若手招待講演　Early Research in Biophysics Award

第 1 日目（10 月 30 日（金））/ Day 1 (Oct. 30, Fri.)

13:00～15:30　C1 会場/ Room C1

1YP1　日本生物物理学会若手奨励賞選考会

Early Research in Biophysics Award Candidate Presentations

オーガナイザー：男女共同参画・若手問題検討委員会

Organizer: The Committee of Promoting Gender Equality and Young Scientists

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In 2005, the Biophysical Society of Japan has established Early Research in Biophysics Award to recognize distinguished research work by young members of the BSJ. In this fifth year, we received thirty eight highly qualified applications. After extremely competitive first round of screening, which is based on written evaluation, the following ten applicants were chosen as the "young guest lecturers". For the second round of screening, each "guest lecturers" will be asked to make a 10-minute presentation followed by 3 minutes of Q&A discussion. At the conclusion of this round, up to five award winners will be selected. The award winners will be announced at the banquet in the evening of Saturday, October 31st.We urge all the BSJ members to attend the oral presentations on Friday, October 30th at Early Research in Biophysics Award Candidate Presentations, since these lecturers and their researches represent the future of biophysics.

13:00　市橋 伯一　　2P-228

1YP1-01　再帰的な遺伝情報の自己複製システムが in vitro で実現する条件を知る

What is the condition of realizing a self-replication system of genetic information in vitro?

○市橋 伯一 (1), 松浦 友亮 (3), 四方 哲也 (2) ((1) 大阪大学大学院情報科学研究科: (2) 大阪大学大学院情報科学研究科；生命機能研究科；科学技術振興機構 ERATO: (3) 大阪大学大学院情報科学研究科)

Norikazu Ichihashi (1), Tomoaki Matsuura (3), Tetsuya Yomo (2) ((1) Graduate School of Information Science and Technology, Osaka University: (2) Graduate School of Information Science and Technology; Graduate School of Frontier Bioscience, Osaka University; ERATO, JST: (3) Graduate School of Information Science and Technology, Osaka University)

13:15　鎌形 清人　　1P-057

1YP1-02　キャピラリー内トラップによる一分子の長時間観察：蛋白質の折り畳みへの応用

Long-time observation of a single molecule trapped in a capillary cell: application for protein folding

○鎌形 清人 (1), 後藤 祐児 (2), 高橋 聡 (3) ((1) 東北大学多元物質科学研究所: (2) 大阪大学蛋白質研究所: (3) 東北大学多元物質科学研究所；CREST, JST)

Kiyoto Kamagata (1), Yuji Goto (2), Satoshi Takahashi (3) ((1) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University: (2) Institute for Protein Research, Osaka University: (3) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University; CREST, JST)

13:30　柴田 幹大　　1P-226

1YP1-03　高速原子間力顕微鏡（AFM）を用いたバクテリオロドプシンの光励起に伴う動態観察

High-speed atomic force microscopy visualization reveals dynamic molecular processes in photo-activated bacteriorhodopsin

○柴田 幹大 (1), 山下 隼人 (1), 内橋 貴之 (2), 神取 秀樹 (3), 安藤 敏夫 (2) ((1) 金沢大学: (2) 金沢大学；戦略的創造研究推進事業: (3) 名古屋工業大学)

Mikihiro Shibata (1), Hayato Yamashita (1), Takayuki Uchihashi (2), Hideki Kandori (3), Toshio Ando (2) ((1) Kanazawa University: (2) Kanazawa University;　JST/CREST: (3) Nagoya Institute of Technology)

13:45　遠山 祐典

1YP1-04　細胞死の新しい役割：胚発生におけるアポトーシス（プログラム細胞死）の力学的寄与

Mechanical Forces Due to Cell Destruction: Biophysical Investigation of the Role of Apoptosis (Programmed Cell Death) in Tissue Dynamics

○遠山 祐典 (1), Peralta Xomalin (1), Wells Adrienne (2), Kiehart Daniel (2), Edwards Glenn (1) ((1) デューク大学 物理: (2) デューク大学 生物)

Yusuke Toyama (1), Xomalin Peralta (1), Adrienne Wells (2), Daniel Kiehart (2), Glenn Edwards (1) ((1) Duke University Physics Department: (2) Duke University Department of Biology)

14:00　西山 雅祥　　1P-126

1YP1-05　バクテリアべん毛モーターの熱力学的コントロール

Thermodynamic control of bacterial flagellar motors

○西山 雅祥 (1), 曽和 義幸 (2), 熊崎 茂一 (3), 木村 佳文 (3), 本間 道夫 (4), 石島 秋彦 (5), 寺嶋 正秀 (3) ((1) 京大院理 & 科技振: (2) 法政大: (3) 京大: (4) 名大: (5) 東北大)

Masayoshi Nishiyama (1), Yoshiyuki Sowa (2), Shigeichi Kumazaki (3), Yoshifumi Kimura (3), Michio Homma (4), Akihiko Ishijima (5), Masahide Terazima (3) ((1) Kyoto Univ. & JST: (2) Hosei Univ.: (3) Kyoto Univ.: (4) Nagoya Univ.: (5) Tohoku Univ.)

14:15　日比野 佳代　　3P-152

1YP1-06　情報伝達タンパク質 Ras、RAF 間の分子認識と細胞内信号伝達制御

Mutual molecular recognition of Ras and RAF for accurate signal transduction

○日比野 佳代 (1), 佐甲 靖志 (1) ((1) 独立行政法人理化学研究所)

Kayo Hibino (1), Yasushi Sako (1) ((1) RIKEN)

14:30　古川 亜矢子　　1P-024

1YP1-07　抗 HIV 活性を有する天然型 APOBEC3G タンパク質の構造、１本鎖 DNA との相互作用及び酵素反応のリアルタイムモニタリング

Structure, interaction with single-stranded DNA, and real-time monitoring of the enzymatic reaction of wild-type APOBEC3G possessing anti-HIV activity

○古川 亜矢子 (1), 永田 崇 (1), 杉山 隆一 (2), 高久 洋 (2), 片平 正人 (1) ((1) 横浜市立大学: (2) 千葉工業大学)

Ayako Furukawa (1), Takashi Nagata (1), Ryuichi Sugiyama (2), Hiroshi Takaku (2), Masato Katahira (1) ((1) Yokohama City University: (2) Chiba Institute of Technology)

14:45　古川 良明　　1P-058

1YP1-08　ポリグルタミン病の新たな分子病理メカニズムータンパク質線維の構造伝播による発症制御の可能性

Cross-seeding fibrillation of Q/N-rich proteins offers new pathomechanism of polyglutamine diseases

○古川 良明 (1), 金子 貢巳 (1), 黒沢 大 (1), 松本 弦 (1), 貫名 信行 (1) ((1) 理化学研究所脳科学総合研究センター)

Yoshiaki Furukawa (1), Kumi Kaneko (1), Masaru Kurosawa (1), Gen Matsumoto (1), Nobuyuki Nukina (1) ((1) RIKEN, Brain Science Institute)

15:00　前田 将司

1YP1-09　ヒト由来コネキシン 26 ギャップ結合チャネルのＸ線結晶構造

Crystal structure of human connexin 26 gap junction channel

○前田 将司 (1), 中川 宗 (1), 菅 倫寛 (1), 山下 栄樹 (1), 大嶋 篤典 (3), 藤吉 好則 (3), 月原 冨武 (2) ((1) 大阪大学: (2) 兵庫県立大学: (3) 京都大学)

Shoji Maeda (1), So Nakagawa (1), Michihiro Suga (1), Eiki Yamashita (1), Atsunori Oshima (3), Yoshinori Fujiyoshi (3), Tomitake Tsukihara (2) ((1) Osaka University: (2) University of Hyogo: (3) Kyoto University)

15:15　山口 繁生　　2P-207

1YP1-10　Photoactive Yellow Protein の低障壁水素結合

Low-barrier hydrogen bond in Photoactive Yellow Protein

○山口 繁生 (1), 上久保 裕生 (1), 栗原 和男 (2), 黒木 良太 (2), 山崎 洋一 (1), 片岡 幹雄 (3) ((1) 奈良先端科学技術大学院大学: (2) 日本原子力研究開発機構: (3) 奈良先端科学技術大学院大学; 日本原子力研究開発機構)

Shigeo Yamaguchi (1), Hironari Kamikubo (1), Kazuo Kurihara (2), Ryota Kuroki (2), Yoichi Yamazaki (1), Mikio Kataoka (3) ((1) Nara Institute of Science and Technology: (2) Japan Atomic Energy Agency: (3) Nara Institute of Science and Technology; Japan Atomic Energy Agency)

（アイウエオ順）

シンポジウム　Symposia

第 1 日目(10 月 30 日 (金)) / Day 1 (Oct. 30, Fri.)

9:00～11:30　FL 会場/ Room FL

1SA1　タンパク質間相互作用研究の手法としての共進化解析
Co-evolutionary analyses as the methods to investigate protein-protein interaction

オーガナイザー：由良 敬 (お茶の水女子大), 白井 剛(長浜バイオ大)
Organizer: Kei Yura (Ochanomizu University), Tsuyoshi Shirai (Faculty of Bioscience, Nagahama Institute of Bio-Science and Technology)

It is known that the genes of interacting proteins often have simiar evolutionary rates, or accumulate mutations in a compensatory manner at protein level. The phenomenon is called co-evolution. Co-evolution is one of the most important topics in current evolutionary study, because it represents the evolutionary aspect of systems or omics biology. Co-evolutionary events are thought to be responsible for establishing specificity between proteins and organisms, and can be used to predict protein-protein interactions, or to elucidate the history of molecular system. In this symposium, we would like to introduce and discuss the recent achievements in the co-evolutionary study, from the theoretical studies to the experimental applications.

1SA1-01　タンパク質共進化と分子進化速度の共変動
Co-evolution of proteins and covariation of evolutionary rate
○岸野 洋久 (東京大学農学生命科学研究科)
Hirohisa Kishino (University of Tokyo)

1SA1-02　バルナーゼとバルスターの相互作用の共進化解析
Co-evolutionary analyses of interactions between barnase and barstar
○伊倉 貞吉, 浦久保 良昭, 伊藤 暢聡 (東京医科歯科大学)
Teikichi Ikura, Yoshiaki Urakubo, Nobutoshi Ito (Tokyo Medical and Dental University)

1SA1-03　共進化情報によるタンパク質間相互作用予測
Prediction of protein-protein interaction with co-evolutionary information
○藤 博幸, 佐藤 哲也 (九州大学生体防御医学研究所)
Hiroyuki Toh, Tetsuya Sato (Medical Institute of Bioregulation, Kyushu University)

1SA1-04　BPTI 変異体の熱安定性とタンパク質間相互作用の共進化的視点からの解析
Analysis of thermal stability and protein-protein interaction in BPTI from a co-evolutionary viewpoint
○黒田 裕 (東京農工大学)
Yutaka Kuroda (Tokyo University of Agriculture and Technology (TUAT))

1SA1-05　タンパク質共進化機構の集団遺伝学的考察
Population gentical study on the mechanism of co-evolution of proteins
○飯塚 勝 (九州歯科大学)
Masaru Iizuka (Kyushu Dental College)

9:00～15:30　S1 会場/ Room S1

1SA2　プリオンとウィルスの感染(BSJ&ABA 連携国際シンポジウム)
BSJ&ABA Joint Symposium，”Prion and Virus Infections”

オーガナイザー：永山 國昭 (岡崎統合バイオサイエンスセンター), 曽我部 正博 (名古屋大), 片岡 幹雄 (奈良先端大)
Organizer: Kuniaki Nagayama (Okazaki Institute for Integrative Bioscience), Masahiro Sokabe (Nagoya Univ.), Mikio Kataoka (Nara Institute of Science and Technology)

Protein-conformation diseases have been attractive to same range of biophysicists by its vivid connection to structural biophysics. Among them, prion and Alzheimer diseases are studied from the aspect of infectious structures particularly in this society. As one of major targets of structural biology, virus structures have also been widely studied in the world-scene of biophysics. Unfortunately they have no common ground to be discussed together till now though the prion disease had once been considered to belong to slow

virus diseases. In this joint symposium we will invite active scientists from the two fields to discuss "what is the infectious processes in common". A big mystery still exists in the prion infection or its disease initiation. On the other hand the virus infection has been well understood and even engineered now for particular genes to be uptaken into cells. By giving a light to the prion infection from the angle of virus infection or vise versa, we can see an interesting novel encounter productive to both fields.

1SA2-01 Opening address
○永山 國昭 (岡崎統合バイオサイエンスセンター)
Kuniaki Nagayama (Okazaki Institute for Integrative Bioscience)

1SA2-02 Intracellular localization of abnormal isoform of prion protein
○堀内 基広 (北海道大学大学院獣医学研究科プリオン病学講座)
Motohiro Horiuchi (Hokkaido Univ.)

1SA2-03 Investigating the role of exosomes in the processing of proteins associated with prion and Alzheimer's diseases
○Andrew F. Hill (Prion, Univ. Melbourne, Australia)

1SA2-04 プリオン感染における株多様性の存在と株間干渉現象の意義
Meaning of Strain diversity and Interference Seen in Prion Infection
○西田 教行 (長崎大大学院医歯薬学総合研究科感染免疫学講座)
Noriyuki Nishida (Nagasaki Univ)

1SA2-05 強い神経細胞死活性を持つアルツハイマー病患者に由来するアミロイドβ凝集体
High-mass amyloid beta-protein assembly with a unique toxic surface from Alzheimer's disease brains
○星 美奈子 (京都大学大学院医学研究科腫瘍生物学講座)
Minako Hoshi (Kyoto Univ.)

1SA2-06 Implication of endogenous retrovirus in prion diseases
○Yong-Sun Kim (Prion Ilsong Institute of Life Science, