面上の DNA ハイブリダイゼーションの反応速度論解析
Kinetic investigation of DNA hybridization on surface using single-molecule conductance measurement
Takanori Harashima, Yuki Jono, Tomoaki Nishino (*Sch. Sci., TokyoTech.*)

1Pos282* 制御・情報技術の統合による集団内細胞行動特徴の定量解析
Quantitative analysis of collective cell migration by integration of controlled in vitro experiment and information processing
Asuka Yamaguchi[1], Masakazu Akiyama[2], Ikuhiko Nakase[3], Masaya Hagiwara[4] ([1]*Sch. Sci., Osaka Pref. Univ.*, [2]*MIMS, Meiji Univ.*, [3]*Grad. Sch. Sci., Osaka Pref. Univ.*, [4]*RIKEN, CPR*)

1Pos283* 分散培養心筋細胞と心臓組織片の電気生理学的信号の同期
Synchronization of electrophysiological signal between dispersed cardiomyocytes and cardiac tissue piece
Toru Nakamura, Chiho Nihei, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell biology, Department of Frontier Bioscience, Hosei University, Grad. School of Science and Engineering*)

1Pos284 DNA ナノデバイスを制御する DNA 生成回路の検証
Characterization of DNA Generation Circuits for Controlling DNA Nanodevices
Ken Komiya, Teruya Enomoto, Masayuki Yamamura (*Sch. Comp., Tokyo Tech.*)

1Pos285 Photo-control of Ras nucleotide exchange reaction using the inhibitor peptides modified with spiropyran derivative
Kenichi Taii[1], Nobuyuki Nishibe[1], Kei Sadakane[2], Shinsaku Maruta[1,2] ([1]*Dept. of Bioinfo., Grad. Sch. of Eng., Soka Univ.*, [2]*Dept. of Sus. Inno., Fac. of Sci. and Eng., Soka Univ.*)

結晶成長・結晶化技術／Crystal growth & Crystallization technique

1Pos286 アポフェリチンを使ったマグネタイト単結晶ナノ粒子の作製
Synthesis of single crystal magnetite nanoparticles in apoferritin cavity
Tomoko Kanamaru, Daisuke Katayama, Naoki Takasihima, Takeshi Narusima, **Hideyuki Yoshimura** (*Dpt. Phys., Meiji University*)

その他／Miscellaneous topics

1Pos287 (1SCA-5) 光からエネルギーを合成しタンパク質合成をする人工光合成細胞の構築
(1SCA-5) Artificial photosynthetic cell producing energy for protein synthesis
Samuel Berhanu[2], Takuya Ueda[3], **Yutetsu Kuruma**[1] ([1]*JAMSTEC*, [2]*ELSI, Titech*, [3]*Grad. Sch. of Front. Sci., Univ. of Tokyo*)

1Pos288 人工細胞-生細胞ハイブリッドバイオシステムの創成
Synthesis of artificial/living cell hybrid biosystems
Masamune Morita, Kaoru Katoh, Naohiro Noda (*Biomed. Res. Inst. (BMRI), AIST*)

1Pos289 *Mycolicibacterium smegmatis* のストラクトーム解析
Structome analysis of *Mycolicibacterium smegmatis*
Hiroyuki Yamada[1], Masashi Yamaguchi[2] ([1]*Res. Inst. Tuberculosis., JATA.*, [2]*Mycol. Res. Cent., Chiba*)

1Pos290 Identification of lipid interactions in the transmembrane regions of human Na+, K+-ATPase
Dhani Ram Mahato, Magnus Andersson (*Dept. Che., Ume Univ.*)

2 日目（9 月 25 日（水））／Day 2（Sep. 25 Wed.）
4F 天瑞・ホワイエ／4F TENZUI・Foyer

蛋白質：構造／Protein: Structure

2Pos001* Mycoplasma mobile のモーターを構成するタンパク質 MMOB1620 の構造解析
Structural analysis of MMOB1620 which composes Mycoplasma mobile's motor
Hiroki Sato[1], Aya Kodama[2], Hisashi Kudo[3], Koji Ooka[4], Syunji Suetaka[3], Yuuki Hayashi[3], Munehito Arai[3,4], Makoto Miyata[1,2] ([1]*Graduate School of Science, Osaka City University*, [2]*Faculty of Science, Osaka City University*, [3]*Dept. Life Sci., Univ. Tokyo*, [4]*Dept. Phys., Univ. Tokyo*)

2Pos002* 異なる長さの C 末端領域を持つテロメア繰り返し配列結合タンパク質 AtTRP1 の DNA 結合領域に対する構造研究
Structural studies for DNA binding domain of telomere repeat binding protein, AtTRP-1 with different size of C-terminal region
Shunta Kojima[1], Hayato Morita[2] ([1]*Grad. Sch. Sci., Josai.Univ*, [2]*Fac.Sci., Josai.Univ*)

2Pos003* PaCS-MD によるタンパク質−タンパク質複合体の解離シミュレーション
Protein-protein complexes dissociation simulated by Parallel Cascade Selection Molecular Dynamics
Yoshiki Miyazawa[1], Duy Phuoc Tran[2], Kazuhiro Takemura[2], Akio Kitao[2] ([1]*Grad. Sch. LST.,Tokyo Tech*, [2]*Sch. LST.,Tokyo Tech*)

2Pos004 Deep-Autoencoder に基づいたホモロジーモデリングソフトウェアの開発
Development of Deep-Autoencoder based Homology Modeling software
Masaya Furue, Mitsutaka Nemoto, Lisa Matsukura, Naoyuki Miyashita (*BOST KINDAI Univ.*)

2Pos005 Caged-GTP を用いたがん遺伝子産物 Ras の SACLA, SPring-8, NMR による GTP 加水分解過程の構造変化の解明
Structural changes on GTP hydrolysis of oncogene product Ras revealed by SACLA, SPring-8 and NMR using photo-controllable caged-GTP
Yoshiteru Makino[1], Takashi Kawamura[2], Shigeyuki Matsumoto[1], Eriko Nango[3], So Iwata[3], Takashi Kumasaka[2], Fumi Shima[4] ([1]*Grad. Sch. Med., Kobe. Univ.*, [2]*Protein Cryst. Anal. Div., JASRI.*, [3]*Grad. Sch. Med., Kyoto Univ.*, [4]*Grad. Sch. Sci. Tec. Innov., Kobe Univ.*)

2Pos006 アブラナ科植物の自家不和合性を制御するタンパク質 SRK/SP11 複合体の Rosetta と accelerated MD を用いた構造モデリング
Computational modeling of SRK/SP11 protein complexes using Rosetta and accelerated MD simulations
Yoshitaka Moriwaki[1], Tohru Terada[1,2], Koji Murase[1], Kentaro Shimizu[1] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

2Pos007 粗視化シミュレーションによる CDK4 の構造変化に関する研究
Conformational transition of CDK4 by using coarse-grained simulations
Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

2Pos008 Single particle analysis of silkworm lipid transfer protein complex, lipophorin
Shunsuke Kita[1], Kazuhiro Mio[2], Mika Hirose[3], Kenji Iwasaki[4], Naruhiko Adachi[5], Toshio Moriya[5], Masato Kawasaki[5], Katsumi Maenaka[1] ([1]*Fac. of Pharm. Sci., Hokkaido Univ.*, [2]*Operand OIL, AIST*, [3]*IPR, Osaka Univ.*, [4]*TARA, Univ. of Tsukuba*, [5]*SBRC, KEK*)

2Pos009 HIV-2 糖タンパク質の構造機能解析
Structure and functional analysis of human immunodeficiency virus type-2 (HIV-2) envelope glycoprotein
Yuki Anraku[1], Shunsuke Kita[2], Hideo Hukuhara[2], Simon Davis[3], Atsushi Hurukawa[2], Thushan de Silva[3], James Robinson[4], Yuguang Zhao[3], Yvonne Jones[3], David Stuart[3], Juha Huiskonen[3], Sarah Rowland-Jones[3], Katsumi Maenaka[2] ([1]*Grad. Sch. Life Sci., Univ. Hokkaido*, [2]*Faculty of Pharm Sci., Univ. Hokkaido*, [3]*Univ. Oxford*, [4]*Univ. Tulane*)

2Pos010 分子動力学シミュレーションを用いたαシヌクレインアミロイドの構造解析
Structural analysis of α-synuclein amyloids using molecular dynamics simulation
Hiroki Otaki, Yuzuru Taguchi, Noriyuki Nishida (*Grad. Sch. Biomedical Sci., Nagasaki Univ.*)

2Pos011 翻訳後修飾によってシトルリン化したヒト S100A3 蛋白質の擬似体の探索
Exploring the posttranslational modification of human S100A3 protein using citrullination mimics
Kenji Ite[1,2], Kenji Kizawa[3], Kenichi Kitanishi[4], Masaki Unno[1,2] ([1]*Graduate School of Science and Engineering, Ibaraki University*, [2]*Frontier Research Center for Applied Atomic Sciences, Ibaraki University*, [3]*Kao Corporation*, [4]*Department of Chemistry, Faculty of Science, Tokyo University of Science*)

2Pos012 機械学習を用いたタンパク質主鎖構造における 2 面角の再分類
Reclassification of dihedral angles in protein backbone structures using machine learning
Hiroto Murata, George Chikenji (*Dept. Appl. Phys., Nagoya Univ.*)

2Pos013 糖化が LDL の物性に与える影響について
Effect of glycation on the physical properties of low density-lipoprotein
Seiji Takeda[1], Toshihiro Sakurai[1], Shu-Ping Hui[1], Hitoshi Chiba[2] ([1]*Faculty of Health Sciences, Hokkaido Univ.*, [2]*Faculty of Health Science, Sapporo University of Health Sciences*)

2Pos014 酵母プリオン Sup35 の液-液相分離と線維化に対する共溶質の影響
Effects of co-solutes on liquid-liquid phase separation and fibrillization of yeast prion Sup35
Suguru Nishinami[1], Yumiko Ohhashi[2], Kentaro Shiraki[1] ([1]*Pure and Appl. Sci., Univ. Tsukuba*, [2]*Grad. Sch. Sci., Univ. Kobe*)

2Pos015 局所クラスター間構造コンプライアンスに基づくタンパク質の形状に内在する変形伝播特性の解析
Analysis of the Deformation Transmission Properties in Protein Shapes based on the Structural Compliance between Localized Clusters
Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

2Pos016 フェレドキシン構造とそのリバース構造の、PDB における発生頻度が異なるのはなぜか？
Why occurring frequencies of ferredoxin and its reverse fold in PDB are largely different?
Megumi Nakajima, George Chikenji (*Nagoya University Graduate School of Engineering Department of Applied Physics Sasai Laboratory*)

2Pos017 Structural Characterization of β_2 Microglobulin Core Fragments in Amyloid Fibrils using Circular Dichroism Theory and Molecular Dynamics
Koichi Matsuo[1,3], Hirotsugu Hiramatsu[2], Robert W. Woody[3] ([1]*Hiroshima Synchrotron Radiation Center, Hiroshima University*, [2]*Department of Applied Chemistry, National Chiao Tung University*, [3]*Department of Biochemistry and Molecular Biology, Colorado State University*)

2Pos018 B 型肝炎ウイルス(HBV)への逆転写阻害薬剤分子のカプシド内部の自由エネルギー計算
Calculation of free energy of transfer of a reverse transcription inhibitor to the inside of Hepatitis B Virus (HBV) capsid
Ryo Urano[1], Kazushi Fujimoto[1], Yoshimichi Andoh[2], Noriyuki Yoshii[2], Wataru Shinoda[1], Susumu Okazaki[1] ([1]*Grad. Sch. Eng., Nagoya Univ.*, [2]*Center Comput. Sci. Grad. Sch. Sci., Nagoya Univ.*)

2Pos019 アンチパラレル β シート中のジスルフィド結合が分泌タンパク質ホールディングに及ぼす影響
The effect of disulfide bonds in anti-parallel β-sheets on secreted protein folding
Hiromi Suzuki (*School of Agri., Meiji Univ.*)

2Pos020 エンドセリン B 受容体の分子動力学シミュレーション
Molecular dynamics simulations of human endothelin B receptor
Koichi Abe[1], Yoshitaka Moriwaki[1], Kentaro Shimizu[1,2], Tohru Terada[2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

2Pos021 クライオ電子顕微鏡単粒子解析法を用いた KcsA の構造解析
Structural Analysis of KcsA by Cryo-EM Single Particle Analysis
Hiroko Takazaki[1], Hirofumi Shimizu[2], Takuo Yasunaga[1] ([1]*Grad. Sch. Comp. Sci. Syst. Eng., KIT*, [2]*Fac. Med. Sci., Univ. Fukui*)

2Pos022 マスク付きセグメンテーション・フィット法による複数サブユニットの電顕マップへの局所重ね合わせ
Masked segmentation fitting of multiple atomic subunits into a local 3D EM density map
Takeshi Kawabata, Haruki Nakamura, Genji Kurisu (*Institute for Protein Research, Osaka University*)

蛋白質：構造機能相関／Protein: Structure & Function

2Pos023* 糸状仮足の構造変化とアクチンフィラメントの分布の相関
Correlation between structural changes of filopodia and distribution of actin filaments
Miho Nakafukasako, Tomoya Higo, Yusuke V. Morimoto, Takuo Yasunaga (*Grad. Sch. Comp. Sci. Syst. Eng., KIT.*)

2Pos024* Does the secondary site of neuraminidase play any significant role in drug resistance of influenza?
Mohini Yadav[1], Manabu Igarashi[2], Norifumi Yamamoto[1] ([1]*Dept. of Engg., Chiba Inst. Tech.*, [2]*Research Center for Zoonosis Control, Hokkaido Univ.*)

2Pos025* 多次元 NMR 分光法を用いたヤエヤマサソリ由来殺虫性ペプチド毒素 LaIT2 の機能領域の溶液構造解析
Structural studies for the functional domains of insecticidal peptide toxin, LaIT2, with heteronuclear multidimensional NMR spectroscopy
Chiharu Tatsushiro[1], Maiki Tamura[2], Hironori Juichi[3], Masahiro Miyashita[3], Hisashi Miyagawa[3], Shinya Ohki[2], Hayato Morita[1,4] ([1]*Fac Sci., Josai Univ*, [2]*Grad. Sch. Mat Sci., JIAST*, [3]*Grad. Sch. Agr., Kyoto Univ*, [4]*Grad. Sch. Sci., Josai Univ*)

2Pos026* 分子動力学計算で探る p53 の C 末端部位の DNA 結合機構
DNA recognition mechanisms of the p53 C-terminal domain Investigated by MD simulation
Yuta Taira[1], Duy Tran[1], Jacob Swadling[2], Akio Kitao[1] ([1]*Tokyo Tech*, [2]*Univ.Tokyo*)

2Pos027* 天然変性タンパク質 Tau の溶液中における過渡的な凝集原繊維構造形成
Intrinsically disordered protein Tau tends to transiently form a part of the protofilament core structure in the soluble state
Ryosuke Kawasaki[1], Shin-ichi Tate[2] ([1]*Dept. MLS, Grad. Sch. Sci., Hiroshima Univ.*, [2]*Prog. MLS, Grad. Sch. Integr. Sci. for Life, Hiroshima Univ.*)

2Pos028 Single-molecule FRET experiments for investigation of DNA single-strand damage recognition mechanism by PARP-1
Anna Sefer[1], Eleni Kallis[1], Tobias Eilert[1], Mara Guariento[1], Nadine Jakobi[1], David Neuhaus[2], Sebastian Eustermann[3], Jens Michaelis[1] ([1]*Ulm University, Institute of Biophysics, Albert-Einstein Allee 11, 89081 Ulm, Germany*, [2]*MRC Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge CB2 0QH, UK*, [3]*Ludwig-Maximilians-University Munich, Gene Center and Department of Biochemistry, Feodor-Lynen-Strasse 25, 81377 Munich, Germany*)

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

2Pos030 Crucial role of conformational excitation in enzyme catalysis of Pin1
Toshifumi Mori[1,2], Shinji Saito[1,2] ([1]*IMS*, [2]*SOKENDAI*)

2Pos031 Weighted ensemble simulations of the cis-trans isomerization in Pin1 enzyme using the QM/MM method
Norifumi Yamamoto[1], Kei Moritsugu[2], Yasushige Yonezawa[3], Shin-ichi Tate[4], Hiroshi Fujisaki[5] ([1]*Chiba Tech*, [2]*Yokohama City Univ*, [3]*Kindai Univ*, [4]*Hiroshima Univ*, [5]*Nippon Med Sch*)

2Pos032 Simulation Study on Atomistic and Physicochemical Properties of Amyloid beta 42
Ikuo Kurisaki, Shigenori Tanaka (*System Info., Grad. Schl., Kobe Univ.*)

2Pos033 敵対的生成ネットワーク（GAN）を用いた新規主鎖構造のタンパク質デザイン
Protein design with novel main-chain structure using Generative Adversarial Networks
Takaaki Sato[1], Yoshitaka Moriwaki[1], Tohru Terada[2], Kentaro Shimizu[1,2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

2Pos034 テルペン環化酵素における基質と反応の選択性に関する計算科学的研究
Computational investigation of the substrate and reaction selectivity of terpene cyclases
Masanobu Arita[1], Keiichi Murai[1], Yoshitaka Moriwaki[1], Tohru Terada[2], Tomohisa Kuzuyama[1], Kentaro Shimizu[1,2] ([1]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [2]*III, Univ. Tokyo*)

2Pos035 Pin1 由来のタンパク質分解酵素のミクロ化
Micronization of a protease derived from Pin1
Teikichi Ikura, Nobutoshi Ito (*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

2Pos036 緑色硫黄細菌 ferredoxin-NADP$^+$酸化還元酵素と基質間の酸化還元反応の特異性
Unique kinetic behavior in the redox reaction catalyzed by ferredoxin-NADP$^+$ oxidoreductase from green sulfur bacteria
Daisuke Seo (*Grd. Sch. Nat. Sci. Tec., Kanazawa Univ.*)

2Pos037 タンパク質キナーゼへの ATP 競合阻害剤結合の自由エネルギー解析
Free energy analysis of ATP competitive inhibitor-protein kinase bindings
Suyong Re, Hiraku Oshima, Yuji Sugita (*RIKEN Center for Biosystems Dynamics Research*)

2Pos038 フォトンファクトリーにおける生体高分子溶液試料の小角 X 線散乱に関する発展
Progress of Biological Small-Angle X-ray Scattering at the Photon Factory
Kento Yonezawa, Masatsuyo Takahashi, Keiko Yatabe, Yasuko Nagatani, **Nobutaka Shimizu** (*KEK, IMSS, PF*)

2Pos039 抗体修飾ナノニードルを用いた生細胞における中間径フィラメントの可動性解析
Mobility analysis of intermediate filament in a living cell using antibody-functionalized nanoneedle and AFM
Ayana Yamagishi[1,2,5], Moe Susaki[1,2], Mei Mizusawa[1,2], Akira Nagasaki[1], Saku Kijima[3], Q.P. Taro Uyeda[1,4], **Chikashi Nakamura**[1,2,5] ([1]*Biomed. Res. Inst., AIST*, [2]*Dept. Biotechnol. & Life Sci., Grad. Sch. Eng., TUAT*, [3]*Bioproc. Res. Inst., AIST*, [4]*Dept. Phys., Sch. Adv. Sci. Eng., Waseda Univ.*, [5]*PhotoBio-OIL, AIST-Osaka Univ.*)

2Pos040 Investigation on the relationship between cytotoxicity and amorphous oligomers
Punitha Velmurugan, Jannatul Aklima, Yoshihiro Ohta, Yutaka Kuroda (*Tokyo university of Agriculture and Technology*)

2Pos041 In vitro ATPase-based screening of circadian clock mutants of KaiC in cyanobacterial circadian clock system
Dongyan Ouyang[1], Atsushi Mukaiyama[1,2], Yoshihiko Furuike[1,2], Kumiko Miwa[3], Takao Kondo[3], Shuji Akiyama[1,2] ([1]*Inst. Mol. Sci.*, [2]*The Grad. Univ. for Adv. Studies*, [3]*Grad. Sch. of Sci., Nagoya Univ*)

2Pos042 構造蛋白質である HIV-1p17 と p24 の動的と静的構造の解析
Dynamic and rigid structures of HIV-1 p17 and p24 proteins
Chiaki Nishimura (*Fac. Pharm. Sci., Teikyo Heisei Univ.*)

2Pos043 アミロイドベータタンパク質を分解する人工ペプチドの設計
Designing artificial peptides that hydrolyze amyloid beta protein
Yoshihiro Iida, Atsuo Tamura (*Kobe Univ, Grad Sch Sci*)

2Pos044 4 つのイントロン位置は、アスパラギン酸アミノ転移酵素立体構造上で平面を形成する。
Four intron positions form a plane in the tertiary structure of aspartate aminotransferase
Michiko Nosaka (*N.I.T., Sasebo College*)

2Pos045 抗微生物ペプチド Cryptdin-4 の多量体の脂質分子存在下における分子シミュレーションによる観察
Antimicrobial peptide Cryptdin-4 oligomers interacting with lipids observed by molecular dynamics simulations
Takao Yoda (*Nagahama Institute of Bio-Science and Technology*)

2Pos046 ヘム ABC インポーター BhuUV-T の構造変化の自由エネルギー解析
Free energy analysis for the conformational changes of a heme ABC importer BhuUV-T
Koichi Tamura[1], Yuji Sugita[1,2,3] ([1]*RIKEN R-CCS*, [2]*RIKEN TMS*, [3]*RIKEN BDR*)

蛋白質：物性・構造／Protein: Property & Structure

2Pos047* トレハロースによるミオグロビンの構造安定化および酸性条件下でのアミロイド形成からの回復作用
Stabilization of the Myoglobin Structure and Restoration from the Amyloid Formation under Acidic Conditions by Trehalose
Satoshi Ajito[1], Mitsuhiro Hirai[1], Nobutaka Shimizu[2], Noriyuki Igarashi[2] ([1]*Grad. Sch. Sci. Tec., Gunma Univ.*, [2]*KEK*)

2Pos048* 異なる緩衝剤中での抗体の安定性と構造変化の関係
Relation between stability and structure of an antibody in different buffers
Hiroaki Oyama[1], Kanta Enomoto[1], Tetsuo Torisu[1], Susumu Uchiyama[1,2] ([1]*Grad. Sch. Eng, Osaka Univ*, [2]*ExCELLS*)

2Pos049* ショウジョウバエ Argonaute2 の N 末端領域はアミロイド繊維を形成する
N-terminal region of Drosophila Argonaute2 can form amyloid fibrils
Haruka Narita, Makoto F. Kuwabara, Tomotaka Komori, Ryo Murakami, Tomohiro Shima, Mikiko C. Siomi, Soutaro Uemura (*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*)

2Pos050* Dynamics of the helix-coil transition of alanine-based polypeptides detected by nanosecond region fluorescence correlation spectroscopy
Supawich Kamonprasertsuk[1,2], Hiroyuki Oikawa[1,2], Satoshi Takahashi[1,2] ([1]*IMRAM.Tohoku Univ.*, [2]*Grad.Sch.Sci.,Tohoku Univ.*)

2Pos051 MD simulation along with MSM analysis reconstructs LPA_6 binding pathway
Rieko Hirota[1], Ryuichiro Ishitani[1], Mizuki Takemoto[1,2], Osamu Nureki[1] ([1]*Dept. of Biosci., Grad Sch. of Sci., Univ. of Tokyo*, [2]*Present address: Preferred Networks, Inc.*)

2Pos052 加熱による中性 pH での β_2 ミクログロブリンのアミロイド線維形成
Heating-induced amyloid formation of β_2-microglobulin at neutral pH
Masahiro Noji[1], Kenji Sasahara[1], Keiichi Yamaguchi[1], Masatomo So[1], Kazumasa Sakurai[2], Jozsef Kardos[3], Hironobu Naiki[4], Yuji Goto[1] ([1]*IPR, Osaka Univ.*, [2]*IAT, Kindai Univ.*, [3]*Dept. Biochem., ELTE*, [4]*Med. Sci., Univ. Fukui*)

2Pos053 Functional Sensitivity and Mutational Robustness of Proteins
Qianyuan Tang, Tetsuhiro Hatakeyama, Kunihiko Kaneko (*Grad. Sch. Art. & Sci., Univ. Tokyo*)

2Pos054 多次元仮想座標とカップルした分子動力学法を用いた mSin3 複合体の立体構造探索
Conformational sampling of an mSin3 complex using multidimensional virtual-system coupled canonical MD
Tomonori Hayami[1,2], Yoshifumi Fukunishi[3], Yoshifumi Nishimura[4], Junichi Higo[5] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Fron. Biosci., Osaka Univ.*, [3]*molprof, AIST*, [4]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [5]*Grad. Sch. Sim. Studies., Univ. Hyogo*)

