ポスター　Poster

＊ 学生発表賞応募演題
＊ Student Presentation Award Application Poster

A. 蛋白質:機能・構造・物性・計測・工学／A. Protein General

20001A* **全原子分子動力学法による維持メチル化酵素(Dnmt1)とその捕因子の動態解析**
Theoretical Analyses on Dynamic Properties of DNA methyltransferase 1 and its Cofactors Based on All-atom Molecular Dynamics Simulations
Takunori Yasuda[1], Yasuteru Shigeta[2], Ryuhei Harada[2] ([1]*College of Biological Sciences, University of Tsukuba*, [2]*Center for Computational Sciences, University of Tsukuba*, [3]*Center for Computational Sciences, University of Tsukuba*)

20002A **3D−RISM 理論を応用した溶液中におけるペプチドの構造揺らぎの解析**
Analysis of structural fluctuations of a small peptide in the solution phase by means of 3D-RISM theory
Masatake Sugita (*Sch. Computing, Tokyo Tech*)

20003A **細菌べん毛形成開始するために 34 個集まってリングになる 2 回膜貫通タンパク質 FliF の N 末端・C 末端細胞質領域欠損体の解析**
Analysis of the cytoplasmic region-deficient mutants of double-transmembrane protein FliF which forms a MS-ring in flagellar formation
Seiji Kojima[1], Mitsuki Kajino[1], Keiichi Hirano[1], Yuna Inoue[1], Tatsuro Nishikino[2], Hiroyuki Terashima[1], **Michio Homma**[1] ([1]*Nagoya Univ, Sch Sci, Div Biol Sci*, [2]*Osaka Univ, Ins Protein Res*)

20004A **Pin1 の変異体 C113A と C113S の構造解析**
Structural analysis of Pin1 mutants C113A And C113S
Teikichi Ikura, Nobutoshi Ito (*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

20005A* Similarity and difference between substrate analogue-induced and spontaneous folding of staphylococcal nuclease
Yujiro Mori[1], Saho Segawa[2], Kosuke Maki[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Sch. Sci., Nagoya Univ.*)

20006A **タンパク質の複合体の界面の相互作用のデータベース解析**
Database analysis of protein-protein interaction
Wataru Sagawa, George Chikenji (*Dept. Appl. Phys., Nagoya Univ.*)

20007A* Cross-seeding of human and bovine insulin amyloid fibrils induces stepwise conformational transition via intermediate states
Keisuke Yuzu[1], Naoki Yamamoto[2], Masahiro Noji[3], Masatomo So[3], Yuji Goto[3], Tetsushi Iwasaki[1,4], Motonari Tsubaki[1], Eri Chatani[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Fac. Med., Jichi Med. Univ.*, [3]*Inst. Protein Res., Osaka Univ.*, [4]*Biosignal Res. Center, Kobe Univ.*)

20008A **低温電子顕微鏡画像を記述する連続関数の計算法：マニフォールドラーニングによる研究**
A Computational Method for Constructing a Continuous Function Describing Cryo-Electron Microscopy Data: A Study using a Manifold Learning
Ryota Kojima, Takashi Yoshidome (*Dep. of Appl. Phys., Tohoku Univ.*)

20009A Unguided Binding MD of Protein-Protein Complexes by PPI-ColDock
Kazuhiro Takemura, Akio Kitao (*Sch. LST, Tokyo Tech*)

20010A* **tRNA 硫黄修飾酵素における鉄硫黄クラスター構造と酵素活性の相関解析**
Correlation between structures of iron-sulfur clusters and enzymatic activity in tRNA thiolation enzymes
Masato Ishizaka[1], Minghao Chen[2], Shun Narai[1], Masaki Horitani[3], Yoshikazu Tanaka[4], Min Yao[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Facul. Adv. Life Sch., Hokkaido Univ.*, [3]*Facul. Agr., Saga Univ.*, [4]*Grad. Sci. Life Sci., Tohoku Univ.*)

20011A Sampling large-scale motions in proteins using a coarse-grained multi-basin Go model
Ai Shinobu[1], Chigusa Kobayashi[1], Yasuhiro Matsunaga[2], Yuji Sugita[1] ([1]*RIKEN*, [2]*Saitama Univ.*)

20012A Visualization of translational GTPase factor-pool formed on the archaeal ribosomal P-stalk by HS-AFM

Hirotatsu Imai[1], Toshio Uchiumi[2], Noriyuki Kodera[1] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*Faculty of Science, Niigata Univ.*)

20013A NMR 解析によるシニョリンとその変異体の立体構造の決定

Determination of structures of chignolin and its mutant by NMR analysis

Shumpei Koroku[1], Ayori Mitsutake[2], Yutaka Maruyama[3], Koh Takeuchi[4] ([1]*Meiji University*, [2]*Meiji University*, [3]*RIKEN*, [4]*AIST*)

20014A 高速 AFM を用いた磁性細菌の細胞骨格結合タンパク質 MamJ の機能解析

Functional analyses of magnetotactic bacterial cytoskeletal binding protein MamJ using high-speed AFM

Takumi Saito[1], Yosuke Kikuchi[2], Yoshihiro Fukumori[3], Azuma Taoka[2,3] ([1]*Graduate School of Natural Science and Technology, Kanazawa University*, [2]*Institute of Science and Engineering, Kanazawa University*, [3]*Nano Life Science Institute (NanoLSI), Kanazawa University*)

20015A* 18 残基チオエーテル結合環状ペプチド群のシミュレーションデータの解析

Analysis of Molecular Dynamics Simulations of 18-residue Thioether Cyclic Peptides

Daiki Noguchi (*Meiji university graduate school*)

20016A グラフ理論に基づくタンパク質立体構造の位相解析への VOLTES 法の応用

Application of VOLTES to topological analyses of protein structures based on graph theory

Anri Terabayashi, Kyousuke Sakata, Toshitaka Shoji, Masaki Kojima (*Sch. Life Sci., Tokyo Univ. Pharm. Life Sci.*)

20017A The molecular basis for the nucleotide selectivity of the ε subunit from bacterial F-type ATP synthases

Alexander Krah[1,2], Roland G. Huber[1], Duncan G. G. McMillan[3], Peter J. Bond[1,4] ([1]*Bioinformatics Institute (BII)*, [2]*Korea Institute for Advanced Study*, [3]*TU Delft*, [4]*Department of Biological Sciences, National University of Singapore*)

20018A Free Energy Calculations of HIV-1 Protease Binding Indinavir and Its Drug-Resistant Mutant

Masahiko Taguchi[1], Ryo Oyama[2], Masahiro Kaneso[2], Shigehiko Hayashi[2] ([1]*Inst. Quant. Life Sci., QST*, [2]*Grad. Sch. Sci., Kyoto Univ.*)

20019A メタゲノムデータベース由来 PET 加水分解酵素の耐熱性および活性の改良

Improvement of thermostability and catalytic activity of a PET degrading enzyme derived from metagenome database

Akihiko Nakamura[1], Naoya Kobayashi[2], Takahiro Kosugi[2], Rie Koga[2], Nobuyasu Koga[2,3], Ryota Iino[2,3] ([1]*Shizuoka Univ.*, [2]*Inst. Mol. Sci.*, [3]*SOKENDAI*)

20020A 心筋カルシウムチャネル Cav1.2 と薬剤間の結合自由エネルギー計算

Calculation of the binding free energy between the Cav1.2 calcium channel and drugs

Tatsuki Negami, Tohru Terada (*Grad. Sch. Agr. Life Sci., Univ. Tokyo*)

20021A 標的空間を 2,3,4 次元とした Dimensional Scaling 法によるフラグメント間相互作用エネルギー行列解析

Analysis of inter fragment interaction energy by Dimensinal Scaling method in 2,3,4 by Dimensional as the target space

Yuki Abe, Masanori Yamanaka (*Univ.Nihon*)

20022A 蛋白質内部で水素結合を形成する荷電残基が示す強力な安定化効果についての熱力学的評価

The thermodynamic characterization of the strong stabilization effect by a buried and charged residue forming hydrogen bonds

Hiroaki Sato, Akiko Nakazawa, Kohei Yamamoto, **Shun-ichi Kidokoro** (*Dept. Bioeng., Nagaoka Univ. Tech.*)

20023A インスリン受容体全長構造モデリングとその分子動力学研究

Computational modeling of full-length insulin receptor and its molecular dynamics

Yoshiharu Mori (*Grad. Sch. of Sys. Info., Kobe Univ.*)

20024A Size evolution of antibody aggregates by the adsorption of serum albumin
Tomohito Nakayama[1,2], Muneaki Hase[1], Atsushi Hirano[2] ([1]*Grad. Sch. Sci. Tech., Univ. Tsukuba*, [2]*NMRI, AIST*)

20025A Theoretical Study on the Transport Cycle of the Heme ABC Transporter BhuUV-T
Koichi Tamura[1], Yuji Sugita[1,2,3] ([1]*RIKEN R-CCS*, [2]*RIKEN BDR*, [3]*RIKEN CPR*)

20026A ヤエヤマサソリ由来殺虫性毒素 LaIT2 の C 末端ドメインの大腸菌大量発現系構築
Constructon of the *E.coli* ovrexpression system for the C-terminal domain of LaIT2, an insecticidal toxin from *Liocheles australasiae*
Chiharu Tatsushiro[1], Maiki Tamura[2], Shinya Ohki[2], Hayato Morita[1,3] ([1]*Grad.Sch.Sci.,Josai Univ*, [2]*Grad.Sch.Mat Sci.,JAIST*, [3]*Fas Sci.,Josai Univ*)

20027A 高密度マイクロウェルアレイによる酵素関連タンパク質のセレクションを目的とした、ペプチドリガーゼによる遺伝子型-表現型対応付け手法の開発
Peptide ligase display (PL display) for selection of enzyme-related protein by combination with high-density microwell array chip
Shingo Ueno[1,2], Shusuke Sato[1,2], Fumi Toshioka[1], Shoichi Tsuchiya[1], Takanori Ichiki[1,2] ([1]*iCONM, Kawasaki Ins. Ind. Prom.*, [2]*Grad. Sch. Eng., Univ. Tokyo*)

20028A 長時間タンパク質ダイナミクスの拡散マップによる解析
Diffusion map analysis of long time protein dynamics
Hiroshi Fujisaki[1], Hiroto Kikuchi[1], Hiromichi Suetani[2], Ayori Mitsutake[3] ([1]*Nippon Medical School*, [2]*Grad. Sch. Eng., Oita Univ.*, [3]*Grad. Sch. Sci., Meiji Univ.*)

20029A Molecular simulation of pH effect on emission color changes through hydrogen-bond networks in firefly luciferase and its mutants
Kota Nosaka[1], Yuto Kudo[2], Naohisa Wada[1] ([1]*Grad. Sch. Life Sci., Univ.Toyo*, [2]*Fac. Food and Nu. Sci., Univ.Toyo*)

20030A Spectroelectrochemical FTIR studies of an electron-bifurcating [FeFe] hydrogenase
Nipa Chongdar[2], Krzysztof Pawlak[2], Olaf Rudiger[2], Edward Reijerse[2], Patricia Rodriguez-Macia[2], Wolfgang Lubitz[2], James Birrell[2], **Hideaki Ogata**[1,2] ([1]*ILTS, Hokkaido Univ.*, [2]*MPI/CEC*)

20031A 演題取り消し

20032A D313Y 変異をもつノーマル型べん毛繊維を用いた多型変換に関与するアミノ酸相互作用の推測
Prediction of amino acid interactions for polymorphic transformation with normal flagellar filaments with the D313Y curly mutation
Ayano Yanagita[1], Minami Oohata[1], Hikaru Tsufuku[1], Shigeru Yamaguchi[1], Fumio Hayashi[2], Kenji Oosawa[1] ([1]*Dept. Chem. & Chem. Biol., Sch. Sci. Technol., Gunma Univ.*, [2]*Ctr. Instr. Anal. Gunma Univ.*)

20033A* 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経路の解析
Protein folding mechanisms predicted by an extended statistical mechanical model
Koji Ooka[1], Munehito Arai[1,2] ([1]*Dept. Phys., Univ. Tokyo*, [2]*Dept. Life Sci., Univ. Tokyo*)

20034A Structural Stability and Unfolding Kinetics of a lytic polysaccharide monooxygenase, CBP21
Yuichi Nakajima, Takeshi Watanabe, Kazushi Suzuki, Hayuki Sugimoto (*Grad. Sch. Sci. & Tech., Niigata Univ.*)

20035A Search for Partial Structural Space of Specific Loop Residues by Hydrogen Bond and Steric Repulsion
Hiroto Murata, George Chikenji (*Dept. Appl. Phys., Nagoya Univ.*)

20036A 機械学習による単粒子 X 線回折像の改善
Improvement for Noisy X-ray Single-Particle Diffraction Pattern using Convolutional Neural Network
Atsushi Tokuhisa[1,2], Yoshinobu Akinaga[1,3], Kei Terayama[1,4], Yasushi Okuno[1,5] ([1]*RIKEN Medical Sciences Innovation Hub Program (MIH)*, [2]*RIKEN Center for Computational Science (R-CCS)*, [3]*VINAS Co.,Ltd.*, [4]*Computational Life Science, Yokohama City Univ.*, [5]*Graduate School of Medicine, Kyoto Univ.*)

20037A* c-Myb-KIX 相互作用を阻害するヘリカルペプチドの合理的設計
Rational design of an α-helical peptide to inhibit 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*)

20038A Optimized Go-MARTINI coarse-grained force field parameters based on structural flexibility of F-BAR protein Pacsin1 on lipid membrane
Md. Iqbal Mahmood[1], Adolfo Poma[2], Kei-ichi Okazaki[1] ([1]*Institute for Molecular Science*, [2]*Institute of Physics, Polish Academy of Sciences, Al. Lotnikow 32/46, 02-668 Warsaw, poland*)

20039A タンパク質脱イミノ化酵素 PAD3 の構造機能相関解明
Elucidation of the structure-function relationship of peptidyl arginine deiminase type 3
Mizuki Sawata[1], Kazuma Funabashi[1], Tetuya Ohwada[1], Hidenari Takahara[2,3], Masaki Unno[1,3] ([1]*Grad. Sch. Sci. Eng., Univ. Ibaraki*, [2]*Sch. Agr., Univ. Ibaraki*, [3]*Frontier., Univ. Ibaraki*)

20040A トキソプラズマ症を引き起こす病原性原虫トキソプラズマの寄生胞膜破壊に関わる Irgb6 の結晶構造
Crystal structure of Irgb6, which is involved in the destruction of a membrane-bound parasitophorous vacuole of Toxoplasma gondii
Yumiko Saijo-Hamano[1], Naoki Sakai[2], Yoshiaki Sakihama[1], Masahiro Yamamoto[3], Ryo Nitta[1] ([1]*Grad. Sch. Med., Kobe Univ.*, [2]*RIKEN, RCS*, [3]*RIMD, Osaka Univ.*)

20041A 糸状仮足観察のための Cryo-CLEM 法の検討
A study of the Cryo-CLEM method for the observation of filopodia
Miho Nakafukasako, Tomoya Higo, Yusuke V. Morimoto, Takuo Yasunaga (*Grad. Sch. Comp. Sci. Syst. Eng., KIT.*)

20042A ヘリオロドプシンおよびシゾロドプシンの構造から明らかになった微生物型ロドプシンの多様性
Structures of heliorhodopsin and schizorhodopsin elucidate the structural diversity of microbial rhodopsins
Wataru Shihoya[1], Keiichi Inoue[2], Singh Manish[3], Akimitsu Higuchi[1], Masae Konno[2], Rei Yoshizumi[3], Takayuki Uchihashi[4], Hideki Kandori[3], Osamu Nureki[1] ([1]*Dept. of Biol., Grad. Sch. Sci, Univ. of Tokyo*, [2]*ISSP, Univ. of Tokyo*, [3]*Life Sci. Appl. Chem., Grad. Sch. Eng., NIT*, [4]*Dept. of Phys., Grad. Sch. Sci, Nagoya Univ.*)

20043A The relationship between designability of protein and preference of local structures: A lattice model study
Kazuma Toko, George Chikenji (*Dept.Appl.Phys.,Nagoya Univ.*)

20044A β ストランドと α ヘリックスをつなぐループが特定の主鎖二面角およびアミノ酸を選択する理由
Why loops connecting a β-strand and an α-helix prefer particular dihedral angles and amino acids
Megumi Nakajima, George Chikenji (*Dept.Appl.Phys.,Nagoya Univ.*)

20045A New insight into ion transport mechanism of the Na+/H+ antiporter PaNhaP revealed by transition path shooting and Markov state model
Titouan Jaunet, Kei-ichi Okazaki (*Institute of molecular science (IMS) okazaki, japan*)

20046A Molecular dynamics simulations of the H.pylori FliG N-terminus
Dagnija Tupina[1,2], Alexander Krah[2], Chrystala I. Constantinidou[1], Peter J. Bond[2] ([1]*Univ. of Warwick*, [2]*A*STAR BII*)

20047A A large-scale structural and evolutionary analysis of protein loop regions
Lin Zhang[1], Hafumi Nishi[1,2] ([1]*Tohoku University*, [2]*Ochanomizu University*)

20048A* Ligand Docking Parallel Cascade Selection Molecular Dynamics (ld-PaCS-MD) の開発と応用
A Development of Ligand Docking Parallel Cascade Selection Molecular Dynamics (ld-PaCS MD) and its applications
Hayato Aida[1,2], Yasuteru Shigeta[2], Ryuhei Harada[2] ([1]*Bio., Degree Programs in Life and Earth Sci., Univ. of Tsukuba.*, [2]*CCS, Univ. of Tsukuba.*)

20049A* アスパラギン酸スキャニングを用いた赤外分光法によるタンパク質内局所的環境変化のマッピング解析
Mapping of the local environmental changes in proteins by FTIR spectroscopy with aspartic acid scanning
Masanori Hashimoto, Kota Katayama, Manish Singh, Yuji Furutani, Hideki Kandori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

20050A Computational Study of Temperature-Dependent Protein Glass Transition under Varying Solvent Compositions
Michelle Yaochai[1,2], Emmanuella Li[2], Joanna Ng[2], Peter J. Bond[2], Alexander Krah[2] ([1]*NUS High Sch.*, [2]*Bioinformatics Inst., A*STAR*)

20051A 計算モデリングを用いた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 複合体の包括的理解
Comprehensive understanding of SRK/SP11 protein complexes of Brassicaceae using computational modeling
Yoshitaka Moriwaki[1], Tohru Terada[1], Koji Murase[2], Seiji Takayama[2], Kentaro Shimizu[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, [2]*Appl. Biol. Chem., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

20052A Effect of the divalent cation for the activity of alcohol dehydrogenase from *Sulfolobus tokodaii*
Shuichiro Goda[1,2], Sho Takashima[2], Kosei Kajiyama[2], Yuka Nagano[2], Takuro Uchida[2], Hideaki Unno[2], Tomomitsu Hatakeyama[2] ([1]*Fuc. Sci. Eng., Soka Univ.*, [2]*Grad. Sch. Eng., Nagasaki Univ.*)

20053A 細菌機械受容チャネル MscL の G46D 変異体を用いた張力感受活性化機構の考察に関するシミュレーション研究
Computational Study Focusing on the Mechano-Gating in the Bacterial Mechanosensitive Channel MscL Using G46D GOF mutant
Yasuyuki Sawada[1], Ken'ichi Hashimoto[2], Hisashi Kawasaki[2], Masahiro Sokabe[3] ([1]*Dept. Nutrition Nagoya Univ. Economics Fac. Human Life Sci.*, [2]*Biotechnology Res Ctr, Univ Tokyo*, [3]*Mechanobiology Lab. Nagoya Univ. Grad. Sch. Med.*)

20054A* LI-cadherin 遺伝子上の SNP に伴う大腸がん転移リスク上昇の分子メカニズム
Molecular basis of increased risk of colorectal cancer metastasis caused by SNPs in LI-cadherin gene
Anna Yui[1], Chika Kikuchi[2], Shuichiro Goda[3], Takahiro Maruno[4], Susumu Uchiyama[4], Makoto Nakakido[1], Daisuke Kuroda[1,5], Satoru Nagatoishi[6], Osamu Arai[7], Hiroko Iwanari[8], Takao Hamakubo[9], Kouhei Tsumoto[1,2,6] ([1]*Dept. of Bioeng., Sch. of Eng., Univ. of Tokyo*, [2]*Dept. of Chem. Biotech., Sch. of Eng., Univ. of Tokyo*, [3]*Grad. Sch. of Sci. Eng., Soka Univ.*, [4]*Dept. of Biotech., Grad. Sch. of Eng., Osaka Univ.*, [5]*Med. Dev. Dev. Reg. Res. Center, Sch. of Eng., Univ. of Tokyo*, [6]*Inst. of Med. Sci., Univ. of Tokyo*, [7]*RCAST, Univ. of Tokyo*, [8]*Inst. of Immunol. Co., Ltd.*, [9]*Nippon Med. Sch.*)

20055A Aβ 産生抑制タンパク質 ILEI の活性中心の同定
Identification of the active center of the Aβ production suppressor protein ILEI
Emi Hibino[1,2], Masaki Nishimura[2] ([1]*Grad. Sch. Pharm. Sci., Nagoya Univ.*, [2]*Mol. Neuro., Shiga Univ. Med. Sci.*)

20056A GTP-チューブリンはどのようにして微小管の核を生成するか? (1) 直線型オリゴマーの形成
How do GTP-tubulins nucleate microtubules? (1)Formation of straight oligomers
Rie Ayukawa[1], Seigo Iwata[1], Hiroshi Imai[2,5], Shinji Kamimura[2], Masahito Hayashi[1], Kien Ngo[1], Itsushi Minoura[1], Seiichi Uchimura[1], Tsukasa Makino[1], Hideki Shigematsu[6], Ken Sekimoto[3], Benoit Gigant[4], Etsuko Muto[1] ([1]*RIKEN CBS*, [2]*Chuo Univ.*, [3]*Paris Univ.*, [4]*Paris-Saclay Univ.*, [5]*Osaka Univ.*, [6]*RIKEN BDR*)

20057A GTP-チューブリンはどのようにして微小管の核を生成するか? (2) オリゴマーのラテラルな相互作用
How do GTP-tubulins nucleate microtubules? (2)Lateral association of oligomers
Seigo Iwata[1], Rie Ayukawa[1], Hiroshi Imai[2,5], Shinji Kamimura[2], Ken Sekimoto[3], Benoit Gigant[4], Etsuko Muto[1] ([1]*CBS, RIKEN*, [2]*Chuo Univ.*, [3]*Paris Univ.*, [4]*Paris-Saclay Univ.*, [5]*Osaka Univ.*)

20058A クライオ電子顕微鏡を用いたシトクロム酸化酵素とシトクロム c の複合体構造解析
The structural analysis of cytochrome *c* oxidase complexed with cytochrome *c* using cryo-electron microscopy
Atsuhiro Shimada[1], Daisuke Kozai[2], Kouki Nishikawa[3,4], Yoshinori Fujiyoshi[3,4], Gyokucho Sho[1], Takumi Mizutani[1], Kazutoshi Tani[5] ([1]*Dept. Appl. Life Sci., Fac. Appl. Biol. Sci., Gifu Univ.*, [2]*Cell. Struct. Phys. Inst., Nagoya Univ.*, [3]*Adv. Res. Inst., Tokyo Med. Dent. Univ.*, [4]*CeSPIA Inc.*, [5]*Grad. Sch. Med., Mie Univ.*)

20059A 重み付きアンサンブル法による Pin1 異性化のパスサンプリング
Obtaining path ensemble of Pin1-catalyzed cis-trans isomerization by weighted ensemble simulation
Kei Moritsugu[1], Norifumi Yamamoto[2], Yasushige Yonezawa[3], Shin-ichi Tate[4], Hiroshi Fujisaki[5] ([1]*Yokohama City Univ.*, [2]*Chiba Tech.*, [3]*Kindai Univ.*, [4]*Hiroshima Univ.*, [5]*Nippon Med. Sch.*)

20060A 水素結合経由の J 値の定量的解析
Quantitative analysis of J value via hydrogen bonds
Hiroki Nakajima[1], Taiki Koizumi[1], Masaki Uuno[2], Masaki Mishima[1] ([1]*Grad.Sch.Sci., Univ,TokyoMetropolitan*, [2]*Grad.Sch.Sci,. Univ,Ibaraki*)

20061A Design of cyclic and linear peptides interacting with transition metal ions
Rikako Morishita, Atsuo Tamura (*Grad. Sch. Sci., Kobe Univ.*)

20062A 細胞壁を持たない細菌のチューブリンの解析
Analysis of bacterial tubulin in cell wall-less bacterium
Taishi Kasai[1], Yuhei Tahara[2], Makoto Miyata[2], Daisuke Shiomi[1] ([1]*Col. Sci., Rikkyo Univ.*, [2]*Grad. sch. Sci., Osaka City Univ.*)

20063A* コレステロールが膜貫通ペプチドの二量体化に与える影響に関する分子動力学的解析
Effect of cholesterol on the dimerization of transmembrane peptides analyzed by the 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.*)

20064A 残基間平均距離統計に基づく方法によるフラボヘモグロビンのフォールディング機構予測
Prediction of folding mechanism of flavohemoglobins using techniques based on inter -residue average residue distance statistics
Maho Osugi, Takeshi Kikuchi (*Dept. Bioinf. Col. Biosci. Ritsumeikan Univ.*)

20065A ドッキングシミュレーションによる Cyclin-dependent kinase-like 5 の基質タンパク質の同定
Identification of Cyclin-dependent kinase-like 5 substrate protein using docking simulation technique
Aya Takahara[1], Shoichi Katayama[2], Takako Kawano[2], Tetsuya Inazu[2], Takeshi Kikuchi[1] ([1]*Dept. Bioinf. Col. Biosci. Ritsumeikan Univ.*, [2]*Col. Pharm.Sci. Ritsumeikan Univ.*)

20066A 構造研究のためのタンパク質連結法の開発
Development of protein ligation techniques for structural studies
Takumi Suzuki (*Grad. Sch. Sci., Univ. TMU*)

20067A* ネガティブ染色電子顕微鏡法により明らかにされた繊毛ダイニンの新規構造
Novel isolated ciliary dynein structure revealed by negative stain EM
Yici Lei[1], Hiroshi Imai[1], Akira Fukunaga[1], Shinji Kamimura[2] ([1]*Dep. Biol. Sci., Grad. Sch. Of Sci., Osaka Univ.*, [2]*Dept. Biol. Sci., Chuo Univ.*, [3]*Dept. Life Sci., Prefect. Univ. Hiroshima*)

20068A カメレオンモデルの二面角ポテンシャルの改良による NtrC の構造転移の解明
Conformational transition of NtrC elucidated by the improvement of dihedral angle potential in chameleon model
Taisei Nagata, Masaki Sasai, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

20069A Expression and Purification of Intact Small Peptides through a Novel Calmodulin-Fusion Protein System
Hao Gu[1], Koki Onuma[1], Takasumi Kato[1], Hiroaki Ishida[2], Yasuhiro Kumaki[1], Takashi Tsukamoto[1,3], Takashi Kikukawa[1,3], Makoto Demura[1,3], Hans J. Vogel[2], Tomoyasu Aizawa[1,3] ([1]*Grad. Sci. Life Sci., Hokkaido univ.*, [2]*Dep. of Biol. Sci., Univ. of Calgary*, [3]*GI-CoRE, Hokkaido univ.*)

20070A RNA 結合タンパク質 FUS の液液相分離を制御するペプチドの探索
Search for peptides to control liquid-liquid phase separation of RNA binding protein FUS
Rika Chiba[1,2], Nanako Iwaki[1,3], Saori Kanbayashi[1], Keisuke Ikeda[4], Tomoshi Kameda[5], Kiyoto Kamagata[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*, [3]*Dep. Chem., Grad. Sch. Sci., Tohoku Univ.*, [4]*Sch. Pharm. Pharm. Sci., Univ. Toyama*, [5]*AIRC, AIST*)

20071A 天然変性タンパク質 LAF-1RGG ドメインの一分子蛍光分光測定による構造特性評価
Conformational properties of the intrinsically-disordered RGG domain of LAF-1 detected by single-molecule fluorescence spectroscopy
Michiko Kimura[1,2], Saya Nakano[1,2], Hiroto Takahashi[1], Hiroyuki Oikawa[1], Satoshi Takahashi[1] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*)

20072A Cryo-EM revealed unique and diverse binding schemes of the microtubule inner proteins at the inner junction region of cilia
Muneyoshi Ichikawa[1], Ahmad Khalifa[2], Daniel Dai[2], Shintaroh Kubo[3], Corbin Black[2], Katya Peri[2], Thomas McAlear[2], Simon Veyron[2], Shun-Kai Yang[2], Javier Vargas[2], Susanne Bechstedt[2], Jean-Francois Trempe[2], Khanh-Huy Bui[2] ([1]*NAIST*, [2]*McGill University*, [3]*Kyoto University*)

20073A 生きた細胞における DXT 法を用いた nAChR のリガンド依存的な分子内部運動の計測
Ligand-dependent intramolecular motion of nAChR in living cells detected by DXT
Koichiro Oishi[1], Yuri Nishino[1], Hiroshi Sekiguchi[2], Yasuhiro Kashino[1], Yuji C. Sasaki[3], Atsuo Miyazawa[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*JASRI*, [3]*Grad. Sch. Sci., The Univ Tokyo*)

20074A Characterization of properties of microtubule inner protein FAP85
Yoshitoki Shibao[1], Corbin Black[2], Muneyoshi Ichikawa[1], Junya Kirima[4], Kazuhiro Oiwa[3], Khanh-Huy Bui[2], Tomoya Tsukazaki[1] ([1]*NAIST*, [2]*McGill University*, [3]*NICT*, [4]*University of Hyogo*)

20075A Binding mode analysis of Hepatitis B virus X protein to DDB1 with Fluorescent based technology detecting Protein-Protein Interactions
Katsumi Omagari (*Department of Virology, Nagoya City University Graduate School of Medical Sciences*)

20076A 大腸菌フェリチン変異体の荷電状態に関する研究
A study on the charge states of Escherichia coli ferritin mutants
Takumi Kuwata, Daisuke Sato, Kazuo Fujiwara, Masamichi Ikeguchi (*Dept. of Biosci., Soka Univ*)

20077A* クライオ電子顕微鏡によるヒト PAC1 受容体の構造解析
Cryo-EM structure of the human PAC1 receptor coupled to an engineered heterotrimeric G protein
Kazuhiro Kobayashi[1], Wataru Shihoya[1], Tomohiro Nishizawa[1], Marie Ngako Kadji Francois[2], Junken Aoki[2], Asuka Inoue[2], Osamu Nureki[1] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Pharm. Sci., Univ. Tohoku*)

20078A Cryo-EM structure of *Thermus thermophilus* V/A-ATPase during the rotary catalysis
Atsuko Nakanishi[1,3], Jun-ichi Kishikawa[2,3], Kaoru Mitsuoka[1], Ken Yokoyama[3] ([1]*Res. Ctr. for UHVEM, Osaka Univ.*, [2]*Inst. for Protein Res., Osaka Univ.*, [3]*Faculty of Life Sci., Kyoto Sangyo Univ.*)

20079A タンパク質における連続する 3 つの残基で構成されるユニットの運動学的特性の解析
Analysis of the Kinematic Properties of Units Comprising Three Consecutive Residues in Proteins
Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

20080A Reconistitution of Cecytb-2 in Phospholipid Bilayer Nanodisc and Meaurments of its Ferric Reductase Activity
Hamed A. Abosharaf[1,2], Yuki Sakamoto[1], Mohammed El behery[1], Thoria Diab[2], Tarek M. Mohamed[2], Tetsunari Kimura[1], Motonari Tsubaki[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Fac. Sci., Tanta Univ.*)

20081A クライオ電子回折法による生体分子微小結晶の高分解能構造解析
High-resolution Structure Determination of Biomolecular Microcrystals by Cryo-Electron Diffraction
Kiyofumi Takaba, Koji Yonekura, Saori Maki-Yonekua (*SPring-8, RIKEN*)

20082A* 液―液相分離によって形成される多相液滴の作成
Multiphase droplet formed by liquid-liquid phase separation
Kanji Tomohara, Yoshihiro Minagawa, Hiroyuki Noji (*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

20083A データベースアノテーションに基づく液滴の分析
Analysis of liquid droplets based on database annotations
Mitsuteru Iwatsuka[1], Motonori Ota[1], Satoshi Fukuchi[2], Hiroto Anbo[2] ([1]*Nagoya university*, [2]*Maebashi Institute of Technology university*)

20084A 免疫阻害機能の異なるリッサウイルス P 蛋白質 C 末端ドメインの構造比較
Structural comparison of the C-terminal domain of functionally divergent lyssavirus P proteins
Aoi Sugiyama[1], Tomo Nomai[1], Xinxin Jiang[1], Miku Minami[1], Min Yao[1], Katsumi Maenaka[1], Naoto Ito[2], Paul Gooley[3], Gregory Moseley[4], Toyoyuki Ose[1,5] ([1]*Faculty of Advanced Life Sci., Hokkaido Univ.*, [2]*Faculty of Appl. Biol. Sci., Gifu Univ.*, [3]*School of Bio21 Mol. Sci. and Biotechnol., Univ. of Melbourne*, [4]*School of Biomed. Sci., Monash Univ.*, [5]*PRESTO, Japan Science and Technology Agency*)

20085A High resolution X-ray analysis reveals a stable structure around the catalytic amino acid Asp52 in lysozyme-sugar complex
Ichiro Tanaka[1,2], Ryota Nishinomiya[1] ([1]*Grad. Sch. Sci. & Eng., Ibaraki Univ.*, [2]*Frontier Ctr, Ibaraki Univ.*)

20086A シトクロム *c* が仲介する多段階電子伝達反応における呼吸鎖超複合体形成の機能的意義
Functional significance of formation of respiratory supercomplex for multiple electron transfer reaction mediated by cytochrome *c*
Wataru Sato, Peter Brzezinski (*Stockholm Univ. Fac. of Nat. Sci.*)

20087A* PaCS-MD/MSM を用いたタンパク質複合体の速度定数評価
Kinetic rate evaluation for protein complexes by PaCS-MD/MSM
Yoshiki Miyazawa, Phouc Duy Tran, Kazuhiro Takemura, Akio Kitao (*Grad. Sch. Life Sci Tech., Tokyo Tech*)

20088A How internal cavities destabilize a protein
Ryo Kitahara[1], Mengjun Xue[2], Takuro Wakamoto[3], Frans A.A. Mulder[4] ([1]*Pharm. Sci., Ritsumeikan Univ.*, [2]*Dep. Chem. Univ. Washington*, [3]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [4]*iNANO, Univ. Aarhus*)

20089A クライオ電子線トモグラフィー法からの糸状仮足中のアクチン繊維とファシンのサブトモグラム平均化
Subtomogram Averaging of F-Actin with Fascin in Filopodia by Cryo-Electron Tomography
Atsuko Nakanishi[1], Naoko Kajimura[1], Shun Kurita[2], Takuo Yasunaga[3], **Kaoru Mitsuoka**[1] ([1]*Res. Ctr. UVHEM, Osaka Univ.*, [2]*Grad. Sch. Eng., Osaka Univ.*, [3]*Grad. Sch. Comp. Sci. Syst. Eng., KIT*)

20090A Could the biogenic zinc oxide nanoparticles inhibit the ATPase activity of ABC transporters?
Aliaa M. Radwan[1,2], Mai M. El-Keiy[2], Tarek M. Mohamed[2], Tetsunari Kimura[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Fac. Sci., Tanta Univ.*)

20091A Cold adaptation and high thermal stability mechanism of glucokinase from psychrophilic bacteria are revealed by spin-labeling ESR
Akane Yato (*Grad. Sch. Adv Hea Sci., Univ. Saga*)

20092A エネルギー準位統計とペプチドの分子進化
Energy level statistics and molecular evolution of peptide
Masanori Yamanaka (*CST, Nihon Univ.*)

20093A ドーパミン制御タンパク質 MAO-B のミトコンドリア膜中でのダイナミクス
The dynamics of dopamine-regulated protein MAO-B in the mitochondrial membrane
Masaki Ottawa[1], Lisa Matsukura[1], Naoyuki Miyashita[1], Ryuichi Harada[2], Yuichi Kimura[1], Shozo Furumoto[3] ([1]*BOST, KINDAI Univ.*, [2]*Med. Tohoku Univ.*, [3]*CYRIC, Tohoku Univ.*)

20094A* 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[1,2], Hiroto Takahashi[1], Satoshi Takahashi[1], Kiyoto Kamagata[1] ([1]*IMRAM, Tohoku University*, [2]*Grad. Sch. Sci., Tohoku University*)

20095A Influence of disulfide-closed loop structures on the stability of alpha-helix
Yuki Yanagida, Masamichi Ikeguchi, Kiyomi Yoshida, Kazuo Fujiwara (*Dept.of Biosci., Soka Univ.*)

20096A CNT aptamers selection and strucuture study
Ting-Chieh Chu, Huanwen Han, Ichiro Yamashita (*Graduate School of Engineering, Osaka University*)

20097A 逆並行 β-シート中の隣接ストランド間の Cα 距離の解析
Analysis of Cα distances between adjacent strands in anti-parallel β-sheets
Hiromi Suzuki (*Sch. Agri., Meiji Univ.*)

20098A A method for producing recombinant cryptdin by enhancing inclusion body formation
Yuchi Song[1], Weiming Geng[1], Shaonan Yan[1], Wendian Yang[1], Yi Wang[1], Tomoyasu Aizawa[1,2] ([1]*Grad. Sch. of Life Sci, Hokkaido Univ.*, [2]*GI-CoRE, Hokkaido Univ.*)

20099A クライオ電顕データを用いた MD 力場の評価
Assessment of force-field accuracy using data of cryogenic electron microscopy
Tomotaka Oroguchi[1,2], Mao Oide[1,2], Taiki Wakabayashi[1,2], Masayoshi Nakasako[1,2] ([1]*Faclt. Sci. Tech., Keio Univ.*, [2]*RIKEN SPring-8 Center*)

20100A* TAT ロドプシン変異体に対する陽イオン結合の分光学的研究
Spectroscopic study of cation binding to a TAT rhodopsin mutant
Teppei Sugimoto, Kota Katayama, Hideki Kandori (*Nagoya institute of technology*)

20101A Structural changes of a-synuclein along the lipid-binding and oligomerization revealed by fluorescence lifetime measurements
Ko Sasada, Ryosuke Matsubara, Koichi Fujii, Tetsunari Kimura (*Kobe Univ., Grad. Sch. of Sci.*)

20102A* 単細胞緑藻由来の葉緑体 ATP 合成酵素完全複合体のワンステップ単離と制御機構の解析
One-step purification and functional analysis of the chloroplast ATP synthase complex
Kentaro Akiyama[1,2], Ken-ichi Wakabayashi[1,2], Toru Hisabori[1,2] ([1]*Grad. Sch. Life Science and Technology, Titech*, [2]*CLS, Titech*)

20103A フォトンファクトリーにおける生体高分子の X 線溶液散乱
Current Status of BioSAXS at the Photon Factory
Nobutaka Shimizu, Kento Yonezawa, Masatsuyo Takahashi, Keiko Yatabe, Yasuko Nagatani (*KEK, IMSS, PF*)

20104A 緩和モード解析を用いた NTL9 のシミュレーションデータの解析
Analysis of simulations of NTL9 using relaxation mode analysis
Ayori Mitsutake (*Dept. of Physics, Meiji Univ.*)

20105A Theoretical Studies of Association-Dissociation of Plastocyanin by Coarse Grain Simulation
Dian Fitrasari, M.S. Arwansyah, Helmia Jayyinunnisya, Kazutomo Kawaguchi, Hidemi Nagao (*Kanazawa University*)

20106A 生体分子構造における形状と機能の関係
Shape similarity and functional similarity in biomolecular structures
Hirofumi Suzuki[1], Takeshi Kawabata[2], Kei Yura[1], Genji Kurisu[2] ([1]*Waseda Univ.*, [2]*IPR, Osaka-univ.*)

20107A Pressure-induced acceleration of the cyanobacterial circadian clock
Keita Mitsuhashi[1], Rina Sakurai[2], Soichiro Kitazawa[2], Kazuki Terauchi[1], Ryo Kitahara[2] ([1]*Grad. Sch. Life Sci., Univ. Ritsumeikan*, [2]*Depart. Pharm., Univ. Ritsumeikan*)

20108A In-cell NMR analysis of an anticancer candidate compound against a chemokine-signaling protein FROUNT
Sosuke Yoshinaga[1], Takafumi Sato[1], Airi Higashi[1], Mitsuhiro Takeda[1], Yuya Terashima[2,3], Etsuko Toda[2,3,4], Kouji Matsushima[2,3], Hiroaki Terasawa[1] ([1]*Fac. Life Sci., Kumamoto Univ.*, [2]*Grad. Sch. Med., Univ. Tokyo*, [3]*RIBS, Tokyo Univ. Sci.*, [4]*Nippon Med. Sch.*)

20109A Intrinsically Disordered Protein Studied by Multi-scale Divide-and-conquer Molecular Dynamics Simulation
Hiromitsu Shimoyama[1], Yasushige Yonezawa[2] ([1]*Kitasato Univ.*, [2]*Kindai Univ.*)

20110A* Saframycin A 生合成関連蛋白質のクライオ電子顕微鏡単粒子解析
Cryo-EM study on saframycin A biosynthesis related protein
Kiichi Honda[1], Takashi Matsui[2], Ryoko Komatsu[3], Ryo Tanifuji[4], Hiroki Oguri[4], Takeshi Yokoyama[1], Yoshikazu Tanaka[1] ([1]*Laboratory of Applied Biological Molecular Science, Graduate School of Life Sciences, Tohoku University*, [2]*Laboratory of Biophysics, Department of Physics, School of Science, Kitasato University*, [3]*Department of Applied Chemistry, Graduate School of Engineering, Tokyo University of Agriculture*, [4]*Department of Chemistry School of Science The University of Tokyo*)

20111A A Singularity-Free Torsion Angle Potential for Coarse- Grained Molecular Dynamics Simulations
Cheng Tan[1], Jaewoon Jung[1,2], Chigusa Kobayashi[1], Yuji Sugita[1,2,3] ([1]*RIKEN Center for Computational Science*, [2]*RIKEN Cluster for Pioneering Research*, [3]*RIKEN Center for Biosystems Dynamics Research*)

20112A* クライオ電子顕微鏡単粒子解析による百日咳壊死毒の構造解析
Cryo-electron microscopy single particle analysis of pertussis dermonecrotic toxin
Atsushi Tsugita[1], Takashi Matsui[2], Yasuhiko Horiguchi[3], Takeshi Yokoyama[1], Yoshikazu Tanaka[1] ([1]*Laboratory of Applied Biological Molecular Science, Graduate School of Life Sciences, Tohoku University*, [2]*Laboratory of Biophysics, Department of Physics, School of Science, Kitasato University*, [3]*Department of Molecular Bacteriology, Research Institute for Microbial Diseases, Osaka University.*)

20113A Biflavonoids that inhibit ATPase and microtubule-gliding activities of mitotic kinesin Eg5
Tomisin H. Ogunwa[1], Sadakane Kei[1], Maruta Shinsaku[1], Miyanishi Takayuki[2] ([1]*Department of Bioinformatics, Graduate School of Engineering, Soka University, Hachioji, Japan*, [2]*Graduate School of Fisheries and Environmental Sciences, Nagasaki University, Nagasaki, Japan*)

20114A 分子動力学シミュレーションを用いた CDR-Grafting による合成 VHH における分子挙動の解析
Molecular dynamics analysis of structural effects of Grafting CDRs in synthetic VHHs
Seisho Kinoshita[1], Makoto Nakakido[1,2], Daisuke Kuroda[1,2], Jose M.M. Caaveiro[3], Kouhei Tsumoto[1,2,4] ([1]*Dept. of Bioeng., Sch. of Eng., Univ. of Tokyo*, [2]*Dept. of Chem. Biotech., Sch. of Eng., Univ. of Tokyo*, [3]*Grad. Sch. of Pharm. Sci., Kyushu Univ.*, [4]*Inst. of Med. Sci., Univ. of Tokyo*)

20115A* 転写コアクチベータ CBP の KIX ドメインと転写因子の相互作用を標的としたペプチド阻害剤の合理的設計
Rational design of the peptide inhibitor targeting the interaction of the KIX domain of CBP with transcriptional activators
Nao Sato[1], Shunji Suetaka[1], Yuuki Hayashi[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

20116A 分布推定アルゴリズムと勾配降下法最適化アルゴリズムによる単粒子解析初期モデル生成
Initial model generation in single particle analysis using Estimation of Distribution Algorithms and gradient descent optimization
Nobuya Mamizu[1,2], Takuo Yasunaga[1] ([1]*Grad. Sch. Comp. Sci., Kyushu Inst. Tech.*, [2]*SYSTEM IN FRONTIER INC.*)

20117A 粗視化ペプチドの安定構造探索に向けたアミノ酸間相互作用ポテンシャルの開発
Amino-Acid Pair Interaction Potentials for Coarse Grained Peptide Folding
Chieko Terashima, Yoshiaki Tanida, Hiroyuki Sato (*Fujitsu Laboratories Ltd.*)

20118A 環状ペプチド中の隣接プロリンに特徴的な異性化
Characteristic isomerization of two adjacent prolines in a cyclic peptide
Yoshiaki Tanida, Chieko Terashima, Hiroyuki Sato (*Fujitsu Labs.*)

20119A* マイコプラズマ・モービレのモーター構成タンパク質 MMOB1620 の SAXS による構造解析
Structural Analysis of MMOB1620, Component Protein of Mycoplasma mobile's Motor, by SAXS
Hiroki Sato[1], Hisashi Kudo[2,3], Yuuki Hayashi[3], Syunji Suetaka[3], Koji Ooka[4], Munehito Arai[3,4], Makoto Miyata[1,5] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Bioengineering center, Kobe Univ.*, [3]*Dept. Life Sci., Univ. Tokyo.*, [4]*Dept. Phys., Univ. Tokyo.*, [5]*OCARINA, Osaka City Univ.*)

20120A Multiscale Modeling Approach for Conformational Search of Macrocyclic Peptides
Hiroyuki Sato, Chieko Terashima, Yoshiaki Tanida (*Fujitsu Laboratories Ltd.*)

20121A 非リボソーム分子機械によるペプチド合成の静電的ラチェット機構
Electrostatic ratcheting mechanism of peptide synthesis by non-ribosomal molecular machine
Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

20122A Local Structural Similarity of Mononucleotide Binding Sites Around Different Chemical Groups in Ligands
Shota Kawakami[1], Hafumi Nishi[2,3], Kengo Kinoshita[1,2] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*Grad. Sch. Info. Sci., Tohoku Univ.*, [3]*Fac. Core. Res., Ochanomizu Univ.*)

20123A* Secondary structure transformation of artificially designed peptide nanofibers
Minami Kurokawa[1], Mika Hirose[2], Akihiro Kawamoto[2], Atsuo Tamura[1] ([1]*Grad. Sch. Sci., Univ. Kobe.*, [2]*IPR,Univ. Osaka.*)

20124A 分子クラウディング環境における光活性化アデニル酸シクラーゼの光反応
Crowding effect on reaction dynamics of photoactivated adenylate cyclase
Hiroto Murakami, Masahide Terazima, Yusuke Nakasone (*Grad. Sch. Sci., Univ. Kyoto*)

20125A 電子伝達系における複数のタンパク質複合体の複合体形成と構造安定性に関する理論的研究
Theoretical study on complex formation and conformational stability of multiple protein complexes in electron transport system
Rena Saito, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Comput. bio., Univ. Kanazawa*)

20126A 高速原子間力顕微鏡を用いたアミロイドβ線維の伸長および抗アミロイドβ抗体による線維伸長阻害の観察
HS-AFM observation of Amyloid β elongation and inhibition by antibodies
Shogo Miyajima[1], Maho Yagi-Utsumi[2], Takayuki Uchihashi[1,2], Koichi Kato[2] ([1]*Dept of Phys, Nagoya univ*, [2]*EXCELLS*)

20127A Bayesian inference and Iterative Boltzmann approach to coarse-grained local potential of disordered proteins
Azuki Mizutani, Shoji Takada, Giovanni B Brandani (*Grad. Sch. Sci, Univ. Kyoto*)

20128A NMR Studies on Cup s 7, an Novel Allergen from Cypress Pollen
Jingkang Zheng[1], Tomona Iizuka[1], Xiaoshaung Lu[1], Tomoyasu Aizawa[1,2] ([1]*Grad. Sci. Life Sci., Hokkaido univ.*, [2]*GI-CoRE Hokkaido univ.*)

20129A* アミノ酸溶媒中における芳香族アミノ酸の溶解度
Solubility of aromatic amino acids in amino acid solutions
Akira Nomoto, Suguru Nishinami, Kentaro Shiraki (*Pure and Appl. Sci, Univ. Tsukuba*)

20130A 経験ベイズ推定を用いた水の効果の最適化によるタンパク質デザイン
Protein design by optimization of role of water using empirical Bayes' estimation
Tomoei Takahashi[1], George Chikenji[2], Kei Tokita[1] ([1]*Grad. Sch. Inform. , Nagoya Univ.*, [2]*Grad. Sch. Eng. , Nagoya Univ.*)

20131A* 脱水に応答して繊維構造を可逆的に形成するクマムシ固有の天然変性タンパク質の解析
Reversible fiber formation of tardigrade-unique intrinsically disordered proteins upon dehydration stress
Akihiro Tanaka, Tomomi Nakano, Takekazu Kunieda (*Dept. of Biol. Sci., Grad. Sch. of Sci., Univ. of Tokyo*)

20132A* スピロプラズマのらせん反転機構
Helical reversal machinery of Spiroplasma
Yuya Sasajima[1], Takayuki Kato[2], Tomoko Miyata[3], Keiichi Namba[3,4,5], Makoto Miyata[1,6] ([1]*Grad. Sch. Sci., Osaka City Univ., Japan*, [2]*IPR., Osaka Univ., Japan*, [3]*Grad. Sch. Front. Biosci., Osaka Univ., Japan*, [4]*BDR & SPring-8 Center, Riken, Japan*, [5]*JEOL Yokogushi Res. Alliance. Lab. Osaka Univ., Japan*, [6]*OCARINA, Osaka City Univ., Japan*)

20133A* 多重平衡状態を持つ光スイッチング蛍光タンパク質「Kohinoor2.0」の開発と、細胞内小器官動態の超解像イメージングへの応用
Photoswitchable fluorescent protein with multiple equilibria states enables super-resolution imaging of intracellular dynamics
Ryohei Noma[1], Tethuichi Wazawa[1], Syusaku Uto[2], Kazunori Sugiura[1], Takeharu Nagai[1] ([1]*Nagai laboratory*, [2]*no affiliation*)

20134A シアノバクテリア由来光受容タンパク質 GAF ドメインの立体構造解析
Structural study of a GAF domain of photosensor protein from Cyanobacteria
Taiki Koizumi[1], Takahiro Aizu[1], Takayuki Nagae[3], Yuu Hirose[2], Masaki Mishima[1] ([1]*Grad. Sch Sci, Tokyo Metropolitan University*, [2]*Department of Environmental and Life Sciences, Toyohashi University of Technology*, [3]*Grad. Sch Eng, Univ.Nagoya*)

B. ヘム蛋白質・膜蛋白質・核酸結合蛋白質／B. Heme-, Membrane- & nucleic acid binding-protein

20135B ウシミトコンドリア呼吸鎖酸素還元酵素の 1.3Å 分解能構造が示唆する二量体化機構
The 1.3 Å resolution structure of bovine mitochondrial respiratory oxygen reductase suggests a dimerization mechanism
Kyoko Shinzawa-Itoh[1], Miki Hatanaka[1], Kazuya Fujita[2], Naomine Yano[1], Yumi Ogasawara[1], Jun Iwata[2], Eiki Yamashita[3], Tomitake Tsukihara[2,3], Shinya Yoshikawa[2], **Kazumasa Muramoto**[1] ([1]*Grad. Sch. Life Sci., Univ. Hyogo*, [2]*Sch. Sci., Univ. Hyogo*, [3]*IPR, Osaka Univ.*)

20136B ゲノム編集酵素の開発に向けたエングレイルドホメオドメインアレイの構造解析
Structural basis for an array of engrailed homeodomains toward the development of genome-editing enzymes
Tomoko Sunami, Yu Hirano, Taro Tamada, Hidetoshi Kono (*iQLS, QST*)

20137B ナノディスクに再構成されたイネキシン 6 ギャップ結合ヘミチャネルの構造
Structures of the Innexin-6 gap junction hemichannels in nanodiscs
Batuujin Burendei[1], Ruriko Shinozaki[2], Masakatsu Watanabe[3], Tohru Terada[4], Kazutoshi Tani[5], Yoshinori Fujiyoshi[6,7], **Atsunori Oshima**[2,8] ([1]*Sch. Sci., Nagoya Univ.*, [2]*Grad. Sch. Pharm. Sci., Nagoya Univ.*, [3]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [4]*III/GSII, Univ. Tokyo*, [5]*Grad. Sch. Med., Mie Univ.*, [6]*Adv. Res., TMDU*, [7]*CeSPIA, Inc.*, [8]*CeSPI, Nagoya Univ.*)

20138B* 分子動力学シミュレーションを用いた、オレキシン 2 受容体の動的性質の研究
Dynamics of Orexin 2 Receptor Using Molecular Dynamics Simulations
Shun Yokoi, Ayori Mitsutake (*Meiji University*)

20139B 酵母の DNA 複製開始機構の一分子観察に向けて
Toward single-molecule observation of yeast pre-replicative complex assembly and firing
Mayu Terakawa S., Tsuyoshi Terakawa (*Dep. Biophys, Grad. Sch. Sci., Kyoto Univ.*)

20140B* β 切断酵素と APP の生体膜中での相互作用と α 切断酵素の構造予測
Interaction Between beta-Secretase and APP in The Biological Membrane, and The Structure Prediction of The TM domain of alpha-Secretase
Kaori Yanagino, Naoyuki Miyashita (*Grad. Sch. BOST, KINDAI Univ.*)

20141B* マラリア原虫のトランスロコンである EXP2 ナノポアのチャネル電流計測
Channel current measurement of EXP2 nanopore as a translocon of the malaria parasite
Mitsuki Miyagi, Sotaro Takiguchi, Kazuaki Hakamada, Masafumi Yoda, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

20142B 四量体と二量体のヘモグロビン平衡混合物の構造の柔らかさの違いによる分離
Separation of tetramer-dimer mixtures mutant hemoglobin by structural flexibility
Shigenori Nagatomo[1], Kitagawa Teizo[2], Nagai Masako[3] ([1]*Dept. Chem., Univ. Tsukuba*, [2]*Grad. Sch.Life Sci., Univ. Hyogo*, [3]*Res. Center Micro-Nano Tech., Hosei Univ.*)

20143B Assembly of a trimeric autotransporter transmembrane domain assisted by BamA embedded into the nanodisc
Eriko Aoki, Kazuo Fujiwara, Masamichi Ikeguchi (*Dept. of Biosci., Soka Univ.*)

20144B ナノディスク再構成型ヘム ABC トランスポーターを用いた基質輸送機構の分光学的解析
Spectroscopic analysis of allocrite transport mechanism using nanodisc-reconstituted heme ABC transporter
Takuya Asada[1], Motonari Tsubaki[1], Yoshitsugu Shiro[2], Hiroshi Sugimoto[3], Tetsunari Kimura[1,4] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Grad. Sch. Life Sci. Univ. of Hyogo*, [3]*RIKEN SPring-8*, [4]*K-CONNEX*)

20145B 膜環境の違いがアルカン水酸化酵素の活性に与える影響について
An effect of membrane environment for the activity of alkane hydroxylase
Takaki Okamoto[1], Tomomi Kikuchi[2], Shingo Nagano[1], **Tomoya Hino**[1] ([1]*Grad. Sch. Eng., Tottori Univ.*, [2]*Grad. Sch. Sus. Sci., Tottori Univ.*)

20146B* Investigating the dissociation process of DBD-p53/DNA complex by PaCS-MD and MSM
Mohamed Marzouk Sobeh[1,2], Akio Kitao[1] ([1]*School of Life Science and Technology, Tokyo Institute of Technology, 2-12-1, Ookayama, Meguro-ku, Tokyo, 152-8550, Japan*, [2]*Physics Department, Faculty of Science, Ain Shams University, 11566, Cairo, Egypt*)

20147B Electrochemical studies of human neuroglobin and cytoglobin using nanostructured electrode
Yasuhiro Mie[1], Kyoka Takahashi[1], Itoga Yuka[2], Kenta Sueyoshi[2], Ryo Torii[2], Jingkai Shen[2], Takumi Tanaka[2], Hirofumi Tsujino[2], Taku Yamashita[3] ([1]*Bioproduction Res. Inst., AIST*, [2]*Grad. Sch. Pharm. Sci., Osaka Univ.*, [3]*Sch. Pharm., Mukogawa Women's Univ.*)

20148B スピンラベル ESR 分光法による HP1 の天然変性領域の動的構造解析： DNA 結合とリン酸化の影響
Structural dynamics of IDP region in heterochromatin protein HP1 by spin-labeling ESR: Effects of DNA binding and phosphorylation
Toshiaki Arata[1,5], Kazunobu Sato[4], Ena Hirai[4], Yuichi Mishima[5], Takeji Takui[4], Toru Kawakami[5], Hironobu Hojo[5], Risa Mutoh[6], Toshimichi Fujiwara[5], Makoto Miyata[1], Isao Suetake[2,3,5] ([1]*Dept. Biol., Grad. Sch. Sci., Osaka City Univ.*, [2]*Nakamura Gakuen Univ.*, [3]*Twin Research Center, Osaka Univ.*, [4]*Dept. Chem., Grad. Sch. Sci., Osaka City Univ.*, [5]*IPR, Osaka Univ.*, [6]*Dept. Phys., Fac. Sci.,Fukuoka Univ.*)

20149B Reactive Coarse-Grained Molecular Dynamics Simulation for the Functional Dynamics of Lambda Exonuclease
Toru Niina, Shoji Takada (*Grad. Sch. Sci. Kyoto Univ.*)

20150B マイクロ秒時間領域で形成される一酸化窒素還元酵素反応中間体の分光解析
Characterization of reaction intermediate formed in the microsecond time domain of the catalytic reaction of nitric oxide reductase
Takehiko Tosha[1], Hanae Takeda[1,2], Tetsunari Kimura[3], Masaki Horitani[4], Yoshitsugu Shiro[2] ([1]*RIKEN SPring-8*, [2]*Univ. of Hyogo*, [3]*Kobe Univ.*, [4]*Saga Univ.*)

20151B PyDISH: Database and analysis tools for heme porphyrin distortion in heme proteins
Yu Takano[1], Hiroko X. Kondo[1,2,3], Yusuke Kanematsu[1,4], Gen Masumoto[5] ([1]*Grad. Sch. Info. Sci. Hiroshima City Univ.*, [2]*Faculty of Eng. Kitami Inst. Tech.*, [3]*RIKEN BDR*, [4]*Grad. Sch. Adv. Sci. Eng. Hiroshima Univ.*, [5]*RIKEN ISC*)

20152B Transient binding and non-rotational coupled motion of p53 revealed by sub-millisecond resolved single-molecule fluorescence tracking
Dwiky Rendra Graha Subekti[1,2], Satoshi Takahashi[1,2], Kiyoto Kamagata[1,2] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Sci. Tohoku Univ.*)

20153B リン脂質二重膜ナノディスクへの再構成に伴うヒト Steap3 の三価鉄還元酵素活性の増強
Enhancement of ferric reductase activity of human Steap3 upon reconstitution into phospholipid bilayer nanodisc
Ayane Nishi[1], Akito Nakata[1], Fusako Takeuchi[2], Tetsunari Kimura[1], **Motonari Tsubaki**[1] ([1]*Dept. of Chem., Grad. Sch. Sci., Kobe Univ.*, [2]*IPHE, Kobe Univ.*)

20154B 分子動力学シミュレーションによって明らかになった SLC26A9 の塩素イオン輸送における細胞質ドメインの役割
Role of the cytoplasmic domains of SLC26A9 in chloride ion transport revealed by the molecular dynamics simulations
Satoshi Omori[1], Yuya Hanazono[2], Hafumi Nishi[1,3], Kengo Kinoshita[1,4,5] ([1]*GSIS, Tohoku Univ.*, [2]*Inst. for Quantum Life Sci., QST*, [3]*Faculty of Core Res., Ochanomizu Univ.*, [4]*ToMMo, Tohoku Univ.*, [5]*Inst. of Dev. Aging and Cancer, Tohoku Univ.*)

20155B Time-resolved spectroscopic measurements on the transport dynamics of ABC transporter
Tetsunari Kimura[1,2], Sae Hayashi[1], Yuka Ikemoto[3], Yoshitsugu Shiro[4], Hiroshi Sugimoto[2] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*RIKEN, SPring-8*, [3]*JASRI*, [4]*Grad. Sch. Sci., Univ. Hyogo*)

20156B 大腸菌 UvrD C 末端 40 アミノ酸欠損変異体の DNA 巻き戻しダイナミクス
DNA-unwinding dynamics of *Escherichia coli* UvrD lacking the C-terminal 40 amino acids
Hiroaki Yokota (*Grad. Sch. Creation New Photon. Indust.*)

20157B 高速原子間力顕微鏡によるタンパク質膜輸送装置 Sec の動態観察
Observation of Substrate Binding Sec Translocon and Structural Change of SecA with HS-AFM
Wataru Nagaike[1], Takamitsu Haruyama[2], Tomoya Tsukazaki[2], Takayuki Uchihashi[1,3] ([1]*Dept of phys, Nagoya univ*, [2]*NAIST*, [3]*EXCELLS*)

20158B Structure of the voltage-dependent potassium channel (hERG) using cryo-electron microscopy
Tatsuki Asai[1], Kano Suzuki[1], Naruhiko Adachi[2], Masato Kawasaki[2], Toshio Moriya[2], Toshiya Senda[2], Satoshi Ogasawara[1], Takeshi Murata[1] ([1]*Grad. Sch. Sci., Univ. Chiba*, [2]*KEK, Tsukuba*)

C. 核酸:構造・物性・相互作用・複合体／C. Nucleic acid

20159C 状態遷移機械を実装する多段階 DNA コンピューティング反応の最適化
Optimization of the multi-step DNA computing reaction that implements a state machine
Shuntaro Sato[1], Masayuki Yamamura[2], Ken Komiya[2] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Sch. Comp., Tokyo Inst. Tech.*)

20160C 演題取り消し

20161C* DNA のメチル化パターン依存的な構造動態の解析
Structural Dynamics of DNA Depending on Methylation-Patterns
Takeru Kameda[1,2], Miho M. Suzuki[3], Akinori Awazu[4], Yuichi Togashi[2,4] ([1]*Graduate School of Science, 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.*)

20162C クロマチンドメインのエントロピー駆動相分離による染色体コンパートメント形成
Entropic phase separation of chromatin domains to form chromosome compartments
Shin Fujishiro, Masaki Sasai (*Grad. Sch. Appl. Phys., Nagoya Univ.*)

20163C* 分子動力学計算による p53-C 末端部位の DNA 結合機構の解明
DNA binding mechanisms of the p53 C-terminal domain elucidated by MD simulation
Yuta Taira, Duy Tran, Akio Kitao (*Titech*)

20164C DNA curtain assay of nucleosome repositioning and collisions induced by translocases
Fritz Nagae, Shoji Takada, Tsuyoshi Terakawa (*Department of Biophysics, Graduate School of Science, Kyoto University*)

20165C 核膜近傍におけるクロマチン構造形成と RNA 輸送モデルの構築
Model construction of chromatin structure formation and RNA transport near the nuclear membrane
Nozomu Imai, Shin Fujishiro, Masaki Sasai (*Dept. Appl. Phys., Nagoya Univ.*)

20166C ArsInsC 配列及び DNA 反復配列の物理的特性・機能性解析
Analysis of physical properties and functionalities of ArsInsC and DNA repeat sequences
Tappei Oda, Masashi Fujii, Naoaki Sakamoto, Akinori Awazu (*Dept. of math. and life sci. Hiroshima Univ.*)

20167C* 並列的な自己集合を基盤とした DNA 演算のナノポアデコーディング
Nanopore decoding for DNA computing based on parallel self-assembly
Sotaro Takiguchi, Ryuji Kawano (*Department of Biotechnology of Life Science, Tokyo University of Agriculture and Technology*)

20168C Local chromatin motion, chromatin quantity and nuclear volume
Shiori Iida[1], Yuji Itoh[2], Kayo Hibino[1,2], Kazuhiro Maeshima[1,2] ([1]*Dept. of Genetics, Sch. of Life Sci., SOKENDAI*, [2]*Genome Dynamics Lab., Natl. Inst. of Genetics*)

20169C* 分子動力学シミュレーションによる転写開始複合体の全原子構造モデリング
Modeling Atomistic Structure of Transcription Initiation Complex with DNA Bubble by Molecular Dynamics Simulation
Genki Shino, Shoji Takada (*Dept. of Biophys., Div. of Bio. Sci., Grad. Sch. of Sci., Kyoto Univ.*)

20170C Toward the construction of artificial organelles with controllability based on liquid-liquid phase separation of DNA nanostructures
Yusuke Sato (*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*)

20171C* DNA によるミクロ相分離 droplet の安定化と新しい人工細胞系の検討
Stabilization of micro phase-separated droplet and examination of new artificial cell system
Moe Yabuta, Yoshihiro Minagawa, Hiroyuki Noji (*Department of Applied Chemistry, Graduate School of Engineering, University of Tokyo*)

20172C* Large scale simulation of DNA hydrogel
Marcos Masukawa[1], Masahiro Takinoue[1,2] ([1]*Tokyo Inst. of Tech., Dept. of Comp. Sci., Sch. of Artif. Intel.*, [2]*Tokyo Inst. of Tech., Dept. of Comput. Intel. and Syst. Sci.*)

D. 電子状態／D. Electronic state

20173D 銅アミン酸化酵素のプロトン化状態についての QM/MM 解析
QM/MM study for the protonation states of copper amine oxidase
Mitsuo Shoji[1,2], Takeshi Murakawa[3], Yasuteru Shigeta[1], Hideyuki Hayashi[3], Toshihide Okajima[3,4] ([1]*Univ. Tsukuba*, [2]*JST-PRESTO*, [3]*Osaka Medical College*, [4]*Osaka Univ.*)

E. 水・水和・電解質／E. Water, Hydration & Electrolyte

20174E Application of a Deep-Learning Technique to Predict the Hydration Structure around Proteins
Kosuke Kawama[1], Takashi Yoshidome[1], Mitsunori Ikeguchi[2,3], Masateru Ohta[2] ([1]*Dep. of Appl. Phys., Tohoku Univ.*, [2]*RIKEN*, [3]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

20175E リガンド結合サイトにおける水和の包括的解析：3D-RISM 理論アプローチ
Comprehensive Analysis of the Hydration of Small Molecule Binding Sites in Ligand-Free Protein Structures: 3D-RISM Approach
Takashi Yoshidome[1], Mitsunori Ikeguchi[2,3], Masateru Ohta[2] ([1]*Dep. of Appl. Phys., Tohoku Univ.*, [2]*RIKEN*, [3]*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

20176E Analysis of urea effect for binding free energy of lysozyme-$(GlcNac)_3$
Simon Hikiri, Nobuyuki Matubayasi (*Grad. Sch. Eng. Sci., Osaka Univ.*)

20177E Simulation-based machine-learning approach for the water dynamics
Taku Muzukami[1], Viet Cuong Nguyen[3], Hieu Chi Dam[2] ([1]*Materials Science, JAIST*, [2]*Knowledge Science, JAIST*, [3]*HPC systems Inc*)

20178E* MED26 による TAF7 と EAF1 認識における多様な結合様式に関する分子動力学研究
Molecular dynamics study on the multiple binding modes of MED26 torecognize EAF1 and TAF7
Satoshi Goto[1], Kota Kasahara[2], Hidehisa Takahashi[3], Hidehisa Takahashi[2] ([1]*Grad. Sch., Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Med., Yokohama City Univ.*)

20179E ヌクレオチド三リン酸の結合による細胞混雑中の蛋白質間相互作用の減少
Reduced protein-protein interactions in the cellular crowding with binding of nucleoside triphosphates
Isseki Yu[1], Michael Feig[2], Yuji Sugita[3] ([1]*Maebashi Institute of Technology*, [2]*Michigan State University*, [3]*RIKEN Theoretical Molecular Science Lab.*)

20180E 異なる配列と構造のペプチド周囲の水和ダイナミクスを MD シミュレーションで明らかにする
MD simulations reveal hydration dynamics around peptides with different sequences and structures
Takuya Takahashi[1], Shingo Nobunaga[1], Takuya Azami[2], Ryoi Ashida[2], Takuya Fujisawa[2], Kota Kasahara[1] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch., Life Sci., Ritsumeikan Univ.*)

20181E 分子動力学法を用いたポリグルタミン酸周囲の水和ダイナミクス解析
Analysis of hydration dynamics around polyglutamic acid using molecular dynamics method
Takuya Fujisawa[1], Takuya Takahashi[2], Kota Kasahara[2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

F. 分子遺伝・遺伝情報・制御・発生・分化／F. Molecular genetics & Development

20182F Loop extrusion of chromatin at surfaces modulates the growth dynamics of transcriptional condensates
Tetsuya Yamamoto[1,2], Helmut Schiessel[3] ([1]*Institute for Chemical Reaction Design and Discovery, Hokkaido University*, [2]*PRESTO, JST*, [3]*Instituut-Lorentz for theoretical physics, Universiteit Leiden*)

20183F* 細胞性粘菌の脱分化過程における細胞質 pH の測定
Measurement of cytosolic pH changes during dedifferentiation of *Dictyostelium* cells
Tomomi Usui[1], Yusuke Morimoto[2] ([1]*Dept. Biosci. Bioinfo., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*Dept. Phys. and Info. Tech., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*)

20184F 合成遺伝子回路における細胞間相互作用依存的な発現と分化多能性
Cell-cell interaction-dependent expression of a synthetic genetic circuit and its relevance to pluripotency
Kei Ikemori[1], Yuichi Wakamoto[2] ([1]*Col. of Art. & Sci., Univ. Tokyo*, [2]*Grad. Sch. of Arts. & Sci., Univ. Tokyo*)

G. 筋肉・分子モーター／G. Muscle & Molecular motor

20185G 小胞輸送を担う分子モーターの分子数とダイニン阻害剤の影響
Effect of the dynein inhibitor dynarrestin on the number of motor proteins transporting synaptic cargos
Kumiko Hayashi[1,3], Miyamoto Miki[1], Shinsuke Niwa[2] ([1]*Grad. Sch. Eng., Tohoku Univ.*, [2]*FIRS, Tohoku Univ.*, [3]*JST, PRESTO*)

20186G X 線繊維回折解析による真核生物鞭毛軸糸の Ca^{2+}濃度依存的らせん対称性変化
[Ca^{2+}]-dependent changes in the helical symmetry of *Chlamydomonas* and *Ciona* flagellar axonemes revealed by X-ray fiber diffraction
Kazuhiro Oiwa[1], Kenta Ishibashi[1,2], Kogiku Shiba[3], Kazuo Inaba[3], Hiroyuki Iwamoto[4], Hitoshi Sakakibara[1] ([1]*Nat. Inst.Info.Commun.Technol*, [2]*Osaka Univ. CiNet*, [3]*Shimoda Marine Res. Cent. Univ. Tsukuba*, [4]*JASRI, SPring-8*)

20187G KIF1A/UNC-104 によるシナプス小胞前駆体輸送の数理モデル 2
Mathematical modeling of synaptic vesicle precursor transport by KIF1A/UNC- 104 2
Ryo Sasaki[1], Ryota Shinagawa[1], Kimiko Nagino[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*)

20188G Computer simulation of molecular shuttles driven by biomolecular motors in external force field
Sweet May[1], Takahiro Nitta[1,2] ([1]*Electronic and Information Systems Engineering Division, Faculty of Engineering, Gifu University*, [2]*Applied Physics Course,Faculty of Engineering, Gifu Univerisity*)

20189G The Impact of Defective Motors on Biosensor Integrated with Actin Filaments and Myosin
Samuel Macharia Kang'iri[1], Takahiro Nitta[1,2] ([1]*ELECTRONICS AND INFORMATION SYSTEMS ENGINEERING DIVISION, FACULTY OF ENGINEERING, GIFU UNIVERSITY*, [2]*APPLIED PHYSICS COURSE, FACULTY OF ENGINEERING, GIFU UNIVERSITY*)

20190G* キネシン分子の空間配置が輸送複合体の運動に与える影響の評価
Molecular layout of kinesin affects the collective movement of DNA origami-based transport complex
Kodai Fukumoto[1], Yuya Miyazono[2], Hisashi Tadakuma[3], Yoshie Harada[1] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*, [3]*SLST, ShanghaiTech Univ.*)

20191G キネシン・ダイニンによる軸索輸送速度の極値統計解析
Extreme value analysis of axonal transport velocity of kinesins and dyneins
Takuma Naoi[1], Kimiko Nagino[1], Kazuo Sasaki[1], Shinsuke Niwa[2], Kumiko Hayashi[1,3] ([1]*Dep. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*, [2]*FRIS, Tohoku Univ.*, [3]*JST, PRESTO*)

20192G 外眼筋の X 線回折像に対する BDM の効果
Effect of BDM on the structure of extraocular muscle revealed by x-ray diffraction
Maki Yamaguchi[1], Tohru Kurihara[1], Naoya Nakahara[1], Tetsuo Ohno[2], Toshiko Yamazawa[1], Hideki Yamauchi[1], Kazuhiro Hirano[1], Takuhiro Kawahara[1], Shigeru Takemori[1] ([1]*Dept. Mol.Physiol., The Jikei Univ. Sch. Med.*, [2]*Sports Med., Teikyo Heisei Univ.*)

20193G 1 分子・多分子実験から迫る、心機能に特化した心筋ミオシンの性質
Molecular properties of single cardiac myosin adapted for heart functions revealed by single- and multi-molecule approaches
Yongtae Hwang[1], Takumi Washio[2,3], Toshiaki Hisada[2], Hideo Higuchi[1], Motoshi Kaya[1] ([1]*Department of Physics, The University of Tokyo*, [2]*Future Center Initiative, The University of Tokyo*, [3]*UT-Heart Inc.*)

20194G ウシミトコンドリア由来 ATP 合成酵素の内在性阻害因子 IF_1 の 阻害機構解明
Elucidation of inhibition mechanism by IF_1, a natural inhibitor protein for bovine mitochondrial ATP synthase
Ryohei Kobayashi, Sougo Mori, Hiroshi Ueno, Hiroyuki Noji (*Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

20195G The N-terminal β-strand of single-headed kinesin-1 is involved in the off-axis force-generation and resultant rotation pitch
Masahiko Yamagishi[1], Shoko Fujimura[2], Mitsuhiro Sugawa[1], Takayuki Nishizaka[2], Junichiro Yajima[1] ([1]*Dept. Life Sci., Grad. Arts & Sci., Univ. Tokyo*, [2]*Dept. Physics, Gakushuin Univ.*)

20196G 心筋サルコメアにおける Fhod3 と cMyBP-C の同定
Identification of Fhod3 and cMyBP-C in cardiac sarcomere
Wataru Kedouin[1], Riho Takiiwa[1], Nao Shimojo[1], Ryu Takeya[2], Takuo Yasunaga[1] ([1]*Kyushu Inst. of Tech.*, [2]*Univ.of Miyazaki*)

20197G キネシンと微小管による印刷可能な人工筋肉のコンピュータシミュレーション
Computer simulation of printable artificial muscles composed of engineered kinesins and microtubules
Yurino Aoyama[1], Yuichi Hiratsuka[2], Takahiro Nitta[3] ([1]*Grad. Sch. Appl. Math. Phys., Gifu Univ.*, [2]*Sch. Materials Sci., JAIST*, [3]*Appl. Phys. Course, Faculty of Eng., Gifu Univ.*)

20198G ウニ胚形態形成の細胞骨格観察に基づくモデル化
Modeling of sea urchin gastrulation based on cytoskeleton imaging
Kaichi Watanabe[1], Yuta Kurose[2], Yuhei Yasui[1], Naoaki Sakamoto[1], Akinori Awazu[1] ([1]*Grad. Sch. of Integrated Sciences for Life, Univ. Hiroshima*, [2]*Grad. Sch. Sci, Univ. Hiroshima*)

20199G ATP 合成酵素の c リングの回転は c サブユニットでのプロトンの受け取りと放出および a サブユニットとの静電相互作用が協調して引き起こされる
Cooperation of proton release/uptake and electrostatic interaction between a subunit and c subunit drive c-ring rotation in ATP synthase
Noriyo Mitome[1,2,3], Shintaroh Kubo[4], Sumie Ohta[2], Hikaru Takashima[3], Yuto Shigefuji[3], Toru Niina[4], Shoji Takada[4] ([1]*Fac. of Educ., Tokoha Univ.*, [2]*Dept. of Chem. and Biochem., Natn. Inst. of Tech., Numazu coll.*, [3]*Dept. of Chem. and Bio. Engin., Natn. Inst. of Tech., Ube coll.*, [4]*Dept. of Biophys., Grad. School of Sci., Kyoto Univ.*)

20200G Performance of step-finding algorithm based on the Schwarz Information Criterion depends on noise and data points per dwell-time

Monique Honsa[1,2], Kimitoshi Takeda[2], Akihiro Otomo[2,3], Hanjin Liu[4], Tomohiro Shima[4], **Ryota Iino**[2,3] ([1]*LMU Munich*, [2]*IMS*, [3]*SOKENDAI*, [4]*U Tokyo*)

20201G 自由エネルギーランドスケープのスイッチングとパワーストローク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 and power stroke

Kaima Matsuda, Masaki Sasai, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya. Univ.*)

20202G 体温に温めた心筋細胞に備わる収縮リズム恒常性

Contraction Rhythm Homeostasis in cardiomyocytes warmed to body temperature

Seine A. Shintani (*Dep. of Biomedical Sci., College of Life and Health Sci., Chubu Univ.*)

20203G 電子顕微鏡構造解析により明らかにされた細胞質ダイニンの休止状態の解除メカニズム

Release mechanism of the shutdown state of cytoplasmic dynein revealed by electron microscopy

Kazuki Iwasaki[1], Yui Kurume[1], Hiroshi Imai[1], Shinji Kamimura[2], Rieko Shimo-kon[1], Ryosuke Yamamoto[1], Takahide Kon[1] ([1]*Grad. Sch. Sci., Osaka Univ*, [2]*Dept.Biol.Sci.,huo Univ.*)

20204G 動く幽霊~高度好塩菌ハロフェラックス・ボルカニ~

Motile ghosts of the halophilic archaeon, Haloferax volcanii

Yoshiaki Kinosita[1,2], Richard Berry[2] ([1]*Molecular Physiology Lab., RIKEN*, [2]*Department of Physics, University of Oxford*)

20205G 汎用 3 次元モデリングソフトウェア Blender を利用したタンパク質超分子構造の動的性質の理解

Understanding Supermolecular Structure and Dynamic Property of Proteins using a general purpose 3D Graphics Modeling Software Blender

Yutaka Ueno[1], Kaoru Katou[1], Akira Kakugo[3], Kento Matsuda[3], Akihiko Konagaya[2] ([1]*AIST Tokyo*, [2]*Tokyo Tech., Dept. of Computer Scinence*, [3]*Hokkaido Univ., Graduate School of Chemical Science and Engineering*)

20206G NMR による海洋性ビブリオ菌べん毛モーターの回転方向を制御する回転子タンパク質 FliG の構造変化の解析

NMR analysis of the conformational change in FliG that switches the rotational direction of the flagellar motor in marine bacterium *Vibrio*

Tatsuro Nishikino[1], Seiji Kojima[2], Michio Homma[2], Yohei Miyanoiri[1] ([1]*Inst. for Protein res., Osaka Univ.*, [2]*Div. Biol. Sci. Grad. Sch. Sci., Nagoya Univ.*)

20207G* Multiple step photo regulation of mitotic kinesin Eg5 using a novel photochromic Inhibitor composed of Spiropyran and azobenzene

Islam Md Alrazi, Kei Sadakane, Happy Ogunwa Tomisin, Shinsaku Maruta (*Soka University, Graduate School of Engineering, Department of Bioinformatics*)

20208G Modeling of condensin hinge/DNA structure by molecular dynamics simulations guided by atomic force microscopy

Hiroki Koide[1], Noriyuki Kodera[2], Shveta Bisht[3], Christian Haering[3], Shoji Takada[1], Tsuyoshi Terakawa[1] ([1]*Department of Biophysics, Graduate School of Science, Kyoto University*, [2]*Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*, [3]*Cell Biology and Biophysics Unit, Structural and Computational Biology Unit, European Molecular Biology Laboratory (EMBL)*)

20209G キネシン 1 二量体の前頭部における微小管からの解離抑制の直接観察

Direct observation of the suppression of the leading head of kinesin-1 dimer from detachment from microtubule

Kohei Matsuzaki[1,2], Michio Tomishige[1] ([1]*Dept. Phys., Col. Sci. Eng., Aoyama Gakuin Univ.*,, [2]*Dept. Appl. Phys., Grad. Sch. Eng., Univ.Tokyo*)

20210G ミオシン VI の歩行運動に対するランドスケープ描像

A landscape-based view on the stepping movement 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.*)

20211G 微小管とキネシンの結合におけるチューブリン C 末端の役割
Role of C-terminal tail of tubulin in microtubule-kinesin binding
Yuta Taguchi, Yukinobu Mizuhara, Jun Ohnuki, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Waseda Univ.*)

20212G* べん毛モーター固定子の協働的な集合によるトルクの自律的制御
Cooperative stator assembly of bacterial flagellar motor for autonomous torque regulation
Kenta Ito, Shuichi Nakamura, Shoichi Toyabe (*Grad. Eng., Tohoku Univ.*)

20213G 光てこによる *Volvox*1 個体が生じる推進力の直接測定
Direct force measurement of a swimming *Volvox* spheroid by a high-speed optical lever system
Katsuya Shimabukuro[1], Kosaku Horinaga[1], Kazumo Wakabayashi[1], Hikaru Emoto[1], Noriko Ueki[2], Ken-ichi Wakabayashi[3], Noriyo Mitome[1,4] ([1]*Chem. Bio. Eng., NIT Ube College*, [2]*Sci. Res. Cent., Hosei Univ*, [3]*CLS, Tokyo Tech*, [4]*Tokoha Univ.*)

20214G 高速イメージングで明らかになった遊泳するボルボックスの速度周期性
Periodic fluctuations detected in the swimming velocity of a *Volvox carteri* spheroid by high speed imaging
Naoki Uemura, Tatsuya Suehiro, Midori Nosaka, Katsuya Shimabukuro (*Chem. Bio. Eng., NIT Ube College*)

20215G* 好熱菌由来 F_1-ATPase の完全な化学力学共役は至適生育温度において破れる
The perfect mechanochemical coupling of thermophilic F_1-ATPase breaks at the optimum growth temperature
Tomoaki Okaniwa[1], Yohei Nakayama[1,2], Eiro Muneyuki[1] ([1]*Grad. Sch. Sci. Eng.*, [2]*Grad. Sch. Eng.*)

20216G ATP 加水分解を選択的に抑制する F_1-ATPase の速度論的制御機構
Kinetic ratchet mechanism of F_1-ATPase selectively suppresses hydrolysis of ATP
Yohei Nakayama, Shoichi Toyabe (*Grad. Sch. Eng., Tohoku Univ.*)

20217G Mixed motility assay を用いたフォトクロミック Eg5 阻害剤の Eg5 阻害機構の解析
Analyze inhibitory mechanism of kinesin Eg5 with photochromic Eg5 inhibitor using mixed-motility assay
Kei Sadakane[1], MD Alrazi Islam[2], Happy Ogunwa Tomisin[2], Shinsaku Maruta[1,2] ([1]*Sci. & Eng., Soka Univ.*, [2]*Grad. Sch. Eng., Soka Univ.*)

20218G DNA ナノチューブ上に構築されたダイニン線形アレイの集団運動性
Collective motility of dynein linear arrays built on DNA nanotubes
Ryota Ibusuki[1], Misaki Shiraga[2], Akane Furuta[1], Maki Yoshio[1], Hiroaki Kojima[1], Kazuhiro Oiwa[1,2], Ken'ya Furuta[1] ([1]*Adv. ICR. Res. Ins., NICT. Kobe*, [2]*Grad. Sch. Sci., Univ. Hyogo*)

20219G Increasing speed of single-molecule kinesin movement in vitro
Keitaro Shibata[1], Misaki Sagawa[2], Hiroaki Kojima[1], Ken'ya Furuta[1] ([1]*Adv. ICT. Res. Ins., NICT*, [2]*Grad. Sch. Sci., Univ. Hyogo*)

20220G Single-molecule analysis of artificial kinesin-1 dimers and trimers with different linker lengths
Kimitoshi Takeda[1], Monique Honsa[1,2], Akihiko Nakamura[3], Jun Ando[4], Ryota Iino[1,5] ([1]*Institute for Molecular Science*, [2]*LMU Munich*, [3]*Dep. Appl. Life Sci. Agr. Shizuoka Univ*, [4]*RIKEN*, [5]*SOKENDAI*)

20221G* バーチャル電極上の電場によるキネシンと微小管の駆動システムの制御
Controlling fundamental functions of the kinesin-microtubule by the electrical field on the virtual cathode
Kenta Hatazawa[1], Ryuzo Kawamura[2], Takayuki Hoshino[1] ([1]*Department of Mechanical Science and Engineering, Science and Technology, Hirosaki Univ.*, [2]*Division of Strangic Research and Development, Graduate School of Science and Engineering, Saitama Univ.*)

20222G* ダイナクチンサイドアームのコンフォメーション多様性
Conformational diversity of dynactin sidearm
Kei Saito[1], Takuya Kobayashi[2], Takashi Murayama[2], Yoko Toyoshima[1] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*Dept. of Pharmacology, Juntendo Univ. Sch. of Med.*)

20223G Constructing a simplified axoneme-like system using *Chlamydomonas* outer arm dynein and DNA nanotubes
Akane Furuta[1,2], Yuka Matsuda[3], Ryota Ibusuki[1], Misaki Sagawa[3], Kazuhiro Oiwa[1,3], Hiroaki Kojima[1], Ken'ya Furuta[1] ([1]*NICT*, [2]*JSPS*, [3]*University of Hyogo*)

20224G V/A-ATPase の膜内在性ドメイン V_o のプロトン漏洩防止機構
Mechanical inhibition of isolated Vo from V/A-ATPase for proton conductance
Jun-ichi Kishikawa[1,2], Atsuko Nakanishi[3], Aya Furuta[2], Takayuki Kato[1], Keiichi Namba[4], Masatada Tamakoshi[5], Kaoru Mitsuoka[2], Ken Yokoyama[2] ([1]*Inst. Prot. Res., Osaka Univ.*, [2]*Dept. Mol. Biosci., Kyoto Sangyo Univ.*, [3]*Res. Ctr. UHVEM., Osaka Univ.*, [4]*Grad. Sch. Frontier. Biosci., Osaka Univ.*, [5]*Dept. Mol. Biol., Tokyo Univ. Pharm. Life Sci.*)

20225G* FliL は低負荷条件下で大腸菌べん毛モーターの回転を支援する
FliL assists flagellar motor rotation in *Escherichia coli* under low load condition
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.*)

20226G *Enterococcus hirae* 由来 V-ATPase のナトリウムイオン濃度に依存した回転運動の 1 分子解析
Single-molecule analysis of rotation of *Enterococcus hirae* V-ATPase depending on sodium ion concentration
Akihiro Otomo[1,2], Tatsuya Iida[1,2], Hiroshi Ueno[3], Takeshi Murata[4], Ryota Iino[1,2] ([1]*Inst. for. Mol. Sci*, [2]*SOKENDAI*, [3]*The Univ. Tokyo*, [4]*Chiba Univ.*)

20227G Autonomous molecular swarm robots realized by sequential transfer of DNA signal
Jakia Jannat Keya[1], Yuta Yamasaki[2], Kazuki Sada[1], Akinori Kuzuya[2], Akira Kakugo[1] ([1]*Hokkaido University*, [2]*Kansai University*)

20228G* 演題取り消し

20229G 鞭毛波形切り替えメカニズムの数理モデル
A mathematical model for mechanism of flagellar waveform change
Kenta Ishibashi[1,2], Hitoshi Sakakibara[3], Kazuhiro Oiwa[2,3,4] ([1]*Osake Univ.*, [2]*NICT-CiNet*, [3]*Advanced ICT Research Institute*, [4]*University of Hyogo*)

20230G The Helical Arrangement of Axonemal Structures Depends on the Region of the Flagellum
Hitoshi Sakakibara[1], Kenta Ishibashi[2], Hiroyuki Iwamoto[3], Hiroaki Kojima[1], Kazuhiro Oiwa[1,4] ([1]*Bio Function PJ, NICT*, [2]*CiNet, Osaka Univ.*, [3]*SPring-8, JASRI*, [4]*Life Sci. Univ. Hyogo*)

20231G ビーズ-DNA 複合体および DNA ナノチューブ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 beads-DNA complex and DNA nanotube
Kohei Arai[1], Kenta Ito[1], Yuki Tsushima[2], Yusuke Sato[1,3], Shoichi Toyabe[1] ([1]*Appl. Phys., Grad. sch. eng., Tohoku univ*, [2]*IIS, Tohoku univ.*, [3]*Front. Res. Inst. Interdiscip. Sci., Tohoku Univ*)

20232G 単極毛性細菌 *Vibrio cholerae* におけるべん毛モーター回転切り替えの協同性
Low cooperativity of flagellar motor switching in *Vibrio cholerae* the bacterium of a single polar flagellum
Hirotaka Tajima[1,2], Masatoshi Nishikawa[1], Yuki Miura[3], Yoshiyuki Sowa[1,2,3], Ikuro Kawagishi[1,2,3] ([1]*Dept. Front. Biosci., Hosei Univ.*, [2]*Res. Cent. Micro-Nano Tech., Hosei Univ.*, [3]*Grad. Sch. Eng., Hosei Univ.*)

20233G CbM4 の持つ時計回りの運動活性の解析
Analysis of the clockwise motility of CbM4
Kohei Yoshimura, Takuma Imi, Takeshi Haraguchi, Masanori Tamanaha, Kohji Ito (*Grad. Sch. Sci., Chiba Univ.*)

20234G* 腸管病原性大腸菌が有するⅢ型分泌装置の ATPase の活性特性評価と HS-AFM を用いた構造ダイナミクスに対する考察
Characterization of the enzymatic property and structural dynamics of the T3SS ATPase from Enteropathogenic Escherichia coli
Aya Suzuki[1], Hiroshi Ueno[1], Ryo Kurosaki[2], Takayuki Uchihashi[2], Hiroyuki Noji[1] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*Grad. Sch. Sci., Univ. Nagoya*)

20235H 演題取り消し

20236H 演題取り消し

20237H Visualizing of neo-self phenomena in chimeric antigen receptor (CAR)-T cells
Hiroaki Machiyama, Ei Wakamatsu, Tadashi Yokosuka (*Dept. Immunol, Tokyo Med. Univ.*)

20238H ストレスファイバーの張力ホメオスタシスに関する研究
Theoretical consideration of homeostasis in stress fibers
Yuika Ueda, Daiki Matsunaga, Tsubasa Matsui, Shinji Deguchi (*Grad. Eng. Sci., Univ. Osaka*)

20239H 支持脂質二重膜に固定したカドヘリンのモノマー・ダイマー間構造変換の高速 AFM による追跡
Chasing the transformation between monomer and dimer structure of cadherin anchored to supported lipid bilayer by high-speed AFM
Shigetaka Nishiguchi[1], Hiroki Oda[3,4], Takayuki Uchihashi[1,2] ([1]*ExCELLS*, [2]*Nagoya Univ.*, [3]*BRH*, [4]*Osaka Univ.*)

20240H 非接着状態がん細胞の転移能上昇に伴う細胞間接着強度の増加
Increase of intercellular adhesion strength of non-adherent cancer cells associated with the upregulation of their metastatic ability
Kenta Ishibashi[1], Chikashi Nakamura[1,2], **Hyonchol Kim**[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Cell. Mol. Biotechnol. Res. Inst., AIST*)

20241H* 損傷した細胞における細胞内粘性と生存確率の関係
Cytoplasmic Viscosity and Cellular Viability of the Damaged Cells
Hideaki Ota, Hideo Higuchi (*Department of Physics, School of Science, The University of Tokyo*)

20242H 繊毛への機械刺激依存的な、マウスノードクラウン細胞における mRNA 分解
Mechanical stimuli to a cilium activate mRNA decay in a mouse nodal crown cell
Takanobu A Katoh[1], Katsutoshi Mizuno[1,2], Hiroshi Hamada[1] ([1]*BDR, Riken*, [2]*School of Medical Sciences, University of Fukui*)

20243H* 運動性細胞における Ras の興奮性制御に関わる GEF の同定
Identification of GEFs regulating the excitability of Ras in motile cells
Koji Iwamoto[1], Satomi Matsuoka[1,2,3], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. Sci., Univ. Osaka*, [2]*Grad. Sch. of Front. Biosci., Univ. Osaka*, [3]*BDR, RIKEN*)

20244H クラミドモナス軸糸運動の再活性化イメージング
High hydrostatic pressure induces vigorous flagellar beating in *Chlamydomonas* non-motile mutants lacking the central apparatus
Toshiki Yagi[1], **Masayoshi Nishiyama**[2] ([1]*Pref. Univ. Hiroshima*, [2]*Kindai Univ.*)

20245H 細菌バイオフィルムと骨代謝の ASEM 免疫電顕と cryo-TEM による観察
Observation of biofilm and bone metabolism in aqueous liquid using immuno-labeled ASEM and cryo-TEM
Chikara Sato[1], Shinya Sugimoto[2], Eiko Sakai[3], Mari Sato[1], Naoki Kasahata[1], Masami Naya[1] ([1]*Health & Medical Res.Inst, AIST.*, [2]*Dept. Bacteriol., The Jikei Univ. Sch. Med.*, [3]*Dental Pharmacology,Nagasaki Univ.*)

20246H Tension at adherens junction inhibits proliferation and promotes differentiation of keratinocyte carcinoma cells
Oleg Dobrokhotov, Masahiro Sokabe, Hiroaki Hirata (*Grad. Sch. Med., Nagoya Univ.*)

20247H 細胞質中における p52SHC は GRB2 の細胞膜移行を負に制御する
p52SHC in the cytoplasm negatively regulates GRB2 translocation to the plasma membrane
Ryo Yoshizawa[1,2], Nobuhisa Umeki[2], Masayuki Murata[1], Yasushi Sako[2] ([1]*Grad.sch.arts and ahi., the univ. Tokyo*, [2]*Wako Inst., Riken*)

20248H 細胞内脂肪滴の普遍的相挙動
Liquid-liquid crystal phase transitions in intracellular lipid droplets
Shunsuke F. Shimobayashi[1], Yuki Ohsaki[2] ([1]*Chemical Biological Engineering, Princeton Univ.*, [2]*Grad. Sch. Med., Nagoya Univ.*)

20249H 陰圧条件下における金魚ケラトサイト細胞の移動速度の上昇
Enhanced movement of fish keratocyte cells under negative pressure conditions
Akihiro Yamazaki, Hitoshi Tatsumi (*Kanazawa Inst. of Technology*)

20250H 1 細胞自律的な細胞内温度制御の分子機構
A cell-autonomous control of intracellular temperature by mitochondrial thermogenesis
Akira Murakami[1,2], Kohjiro Nagao[1], Reiko Sakaguchi[1], Kohki Okabe[2], Harada Yoshie[3], Masato Umeda[1] ([1]*Dept. of Synth. Chem. And. Biol. Chem., Grad. Sch. of. Eng., Kyoto Univ.*, [2]*Grad. Sch. of Pharm. Sci., Univ. of Tokyo*, [3]*Inst. for Protein Res., Osaka Univ.*)

20251H 蛍光顕微鏡法による単一デスミンフィラメントの可視化
Visualization of single desmin filaments by fluorescence microscopy in vitro
Masashi Sato, Keigo Murakami, **Kuniyuki Hatori** (*Grad. Sch. Sci. Eng., Yamagata Univ.*)

20252H* 収縮するアクトミオシン構造の綱引きで決まる細胞サイズ液滴内の位置対称性
A tug-of-war between contractile actomyosin structures determines the positioning symmetry in cell-sized droplets
Ryota Sakamoto[1], Tetsuya Hiraiwa[2,3], Masatoshi Tanabe[4], Kazuya Suzuki[4,5], Shin'ich Ishiwata[4], Yusuke Maeda[1], Makito Miyazaki[6,7,8] ([1]*Dept. Phys., Kyushu Univ.*, [2]*Dept. Phys., Tokyo Univ.*, [3]*Mechanobio. Inst., Nat. Univ. Singapore*, [4]*Dept. Phys., Waseda Univ.*, [5]*Cent. Lab., Hamamatsu Photonics K.K*, [6]*Hakubi Cent., Kyoto Univ.*, [7]*Dept. Phys., Kyoto Univ.*, [8]*Curie Inst.*)

20253H* NF-κB mediated transcriptional regulation in B-cell
Johannes Nicolaus Wibisana[1], Takehiko Inaba[2], Yasushi Sako[2], Mariko Okada[1] ([1]*IPR Osaka Univ.*, [2]*RIKEN*)

20254H 神経シナプスでの AMPA 受容体数密度の動的制御：1 分子イメジングによる解明
Dynamic regulation of the AMPA receptor number density in the neuronal synapse as revealed by single-molecule imaging
Yuri L. Nemoto[1], Kazuma Naito[2], Hiroko Hijikata[1], Taka A. Tsunoyama[1], Nao Hiramoto-Yamaki[2], Rinshi S. Kasai[3], Yuki M. Shirai[2], Manami S. Miyahara[2], Takahiro K. Fujiwara[2], Akihiro Kusumi[1,2,3] ([1]*OIST*, [2]*Kyoto University, WPI-iCeMS*, [3]*Kyoto University, Institute for Frontier Life and Medical Sciences*)

20255H γ-tubulin は中心子トリプレット微小管形成に寄与する
γ-tubulin functions in assembling centriolar triplet microtubules
Yuki Nakazawa[1,2], Mao Horii[3], Saki Watanabe[2], Moeko Otsuki[2], Akira Noga[3], Ken-ichi Wakabayashi[4], Masafumi Hirono[2] ([1]*Science and Technology Group, OIST*, [2]*Dept. Frontier Biosci.,Fac. Biosci. Appl. Chem., Hosei Univ.*, [3]*Dept. Biosci., Grad. Sch. Sci., Univ. Tokyo*, [4]*Inst. Innov. Res., Tokyo Inst. Tech.*)

20256H 2 本の内べん毛の同調した回転は細菌の遊泳を制御する
Coordinated rotation of dual endo-flagella controls bacterial swimming
Toshiki Kuribayashi, Shuichi Nakamura (*Grad. Sch. Eng., Tohoku Univ.*)

20257H 細胞の間隙で働く接着性 GPCR の蛍光 1 分子観察
Single molecule observation of adhesion GPCR accumulated at the cell-cell interface
Rinshi Kasai[1], Yuri Nemoto[2] ([1]*Inst. Front. Life. Med. Sci., Kyoto Univ.*, [2]*OIST*)

20258H* マイクロ構造化ハイドロゲル上を移動する細胞の核形態変化の定量解析
Quantitative analysis of dynamic changes in nuclear morphology in cells migrating on microstructured gelatin hydrogel
Ryo Ishida[1], Tomoko Oyama G[2], Kotaro Oyama[2], Mitsumasa Taguchi[2], Hiromi Miyoshi[1] ([1]*Grad. Sch. Syst., Univ. Tokyo. MetroSyst*, [2]*QuBS., QST*)

20259H ADP により調節されるマウス気管繊毛の運動活性
Motility of murine tracheal cilia modulated by ADP
Masashi Iwata[1], Keiju Kawano[1], Masayuki Shiina[1], Toshihito Iwase[1], Nobukiyo Tanaka[1], Koji Ikegami[2], Tomoko Masaike[1] ([1]*Dept. of Appl. Biol. Sci., Tokyo Univ. of Science*, [2]*Grad. Sch. of Biomedical & Health Sci., Hiroshima Univ.*)

20260H 熱量および蛍光滴定により推定されたタウ-DNA 結合熱
Tau-DNA binding heat estimated by calorimetric and fluorescence titrations
Kan Matsuda, Junta Kashima, Hideyuki Komatsu (*Dept. Biosci. Bioinf., Kyushu Inst. Tech.*)

20261H* クラミドモナス繊毛交互打ち変異株の単離と解析
Isolation and analysis of Chlamydomonas mutants showing alternate ciliary beatings
Kazuma Sakamoto[1,2], Toru Hisabori[1,2], Ken-ichi Wakabayashi[1,2] ([1]*CLS, Tokyo Tech.*, [2]*Sch. Life Sci. Tech., Tokyo Tech.*)

20262H Response of plural phagocytosis is regulated by the attached order of antigens as far as macrophages can recognize the time differences
Tomoyasu Sakaguchi[1], Yuya Hurumoto[1], Tosiki Azuma[1], Amane Yosida[1], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

20263H Dominant factor for cease phagocytosis after excess intake of antigens is explained by the volume regulation with 0.62-μm encapsulation
Toshiki Azuma[1], Yuya Furumoto[1], Amane Yoshida[1], Tomoyasu Sakaguchi[1], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Phys., Sch. Adv. Sci. & Eng., Waseda Univ*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

20264H Measurement of the temporal rotation change of individual cells' trajectory in collective cell migration in agarose microchannels
Shun Koide[1], Mitsuru Sentoku[1], Kento Iida[2], Hiromichi Hashimoto[2], Masao Odaka[3], Akihiro Hattori[3], Kenji Yasuda[1,2,3] ([1]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda U niv.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

20265H Maximum limit of phagocytosis is explained by the shortage of consumable cell membrane with 0.9 μm envelope in phagosome
Dan Horonushi[1], Yuya Furumoto[2], Toshiki Azuma[2], Amane Yoshida[2], Tomoyasu Sakaguchi[2], Yumeno Tanaka[1], Kenji Yasuda[1,2,3] ([1]*Dept. 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*)

20266H Velocity split after passing through the wide-narrow-wide capillary tube caused by short-term memory in collective cell migration
Mitsuru Sentoku[1], Hiromichi Hashimoto[2], Kento Iida[2], Kenji Yasuda[1,2,3] ([1]*Dept. 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.*)

20267H PM2.5 antigens maintains efficiency of engulfment ability in serial phagocytosis of single macrophages with on-chip free-flow method
Yuya Furumoto[1], Toshiki Azuma[1], Amane Yoshida[1], Tomoyasu Sakaguchi[1], Yumeno Tanaka[2], Dan Horonushi[2], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

20268H 好気及び嫌気性条件で酸化及び還元型αディフェンシン cryptdin-4 の抗菌メカニズムの検討
Antibacterial mechanism of an α-defensin, cryptdin-4 in redox status under aerobic and anerobic conditions
Yi Wang[1], Weiming Geng[1], Rina Hiramine[1], Chisato Toyokawa[1], Tomoyasu Aizawa[1,2] ([1]*Grad. Sci. Life Sci., Hokkaido Univ.*, [2]*GI-CoRE, Hokkaido Univ.*)

20269H 多電極電位システムを用いたハイスループット心毒性検査法の実用化を目指した少数心筋細胞集団薬剤応答の解析
Analysis of small size of cardiomyocyte population's drug response for high-throughput cardiotoxicity test using multi-electrode system
Kentaro Kito, Naoki Tadokoro, Masahito Hayashi, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell biology, Department of Frontier Bioscience, Hosei University*)

20270H 大腸菌走化性応答適応過程の高い再現性を実現する簡易培養方法の構築
Construction of simple culture method that realizes high reproducibility of Escherichia coli chemotaxis response adaptation process
Hiroto Tanaka, Yasuaki Kazuta, Amina Yano, Hiroaki Kojima (*Adv ICT Res Inst, NICT*)

20271H Hysteresis is not remained in macrophages after engulfment in fluctuation of movement angles with a single-point series phagocytosis assay

Yumeno Tanaka[1], Yuya Furumoto[2], Toshiki Azuma[2], Amane Yoshida[2], Tomoyasu Sakaguchi[2], Dan Horonushi[1], Kenji Yasuda[1,2,3] ([1]*Dept. 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.*)

20272H* アガロース微細加工技術を用いた環状心筋細胞ネットワークによる伝導異常モデルの構築
Construction of conduction abnormality model by circular cardiomyocyte network using agarose microfabrication technology

Koji Emura, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad.Sci&Eng, Hosei Univ.*)

20273H Width-dependent concave velocity distribution in collective migration is explained by two fluid-like behavior rules

Hiromichi Hashimoto[1], Mitsuru Sentoku[2], Syun Koide[2], Kento Iida[1], Kenji Yasuda[1,2,3] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*)

20274H 高静水圧によるウニ精子細胞内カルシウム濃度への影響
Effects of high hydrostatic pressure on intracellular Ca2+ concentration of sea urchin swimming live sperm

Hiroshi Imai[1,2], Masayoshi Nishiyama[3], Yumiko Kaminoe[3], Yoshie Harada[4], Takahide Kon[1], Shinji Kamimura[2] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Dept. Biol. Sci., Chuo Univ.*, [3]*Dep. Phys., Kindai Univ.*, [4]*IPR, Osaka Univ.*)

20275H 生細胞における 1 分子イメージングと超解像顕微鏡法を用いた動態と相互作用の定量解析
Quantification of dynamics and kinetics using single-molecule and super-resolution imaging in living cells

Yuma Ito, **Makio Tokunaga** (*Sch. Life Sci. Tech., Tokyo Tech.*)

20276H 1 分子イメージングで明らかになった糖鎖によるエクソソーム機能制御
Regulation of exosome function by glycans as revealed by single-molecule imaging

Tatsuki Isogai[1], Koichiro M. Hirosawa[2], Yasuhiko Kizuka[2,3], Yasunari Yokota[4], Kenichi G. N. Suzuki[2,3] ([1]*Grad. Sch. Nat Sci Tech.*, [2]*iGCORE, Gifu. Univ.*, [3]*CREST, JST*, [4]*Dept. Eng., Gifu Univ.*)

20277H アクチンの重合と脱重合の熱測定
Calorimetry of actin polymerization and depolymerization

Shouron Kure, Hideyuki Komatsu (*Dept. Biosci. Bioinf., Kyushu Inst. Tech*)

20278H 線虫 MEC-2 および相互作用チャネル蛋白質の構造・生化学的解析
The structural and biochemical analyses of MEC-2 and its partner channel proteins in *C. elegans*

Norihiro Takekawa[1], Maria Uehori[2], Shunji Nakano[3], Ikue Mori[3], Michio Homma[4], Katsumi Imada[1] ([1]*Dept. of Macromol. Sci., Grad. Sch. of Sci., Osaka Univ.*, [2]*Dept. of Chem., Fac. of Sci., Osaka Univ.*, [3]*NSI, Grad. Sch. of Sci., Nagoya Univ.*, [4]*Div. of Biol. Sci., Grad. Sch. of Sci., Nagoya Univ.*)

20279H ヒト iPS 細胞を用いた原腸形成時の自己組織化運動
Self-organizing movement during gastrulation using human iPS cells

Ryo Kobayashi[1], Chihiro Takeuchi[2], Kiyoshi Ohnuma[3] ([1]*Grad. Sch. Eng., Univ. Nagaoka Tech.*, [2]*Eng., Univ. Nagaoka Tech.*, [3]*Inn., Univ. Nagaoka Tech*)

20280H マウス気管の繊毛運動による喘息原因物質キチンの輸送
Observation of ciliary motility of murine trachea and epithelial transport of chitin involved in the development of asthma

Arata Imaizumi[1], Keiju Kawano[1], Nobukiyo Tanaka[1], Susumu Nakae[2], Koji Ikegami[3], Tomoko Masaike[1] ([1]*Dept. Appl. Biol. Sci. Tokyo Univ. Sci.*, [2]*Grad. Sch. of Integrated Sci. for Life, Hiroshima Univ.*, [3]*Grad. Sch. of Biomedical & Health Sci., Hiroshima Univ.*)

20281H リアルタイムフィードバック制御による機械的刺激に影響を受けた心筋細胞の拍動
Beat sequence of cardiomyocytes affected by to mechanical stimulus with real-time feedback control

Shota Nozaki, Kazuki Mammoto, Takashi Miyazawa, Ryuta Watanabe, Yuta Moriyama, Ryu Kidokoro, Toshiyuki Mitsui (*Aoyama Gakuin University*)

20282H 心筋梗塞の治療のための in vitro 移植モデルにおけるペースメーカーの入れ替わり
Pacemaker switching of in vitro transplantation model for heart infarction
Toru Nakamura, Chiho Nihei, Masahito Hayashi, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell biology, Department of Frontier Bioscience, Hosei University, Grad. School of Science and Engineering*)

20283H 圧力がミトコンドリアの機能に及ぼす影響
Effects of pressure on mitochondrial activity
Yoshiki Oie[1], Yoshihiro Ohta[2] ([1]*Grad. Sch. Sci., Tokyo University of Agriculture and Technology*, [2]*Tokyo University of Agriculture and Technology*)

20284H タウ–微小管とタウ–ヘパリン相互作用の等温滴定熱測定の比較
Comparative analysis between isothermal titration calorimetries of tau–microtubule and tau–herparin interactions
Junta Kashima, Rio Okamoto, Hideyuki Komatsu (*Dept. Biosci. Bioinf., Kyushu Inst. Tec*)

20285H ミトコンドリア電子伝達系のプロトンポンプ活性の単一細胞検出
Detection of proton pump activities in mitochondrial electron transfer chain in a single cell level
Yoshiki Suganuma, Masato Miura, Hiroko Kashiwagi, Yoshihiro Ohta (*Tokyo University of Agriculture and Technology, Department of Biotechnology and Life Sciences.*)

20286H 単細胞 FRET とべん毛モーター回転による CheYp 濃度の同時観察による適応系のメカニズム解明
Elucidation of mechanism for adaptation system through the simultaneous observation CheYp by single cell FRET and flagellar motor rotation
Takuma Nakagawa, Tatsuya Yamakoshi, Che Yong-Suk, Hajime Fukuoka, Akihiko Ishijima (*Grad. Sch. Frontier Biosci. Osaka Univ.*)

20287H Simultaneous observation of chemotactic response and intracellular behavior of chemotaxis proteins at single *E. coli* cell
Taro Yuri, Takuma Nakagawa, Keisuke Nishitani, Yong-Suk Che, Yumiko Uchida, Akihiko Ishijima, **Hajime Fukuoka** (*Grad. Sch. Frontier Biosci., Osaka Univ.*)

20288H CheB の細胞内動態とべん毛モーター回転の同時計測
Simultaneous measurement of flagellar motor rotation and Dynamics of CheB localization during chemotactic response
Keisuke Nishitani[1], Tatsuki Hamamoto[2], Yong-Suk Che[1], Akihiko Ishijima[1], Hajime Fukuoka[1] ([1]*Grad. Sch. Frontier Biosci. Osaka Univ.*, [2]*OIST. Grad. Univ.*)

20289H 回転方向に依存したべん毛モーターの回転揺らぎの高時間分解能測定。
High temporal resolution measurement of rotational fluctuation of flagellar motor depending on rotational direction
Koki Murai, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci. Osaka Univ.*)

20290H 心筋細胞における拍動間隔の温度依存性
Temperature dependence of beating rate in cardiomyocytes
Kohei Oyama, Masahito Hayashi, Tomoyuki Kaneko (*Laboratory for Reconstructive Cell Biology, Department of Frontier Bioscience, Hosei University, Grad School of Science and Engineering*)

20291H 走化性タンパク質 CheRCheB の存在と大腸菌スイッチング同調
Requirement for Chemotaxis Protein CheR and CheB for the switching coordination between two flagellar motors on E. coli cell
Tatsuki Hamamoto[2], **Yumiko Uchida**[1], Yong-Suk Che[1], Akihiko Ishijima[1], Hajime Fukuoka[1] ([1]*Grad. Sch. Frontier Biosci. Osaka Univ*, [2]*OIST Grad. Univ*)

20292H* レプトスピラ経皮侵入に関わる運動の重要性
Significance of motility for percutaneous invasion of the spirochete *Leptospira*
Keigo Abe[1], Toshiki Kuribayashi[1], Kyosuke Takabe[2], Shuichi Nakamura[1] ([1]*Department of Applied Physics, Graduate School of Engineering, Tohoku University*, [2]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

20293H* 蛍光および反射干渉顕微鏡による細胞ー基板界面でのがん細胞膜の分子パッキングの評価
Evaluation of molecular packing of cancer cell membrane at cell-substrate interface by fluorescence and interference reflection microscopy
Hayata Noro[1], Mai Fujii[1], Shodai Togo[1], Mami Watanabe[1], Masami Suganuma[2], Naritaka Kobayashi[2], Ryozo Kawamura[1,2], Seiichiro Nakabayashi[1,2], Takahisa Matsuzaki[2], Hiroshi Yoshikawa[1,2] ([1]*Dept. of Chem., Saitama Univ.*, [2]*Div. of Strateg. Res. and Dev., Grad. Sch. of Sci. and Eng., Saitama Univ.*)

20294H* 細胞接着界面の膜分子配列性の評価：がん細胞と正常細胞の比較
Characterization of molecular packing of cell membranes at cell-substrate interface:Comparison between cancer cells and normal cells
Mai Fujii[1], Hayata Noro[1], Syodai Togo[1], Mami Watanabe[1], Masami Suganuma[2], Naritaka Kobayashi[2], Ryuzo Kobayashi[1,2], Seiichiro Nakabayashi[1,2], Takahisa Matsuzaki[2], Hiroshi Y. Yoshikawa[1,2] ([1]*Grad. Chem., Univ. Saitama*, [2]*Division of Strategic Research and Development, Grad. Sci. Eng., Univ. Saitama*)

20295H 人工多細胞型分子ロボットの自動生産に関する研究
Toward Automated Production of Multicellular Molecular Robots
Ryo Shimizu[1], Satoshi Murata[1], Shin-ichiro Nomura[1], Yuki Suzuki[4], Ibuki Kawamata[1], Gen Hayase[3], Taro Toyota[2] ([1]*Murata/Nomura Lab, Univ. Tohoku*, [2]*Toyota Lab, Univ. Tokyo*, [3]*MANA*, [4]*FRIS, Univ. Tohoku*)

20296H 繊毛の初期屈曲形成に重要な根元局在型マイナーダイニン
Requirement of minor-type axonemal dyneins localized to the proximal region for the initial bend formation of cilia
Tomohiro Komatsu, Ayuna Sahara, Yusuke Kondo, **Toshiki Yagi** (*Dept. Life Sci. Prefectural Univ. Hiroshima*)

20297H Formation of actin cortex structure by myosin motor activity
Mitsusuke Tarama, Tatsuo Shibata (*RIKEN BDR*)

I. 生体膜・人工膜／I. Biological & Artificial membrane

20298I* 抗菌ペプチド・マガイニン 2 と脂質膜の相互作用に対する膜電位の効果
Effect of Membrane Potential on Interaction of Antimicrobial Peptide (AMP) Magainin 2 (Mag) with Single GUVs
Or Rashid Md. Mamun[1], Moghal Md. Mizanur[1], Billah Md. Masum[1], Hasan Moynul[1], Yamazaki Masahito[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

20299I* 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 の巨大リポソーム内腔への侵入の検出
Detection of the Entry of Nonlabeled Cell-Penetrating Peptide (CPP) Transportan 10 (TP10) into Single Giant Unilamellar Vesicles (GUVs)
Madhabl Lata 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.*)

20300I* 脂質分子の二分子層膜横断（フリップ・フロップ）に対する浸透圧の効果
The effect of osmotic pressure on the transbilayer movement (flip-flop) of lipid molecules
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.*)

20301I 脂質・コレステロールによって制御される上皮成長因子受容体の膜貫通・膜近傍ドメインの多量体形成機構
Lipid-cholesterol regulation of the oligomerization in transmembrane and juxtamembrane domains of epidermal growth factor receptor
Ryo Maeda[1], Takeshi Sato[2], Yasushi Sako[1] ([1]*Cellular Informatics Lab., RIKEN*, [2]*Kyoto Pharmaceutical Univ.*)

20302I* 抗菌ペプチド・ラクトフェリシン B(4-9)の大腸菌、スフェロプラスト、および巨大リポソームの内腔への侵入に対する膜電位の効果
Effect of Membrane potential on Entry of Antimicrobial Peptide (AMP) LfcinB (4-9) into Single *E. coli* Cells, Spheroplasts, and GUVs
Farzana Hossain[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.*)

20303I* アミロイド線維形成とリン脂質二分子膜破壊との関係性の解明
Investigation of relationships between amyloid fibril formation and phospholipid bilayer destruction
Hiroki Takayama[1], Kaori Mageshi[1], Kenichi Morigaki[2], Eri Chatani[1] ([1]*Graduate School of Science, Kobe University*, [2]*Biosignal research center, Kobe University*, [3]*Graduate School of Agricultural Science, Kobe University*)

20304I Regulation of actin dynamics by phosphoinositides
Yosuke Senju (*RIIS, Univ. Okayama*)

20305I 高速 AFM によるハブ毒液由来脂質分解酵素 PLA2 の膜認識機構の解明
Membrane recognition mechanism of phospholipase A_2 from habu snake venom revealed by high-speed AFM (HS-AFM)
Magoto Kamiya[1], Mikihiro Shibata[2,3], Naoko Oda-Ueda[4], Ayumi Sumino[2,3] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*, [3]*InFiniti, Kanazawa Univ.*, [4]*Dept. Pharm. Sci., Sojo Univ.*)

20306I 2 種類のリン脂質種からなるモデル生体膜の構造に対するコレステロールとラノステロールの影響の比較
Comparative study of the effects of cholesterol and lanosterol on the structure of model biomombrane formed by two phospholipid species
Akira Matsumoto, Hiroshi Takahashi (*Grad. Sch. Sci and Tech., Gunma University*)

20307I* 細胞サイズ閉じ込め中の拡散に対する界面の効果
Effects of membrane interface properties on diffusion in cell-sized confinement
Kanae Harusawa[1,2], Chiho Watanabe[2], Akira Kitamura[3], Masataka Kinjo[3], Miho Yanagisawa[2] ([1]*Grad. Sch. Eng., Tokyo Univ. of Agri. and Technol.*, [2]*Grad. Sch. Arts and Sci., The Univ. of Tokyo*, [3]*Grad. Sch. Life Sci., Hokkaido Univ.*)

20308I 相分離リポソームを用いた膜タンパク質の高濃度再構成
High-density reconstitution of membrane protein into phase-separated liposome
Mizuki Kobayashi[1,2], Kei Fujiwara[3], Chiho Watanabe[2], Miho Yanagisawa[2] ([1]*Grad. Sch. Eng., Tokyo Univ. of Agri. and Tech*, [2]*Grad. Sch. Arts and Sci., The Univ. of Tokyo*, [3]*Sch and Tech.Biosciences and Informatics., Keio Univ*)

20309I 鞭毛で泳ぐ単細胞緑藻クラミドモナスを用いて巨大リポソームを内側から動かす
Driving a giant liposome from inside by a flagellating unicellular green algae *Chlamydomonas*
Shunsuke Shiomi[1], Masahito Hayashi[1], Tomohiro Uemura[2], Tomoyuki Kaneko[1] ([1]*LaRC, FB, Hosei Univ.*, [2]*FB, Hosei Univ.*)

20310I ラベルされていない抗菌ペプチド・PGLa と単一 GUV との相互作用
Interaction of Nonlabeled Antimicrobial Peptide PGLa with Single Giant Unilamellar Vesicles (GUVs)
MD Hazrat Ali[1], Madhabl Lata Shuma[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.*)

20311I Epigallocatechin gallate induces the burst of giant unilamellar vesicles in the tension-dependent manner
Naoya Sugita[1], Mika Terada[1], Yukihiro Tamba[1], Masahito Yamazaki[2] ([1]*Natl. Inst. Tech., Suzuka Coll.*, [2]*Shizuoka Univ.*)

20312I 筋小胞体 Ca ポンプの M2 ヘリックス:膜貫通部分のエネルギー共役における役割
Role of transmembrane portion of M2 helix in energy coupling of sarcoplasmic reticulum Ca pump
Takashi Daiho, Kazuo Yamasaki, Satoshi Yasuda, Jun-ichi Kawabe (*Asahikawa Med. Univ. Biochem.*)

20313I* 脂質分子混み合い効果によるバクテリオロドプシン間実行相互作用の解析
Crowding effects induced by lipid molecules on effective interactions between bacteriorhodopsins
Keiju Suda[1], Ayumi Suematsu[2], Rho Akiyama[1] ([1]*Kyushu University, science faculty, department of chemistry*, [2]*Kyushu sangyo University*)

20314I* ナノサイズリポソームの脂質膜への融合条件の調査
Examination of fusion condition of nano-sized liposome to lipid membrane
Chika Arisaka, Kouki Kamiya (*Grad. Sch. Sci and Tec., Univ. Gunma*)

20315I ハイドロゲル固体試料中で見られた紫膜の特異な積層構造の形成機構
Formation Mechanisms of Anomalous Purple Membrane Stacking in Hydrogels
Yasunori Yokoyama[1], Riku Kurita[1], Shunsuke Yano[1], Koshi Takenaka[1], Hiroshi Takahashi[2], Masashi Sonoyama[2,3,4] ([1]*Grad. Sch. Eng., Nagoya Univ.*, [2]*Grad. Sch. Sci. & Tech., Gunma Univ.*, [3]*GIAR, Gunma Univ.*, [4]*GUCFW, Gunma Univ.*)

20316I ベシクル凝集構造の力学モデル
Mechanical Model of Vesicle Aggregates
Toshikaze Chiba[1], Masayuki Imai[1], Primoz Ziherl[2,3] ([1]*Grad. Sch. Sci., Tohoku Univ*, [2]*Jozef Stefan Inst*, [3]*Ljubljana Univ*)

20317I In vitro selection using cDNA display for liposome binding peptides to generate antibacterial peptides
Takeru Yoshinobu, Naoto Nemoto (*Graduate School of Science & Engineering, Saitama University*)

20318I* Pattern Formation by Mechanochemical Feedback between Membrane Deformation and the Brusselator Model
Naoki Tamemoto, Hiroshi Noguchi (*ISSP, Univ. Tokyo*)

20319I ナノサイズリポソーム融合による細胞サイズ GM1 非対称膜リポソームの構築
Construction of cell-sized GM1 asymmetric vesicles using nano-sized vesicle fusion method
Masato Suzuki[1], Kouki Kamiya[1,2] ([1]*Sci. & Tech., Univ. Gunma*, [2]*Grad. Sci. & Tech., Univ. Gunma*)

20320I 電位依存性プロトンチャネルの細胞内側からの制御
Intracellular regulation of the voltage-gated proton channel
Akira Kawanabe, Yuichiro Fujiwara (*Kagawa Univ.*)

20321I Artificial bilayers on hydrogel for channel current recordings
Toru Ide[1,2], Minako Hirano[2], Daiki Yamamoto[1], Mami Asakura[3], Yuki Kitamura[3] ([1]*Grad Schl Health Systems Okayama Univ*, [2]*GPI*, [3]*Fac Eng Okayama Univ*)

20322I イノシトールリン脂質による KcsA の制御
Functional coupling between phosphoinositides and KcsA studied by lipid-bilayer recording
Takunari Kiya, Akira Kawanabe, Yuichiro Fujiwara (*Kagawa Univ.*)

20323I* 自動顕微鏡計測により見出された，定常流れ場における細胞サイズのリポソームへの分子濃縮
Automated direct observation unveiled hydrodynamic accumulation of molecules into cell-sized liposomes against a concentration gradient
Hironori Sugiyama[1], Toshihisa Osaki[2,3], Shoji Takeuchi[2,4], Taro Toyota[1,5] ([1]*Grad. Sch. Arts and Sci., The University of Tokyo*, [2]*IIS, The University of Tokyo*, [3]*KISTEC*, [4]*Grad. Sch. Info. Sci. Tech., The University of Tokyo*, [5]*UBI, The University of Tokyo*)

20324I 平面脂質膜の組成の違いによる OmpG の膜への挿入の違いについて
Differences of OmpG into the planar lipid membranes with various compositions
Toshiyuki Tosaka[1], Koki Kamiya[2] ([1]*Sci. & Tech., Univ. Gunma*, [2]*Grad. Sci. & Tech., Univ. Gunma*)

20325I 油中水滴エマルションにおけるヒドロキシプロピルセルロースのパターン形成とダイナミクス
Pattern formation and dynamics of hydroxypropyl cellulose in water-in-oil emulsion
Kazunari Yoshida[1], Keitaro Horii[2], Azusa Saito[2], Akito Takashima[2], Izumi Nishio[2] ([1]*Grad. Sch. Sci. Eng., Yamagata Univ.*, [2]*Col. Sci. Eng., Aoyama Gakuin Univ.*)

20326I Effect of lipid quality on the association of membrane bound proteins with phosphoinositide-containing membranes
Eiji Yamamoto[1], Junko Sasaki[2], Takehiko Sasaki[2], Mark S. P. Sansom[3] ([1]*Department of System Design Engineering, Keio University*, [2]*Medical Research Institute and Graduate School of Medical and Dental Sciences, Tokyo Medical and Dental University*, [3]*Department of Biochemistry, University of Oxford*)

20327I 気液界面における人工肺サーファクタント膜へのコレステロールの影響
Effect of cholesterol on a model lung surfactant monolayer at the air-water interface
Masahiro Hibino[1], Saki Izumi[2] ([1]*Div. Sustain. Environ. Eng., Muroran Inst. Tech.*, [2]*Dept. Appl. Sci., Muroran Inst. Tech.*)

20328I 自動生成される人工多細胞体とその電気的活性について
On multicellular lipid compartments and their electrical activity
Shin-ichiro Nomura (*Dep. Robotics, TOHOKU Univ.*)

20329I 分子シミュレーションによるリポソームにおける膜タンパク質拡散解析
Molecular dynamics simulation of the diffusion of membrane proteins on vesicles
Diego Ugarte, Shoji Takada (*Dept. Biol., Sch. Sci., Kyoto Univ., Japan*)

20330I* Observation Protein-Protein Interactions in α-hemolysin
Misa Yamaji, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

20331I* Outer membrane phospholipaseA (OmpLA)を用いた細胞モデルの構築
Creation of complex-functional cell model using outer membrane phospholipase A
Seren Ohnishi, Koki Kamiya (*Grad. Sci., Univ.Gunma*)

20332I* α-ヘモリシンナノ空間における β ヘアピンペプチドのイオン電流記録
Ion current recording of a β-hairpin peptide in confined α-hemolysin nanospace
Miyu Fukuda, Misa Yamaji, Ryuji Kawano (*Department of biotechnology and life science, Tokyo University of Agriculture and Technology*)

20333I 大腸菌が引き起こすリポソームの形態変化パターン解析
Analysis of morphological change patterns of liposomes driven by encapsulated *E. coli*
Mai Hayakawa, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

20334I* Construct analysis system between peptide local structure in lipid membrane and membrane deformation
Kayano Izumi, Ryuji Kawano (*Department of Biotechnology and Life science, Tokyo University of Agriculture and Technology*)

20335I サイズ選択性を有する DNA オリガミ人工チャネル
Size-selective molecular transportation by DNA origami channel
Shoji Iwabuchi[1], Ibuki Kawamata[1,2], Satoshi Murata[1], M. Shin-ichiro Nomura[1] ([1]*Rob. Eng., Univ. Tohoku*, [2]*Nat. Sci., Fuc. Core Res., Univ. Ochanomizu*)

20336I* Protein crowder as a modulator of Min wave generation for cell division
Saki Nishikawa, Shunshi Kohyama, Nobuhide Doi, Kei Fujiwara (*Faculty of science and technology, Keio University*)

20337I 脂質二分子膜に働く光捕捉力の検証
Lateral diffusion in lipid bilayers biased by optical forces
Yuto Ishihara[1], Tutsunori Kishimoto[1,2], Fuko Kueda[3,4], Suguru N. Kudoh[2], Kenichi Morigaki[3,4], Chie Hosokawa[1,5] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*Grad. Sch. Sci. Tech., Kwansei Gakuin Univ.*, [3]*Grad. Sch. Agr., Kobe Univ.*, [4]*Biosignal., Kobe Univ.*, [5]*PhotoBIO-OIL, AIST*)

20338I* 細胞膜の物理的状態の制御に向けた生物活性ナノ材料の設計並びに評価
Design and Evaluation of Bioactive Nanomaterials toward Control of Physical Properties of Plasma Membrane
Tomohiro Nobeyama[1], Hyungjin Kim[2], Kazuki Shigyo[3], Hirotaka Nakatsuji[4], Hiroshi Sugiyama[5], Naoko Kawamura[6,7], Hiromune Ando[6,7], Tatsuya Murakami[1,8,9] ([1]*Grad. Sch. of Eng., Toyama Prefectural Univ.*, [2]*Grad. Sch. of Med., Yamaguchi Univ.*, [3]*Grad. Sch. of Integrated Sciences for Life., Hiroshima Univ*, [4]*Grad.Sch. of Eng., Osaka Univ.*, [5]*Grad.Sch.of Sci., Kyoto Univ.*, [6]*G-CHAIN., Gifu Univ*, [7]*iGCORE.,Tokai National Higher Education and Research System*, [8]*Fac.of.Eng., Toyama Prefectural Univ.*, [9]*KUIAS.,Kyoto Univ*)

J. 化学受容・神経／J. Chemoreception,Neuroscience & Sensory systems

20339J* 線虫の低温耐性を制御する新規の GPCR 型温度センサー分子
Novel GPCR-type temperature receptor in cold tolerance of *C. elegans*
Kohei Ohnishi, Toru Miura, Tomoyo Ujisawa, Akane Ohta, Atsushi Kuhara (*Inst. for Integrative Neurobiology, Konan Univ., Japan*)

20340J* ヒトムスカリン性アセチルコリン受容体 (M_2) のリガンド認識機構の理解に向けた赤外分光研究
Infrared spectroscopic study for elucidating ligand recognition mechanism of human M_2 muscarinic acetylcholine receptor
Kohei Suzuki[1], Kota Katayama[1], Ryoji Suno[2], Yuji Sumii[1], Norio Shibata[1], Hideki Kandori[1] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech*, [2]*Kansai Medical University. Medical.*)

20341J Clostridium 属細菌の走化性アッセイ法の確立
Establishment of Methods for Chemotaxis Assays of *Clostridium* spp.
So-ichiro Nishiyama, Susumu Oogoshi, Hiroshi Urakami (*Fac. App. Life Sci., Niigata Univ. Pharm. App. Life Sci.*)

20342J* 非平衡流動場における脂質膜へのアミロイド β 凝集の単分子観察
Single Molecule Observation of Amyloid β Aggregation to Lipid Membrane under Non-equilibrium Fluidic Condition
Akane Iida[1], Hideki Nabika[2] ([1]*Grad. Sch. of Sci. and Eng., Yamagata Univ.*, [2]*Fac. of Sci., Yamagata Univ.*)

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

20343K 線虫 *C. elegans* を用いた異なる感覚情報の統合に関わる神経回路モデル
The model of neural circuit integrating different sensory information in *C. elegans*
Misaki Okahata[1], Aguan D. Wei[2], Akane Ohta[1], Atsushi Kuhata[1,3] ([1]*Inst. for Integrative Neurobio., Konan Univ.*, [2]*SEA Children's Research Inst.*, [3]*AMED-PRIME*)

20344K 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[1,2], Mari Ikeda-Ogiue[1,2], Minoru Saito[2] ([1]*Dep. Urology, Grad Sch Medicine, Juntendo Univ.*, [2]*Dep. Life sciences, College Humanities and Sciences, Nihon Univ.*)

20345K 線虫において脂肪酸代謝経路の β 酸化で働く HADH が低温馴化を制御する
HACD-1 that is beta-oxidation of fatty acid metabolism regulates cold acclimation in intestine and sensory neurons in C. elegans
Akihisa Fukumoto[1], Atushi Kuhara[1], Akane Ohta[1], Misaki Okahata[1], Youhei Minakuti[2], Atushi Toyoda[2] ([1]*Inst. for Integrative Neurobio., Konan Univ.*, [2]*NIG, Japan*)

20346K 細胞間の活動同期性に基づく神経クラスタの統計的推測
Statistical inference of neuronal ensembles based on synchronous activity among neurons
Shun Kimura, Koujin Takeda, Yuishi Iwasaki (*Grad. Sch. Sci. Eng., Univ. Ibaraki*)

20347K Integrated signaling from thermosensoryneurons at a tail interneuron regulates cold acclimation
Haruka Motomura, Satoko Fujii, Makoto Ioroi, Atsushi Kuhara, Akane Ohta (*Institute for integrative Neurobiology, Konan Univ.*)

20348K 内因性カンナビノイドによる小脳 GABA シナプス伝達のシナプスタイプ別制御
Endocannabinoids regulate cerebellar GABAergic transmission in a synapse type-dependent manner
Moritoshi Hirono[1,2], Yuchio Yanagawa[3] ([1]*Dep. Physiol., Wakayama Med. Univ. Sch. Med.*, [2]*Grad. Sch. Brain Sci., Doshisha Univ.*, [3]*Dep. Genetic and Behav. Neurosci., Gunma Univ. Grad. Sch. Med.*)

20349K A method to differentiate neurite non-invasively with needle agarose microfabrication technology
Yuhei Tanaka, Haruki Watanabe, Kenji Shimoda, Kenji Yasuda (*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

20350K 微小多電極解析のための神経細胞の 1 細胞レベル長期培養環境の最適化
Optimization of the long-term cultural environment of isolated single neurons for micro-multielectrode analysis
Kenji Shimoda, Yuhei Tanaka, Haruki Watanabe, Kenji Yasuda (*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

20351K 1 神経突起の伸長を長期間観察さるための改良された μm 分解能のアガロース微細加工技術の評価
Evaluation of an improved μm resolution agarose microfabrication technology for long-term individual neurite elongation observation
Haruki Watanabe[1], Yuhei Tanaka[1], Kenji Shimoda[1], Kenji Yasuda[1] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [3]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [4]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

20352K マウス海馬の長期増強を膜電位感受色素によるイメージングで観察する
Imaging analysis of the long-term potentiation of the mouse hippocampal activity
Yoko Tominaga, Makiko Taketoshi, **Takashi Tominaga** (*Inst Neurosci Tokushima Bunri Univ.*)

20353K プリオンタンパク質ノックアウトマウスにおける小脳長期抑圧障害
Impairment of cerebellar long-term depression in prion protein-deficient mice ectopically expressing PrPLP/Dpl
Yasushi Kishimoto[1], Moritoshi Hirono[2], Ryuichiro Atarashi[3], Suehiro Sakaguchi[4], Tohru Yoshioka[5], Shigeru Katamine[6], Yutaka Kirino[1] ([1]*Kagawa Sch. Pharm. Sci., Tokushima Bunri Univ.*, [2]*Dep. Physiol., Wakayama Med. Univ. Sch. Med.*, [3]*Fac. Med., Univ. of Miyazaki*, [4]*KOSOKEN, Tokushima Univ.*, [5]*Kaohsiung Medical Univ.*, [6]*CICORN, Nagasaki Univ.*)

20354K ミミズ短期記憶におけるセロトニンの関与
Involvement of serotonin in short-term memory of earthworms
Yoshiichiro Kitamura, Toshiaki Nakahara, Hikaru Takahashi (*Dept Math Sci Phys, Col Sci Eng, KGU*)

L. 行動／L. Behavior

20355L 蟻はピンクノイズで探索する
Ants run on a treadmill with the pink noise
Tomoko Sakiyama[1], Naohisa Nagaya[2], Ryusuke Fujisawa[3] ([1]*Soka University*, [2]*Kyoto Sangyo University*, [3]*Kyushu Institute of Technology*)

20356L* 隠れマルコフモデルと逆強化学習法による生物複数戦略の同定
Identification of multiple strategies by inverse reinforcement learning with hidden-Markov model
Kohei Morimoto[1,2], Muneki Ikeda[3,4], Yuki Tsukada[3], Nakano Shunji[3], Ikue Mori[3,4], Naoki Honda[2,5,6] ([1]*Undergrad. Info. and Math., Kyoto Univ.*, [2]*Grad. Bio., Kyoto Univ.*, [3]*Grad. Sci., Nagoya Univ.*, [4]*CBS., Riken*, [5]*Research Center for Dynamic Living Systems, Kyoto Univ.*, [6]*ExCELLS, NINS.*)

20357L 睡眠の剥奪はショウジョウバエによる食物臭の嗜好性を変化させる
Sleep deprivation alters food odor preference in Drosophila
Fuminori Tanizawa[1,2], Hiroyuki Takemoto[3] ([1]*Kaisei Senior High School*, [2]*Future Scientists' School, Shizuoka University*, [3]*Research Institute of Green Science and Technology, Shizuoka University*)

20358L 壁近くのゾンビ化した単鞭毛クラミドモナスの遊泳
Swimming of zombifield monoflagellated Chlamydomonas near wall
Ken Nagai (*JAIST*)

20359L* 報酬と好奇心によって駆動される行動を表現する意思決定モデル
A decision-making model for reward and curiosity-driven behavior
Yuki Konaka[1,2], Naoki Honda[1,2] ([1]*Graduate School of Biostudies, Kyoto university.*, [2]*Theoretical Biology Research Group, Exploratory Research Center on Life and Living Systems (ExCELLS), National Institutes of Natural Sciences.*)

M. 光生物:視覚・光受容・光合成・光制御／M. Photobiology

20360M マウス桿体視細胞においてロドプシンを介するが光オフで生じるプロテインキナーゼ A の活性化
Rhodopsin-mediated Light-off-induced Protein Kinase A Activation in Mouse Rod Photoreceptor Cells
Shinya Sato[1], Takahiro Yamashita[2], Michyuki Matsuda[1,3] ([1]*Grad. Sch. Biostud., Univ. Kyoto*, [2]*Grad. Sch. Sci., Univ. Kyoto*, [3]*Grad. Sch. Med., Univ. Kyoto*)

20361M 光合成酸素発生系における *g*=5 S_2 状態の分子構造
Molecular Structure of the S_2 State with a *g*=5 Signal in the Oxygen Evolving Complex of Photosystem II
Hiroyuki Mino, Shota Taguchi, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Uni.*)

20362M QM/MM-MD による光回復酵素-紫外線損傷 DNA 複合体の逐次修復反応中における反応中間体の観測に成功
QM/MM-MD approach for photolyase-UV-damaged DNA complex achieved that observe an intermediate in the successive DNA repair reactions
Ryuma Sato[1], Hiroshi Watanabe[2,3], Junpei Yamamoto[4], Makoto Taiji[1] ([1]*RIKEN*, [2]*Keio univ, KQCC*, [3]*PRESTO JST*, [4]*Osaka univ*)

20363M 光化学系Ⅱにおける D1-Asp170 の His 変異体の新規なアミノ酸変換
Novel amino acid conversion of a His mutant of D1-Asp170 in photosystem II
Yuichiro Shimada[1], Tomomi Kitajima-Ihara[1], Ryo Nagao[1,2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Res. Inst. Interdiscip. Sci., Okayama Univ.*)

20364M Clarification of proton transfer pathways in water photolysis in photosystem II
Ayane Sugiyama, Yuichiro Shimada, Takumi Noguchi (*Division of Material Science, Graduate School of Science, Nagoya University, Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan*)

20365M 光化学系Ⅱの第二キノン電子授与体 Q_B の反応における D1-His252 の役割
Role of D1-His252 in the reaction of the secondary quinone electron accepter Q_B in photosystem II
Tomoyuki Kobayashi[1], Yuichiro Shimada[1], Ryo Nagao[2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci, Nagoya Univ.*, [2]*Res. Inst. Interdiscip. Sci., Okayama Univ.*)

20366M 光化学系Ⅱにおけるキノン電子受容体 Q_A・Q_B 間の電子移動の時間分解赤外分光検出
Time-resolved infrared detection of electron transfer between quinone electron acceptors Q_A and Q_B in photosystem II
Honami Ito, Yuki Kato, Takumi Noguchi (*Grad. Sch. Sci, Nagoya Univ.*)

20367M Mutational analysis of the mechanism of an absorption red shift in a marine bacterial Cl^--pumping rhodopsin
Takashi Nagata[1,2], Masayuki Karasuyama[2,3], Ichiro Takeuchi[3,4,5], Yu Nakajima[6], Susumu Yoshizawa[7], Keiichi Inoue[1,4] ([1]*Inst. Solid State Phys., Univ. Tokyo*, [2]*PRESTO, JST*, [3]*Dept. Computer Sci., Nagoya Inst. Tech.*, [4]*RIKEN Center for Advanced Intelligence Project*, [5]*OptoBioTechnology Research Center, Nagoya Inst. Tech.*, [6]*Bioproduction Res. Inst., Nat. Inst. Adv. Indust. Sci. Tech.*, [7]*Atmosphere and Ocean Res. Inst., Univ. Tokyo*)

20368M FTIR spectroelectrochemical study on the mechanism of the pH dependence of the redox potential of the non-heme iron in photosystem II
Yuki Kato, Hiroki Watanabe, Takumi Noguchi (*Grad. Sch. Sci., Nagoya Univ.*)

20369M Spectroscopic properties and energy transfer dynamics of two different forms of acpPC from dinoflagellate *Symbiodinium*

Hayata Yamamoto[1], Keisuke Kawakami[2], Hiroko Uchida[3], Akio Murakami[3], Nobuo Kamiya[4], Daisuke Kosumi[5] ([1]*Dept. of Sci. and Tech., Kumamoto Univ.*, [2]*RIKEN*, [3]*Research Center of Island Seas, Kobe Univ.*, [4]*ReCAP, Osaka City Univ.*, [5]*IINA, Kumamoto Univ.*)

20370M Energy transfers in PSI of cyanobacterium, red alga, and dinoflagellate

Hiroki Serikawa[1], Hayata Yamamoto[1], Keisuke Kawakami[2], Hiroko Uchida[3], Akio Murakami[3], Kimiko Nagayoshi[4], Toshinari Kuroki[4], Susumu Takio[5], Nobuo Kamiya[6], **Daisuke Kosumi**[7] ([1]*Dept. of Sci. and Tech., Kumamoto Univ.*, [2]*RIKEN*, [3]*Research Center of Island Seas, Kobe Univ.*, [4]*Daiichi Seimou Co., Ldt.*, [5]*CWMD, Kumamoto Univ.*, [6]*ReCAP, Osaka City Univ.*, [7]*IINa, Kumamoto Univ.*)

20371M 新しいタイプの光サイクル型動物オプシンの創製

Construction of a novel type of photocycle animal opsin

Kazumi Sakai[1], Yoshinori Shichida[2], Yasushi Imamoto[1], Takahiro Yamashita[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Res. Org. for Sci. and Tech., Univ. Ritsumeikan*)

20372M AUREO1-LOV ドメインの光誘起構造変化

Light-induced conformational switching of the LOV domain in aureochrome-1

Itsuki Kobayashi, Hiroto Nakajima, **Osamu Hisatomi** (*Grad. Sch. Sci., Osaka Univ.*)

20373M* 演題取り消し

20374M* 低温赤外分光測定による(6-4)光回復酵素の修復メカニズム解明

Elucidation of the repair mechanism of (6-4) photolyase by low-temperature FTIR spectroscopy

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.*)

20375M* カチオンチャネルロドプシン *Ts*_Rh3 における C 末端領域の重要性

Importance of the C-terminal region in cation channel rhodopsin *Ts*_Rh3

Rintaro Tashiro[1], Kumari Sushmita[2], Suneel Kateriya[2], Hideki Kandori[1], Satoshi Tsunoda[1,3] ([1]*Nagoya Inst. Tech.*, [2]*Jawaharlal Nehru Univ.*, [3]*JST PRESTO*)

20376M 高速 AFM によるロドプシンクラスター上トランスデューシン動的過程の観察

Dynamic process of G protein transducin on rhodopsin cluster observed by high-speed AFM

Kazuhiko Hoshikaya[1], Hayato Yamashita[1], Fumio Hayashi[2], Kenichi Morigaki[3,4], Masashi Fujii[5,6], Akinori Awazu[5,6], Masayuki Abe[1] ([1]*Graduate School of Engineering Science, Osaka University*, [2]*Graduate School of Science, Kobe University*, [3]*Biosignal research center, Kobe University*, [4]*Graduate School of Agricultural Science, Kobe University*, [5]*Graduate School of Science, Hiroshima University*, [6]*Graduate School of Integrated Sciences for Life, Hiroshima University*)

20377M Biophysical characterization of different members of TAT rhodopsins: a new group of microbial rhodopsins

Kentaro Mannen[1], Takashi Nagata[1,2], Oded Béjà[3], Keiichi Inoue[1] ([1]*Inst. Solid State Phys., Univ. Tokyo*, [2]*PRESTO, JST*, [3]*Biol., Israel Inst. Tech.*)

20378M Actinotalea fermentans におけるヘリオロドプシンの発現

Expression of Heliorhodopsin in Actinotalea fermentans

Rei Abe-Yoshizumi, Ai Muto, Hideki Kandori (*Nagoya Inst. Tech.*)

20379M 絶対嫌気性緑色硫黄光合成細菌における Rieske/cyt*b* 複合体と *c* 型シトクロム間の相互作用解析

Studies on interaction between Rieske/cyt*b* complex and *c*-type cytochromes in strictly anaerobic photosynthetic green sulfur bacteria

Hiraku Kishimoto[1], Takahiro Nagaoka[1], Chihiro Azai[2], Risa Mutoh[3], Hideaki Tanaka[4], Yohei Miyanoiri[4], Genji Kurisu[4], Hirozo 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.*)

20380M 脊椎動物の非視覚オプシン Opn5 の多様化の起源の探索

Origin of diversification of vertebrate non-visual opsin Opn5

Takahiro Yamashita[1], Kengo Fujii[1], Kazumi Sakai[1], Yasushi Imamoto[1], Hideyo Ohuchi[2], Yoshinori Shichida[3] ([1]*Grad. Sch. of Sci., Kyoto Univ.*, [2]*Grad. Sch. of Med., Dent. and Pharm. Sci., Okayama Univ.*, [3]*Ritsumeikan Univ.*)

20381M* アニオンチャネルロドプシン吸収波長制御機構の解明
Mechanism of absorption wavelength shifts in anion channelrhodopsin mutants
Masaki Tsujimura[1], Tomoyasu Noji[1,2], Keiichi Kojima[3], Yuki Sudo[3], Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*RCAST., Univ. Tokyo*, [3]*Grad. Sch. Med. Dent.& Pharm., Okayama Univ.*)

20382M AUREO1-LOV の光誘起構造変化に関与する水素結合
Hydrogen bonds involved in the light-induced conformational switching of AUREO1-LOV
Yumiko Adachi, Hiroto Nakajima, Osamu Hisatomi (*Graduate School of Science, Osaka University*)

20383M* 新たに同定した水素結合ネットワークによる植物由来(6-4)光回復酵素の補因子 FAD の光依存的還元反応の制御
A newly identified hydrogen-bonding network modulates photoreduction of the flavin cofactor in plant (6-4) photolyase
Yuhei Hosokawa[1], Ryuma Sato[2], Martin Saft[3], Pavel Muller[4], Klaus Brettel[4], Lars-Oliver Essen[3], Shigenori Iwai[1], Junpei Yamamoto[1] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*Riken*, [3]*Dept. Chem., Philipps Univ.*, [4]*I2BC, CEA, CNRS*)

20384M* 分光学的手法による霊長類青感受性視物質の光反応構造解析
Photochemical dynamics 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]*Grad. Sch. Eng., Nagoya Inst. Tech*, [2]*Prim. Res. Inst. Kyoto Univ.*)

20385M* Rhodococcus 属細菌が有するヘリオロドプシンの物性および生理機能の探索
Study on physiological functions and physical properties of heliorhodopsin possessed by Rhodococcus bacteria
Ai Muto, Rei Abe-Yoshizumi, Hideki Kandori (*Nagoya Inst. Tech.*)

20386M 光応答転写因子 Photozipper における二量体形成過程の高速 AFM 観察
High-speed AFM observation on dimer formation of a light-sensing transcription factor, Photozipper
Akihiro Tsuji[1], 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.*)

20387M 光による植物細胞の膜電位制御系の開発
Development of an light regulatory system of membrane potential in plant cell
Masae Konno[1,2], Hiromu Yawo[1], Hideki Kandori[3,4], Keiichi Inoue[1] ([1]*ISSP, Univ. Tokyo*, [2]*JST, PRESTO*, [3]*Life Sci. Appl. Chem., Grad. Sch. Eng., NIT*, [4]*OBTRC, NIT*)

20388M* ビブリオ属のブループロテオロドプシンが示す異常な pH 依存的吸収変化のメカニズム
Mechanism of unusual pH-dependent color change in blue-proteorhodopsin from *Vibrio califitulae*
Mizuki Sumikawa (*Nagoya Inst. Tech*)

20389M* 新規ロドプシンフォスホジエステラーゼ（Rh-PDE）8 種の分子特性
Molecular properties of eight novel rhodopsin phosphodiesterases (Rh-PDEs)
Masahiro Sugiura[1], Satoshi Tsunoda[1], Masahiko Hibi[2], Hideki Kandori[1] ([1]*Nagoya Institute of Technology*, [2]*Graduate School of Science, Nagoya University*)

20390M* 内外の配向でのセンサリーロドプシン II の表面増強赤外分光法
Surface-enhanced infrared spectroscopy on sensory rhodopsin 2 tethered with the inside or outside facing orientation
Jingyi Tang[1], Insyeerah Binti Muhammad Jauhari[1], Yuji Furutani[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*OptoBioTech. Research Center, Nagoya Inst. Tech.*)

20391M 電子励起状態における、フィコシアノビリンの構造変化に関する理論的研究
Exploring the structural changes of phycocyanobilin in the excited states
Kenji Mishima[1], Mitsuo Shoji[1,2], Yasufumi Umena[3], Yasuteru Shigeta[1] ([1]*CCS. Univ. Tsukuba*, [2]*JST-PRESTO*, [3]*Jichi Medical University*)

20392M 対称 I 型ヘリバクテリア反応中心光捕集過程の理論解析と光化学系 I との比較
Theoretical analysis of light harvesting mechanism of homodimeric type-I Heliobacterial reaction center: comparison to PSI
Akihiro Kimura[1], Hirotaka Kitoh[2,3], Yasuteru Shigeta[3], Shigeru Itoh[1] ([1]*Department of Physics, Graduate School of Science, Nagoya University*, [2]*JST, PRESTO*, [3]*Center for Computational Sciences, University of Tsukuba*)

20393M 錐体・桿体視細胞の外節における脂質環境の解析
Analysis of the lipid environment in outer segment membranes of rod and cone photoreceptor cells
Shuji Tachibanaki[1], Keiji Seno[2], Tateki Matsui[1], Masahiro Ueda[1] ([1]*Grad. Sch. of Frontier Biosci., Osaka Univ.*, [2]*Facultiy of Med., Hamamatsu Univ. Sch. of Med.*)

20394M 固体 NMR による内向きプロトンポンプロドプシン Schizorhodopsin のレチノール発色団の構造解析
Structure of retinal chromophore in Schizorhodopsin as studied by solid-state NMR
Seiya Tajima[1], Hideki Kandori[2], Keiichi Inoue[3], Izuru Kawamura[1] ([1]*Grad. Sch. Eng. Sci, Yokohama Nat. Uni.*, [2]*Nagoya Inst. Tech.*, [3]*Inst. Solid. State. Phys., Univ. Tokyo*)

20395M 共役二重結合系を延長したレチナールアナログによる赤色感受性チャネルロドプシンの更なる長波長シフト
Red-Shift of Red-Activatable Channelrhodopsin Using One-Double-Bond-Inserted Retinal Analogs
Yasushi Imamoto[1], Yi-Chung Shen[1], Toshikazu Sasaki[1], Takahiro Yamashita[1], Takashi Okitsu[2], Yumiko Yamano[2], Akimori Wada[2], Yoshinori Shichida[3] ([1]*Kyoto Univ.*, [2]*Kobe Pharm. Univ.*, [3]*Ritsumeikan Univ.*)

20396M 紅色光合成細菌の LH2 タンパク質の色素改変：色素のサイトエネルギーとタンパク質内励起エネルギー移動への影響
Pigment modification in LH2 proteins from purple photosynthetic bacteria: effects on pigment site-energy and intracomplex energy transfer
Yoshitaka Saga[1], Yuji Otsuka[1], Madoka Yamashita[1], Shiori Nakagawa[1], Yuto Masaoka[2], Tsubasa Hidaka[2], Yutaka Nagasawa[2] ([1]*Fac. Sci. Eng., Kindai Univ.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ.*)

20397M* Aureochrome-1 における LOV コアから活性ドメインへの情報伝達機構
Signal transduction from LOV core to effector domain in Aureochrome-1
Hiroto Nakajima, Itsuki Kobayashi, Osamu Hisatomi (*Grad. Sci. Sci., Univ. Osaka*)

20398M 天然アニオンシャネルロドプシン GtACR1 の分子機構に関する理論的研究
Theoretical study on molecular mechanics of natural anion channel rhodopsin GtACR1
Takafumi Shikakura, Cheng Cheng, Shigehiko Hayashi (*Kyoto Univ. Graduate School of Science*)

20399M Theoretical study of electron transport between cytochrome f and plastocyanin by using a coarse-grained simulation
Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

20400M 緑色硫黄細菌のルブレドキシン-酸素酸化還元酵素への電子供与系
Electron transfer path to the rubredoxin-oxygen oxidoreductase in green sulfur bacteria
Wanwipa Ittarat[2,4], Takeshi Sato[3], Masaharu Kitashima[2], Hidehiro Sakurai[2,3], Kazuhito Inoue[2,3], **Daisuke Seo**[1] ([1]*Grad Sch Nat Sci&Tec, Kanazawa Univ*, [2]*Dep Biol, Fac Sci, Kanagawa Univ*, [3]*Res Ins Int Sci, Fac Sci, Kanagawa Univ*, [4]*BIOTEC, NSTDA, Thailand*)

20401M *Heliobacterium modesticaldum* 由来反応中心における励起エネルギー移動および初期電荷分離に関する研究
Studies on excitation energy transfer and primary charge separation in the reaction center complex from *Heliobacterium modesticaldum*
Risa Kojima[1], Hayata Yamamoto[2], Chihiro Azai[3], Chiasa Uragami[4], Hideki Hashimoto[4], Daisuke Kosumi[5], Hirozo Oh-oka[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Sci & Tech., Kumamoto Univ.*, [3]*Coll. Life Sci., Ritsumeikan Univ.*, [4]*Fac. Sci & Tech., Kwansei Gakuin Univ.*, [5]*IINA, Kumamoto Univ.*)

20402M 光吸収計算によって現れた C-フィコシアニンの 6 量体構造の機能的な意味
Functional meaning of hexamer structure of C-phycocyanin revealed by calculation of absorption wavelength
Hiroto Kikuchi (*Dept. of Phys. Nippon Med. Sch.*)

20403M Connecting the spectral properties to the structure of photosystem I containing Chlorophyll-*f*
Rin Taniguchi[1], **Yutaka Shibata**[1], Toshiyuki Shinoda[2], Tatsuya Tomo[2], Shen Ye[1] ([1]*Tohoku Univ., Grad. Sch. Sci.*, [2]*Tokyo Univ. Sci., Fac. Sci.*)

20404M 海洋性藻類 *Guillardia theta* における微生物ロドプシンの遺伝子発現解析
Gene expression analysis of microbial rhodopsins from marine algae *Guillardia theta*
Yumeka Yamauchi[1], Masae Konno[1,2], Keiichi Inoue[1,2], Hideki Kandori[1,3] ([1]*Life Sci. & Appl. Chem., Nagoya Inst. Tech.*, [2]*ISSP, Univ. Tokyo*, [3]*OBTRC, Nagoya Inst. Tech.*)

20405M Theoretical study on molecular mechanism of a light-driven ion transport of Halorhodopsin
Ryo Oyama, Taisuke Hasegawa, Shigehiko Hayashi (*Grad. Sch. Sci., Kyoto Univ.*)

20406M Disruption of water-mediated H-bond network in rhodopsin mutations cause night blindness
Kota Katayama[1], Yuri Takeyama[1], Akiko Enomoto[1], Hiroo Imai[2], Hideki Kandori[1] ([1]*Grad.Sch.Eng., Nagoya Inst. Tech*, [2]*Primate Res. Inst. Kyoto Univ*)

20407M クロロフィル *f* をもつ光化学系 I 複合体の構造
Structural of photosystem I complex with chlorophyll *f*
Toshiyuki Shinoda[1], Koji Kato[2], Ryo Nagao[2], Seiji Akimoto[3], Jian-Ren Shen[2], Fusamichi Akita[2,4], Naoyuki Miyazaki[5,6], Tatsuya Tomo[1] ([1]*Fac. Sci., Tokyo Univ. Sci.*, [2]*RIIS., Okayama Univ.*, [3]*Grad. Sch. Sci., Kobe Univ.*, [4]*PRESTO, JST*, [5]*IPR., Osaka Univ.*, [6]*TARA., Tsukuba Univ.*)

20408M* In situ visualization of reversible state transition in live *Chlamydomonas* cells by noninvasive excitation spectral microscopy
Xianjun Zhang[1], Yuki Fujita[1], Ryutaro Tokutsu[2], Jun Minagawa[2], Shen Ye[1], Yutaka Shibata[1] ([1]*Tohoku Univ., Grad. Sch. Sci.*, [2]*NIBB, Div. Environ. Photobiol.*)

20409M Anion binding to mutants of the Schiff base counterion in heliorhodopsin
Anion binding to mutants of the Schiff base counterion in heliorhodopsin
Manish Singh[1], Kota Katayama[1], Oded Beja[2], Hideki Kandori[1] ([1]*Nagoya Inst. Tech*, [2]*Israel Inst. Tech*)

20410M* 光化学系 I 反応中心の電子移動におけるクロロフィルエピマー化の影響
Effect of chlorophyll epimerization on the electron transfer in photosystem I reaction center
Koji Mitsuhashi[1], Keisuke Saito[1,2], Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*)

20411M* 光化学系 II 水分解触媒部位の交換カップリングの起源
Origin of exchange couplings of the Mn_4CaO_5 cluster in photosystem II
Shunya Nishio[1], Keisuke Saito[1,2], Hiroshi Ishikita[1,2] ([1]*Fac. Eng., Univ. Tokyo*, [2]*RCAST., Univ. Tokyo*)

20412M Simultaneous Mapping of Fluorescence Spectra and Lifetimes of Chlorophylls Revealed Accumulation of Quenched LHCII
Yuki Fujita, Xianjun Zhang, Touru Kondou, Yutaka Shibata (*Organic Physical Chemistry Lab., Tohoku Univ.*)

20413M アゾベンゼン挿入 DNA と T7RNA ポリメラーゼの光転写制御ダイナミクス
Dynamics of photo-regulated transcription reaction of T7 RNA polymerase and azobenzene-tethered DNA
Gennosuke Takekawa (*Grad. Sch. Sci., Kyoto Univ.*)

20414M 青色光センサータンパク質 VVD の光反応ダイナミクス
Photoreaction dynamics of blue light sensor protein VVD
Takafumi Nakayama, Andrea Mussini, Yusuke Nakasone, Masahide Terajima (*Grad. Sch. Sci., Univ. Kyoto*)

20415M* The gate-keeper role of a highly conserved helix-3 tryptophan for ion transport of the channelrhodopsin chimera, C1C2/ChRWR
Yujiro Nagasaka[1], Shoko Hososhima[2], Keiichi Inoue[1], Hideki Kandori[2,3], Hiromu Yawo[1] ([1]*ISSP., Univ. Tokyo*, [2]*Grad. Sch. Eng., Nagoya Inst. of Tech*, [3]*Optobio., Nagoya Inst. of Tech*)

20416O 演題取り消し

20417O 天然の原核生物由来カルシウムチャネルにおけるイオン透過選択性の進化とその決定残基の同定
The selectivity determinant and evolution of a native prokaryotic voltage-dependent calcium channel
Katsumasa Irie[1], Takushi Shimomura[1,3], Yoshiki Yonekawa[2], Hitoshi Nagura[1], Michihiro Tateyama[3], Yoshinori Fujiyoshi[4] ([1]*CeSPI, Nagoya univ.*, [2]*Grad. Pharm. Med. Sci., Nagoya univ.*, [3]*Div. Biophys. Neurobio., NIPS*, [4]*CeSPL,TMDU*)

20418O* Effects of Oligopeptides on Growth of Primitive Vesicles
Akiko Baba[1], Kazuki Yokoyama[1], Ulf Olsson[2], Masayuki Imai[1] ([1]*Department of Physics, Faculty of Science, Tohoku University*, [2]*Department of Chemistry, Faculty of Science, Lund University*)

20419O* ベシクル表面上での情報分子成長
Growth of Information Molecules on Vesicle Surface
Yuto Hachiya[1], Hikaru Hatori[1], Syoichi Toyabe[2], Steen Rasmussen[3], Masayuki Imai[1] ([1]*Phys, Tohoku Univ.*, [2]*Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*, [3]*Phys, Chem Pharm, Univ. Southern Denmark*)

20420O 膜のないドロップレット内での RNA ゲノムの自己複製
Translation-coupled RNA replication in membrane-free droplets
Ryo Mizuuchi[1,2], Norikazu Ichihashi[1] ([1]*Komaba Institute for Science, Univ. Tokyo*, [2]*JST PRESTO*)

20421O Study on evolutionary fluctuation-response relationship in multicellular development
Chikara Furusawa[1,2] ([1]*BDR, RIKEN*, [2]*UBI, Graduate School of Science, The University of Tokyo*)

20422O* 膜面上の高分子合成と連携した持続的なベシクルの自己生産
Sustainable Reproduction of Vesicles coupled with a Surface-Confined Template Polymerization
Minoru Kurisu[1], Harutaka Aoki[1], Takehiro Jimbo[1], Yuka Sakuma[1], Sandra Luginbuhl[2], Peter Walde[2], Masayuki Imai[1] ([1]*Dept. of Phys., Tohoku Univ.*, [2]*Dept. of Mater., ETH*)

20423O How combination of DNA recombination and translation error allows efficient evolution?
Kenta Mitsutomi, **Daisuke Kiga** (*Waseda Univ, Dept Electrical Eng and Biosci*)

20424O* 進化実験による最も単純な等温条件下 DNA 複製機構の探索
Minimization of Elements for Isothermal DNA Replication by an Evolutionary Approach
Hiroki Okauchi[1], Yoshihiro Sakatani[2], Kensuke Otuka[2], Norikazu Ichihashi[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Bioinfo. Eng., Univ. Osaka*)

20425O ホストパラサイト相互作用による表現型可塑性の進化
Evolution of Phenotypic Plasticity in Host-Parasite Interactions
Naoto Nishiura, Kunihiko Kaneko (*The University of Tokyo Graduate School of Arts and Sciences*)

20426O* 高分子混雑環境下でのミクロ相分離が創成する細胞様構造体
Emergence of cell-like structure through micro phase separation in a crowding macromolecular solution
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.*)

20427O* 人工膜小胞内リン脂質合成による自律的細胞分裂機構の構築
Development of a self-reproducing vesicular system driven by internal phospholipid synthesis
Kota Nakajima[1], Shunsuke Okada[2], Hiroshi Ueno[1], Naoki Soga[1], Takahiro Muraoka[2], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Dept. Appl. Chem., Grad. Sch. Eng., Tokyo Univ. Agri. Tech.*)

20428O* 細菌アクチン MreB からスピロプラズマ遊泳モーターへの進化
Development of *Spiroplasma* swimming motor from bacterial actin, MreB
Daichi Takahashi[1], Ikuko Fujiwara[1,2], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci., Osaka City Univ.*, [2]*OCARINA, Osaka City Univ.*)

20429O 遺伝暗号における適応度地形の解析
Analysis of the fitness landscape of the genetic code
Yuji Omachi[1], Nen Saito[1], Chikara Furusawa[1,2] ([1]*Grad. Sch. Sci. UTokyo*, [2]*RikenBDR*)

20430O ~Parasite による Host 多様化の促進~ 原始的な多様性は如何にして生まれたか？
Host diversification promoted by parasites: prebiotic diversity in evolution
Rikuto Kamiura[1,2], Norikazu Ichihashi[1,2] ([1]*Graduate School of Arts and Science, The University of Tokyo*, [2]*Komaba Institute of Science, The University of Tokyo*)

P .ゲノム生物学・生命情報科学: ゲノミクス・分子進化／P. Genome biology & Bioinformatics

20431P Selection originating from protein stability/foldability: Relationships between protein folding free energy, sequence ensemble and fitness
Sanzo Miyazawa

20432P 自己集合ペプチドのオリゴマー形成に関する分子動力学的解析
Capturing oligomerization process of self-assembly peptides by using molecular dynamics simulations
Kota Kasahara[1,3], Junya Okigawa[1], Hiroki Terazawa[2], Qilin Xie[3], Satoshi Goto[2], Hayato Itaya[2], Katsufumi Nakayama[3], Takuya Takahashi[1] ([1]*Coll. Life. Sci., Ristumeikan Univ.*, [2]*Grad. Sch. Life Sci, Ritsumeikan Univ.*, [3]*Coll. Pharm. Sci., Ritsumeikan Univ.*)

20433P* Protein Data Bank に基づくタンパク質-ペプチド結合予測のための相互作用パターンの網羅的な分類と分析
Comprehensive classification and analysis of interaction patterns for protein-peptide binding prediction based on the Protein Data Bank
Keiichiro Sato[1], Kota Kasahara[1,2], Takuya Takahashi[1,2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

20434P 演題取り消し

20435P* 荷電性残基の分布がタンパク質の液-液相分離に与える影響の解明に向けた分子動力学シミュレーション
Molecular dynamics simulations to dissect effects of charge distributions in protein sequence on the liquid-liquid phase separation
Hiroki Terazawa[1], Junya Okigawa[2], Kota Kasahara[2], Hiroshi Imamura[2], Minoru Kato[2], Takuya Takahashi[2] ([1]*Grad. Sch. Life Sci, Ritsumeikan Univ.*, [2]*Coll. Life Sci, Ritsumeikan Univ.*)

20436P 分子動力学シミュレーションによるアクチン構造ゆらぎの解析
Structural flexibility of actin studied by molecular dynamics simulation
Ryotaro Koike, Motonori Ota (*Grad. Sch. Info., Nagoya Univ.*)

20437P* PC4 天然変性領域の VP16 結合の制御メカニズムの解明
Simulation study of the mechanism of PC4 unstructured region which regulates binding with VP16
Qilin Xie[1], Kota Kasahara[2], Masafumi Nakayama[1], Takuya Takahashi[2] ([1]*Coll. Pha Sci., Ritsumeikan Univ.*, [2]*Coll. Life Sci., Ritsumeikan Univ.*)

20438P ウニ初期胚の核及び核内動態の蛍光イメージング観察・解析
Imaging analysis of inter- and intra-nuclear dynamics of sea urchin embryo
Miko Imada[1], Ayaka Sugiyama[2], Sayaka Hayashi[2], Kaichi Watanabe[1], Yuhei Yasui[1], Naoaki Sakamoto[1], **Akinori Awazu**[1] ([1]*Dept. Math and Life Sciences*, [2]*Dept. Math and Life Sciences*)

20439P 不凍タンパク質の予測及び解析
Prediction and analysis of antifreeze protein
Ryosuke Miyata, Kentaro Shimizu, Tohru Terada, Yoshitaka Moriwaki (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

20440P 酵母の胞子形成の時系列マイクロアレイデータに対する効果的な非階層的クラスタリング手法開発の検討
Consideration of efficient non-hierarchical clustering method for time series microarray data of sporulation of S. cerevisiae
Aoi Tani[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Fac. Adv. Math. Sci., Meiji Univ.*, [2]*RDCMIT, Tokyo Med. Univ.*)

20441P DTX: 新規ヒト創薬ターゲット探索のための統合化ウェブツールの開発
DTX: An integrative web tool for exploring new potential drug targets in humans
Atsushi Hijikata, Masafumi Shionyu, Tsuyoshi Shirai (*Facult. Biosci, Nagahama Inst. Bio-Sci. Tech.*)

20442P DR-SIP: Predicting the Quaternary Structures of Homo-oligomeric Transmembrane Proteins
Wai Soon Chan[1,2,3], Jinhao Zhou[2,4], Christopher Llynard Ortiz[2], Chi-Hong Chang Chien[2], Rong-Long Pan[2], Lee-Wei Yang[2,3,5] ([1]*BioMol. Sim. Grp., Kansai Photon Sci. Inst., QST, Japan*, [2]*Inst. of BioInfo. and Struct. Bio., Nat. Tsing Hua Uni., Taiwan*, [3]*BioInfo., TIGP, Inst. of Info. Sci., Academia Sinica, Taiwan*, [4]*UTHealth Grad. Sch. of Biomed. Sci., Uni. of Texas, USA*, [5]*Phys. Div., Nat. Center for Theoretical Sci., Nat. Tsing Hua Uni., Taiwan*)

20443P 機械学習を利用した scRNAseq からの空間的遺伝子発現パターンの再構成
Prediction of spatial gene expressions from scRNAseq data by machine learning
Yasushi Okochi[1,2], Shunta Sakaguchi[3], Ken Nakae[4], Takefumi Kondo[3,5], Naoki Honda[1,6,7] ([1]*Laboratory for Theoretical Biology, Graduate School of Biostudies, Kyoto University*, [2]*Faculty of Medicine, Kyoto University*, [3]*Laboratory for Cell Recognition and Pattern Formation, Graduate School of Biostudies, Kyoto University*, [4]*Graduate School of Informatics, Kyoto University*, [5]*K-CONNEX*, [6]*Research Center for Dynamic Living Systems, Kyoto University*, [7]*Theoretical Biology Research Group, ExCELLS*)

20444P 蛍光増強 RNA アプタマーと cDNA ディスプレイを用いた高感度抗原検出法の開発
Development of a highly sensitive antigen detection method using fluorescence-enhanced RNA aptamer and cDNA display
So Higashide, Naoto Nemoto (*Graduate School of Science & Engineering, Saitama-University*)

20445P 機械学習を用いた PLP 結合タンパク質の予測
Prediction of PLP-binding proteins by using machine learning-based methods
Masafumi Shionyu, Tomohiro Hatta, Atsushi Hijikata (*Fac. Biosci., Nagahama Inst. Bio-Sci. Tech.*)

20446P Formation of chromatin remodeler Chd1-ADP-Pi analogues ternary complexes which mimic transient states in ATPase cycle
MD Noor A Alam, Sadakane Kei, Maruta Shinsaku (*SOKA UNIVERSITY*)

20447P 細胞イメージングへの応用のための蛍光増強アプタマーの開発
Development of fluorescence enhancement aptamers of dye for cell imaging applications
Tomoyuki Koike[1], Takashi Kubo[1], Kenjiro Hanaoka[2], Mitsuyoshi Ueda[3], Koichi Kuroda[3], Naoto Nemoto[1] ([1]*Graduate School of Science and Engineering, Saitama University.*, [2]*Graduate School of Pharmaceutical Sciences, The University of Tokyo.*, [3]*Graduate School of Agriculture, Kyoto University.*)

20448P* マルチタスク学習を用いたタンパク質-リガンド結合部位の統合的な予測
Integrated prediction of protein-ligand binding sites using multi-task learning
Haruka Nakashima, Yoshitaka Moriwaki, Tohru Terada, Kentaro Shinizu (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*)

20449P 電顕フィッティング計算のための高速な原子モデルの GMM への変換：PCA ボックスダウンサンプル法
Fast calculation of Gaussian mixture models for atomic models to fit them on electron microscopy map: PCA-box down-sampling method
Takeshi Kawabata, Haruki Nakamura, Genji Kurisu (*IPR, Osaka U.*)

20450P* GPCR オリゴマーに影響を及ぼすがん関連ホットスポット変異の予測
Prediction of cancer associated hotspot mutations that affect GPCR oligomerization
Sakie Shimamura[1], Vachiranee Limviphuvadh[2], Hiroyuki Toh[3], Wataru Nemoto[1] ([1]*Dept. Sch. & Tech., Tokyo Denki Univ.*, [2]*A*STAR, BII.*, [3]*Sch. of Sci. & Tech., Kwansei Gakuin Univ.*)

20451P Remodelers exploit spontaneous nucleosome fluctuations to reorganize chromatin
Giovanni Brandani, Shoji Takada (*Kyoto University, School of Science*)

20452P 電顕画像と立体構造情報との照合による膜タンパク質ファミリーの判別技術開発
Development of membrane protein family identifier by collating EM images and atomic coordinate data
Ryuji Shinozaki[1], Masami Ikeda[2], Chikara Sato[3], **Makiko Suwa**[1] ([1]*College of Sci. and Eng., Aoyamagakuin Univ.*, [2]*AIRC, AIST*, [3]*Health med., AIST*)

20453P Analysis of Genetic Variants Through Protein and Residue Sociability
Hafumi Nishi[1,2], Yuki Kagaya[1], Matsuyuki Shirota[3], Kengo Kinoshita[1] ([1]*Grad. Sch. Info. Sci., Tohoku Univ.*, [2]*Faculty Core Res., Ochanomizu Univ.*, [3]*Sch. Med., Tohoku Univ.*)

20454P* タンパク質機能部位予測に適切な相同配列群選択手法の構築
Construction of a set of appropriate homologous sequences to predict functional regions of a protein
Yuto Takahashi[1], Shoichiro Kato[1], Hiroyuki Toh[2], Wataru Nemoto[1] ([1]*Dept. Sch. & Tech., Tokyo Denki Univ.*, [2]*Sch. of Sci. & Tech., Kwansei Gakuin Univ.*)

20455P* 転写翻訳系とゲノムが同種の無細胞ゲノム転写翻訳系の確立
In vitro genome transcription-translation system using Escherichia coli systems
Yukino Matsui, Tatsuki Deyama, Nobuhide Doi, Kei Fujiwara (*Dept. Biosci. Info., Keio univ.*)

20456P A comparative study of external morphology and phylogeny in the two species of earthworms
Hayato Endou (*Oyama Highschool*)

20457P Protein-Protein interaction patterns distinguish the hearing-loss phenotype between syndromic and non-syndromic types
Thi Thu Ha Duong[1,2], Kei Yura[1,3,4] ([1]*Graduate School of Humanities and Sciences, Ochanomizu University, 2-1-1 Otsuka, Bunkyo, Tokyo 112-8610, Japan*, [2]*nstitute of Genome Research, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Cau Giay, Ha Noi, Vietnam*, [3]*Center for Interdisciplinary AI and Data Science, Ochanomizu University, 2-1-1 Otsuka, Bunkyo, Tokyo 112-8610, Japan*, [4]*Graduate School of Advanced Science and Engineering, Waseda University, 3-4-1 Okubo, Shinjuku, Tokyo 169-8555, Japan*)

20458P* PLA2 産生に関与する遺伝子と経路の同定
Identification of the genes and pathways responsible for PLA2 production
Eri Hayashi[1], Yuto Kimura[1], Shuichi Hirose[2], Satoko Nakamura[3], Norimasa Kashiwagi[3], Chiaki Ogino[3,4], Wataru Nemoto[1] ([1]*Dept. Sch. & Tech., Tokyo Denki Univ.*, [2]*NAGASE R&D Center*, [3]*hem Sci. & Eng., Grad. Sch. of Eng., Kobe Univ.*, [4]*Org. of Adv Sci & Tec., Kobe Univ.*)

Q. 生態・環境／Q. Ecology & Environment

20459Q 栄養構造を持つ 12 種微生物の人工生態系における確率現象
Stochastic phenomena in synthetic ecosystems of 12 microbial species with a trophic structure
Kazufumi Hosoda[1], Naomi Murakami[1], Shigeto Seno[2], Yutaka Osada[3], Hideo Matsuda[2], Chikara Furusawa[4], Michio Kondoh[5] ([1]*ITGP, Osaka univ.*, [2]*IST, Osaka univ.*, [3]*FRA*, [4]*Sci, Univ. Tokyo / BDR, Riken*, [5]*Life sci, Tohoku univ.*)

20460Q 蝶の模様の多様性と複雑性は、やわらかい要素やかたい要素を組み合わせて進化してきた
Combinations of flexible and fixed components facilitate colorful divergence and complexity in butterflies
Takao Suzuki (*Grad. Sch. Sci., Univ. Tokyo*)

20461Q 大阪府の石川における外来のアメリカツノウズムシの繁殖生態
The breeding ecology of the invasive alien Planaria, Girardia dorotocephala, in the middle reaches of the Isikawa river in Osaka Pref
Sakura Takahashi (*Osaka Pref. Tondabayashi H.S.*)

20462Q マミズクラゲの無性世代の 2 つの芽体を決める生息条件について
The habitat conditions determined two types of sprout formation of the asexual generation of Freshwater jellyfish, Craspedacusta sowerbii
Yuki Tanino, Yuta Hirayama, Sota Moriyama (*Osaka Pref.Tondabayashi H.S.*)

20463Q 金剛山地(大阪府)におけるヨツワクガビルの生息環境について
The Habitat of the Orobdella whitmani Oka in the Kongo Mountains (Osaka pref.)
Yuya Uenishi (*Osaka pref. Tondabayshi H.S.*)

20464Q 大阪府で初めて繁殖を確認したイワナ Salvelinus leucomaenis の生態とその由来の研究
The study of the ecology and origin of Salvelinus leucomaenis that has been confirmed to breed for the first time in Osaka prefecture
Kanato Nakamura, **Kaito Oana** (*Osaka pref. Tondabayashi H.S.*)

20465Q 三面コンクリート張り水路でゲンジボタルが生息できる理由
Reasons why Japanese Firefly, Luciola cruciate, can inhabit in a three-sided concrete channel
Takumi Matsuo, Tomoki Ikegawa (*Osaka Pref. Tondabayashi H.S.*)

20466Q 海浜植物のハマヒルガオが浜辺で生育できる理由
Reasons why the beach plant, Calystegia Soldanella, can grow on the beach
Kei Yanazawa (*Osaka Pref. Todabayashi H.S.*)

20467Q ドジョウの繁殖行動を誘発するトリガーについて
Triggers that trigger breeding behavior in loaches, Misgurnus anguillicaudatus,
Yohei Okugawa (*Osaka Pref. Tondabayashi H.S.*)

R. 数理生物学・非平衡・生体リズム／R. Mathematical biology, Nonequilibrium state & Biological rhythm

20468R Fisher 情報量による ERK リン酸化ダイナミクスの熱力学的性質の解明
The Fisher information of time reveals the thermodynamic property of ERK phosphorylation dynamics
Keita Ashida[1], Yohei Kondo[2,3,4], Kazuhiro Aoki[2,3,4], Sosuke Ito[1,5] ([1]*Universal Biology Institute, The University of Tokyo*, [2]*Exploratory Research Center on Life and Living Systems (ExCELLS), National Institutes of Natural Science*, [3]*National Institute for Basic Biology, National Institutes of Natural Sciences*, [4]*Department of Basic Biology, School of Life Science, SOKENDAI*, [5]*JST, PRESTO*)

20469R Life-logger, 1000 匹の線虫の寿命時間スケールでの行動動態を計測するためのビデオ撮影装置の開発
Life-logger, a video-recorder of crawling motion of 1,000 *C. elegans* individuals during their lifespan
Yukinobu Arata, Peter Jurica, Yasishi Sako (*Cellular Informatics Laboratory, Riken*)

20470R 度数情報だけで再訪性を判断するエージェントのネットワーク探索
A Random walk model on the Scale-Free Network with the Cognitive Biases
Koji Takashima, Tomoko Sakiyama (*Soka University*)

20471R* 遺伝子発現レベルの情報から ErbB シグナルの動態を予測する数理モデリング基盤の開発
Model-based prediction of ErbB signaling dynamics solely from the information about gene expression levels
Hiroaki Imoto, Marie Maeda, Suxiang Zhang, Mariko Okada (*IPR, Osaka Univ.*)

20472R Approximation of transition density of the conductance based neuronal model with noise
Takanobu Yamanobe (*Sch. Med., Hokkaido Univ.*)

20473R 人工トリペプチドからなる自己集合性ナノファイバーの進行波による力発生
Force generation by a propagating wave of artificial tripeptide-based fibrous assemblies
Ryou Kubota[1], Masahiro Makuta[2], Ryo Suzuki[3], Masatoshi Ichikawa[2], Motomu Tanaka[3], Itaru Hamachi[1,4] ([1]*Grad. Eng., Kyoto Univ.*, [2]*Grad. Sci., Kyoto Univ.*, [3]*Inst. Adv. Stud., Kyoto Univ.*, [4]*JST ERATO*)

20474R Quantifying expressive power of gene regulatory systems
Yohei Kondo[1,2], Kazuhiro Aoki[1,2,3] ([1]*ExCELLS*, [2]*SOKENDAI*, [3]*NIBB*)

20475R 質量保存を満たす反応拡散系にみられる相分離的な挙動
Phase-separation like behavior in mass-conserved reaction diffusion systems
Michio Tateno, Shuji Ishihara (*Shuji Ishihara Lab., Graduate School of Arts and Sciences, The University of Tokyo*)

20476R Investigation of related genes in the development of atopic dermatitis by geometric feature extraction from gene expression patterns
Takuya Hasebe[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ*, [2]*RDCMIT, Tokyo Med. Univ*)

20477R 脳神経系の可塑的結合力学系モデルにおける自己組織的ネットワーク
Self-organized network structures in coupled dynamical system with connection plasticity inspired by cerebral nervous system
Amika Ohara, Masashi Fujii, Akinori Awazu (*Dept. of math. and life sci. Hiroshima univ.*)

20478R ディープラーニング及びオートエンコーダーを用いた乳癌組織中の DEGs からの特徴抽出と予後予測
Feature extraction and prognosis prediction from DEGs in breast cancer tissue using Deep learning and Autoencoder
Yusuke Mizukoshi[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Fac. Adv. Math. Sci., Meiji Univ.*, [2]*RDCMIT, Tokyo Med. Univ.*)

20479R Determination of the interacting time between KaiA and KaiB during clock oscillation
Risa Mutoh[1], Takahiro Iida[1], Mino Hiroyuki[2] ([1]*Faculty of Sci. Fukuoka Univ.*, [2]*Grad. Sch. of Sci., Nagoya Univ.*)

20480R オンチップ単一細胞培養システムによる 3 細胞系心筋ネットワークの拍動同期過程の観察
Observation of synchronized beating cycles of cardiomyocytes during three cell network formation in on-chip single cell measurement assay
Yoshitsune Hondo[1], Kazufumi Sakamoto[1], Rikuto Sekine[2], Yuhei Tanaka[1], Haruki Watanabe[1], Kenji Shimoda[1], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

20481R Active Inference of Gradient in Reward-oriented Behavior
WeiQing Chen[1], Naoki Honda[1,2] ([1]*Grad. Sch. Bio., Univ. Kyoto*, [2]*Theoretical Biology Research Group, Exploratory Research Center on Life and Living Systems (ExCELLS), National Institutes of Natural Sciences, Okazaki, Aichi, Japan.*)

20482R 膜タンパク質のクラスター形成機構の数理的研究
A Mathematical study on the mechanism of cluster formation of membrane proteins
Hiroaki Takagi (*Sch. Med., Nara Med. Univ.*)

20483R ES 細胞分化初期における染色体動態
The dynamics of chromosomes on early differentiation stage from ES cell
Tetsushi Komoto, Masashi Fujii, Akinori Awazu (*Hiroshima univ. Grad. Sch. Integrated Sciences for Life*)

20484R* Inferring domain of Interactions among Dictyostelium discoideum colony from the Ensemble of Trajectories of cells
Udoy S. Basak[1,2], Sulimon Sattari[1], Md. Motaleb Hossain[1], Kazuki Horikawa[3], Tamkiki Komatsuzaki[1] ([1]*Hokkaido University*, [2]*Pabna University of Science and Technology*, [3]*Tokushima University*)

20485R 栄養の枯渇が引き起こす酵母の解糖系振動現象
Glycolytic Oscillation in Yeast Induced by Nutrient Depletion
Seiji Hatano[1], Noboru Nagata[1], Yutetsu Kuruma[2], Toshihiro Kawakatsu[1], Masayuki Imai[1] ([1]*Grad. Sch. Sci., Tohoku Univ.*, [2]*ELSI, Tokyo Inst. Tech.*)

20486R ミトコンドリア呼吸鎖エナジェティクスの速度論的解析
Kinetic analysis of energetics in mitochondrial respiratory chain
Ikuo Kujiraoka[1], Kotaro Takeyasu[2,3], Junji Nakamura[2,3] ([1]*Graduate school of science and technology, Univ. Tsukuba*, [2]*Faculty of pure and applied sciences, Univ. Tsukuba*, [3]*Tsukuba research center for energy materials science, Univ. Tsukuba*)

20487R Chromatin dynamics in Hox-mediated animal body development
Yoshifumi Asakura[1], Naoki Honda[1,2] ([1]*Grad. Sch. Biostudies, Univ. Kyoto*, [2]*ExCELLS, NINS*)

20488R エピジェネティック修飾の変化の影響を考慮した EM 遷移のシミュレーション
A model on the effects of epigenetic modification on epithelial-mesenchymal transitions (EMT)
Kenichi Hagiwara, Masaki Sasai (*Dept.Appl.phys.,Nagoya Univ.*)

20489R Length scale-dependent relaxation in chromatin with and without the transcription factory
Ashwin S. S[1], Yuji Itoh[2], Kazuhiro Maeshima[2], Masaki Sasai[1] ([1]*Department of Applied Physics, Nagoya University, Nagoya, JAPAN*, [2]*Structural Biology Center, National Institute of Genetics, Mishima, JAPAN*)

20490R 出芽酵母の DNA 二本鎖切断時における染色体動態の数理モデル
A mathmatical model of chromosomal dynamics in budding yeast during DNA double strand break
Shinjiro Nakahata, Akinori Awazu, Masashi Fujii (*Hiroshima univ. Grad. Sch. Integrated Sciences for Life*)

20491R Quantifying the length- and time-scales of influence of cells in collective motion
Sulimon Sattari[1], Udoy Basak[1], Md. Hossain Motaleb[1], Kazuki Horikawa[2], Tamiki Komatsuzaki[1] ([1]*Hokkaido University Research Institute for Electronic Science*, [2]*Tokushima Unviersity, Institute of Biomedical Sciences*)

20492R Circular probability currents and correlation functions for gene switching coupled with epigenetic dynamics
Bhaswati Bhattacharyya, Masaki Sasai (*Department of Applied Physics, Graduate School of Engineering, Nagoya University*)

20493R 植物のストレス応答を担う植物ホルモン時空間動態の数理モデル
Mathematical model of spatiotemporal dynamics of plant hormones responsible for plant stress response
Mariko Arimoto, Akinori Awazu, Masashi Fujii (*Grad. Sch. Sci., Univ. Hiroshima*)

20494R 協同的に振る舞う遺伝子発現制御ネットワークの定量的解析
Quantitative analysis of cooperative network from sloppy gene expression dynamics
Masayo Inoue[1], Kunihiko Kaneko[2] ([1]*IMS, Meiji Univ.*, [2]*Univ. of Tokyo*)

20495R ヒトゲノム中の 3 塩基リピート配列周辺エピゲノムとクロマチン構造のゲノムワイドな解析
Genome-wide analysis of epigenetic and chromatin-structural features around triplet repeat sequences in human genome
Kenji Ojima[1], Yuudai Hirose[2], Masashi Fujii[1], Akinori Awazu[1] ([1]*Department of Mathematical and Life Sciences, Graduate School of Integrated Sciences for Life, Hiroshima University*, [2]*Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University*)

20496R バクテリアの集団運動による走性の変化
Enhanced bacterial taxis by collective movement
Tatsuro Kai, Takahiro Abe, Shuichi Nakamura, Seishi Kudo, Shoichi Toyabe (*Department of Applied Physics, Graduate School of Engineering, Tohoku University*)

20497R Fluctuation distribution of propagation time was conserved during excitation conduction in lined-up cardiomyocyte networks
Kazufumi Sakamoto[1], Yoshitsune Hondo[1], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

20498R Vector analysis of amoeba motion with respect to the propagation of chemoattractant cyclic-AMP
Vector analysis of amoeba motion with respect to the propagation of chemoattractant cyclic-AMP
Md. Motaleb Hossain[1,2], Sulimon Sattari[1], Udoy S Basak[1], Kazuki Horikawa[3], Tamiki Komatsuzaki[1] ([1]*Hokkaido University*, [2]*University of Dhaka*, [3]*Tokushima University*)

20499R* 免疫系の記憶ダイナミクスにおける適応的な抗原の有害・無害識別
Adaptive Discrimination of Risk of Antigens in Immune Memory Dynamics
Kana Yoshido[1], Naoki Honda[1,2] ([1]*Grad. Sch. Biostudies, Univ. Kyoto*, [2]*ExCELLS, NINS*)

20500R* ERK シグナル伝達系の進化生化学
Evolutionary biochemistry of ERK signaling network
Masaya Mukai[1,2,3], Yohei Kondo[2,3], Kazuhiro Aoki[1,2,3] ([1]*Division of Quantitative Biol., NIBB*, [2]*Quantitative Biol. Group, ExCELLS*, [3]*Dept. of Basic Biol., Sch. of Life Sci., SOKENDAI*)

20501S BSA における AQDS 結合サイトの光誘起電子電子二重共鳴(DEER)計測
Light-induced DEER measurement on the AQDS-binding site in Bovine Serum Albumin
Hiroki Nagashima, Lewis Antill, Kiminori Maeda (*Dep. Chem., Grad. Sch. Sci., Saitama University*)

20502S ヒト皮膚または培養皮膚に貼付したセラミド含有粘着性ゲルシートからのセラミド放出のマイクロ FT-IR 分光法による計測
Micro FT-IR Spectroscopic Study on Ceramide-release from Ceramide-Containing Adhesive Gel Sheet Affixed to Human Skin or Cultured Skin
Hiroshi Takahashi[1], Ryota Watanabe[2], Kenichi Nishimura[2], Taro Moriwaki[3] ([1]*Grad Sci Sci.&Tech., Gunma Univ.*, [2]*ALCARE Co., Ltd.*, [3]*JASRI/SPring-8*)

20503S ウニの発生初期における核内染色体構造の動的および細胞特異的変化
Dynamic and cell specific changes in intranuclear chromosomal structures during early development of sea urchin
Yuhei Yasui, Ayaka Sugiyama, Naoaki Sakamoto, Akinori Awazu (*Integrated science for life, Hiroshima University*)

20504S 伝導度計測を用いたペプチドのリン酸化の単一分子検出
Single-molecule detection of peptide phosphorylation using electrical conductance measurement
Takanori Harashima[1], Yoshiyuki Egami[2], Tomoya Ono[3], Tomoaki Nishino[1] ([1]*School of Science, Tokyo Institute of Technology*, [2]*Faculty of Engineering, Hokkaido University*, [3]*Department of Electrical and Electronic Engineering, Kobe University*)

20505S* イオン液体-スピン乾燥法で走査型電子顕微鏡の試料作製を容易にする
A simple and quick method to prepare biological specimens for scanning electron microscopy by an ionic liquid
Tatsuya Suehiro, Naoki Uemura, Saki Taguchi, Katsuya Shimabukuro (*Chem. Bio. Eng., NIT Ube College*)

20506S 短波赤外光を発する量子ドットによる無侵襲マウス脳表血管造影とその焦点合わせについて
Novel angiography for mouse cerebral vasculature using short-wave infrared light emitting quantum dots and its focusing
Tatsuto Iida[1], Hiro Yamato[1], Takashi Jin[2], **Yasutomo Nomura**[1,2] ([1]*Department of Systems Life Engineering, Maebashi Institute of Technology*, [2]*RIKEN Center for Biosystems Dynamics Research*)

20507S Variogram/Correlogram 法を使った生物対流解析
Variogram and correlogram assay of cell motility: Bioconvection in harmful algae *Chattonella*
Mina Nakahara, Atsuto Kobayashi, **Shinji Kamimura** (*Dept. Biol. Sci., Fac. Sci. & Eng., Chuo Univ.*)

20508S 分裂期の染色体の 3D-AFM 像の理論予測と実測との比較
A theoretical prediction of 3D atomic force microscopy image of chromosomes in mitotic phase and its comparison with experiments
Takashi Sumikama[1], Keisuke Miyazawa[1,2], Makiko Meguro-Horike[3], Ryohei Kojima[2], Naoko Okano[2], Shin-ichi Horike[3], Adam S. Foster[1,4], Takeshi Fukuma[1,2] ([1]*Nano Life Sci. Inst. (WPI-NanoLSI), Kanazawa Univ.*, [2]*Grad. Sch. of Nat. Sci. and Tech., Kanazawa Univ.*, [3]*Div. of Func. Gen., Adv. Sci. Res. Center, Kanazawa Univ.*, [4]*Dept. of Appl. Phys., Aalto Univ.*)

20509S 原子間力顕微鏡の位相イメージングを用いた *Paracoccus denitrificans* 細胞に結合した膜小胞の解析
Analysis of bacterial extracellular membrane vesicles bound to *Paracoccus denitrificans* cell by atomic force microscopy phase imaging
Yousuke Kikuchi[1], Yuuki Ichinaka[1], Masanori Toyofuku[2,3], Nozomu Obana[3,4], Nobuhiko Nomura[2,3], Azuma Taoka[1,5] ([1]*Col. of Sci. and Eng., Kanazawa Univ.*, [2]*Life and Env. Sci., Tsukuba Univ.*, [3]*MiCS, Tsukuba Univ.*, [4]*Trans. Med. Res., Tsukuba Univ.*, [5]*WPI-NanoLSI, Kanazawa Univ.*)

20510S 神経細胞分化における細胞内温度の関与
Involvement of intracellular temperature in neuronal differentiation
Shunsuke Chuma[1], Kohki Okabe[2,3], Yoshie Harada[1,4] ([1]*IPR, Osaka Univ.*, [2]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [3]*PRESTO, JST*, [4]*QIQB, OTRI, Osaka Univ.*)

20511S 原子間力顕微鏡と多孔窒化シリコン薄膜を用いた生きた細胞表面の高分解能観察方法の開発
Development of high-resolution observation method of living cell surface in atomic force microscope using porous silicon nitride membrane
Takehiko Ichikawa[1], Taiki Kitamura[2], Dong Wang[1,3], Hiroko Oshima[3], Masanobu Oshima[1,3], Takeshi Fukuma[1,2] ([1]*NanoLSI, Kanazawa Univ.*, [2]*College of Science and Engineering, Kanazawa Univ.*, [3]*Cancer Research Institute, Kanazawa Univ.*)

20512S 自動イオンチャネル電流測定装置の開発
Development of a system for automated ionic current measurement
Minako Hirano[1], Masahisa Tomita[2], Chikako Takahashi[1], Nobuyuki Kawashima[2], Toru Ide[3] ([1]*Grad. Sch. Creation Photon Indust.*, [2]*SYSTEC Corporation*, [3]*Okayama Univ.*)

20513S 上皮成長因子受容体癌変異への自動化 1 分子解析の薬理学的応用
Pharmacological application of automated single-molecule analysis for EGFR cancerous mutants
Michio Hiroshima[1,2], Daisuke Watanabe[3], Masahiro Ueda[1,3] ([1]*RIKEN BDR*, [2]*RIKEN CPR*, [3]*FBS, Osaka Univ.*)

20514S 生細胞 1 分子超解像イメージングによるヒストンバリアントのナノスケール局在解析
Nano-scale localization analysis of histone variants in living cells using single-molecule super-resolution imaging
Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech*)

20515S サブミリ秒光波面シェイピングシステムによる厚さ 2mm の鶏肉を通した光集束及び蛍光イメージング
Optical focusing and fluorescence imaging through a 2mm thick chicken tissue slice by submillisecond wavefront shaping system
Atsushi Shibukawa, Keiichi Kojima, Yuki Sudo (*Grad. Sch. of Med. Dent. Pharm. Sci., Okayama Univ.*)

20516S Development of continuous non-clogging cell fractionation technique using pillar arrangement and AC electric field
Kaito Asahi[1], Moe Iwamura[2], Masao Odaka[3,4], Akihiro Hattori[3,4], Kenji Yasuda[1,2,3,4] ([1]*Dept. 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*)

20517S Interaction of nicked-DNA with solid state nanopores
Shimba Ichino, Kento Lloyd, Takumi Yoshikawa, Ryoma Omori, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ.*)

20518S Simple precise flow speed measurement in an on-chip flow cytometer with simultaneous two-wavelength differential image analysis
Toshinosuke Akimoto[1], Shuya Sawa[1], Masao Odaka[3], Akihiro Hattori[3], Mitsuru Sentoku[1], Hiromiti Hasimoto[2], Kaito Asahi[1], Kenji Yasuda[1,2,3] ([1]*Dept. 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.*)

20519S 多次元デジタルバイオアッセイで明らかになった、インフルエンザウイルスにおける粒子ごとの薬剤応答の多様性
Multi-Dimensional (MD) Digital Bioassay unveils heterogeneous drug-susceptibility of influenza A virus in a single-virus resolution
Shingo Honda[1], Kazuhito V. Tabata[2], Yoshihiro Minagawa[2], Hiroyuki Noji[1,2] ([1]*Dept. Bioeng., Grad. Sch. Eng., Univ. Tokyo*, [2]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

20520S Ligand is not necessary for progress of engulfment in IgG-coated and non-coated mixture of antigen cluster
Amane Yoshida[1], Yuya Furumoto[1], Toshiki Azuma[1], Tomoyasu Sakaguchi[1], 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]*WASEDA Biosci. Res. Ins. in Singapore (WABIOS)*)

20521S 光ファイバー型蛍光相関分光装置を用いたエクソソームの同定
Identification of exosome by using optical fiber based fluorescence correlation spectroscopy
Misato Osaka[1], Johtaro Yamamoto[2,3], Masataka Kinjo[3] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Health & Med. Res. Inst., AIST*, [3]*Fac. of Adv. Life Sci., Hokkaido Univ.*)

20522S 最大エントロピー法と変分ベイズクラスタリングを用いた 1 分子 FRET データ解析による細胞質中 RAF のダイマー化状態の検出
Dimer formation of cytosolic RAF detected by single-molecule FRET analysis based on maximum entropy and variational Bayes-culstering
Kenji Okamoto, Yasushi Sako (*RIKEN CPR*)

20523S Investigation of automatic single-molecule tracking method for large-scale single-molecule imaging analysis
Sotaro Mori[1], Masato Yasui[4], Satomi Matsuoka[1,2,3,5], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. Sci., Univ. Osaka*, [2]*Grad. Sch. Sci. of Front. Biosci., Univ. Osaka*, [3]*BDR, RIKEN*, [4]*ZIDO Corp.*, [5]*PRESTO, JST*)

20524S* ヨーロッパモノアラガイの咀嚼神経系の蛍光 NO イメージング ー味覚嫌悪学習前後の NO 放出の比較
Fluorescence NO imaging for feeding nervous system of the pond snail-Comparison of NO release before and after taste-aversive conditioning
Ayaka Itoh[1], Yoshimasa Komatsuzaki[2], Minoru Saito[1] ([1]*Grad. Sch. of Int. Bas. Sci., Nihon Univ.*, [2]*Coll. Sci. Tech., Nihon Univ.*)

20525S DNA ナノデバイスを用いた細胞の機械シグナルイメージング技術開発
Development of mechanical signal imaging technique using DNA nano-device
Hiroki Fukunaga[1], Takahiro Saito[1], Satiko Onishi[2], Mitsuhiro Iwaki[1,2] ([1]*FBS, Univ. Osaka*, [2]*BDR, Riken*)

20526S クロモセンター領域内外におけるヘテロクロマチンタンパク質 HP1α 動態の生細胞 1 分子イメージング定量解析
Dynamics of Heterochromatin protein 1α inside and outside chromocenter domain in living cells using single-molecule imaging
Masanori Nakano[1], Yuma Ito[1], Takahiro Maeda[1], Chikashi Obuse[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Inst. Tech.*, [2]*Biosci. Grad Sch Sci., Osaka Univ*)

20527S 補償光学系を用いた 1 分子イメージングにおける収差補正のシミュレーション
Light field simulation of single-molecule imaging for aberration correction using adaptive optics
Xiang Zhou, Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech.*)

20528S 核小体タンパク質の多色超解像 1 分子イメージング解析
Multicolor single-molecule imaging analysis of the nucleolar proteins
Supanut Sirisukhodom[1], Yuma Ito[1], Noriko Saitoh[2], Makio Tokunaga[1] ([1]*Sch. Life Sci. Tech., Tokyo Tech.*, [2]*Div. of Cancer Biol., The Cancer Inst. JFCR.*)

20529S Development of an enzyme-coupled fluorometric digital bioassay for ATPase
Hiroshi Ueno, Mayu Hara, Mio Sano, Hiroyuki Noji (*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

20530S 2 光子生体イメージングでみるインフルエンザウイルス感染肺
In vivo imaging of the cellular pathophysiology in influenza virus-infected mouse lung
Hiroshi Ueki[1], Yoshihiro Kawaoka[1,2,3] ([1]*Division of Virology, Department of Microbiology and Immunology, Institute of Medical Science, University of Tokyo*, [2]*Department of Special Pathogens, International Research Center for Infectious Diseases, Institute of Medical Science, University of Tokyo*, [3]*Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison*)

20531S Direct observation of force-induced release of SecM translation arrest
Zhuohao Yang[1], Ryo Iizuka[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. Pharm. Sci., The Univ. Tokyo.*, [2]*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

20532S パッチクランプ AFM の開発に向けて
Toward the development of Patch Clamp Atomic Force Microscopy
Takeru Matsubara[1], Shinji Watanabe[2], Toshio Ando[2], Noriyuki Kodera[2] ([1]*Grad. Sch. NanoLS., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

20533S* Biophysical analysis of pH-dependent conformational change of LDLR family members in ligand capture and release

Aki Shiozawa[1], Noriyuki Kodera[2], Terukazu Nogi[1] ([1]*Grad. Sch. of Med. Lif. Sci., Yokohama City Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

20534S* 客観的な生物物理学データ解析に向けた初期パラメータ設定を必要としない隠 れマルコフモデルフィッティング手法の開発

Development of a new hidden Markov model fitting algorithm without predefinition of parameters for objective biophysical data analysis

Hanjin Liu, Tomohiro Shima, Sotaro Uemura (*Sch. Sci., Univ. Tokyo*)

20535S DNA motions near geometrically anisotropic nanopores

Takumi Yoshikawa, Ryoma Omori, Shimba Ichino, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ.*)

20536S* 統計的蛍光画像解析による濃度分布イメージング

Fluorescence Imaging for Concentration Based on Statistical Analysis

Ryosuke Fukushima[1], Johtaro Yamamoto[2,3], Masataka Kinjo[3] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Health & Med. Res. Inst., AIST*, [3]*Fac. of Adv. Life Sci., Hokkaido Univ.*)

20537S* Hybrid Photon Counting (HPC)検出器の microED 法への応用

Hybrid Photon Counting (HPC) detector application for microED method

Keigo Takahira[1,2], Kotaro Tanaka[1], Takeyoshi Taguchi[2], Hiroyuki Kanda[2], Akihito Yamano[2], Takuo Yasunaga[1] ([1]*Grad.Sch.Comp.Sci.Syst.Eng.,KIT,Fukuoka,Japan*, [2]*Rigaku Corporation,Tokyo,Japan*)

20538S* 環境の温度変化に対する RNA の状態変化を介した細胞応答の解明

Investigating cell response to environmental temperature change via RNA state changes

Hiroki Shibata[1], Kohki Okabe[1,2], Takashi Funatsu[1] ([1]*Grad. Sch. of Pharm. Sci., The Univ of Tokyo*, [2]*PRESTO, JST*)

20539S* 繊毛虫 *Tetrahymena* による遊泳軌跡の三次元定量

Three-dimensional analysis of the swimming trajectories of *Tetrahymena*

Akisato Marumo, Kyohei Matsuda, Masahiko Yamagishi, Mitsuhiro Sugawa, Junichiro Yajima (*Dept. Life Sci., Grad. Arts & Sci., Univ. Tokyo*)

20540S 相関顕微鏡法（CLEM）による同一試料観察に向けた相関・位置合わせ精度の改善

Improvement of correlation and alignment accuracy toward the same sample observation by CLEM

Yuki Gomibuchi[1], Risa Ezoe[2], Hiroko Takazaki[1,3], Yasuhisa Honda[2], Yusuke V. Morimoto[1], Takuo Yasunaga[1] ([1]*Dept. of Phys. Info. Tech., Kyushu Inst. Tech*, [2]*Dept. of Biosci. Bioinfo., Kyushu Inst. Tech.*, [3]*IPR. Osaka Univ.*)

20541S 画像解析システム Eos の次世代開発に向けて

Approach to the next generation of our developing image processing system, Eos

Takuo Yasunaga (*Comp. Sci and Sys. Eng., Kyutech*)

20542S 高速原子間力顕微鏡データと分子シミュレーションのデータ同化によるミオシン V の動的構造解析

Dynamic structure analysis of myosin V by data assimilation combining HS-AFM data and molecular simulations

Sotaro Fuchigami[1], Rie Koga[2], Shoji Takada[1] ([1]*Grad. Sch. of Science, Kyoto Univ.*, [2]*ExCELLS, NINS*)

20543S 水素化アモルファスシリコンと有機半導体で増強された分子薄膜を用いた揮発性 化合物のセンサシステム

A sensor system for volatile organic compound using molecular film enhanced by hydrogenated amorphous silicon and organic semiconductor

Hikaru Hatakeyama[1], Kisiro Seino[1], Shu Mugita[1], Kairi Shimazaki[1], Hiroshi Masumoto[2], Yutaka Tsujiuchi[1] ([1]*Material Science and Engineering, Akita University*, [2]*Frontier Research Institute for Interdisciplinary, Tohoku University*)

20544S 水素化アモルファスシリコンの上に積層したバクテリオロドプシンの分子間相互作用と構造変化
Inter molecular interaction and structural change of bacteriorhodopsin film laminated on hydrogenated amorphous silicon film
Yutaka Tsujiuchi[1], Hikaru Hatakeyama[1], Koki Shimanaka[1], Hiroshi Masumoto[2] ([1]*Mat.Sci.AkitaUNIV*, [2]*Fris.TohokuUNIV*)

20545S 粒子フィルター MD シミュレーションによる高速 AFM の非斉時ビデオのデータ同化
Particle-filter MD simulations to assimilate asynchronous video data of high-speed AFM
Suguru Kato, Sotaro Fuchigami, Shoji Takada (*Kyoto University*)

20546S HPD を用いた広視野蛍光 1 分子検出による局所環境変化のモニタリング
Local ambient condition monitoring by hybrid photo-detector (HPD)-based wide-field single-molecule fluorescence detection
Atsuhito Fukasawa[1], Gaku Nakano[1], Takayasu Nagasawa[1], Minako Hirano[2], Toru Ide[3], Hiroaki Yokota[2] ([1]*Hamamatsu Photonics K.K.*, [2]*Grad. Sch. Creation Photon Indust.*, [3]*Grad. Sch. Interdiscip. Sci. Eng. Health Sys.*)

20547S 多様な構造をもつタンパク質複合体の単粒子解析を改善する方法の調査研究
A survey and investigation on methods to improve single particle analysis of heterogeneous protein complexes
Kotaro Tanaka, Takuo Yasunaga (*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech*)

20548S 生物発光共鳴エネルギー移動による発光バクテリアルシフェラーゼの高輝度化
Enhanced brightness of bacterial luciferase by bioluminescence resonance energy transfer
Tomomi Kaku, Megumi Iwano, Tetsuyuki Entani, Kenji Osabe, Takeharu Nagai (*The Institute of Scientific and Industrial Reseach, Osaka University*)

20549S* Wash-free デジタルバイオ計測のための split enzyme の開発
Development of a split enzyme for wash-free digital bioassay
Yanbo Ma, Hiroshi Ueno, Hiroyuki Noji (*Department of Applied Chemistry, Graduate School of Engineering, University of Tokyo*)

20550S Raman imaging for cancer diagnosis
Clement Jean-Emmanuel[1], Mochizuki Kenntaro[2], Fujita Katsumasa[3], Komatsuzaki Tamiki[1] ([1]*RIES Hokkaido University*, [2]*Kyoto University*, [3]*Osaka University*)

T .バイオエンジニアリング・結晶成長・結晶化技術／T. Bioengineering, Crystal growth & Crystallization technique

20551T FRAP 法と遺伝子組換えを併用した反応拡散分子の細胞内動態解析
FRAP combined with genetic manipulation reveals the kinetics of actin-binding proteins in cells
Takumi Saito[1,2], Daiki Matsunaga[1], Tsubasa Matsui[1], Kentaro Noi[1], Shinji Deguchi[1] ([1]*Grad. Sch. Eng. Sci., Osaka uni.*, [2]*JSPS Research Fellow*)

20552T 高汎用性を目指した改良凝固ゲル中結晶化法の開発と評価
Development and evaluation of the high-strength hydrogel method for high versatility
Taichi Naruse[1], Mihoka Amano[1], Noriaki Kunimune[2], Tsuguo Nagasawa[2], Hiroaki Adachi[3], Yusuke Mori[4], Shigeru Sugiyama[5] ([1]*Grad. Sch. Sci., Kochi Univ.*, [2]*KUNIMUNE Inc.*, [3]*SOSHO Inc.*, [4]*Grad. Sch. Eng., Osaka Univ.*, [5]*Fac. Sci. & Tec., Kochi Univ.*)

20553T DNA オリガミによる人工 γ-TuRC
Artificial γ-TuRC made by DNA origami
Daisuke Inoue (*Kyushu University*)

20554T 集光レーザービームによる動的微小管ネットワークの形成
Formation of dynamic microtubule networks by focused laser beam
Kei Takano[1], Takuya Takeshige[1], Humika Kiryu[1], Ryuzo Kawamura[1], Chi-shiun Wu[2], Shih Yang-Hshin[2], Seiichiro Nakabayashi[1], Teruki Sugiyama[2,3], Hiroshi Yoshikawa[1] ([1]*Grad. Chem., Saitama Univ.*, [2]*App. Chem., National Chiao Tung Univ.*, [3]*Mate. Sci., Nara Inst. Sci. Tech. Univ.*)

20555T Combination approach for identification of highly-active mutant of processive chitinase
Akasit Visootsat[1,2], Akihiko Nakamura[3], Tak-Wai Wang[4], Ryota Iino[1,2] ([1]*Department of Functional Molecular Science, School of Physical Sciences, The Graduate University for Advanced Studies*, [2]*Institute for Molecular Science*, [3]*Department of Applied Life Sciences, Faculty of Agriculture, Shizuoka University*, [4]*Chimie ParisTech*)

20556T Culture-independent method for screening macromolecule-degrading microbes using deformability-based microfluidic microdroplet sorting
Mikihisa Muta[1], Kai Saito[1], Ryo Iizuka[1], Wataru Kawakubo[2], Hyun Yoon Dong[3], Tetsushi Sekiguchi[3], Shuichi Shoji[2], 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.*)

20557T 方向性を持った運動をするアメーバ型分子ロボットの開発
Toward vector motion of the cell-sized motorized molecular
Noriki Fukami[1], Yuichi Hiratsuka[2], Ibuki Kawamata[1], Yuki Suzuki[1,3], Satoshi Murata[1], Shin-ichiro Nomura[1] ([1]*Department of Robotics, Graduate School of Engineering, Tohoku University, Sendai 980-8579, Japan.*, [2]*Japan Advanced Institute of Science and Technology*, [3]*Frontier Research Institute for Interdisciplinary Sciences, Tohoku University*)

U. その他／U. Other topics

20558U Topological Data Analysis of Large-scale Multicellular Networks
Suguru Shimomura[1], Satoru Iwasaki[1], Tadashi Nakano[2] ([1]*Graduate School of Information Science and Technology, Osaka University*, [2]*Institute for Datability Science, Osaka University*)

20559U Observation of floating phenomenon of *Cyclotella meneghiniana* by direct microscope: Temperature dependence analysis using a heater
Yuki Ide[1], Yuji Matsukawa[1], Daisuke Miyashiro[1], Shigeki Mayama[2], Matthew L. Julius[3], Kazuo Umemura[1] ([1]*Tokyo Univ. Sci.*, [2]*Tokyo Gakugei Univ.*, [3]*St. Cloud State Univ.*)

20560U 矢が優れた飛び道具である理由ー自作風洞実験装置を用いた飛行する矢に働く力の分析ー
The reason why the arrow is superior flying tool - Analysis of forces acting on flying arrows by using a home-made wind tunnel device -
Haruto Tgawa, Akito Wada, Hinata Furuya, Ayumu Yamamori (*Osaka Pref. Tondabayashi H.S.*)

20561U 一本鎖 DNA を被覆した単層カーボンナノチューブと細胞膜間の力学的相互作用
Mechanical interaction between single-strand DNA wrapped single-walled carbon nanotubes and cell membrane
Daisuke Miyashiro[1,2], Ryo Hamano[1], Kazuo Umemura[1] ([1]*Tokyo University of Science*, [2]*ESTECH CORP.*)

20562U 二本鎖 DNA とカルボキシメチルセルロースで分散した単層カーボンナノチューブの吸光度特性
Absorption properties of single-walled carbon nanotubes dispersed with double-stranded DNA and carboxymethylcellulose
Ryo Hamano[1], Daisuke Miyashiro[1,2], Kazuo Umemura[1] ([1]*Tokyo Univ. Sci.*, [2]*ESTEC CORP.*)

20563U 空気の抵抗が雷の発生と発光に及ぼす影響
Effect of air resistance on the generation and lightning of thunderbolt
Shingo Iwasaki (*HatusibaTondabayasi H.S.*)

20564U 基準振動解析を用いたロドプシンの動態予測と機能の連関
Relationship between function and dynamics of rhodopsin using normal mode analysis
Yukito Kaneshige[1], **Masashi Fujii**[1,2], Fumio Hayashi[3], Kenichi Morigaki[4], Hayato Yamashita[5], Akinori Awazu[1,2] ([1]*Dept. Math. Sci., Grad. Sch. Sci., Hiroshima Univ.*, [2]*Dept. Math. Sci., Grad. Integ. Sci. Life, Hiroshima Univ.*, [3]*Grad. Sch. Sci., Kobe Univ.*, [4]*Biosignal Research Center, Kobe Univ.*, [5]*Grad. Sch. Eng. Sci., Osaka Univ.*)

20565U Attempts at CA-type formal analysis of fibrous assembly of particles
Takashi Konno (*Math. Biol. Med. Univ. Fukui*)

20566U Formation of small G-protein Ras multimer induced by chemical modification of HVR domain
Rufiat Nahar[1], Maruta Shinsaku[2] ([1]*NAHAR RUFIAT*, [2]*SHINSAKU MARUTA*)

20567U 模型飛行機の主翼長が滑空性能に与える影響
The Effect of Wing Length on Gliding Performance of Model Airplanes
Fumiya Yamanaka (*Osaka Pref. Tondabayashi H.S.*)

20568U 円環気流接合殺菌法によるウイルス感染ルートの遮断
Blocking virus infection routes by CARS-sterilizattion
Kuniaki Nagayama[1], Ryoichi Matsuda[2] ([1]*N-EM Labs.*, [2]*Grad. Sch. Sci., Tokyo Univ. Sci.*)

20569U* Self-Assembly of Flexible DNA Ring Motif
Shiyun Liu[1], Ibuki Kawamata[1,2], Satoshi Murata[1] ([1]*Grad. Sch. Eng., Univ. Tohoku*, [2]*Div. Natural Sci. Fac. Core Research, Univ. Ochanomuzu*)

20570U 分子スウォームの自動制御のための DNA 反応回路の最適化
Optimization of the molecular circuit for automatic controlling movement of microtubules
Daiki Matsumoto[1], Ibuki Kawamata[1], Yuki Suzuki[1,2], Satoshi Murata[1], Jakia Jannat Keya[3], Akira Kakugo[3], Shin-ichiro Nomura[1] ([1]*Department of Robotics, Graduate School of Engineering, Tohoku University, Japan*, [2]*Creative Interdisciplinary Research Division,Frontier Research Institute for Interdisciplinary Sciences,Tohoku University*, [3]*Department of Chemistry, Faculty of Science, Hokkaio University*)

20571U 機械学習を用いた生物形態の定量化とその応用
Characterization of biological morphology by using machine learning
Masato Tsutsumi[1], Nen Saito[1,2], Chikara Furusawa[1,2,3] ([1]*Dept. of Physics,Grad School of Science, The Univ. of Tokyo*, [2]*Universal Biology Institute, The Univ. of Tokyo*, [3]*Center for Biosystems Dynamics Research, RIKEN*)

20572U Circularization in coding regions of Flaviviruses are crucial for viral fitness
Roland G. Huber (*A*STAR BII*)