2Pos055 アデニル酸キナーゼの構造転移の改良カメレオンモデルによる研究
Conformational transition of adenylate kinase studied with the improved chameleon model
Ryota Mori, Masaki Sasai, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

2Pos056 Spectroscopic analysis of protein crowded environments using the charge-transfer fluorescence probe ANS
Chikashi Ota[1], **Kazufumi Takano**[2] ([1]*Ritsumeikan Univ.*, [2]*Kyoto Pref. Univ.*)

蛋白質：機能／Protein: Function

2Pos057 (2SHA-6) ダイナミン GTP アーゼはアクチン線維の束化と分散を機械的に制御する
(2SHA-6) Dynamin GTPase mechanically regulates bundling and unbundling of actin filaments
Kohji Takei[1], La The Mon[1], Tadashi Abe[1], Tetsuya Takeda[1], Ikuko Fujiwara[2], Akihiro Narita[3] ([1]*Grad.Sch. Med.Dent. Pharm.Sci., Okayama Univ.*, [2]*Dept. Biol.Facul.Sci., Osaka City Univ.*, [3]*Struct. Biol. Res. Ctr and Divi. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

2Pos058 FRET リアルタイム活性測定系を用いた大腸菌 S2P ファミリー膜内切断プロテアーゼ RseP の kinetics 解析
Kinetic analysis of the proteolytic reaction catalyzed by S2P family intramembrane protease RseP using a FRET-based real-time assay system
Yohei Hizukuri, Yoshinori Akiyama (*Inst. Front. Life Med. Sci., Kyoto Univ.*)

2Pos059 Recognition mechanism of proteins which bind to versatile amino acid sequences
Katsumi Omagari (*Dept. of Virology, Medical School, Nagoya City University*)

2Pos060 呼吸鎖超複合体形成タンパク質によって制御される Cyt *c* のパートナータンパク質認識機構
The mechanism of cytochrome *c*-redox partner proteins recognition regulated by the respiratory supercomplex factor protein
Wataru Sato[1], Koichiro Ishimori[2], Peter Brzezinski[1] ([1]*Stockholm Univ. Fac. of Nat. Sci.*, [2]*Hokkaido Univ. Fac. of Sci.*)

2Pos061 QM/MM 法によるニワトリ卵白リゾチームの糖加水分解反応シミュレーション
QM/MM Study on Hydrolysis of Polysaccharides in Hen Egg-White Lysozyme
Takuya Uto[1], Yoshiki Mitani[2], Toshifumi Yui[2] ([1]*Organization for Promotion of Tenure Track, University of Miyazaki*, [2]*Faculty of Engineering, University of Miyazaki*)

蛋白質：計測・解析／Protein: Measurement & Analysis

2Pos062 幾何学に基づく新しいタンパク質構造解析プログラム
A new program to analyze protein structures based on the geometric context
Anri Terabayashi[1], Momoka Nakamura[1], Kyosuke Sakata[1], Takuya Miyakawa[2], Masaru Tanokura[2], Tohru Terada[3], Masaki Kojima[1] ([1]*Sch. Life Sci., Tokyo Univ. Pharm. Life Sci.*, [2]*Grad. Sch. Agric. Life Sci. Univ. Tokyo*, [3]*III, Univ. Tokyo*)

2Pos063 細胞質中 RAF 分子の構造およびダイマー化状態を捉える 1 分子計測
Conformational and dimeric states of cytosolic RAF detected by single-molecule measurements
Kenji Okamoto[1], Kayo Hibino[2], Yasushi Sako[1] ([1]*RIKEN CPR*, [2]*NIG*)

2Pos064 信号変化の順序決定の自動化およびタンパク質 HD 交換ダイナミクスの振動バンドへの応用
Automatic determination of the sequential order of signal changes and its application to vibrational bands of protein H-D exchange process
Daisuke Miyata[1], Takakazu Nakabayashi[1], Shinichi Morita[2] ([1]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [2]*Graduate School of Science, Tohoku University*)

2Pos065 水素高感度解析を実現するタンパク質中性子回折実験の進歩
Progress of the protein neutron diffractometry to realize hydrogen high sensitivity analysis
Ichiro Tanaka (*Graduate School of Science and Engineering, Ibaraki University*)

2Pos066 Flexible Fitting of Biomolecular Structures to Atomic-Force-Microscopy Images via Biased Molecular Simulations
Toru Niina, Sotaro Fuchigami, Shoji Takada (*Grad. Sch. Sci. Univ. Kyoto*)

2Pos067 Deep convolutional neural networks for identifying cryo-EM grid holes suitable for particle collection
Yuichi Yokoyama[1], Tohru Terada[3], Kentaro Shimizu[2,3], Kazutoshi Tani[4] ([1]*GSII, Univ. Tokyo*, [2]*Grad. Sch. Agr. Life Sci., Univ. Tokyo*, [3]*III, Univ. Tokyo*, [4]*Grad. Sch. Med., Univ. Mie*)

2Pos068 アクチン線維に張力を発生させると線維の長軸まわりのねじれは減少する
Mechanical stress declined the amplitude of the torsional fluctuations of single actin filaments
Kaoru Okura, Takumi Fukuda, Hitoshi Tatsumi (*Department of Applied Bioscience, Kanazawa Inst. of Technol., Ishikawa, Japan*)

2Pos069 高速 AFM 画像のドリフト除去法の応用
Application of drift elimination method for high-speed AFM images
Shotaro Tsujioka[1], Hideji Murakoshi[2], Mikihiro Shibata[3,4] ([1]*Division of Transdisciplinary Sciences,Graduate School of Frontier Initiative,Kanazawa University*, [2]*National Institute for Physiological*, [3]*WPI Nano Life Science Institute (WPI-NanoLSI),Kanazawa University*, [4]*Institute for Frontier Science Initiative,Kanazawa University*)

蛋白質工学／Protein: Engineering

2Pos070* ポリプロリンロッドの挿入によるドメインスワッピング二量体のデザイン
Poly-proline rod insertion for the design of domain-swapped dimer
Shota Shiga[1], Masaru Yamanaka[2], Wataru Hujiwara[1], Shun Hirota[2], Shuichiro Goda[3], Koki Makabe[1] ([1]*Graduate School of Science and Engineering, Yamagata University*, [2]*Division of Materials Science, Nara Institute of Science and Technology*, [3]*Graduate School of Engineering, Nagasaki University*)

2Pos071* c-Myb-KIX 相互作用を阻害するペプチドの計算機によるデザイン
Computational design of a peptide inhibitor targeting c-Myb-KIX interaction
Shunji Suetaka[1], Yoshiki Oka[1], Tomoko Kunihara[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

2Pos072* 超安定タンパク質構造のゼロからの合理設計とその融合による、GPCR 構造の合理的安定化
Tailor-made design of superstable proteins from scratch for rational stabilization of GPCR
Masaya Mitsumoto[1,2], Nanao Suzuki[3], Ryosuke Nakano[3], Takahiro Kosugi[1,2,4], Takeshi Murata[3], Nobuyasu Koga[1,2,4] ([1]*ExCELLS, NINS*, [2]*SOKENDAI*, [3]*Fac. of Sci., Chiba Univ.*, [4]*IMS, NINS*)

2Pos073* 理論的飽和変異解析によるジヒドロ葉酸還元酵素の高活性化
Improving activity of dihydrofolate reductase by theoretical saturation mutagenesis
Kazuhisa Ohara[1], Yoshiki Oka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

2Pos074* Engineering of genome editing protein Cas9 that slides along DNA faster and might enable efficient target search
Trishit Banerjee[1,2], Dwiky Rendra Graha Subekti[1,3], Hiroto Takahashi[1], Satoshi Takahashi[1], Kiyoto Kamagata[1] ([1]*IMRAM, Tohoku Uni.*, [2]*Fac. of Sci., Tohoku Uni.*, [3]*Grad. Sch. of Sci., Tohoku Uni.*)

2Pos075 (2SGP-8) 天然変性タンパク質 p53 を標的としたペプチドの人工設計ー液液相分離の制御ー
(2SGP-8) Rational design of peptide targeting intrinsically disordered protein p53—regulation of function and phase-phase separation—
Kiyoto Kamagata[1], Eriko Mano[1], Yuji Itoh[1], Saori Kanbayashi[1], Masaya Honda[1], Ryo Kitahara[2], Tomoshi Kameda[3] ([1]*IMRAM, Tohoku Univ.*, [2]*Coll. Pharmacy Sci., Ritsumeikan Univ.*, [3]*AIRC, AIST*)

2Pos076 膜内・膜外領域の改変によるサーモフィリックロドプシンの熱安定化
Further Thermo-Stabilization of Thermophilic Rhodopsin through Engineering in Intramembrane and Extramembrane Regions
Tomoki Akiyama[1], Naoki Kunishima[2], Masako Hirose[3], Sayaka Nemoto[4], Stoshi Yasuda[4,5,6], Yuki Sudo[7], Takeshi Murata[4,6] ([1]*Grad. Sch. Sci. & Eng., Univ. Chiba*, [2]*RIKEN RSC-Rigaku Collaboration Center*, [3]*Malvern Panalytical division of Spectris Co., Ltd*, [4]*Grad. Sch. Sci., Univ. Chiba*, [5]*Inst. Advanced Energy, Univ. Kyoto*, [6]*Molecular Chirality Research Center, Chiba University*, [7]*Grad. Sch. Med. Dent. Pharm. Sci., Univ. Okayama*)

2Pos077 麹菌菌体外放出系の高機能化
Improvement of exocytotic secretion system of *Aspergillus oryzae*
Mone Kogure, Kensuke Nakajima, Yoshinori Tsuji, Yusuke Matsuda (*Dept.Biosci., Grad.Sch.Sci.Tech., Kwansei Gakuin Univ.*)

2Pos078 細胞特異的ゲノム編集を目的とした核酸をデリバリーする新規一本鎖抗体 scFv の作製
Preparation of a novel single chain variable fragment (scFv) which delivers nucleic acid for cell-specific genome editing
Haruka Nasu[1], Yuji Sato[1], Takashi Tsukamoto[2,3], Takashi Kikukawa[2,3], Makoto Demura[2,3], Tomoyasu Aizawa[2,3] ([1]*Grad. Sch. Life Sci. Hokkaido Univ.*, [2]*Fac. Adv. Life Sci. Hokkaido Univ.*, [3]*GSS, GI-CoRE*)

ヘム蛋白質／Heme proteins

2Pos079 生体反応場におけるシトクロム c 内多核ヘムの空間配置・酸化還元状態の変化
Cellular environment modulates geometry and redox state of deca-heme cofactors in bacterial surface cytochromes
Yoshihide Tokunou[1,2,3], Shingo Hattori[4], Thomas Clarke[5], Liang Shi[6], Kazuyuki Ishii[4], Akihiro Okamoto[2] ([1]*Faculty of Life. Environ. Sci., Uni. Tsukuba*, [2]*NIMS*, [3]*Research Fellow of JSPS*, [4]*Inst. Indust. Sci., Univ. Tokyo*, [5]*Centre for Molecular and Structural Biochemistry, Univ. East Anglia*, [6]*Dept. of Biological Sciences, China Univ. of Geosciences*)

2Pos080 NO-binding and protonation process in the catalytic reaction of the bacterial NO reductase as established by time-resolved spectroscopy
Hanae Takeda[1,2], Tetsunari Kimura[3], Takashi Nomura[1], Takehiko Tosha[2], Yoshitsugu Shiro[1], Minoru Kubo[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*RIKEN, SPring-8 Center*, [3]*Grad. Sch. Sci., Kobe Univ*)

2Pos081 Anodized gold surface enables mediator-free bioelectrocatalysis of redox enzymes
Yasuhiro Mie, Yoshiaki Yasutake, Mashiki Ikegami, Tomohiro Tamura (*Bioproduction Res. Inst., AIST*)

膜蛋白質／Membrane proteins

2Pos082* 膜蛋白質複合体の構造ダイナミクスへコレステロールが及ぼす影響に関する分子動力学的解析
Influences of cholesterol on structural dynamics of membrane protein complexes studied by molecular dynamics simulations
Hayato Itaya[1], Kota Kasahara[2], Yoshiaki Yano[3], Katsumi Matsuzaki[3], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Pharm.Sci., Kyoto Univ*)

2Pos083* Observation of a β-Hairpin Peptide in α-Hemolysin Nanopore
Misa Yamaji, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

2Pos084* 表面プラズモン共鳴法を用いた膜タンパク質に特異的な脂質の同定: 脂質の生理機能解明を目指して
Identification of membrane proteins-specific lipids using surface plasmon resonance analysis: For elucidating the physiology of lipids
Masataka Inada[1], Masanao Kinoshita[1], Masayuki Iwamoto[2], Shigetoshi Oiki[2], Nobuaki Matsumori[1] ([1]*Grad. Sch. Sci., Kyushu Univ.*, [2]*Fac. Med. Sci., Univ. Fukui*)

2Pos085 クライオ電子顕微鏡による組換リアノジン受容体の高分解能構造
High-resolution cryo-EM structures of recombinant ryanodine receptors
Takuya Kobayashi[2], Akihisa Tsutsumi[3], Kei Saito[4], Takashi Sakurai[2], Masahide Kikkawa[3], Takashi Murayama[2], **Haruo Ogawa**[1] ([1]*IQB, The Univ. Tokyo*, [2]*Juntendo Univ. Grad. Sch. Med.*, [3]*Grad. Sch. Med., Univ. Tokyo*, [4]*Grad. Sch. Arts Sci., Univ. Tokyo*)

2Pos086 Exploring Structural Dynamics of Bacterial ABC Transporter MsbA by High Speed AFM
Kien X. Ngo, Holger Flechsig, Noriyuki Kodera, Toshio Ando (*WPI Nano Life Science Institute, Kanazawa University*)

2Pos087 Corynebacterial “Force-From-Lipids” mechanosensation for glutamate production
Yoshitaka Nakayama[1], Ken-ichi Hashimoto[2,3], Hisashi Kawasaki[2,3], Boris Martinac[1,4] ([1]*Victor Chang Cardiac Research Institute*, [2]*Biotech. Res. Cen., Univ. Tokyo*, [3]*Collab. Res. Ins. Inno. Microbiol., Univ. Tokyo*, [4]*University of New South Wales*)

2Pos088 The assembly of the trimeric autotransporter transmembrane domain into BamA-embedded nanodiscs
Eriko Aoki, Kazuo Fujiwara, Masamichi Ikeguchi (*Dept. of Bioinfo., Soka Univ.*)

核酸結合蛋白質／Nucleic acid binding proteins

2Pos089 CRISPR Cas3 と Cse1 複合体の分子動力学シミュレーション
Molecular dynamics simulations of CRISPR Cas3 and Cse1 complex
Tomohiro Yamaguchi, Yui Taketomo, Naoyuki Miyashita (*BOST KINDAI Univ.*)

2Pos090 Identification of proteins that interact with nucleosomes by Quantitative Proteomics
Lumi Negishi[1], Hiroki Tanaka[2], Rina Hirano[1], Tomoya Kujirai[1], Hitoshi Kurumizaka[1] ([1]*IQB, Univ. Tokyo*, [2]*Grad. Adv. Sci. Eng., Waseda Univ.*)

2Pos091 転写因子の振る舞いとクロマチンのゆらぎの関係性を 1 分子計測によって解析する
Single molecular dynamics of transcription factors are controlled by diffusion movement of chromatin
Kazuko Okamoto[1], Yasushi Okada[1], Kuniya Abe[2], Tomonobu M Watanabe[1] ([1]*RIKEN BDR*, [2]*RIKEN BRC*)

2Pos092 DNA 二重鎖切断に応答した DNA トポイソメラーゼ 2B の核内挙動
Dynamic behavior of DNA topoisomerase 2B in response to DNA double-strand breaks
Ken ichi Yano, Keiko Morotomi-Yano (*IPPS, Kumamoto Univ.*)

核酸／Nucleic acid

2Pos093* 人工細胞デバイス内に封入した長鎖 DNA 1 分子からの遺伝子発現
Gene expression from a single large DNA encapsulated in artificial cell device
Yuto Ochiai[1], Hiroshi Ueno[1], Masayuki Su'etsugu[2], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Dept. Life Sci., Col. Sci., Rikkyo Univ.*)

2Pos094* 生体ナノポアフィルタを用いた DNA の一分子分離
Separation of a single molecule DNA using biological nanopore filter
Asuka Tada, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

2Pos095* DETECTION OF DNA-POINT-MUTATION USING BIOLOGICAL NANOPORE
Ping Liu, Keisuke Shimizu, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

2Pos096 DNA を利用した人工分子モーターの実現を目指して
Towards the realization of artificial molecular motor using DNA molecules
Kohei Arai, Yuki Tsushima, Shoichi Toyabe (*Appl. Phys., Tohoku Univ.*)

2Pos097 染色体脱凝縮シミュレーションによるヒト間期核組織化の理解
Organization of interphase human nucleus via simulated chromosome decondensation
Shin Fujishiro, Masaki Sasai (*Dept. Appl. Phys., Nagoya Univ.*)

2Pos098 クロマチン構造と RNA 輸送経路が協調して形成される過程
Cooperative formation of RNA transporting pathway and chromatin structure
Nozomu Imai, Shin Fujishiro, Masaki Sasai (*Dept. Appl. Phys., Nagoya Univ.*)

2Pos099 染色体のナノスケール 3 次元内部構造を可視化するための液中 3 次元原子間力顕微鏡（3D-AFM）の開発
Development of 3D-AFM to visualize nanometer-scale three-dimensional structures of chromosomes in liquid
Keisuke Miyazawa[1], Makiko Meguro-Horike[2], Shin-ichi Horike[2], Takashi Sumikama[3], Taku Higasayama[1], Masayuki Harada[1], Takeshi Fukuma[1,3] ([1]*Kanazawa Univ.*, [2]*Division of Functional Genomics, Advanced Science Research Center, Kanazawa Univ.*, [3]*Nano Life Science Institute (WPI-NanoLSI), Kanazawa Univ.*)

2Pos100 染色体の 3D-AFM 像と実像の関係の理論的解明
A theoretical study on a relationship between 3D atomic force macroscopy image and structure of chromosomes
Takashi Sumikama[1], Keisuke Miyazawa[4], Adam Foster[1,2,3], Takeshi Fukuma[1,4] ([1]*Nano Life Sicence Institute (WPI-NanoLSI), Kanazawa University*, [2]*Department of Applied Physics, Aalto University*, [3]*Graduate School Materials Science in Mainz*, [4]*Division of Electrical Engineering and Computer Science, Kanazawa University*)

2Pos101 FRET study on sequence-dependent unwrapping of nucleosomal DNA
Tomoko Sunami, Di Luo, Hidetoshi Kono (*MMS, iQLS, QST*)

2Pos102 DNA メチル化に依存したヌクレオソームのスライディング動態の解析
Computational Analysis of the Nucleosome Sliding Dynamics Depending on DNA Methylation
Takeru Kameda[1,2], Miho Suzuki[3], Akinori Awazu[1,4], Yuichi Togashi[1,2,4] ([1]*Department of Mathematical and Life Sciences, Hiroshima University*, [2]*RIKEN Center for Biosystems Dynamics Research.*, [3]*Graduate School of Medicine, Nagoya University*, [4]*Graduate School of Integrated Sciences for Life, Hiroshima University.*)

分子遺伝・遺伝情報制御／Molecular genetics & Gene expression

2Pos103* 微小空間内における 1 分子からの長鎖 DNA 複製
Large DNA amplification from single molecule in micro-sized droplet
Hiroki Sawada[1], Naoki Soga[1], Seia Nara[2], Masayuki Su'etsugu[2], Kazuhito V. Tabata[1], Hiroyuki Noji[1] ([1]*Dept. App. Chem, Univ. Tokyo.*, [2]*Dept. Life. Sci., Sol. Sci., Rikkyo Univ.*)

発生・分化／Development & Differentiation

2Pos104* Piezo1 はリンパ管弁形成過程におけるカルシウムシグナルに必要である
Piezo1 is required for calcium signaling during lymphatic valve morphogenesis
Hiroki Katsuta[1,2], Keiko Nonomura[2], Akemi Kanie[2], Takaki Miyata[1], Toshihiko Fujimori[2] ([1]*Grad. Sch. Med. Nagoya Univ. Cell Biol.*, [2]*NIBB Embryology*)

2Pos105 血管新生における血管内皮細胞の往復運動
Linear reciprocating movement of vascular endothelial cells in angiogenesis
Naoko Takubo[1], Kazuaki Naemura[2], Ryo Yoshida[3], Terumasa Tokunaga[4], Hiroki Kurihara[2] ([1]*Isotope Science Center, Univ. Tokyo*, [2]*Grad. Sch. Med., Univ. Tokyo*, [3]*Inst. Statistical Mathematics*, [4]*Faculty of Computer Science and Systems Engineering, Kyushu Inst. Tec.*)

2Pos106 ドリフトのあるランダム運動がヒトの胚葉形成には必要である
Brownian motion with drift is essential for forming human germ layers
Kenshiro Maruyama, Ryo Kobayashi, Haru Hikita, Tadashi Tsubone, **Kiyoshi Ohnuma** (*Nagaoka University of Technology*)

2Pos107 確率的な細胞たちが協調して正確な大きさの体節を作る仕組み ～分節時計によるノイズキャンセル機構～
Noise-resistant developmental reproducibility in vertebrate somite formation
Naoki Honda[1,2], Ryutaro Akiyama[2], Dini WK Sari[2], Bessho Yasumasa[2], Takaaki Matsui[1,2] ([1]*Grad. Sch. Biostudies., Kyoto Univ.*, [2]*NAIST*)

2Pos108 エネルギー地形アプローチに基づく組織形態形成の多様性と安定性の探求
Exploring variety and robustness in tissue morphogenesis based on energy landscape approach
Yoshitaka Kameo[1,2,3], Hironori Takeda[2], Taiji Adachi[1,2,3] ([1]*IFLMS, Kyoto Univ*, [2]*Grad Sch Eng, Kyoto Univ*, [3]*Grad Sch Bio, Kyoto Univ*)

2Pos109 三次元粒子画像流速測定法によるノード流の解析
Analysis of nodal flow by three-dimensional particle image velocimetry
Atsushi Taniguchi[1,2], Yukinori Nishigami[3], Shigenori Nonaka[1,2] ([1]*Spatiotemp. Reg., NIBB*, [2]*ExCELLS*, [3]*RIES, Hokkaido Univ.*)

筋肉／Muscle

2Pos110 Mechanical stress-responsive membrane remodeling in muscle cells
Kenshiro Fujise, Hiroshi Yamada, Kohji Takei, **Tetsuya Takeda** (*Okayama Univ. Grad. Sch. Med. Dent. Pharm. Sci.*)

2Pos111 無機ポリリン酸存在下でのアクチン重合
Polymerization of actin molecules in the presence of inorganic polyphosphate
Koji Ito, Kuniyuki Hatori (*Grad. Sch. Sci. Eng. Yamagata Univ.*)

2Pos112 Visualization of Ca2+ regulated structural change in muscle thin filament by cryoEM
Yurika Yamada, Keiichi Namba, Takashi Fujii (*Grad. Sch. of Frontier Biosci., Osaka Univ.*)

2Pos113 Fhod3 と cMyBP-C による心筋サルコメアの形成および維持機構
Mechanism of construction and maintenance of cardiac sarcomeres by Fhod3 and cMyBP-C
Wataru Kedouin[1], Riho Takiiwa[1], Nao Shimojo[1], Ryu Takeya[2], Takuo Yasunaga[1] ([1]*Grad. Sch. of Comp. Sci. and Sys. Eng., Kyushu Inst. of Tech.*, [2]*Dept. of Pharma., Univ. of Miyazaki*)

2Pos114* DNA オリガミを用いたナノバネ結合心筋ミオシンフィラメントの 1 分子解析
Single molecule analysis of DNA origami-based cardiac myosin filaments attached with Nanospring
Hiroki Fukunaga[1], Masashi Ohmachi[2], Keisuke Fujita[2], Keigo Ikezaki[3], Toshio Yanagida[1,2], Mitsuhiro Iwaki[1,2] ([1]*FBS, Univ. Osaka*, [2]*BDR, Riken*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

2Pos115* 細胞質ダイニンの運動方向性を左右するアミノ酸の同定
Key residues on cytoplasmic dynein for asymmetric unbinding from microtubule
Shintaroh Kubo[1], Tomohiro Shima[2], Takahide Kon[3], Shoji Takada[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Grad. Sch. Sci., Tokyo Univ.*, [3]*Grad. Sch. Sci., Univ. Osaka*)

2Pos116* 好熱菌由来 F_1-ATPase の至適生育温度における力学的仕事の測定
The Measurement of Mechanical Work of Thermophilic F_1-ATPase at the Optimum Growth Temperature
Tomoaki Okaniwa[1], Yohei Nakayama[2], Naoya Terahara[1], Eiro Muneyuki[1] ([1]*Dept. Phys., Graduate School of Science and Engineering, Chuo Univ.*, [2]*Dept. Appl. Phys., Graduate School of Engineering, Tohoku University*)

2Pos117* 中間鎖をアンカーとした新しい運動アッセイ法によるクラミドモナス軸糸ダイニン集団の運動特性の計測
Collective motility of Chlamydomonas outer arm dynein measured using its intermediate chain as a scaffold for motility assays
Yuka Matsuda[1], Akane Furuta[2], Hiroaki Kojima[2], Kazuhiro Oiwa[1,2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICT Res. Inst., NICT*)

2Pos118 The combination of high-speed atomic force microscopy and X-ray crystallography reveals rotary catalysis of a shaftless V1 motor
Shintaro Maruyama[1], Motonori Imamura[2], Takayuki Uchihashi[3,4], Kazuya Nakamoto[1], Kenji Mizutani[5], Lica Fabiana Imai[1], Kano Suzuki[1], Yoshiko Ishizuka-Katsura[6], Tomomi Someya-Kimura[6], Mikako Shirouzu[1,6,7], Ichiro Yamato[1,7], Toshio Ando[2], Takeshi Murata[1,8] ([1]*Grad. Sch. Sci., Univ. Chiba*, [2]*WPI Nano Life Sci. Inst., Univ. Kanazawa*, [3]*JST, CREST*, [4]*Dep. Phys., Univ. Nagoya*, [5]*Grad. Sch. Med. Life. Sci., Univ. Yokohama*, [6]*DSSB, RIKEN*, [7]*Ind. Sci. Tokyo Univ. Sci.*, [8]*PREST, JST*)

2Pos119* Measurement of force generation by dynein ensemble on a doublet microtubule obtained from sperm flagella
Takashi Fujiwara[1], Chikako Shingyoji[1], Hideo Higuchi[2] ([1]*Dept. Biol. Sci., Grad. Sch. Sci., Univ. Tokyo*, [2]*Dept. Phys., Grad. Sch. Sci., Univ. Tokyo*)

2Pos120* 1 分子計測による腸内連鎖球菌由来の回転分子モーター V_1-ATPase の化学力学共役機構の解明
Chemo-mechanical coupling scheme of rotary molecular motor *Enterococcus hirae* V_1-ATPase revealed by single-molecule analysis
Tatsuya Iida[1,2], Yoshihiro Minagawa[3], Hiroshi Ueno[3], Fumihiro Kawai[4], Takeshi Murata[5], Ryota Iino[1,2] ([1]*SOKENDAI (The Grad. Univ. for Adv. Stud.)*, [2]*Inst. for Mol. Sci.*, [3]*The Univ. of Tokyo*, [4]*Yamagata Univ.*, [5]*Chiba Univ.*)

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

2Pos122 アクチンの pH 依存的な荷電状態と分子間相互作用
pH-dependent charge-state and intermolecular interaction of actin
Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

2Pos123 枯草菌べん毛モーターの回転ステップ解析
Step analysis of the *Bacillus* Na^+-driven flagellar motor
Naoya Terahara[1,2], Miku Yoh[3], Eiro Muneyuki[1], Keiichi Namba[2,4], Tohru Minamino[2] ([1]*Dept. Phys., Chuo Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*Fac. Human Life Sci., Doshisha Women's Col.*, [4]*BDR/RSC, Riken*)

2Pos124 アクチン繊維の集団運動により形成されるベルトパターンはリング状に変化する
Transformation of belt-like to ring patterns of a quasi-concentrated solution of F-actin driven by myosin-coated surface
Kentaro Ozawa[1], Mikiya Amano[1], Hirotaka Taomori[1], Itsuki Kunita[2], Shigeru Sakurazawa[3], Hajime Honda[1] ([1]*Dept. Bioeng., Nagaoka Univ. Tech.*, [2]*Univ. Ryukyus*, [3]*Future Univ. Hakodate*)

2Pos125 Myosin II decreases the connectivity of an actin network using two different mechanisms depended on concentration of crosslinking protein
Kyohei Matsuda[1], Takuya Kobayashi[1,2], Mitsuhiro Sugawa[1], Masahiko Yamagishi[1], Yoko Y. Toyoshima[1], Junichiro Yajima[1] ([1]*Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo*, [2]*Juntendo University*)

2Pos126 Developing the detection system of the conformational change in rotating flagellar motor by single motor FRET
Takuma Nakagawa, Tatsuya Yamakoshi, Yong-Suk Che, Akihiko Ishijima, **Hajikme Fukuoka** (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

2Pos127 ダイニン・微小管・DNA 折り紙複合体の振動的運動
Oscillatory movement of the dynein-microtubule complex crosslinked with DNA-origami
Shimaa A. Abdellatef[1], Hisashi Tadakuma[2], Yuichi Kondo[3], Kangmin Yan[1], Hideo Higuchi[3], **Keiko Hirose**[1] ([1]*Biomed. Res. Inst., AIST*, [2]*IPR, Osaka Univ.*, [3]*Grad. Sch. Sci., Univ. Tokyo*)

2Pos128 Ca2+濃度変化による真核生物鞭毛軸糸の構造変化の X 線繊維回折解析
Structural changes of Chlamydomonas and Ciona flagellar axonemes coupled with the change in [Ca2+] studied with X-ray fiber diffraction
Kazuhiro Oiwa[1], Hiroyuki Iwamoto[2], Kogiku Shiba[3], Kazuo Inaba[3], Hitoshi Sakakibara[1] ([1]*Adv. ICT Res. Inst., NICT*, [2]*JASRI*, [3]*Shimoda Marine Res. Cent. Univ. Tsukuba*)

2Pos129 新規繊毛ダイニン軽鎖 MOT7 の構造機能解析
Structural/functional analyses on MOT7, a novel light chain of ciliary dynein f/I1
Ryosuke Yamamoto[1], Yuuhei Nakagiri[1], Osamu Kutomi[2], Hiroshi Imai[1], Chihong Song[3], Kazuyoshi Murata[3], Ken-ichi Wakabayashi[4], Takashi Ishikawa[5], Kazuo Inaba[6], Takahide Kon[1] ([1]*Osaka Univ.*, [2]*Univ. of Yamanashi*, [3]*NIPS*, [4]*Tokyo Tech*, [5]*PSI*, [6]*Univ. of Tsukuba*)

2Pos130 全反射赤外分光法を用いた共役イオン結合による Na^+駆動型モーター固定子の構造変化の解明
The cation-induced structural changes in the Na^+-driven flagellar stator studied by ATR-FTIR
Masayo Iwaki[1], Tatsuro Nishikino[2], Hiroyuki Terashima[2], Michio Homma[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Nagoya Univ.*)

2Pos131 2 つのアゾベンゼンを持つフォトクロミック Eg5 阻害剤存在下における Eg5 活性の光制御機構の研究
Study on inhibitory mechanism of kinesin Eg5 with photochromic Eg5 inhibitor composed of two azobenzene
Kei Sadakane[1], Islam MD Alrazi[2], Kenichi Taii[2], Tomisin H. Ogunwa[3], Shinsaku Maruta[1,2] ([1]*Sci. & Eng., Soka Univ.*, [2]*Grad. Sch. Eng., Soka Univ.*, [3]*Grad. Sch. Fisheries and Environmental Sci., Nagasaki Univ.*)

2Pos132 結晶性キチン加水分解酵素は背水の陣で進むブラウニアンモーターである
Crystalline chitin hydrolase is a Burnt-bridge Brownian motor
Akihiko Nakamura[1,2], Kei-ichi Okazaki[1], Tadaomi Furuta[3], Minoru Sakurai[3], Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*, [3]*Tokyo Institute of Technology*)

2Pos133 プログラマブルな DNA オリガミによる微小管格子構造の制御
Defining microtubule lattice structure using programmable DNA-origami seeds
Daisuke Inoue, Franky Djutanta, Rizal Hariadi (*Biodesingn Institute, Arizona State Univ.*)

2Pos134 Plus-end directionality is present in the conserved catalytic motor core of kinesin-14 minus-end directed motors
Masahiko Yamagishi, Junichiro Yajima (*Dept. Life Sci., Grad. Arts & Sci., Univ. Tokyo*)

2Pos135 DNA オリガミの分子配置技術を用いたキネシン分子の協調性評価
Evaluating coordination between kinesin motors using DNA origami-based transport complex
Kodai Fukumoto[1], Yuya Miyazono[2], Hisashi Tadakuma[1], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

2Pos136 KIF1A/UNC-104 によるシナプス小胞前駆体輸送の数理モデル
Mathematic modeling of synaptic vesicle precursor transport by KIF1A/UNC-104
Ryo Sasaki[1], Ryota Shinagawa[1], Kazuo Sasaki[1], Shinsuke Niwa[2], Kumiko Hayashi[1,3] ([1]*Dep. Appl. Phys., Grad. Sch. of Eng., Tohoku Univ.*, [2]*FRIS, Tohoku Univ.*, [3]*JST, PRESTO, Tokyo, Japan*)

2Pos137 遺伝性痙性対麻痺を引き起こす変異型ヒト KIF1A の運動特性
Motility characteristics of human KIF1A mutants in hippocampal neurons in relation to hereditary spastic paraplegia
Shiori Matsumoto[1], Kyoko Chiba[2], Shinsuke Niwa[3], Kumiko Hayashi[1,4] ([1]*Dep. Appl. Phys., Grad. Sch. of Eng., Tohoku Univ.*, [2]*Col. Biol. Sci., UC Davis*, [3]*FRIS, Tohoku Univ.*, [4]*PRESTO, JST*)

2Pos138 キネシン 1 の連続的移動距離を決める要因の高速一分子観察
Determinant of the processivity of kinesin-1 as studied using high-speed single-molecule observations
Tsukasa Enomoto[1], Kohei Matsuzaki[2], Michio Tomishige[2] ([1]*Grad. Sch. Sci. Eng., Aoyama Gakuin Univ.*, [2]*Dept. Math. Phys., Col. Sci. Eng., Aoyama Gakuin Univ.*)

細胞生物的課題／Cell biology

2Pos139* 集団運動する神経幹細胞で測定された牽引力の、細胞配向場によるモデリング
Traction Force of Neural Stem Cells under Collective Migration was Modeled using the Orientation Field of Cell Alignment
Masahito Uwamichi[1], Kyogo Kawaguchi[2], Masaki Sano[3,4] ([1]*Dept. of Phys, Univ. of Tokyo*, [2]*RIKEN BDR*, [3]*IIAS*, [4]*TOKYO COLLEGE*)

2Pos140* 細胞集団の 3D 自己組織化: 高分子溶液の水／水ミクロ相分離の活用
Self-Generating 3D Cellular Assembly: Aqueous/Aqueous Micro Droplet as a Non-invasive Scaffold
Ritsuki Ito, Toshifumi Kishimoto, Takahiro Kenmotsu, Koichiro Sadakane, Kenichi Yoshikawa (*Graduate School of Life Medical Science, Doshisha University*)

2Pos141* ナノ粒子を用いた細胞内局所加熱に対する細胞の応答
Responses of cells to local heating in cells using a nanoparticle
Hideaki Ota, Hideo Higuchi (*Phys., Grad. Sci., Univ. Tokyo*)

2Pos142* Quantitation of cell shape by machine learning
Masato Tsutsumi[1], Chikara Furusawa[2,3], Satoshi Sawai[4], Nen Saito[2] ([1]*Grad School of Science, The Univ. of Tokyo*, [2]*Universal Biology Institute, The Univ. of Tokyo*, [3]*Center for Biosystems Dynamics Research, RIKEN*, [4]*Graduate School of Arts and Sciences, The Univ. of Tokyo*)

2Pos143* 細胞接着形態振動を駆動するグラフトポリマー層の垂直/水平変形性とその相関解析
Dual characterizations of vertical/lateral deformation of grafted-polymer layer driving cell-shape oscillation
Sayaka Masaike[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

2Pos144* 鍵アミノ酸残基を含む領域に変異をもつべん毛繊維の in vitro 多型変換実験
In vitro polymorphic transformation of flagellar filaments with mutations in a domain including the key amino acids
Shiori Hirose[1], Hidetoshi Tomaru[1], Yuuka Sashida[1], Yuka Kobayashi[1], Kana Horiguchi[1], Mikako Tsubaki[1], Fumio Hayashi[2], Kenji Oosawa[1] ([1]*Gunma Univ, Grad. Sch. Sci. Technol*, [2]*Gunma Univ, Ctr. Instr. Anal*)

2Pos145* マイコプラズマニューモニエの走流性
Rheotaxis in *Mycoplasma pneumoniae*
Yoshiki Kabata, Daisuke Nakane, Takayuki Nishizaka (*Department of Physics, Gakushuin University*)

2Pos146* 細胞内で LLPS 現象を観察する簡単な方法の開発
Development of a simple method to observe LLPS in cells
Chaieun Kim[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo.*, [2]*PRESTO, JST*)

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

2Pos148 バクテリア集団運動の揺らぎと応答の測定
Measurement of fluctuation and response of bacterial collective motion
Tatsuro Kai, Takahiro Abe, Shuichi Nakamura, Seishi Kudo, Shoichi Toyabe (*Appl. Phys., Tohoku Univ.*)

2Pos149 細胞運動のメカノケミカルモデル
Mechanochemical modelling of crawling cells
Mitsusuke Tarama[1], Kenji Mori[2], Ryoichi Yamamoto[2,3] ([1]*RIKEN BDR*, [2]*Dep Chem Eng, Kyoto Univ*, [3]*IIS, Univ Tokyo*)

2Pos150 Quantitative Analysis of Signal-dependent Cell Cycle Regulation
Kyoichi Ebata, Hiroaki Imoto, Sawa Yamashiro, Mariko Okada (*IPR, Osaka Univ.*)

2Pos151 飢餓状態への過渡期における大腸菌集団の束状凝集と一細胞形態
Bundle structure and single-cell morphology in E. coli populations during transient to a starvation condition
Takuro Shimaya[1], Reiko Okura[2], Yuichi Wakamoto[2], Kazumasa A. Takeuchi[1,3] ([1]*Dept. of Phys., Univ. Tokyo*, [2]*Dept. of Basic Sci., Univ. Tokyo*, [3]*Dept. of Phys., Tokyo Tech*)

2Pos152 Adaptability and robustness of cell migration realized by size-dependent polarity dynamics
Akihiko Nakajima[1,2], Motohiko Ishida[2], Satoshi Sawai[2,3] ([1]*Dept. Gen. Sys. Studies, Grad. Sch. Arts & Sci., Univ. Tokyo*, [2]*Res. Cent. Comp. Sys. Biol., Univ. Tokyo*, [3]*Dept. Basic Sci, Grad. Sch. Arts & Sci., Univ. Tokyo*)

2Pos153 3 次元毛細管構造のトポロジーが血管内皮細胞のシート展開の振る舞いを決定する
Topology of three-dimensional capillary structure determines blood vein sheet extension behavior
Kento Iida[1], Hiromichi Hashimoto[1], Masao Odaka[2], Akihiro Hattori[2], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Org. Univ. Res. Initiatives, Waseda Univ.*)

2Pos154 血管内皮細胞の二次元平面構造内における単一細胞の運動特性の観察
Behavior of single vascular endothelial cells in 2D structures
Hiromichi Hashimoto[1], Yuki Yamanaka[1], Ryuji Takano[2], Kento Iida[1], Masao Odaka[3], Kenji Matsuura[3], Akihiro Hattori[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

2Pos155 FRET を用いた「CheYp 濃度変化」と「べん毛モーターの回転方向」の同時計測
Simultaneous measurement of flagellar motor rotation and CheYp concentration via single cell FRET
Tatsuya Yamakoshi, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad.Sch.Frontier.Osaka Univ.*)

2Pos156 低浸透圧下における金魚ケラトサイト細胞シートの移動速度の上昇
Enhanced movement of fish keratocytes cell-sheet under low osmotic conditions
Naoto Ishijima, Hitoshi Tatsumi (*Human Information Systems Laboratory, Kanazawa Institute of Technology*)

2Pos157 A multi-omic approach to predict gene expression and metabolic functions from label-free spectral imaging of living cells
Arno Germond, Vipin Kumar, Tomonobu M. Watanabe (*RIKEN BDR*)

2Pos158 Conduction Pathway Analysis of Line-Networked Cardiomyocytes By using Multi-Electrode Array System
Tetsuro Yoshida, Tomoyuki Kaneko (*LaRC, FB, Grad. Sci.&Eng., Hosei Univ.*)

2Pos159 原子間力顕微鏡を用いた悪性度が異なるがん細胞の細胞間接着強度の比較
Comparison of intercellular adhesion strengths of cancer cells having different malignancies studied by atomic force microscopy
Kenta Ishibashi[1,2], Tomoko Okada[1], Chikashi Nakamura[1,2,3], Hyonchol Kim[1,2,3] ([1]*Biomed. Res. Inst., AIST*, [2]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [3]*PhotoBio-OIL, AIST-Osaka Univ.*)

2Pos160 Analysis of Physical Effect on Macrophage with Agarose Microchamber
Tomoyuki Irisawa, Nami Morizino, Tomohiro Saito, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

2Pos161 擬似心臓モデルとしての直線状心筋・線維芽細胞ネットワークの再構成および電気生理学性質の評価
Reconstruction of cardiac tissue-like cell structure and electrophysiological property evaluation
Koki Fujii, Tomoyuki Kaneko (*Grad. Sch. FB LaRC, Hosei Univ.*)

2Pos162 多電極電位システムを用いた赤外線レーザー照射による心臓組織片の拍動変化
Beating rate change of heart tissue piece by infrared laser irradiation using Multi Electrode Array system
Koji Emura, Tomoyuki Kaneko (*LaRC, FB, Grad.Sci&Eng, Hosei Univ.*)

2Pos163 ニワトリ胚由来心筋細胞を低温から温度を上げた際の拍動周期の変化
Beating rate change of chick embryonic cardiomyocytes heated up from low temperature
Kohei Oyama, Wei Wang, Tomoyuki Kaneko (*LaRC, FB, HOSEI unv.*)

2Pos164 心臓組織片の薬剤感受性におけるサイズ依存性の分析
Analysis of sensitivity for drugs depending size of cardiac tissue
Ryohei Kobayashi, Koji Emura, Tomoyuki Kaneko (*LaRC,FB,Hosei Univ.*)

2Pos165 ハイドロゲル上でのマスト細胞の脱顆粒抑制機構の研究
Inhibition of degranulation in mast cells attached to a hydrogel through defective microtubule tracts
Tadahide Furuno, Atsushi Shiki, Satoru Yokawa, Yoshikazu Inoh (*Sch. Pharm., Aichi Gakuin Univ.*)

生体膜・人工膜／Biological & Artificial membrane: Structure & Property

2Pos166 局所麻酔薬によるラフト様/非ラフト様相分離の解消とその機序
Mechanism of the local anesthetics-induced perturbation of raft-like ordered membrane domains
Masanao Kinoshita, Takeshi Chitose, Nobuaki Matsumori (*Kyushu University*)

2Pos167 Comparative study on organizations of human stratum corneum intercellular lipids collected from various body sites
Kenta Moriwaki, Hiromitsu Nakazawa, Satoru Kato (*Grad. Sch. Sci & Tech., Univ. Kwansei Gakuin*)

2Pos168* 回折 X 線ブリンキング法を用いた生細胞上の GPCR 分子内部運動の決定
Determining Intramolecular Motion of GPCRs on Live Cells using Diffracted X-ray Blinking Technique
Masaki Ishihara[1,2], Shoko Fujimiura[2], Kohei Ichiyanagi[3,4], Shunsuke Nozawa[3], Shinichi Adachi[3], Ryo Fukaya[3], Masahiro Kuramochi[1,2], Kazuhiro Mio[2], Yuji Sasaki[1,2] ([1]*Grad Sch. of Fron. Sci., Univ. of Tokyo*, [2]*Univ. of Tokyo - AIST OIL*, [3]*KEK*, [4]*Jichi Med. Univ*)

2Pos169* 大腸菌の封入密度に依存したリポソームの形態変化
Morphological changes of liposomes depending on density of encapsulated E. coli
Mai Hayakawa, Hazuki Terajima, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

2Pos170* 抗菌ペプチド・ラクトフェリシン B が誘起する細胞膜や脂質膜の急速な膜透過には膜電位が重要な役割を果たす
Membrane potential is vital for rapid permeabilization of plasma membranes and lipid bilayers by the antimicrobial peptide lactoferricin B
Farzana Hossain[1], Md. Mizanur Moghal[1], Md. Zahidul Islam[1], Md. Moniruzzaman[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos171* 細胞透過ペプチド・トランスポータン 10 の単一ベシクル内腔への侵入に対する膜電位の効果とそのメカニズム
Effect of membrane potential on the entry of cell-penetrating peptide transportan10 into the lumen of single vesicles and its mechanism
Md. Mizanur Moghal[1], Md. Zahidul Islam[1], Samiron Kumar Saha[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos172 膜タンパク質の分子内部動態解析技術の開発
Understanding intramolecular dynamics of membrane proteins using X-ray based analysis techniques
Kazuhiro Mio[1], Shoko Fujimura[1], Masaki Ishihara[2], Muneyo Mio[1], Masahiro Kuramochi[2], Hiroshi Sekiguchi[3], Tai Kubo[1], Yuji C. Sasaki[2] ([1]*Operand OIL, AIST*, [2]*Grad. Sch. of Front. Sci., The Univ of Tokyo*, [3]*JASRI*)

2Pos173 リン脂質とアクチンとビーズの互いに結合しないもの同士によるリポソームの形態形成
Liposome morphogenesis by phospholipid, actin filament and polystyrene bead that are not bound to each other
Ryota Kojima[1], Tomo Shibuya[2], Yutaka Sumino[2], Shunsuke Tanaka[1], Masahito Hayashi[1], **Kingo Takiguchi**[1] ([1]*Department of Biological Science, Graduate School of Science, Nagoya University*, [2]*Department of Applied Physics, Tokyo University of Science*)

2Pos174 タンパク質吸着による脂質膜の基板からの剥離
Membrane detachment from substrate induced by protein adhesion
Hiroshi Noguchi (*ISSP, Univ. Tokyo*)

2Pos175 エピガロカテキンガレートが誘起する GUV の破裂のメカニズム
Mechanism of the burst of giant unilamellar vesicles induced by epigallocatechin gallate
Yukihiro Tamba[1], Mika Terada[1], Naoya Sugita[1], Masahito Yamazaki[2] ([1]*Natl Inst Tech, Suzuka Coll*, [2]*Shizuoka Univ*)

2Pos176 平面型人工脂質二分子膜への昆虫細胞由来出芽ウイルスの融合観察
Observation of fusion between baculovirus budded virus envelopes and artificial planar bilayer lipid membrane
Azusa Oshima[1], Nahoko Kasai[1], Hiroshi Nakashima[1], Kanta Tsumoto[2], Koji Sumitomo[3] ([1]*NTT Basic Res. Labs.*, [2]*Mie Univ.*, [3]*Univ. Hyogo*)

2Pos177 赤外レーザー照射によるリポソームの形態変化
Morphological changes of liposomes by infrared laser irradiation
Tomoyuki Kaneko, Akira Oguri, Shunsuke Shiomi, Mai Hayakawa, Masahito Hayashi (*LaRC, FB, Hosei Univ.*)

2Pos178 抗菌ペプチド・マガイニン 2 が誘起するポア形成に対する膜電位の効果
Effect of membrane potential on antimicrobial peptide magainin 2 (mag)-induced pore formation in lipid bilayers
Md. Mamun Or Rashid[1], Md. Mizanur Moghal[1], Moynul Hasan[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos179 蛍光プローブでラベルされていない細胞透過ペプチド・トランスポータン 10 と単一巨大リポソームとの相互作用
Interaction of non-fluorescent probe-labelled cell-penetrating peptide transportan 10 with single giant unilamellar vesicles (GUVs)
Madhabi Shuma[1], Md. Mizanur Moghal[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos180 浸透圧により DOPG/DOPC-GUV に誘起される膜張力の評価
Estimation of Membrane Tension of DOPG/DOPC-GUVs Induced by Osmotic Pressure
Samiron Kumar Saha[1], Sayed Ul Alam Shibly[1], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos181 抗菌性オリゴ糖が誘発する脂質二分子膜の多層化
An antibacterial oligosaccharide makes lipid bilayer multi-layered
Ayumi Sumino[1,2], Tatsuya Hagiwara[3], Hatsuo Yamamura[3] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*InFiniti, Kanazawa Univ.*, [3]*Grad. Sch. Eng., Nagoya Inst. Tech.*)

2Pos182 Leaflet-specific lipid diffusions in supported lipid bilayers
Takuhiro Otosu, Shoichi Yamaguchi (*Saitama Univ.*)

2Pos183 インクジェット塗布を用いたパターン化人工生体膜の開発
Inkjet-printed and dried lipid membrane arrays for the biophysical studies and biosensing applications
Yasushi Tanimoto[1], Misato Yamada[2], Fumio Hayashi[3], Kenichi Morigaki[1,2] ([1]*Biosignal, Kobe Univ.*, [2]*Grad. Sch. Agr., Univ. Kobe*, [3]*Grad. Sch. Sci., Univ. Kobe*)

2Pos184 Multiscale molecular dynamics simulations of F-BAR protein Pacsin1: Assembly and curvature preference on lipid membrane
Md. Iqbal Mahmood[1], Hiroshi Noguchi[2], Kei-ichi Okazaki[1] ([1]*Institute for Molecular Science, Okazaki*, [2]*Institute for Solid State Physics, University of Tokyo, Kashiwa, Chiba*)

2Pos185 高速 AFM によるハブ毒液由来のホスホリパーゼ A_2 によって引き起こされる膜分解の動態観察
Membrane degradation dynamics by phospholipase A_2 from snake venom observed by high-speed AFM
Magoto Kamiya[1], Naoko Oda-Ueda[2], Ayumi Sumino[3,4] ([1]*Division of Mathematical and Physical Sciences, Graduate School of Natural Science and Technology, Kanazawa University*, [2]*Department of Pharmaceutical Sciences, Sojo University*, [3]*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*, [4]*Institute for Frontier Science Initiative, Kanazawa University*)

神経回路・脳の情報処理／Neuronal circuit & Information processing

2Pos186 グラフニューラルネットワークを用いた運動想起時脳波分類
Classification of Motor Imagery Using Graph Neural Networks
Ryo Nakajima[1], Hideo Mukai[2] ([1]*Comp. Sci. Prog., Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Dept. Comp. Sci., Sch. Sci. & Tech., Meiji Univ.*)

2Pos187 運動想起時脳波の時間周波数解析とニューラルネットワークによる識別
Time-Frequency and neural network analysis for classification motor imagery EEG
Azumi Ohno[1], Hideo Mukai[1,2] ([1]*Comp. Sci. Prog., Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Dept. Comp. Sci., Sch. Sci. & Tech., Meiji Univ.*)

2Pos188 深層畳み込みニューラルネットワークを用いたマウスの社会的行動の自動検出
Automated detection of social behavior in mice using deep convolutional neural network
Hideo Mukai[1,2], **Kenji Takemoto**[1] ([1]*Comp. Sci. Prog., Grad. Sch. Sci. & Tech., Meiji Univ.*, [2]*Dept. Comp. Sci., Sch. Sci. & Tech., Meiji Univ.*)

2Pos189 仮想空間を用いた EEG による運動想起フィードバック訓練システムの構築
EEG-Based motor imagery feedback training system on VR environment
Hideo Mukai[1,2], **Kazuki Kobayashi**[1] ([1]*Comp. Sci. Prog., Grad. Sch. Sci. & Tech.,Meiji Univ.*, [2]*Dept. Comp.Sci., Sch. Sci & Tech., Meiji Univ*)

2Pos190 線虫 C.elegans の学習行動を制御する神経回路のシナプス可塑性
Mechanisms of Synaptic Plasticity in a Neural Circuit that Regulates Memory Dependent Behavior in C. elegans
Llian Mabardi, Hirofumi Kunitomo, Hirofumi Sato, Yu Toyoshima, Yuichi Iino (*Tokyo University School fo Science Department of Biology*)

2Pos191 海馬で合成される男性・女性ホルモンやストレスホルモンによる記憶シナプスの早い non-genomic な制御
Rapid non-genomic modulation of synapses by hippocampus-synthesized androgen, estrogen and stress steroid
Suguru Kawato[1,2], Mika Soma[1], Mari Ogiue-Ikeda[1] ([1]*Dep. Cognitive Neuroscience, Fac. Pharma-Science, Teikyo Univ.*, [2]*Dep. Urology, Grad Sch Medicine, Juntendo Univ.*)

行動／Behavior

2Pos192 A leadership-based phase transition in a flocking model with activated and un-activated agents
Sulimon Sattari[1], Tamiki Komatusaki[1], Mikito Toda[2], Sky Nicholson[3], Jason Green[3], Udoy Basak[1] ([1]*Hokkaido University, Research Institute for Electronic Science*, [2]*Nara Women's University*, [3]*University of Massachusetts, Boston*)

光生物学：視覚・光受容／Photobiology: Vision & Photoreception

2Pos193* レチナールを結合するリジンを保存しない微生物型ロドプシンの光応答性機能獲得
Engineering microbial rhodopsin without retinal-binding lysine to gain photosensitive function
Yumeka Yamauchi[1], Masae Konno[1,2], Daichi Yamada[1,3], Kei Yura[4,5,6], Keiichi Inoue[1,7], Oded Béjà[8], Hideki Kandori[1,2] ([1]*Life Sci. Appl. Chem., Nagoya Inst. Tech.*, [2]*OBTRC, Nagoya Inst. Tech.*, [3]*Grad. Sch. Life Sci., Univ. Hyogo*, [4]*Grad. Sch. Hum. Sci., Ochanomizu Univ.*, [5]*Sim. Inf. Bio., Ochanomizu Univ.*, [6]*Sch. Adv. Sci. Eng., Waseda Univ.*, [7]*ISSP, Univ. Tokyo*, [8]*Technion - Israel Inst. Tech.*)

2Pos194* T(6-4)C の同位体標識を用いた(6-4)光回復酵素の低温における DNA 修復中間体の赤外分光測定
Low-temperature FTIR study of the repair intermediates of T(6-4)C/photolyase using isotope labeling
Katsuya Maeda[1], Mai Kumagai[1], Daichi Yamada[2], Yuma Terai[3], Junpei Yamamoto[3], Hideki Kandori[1] ([1]*Nagoya Inst. Tech*, [2]*Univ. Hyogo.*, [3]*Osaka Univ.*)

2Pos195* シネコシスティスハロロドプシン（SyHR）のアニオン輸送における 塩基性アミノ酸の機能的役割
Functional roles of basic amino acids on the anion transport in *Synechocystis* halorhodopsin (SyHR)
Masaki Nakama[1], Keiichi Kojima[1], Marie Kurihara[1], Susumu Yoshizawa[2], Yuki Sudo[1] ([1]*Grad. Sch. of Med. Dent.& Pharm. Sci. Okayama Univ.*, [2]*AORI, UTokyo*)

2Pos196* Molecular characterization of heliorhodopsin from marine giant virus light-dependently infecting to *Emiliania huxleyi*
Ritsu Mizutori[1], Masae Konno[1,2], Keiichi Inoue[1,3], Oded Beja[4], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*OBTRC, NIT*, [3]*ISSP, Univ. Tokyo*, [4]*Technion-Israel Inst. Tech.*)

2Pos197* 分光学的手法による霊長類青感受性視物質の光反応中間体解析
Photochemical reactions of a primate blue-sensitive pigment by spectroscopic study
Shunpei Hanai[1], Kota Katayama[1], Takuma Sasaki[1], Hiroo Imai[2], Hideki Kandori[1] ([1]*Nagoya Institute of Technology*, [2]*Primate Research Institute, Kyoto University*)

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

2Pos199 ロドプシンクラスター上におけるトランスデューシンの動的過程の高速 AFM 観察
High-speed AFM observation of the dynamic process of transducin on rhodopsin cluster
Kazuhiko Hoshikaya[1], Yasushi Tanimoto[2], Hayato Yamashita[1], Kenichi Morigaki[2,3], Fumio Hayashi[4], Masayuki Abe[1] ([1]*Graduate School of Engineering Science, Osaka University*, [2]*Biosignal research center, Kobe University*, [3]*Graduate School of Agricultural Science, Kobe University*, [4]*Graduate School of Science, Kobe University*)

2Pos200 網膜桿体細胞内円盤膜上での脂質-光受容タンパク質秩序形成の数理モデル
A mathematical model of pattern formation of lipid-photoreceptor proteins on disk membranes of retinal cells
Yukito Kaneshige[1], Yasushi Tanimoto[2], Hiraku Nishimori[1], Kenichi Morigaki[2], Fumio Hayashi[3], Akinori Awazu[1] ([1]*Dept. of Math. & Sci. Hiroshima Univ.*, [2]*Dept. of Agri. Kobe Univ.*, [3]*Dept. of Sci. Kobe Univ.*)

2Pos201 新奇チャネルロドプシン Ts_Rh3 の電気生理学的解析
Electrophysiological analysis of a novel channelrhodopsin Ts_Rh3
Rintaro Tashiro[1], Kumari Sushmita[2], Suneel Kateriya[2], Hideki Kandori[1], Satoshi Tsunoda[1,3] ([1]*Nagoya Institute of Technology*, [2]*Jawaharlal Nehru University*, [3]*JST PRESTO*)

2Pos202 リン酸化ロドプシン･アレスチン複合体は視細胞円板膜切れ込み部に集まる
Phosphorylated-rhodopsin/arrestin complex assembles to disc incisures
Fumio Hayashi[1], Fuko Kueda[2], Kenichi Morigaki[2,3], Keiji Seno[4] ([1]*Kobe Univ, Sci, Biology*, [2]*Kobe Univ, Agri*, [3]*Kobe Univ, Biosignal*, [4]*Hamamatsu Univ Sch Med*)

2Pos203 ボルボックスの光驚動反応における鞭毛運動の照度依存性
Light intensity dependence of adaptive photo-response of Volvox
Yukariko Komasaka, Yoshihiro Murayama (*Department of Applied Physics, Tokyo University of Agriculture and Technology*)

2Pos204 共鳴ラマン分光法と MD + QM/MM 計算を用いたシアノバクテリオクロム発色団の脱プロトン化部位の同定
Identification of the Deprotonated Pyrrole Nitrogen of the Bilin-Based Photoreceptor by Raman Spectroscopy with MD+QM/MM Analysis
Risako Miyoshi[1], Shinsuke Osoegawa[1], Kouhei Watanabe[1], Yuu Hirose[2], Tomotsumi Fujisawa[1], Masahiko Ikeuchi[3], Masashi Unno[1] ([1]*Dept. Chem. & Appl. Chem., Saga Univ.*, [2]*Dept. of Appl. Chem. & Life Sci., Toyohasi Univ. of Tech.*, [3]*Dept. Life Sci. (Biology), Univ. of Tokyo,*)

2Pos205 ビリベルジン結合型シアノバクテリオクロムの遠赤／橙色光変換過程での構造変化の検出
Detection of structural change during far-red/orange reversible photoconversion of biliverdin-binding cyanobacteriaochrome
Yuka Takeda, Keiji Fushimi, Rei Narikawa (*Grad. Sch. Sci., Univ. Shizuoka*)

2Pos206 赤外分光法によって明らかになった色覚視物質とロドプシンの構造ダイナミクスの違い
Different structural dynamics between cone pigments and rhodopsin revealed by FTIR spectroscopy
Takuma Sasaki[1], Kota Katayama[1], Hiroo Imai[2], Hideki Kandori[1] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Primate Res. Inst., Kyoto Univ.*)

2Pos207 An Anion Channelrhodopsin with a Naturally Super-Slow Photocycle
Takahiro Kitahara[2], Hina Kurane[3], Chihiro Kikuchi[2], Tomoyasu Aizawa[1,4], Takashi Kikukawa[1,4], Makoto Demura[1,4], **Takashi Tsukamoto**[1,4] ([1]*Fac. Adv. Life Sci., Hokkaido Univ.*, [2]*Grad. Sch. Life Sci., Hokkaido Univ.*, [3]*Sch. Sci., Hokkaido Univ.*, [4]*GSS, GI-CoRE, Hokkaido Univ.*)

2Pos208 赤外分光法により明らかとなった酵素型ロドプシンの構造的特徴
Structural features of enzyme rhodopsins revealed by infrared spectroscopy
Masahito Watari[1], Tatsuya Ikuta[2], Haon Hutamata[2], Daichi Yamada[1], Wataru Shihoya[2], Kazuho Yoshida[1], Yuji Hurutani[1], Satoshi Tsunoda[1,3], Osamu Nureki[2], Hideki Kandori[1] ([1]*Life Sci. Appl. Chem., Nagoya Inst. Tech.*, [2]*Grad. Sch. Sci., Univ. Tokyo.*, [3]*PREST, JST*)

2Pos209 *Mastigocladopsis repens* halorhodopsin の Cl^-ポンプ活性における His166 の重要性
Importance of His166 for Cl^--pump activity of *Mastigocladopsis repens* halorhodopsin
Kento Iwama[1], Yumi Watanabe[1], Takashi Tsukamoto[1,2,3], Tomoyasu Aizawa[1,2,3], Makoto Demura[1,2,3], Takashi Kikukawa[1,2,3] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*, [3]*GSS, GI-CoRE, Hokkaido Univ.*)

2Pos210 時間分解フーリエ変換赤外分光法による KR2 のナトリウムおよびリチウムイオン輸送の分子機構研究
Time-resolved FTIR spectroscopy for studying molecular mechanisms of sodium and lithium ion transportation of *Krokinobacter* rhodopsin 2
Sahoko Tomida[1], Hideki Kandori[1], Yuji Furutani[1,2] ([1]*Nagoya Inst. Tech.*, [2]*Inst. Mol. Sci.*)

2Pos211 Rc-PYP の多量体複合体形成における K72 の役割
Functional role of a residue K72 of Rc-PYP in light dependent oligomeric complex formation process
Yoichi Yamazaki[1], Natsuki Oka[1], Yugo Hayashi[1], Hironari Kamikubo[1,2] ([1]*Div. Mat. Sci. NAIST*, [2]*IMSS,KEK*)

光生物学：光合成／Photobiology: Photosynthesis

2Pos212 FTIR study on the localization of the excited triplet state of chlorophyll in photosystem II
Taichi Hayase[1], Yuichiro Shimada[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*RIIS, Okayama Univ.*)

2Pos213 緑色イオウ細菌 Chlorobaculum tepidum からの反応中心複合体標品の改良
Improved preparation of the reaction center complex from the green sulfur bacterium *Chlorobaculum tepidum*
Koki Wada[1], Chihiro Azai[2], Tetsuko Nakaniwa[3], Genji Kurisu[3], **Hirozo Oh-oka**[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Inst. Protein Res., Osaka Univ.*)

2Pos214 Carotenoid glycoside quenches bacteriochlorophyll *a* fluorescence in the photosynthetic reaction center complex of green sulfur bacteria
Chihiro Azai[1], Jiro Harada[2], Takumi Inoue[1], Shogo Fujimoto[3], Shinji Masuda[4], Daisuke Kosumi[3,5] ([1]*Col. Life Sci., Ritsumeikan Univ.*, [2]*Dept. Med. Biochem., Kurume Univ. Sch. Med.*, [3]*Grad. Sch. Sci. & Tech., Kumamoto Univ.*, [4]*Cent. Biol. Res. & Info., Tokyo Inst. Tech.*, [5]*IPPS, Kumamoto Univ.*)

2Pos215 Isolation of the Rieske/cytochrome *b* complex from green sulfur bacteria and interaction of the Rieske protein with cytochrome *c*-556
Hiraku Kishimoto[1], Takahiro Nagaoka[1], Chihiro Azai[2], Risa Mutoh[3], Hideaki Tanaka[4], Yohei Miyanoiri[4], Genji Kurisu[4], Hirozou Oh-oka[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Col. Life Sci. Ritsumeikan Univ.*, [3]*Fac. Sci., Fukuoka Univ.*, [4]*Inst. Protein Res., Osaka Univ.*)

2Pos216 Spectroscopic characterization of a bacteriochlorophyll b-based LH1-RC complexes from thermophilic purple bacterium Blactochloris tepida
Yukihiro Kimura[1], Ryuta Seto[1], Tomoaki Kawakami[2], Rikako Kishi[1], Michie Imanishi[1], Shinichi Takaichi[3], Shinji Takenaka[1], Michael T. Madigan[4], Seiu Otomo[2] ([1]*Grad. Sch. Agri. Sci., Kobe Univ.*, [2]*Ibaraki Univ.*, [3]*Tolyo Univ. of Agri.*, [4]*Southern Illinois Univ.*)

2Pos217 光感受性アデニル酸シクラーゼ OaPAC の活性制御部位の同定
Identification of the activity-regulating site in the photoactivated adenylate cyclase (OaPAC)
Minako Hirano[1], Tomoya Ishido[2], Masumi Takebe[3], Toru Ide[2], Shigeru Matsunaga[3] ([1]*Grad. Sch. Creation Photon Indust.*, [2]*Okayama Univ.*, [3]*Hamamatsu Photonics K.K.*)

2Pos218 Light-dependent structural states of OaPAC
Tomoya Ishido[1], Toru Ide[1], Minako Hirano[2] ([1]*Okayama University*, [2]*GPI*)

2Pos219 タイプ 1 ロドプシンの L/Q スイッチがヘリオロドプシンの波長制御に及ぼす影響
Effects of the L/Q switch on color tuning of heliorhodopsin
Yuta Nakajima, Hideki Kandori (*Grad. Sch. Eng., NIT*)

2Pos220 クリプト藻由来のカチオンチャネルロドプシン Gt_CCR4 のオプトジェネティクスに向けた電気生理学的研究
Study of cation channelrhodopsin Gt_CCR4 from cryptophyte for optogenetics
Shunta Shigemura[1], Shoko Hososhima[1], Hideki Kandori[1], Satoshi Tsunoda[1,2] ([1]*Grad. Sch. Eng., NIT*, [2]*JST PRESTO*)

2Pos221 中赤外レーザーの神経系培養細胞のカルシウム濃度および膜電位への影響
The influence of mid-infrared laser on Ca2+ concentration and membrane potential of neuron-like cells
Yoshiyuki Shimizu, Toyohiko Yamauchi, Tatsuo Dougakiuchi, Gen Takebe (*Hamamatsu Photonics K.K.*)

2Pos222 中赤外光照射による細胞のアポトーシスシグナル誘導
Induction of intracellular apoptotic cell signaling by mid-infrared laser exposure
Gen Takebe, Yoshiyuki Shimizu, Toyohiko Yamauchi, Tatsuo Dougakiuchi (*Hamamatsu Photonics K.K. Central Research Laboratory*)

2Pos223 生体エネルギーを浪費する光駆動内向きプロトンポンプロドプシンの電気生理学研究と光遺伝学への応用
Electrophysiological study and optogenetics application of inward-directed proton-pumping rhodopsin, NsXeR
Satoshi Tsunoda[1,2], Shoko Hososhima[1], Hideki Kandori[1] ([1]*Nagoya Institue of Technology*, [2]*JST PRESTO*)

2Pos224 Photo-regulate small GTPase Ras using photochromic peptide inhibitor
Nobuyuki Nishibe[1], Kenichi Taii[1], Toshio Nagashima[2], Toshio Yamazaki[2], Kazunori Kondoh[1], Shinsaku Maruta[1] ([1]*Depertment of Bioinformatics, Soka University Graduate School of Engineering, Hachioji, Japan*, [2]*Center for Life Science Technologies, RIKEN, Yokohama, Japan*)

放射線生物：活性酸素／Radiobiology & Active oxygen

2Pos225 プリオンペプチド銅錯体のレドックスポテンシャル
Redox potential of copper-binding prion peptide
Shuhei Murakami, Wakako Hiraoka (*Grad.Sch.of Sci.& Tech.,Meiji Univ*)

2Pos226 低酸素下での X 線誘発 DSB の修復効率
Rejoining efficiency of X-ray-induced DSBs in hypoxia
Ryoichi Hirayama, Akiko Uzawa, Yoshiya Furusawa, Sumitaka Hasegawa (*NIRS, QST*)

2Pos227 低線量放射線に曝露された細胞の運命決定における ATM を介した細胞質の放射線応答重要性
Importance of ATM-mediated cytoplasmic radiation response in determining the fate of cells exposed to low-dose radiation
Munetoshi Maeda[1], Hideki Matsumoto[2], Masanori Tomita[3] ([1]*Proton Medic. Res. Div., R&D Dept., WERC*, [2]*Dept. Exp. Radiol. Health Phys., Sch. Med. Sci., Univ. Fukui*, [3]*Radiat. Safety Res. Center, NTRL, CRIEPI*)

2Pos228 酸化ストレスが引き起こす HeLa 細胞ミトコンドリア電子伝達系の機能増幅
Oxidative stress-induced enhancement of mitochondrial electron transport chain in HeLa cells
Wakako Hiraoka, Shuhei Murakami (*Department of Physics, Meiji University*)

生命の起源・進化／Origin of life & Evolution

2Pos229* **DNA を自発的に取り込んだ細胞サイズ液滴**
Aqueous polymer solutions create stable cell-sized sphere entrapping DNA: A novel scenario of de novo cell
Fumika Fujita[1], Hiroki Sakuta[1], Kanta Tsumoto[2], Takahiro Kenmotsu[1], Kenichi Yoshikawa[1] ([1]*Facul. Life Med. Sci., Doshisha Univ.*, [2]*Facul. Eng., Mie Univ.*)

2Pos230* **遺伝子破壊変異の頻度が調節可能な系の構築およびそのゲノム縮小の進化実験への応用**
Construction of a Genetic Tool for Tuning Gene-Inactivating Mutations and its Application to Experimental Evolution of Genome Reduction
Yuki Kanai[1], Saburo Tsuru[2], Chikara Furusawa[2,3] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*UBI, Univ. Tokyo*, [3]*BDR, RIKEN*)

2Pos231 Membraneless Polyester Microdroplets as Primordial Compartments at the Origins of Life
Tony Z Jia[1], Kuhan Chandru[1], Yayoi Hongo[1], Rehana Afrin[1], Tomohiro Usui[1], Kunihiro Myojo[2], Po-Hsiang Wang[1], H. James Cleaves[1] ([1]*Earth-Life Science Institute, Tokyo Institute of Technology*, [2]*Tokyo Institute of Technology Department of Earth and Planetary Science*)

2Pos232 **情報高分子と連携したベシクルの自己生産**
Reproduction of Vesicles coupled with Template Polymerization
Minoru Kurisu[1], Harutaka Aoki[1], Takehiro Jimbo[1], Yuka Sakuma[1], Masayuki Imai[1], Sandra Luginbuhl[2], Peter Walde[2] ([1]*Grad. Sch. Sci., Univ. Tohoku*, [2]*dep. Material, ETH*)

2Pos233 Laboratory evolution of Escherichia coli reveals constrained evolutionary states for antibiotic resistance
Junichiro Iwasawa[1], Tomoya Maeda[2], Takaaki Horinouchi[2], Chikara Furusawa[1,2,3] ([1]*Dept. of Physics, Univ. of Tokyo*, [2]*RIKEN BDR*, [3]*UBI, Univ. of Tokyo*)

2Pos234 Fitness landscape of antibiotic-resistance evolution
Masayoshi Hiranaka[1], Nen Saito[2], Chikara Furusawa[2,3] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*UBI, Univ. Tokyo*, [3]*BDR, RIKEN*)

2Pos235 Relationship between fluctuation of single-enzyme activity and evolvability
Hiroshi Ueno[1], Morito Sakuma[1], Yoshihiro Minagawa[1], Kazuhito Tabata[1], Kentaro Miyazaki[2,3], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*AIST*, [3]*Grad. Sch. Front. Sci., Univ. Tokyo*)

ゲノム生物学／Genome biology

2Pos236 **数理モデルとライブイメージングデータを用いた分裂酵母間期核内構造の解析**
Analysis of fission yeast interphase intranuclear structure by mathematical model and live imaging data
Yuki Takayama[1], Hisamichi Senda[2], Koki Ito[3], Hiraku Nishimori[3], Masaru Ueno[3], Akinori Awazu[3] ([1]*Grad. Sch. Sci., Univ. Hiroshima*, [2]*Grad. Sch. Advanced Sciences of Matter, Univ. Hiroshima*, [3]*Grad. Sch. Integrated Sciences for Life, Univ. Hiroshima*)

2Pos237 Dynamical chromatin organization during transcription
Ashwin S. Selvarajan[1], Kayo Hibino[2], Yuji Itoh[2], Kazuhiro Maeshima[1,2], Masaki Sasai[2] ([1]*Dept of Applied Physics, Nagoya University, Nagoya, Japan*, [2]*Structural Biology Center, National Institute of Genetics, Mishima, Shizuoka, Japan*)

生命情報科学／Bioinformatics

2Pos238 機械学習を用いたタンパク質部分配列の構造及び機能の解析
Analysis of structural and functional propensities for subsequences of proteins by using machine learning
Ryohei Kondo[1], Kota Kasahara[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

2Pos239 GPCR ー G タンパク質の結合選択性に関わる部位同定および結合 G タンパク種予測への応用
Determination of key regions relating GPCR-Gprotein coupling selectivity and their application for predicting coupling G-protein kinds
Mayu Kawamura[1], Risako Kasado[1], Tomomi Manaka[1], Ryuuji Shinozaki[1,2], Masami Ikeda[3], **Makiko Suwa**[1,2] ([1]*Aoyamagakuin Univ. College of Sci. and Eng.*, [2]*Aoyamagakuin Univ. Grad. School. Sci. and Eng.*, [3]*AIST AIRC*)

2Pos240 デノボデザインによる新規 αβ 型蛋白質フォールドの探査
Exploration of novel alpha-beta protein folds by de novo design
Shintaro Minami[1], Rie Koga[1], George Chikenji[2], Toshihiko Sugiki[3], Naohiro Kobayashi[4], Nobuyasu Koga[1] ([1]*NINS, ExCELLS*, [2]*Grad. Shc. of Eng., Nagoya Univ.*, [3]*Inst. for Prot. Res., Osaka Univ.*, [4]*RIKEN, RSC*)

2Pos241 アンサンブルドッキングによるタンパク質の相互作用面の解析
Analysis of protein interaction surfaces using ensemble rigid-body docking process
Nobuyuki Uchikoga[1], Yuri Matsuzaki[2] ([1]*Dept. of Network Design, Sch. of Interdiscip. Math. Sci., Meiji Univ.*, [2]*ToTAL, TITech*)

2Pos242 転写因子 Med26 における天然変性蛋白質認識メカニズムの分子動力学的検討
Molecular dynamics study for elucidation of recognition mechanism of intrinsically disordered proteins by transcription factor Med26
Satoshi Goto[1], Takuya Takahashi[2], Kouta Kasahara[3] ([1]*Coll Life Sci., Ritsumeikan Univ*, [2]*Prof. Univ.Ritsumei*, [3]*Ass.Prof. Univ.Ritsumei*)

数理生物学／Mathematical biology

2Pos243* (2SCP-6) 上皮メカノケミカル動態の同定
(2SCP-6) System identification of mechano-chemical epithelial sheet dynamics
Yoshifumi Asakura[1], Yohei Kondo[2], Kazuhiro Aoki[2], Naoki Honda[1] ([1]*Grad. Sch. Biostudies, Univ. Kyoto*, [2]*Div. Quantitative Biol. ExCELLS, NIBB.*)

2Pos244* 細胞周期の不均一性に関する網羅的数理モデルの構築
A comprehensive model of heterogeneous cell cycle responses
Hiroaki Imoto, Kyouichi Ebata, Shigeyuki Magi, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

2Pos245* 真性粘菌変形体の走磁性とその探索行動への寄与
Magnetotaxis of Physarum plasmodium and its contribution to exploration
Michinori Muro, Hiroshi Sato, Tomohiro Shirakawa (*Natl Def Acad Japan*)

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

2Pos247 BOID における第 4 のルール：他個体への注目は一定時間毎に一定の確率で失われる
The fourth rule of BOID: attention to the other individuals is lost with fixed probability every fixed time
Tomohiro Shirakawa, Hiroshi Sato, Takuya Matsuo (*Natl. Def. Acad. Japan*)

2Pos248 An Information-theoretic approach toward identifying the leader(s) and aggregation place in Dictyostelium Discoideum colony
Udoy Sankar Basak[1], Sulimon Sattari[1], Kazuki Horikawa[2], Tamiki Komatsuzaki[1] ([1]*Hokkaido University*, [2]*Tokushima University*)

2Pos249 細胞内共生進化への理論的アプローチ
Theoretical approach to evolution of intracellular symbiosis
Sakura Aoki, Kunihiko Kaneko (*The University of Tokyo Graduate School of Arts and Scienses*)

2Pos250 Asymptotic expansion of a stochastic FitzHugh-Nagumo model
Takanobu Yamanobe (*Sch. Med., Hokkaido Univ.*)

非平衡・発生リズム／Nonequilibrium state & Biological rhythm

2Pos251 光応答性を持った C. elegans の集団運動
Collective motion of optically susceptible C. elegans
Ken Nagai[1], Hiroshi Ito[2], Takuma Sugi[3] ([1]*JAIST*, [2]*Kyushu Univ.*, [3]*Shiga Univ. Med. Sci.*)

2Pos252 逆ミセルを用いたフレーリッヒ凝縮の研究 (I)
Studies of Frohlich condensation using reverse micelles. I
Hiroshi Murakami (*QST*)

2Pos253 孤立した粒子の運動解析を基とした、回転する自走粒子の集団運動を表す数理モデルの推定
Estimation of mathematical model representing collective motion of rotating self-propelled particle
Tadashi Sakaguchi[1], Kazuhiro Oiwa[2], Hitoshi Sakakibara[2], Ken Nagai[1] ([1]*JAIST*, [2]*NICT*)

2Pos254 抗原識別における確率的ノイズの役割
A role of stochastic noise in ligand discrimination
Masashi K. Kajita, Kazuyuki Aihara, Tetsuya J. Kobayashi (*IIS, University of Tokyo*)

2Pos255 Theoretical model of dynamics of epithelial tissue with cellular chirality
Takaki Yamamoto[1], Tetsuya Hiraiwa[2], Tatsuo Shibata[1] ([1]*RIKEN BDR*, [2]*Mechanobiology Institute, National University of Singapore*)

計測／Measurements

2Pos256* 細胞内温度場は高分子に依存する
Intracellular temperature field depends on polymers
Masaharu Takarada[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ of Tokyo*, [2]*PRESTO, JST*)

2Pos257* インフルエンザウイルス多様性解析に向けた、多次元デジタル計測技術の開発
Multi-Dimensional (MD) digital assay for analysis of influenza virus heterogeneity
Shingo Honda[1], Yoshihiro Minagawa[2], Kazuhito V. Tabata[2], Hiroyuki Noji[2] ([1]*Dept. Bioeng., Grad. Sch. Eng., Univ. Tokyo*, [2]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

2Pos258* Development of a method for quantitative profiling of microRNAs in single exosomes
Cinya Chung, Ryo Iizuka, Takashi Funatsu (*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*)

2Pos259* 光ファイバーを用いた蛍光相関分光法の開発とエクソソーム研究への応用
Development of optical fiber based fluorescence correlation spectroscopy and application to exosome study
Misato Osaka[1], Johtaro Yamamoto[2,3], Masataka Kinjo[3] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Biomed. Res. Inst., AIST.*, [3]*Fac. of Adv. Life Sci., Hokkaido Univ.*)

2Pos260* 細胞内温度変動に関与する分子のスクリーニング法の開発
Development of a method to screen molecules related to intracellular temperature variation
Takashi Mitsubori[1], Kohki Okabe[1,2], Fumi Kano[3], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*, [2]*PRESTO, JST*, [3]*IIR, Tokyo Inst. of Tech.*)

2Pos261 Optical tweezers with red laser for new applications
Tomohiro Masuda, Wataru Nakashima, Kazuki Nakajima, Shin Yamaguchi, Takashi Sagawa, **Yuichi Inoue** (*SIGMAKOKI CO., LTD.*)

2Pos262 赤外超解像顕微鏡によるガチョウおよびペンギン羽毛の内部構造観察
Orientation-sensitive molecular imaging of keratin proteins of goose and penguin feathers by an IR super-resolution micro-spectroscopy
Hirona Takahashi, Koki Kimura, **Makoto Sakai** (*Faculty of Science, Okayama University of Science*)

2Pos263 ミクロゲルの粘弾性特性の測定
Viscoelastic measurement of a biopolymer microgel by microcapillary aspiration
Atsushi Sakai[1,2], Yoshihiro Murayama[1], Miho Yanagisawa[2] ([1]*Tokyo Univ. of Agri. & Technol.*, [2]*Komaba Inst. Sci., The Univ. Tokyo.*)

バイオイメージング／Bioimaging

2Pos264* 高速イオン伝導顕微鏡による表面電荷のマッピング
Mapping of surface charge by high speed ion conductance microscopy
Shusei Kaihatsu[1], Kazuki Shigyo[2], Toshio Ando[2], Shinji Watanabe[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

2Pos265* マニピュレーター付き高速 AFM スキャナーの改良
Improvement of high-speed AFM scanner with manipulator
Jun Takano[1], Shun Aoki[2], Kazuki Shigyo[3], Shinji Watanabe[3], Toshio Ando[3,4], Noriyuki Kodera[3,4] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Sch. Math. & Phys., Kanazawa Univ.*, [3]*WPI-NanoLSI, Kanazawa Univ.*, [4]*CREST, JST*)

2Pos266* タンパク質オリゴマー分布イメージング：生細胞内で空間的に不均一なオリゴマーの分布可視化に向けて
Protein Oligomer Imaging: towards Visualization of Spatially Heterogeneous Oligomer Distribution in Living Cell
Ryosuke Fukushima[1], Johtaro Yamamoto[2,3], Masataka Kinjo[2] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [3]*Biomed. Res. Inst., AIST*)

2Pos267* A ratiometric bioluminescent indicator for water hardness in living specimen
Md Nadim Hossain[1,2], Ryuichi Ishida[2], Mitsuru Hattori[1,2], Tomoki Matsuda[1,2], Takeharu Nagai[1,2] ([1]*Graduate School of Engineering, Osaka University*, [2]*ISIR, Osaka University*)

2Pos268 (2SHP-4) 大気圧走査電子顕微鏡 ASEM による骨組織再構築の水中免疫電顕法と cryo-TEM 観察
(2SHP-4) Observation of unstained bone tissues and immuno-EM in liquid by ASEM and cryo-TEM
Chikara Sato[1], Shinya Sugimoto[2], Yuri Hatano[1], Mari Sato[1], Eiko Sakai[3] ([1]*Biomedical Res. Inst., AIST*, [2]*Dept. Bacteriol., The Jikei Univ. Sch. Med.*, [3]*Dental Pharmacology, Nagasaki Univ.*)

2Pos269 (2SEA-5) G1 期酵母細胞核内における核酸分布の XFELX 線回折イメージング
(2SEA-5) Distribution of nucleic acids in yeast nucleus of G1 phase visualized by X-ray diffraction imaging using X-ray free electron laser
Masayoshi Nakasako[1,2], Takahiro Yamamoto[1,2], Amane Kobayashi[1,2], Mao Oide[1,2], Koji Okajima[1,2], Yuki Takayama[1,2,3], Tomotaka Oroguchi[1,2], Masaki Yamamoto[2] ([1]*Keio University*, [2]*RIKEN*, [3]*University of Hyogo Prefecture*)

2Pos270 ホウレンソウグラナ膜における光化学系 II 分子間相互作用の高速 AFM による解析
HS-AFM imaging and analyses of intermolecular interaction of photosystem II in grana membrane from spinach
Daisuke Yamamoto (*Fuc. Sci. Fukuoka Univ.*)

2Pos271 光照射でタンパク質機能阻害・細胞死を誘導する単量体光増感緑色蛍光タンパク質の開発
Monomeric green fluorescent protein based photosensitizer for photo-inducible protein inactivation and cell death
Tomoki Matsuda[1], Yemima Dani Riani[1], Kiwamu Takemoto[2], Takeharu Nagai[1] ([1]*ISIR, Osaka Univ.*, [2]*Grad Sch. of Med., Yokohama City Univ.*)

2Pos272 RNA ポリメラーゼ II により制御されるクロマチンダイナミクス
Chromatin dynamics regulated by RNA polymerase II
Yuji Itoh, Michael Babokhov, Kayo Hibino, Kazuhiro Maeshima (*NIG*)

2Pos273 電子顕微鏡トモグラフィ像への構造フィッティング
Fitting atomic structure to Electron Microscopy Tomography
Yuki Mori, Suguru Kato, Toru Niina, Shoji Takada (*Kyoto University*)

2Pos274 高輝度なポジティブ型光スイッチング蛍光タンパク質 Kohinoor 2.0 の開発
Development of a highly-bright positively reversibly photoswitchable fluorescent protein Kohinoor 2.0 for super-resolution microscopy
Tetsuichi Wazawa[1], Shusaku Uto[1], Kazunori Sugiura[1], Shunsuke Maeda[2], Katsumasa Fujita[2], Takashi Washio[1], Takeharu Nagai[1] ([1]*ISIR, Osaka Univ*, [2]*Grad Sch of Engin, Osaka Univ*)

2Pos275 プラズモニックナノ粒子を用いた高速マルチカラー生体 1 分子イメージング
Multi-color and high-speed imaging of single biomolecules with plasmonic nanoparticles
Jun Ando[1,2], Akihiko Nakamura[1,2], Mayuko Yamamoto[1], Ryota Iino[1,2] ([1]*IMS, NINS*, [2]*SOKENDAI*)

2Pos276 Characterizing the spatio-temporal heterogeneity on biomolecular concentration, mobility and local environment in live cells
Sho Oasa[1], Aleksandar J. Krmpot[1,2], Stanko N. Nikolic[1,2], Lars Terenius[1], Rudolf Rigler[1,3], Vladana Vukojevic[1] ([1]*Dept. of Clin. Neurosci., Center for Mol. Med., Karolinska Inst.*, [2]*Inst. of Physics, Univ. of Belgrade*, [3]*Dept. of Med. Biochem. and Biophys., Karolinska Inst.*)

2Pos277 Mapping of mechanical property on live cell surface by scanning ion conductance microscope
Satoko Kitazawa[1], Linhao Sun[2], Ayako Housaka[2], Takahiro Watanabe-Nakayama[2], Hiroki Konno[2], Mikihiro Shibata[2], Shinji Watanabe[2] ([1]*Grad. Sch. Math. &Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

2Pos278 定量的 ATP イメージングを用いた細胞の代謝状態の空間的相関の解析
Spatial correlation of metabolic states in mammalian cells revealed by quantitative single-cell ATP imaging
Hideyuki Yaginuma[1,2], Yasushi Okada[1,3] ([1]*BDR, Riken*, [2]*Grad. Sch. of Eng., Univ. of Tokyo*, [3]*Grad. Sch. of Sci., Univ. of Tokyo*)

2Pos279 局所特徴モーフィングした補間による深さ解像度の低い 3 次元画像の改善
Feature based local morphing improved interpolation of 3D stack images at low depth resolution
Yutaka Ueno[1], Takashi Kawasaki[2], Totai Mitsuyama[1] ([1]*AIST Tokyo*, [2]*AIST Kansai*)

2Pos280 スマートフォン発光顕微鏡による 1 細胞イメージング
Smartphone based chemiluminescence microscope for single cell imaging
Mitsuru Hattori[1], Sumito Shirane[2], Kuniaki Nagayama[2], Takeharu Nagai[1] ([1]*ISIR, Osaka Univ.*, [2]*Life is small. Company*)

2Pos281 鱗翅目昆虫の変態過程における極微弱バイオフォトン発光の連続画像計測
Continuous imaging of biophoton emission of lepidopterous insects during
Shoko Usui[1], Mika Tada[2], Masaki Kobayashi[1] ([1]*Grad. Sch. Elec., Tohtech*, [2]*Center for General Education., Tohtech*)

2Pos282 Construction of a millisecond structured illumination microscope and its application to ultrafast super-resolution live cell imaging
Shinji Kajimoto[1], Tomu Suzuki[1], Narufumi Kitamura[2], Mayumi Takano[2], Naoko Furusawa[3], Yasushi Nakano[3], Kohsuke Gonda[2], Takakazu Nakabayashi[1] ([1]*Grad. Sch. Pharm. Sci., Tohoku Univ.*, [2]*Grad. Sch. Med., Tohoku Univ.*, [3]*Konica Minolta Inc.*)

バイオエンジニアリング／Bioengineering

2Pos283* DNA を用いた反応拡散系のプログラムによるハイドロゲル中におけるパターン形成
Programmable reaction-diffusion system using synthetic DNA for pattern formation in hydrogel medium
Keita Abe, Ibuki Kawamata, Shin-ichiro Nomura M., Satoshi Murata (*1Department of Robotics, Graduate School of Engineering, Tohoku University, Japan*)

2Pos284* マイクロドロップレットを用いた G タンパク質共役型受容体ペプチドアゴニスト探索法のフィジビリティスタディ
Feasibility study of the method to obtain peptide agonists for G protein-coupled receptors using water-in-oil microdroplets
Anna Matsueda[1], Takashi Sakurai[1], Ryo Iizuka[1], Yasuyuki Nakamura[2,3], Jun Ishi[2,3], Akihiro Kondo[2,3], Dong Hyun Yoon[5], Tetsushi Sekiguchi[5], Syuichi Syoji[4], Soichiro Tsuda[6], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*, [2]*Eng. Biol. Res. Cent., Kobe Univ.*, [3]*Grad. Sch. of Sci., Technol. and Innov., Kobe Univ.*, [4]*Dept. of Nanosci. and Nanoeng., Waseda Univ.*, [5]*Res. Org. for Nano & Life Innov., Waseda Univ.*, [6]*On-chip Biotechnol. Co., Ltd.*)

2Pos285* 高分子分解酵素産生微生物の取得のための液滴の変形能を利用したスクリーニング法
Deformability-based microfluidic droplet screening to obtain microbes producing macromolecule-degrading enzymes
Mikihisa Muta[1], Kai Saito[1], Ryo Iizuka[1], Wataru Kawakubo[2], Dong Hyun Yoon[3], Tetsushi Sekiguchi[3], Shuichi Shoji[3], Mei Ito[4], Yuji Hatada[4], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*, [2]*Dept. of Nanosci. and Nanoeng., Waseda Univ.*, [3]*Res. Org. for Nano & Life Innov.*, [4]*Dept. of Life Sci. and Green Chem., Saitama Inst. of Technol.*)

2Pos286 カップ形状微小電極の開発と 1 細胞発現分子計測への応用
Development of cup-shaped microelectrode and its application for detection of expressed biomolecules in single cell level
Airi Kuriyama[1,2], Tomoyuki Kamata[1], Dai Kato[1], Naoshi Kojima[1], Shohei Yamamura[3], **Hyonchol Kim**[1,2,4] ([1]*Biomed. Res. Inst., AIST*, [2]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [3]*Health Res. Inst., AIST*, [4]*PhotoBio-OIL, AIST-Osaka Univ.*)

2Pos287 太陽光に依存しない細胞内生物発光による光合成
Sunlight independent plant cell photosynthesis by self-contained bioluminescence
Kenji Osabe[1], Megumi Iwano[2], Ryuichi Nishihama[2], Kazushi Suzuki[1], Sakiko Ishida[2], Tomomi Kaku[1], Takayuki Kohchi[2], Takeharu Nagai[1] ([1]*Osaka Univ., I.S.I.R.*, [2]*Kyoto Univ., Grad. Sch. Biost.*)

2Pos288 (2SEP-7) グラフェン電界効果トランジスタとフェムトリットルチャンバーを用いたデバイ遮蔽を超える電気的バイオセンシング
(2SEP-7) Electrical Biosensing beyond the Debye Screening Length Using Graphene Field-Effect Transistor in Femtoliter Microchamber
Takao Ono[1], Yasushi Kanai[1], Koichi Inoue[1], Yohei Watanabe[2], Shin-ichi Nakakita[3], Toshio Kawahara[4], Yasuo Suzuki[4], Kazuhiko Matsumoto[1] ([1]*ISIR, Osaka Univ.*, [2]*Kyoto Pref. Univ of Med.*, [3]*Kagawa Univ.*, [4]*Chubu Univ.*)

3 日目（9 月 26 日（木））／Day 3（Sep. 26 Thu.）
4F 天瑞・ホワイエ／4F TENZUI・Foyer

蛋白質：構造／Protein: Structure

3Pos001 Dynamic docking between a flexible enzyme and its inhibitor using multicanonical MD simulations and binding free energy calculations
Narutoshi Kamiya[1], Gert-Jan Bekker[2] ([1]*Sim. Stu., Univ. Hyogo*, [2]*IPR, Osaka Univ.*)

3Pos002 Biological Structure Model Archive: 計算機で得られた生体分子モデルのアーカイブ
Biological Structure Model Archive: An archive for computationally obtained data
Gert-Jan Bekker, Takeshi Kawabata, Genji Kurisu (*Osaka University, IPR*)

3Pos003 Nanodisc に再構成した好熱菌由来 V-ATPase の単粒子解析
Single-particle analysis of the lipid nanodisc-reconstituted V-type ATPase/synthase from *Thermus thermophilus*
Atsuko Nakanishi[1], Jun-ichi Kishikawa[1], Kaoru Mitsuoka[2], Ken Yokoyama[1] ([1]*Faculty of Life Sci. Kyoto Sangyo Univ.*, [2]*Res. Ctr. for UHVEM. Osaka Univ.*)

3Pos004 Prediction of ligand distribution around a protein by 3D-RISM theory
Masataka Hamano, Masatake Sugita, Takeshi Kikuchi, Fumio Hirata (*Dept. Bioinfo., Coll. Biosci., Ritsumeikan Univ*)

3Pos005 アミノ酸配列情報からのフラボヘモグロビンのフォールディング機構予測
Prediction of the folding mechanism of flavohemoglobin based on average distance statitistical method
Maho Osugi, Takeshi Kikuchi (*Dept. Bioinfo., Coll. Biosci., Ritsumeikan Univ.*)

3Pos006 分布推定アルゴリズムによる単粒子解析投影パラメーター決定
Determination of projection parameters in single particle analysis using Estimation of Distribution Algorithms
Nobuya Mamizu[1,2], Takuo Yasunaga[1] ([1]*Kyushu Institute of Technology*, [2]*SYSTEM IN FRONTIER INC.*)

3Pos007 連続滴定小角 X 線散乱測定を用いた KaiC に対する KaiA の滴定挙動解析
Titration analysis of KaiA for KaiC using continuous titration small angle X-ray scattering
Risako Aoyama[1], Yoichi Yamazaki[1], Kento Yonezawa[2], Atsushi Mukaiyama[3], Yugo Hayashi[1], Sachiko Toma-Fukai[1], Nobutaka Shimizu[2], Shuji Akiyama[3], Hironari Kamikubo[1,2] ([1]*Div. Mat. Sci., NAIST*, [2]*IMSS, KEK*, [3]*CIMoS, IMS*)

3Pos008 Folding properties prediction of ribonuclease and chymotrypsin based on inter-residue average distance statistics
K M Ahsanul Kabir, Takeshi Kikuchi (*Dept. Bioinfo., Grad. Sch. of Life Sci., Ritsumeinkan Univ., Computational Biomolecular Chemistry lab.*)

3Pos009 The off-axis rotor of *Enterococcus hirae* V-type ATPase by Volta phase contrast cryo-EM
Raymond N. Burton-Smith[1], Jun Tsunoda[1], Yu Yamamori[2], Naoyuki Miyazaki[3], Fabiana L. Imai[4], Chihong Song[1], Kentaro Tomii[2], Kenji Iwasaki[3], Junichi Takagi[5], Hiroshi Ueno[7], Takeshi Murata[4], Ryota Iino[6], Kazuyoshi Murata[1] ([1]*NIPS*, [2]*AIST*, [3]*Univ. Tsukuba*, [4]*Chiba Univ.*, [5]*Osaka Univ.*, [6]*IMS*, [7]*Univ. Tokyo*)

3Pos010 GTP 結合型および GDP 結合型微小管におけるチューブリン C 末端構造分布差の分子動力学計算による解析
Simulation study for conformational difference of tubulin C-terminal tails in GTP-bound and in GDP-bound microtubule
Takuma Todoroki[1], Yukinobu Mizuhara[2], Jun Ohnuki[2], Mitsunori Takano[2], Koji Umezawa[1,3] ([1]*Grad. Sch. Of Sci. & Tech., Shinshu Univ.*, [2]*Grad. Sch. of Adv. Sci. & Eng., Waseda Univ.*, [3]*IBS, Shinshu Univ.*)

3Pos011 距離依存誘電率および溶媒接触表面積を取り込んだ SAAP 力場を用いたトリプケージの分子シミュレーション
Molecular simulation of Trp-cage using the SAAP force field with Distance-Dependent Dielectric and Solvent Accessible Surface Area
Koji Yoshida, Taku Shimosato, **Michio Iwaoka** (*Tokai Univ., Depart. Chem.*)

3Pos012 asymmetry of psi-loop motifs
Koki Fukuda, George Chikenji (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

3Pos013 溶液 NMR による水素結合の直接観測
Direct observation of hydrogen bonds by solution NMR
Taiki Koizumi, Hiroki Nakajima, Yutaka Ito, Masaki Mishima (*Grad. Sch. Sci., TMU*)

3Pos014 (3SHA-5) STAP-2 により Breast tumor kinase が活性化する機構の解明
(3SHA-5) Molecular basis of Breast tumor kinase by an adaptor protein, STAP-2
Junki Nakasako[1], Yuki Matsuo[2], Ryo Kanda[2], Yoshino Tanaka[2], Min Yao[3], Tadashi Matsuda[2], Katsumi Maenaka[2], Toyoyuki Ose[2,3,4] ([1]*Graduate school of Life Science*, [2]*Faculty of Pharm.*, [3]*Faculty of Advanced Life Science, Hokkaido University*, [4]*JST PRESTO*)

3Pos015 分子シミュレーションで探る angiotensin II type 1 receptor（AT1R）の活性化メカニズム
Activation mechanism of the angiotensin II type 1 receptor (AT1R) explored by molecular simulations
Yuichiro Kanamori, **Tadaomi Furuta**, Minoru Sakurai (*Center for Biol. Res. & Inform., Tokyo Tech*)

3Pos016 クライオ電子顕微鏡による多剤排出ポンプ複合体 MexAB–OprM の構造解析
The wild-type structures of MexAB-OprM multidrug efflux pump revealed by cryo-electron microscopy
Kenta Tsutsumi[1], Ryo Yonehara[1], Etsuko Ishizaka-Ikeda[1], Naoyuki Miyazaki[1,2], Shintaro Maeda[1,3], Kenji Iwasaki[1,2], Atsushi Nakagawa[1], Eiki Yamashita[1] ([1]*IPR, Univ. Osaka*, [2]*TARA, Univ. Tsukuba*, [3]*The Scripps Research Inst.*)

3Pos017 IgG 抗体の Fv フラグメントはドメイン運動に伴う水和構造変化によって抗原認識ループの構造変化を制御する
Domain motion of Fv-fragment in antibody immunoglobulin G controls conformation of antigen-recognizing loop through hydration structure
Tomotaka Oroguchi[1,2], Masayoshi Nakasako[1,2] ([1]*Faclt. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 Center*)

3Pos018 3D−RISM 理論を応用した溶液中における Met−enkephalin の構造揺らぎの解析
Analysis of structural fluctuations of Met-enkephalin in the solution phase by means of 3D-RISM theory
Masatake Sugita[1], Fumio Hirata[2] ([1]*Dept. of Bioinfo., Col. of Life Sci., Ritsumeikan Univ.*, [2]*Toyota Phys. & Chem. Res. Inst.*)

3Pos019 網羅的構造解析による酵素機能関連天然変性蛋白質の探索
Exploration of disordered proteins associated with enzymatic functions by comprehensive structural search
Satoshi Omori[1], Hafumi Nishi[1], Kengo Kinoshita[1,2] ([1]*GSIS, Tohoku Univ.*, [2]*ToMMo, Tohoku Univ.*)

3Pos020 A local structural environment descriptor toward evaluating impact of rare variants in humans on protein structures and functions
Atsushi Hijikata, Masafumi Shionyu, Tsuyoshi Shirai (*Nagahama Inst. Bio-Sci. Tech.*)

3Pos021 A new MD integration enabling large time step from accurate temperature and pressure evaluations
Jaewoon Jung[1,2], Hiraku Oshima[3], Kento Kasahara[3], Chigusa Kobayashi[1], Takaharu Mori[2], Yuji Sugita[1,2,3] ([1]*RIKEN Center for Computational Science*, [2]*RIKEN Cluster for Pioneering Research*, [3]*RIKEN Center for Biosystems Dynamics Research*)

3Pos022 Protein interactions in the *in vitro* cyanobacterial circadian clock system revealed by SDSL-ESR
Risa Mutoh[1], Takahiro Iida[1], Hiroyuki Mino[2], Masahiro Ishiura[3] ([1]*Faculty of Sci, Fukuoka Univ.*, [2]*Dep. Sch. of Sci., Nagoya Univ.*, [3]*CGR, Nagoya Univ.*)

3Pos023 Investigation of formation mechanism of Prx high molecular weight complexes
Mami Jindai[1], Rino Sasaki[1], Noriyuki Kodera[2], Toshio Ando[2], **Hiroki Konno**[2] ([1]*Sch. of Nat. Syst., Coll. of Sci. & Eng., Kanazawa Univ.*, [2]*WPI Nano Life Sci. Inst. (WPI-NanoLSI), Kanazawa Univ.*)

3Pos024 Time-localised Predictions of Conformational Transitions in Protein Dynamics
Ryuhei Harada[1], Vladimir Sladek[2], Yasuteru Shigeta[1] ([1]*CCS, Unv. of Tsukuba*, [2]*Slovak Academy of Sciences*)

3Pos025 フレキシブルドッキングによる結合自由エネルギーと速度定数計算
Calculation of binding free energy and kinetic rates with flexible protein docking
Duy Tran, Akio Kitao (*Tokodai, Grad. Life Sci. Tech.*)

3Pos026 Evolutionary diversity of Kai-protein clock system in cyanobacteria
Atsushi Mukaiyama[1,2], Dongyan Ouyang[1], Yoshihiko Furuike[1,2], **Shuji Akiyama**[1,2] ([1]*IMS*, [2]*SOKENDAI*)

3Pos027 Hierarchical classification method of protein-protein interfaces based on their secondary structures
Takashi Fujii, Kazuo Fujiwara, Masamichi Ikeguchi (*Grad. Sch. of Eng., Soka Univ*)

3Pos028 タンパク質ダイナミクスに対する拡散マップ法の適用
Applications of a diffusion map method to protein dynamics
Hiroto Kikuchi[1], Ayori Mitsutake[2], Hiroshi Fujisaki[1] ([1]*Dept. of Phys. Nippon Med. Sch.*, [2]*Dept. of Phys. Meiji Univ.*)

3Pos029 myPresto, computer-aided drug development software
Shinji Iida[1,11], Ikuo Fukuda[2], Junichi Higo[2], Kota Kasahara[3], Takashi Kurosawa[4], Tadaaki Mashimo[5], Kiyotaka Misoo[5], Yoshinori Wakabayasi[6], Ryuta Murakami[1,7], Chisato Kanai[1,7], Yusuke Sugihara[8], Mitsuhito Wada[1], Hironori Nakamura[9], Yoshifumi Fukunishi[10] ([1]*NNPC*, [2]*Grad. Sch. Sim. Hyogo Univ.*, [3]*Col. of Life Sci., Ritsumeikan Univ.*, [4]*Hitachi Solutions East Japan, Ltd.*, [5]*IMSBIO Co., Ltd.*, [6]*BY-HEX LLP*, [7]*INTAGE Healthcare Inc. Drug Discovery Suport Department*, [8]*Fujitsu Kusyu Systems Ltd.*, [9]*Biomodeling Research Co., Ltd.*, [10]*AIST, molprof*, [11]*JBiC*)

3Pos030 十二量体フェリチン様 Dps の希土類バイオミラリゼーションにおける構造基盤
Structural basis of rear-earth metal biomineralization in dodecameric ferritin-like protein, Dps
Mitsuhiro Okuda[1,2], Pretre Gabriela[1], Kornelius Zeth[3] ([1]*CIC nanoGUNE*, [2]*Ikerbasque*, [3]*Roskilde University*)

3Pos031 演題取り消し

蛋白質：物性・構造／Protein: Property & Structure

3Pos032 天然構造が極めて類似したタンパク質の熱変性：遷移構造が異なる分子起源の理論研究
A theoretical study for thermal unfolding of proteins with quite similar native structure and different transition structures
Ken Tomihara, Takashi Yoshidome (*Department of Applied Physics, Tohoku University*)

3Pos033 分子動力学法と機械学習を用いたテトラペプチドの凝集性の評価
Evaluating aggregation propensity of tetra-peptide using MD and machine learning
Yoichi Kurumida, Yutaka Saito, Tomoshi Kameda (*AIRC, AIST*)

3Pos034 Molecular evolution of the structure elements in the TIM barrel family proteins
Yasumichi Takase[1], Yugo Hayashi[1], Yoichi Yamazaki[1], Sachiko Toma-Fukai[1], Hironari Kamikubo[1,2] ([1]*Div. Mat. Sci., NAIST*, [2]*IMSS KEK*)

3Pos035 メタノール中アラメチシンのヘリックス構造熱安定性
Thermal stability of helical conformation of alamethicin in methanol
Yoshinori Miura (*Center for Advanced Instrumental Analysis, Univ. Kyushu*)

3Pos036 ヨウ素染色を用いた種の異なるインスリンアミロイド構造の識別及びシード依存的構造伝播の追跡
Structural difference and its seed-dependent propagation of human/bovine insulin amyloid fibrils as detected by iodine staining
Keisuke Yuzu, Eri Chatani (*Grad. Sch. Sci., Kobe Univ.*)

3Pos037 Examination of the possibility of the formation of transmissible transthyretin amyloid fibrils by the use of proteolysis
Misato Matsumura[1], Naoki Yamamoto[2], Keiichi Yamaguchi[3], Masatomo So[3], Yuji Goto[3], Eri Chatani[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Fac. Med., Jichi Med. Univ.*, [3]*Inst. Protein Res., Osaka Univ.*)

3Pos038 The mechanisms underlying the inhibition of amyloid formation by polyphenol
Yuto Kimura, Masatomo So, Yuji Goto (*IPR, Osaka Univ.*)

蛋白質：機能／Protein: Function

3Pos039 In vitro assembly of metabolon by liquid-liquid phase separation
Tomoto Ura, Kentaro Shiraki (*Pure and Appl.Sci.,Univ.Tsukuba*)

3Pos040 Binding properties of heart-type Fatty-Acid-Binding Protein proved by 1,8-ANS displacement assay
Shun Tokudome[1], Mai Nomura[1], Fumio Hayashi[2], Shigeru Sugiyama[3], Shigeru Matsuoka[4], Michio Murata[5], Masashi Sonoyama[1,6,7] ([1]*Grad Sch. Sci-Tech., Univ. Gunma*, [2]*Ctr. Inst. Analysis, Univ. Gunma*, [3]*Sch. Sci-Tech., Univ. Kochi*, [4]*Grad Sch. Med., Univ. Ooita*, [5]*Grad Sch. Sci., Univ. Osaka*, [6]*GIAR., Univ. Gunma*, [7]*GUCFW., Univ. Gunma*)

3Pos041 混雑環境系におけるタンパク質ーリガンド結合機構の速度論的解析
Crowder effects on a protein-ligand binding process
Kento Kasahara[1], Suyong Re[1], Hiraku Oshima[1], Isseki Yu[4], Grzegorz Nawrocki[5], Michael Feig[5], Yuji Sugita[1,2,3] ([1]*RIKEN BDR*, [2]*RIKEN R-CCS*, [3]*RIKEN CPR*, [4]*Maebashi Inst. of Tech.*, [5]*Michigan State Univ.*)

蛋白質：計測・解析／Protein: Measurement & Analysis

3Pos042 マニフォールドラーニングを用いた低温電子顕微鏡 4 次元イメージング法の確立に向けて
Toward constructing a four-dimensional imaging technique for cryo-electron microscopy with manifold learning
Takashi Yoshidome (*Department Applied Physics, Tohoku University*)

3Pos043 投影方向に偏りがある低温電子顕微鏡像の全投影方向の像の回復に向けて
Toward a recovery of images from all irradiation directions using cryo-electron microscopy data with biased irradiation directions
Ryota Kojima, Takashi Yoshidome (*Department of Applied Physics, Tohoku University*)

3Pos044 バイオ医薬品のプロセス開発および QC における MAM のためのワークフロー駆動型プラットフォームソリューション
A workflow driven platform solution for MAM-based critical quality attribute monitoring of biotherapeutics in process development and QC
Kenji Hirose[1], Maki Terasaki[1], Shota Nakamura[1], Nilini Ranbaduge[2], Henry Shion[2], Ying Qing Yu[2], Min Du[2], Weibin Chen[2] ([1]*Nihon Waters*, [2]*Waters*)

3Pos045 カチオンイオン交換と超小型飛行時間型質量分析計を用いたオンライン IEX-MS による モノクローナル抗体チャージバリアントの特性解析とモニタリング
Online IEX-MS Characterization and Monitoring of mAb Charge Heterogeneity Us ing an Optimized Cation Exchange Resin and Compact TOF MS
Maki Terasaki[1], Shota Nakamura[1], Kenji Hirose[1], Samantha Ippoliti[2], Wang Qi[2], Yu Ying Qing[2], Lauber Matthew A.[2] ([1]*Nihon Waters K. K.*, [2]*Waters Corporation*)

3Pos046 DFA イオンペア試薬、高密度フェニル結合充填剤による ADC の高感度 LC-MS プロファイリング
High sensitivity LC-MS profiling of ADC with difluoroacetic acid ion pairing and a high coverage phenyl-bonded stationary phase
Hiroko Iwasaki[1], Kenji Hirose[1], Jennifer Nguyen[2,3], Jacquelynn Smith[4], Olga V. Friese[4], Jason C. Rouse[4], Daniel P. Walsh[2], Matthew A. Lauber[2] ([1]*Nihon Waters K. K.*, [2]*Waters Corporation*, [3]*Univ. of Copenhagen*, [4]*Biotherapeutics Pharm, Sci., Pfizer WRD*)

3Pos047 ポリリン酸による鶏リゾチームの凝集
Polyphosphate-induced aggregation of hen lysozyme
Kenji Sasahara, Keiichi Yamaguchi, Masatomo So, Yuji Goto (*IPR Osaka university*)

3Pos048 超小型高分解能質量分析計の導入によるバイオ医薬品開発の課題の解決
Meeting Challenges of Implementing Accurate-Mass Mass Spectrometry for Biotherapeutic Development in Regulated/non-Regulated Environments
Shota Nakamura[1], Taiji Kawase[1], Maki Terasaki[1], Kenji Hirose[1], Henry Shion[2], Mellisa Ly[2], Nilini Ranbaduge[2], Ximo Zhang[2], Yun Alelyunas[2], Jonathan Pugh[2], Robert Lewis[2], Jill Lord[2], Mark Halifax[2], Nick Tomczyk[2], Dale Cooper-Shepherd[2], Laetitia Denbigh[2], Ying Qing Yu[2], Jason Rouse[3], Weibin Chen[2] ([1]*Nihon Waters K.K.*, [2]*Waters Inc.*, [3]*Pfizer Inc.*)

蛋白質工学／Protein: Engineering

3Pos049 珪藻殻への有用タンパク質提示発現による機能性材料開発
Protein display on the silica frustules of a marine diatom
Natsuki Onishi, Kensuke Nakajima, Yoshinori Tsuji, Yusuke Matsuda (*Dept.Biosci., Grad.Sch.Sci.Tech., Kwansei Gakuin Univ.,*)

3Pos050 Development of the engineered trimeric single-chain Fv fragment of the therapeutic antibody
Takashi Tadokoro, Kota Nakamura, Harumi Tsuboi, Katsumi Maenaka (*Faculty of Pharmaceutical Sciences, Hokkaido University*)

3Pos051 多様なユビキチン鎖のロバストな合成法
Robust synthesis methods of various ubiquitin chains
Takumi Suzuki, Takahiro Aizu, Yutaka Ito, Masaki Mishima (*Grad. Sch. Sci., TMU*)

3Pos052 De novo design of protein structures with Ploop-motif for ATP binding
Hiroko Yamada[1], Kengo Nakamura[1], Takahiro Kosugi[1,2,3], Nobuyasu Koga[1,2,3] ([1]*SOKENDAI*, [2]*NINS IMS*, [3]*NINS ExCELLS*)

ヘム蛋白質／Heme proteins

3Pos053 金属タンパク質における酸化還元電位の第一原理計算法の開発
An ab initio method of evaluating redox potential for metalloprotein
Cheng Cheng, Shigehiko Hayashi (*Kyoto Univ*)

3Pos054 ウシミトコンドリア由来酸素還元酵素の活性型の単量体構造
Monomeric structure of an active form of respiratory oxygen reductase from bovine mitochondria
Kyoko Shinzawa-Itoh[1], Takashi Sugimura[2], Tomonori Misaki[2], Yoshiki Tadehara[1], Shogo Yamamoto[1], Makoto Hanada[1], Naomine Yano[1], Tetsuya Nakagawa[3], Shigefumi Uene[1], Takara Yamada[3], Hiroshi Aoyama[4], Eiki Yamashita[5], Tomitake Tsukihara[1,5], Shinya Yoshikawa[1], **Kazumasa Muramoto**[1] ([1]*Graduate School of Life Science, University of Hyogo*, [2]*Graduate School of Material Science, University of Hyogo*, [3]*School of Life Science, University of Hyogo*, [4]*Graduate School of Pharmaceutical Sciences, Osaka University*, [5]*Institute for Protein Research, Osaka University*)

膜蛋白質／Membrane proteins

3Pos055 脂質・コレステロール・タンパク間の協同性による上皮成長因子受容体の膜近傍ドメイン 2 量体形成機構
Lipid-cholesterol-protein interaction in the dimerization of juxtamembrane domains of epidermal growth factor receptor
Ryo Maeda[1], Yasushi Sako[1], Takeshi Sato[2] ([1]*Cellular Informatics Lab., RIKEN*, [2]*Kyoto Pharmaceutical Univ.*)

3Pos056 バクテリオルベリン及びその前駆体の膜タンパク質ハロロドプシンへの結合特異性
Binding specificity of bacterioruberin and its precursors to membrane protein halorhodopsin
Fumiya Hattori, Takanori Sasaki (*Grad.Sch.Adv.Math.Sci.,Meiji Univ*)

3Pos057 細胞膜上 Akt の 1 分子イメージングによるシグナル伝達機構の研究
A single molecule imaging approach to understand signal transduction mechanism through Akt on the plasma membrane
Hideaki Yoshimura, Takeaki Ozawa (*Sch. Sci., Univ. Tokyo*)

3Pos058 Triton X-100 により可溶化した Proteorhodopsin の光機能中間体の速度論的解析
Kinetic analysis of photointermediates of Proteorhodopsin solubilized with Triton X-100
Airi Yamamoto[1], Fumio Hayashi[2], Takashi Kikukawa[3,4], Masashi Sonoyama[1,5,6] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Inst. Anal. Cent., Gunma Univ.*, [3]*Fac. Adv. Life Sci., Hokkaido Univ.*, [4]*GI-CoRE, Hokkaido Univ.*, [5]*GIAR., Gunma Univ.*, [6]*GUCFW., Gunma Univ.*)

3Pos059 1 分子イメージングによる TRPV1 チャネル・脂質間相互作用の時空間動態解析
Spatiotemporal analysis of TRPV1 channel-lipid interaction by single molecule imaging
Yutaro Kuwashima[1,2], Masataka Yanagawa[2], Mitsuhiro Abe[2], Yasushi Sako[2], Ryohei Aoyagi[1], Makoto Arita[1] ([1]*Grad. Sch. Pharm., Univ. Keio*, [2]*Wako Inst., Riken*)

核酸結合蛋白質／Nucleic acid binding proteins

3Pos060 The effect of the distance between the RNA sequences recognized by two RNA-binding domains on the affinity of the MSI1-RNA interaction
Wei Hsun Tu[1,2], Keisuke Kamba[1], Takashi Nagata[1,2], Masato Katahira[1,2] ([1]*Inst. of Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Energy Sci., Kyoto Univ.*)

3Pos061 Computational insights into DNA binding affinity and its repair activity for photolyase/cryptochrome superfamily
Ryuma Sato[1], Yoshiharu Mori[2], Noriaki Okimoto[1], Makoto Taiji[1] ([1]*RIKEN*, [2]*Kitasato univ*)

3Pos062 The directionality regulation mechanism of serine recombinase
Hsiu-Fang Fan (*NSYSU*)

3Pos063 Single-molecule studies of how polyamines stimulate RecA-mediated recombination
Naciye Esma Tirtom[1], Yang Hsu[2], Hung-Wen Li[1] ([1]*NTU*, [2]*NTNU*)

核酸／Nucleic acid

3Pos064 (3SEA-3) 温度上昇とテラヘルツ光照射は転写反応に異なる影響を及ぼす。
(3SEA-3) Terahertz radiation and temperature increase differently affect transcription by RNA polymerase
Masahiko Imashimizu[1], Masahito Tanaka[1], Hiromichi Hoshina[2], Koh Takeuchi[1] ([1]*AIST*, [2]*RIKEN*)

3Pos065 液体状 DNA の相分離を利用したドメインを持つマイクロゲルカプセルの構築
Construction of hydrogel microcapsules with domain by using phase separation of liquid-like DNA
Yuji Nakashima, Yusuke Sato, Masahiro Takinoue (*Dept. of Comp. Sci., Tokyo Tech.*)

3Pos066 DNA 液滴を用いた液-液相分離による動的システム
Dynamic system by liquid-liquid phase separation using DNA droplet
Nozomi Tsumura, Yusuke Sato, Yuji Nakashima, Masahiro Takinoue (*Tokyo Tech*)

3Pos067 DNA 液滴ポーラスマイクロ構造の形成
Porous microstructure formation of DNA droplet
Tetsuro Sakamoto, Yusuke Sato, Masahiro Takinoue (*Tokyo Institute of Technology*)

3Pos068 DNA ゲルの相転移のシミュレーションモデルと解析
Simulation model and analysis of phase transition of DNA gel
Akihiro Yamamoto, Tetsuro Sakamoto, Yusuke Sato, Masahiro Takinoue (*School of Computing, Tokyo Institute of Technology*)

3Pos069 捩じれストレス下におけるヌクレオソーム DNA 解離および H2A/H2B2 量体脱離の自由エネルギープロファイル
Free energy profiles of unwrapping nucleosomal DNA under torsional stress and eviction of the H2A/H2B dimer
Hisashi Ishida, Hidetoshi Kono (*Institute for Quantum Life Science, QST*)

3Pos070 転写開始複合体における DNA 開裂に関連した DNA・タンパク質間相互作用の検討
DNA-Protein Interaction Related to DNA Opening in Transcription Initiation Complex
Genki Shino, Masahiro Shimizu, Shintaroh Kubo, Toru Niina, Shoji Takada (*Dept. of Biophys., Div. of Bio. Sci., Grad. Sch. of Sci., Univ. of Kyoto*)

水・水和／電解質／Water & Hydration & Electrolyte

3Pos071 Poly(*N*-isopropylacrylamide)のコイル-グロビュール転移に伴う水への溶解度の劇的低下の物理
Physics of drastic decrease in water solubility upon coil-to-globule transition of poly(*N*-isopropylacrylamide)
Masao Inoue, Tomohiko Hayashi, Simon Hikiri, Masahiro Kinoshita (*Inst. Adv. Energ., Kyoto Univ.*)

3Pos072 Water-protein interactions coupled with protein conformational transition
Soichiro Kitazawa[1], Takuro Wakamoto[2], Ryo Kitahara[1] ([1]*College of Pharmaceutical Sciences, Rtisumeikan Univ.*, [2]*Graduate School of Life Sciences, Ritsumeikan Univ.*)

3Pos073 SASA モデルにおける蛋白質間相互作用の過安定化
Over-stabilization of protein-protein interaction in solvent accessible surface area model
Kohei Kuroishi, Dan Parkin, Akira Yodogawa, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

3Pos074 Machine-learning approach for water dynamics
Taku Mizukami[1], Viet Cuong Nguyen[3], Hieu Chi Dam[2] ([1]*JAIST, Materials*, [2]*JAIST, Knowledge*, [3]*HPC.Inc*)

発生・分化／Development & Differentiation

3Pos075 (3SFA-7) 三次元構造モデルから発生過程における細胞機能の理解を試みる
(3SFA-7) Attempt to understand the cellular function during developmental process from 3D structural model
Junpei Kuroda[1,4], Takeshi Itabashi[1,2,3], Takako M. Ichinose[1], Shigeru Kondo[4], **Atsuko H. Iwane**[1,2,3] ([1]*Cell Field Struc., BDR, Riken*, [2]*Grad. sch. Integ. Sci. Life, Hiroshima Univ.*, [3]*Spec. Res. Promot. Group, Grad. Sch. Fronti., Biosci., Osaka Univ.*, [4]*Pattern formation, Grad. Sch. Fronti., Biosci., Osaka Univ.*)

3Pos076 脳形態形成におけるニューロン移動と大脳成長の連成数理モデリング
A coupled mathematical modeling for neuronal migration and cerebral growth in brain morphogenesis
Hironori Takeda[1], Yoshitaka Kameo[1,2,3], Taiji Adachi[1,2,3] ([1]*Grad. Sch. Eng, Kyoto Univ.*, [2]*Inst. Front. Life Med Sci., Kyoto Univ.*, [3]*Grad. Sch. Biostudies, Kyoto Univ*)

3Pos077 Modeling of sea urchin gastrulation based on cytoskeleton imaging
Kaichi Watanabe, Naoaki Sakamoto, Akinori Awazu (*Integrated Sciences for Life in Hiroshima University*)

3Pos078 細胞分裂に関わるキネシン 5 の頭部間協調におけるネック領域の役割の高速一分子観察
High-speed single molecule studies for the role of the neck region on the head-head coordination of mitotic kinesin-5
Taiga Yamada[1], Kohei Matsuzaki[2], Michio Tomishige[2] ([1]*Grad. Sch. Sci. Eng., Aoyama Gakuin Univ.*, [2]*Dept. Math. Phys., Col. Sci. Eng., Aoyama Gakuin Univ.*)

3Pos079 DNA ナノスプリングによる負荷を受けながら運動するキネシン 1 の高速一分子観察
High-speed single-molecule observations of kinesin-1 moving under a load from DNA origami nanospring
Kohei Matsuzaki[1], Mitsuhiro Iwaki[2], Michio Tomishige[1] ([1]*Dept. Phys., Col. Sci. Eng., Aoyama Gakuin Univ.*, [2]*BDR, Riken*)

3Pos080 Kinetic parameters and reaction scheme of high and low activity mutants of Serratia marcescens chitinase A
Akasit Visootsat[1,2], Paul Vignon[3], Akihiko Nakamura[1,2], Takayuki Uchihashi[4,5], Hiroki Watanabe[4,5], Ryota Iino[1,2] ([1]*IMS*, [2]*SOKENDAI*, [3]*ParisTECH*, [4]*Nagoya University*, [5]*ExCELLS*)

3Pos081 高速原子間力顕微鏡により観察された微小管上の外腕ダイニン
High-speed atomic force microscopy on outer dynein arms aligned on microtubules
Kenta Ishibashi[1,2], Kazuhiro Oiwa[2,3,4] ([1]*Osaka Univ.*, [2]*NICT-CiNet*, [3]*Advanced ICT Research Institute*, [4]*University of Hyogo*)

3Pos082 Development of novel Photochromic inhibitors for kinesin Eg5 which form multiple isomerization states utilizing azobenzene and spiropyran
Islam Md Alrazi, Kei Sadakane, Shinsaku Maruta (*Department of Bioinformatics, Graduate School of Engineering, Soka University, Hachioji, Tokyo , Japan*)

3Pos083 回転子変異体を用いたべん毛モータースイッチ機構の解析
Analysis of the bacterial flagellar switch using mutant rotor components
Mai Kato[1], Tsubasa Ishida[1], Myu Yoshida[2], Yoshisyuki Sowa[1,2,3] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*,, [2]*Dept. Frontier Biosci., Hosei Univ*, [3]*Micro-nano Tech., Hosei Univ*)

3Pos084 細菌べん毛モーターの回転を支える回転軸-軸受間相互作用の解析
Analysis of shaft-bearing interactions that support the smooth rotation of bacterial flagellar motors
Yumi Kumazaki[1], Tsubasa Ishida[1], Myu Yosida[2], Yoshiyuki Sowa[1,2,3] ([1]*Grad. Sch. Sci. & Eng, Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Micro-nano Tech., Hosei Univ.*)

3Pos085 Controlling the rotation speed of the bacterial flagellar motor with light-driven rhodopsin
So Hasegawa[1], Rei Abe-Yoshizumi[2], Keiichi Inoue[3], Hideki Kandori[2], Yoshiyuki Sowa[4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ*, [2]*Grad. Sch. Eng., Nagoya Inst. Tech*, [3]*Inst. Solid State Phys., Univ. Tokyo*, [4]*Dept. Frontier Biosci., Hosei Univ*)

3Pos086 *Paenibacillus* sp. TCA20 と大腸菌に由来するべん毛モーターキメラ固定子のイオン選択性
Ion specificity of chimeric stator proteins between *Paenibacillus* sp. TCA20 MotB1 and *Escherichia coli* MotB
Sakura Onoe[1], Myu Yoshida[2], Masahiro Ito[3], Yoshiyuki Sowa[1,2,4] ([1]*Grad. Sch. Sci. & Eng., Hosei Univ.*, [2]*Dept. Frontier Biosci., Hosei Univ.*, [3]*Grad. Sch. Life Sci. Toyo Univ.*, [4]*RC. Micro-nano Tech., Hosei Univ.*)

3Pos087 DNA オリガミを用いた野生型と変異体キネシン二分子による協調運動の観察
Cooperative transport by wild-type and mutant kinesin motors as studied by using programmable DNA origami
Shu Takano[1], Ryosuke Masuda[3], Kohei Matsuzaki[2], Mitsuhiro Iwaki[4], Michio Tomishige[2] ([1]*Grad. Sch. Sci. Eng., Aoyama Gakuin Univ.*, [2]*Dept. Math. Phys., Col. Sci. Eng., Aoyama Gakuin Univ.*, [3]*Dept. Appl. Phys., Grad. Sch. Eng., Univ. Tokyo*, [4]*BDR, Riken*)

3Pos088 INHIBITION OF MITOTIC KINESIN EG5 BY KOLAFLAVANONE

Tomisin Ogunwa[3], Kei Sadakane[1], Ayodele O. Kolawole[4], Olusola O. Elekofehinti[4], Afolabi C. Akinmoladun[4], Olaposi I. Omotuyi[5], Takayuki Miyanishi[3], **Shinsaku Maruta**[1,2] ([1]*Sci. & Engin., Soka University*, [2]*Grad. Sch. Engin., Soka Unive.*, [3]*Grad. Sch. Fisheries and Environmental Sci, Nagasaki Unive.*, [4]*Dept. of Biochem., The Federal Unive. of Tech.*, [5]*Centre for Biocomputing and Drug Design, Adekunle Ajasin Unive.*)

3Pos089 F_1-ATPase の軸とシリンダーの結合寿命の測定

Single-molecule pull-out manipulation of the shaft of the rotary motor F_1-ATPase

Tatsuya Naito[1], Tomoko Masaike[2], Daisuke Nakane[1], Mitsuhiro Sugawa[3], Takayuki Nishizaka[1] ([1]*Dept. Phys., Gakushuin Univ.*, [2]*Dept. Appl. Biol. Sci., Tokyo Univ. Sci.*, [3]*Grad school of arts and sciences, Univ. of Tokyo,*)

3Pos090 Does giraffe kinesin move faster than mouse?

Taketoshi Kambara[1], Yasushi Okada[1,2] ([1]*RIKEN BDR*, [2]*U. of Tokyo, Grad. Sci.*)

3Pos091 Microsecond-resolved observation of F_1-ATPase conformational changes by single molecular fluorescence spectroscopy

Hiroki Senmaru[1], Hiroyuki Oikawa[2], Mitsuhiro Sugawa[3], Satoshi Takahashi[2] ([1]*Tohoku University Graduate school of life sciences*, [2]*Tohoku university IMRAM*, [3]*Tokyo university graduate school of Arts and Sciences*)

3Pos092 遺伝子工学的に人工的に設計したモータタンパク質収縮ネットワークの性能向上

Improvement of a genetically-engineered microtubule contractile protein network

Zhao Du[1], Takahiro Nitta[3], Yingzhe Wang[2], Keisuke Morishima[2], Yuichi Hiratsuka[1] ([1]*JAIST, Sch. of Mat. Sci.*, [2]*Osaka Univ., Grad. Sch. of Eng., Dep. Mech. Eng.*, [3]*Gifu Univ., Grad. Sch. of Eng., Dep. of EECE*)

3Pos093 暗視野顕微鏡を用いた微小管混雑時における細胞質ダイニンのステップの高時間分解能観察

Cytoplasmic dynein stepping on crowded microtubules resolved using dark-field imaging with high spatio-temporal resolution

Yusuke Kumagai[1], Keitaro Shibata[2], Ken'ya Furuta[2], Hajime Honda[1], Hiroaki Kojima[2] ([1]*Dep. Bioeng., Nagaoka Univ.*, [2]*Adv. ICT Res. Ins., NICT*)

3Pos094 共通祖先型 F_1-ATPase の一分子回転解析

Reconstruction and Characterization of Ancestral F_1-ATPase

Nanako Nakama[1], Hiroshi Ueno[1], Ryutaro Furukawa[2], Ryohei Kobayashi[1], Ryo Watanabe[1], Satoshi Akanuma[2], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Facul. Human Sci., Univ. Waseda*)

3Pos095 クラミドモナス軸糸ダイニン集合体の外部負荷に対する応答を測定する

Measuring mechanical responses of Chlamydomonas axonemal dynein arrays to external load

Misaki Sagawa[1], Akane Furuta[2], Hiroaki Kojima[2], Kazuhiro Oiwa[1,2], Ken'ya Furuta[2] ([1]*Grad. Sch. of Life Science, Univ. Hyogo*, [2]*Adv. ICT Res. Inst., NICT*)

細胞生物的課題／Cell biology

3Pos096 (3SHA-4) 過渡的に形成される GPCR ダイマーの研究：細胞内蛍光 1 分子観察によるアプローチ

(3SHA-4) Examining the transiently formed GPCR dimer: an approach by single fluorescent molecule observation in living cells

Rinshi Kasai (*Inst. Front. Life. Med. Sci., Kyoto Univ.*)

3Pos097 微小管結合蛋白質を介したアクチンフィラメントと微小管との束化が細胞突起に与える影響

The role of microtubule-associated protein mediated bundle formation between actin filaments and microtubule on cell process formation

Chihiro Doki[1], Masahiro Kuragano[1], Kohei Nishida[1], Shoma Saito[1], Susumu Kotani[2], Kiyotaka Tokuraku[1] ([1]*Grad.Sch.Eng.,Muroran Inst.Tech.*, [2]*Fac. Sci., Kanagawa Univ*)

3Pos098 デスミンとアクチンを包含する液滴のそれらの集合により誘発される変形
Deformations of droplets containing desmin and actin caused by their assembly
Yoshiya Miyasaka, Keigo Murakami, Kuniyuki Hatori (*Grad. Sch. of Sci. and Eng., Yamagata Univ.*)

3Pos099 S1P 修飾弾性率可変ゲルを用いた Muse 細胞ホーミング及び力学場応答性の解析
Homing and mechano-response of Muse cells analyzed on S1P-modified hydrogel with tunable elasticity
Lei Guo[1], Yukie Tsuji[2], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

3Pos100 細胞の突起形成における MAP4 の局在と機能
Localization and function of microtubule-associated protein (MAP) 4 in cell protrusion formation
Kohei Nishida[1], Masahiro Kuragano[1], Chihiro Doki[1], Susumu Kotani[2], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Eng., Muroran Inst. Tech.*, [2]*Fac. Sci., Kanagawa Univ.*)

3Pos101 F-actin に沿った Fimbrin の協同的クラスター形成の方向性
Direction of the cooperative cluster formation of fimbrin along actin filaments
Naoki Hosokawa[1], Masahiro Kuragano[1], Keitaro Shibata[2], Taro Q.P. Uyeda[3], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Eng., Muroran Inst. Tech.*, [2]*NICT*, [3]*Dep. of Physics, Fac. Sci. Engin., Waseda Univ.*)

3Pos102 非凍結温度において氷結合タンパク質は線虫の低温耐性を改善する
Ice-Binding Proteins Improves the Survival Rate of *Caenorhabditis elegans* at Non-freezing Temperature
Masahiro Kuramochi[1,2,3], Geikaku Tou[1], Chiaki Takanashi[1], Motomichi Doi[3], Kazuhiro Mio[2], Sakae Tsuda[4], C. Yuji Sasaki[1,2] ([1]*University of Tokyo*, [2]*AIST-UTokyo OIL*, [3]*Biomedical R.I., AIST*, [4]*Bioproduct R.I., AIST*)

3Pos103 フェムト秒レーザー誘起衝撃力と反射干渉顕微鏡による細胞接着強度の定量評価手法の確立
Quantitative evaluation of cell adhesion strength by reflection interference contrast microscopy combined with femtosecond laser impulse
Yukiko Yoshimura, Sohei Yamada, Yoichiroh Hosokawa, Ryohei Yasukuni, Kazunori Okano (*Division of Materials Science, Nara Institute of Science and Technology*)

3Pos104 アクチンネットワーク上におけるアクチン結合タンパク質の局在形成における自律的制御機構
Self-regulatory mechanisms for the segregation of actin binding proteins on actin network
Yosuke Yamazaki, Taro QP Uyeda (*Dep. Phys., Waseda Univ.*)

3Pos105 iPS 細胞は最適弾性領域に移動し、増殖促進と高質な幹細胞性保持を示す
iPS cells show mechanotactic accumulation, higher proliferation and expression of stemness marker in optimal region of matrix elasticity
Mengfan Wang[1], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu. Univ.*, [2]*IMCE, Kyushu Univ.*)

3Pos106 分化フラストレート MSC における APC 発現調節の上流機構の検証
Investigation of upstream regulatory factors of APC expression in the MSCs in frustrated differentiation
Misaki Kaneshiro[1], Thasaneeya Kuboki[2], Satoru Kidoaki[2] ([1]*Grad. Sch. Eng., Kyushu Univ.*, [2]*IMCE, Kyushu Univ.*)

3Pos107 Ca^{2+} 存在下/非存在下における mbo1（後退運動変異株）の鞭毛波形
The flagellar waveforms of *mbo1*, a mutant moving backward only, in the presence/absence of Ca^{2+}
Hitoshi Sakakibara, Hiroaki Kojima, Kazuhiro Oiwa (*Adv. ICT Res. Inst., NICT*)

3Pos108 アクチン結合タンパク質 Rng2 がアクトミオシン in vitro 運動を協同的に阻害するメカニズム
The mechanism of cooperative inhibition of actomyosin movement in vitro by the actin binding protein Rng2
Yuuki Hayakawa[1], **Yosuke Kakuta**[1], Ngo Kien X.[2], Noriyuki Kodera[2], Taro QP Uyeda[1] ([1]*Department of Physics, Faculty of Advanced Science and Engineering, Waseda University*, [2]*Bio-AFM Res. Ctr., Kanazawa Univ.*)

3Pos109 二種の異なるアクチン結合タンパク質のアクチンへの結合が相互排他的かまたは協調的かを評価する観察系の構築
Establishment of observation system to evaluate whether two different actin binding proteins bind to actin mutually or accommodative
Tenji Yumoto, Taro QP Uyeda (*Dept. Physics, Waseda Univ.*)

3Pos110 動的な誘引物質濃度勾配における好中球様 HL60 細胞の運動方向決定
Decision making of migratory direction of neutrophil-like HL60 cells in dynamical chemoattractant gradient
Motohiko Ishida[1], Akihiko Nakajima[2,3], Satoshi Sawai[1,3] ([1]*Dept. Basic Sci., Grad. Sch. of Arts & Sci., Univ. of Tokyo, Japan*, [2]*Dept. General Systems Studies, Grad. Sch. of Arts & Sci., Univ. of Tokyo, Japan*, [3]*Comp. Sys. Biol. Cent., Grad. Sch. of Arts & Sci., Univ. of Tokyo, Japan*)

3Pos111 タウ–微小管相互作用の等温滴定熱測定
Isothermal titration calorimetry of tau-microtubule interaction
Junta Kashima, Hiroshi Sakamoto, Junichi Taira, Hideyuki Komatsu (*Biosci. Bioinf., Kyushu Inst. Tech.*)

3Pos112 Rhodamine-phalloidin と Lifeact-GFP のアクチン結合の相互排他性
Mutual Exclusion of Actin Binding between Rhodamine-phalloidin and Lifeact-GFP
Saku Kijima[2], **Yuuya Aoki**[1], Taro QP Uyeda[1] ([1]*Dept. Physics, Waseda Univ*, [2]*Biopro. Res. Inst., AIST*)

3Pos113 RhPh 染色したアクチンフィラメントの 3 つの蛍光の明滅パターンの解析
Analysis of three distinct blinking patterns of RhPh fluorescence along actin filaments
Kazunori Ono, Ryuichi Kaneda, **Syunsuke Ando**, Koki Arai, Yosuke Yamazaki, Taro QP Uyeda (*Dept. Physics, Waseda Univ*)

3Pos114 らせん型細菌スピロヘータの遊泳の力と速度の関係
Force-velocity relationship of the spirochete *Leptospira* swimming
Keigo Abe[1], Kyosuke Takeba[2], Shuichi Nakamura[1] ([1]*Grad.Sch.Eng., Tohoku Univ.*, [2]*Life and Env.Sci., Tsukuba Univ.*)

生体膜・人工膜／Biological & Artificial membrane: Dynamics

3Pos115 Effect of sucrose on the diffusion of proteins tethered in a glass-supported lipid bilayer
Hiromitsu Hariu (*Saitama Univ.*)

3Pos116 分子ツールとしての電位依存性ホスファターゼの改良
Improvement of voltage-sensing phosphatase as a molecular tool of phosphoinositide depletion in living cells
Akira Kawanabe[1,2], Natsuki Mizutani[2], Tomoko Yonezawa[2], Yasushi Okamura[2] ([1]*Fac. Med., Kagawa Univ.*, [2]*Grad. Sch. Med., Osaka Univ.*)

3Pos117 油中水滴接触膜張力の定量的操作法とチャネル研究への応用
Manipulation and quantitative evaluation of membrane tension during single-channel current recordings in the contact bubble bilayer
Masayuki Iwamoto[1], Shigetoshi Oiki[2] ([1]*Dept. Mol. Neurosci., Univ. Fukui. Facul. Med. Sci.*, [2]*Biomed. Imaging Res. Center, Univ. Fukui*)

3Pos118 細菌機械受容チャネル MscL の脂質膜環境変化に対する応答のシミュレーション研究
Computational Study Focusing on the Response to Changes of Membrane Environment in Gating of the Bacterial Mechanosensitive Channel MscL
Yasuyuki Sawada[1], Ken'ichi Hashimoto[2], Hisashi Kawasaki[2], Masahiro Sokabe[3] ([1]*Dept. Nutrition, Nagoya Univ. Eco.*, [2]*Biotech. Res. Ctr., Tokyo Univ.*, [3]*Mechanobiology Lab, Nagoya Univ. Grad. Sch. Med.*)

3Pos119 A gold nano-electrode for single channel detection
Toru Ide[1,2], Minako Hirano[2], Kota Kaneko[1], Huimin Ma[1] ([1]*Fac. Engn. Okayama Univ.*, [2]*Photo-Bio. GPI*)

3Pos120 全自動パッチクランプシステムによる、アダプティブコントロールを用いた正確な 50%不活性化状態制御実験の実現
Adaptive voltage control ensures the precise half inactivation application of voltage gated channels on automated patch clamp system
Kazuya Tsurudome (*Sophion Bioscience K.K.*)

3Pos121 人工イオンチャネルの分子動力学シミュレーション
All-atom molecular dynamics simulations of artificial ion channels
Takahiro Osamura[1], Toru Ekimoto[1], Tsutomu Yamane[1], Takahiro Muraoka[2], Kazushi Kinbara[3], Mitsunori Ikeguchi[1,4] ([1]*Grad. Sch. Med Life Sci., Yokohama City Univ.*, [2]*Grad. Sch. Global Innov., Tokyo Univ. of Agri. and Tech.*, [3]*Grad. Sch. Life Sci. and Tech., Tokyo Tech*, [4]*Med. Sci. Innov. Hub., Riken*)

3Pos122 筋小胞体カルシウムポンプの Ca^{2+}結合に及ぼす界面活性剤の効果
Effect of solubilization with a detergent on sarcoplasmic reticulum Ca^{2+}-ATPase
Takashi Daiho, Stefania Danko, Kazuo Yamasaki, Satoshi Yasuda, Hiroshi Suzuki (*Asahikawa Medical Univ.*)

3Pos123 プロトニック有機電極によるミトコンドリアの ATP 合成操作
Control of mitochondrial ATP synthesis with a protonic biotransducer
Momoka Takahashi[1], Mingyin Cui[2], Hiroko Kashiwagi[1], Takeo Miyake[2], Yoshihiro Ohta[1] ([1]*Grad. Sch. Biotech., TUAT*, [2]*Grad. Sch. Info., Univ. Waseda*)

3Pos124 Toward the construction of DNA origami artificial channel with selective transport function
Shoji Iwabuchi[1], Ibuki Kawamata[1], Yuki Suzuki[2], Satoshi Murata[1], M. Shinichiro Nomura[1] ([1]*Grad. Eng., Univ. Tohoku*, [2]*FRIS, Univ. Tohoku*)

3Pos125 上皮成長因子受容体クラスターによる EGF シグナル伝達の調節
Regulation of downstream signaling by clusters of epidermal growth factor receptor
Michio Hiroshima[1,2], Nario Tomishige[3], Masahiro Ueda[1], Toshihide Kobayashi[3], Yasushi Sako[2] ([1]*RIKEN BDR*, [2]*RIKEN CPR*, [3]*Univ. of Strasbourg*)

3Pos126 p52Shc は時間依存的に Grb2 のシグナル伝達ダイナミクスを制御する
p52Shc regulates Grb2 signaling dynamics in a time dependent manner after cell stimulation
Ryo Yoshizawa[1], Nobuhisa Umeki[2], Masataka Yanagawa[2], Masayuki Murata[1], Yasushi Sako[2] ([1]*Grad.sch.arts and ahi., the univ. Tokyo*, [2]*Wako Inst., Riken*)

3Pos127 Analysis of electrostatic interaction of acidic glycolipid with transmembrane peptide of insulin receptor
Yuka Nimura[1], Kazuya Kabayama[1,2,3], Yuya Asahina[4], Shinya Hanashima[1], Hironobu Hojo[4], Michio Murata[1], Koichi Fukase[1,2,3] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*MS-CORE, PRC, Grad. Sch. of Sci., Osaka Univ.*, [3]*Inst. for Radiation Sciences, Osaka Univ.*, [4]*Inst. for Protein Research, Osaka Univ.*)

3Pos128 細胞膜断片ブレブを用いたモデル生体膜への膜タンパク質再構成
Direct reconstitution of membrane proteins from cell membrane blebs into a model biological membrane
Rurika Nagai[1], Yasushi Tanimoto[2], Rinshi Kasai[3], Kenichi Suzuki[4,5], Fumio Hayashi[6], Kenichi Morigaki[1,2] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Biosignal Research Center, Univ Kobe*, [3]*Institute for Frontier Life and Medical Sciences, Univ Kyoto*, [4]*G-chain, Univ. Gifu*, [5]*Grad of Nat. Sci and Tech., Univ Gifu*, [6]*Grad. Sch. Scie, Univ. Kobe*)

神経回路・脳の情報処理／Neuronal circuit & Information processing

3Pos129 アガロース微細構造を用いた海馬細胞から伸長する神経突起の相互作用の解析
Interactions of neurites elongated from isolated hippocampal cells in agarose width-length-controlled microchannels
Yuhei Tanaka[1], Shota Aoki[1], Haruki Watanabe[2], Kenji Shimoda[2], Akihiro Hattori[3], Masao Odaka[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

3Pos130 Implementation of automated driving by deep reinforcement learning on high definition simulator
Shunsuke Isomura[1], **Hideo Mukai**[1,2] ([1]*Comp. Sci. Prog., Grad. Sch. Sci & Tech., Meiji Univ.*, [2]*Dept. Comp. Sci., Sch. Sci & Tech., Meiji Univ.*)

3Pos131 単一の神経突起における伸長特性を測定するためのスポット吸収マイクロニードルを用いた μm 単位の精度のアガロース微細加工技術
Precise μm agarose microfabrication technology with spot absorption microneedle for single neurite elongation property measurement
Haruki Watanabe[1], Yuhei Tanaka[2], Shota Aoki[2], Kenji Simoda[1], Takahito Kikuchi[2], Akihiro Hattori[3,4], Masao Odaka[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

3Pos132 畳み込みニューラルネットワークを用いた脳波解析手法の実装
Implementation of EEG analysis method with Convolutional Neural Networks
Hiroaki Takao[1], Hideo Mukai[1,2] ([1]*Comp. Sci. Prog., Grad Sch. Sci & Tech., Meiji Univ.*, [2]*Dept. Comp. Sci., Sch. Sci. & Tech., Meiji Univ.*)

光生物学：視覚・光受容／Photobiology: Vision & Photoreception

3Pos133 リガンド非結合時のオプシンは稀に光活性化したロドプシンと同等の活性を示す
Apo-opsin exists in equilibrium between a predominantly inactive and a rare highly active state
Shinya Sato[1,2], Beata Jastrzebska[3], Andreas Engel[3], Krzysztof Palczewski[3,4], Vladimir J. Kefalov[1] ([1]*DOVS, Washington Univ.*, [2]*Grad. Sch. Biostudies., Kyoto Univ.*, [3]*Case Western Reserve Univ.*, [4]*UC Irvine*)

3Pos134 天然のバクテリアを用いたヘリオロドプシンの機能研究
Function study of heliorhodopsin using native bacteria
Ai Muto, Rei Abe-Yoshizumi, Hideki Kandori (*Nagoya Inst. Tech.*)

3Pos135 メラノプシンの光活性化機構
Photoactivation process of Melanopsin
Masami Kugo[1], Takahiro Yamashita[1], Yoshinori Shichida[2], Yasushi Imamoto[1] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Ritsumeikan Univ.*)

3Pos136 アミノ酸置換による脊椎動物ロドプシンのバイステーブル特性化
Construction of vertebrate rhodopsin with bistable property by a single mutation
Kazumi Sakai[1], Yoshinori Shichida[2], Takahiro Yamashita[1] ([1]*Graduate School of Science, Kyoto University*, [2]*Research Organization for Science and Technology, Ritsumeikan University*)

3Pos137 高角 X 線散乱法による光活性化ロドプシンの活性構造安定化メカニズムの解析
Stabilization Mechanism of Active Conformation of Photoactivated Rhodopsin Studied by High-Angle X-Ray Scattering
Yasushi Imamoto[1], Keiichi Kojima[2], Toshihiko Oka[3], Ryo Maeda[4], Yoshinori Shichida[5] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*, [4]*RIKEN*, [5]*Ritsumeikan Univ.*)

3Pos138 シアノバクテリオクロム型光受容体のシステイン残基の着脱反応におけるプロトンの役割
Protochromic Absorption Changes in Two-Cys Photocycle of the Blue/Orange Cyanobacteriochrome
Teppei Sato[1,2], Takashi Kikukawa[3], Risako Miyoshi[4], Kosuke Kajimoto[4], Chinatsu Yonekawa[1], Tomotsumi Fujisawa[4], Masashi Unno[4], Toshihiko Eki[1], **Yuu Hirose**[1] ([1]*Toyohashi Univ. of Tech.*, [2]*Nagoya Univ.*, [3]*Hokkaido Univ.*, [4]*Saga Univ.*)

3Pos139 パターン化モデル膜を用いたロドプシンリン酸化とアレスチン結合の解析
Rhodopsin phosphorylation and arrestin binding studied in a patterned model membrane
Fuko Kueda[1], Yasushi Tanimoto[2], Fumio Hayashi[3], Kenichi Morigaki[2,4] ([1]*Fac. Agr., Univ. Kobe*, [2]*Biosignal Research Center, Univ. Kobe*, [3]*Grad. Sch. Scie., Univ. Kobe*, [4]*Grad. Sch. Agr., Univ. Kobe*)

3Pos140 長波長光感受性視物質の塩化物イオン結合における Gln114 の役割
Role of Gln114 in chloride binding of long-wavelength-sensitive visual pigment
Kota Katayama[1], Shunta Nakamura[1], Takuma Sasaki[1], Hiroo Imai[2], Hideki Kandori[1] ([1]*Grad.Sch.Eng., Nagoya Inst. Tech*, [2]*Orimate Res. Inst., Kyoto Univ*)

3Pos141 Comparative Study for Anion Transport Activity of Anion Channelrhodopsins by Using a Simple pH Electrode Method
Chihiro Kikuchi (*Grad. Sch. Life Sci.*)

光生物学：光合成／Photobiology: Photosynthesis

3Pos142 (3SDA-3) 生体組織への応用が期待される光感度の高いチャネルロドプシン
(3SDA-3) Novel optogenetics tool: A light-gated cation channel with high-reactivity to weak light
Shoko Hososhima[1], Shunta Shigemura[1], Hideki Kandori[1], Satoshi Tsunoda[1,2] ([1]*Nagoya Institute of Technology*, [2]*JST, PRESTO*)

3Pos143 光依存的にホモオリゴマー化する植物クリプトクロム 2 の分子特性
Molecular properties of light-dependent homo-oligomerizing *At* CRY2
Kazuya Agata[1], Daichi Yamada[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech., Dept. Life Sci. Appl. Chem.*, [2]*Univ. Hyogo, Dept. Life Sci.*)

3Pos144 光ジッパーを用いた bZIP 型転写因子の標的配列認識の解析
Analyses of the target sequence recognition of a bZIP factor, using a light-activatable Photozipper
Osamu Hisatomi, Samu Tateyama, Itsuki Kobayashi (*Grad. Sch. of Sci., Osaka Univ.*)

3Pos145 光制御型 bZIP 転写因子（フォトジッパー）の β シート疎水面の役割
Hydrophobic residues on the β-sheet of a light-activatable bZIP factor, Photozipper
Hiroto Nakajima, Itsuki Kobayashi, Osamu Hisatomi (*Grad.Sch.of Sci.,Osaka Univ.*)

3Pos146 高速 AFM による DNA 結合光受容タンパク質 Photozipper の 1 分子動態イメージング
Single molecular dynamics imaging of DNA binding photoreceptor protein, Photozipper, by high-speed AFM
Kento Nomura[1], **Hayato Yamashita**[1], Osamu Hisatomi[2], Masayuki Abe[1] ([1]*Grad. Sch. of Eng. Sci., Osaka Univ.*, [2]*Grad. Sch. of Sci., Osaka Univ.*)

3Pos147 Theoretical study on molecular mechanism of a light-driven ion transport of Halorhodopsin from Natronomonas pharaonis
Ryo Oyama, Taisuke Hasegawa, Shigehiko Hayashi (*Grad. Sch. Sci., Univ. Kyoto*)

ゲノム生物学／Genome biology

3Pos148 ウニ初期胚核内構造の発生に伴う動的変化とその細胞特異性
Dynamic and cell specific changes in intranuclear chromosomal
Yuhei Yasui (*Integrated science for life, Hiroshima Univ*)

3Pos149 ヌクレオソーム排他的ループ非形成型インスレーター配列（NENLIS）によるインスレーター活性のゲノムワイド解析
Genome-wide analysis of insulator activity by nucleosome exclusive non-looping insulator sequence (NENLIS)
Yudai Hirose[1], Yuki Matsushima[1], Naoaki Sakamoto[2], Akinori Awazu[2] ([1]*Grad. Sch. Sci., Univ. Hiroshima*, [2]*Grad. Sch. Integrated Sci., Univ. Hiroshima*)

3Pos150 X 染色体不活性化を誘導する染色体動態
The dynamics of chromosomes that trigger X chromosome inactivation
Tetsushi Komoto, Hiraku Nishimori, Akinori Awazu (*Integrated Science for Life in Hiroshima university*)

生命情報科学／Bioinformatics

3Pos151 Machine learning models for predicting ligand-binding sites using residue-wise features
Masafumi Shionyu, Atsushi Hijikata (*Fac. Biosci., Nagahama Inst. Bio-Sci. Tech.*)

3Pos152 モノクローナル抗体の詳細と提供情報のデータベース
Database for information of acquirable monoclonal antibody
Hirofumi Suzuki[1], Mika Kaneko[2], Yukinari Kato[2], Kei Yura[1,3] ([1]*Dept. Life Sci. & Med. Bio., Waseda Univ.*, [2]*Grad. Sch. of Med., Tohoku Univ.*, [3]*Sim. Info. Bio., Ochanomizu Univ.*)

3Pos153 強力な順方向遺伝学による生物システム解析 -Vibrio alginolyticus の走性への応用
Biological system analysis by a strong forward genetics -An application to a taxis in a strain Vibrio alginolyticus
Kunio Ihara[1], Kazuma Uesaka[1], Noriko Nishioka[2], Seiji Kojima[2], Michio Homma[2] ([1]*Nagoya University Cent.Gene Res.*, [2]*Nagoya University Grad. School Sci.*)

3Pos154 時点数の少ないトランスクリプトームデータからのネットワーク推定に適した遺伝子グループ化法
Gene grouping strategy for network inference from a small time-series transcriptome data
Kiyohiro Maeda (*Fujifilm Corporation*)

3Pos155 生物発光タンパク質およびルシフェリンの獲得進化解析
Evolutionary Analysis of Luciferase, Photoprotein and Luciferin
Misato Funahashi[1], Hirofumi Suzuki[2], **Kei Yura**[1,2] ([1]*Grad. Schl Hum. Sci., Ochanomizu Univ.*, [2]*Schl Adv. Sci. Engng., Waseda Univ.*)

数理生物学／Mathematical biology

3Pos156 二倍体遺伝子発現制御系における集合的メンデル遺伝
Group Mendelian Dominance in Diploid Gene Regulatory Network
Kenji Okubo, Kunihiko Kaneko (*Dep. of Basic Sci., Univ. Tokyo*)

3Pos157 不正確な素子から機能的なネットワークをつくる方法
Cooperative architecture for functional network from sloppy gene expression dynamics
Masayo Inoue[1], Kunihiko Kaneko[2] ([1]*IMS, Meiji Univ.*, [2]*Univ. of Tokyo*)

3Pos158 混雑下のナノ～マイクロマシン集団：内部状態と環境の相互干渉
Nano/Micro-machines in the Crowd: Interplay between the Internal State and Surroundings
Yuichi Togashi[1,2] ([1]*RIKEN BDR*, [2]*Grad. Sch. Integ. Sci. Life, Hiroshima Univ.*)

3Pos159 3D phase field simulation for macropinocytosis of amoeboid cells
Nen Saito[1], Satoshi Sawai[2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Arts Sci., Univ. Tokyo*)

3Pos160 Geometric feature extraction from some gene expression pattern for prediction of atopic dermatitis patients
Takuya Hasebe[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, [2]*RDCMIT, Tokyo Med. Univ.*)

3Pos161 増殖系と隠れマルコフモデルの対応に基づく学習の考察
A Study on Learning in Growing Population on the Basis of Hidden Markov Model
So Nakashima[1], Tetsuya J. Kobayashi[2] ([1]*grad. school of IS&T, UTokyo*, [2]*IIS, UTokyo*)

3Pos162 脳神経系の動的ネットワークモデルにおける自発的階層構造形成
Spontaneous hierarchical structure formation in dynamic network model of cerebral nervous system
Amika Ohara, Hiraku Nishimori, Akinori Awazu (*Dept. of math. and life sci. Hiroshima univ.*)

3Pos163 Fitness response relation of a multitype age-structured population dynamics
Yuki Sughiyama[1], So Nakashima[2], Tetsuya Koabayasi[1] ([1]*IIS, The University of Tokyo*, [2]*Department of Mathematical Informatics, The University of Tokyo*)

3Pos164 Simulation and regulation of E.coli which has autonomous diversification ability
Eriko Nakagawa[1], Shotaro Ayukawa[2], Daisuke Kiga[1] ([1]*Department of Electrical Engineering and Bioscience, Waseda University*, [2]*Waseda Research Institute for Science and Engineering, Waseda University*)

3Pos165 Probability landscape of coupled epigenetic and genetic network with eddy-like probability currents
Bhaswati Bhattacharyya, Masaki Sasai (*Department of Applied Physics, Nagoya University*)

3Pos166 ドロップアウトを適用したニューラルネットワークアルゴリズムによる大腸菌の遺伝子制御ネットワークの推定
Inference of gene regulatory network of E.coli by neural network algorithm applied dropout
Yusuke Mizukoshi[1], Masahiro Sugimoto[2], Takanori Sasaki[3] ([1]*Grad. Sch. Adv. Math. Sci., Univ.Meiji*, [2]*RDCMIT, Univ.Tokyo Med*, [3]*Grad. Sch. Adv. Math. Sci., Univ.Meiji*)

非平衡・発生リズム／Nonequilibrium state & Biological rhythm

3Pos167 Active Nematic Sperms in Vivo Mouse
Tsuyoshi Hirashima[1], Kyogo Kawaguchi[2], Takuya Omotehara[3], Masahiro Itoh[3], Kenta Ishimoto[4], Michiyuki Matsuda[1,5] ([1]*Grad Sch Med, Kyoto Univ*, [2]*RIKEN*, [3]*Tokyo Medical University*, [4]*Grad Sch Math Sci, The Univ of Tokyo*, [5]*Grad Sch Biostudies, Kyoto Univ*)

3Pos168 メチルセルロースとの相分離が誘起する重合過程アクチン線維の紡錘形液晶ドメイン自発形成
Emergence of spindle-shaped namatic domains of filamentous actin during polymerization induced by phase-separation from methylcellulose
Masahito Hayashi[1], Tomoyuki Kaneko[1], Kingo Takiguchi[2] ([1]*LaRC, Frontier Biosci., Hosei Univ.*, [2]*Dept. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

3Pos169 Traveling band formation of a mutant *Dictyostelium* cell population induced by contact following of locomotion
Masayuki Hayakawa[1], Tetsuya Hiraiwa[2], Yuko Wada[1], Hidekazu Kuwayama[3], Tatsuo Shibata[1] ([1]*Riken BDR*, [2]*Dept. of Phys, Univ. of Tokyo*, [3]*Faculty of Life and Env. Sci., Univ. of Tsukuba*)

3Pos170 高速 AFM による KaiC、KaiB、SasA 間相互作用のリン酸化状態依存性観察
High-Speed AFM observation of phosphorylation state-dependent interactions between KaiC, KaiB and SasA
Kenta Ueda[1], Tetsuya Mori[2], Shogo Sugiyama[3], Takayuki Uchihashi[1], Carl H. Johnson[2] ([1]*Dept. of Sci, Nagoya Univ*, [2]*UnivDept.of Biol.Sci., Vanderbilt Univ*, [3]*Dept. of Phys, Kanazawa*)

3Pos171 Individual cyanobacterial circadian rhythms under chilly conditions
Hiroshi Ito[1], Hinako Maruayama[1], Irina Mihalcescu[2] ([1]*Grad. Sch. Design., Kyushu Univ.*, [2]*LIPhy, Universite Grenoble Alpes*)

計測／Measurements

3Pos172 多電極システムを用いた心毒性検査のためのハイスループットチャンバーの改良
Improvement of high-throughput chamber for cardio-toxicity testing with multi-electrode array system
Naoki Tadokoro, Tomoyuki Kaneko (*LaRC, FB, Hosei Univ.*)

3Pos173 HPD による広視野蛍光 1 分子偏光検出
Wide-field single-molecule fluorescence polarization detection by hybrid photo-detectors (HPDs)
Atsuhito Fukasawa[1], Gaku Nakano[1], Minako Hirano[2], Toru Ide[3], Hiroaki Yokota[2] ([1]*Hamamatsu Photonics K.K.*, [2]*Grad. Sch. Creation Photon Indust.*, [3]*Grad. Sch. Interdisciplinary Sci. and Engineering in Health Sys.*)

3Pos174 蛍光タンパク質の赤外スペクトル測定ー発色団部位の選択的な観測ー
IR spectra of fluorescent proteins -selective measurement of chromospheres-
Hirona Takahashi, Makoto Sakai (*faculty of Science, Okayama University of Science*)

3Pos175 蛍光計測技術を用いた高分子クラウディングが与える相互作用の評価
Elucidation of the Effect of Macromolecular Crowding to Molecular Interactions using Fluorescence Fluctuation Microscopy Techniques
Fusako Gan[1], Akito Matsui[1], Johtaro Yamamoto[2], Masataka Kinjo[3] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Biomed. Res. Inst., AIST*, [3]*Fac. of Adv. Life Sci., Hokkaido Univ.*)

3Pos176 Examination of backtracking engulfment mechainism in macrophages using on-chip single cell observation assay
Amane Yoshida[1], Yuya Furumoto[1], Toshiki Azuma[1], Takahiro Kitahara[2], Tomoyasu Sakaguchi[2], Masao Odaka[3], Akihiro Hattori[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

3Pos177 キャピラリー吸引法を用いた単一マクロファージの一連の貪食における余分な体積増加について
Extra volume increase of single macrophage during sequential phagocytosis occurred by using micropipette aspiration measurement assay
Toshiki Azuma[1], Yuya Furumoto[1], Amane Yoshida[1], Masao Odaka[2], Akihiro Hattori[2], Tomoyasu Sakaguchi[3], Takahiro Kitahara[3], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Org. Univ. Res. Initiatives, Waseda Univ.*, [3]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ*)

3Pos178 Releasing SecM translation arrest and observing resumed translation using magnetic tweezers
Zhuohao Yang, Ryo Iizuka, Takashi Funatsu (*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*)

バイオイメージング／Bioimaging

3Pos179 (3SGA-5) 転写伸長を制御するメディエーターの 1 分子超解像イメージングによる分子局在と動態の定量解析
(3SGA-5) Molecular localization and dynamics of Mediator regulating transcription elongation using single-molecule and super-resolution microscopy
Yuma Ito[1], Shinnosuke Kunimi[1], Hidehisa Takahashi[2], **Makio Tokunaga**[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

3Pos180 酸性細胞環境内の超解像イメージング応用に向けた耐酸性可逆的光スイッチング緑色蛍光タンパク質の開発
Acid-tolerant Reversibly Switchable Green Fluorescent Protein for Super-resolution Imaging in Acidic Conditions
Hajime Shinoda[1,2], Kai Lu[3], Ryosuke Nakashima[3], Tetsuichi Wazawa[3], Kosuke Noguchi[2], Tomoki Matsuda[2,3], Takeharu Nagai[2,3] ([1]*CPR, Riken*, [2]*Grad. Sch. Eng., Osaka Univ.*, [3]*ISIR, Osaka Univ.*)

3Pos181 Direct observation of heterogeneous starvation response and emergence of surviving subpopulation in the clonal microbial population
Sotaro Takano[1], Miki Umetani[2], Hidenori Nakaoka[2], Yuichi Wakamoto[2,3,4], Ryo Miyazaki[1,5,6] ([1]*AIST, Bioprod. Inst.*, [2]*Grad. Sch. of Arts and Sci., Univ. of Tokyo*, [3]*Universal Biol. Inst., Univ. of Tokyo*, [4]*Res. Center for Complex Syst. Biol., Univ. of Tokyo*, [5]*AIST, CBBD-OIL*, [6]*Life and Env. Sci., Univ. of Tsukuba*)

3Pos182 ヘアレスマウスにおける皮質拡延性抑制の近赤外無侵襲測定
Noninvasive near-infrared monitoring of intrinsic optical signals caused by high K+-induced cortical spreading depression in hairless mice
Hiro Yamato[1], Takashi Jin[2], **Yasutomo Nomura**[1] ([1]*Grad. Eng. Maebashi Inst. Tech.*, [2]*RIKEN BDR*)

3Pos183 1 粒子でナノスケール温度計とナノスケール熱源になる蛍光ナノダイヤモンド
Application of individual fluorescent nanodiamond as nanothermometer and nanoheater
Chongxia Zhong[1], Shingo Sotoma[1,2], Yoshie Harada[1,3], Madoka Suzuki[1] ([1]*Institute for Protein Research (IPR), Osaka University*, [2]*Japan Society for the Promotion of Science(JSPS)*, [3]*QIQB, OTRI, Osaka University*)

3Pos184 粒子フィルター MD シミュレーションによる高速 AFM データからの分子動態推定
Biomolecular dynamics inferred from high-speed AFM data via particle-filter MD simulations
Suguru Kato, Toru Niina, Sotaro Fuchigami, Shoji Takada (*Kyoto University*)

3Pos185 Elucidation of the aggregation of serum amyloid A protein and health diagnosis using a high-throughput screening system
Xuguang Lin[1], Masahiro Kuragano[1], Kenichi Watanabe[2], Kiyotaka Tokuraku[1] ([1]*Dep. of App. Sci. and Eng., Muroran Ins. of Tech.*, [2]*Obihiro Univ. of Agric. Vet. Med.*)

3Pos186 3D time-laps imaging of alpha-synuclein aggregation using quantum-dot nanoprobes
Min Nuo[1], Masahiro Kuragano[1], Q.P Taro Noguchi[2], Kiyotaka Tokuraku[1] ([1]*Dep. of App. Sci.and Eng., Muroran Ins. of Tech.*, [2]*NIT, Miyakonojo College*)

3Pos187 Three-dimensional analysis for formation process of amyloid β_{42} aggregation using quantum dots nanoprobe
Masahiro Kuragano, Kiyotaka Tokuraku (*Div. of Sust. and Env. Eng., Muroran Inst. of Tech.*)

3Pos188 高速 AFM を用いた HECT 型ユビキチンリガーゼのユビキチン化に伴う構造動態の観察
Observation of the structural dynamics associated with ubiquitination of HECT-type ubiquitin ligase using high-speed AFM
Ikumi Mruo[1], Takahiro Watanabe-Nakayama[2], Toshio Ando[2], Hiroki Konno[2] ([1]*Grad. Sch. of Nat. Sci. & Technol., Kanazawa Univ.*, [2]*WPI Nano Life Sci. Inst. (WPI-NanoLSI), Kanazawa Univ.*)

3Pos189 Kinesin transport on microtubules studied by high-speed AFM
Christian Ganser[1], Syeda Rubaiya Nasrin[2], Akira Kakugo[2,3], Ryota Iino[4], Takayuki Uchihashi[5] ([1]*ExCELLS, NINS*, [2]*Grad. Sch. Chem. Sci. Eng., Hokkaido Univ.*, [3]*Fac. Sci., Hokkaido Univ.*, [4]*IMS, NINS*, [5]*Grad. Sch. Sci., Nagoya Univ.*)

3Pos190 鎖の細胞膜提示システムの構築とその機能解析
Construction and functional analysis of the glycan display system on the cell membrane
Ayane Miura[1], Kazuya Kabayama[1,2,3], Syuto Miyake[1], Hiroki Syomura[1], Yoshiyuki Manabe[1], Toshiyuki Yamaji[4], Kentaro Hanada[4], Koichi Hukase[1,2,3] ([1]*Grad. Sch. of Sci., Osaka Univ.*, [2]*MS-CORE, PRC, Grad. Sch. of Sci., Osaka Univ.*, [3]*Inst. for Radiation Sciences, Osaka Univ.*, [4]*NIID*)

3Pos191 分岐鎖アミノ酸に対する遺伝子コード型蛍光バイオセンサー
Genetically encoded fluorescent biosensor for branched-chain amino acids
Hiromi Imamura, Tomoki Yoshida, Hitomi Nakajima, Sena Takahashi, Akira Kakizuka (*Grad. Sch. Biost., Kyoto Univ.*)

3Pos192 Odor-evoked responses in mouse whole brain as detected by BOLD-fMRI analyses with periodic stimulation and independent component analysis
Mitsuhiro Takeda, Fuyu Hayashi, Naoya Yuzuriha, Sosuke Yoshinaga, Hiroaki Terasawa (*Kumamoto University, Faculty of Life Sciences*)

3Pos193 クライオ電子線トモグラフィー法による糸状仮足中のアクチン繊維とファシンの可視化
Visualization of F-Actin with Fascin in Filopodia by electron cryo-tomography
Naoko Kajimura[1], Takuo Yasunaga[2], **Kaoru Mitsuoka**[1] ([1]*Research Center for Ultra-High Voltage EM, Osaka Univ.*, [2]*Grad. Sch. Comp. Sci. Syst. Eng., KIT*)

3Pos194 Fluorescent Ca2+ indicators for multiplexed super-resolution imaging at nanoscopic cellular domain
Kai Lu, Tomoki Matsuda, Tetsuichi Wazawa, Takeharu Nagai (*ISIR, Osaka University*)

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

3Pos196 3D image construction methods for observation of cell with micro manipulation
Masaru Kojima[1], Yuma Takeuchi[1], Yasushi Mae[1], Tatsuo Arai[2,3] ([1]*Grad. Sch. Eng.Sci., Osaka Univ.*, [2]*UEC*, [3]*BIT*)

3Pos197 Distinct morphologies of integrin-targeted peptide co-assemblies in peritumoral space vs physiological ECM
William Cortes, Sona Roy, Sachie Yukawa, **Toshio Sasaki**, Wu Xia, Ye Zhang (*Ye Zhang Unit, Okinawa Institute of Science and Technology*)

3Pos198 環状柔軟多関節 DNA モチーフの自己集合
Self-assembly of a Flexible Multi-joing Ring Motif
Shiyun Liu, Ibuki Kawamata, Shin-ichiro Nomura, Satoshi Murata (*Grad. Sch. Eng., Univ. Tohoku*)

3Pos199 オン・チップマルチイメージングフローサイトメトリーでの血中の循環腫瘍細胞の同定のためのサイズ解析
Size distribution analysis of circulating tumor cell clusters in blood using on-chip multi-imaging flow cytometry
Masao Odaka[1], Akihiro Hattori[1], Kenji Yasuda[1,2] ([1]*Org. Univ. Res. Initiatives, Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos200 アミロイド凝集阻害物質の自動スクリーニングシステムにより見出した高活性天然抽出物の評価
Evaluation of highly active natural extracts found by an automated screening system for amyloid aggregation inhibitors
Rina Sasaki[1], Masahiro Kuragano[1], Kenji Monde[2], Koji Uwai[1], Kiyotaka Tokuraku[1] ([1]*Grad. Sch. Eng., Muroran Inst. Tech.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)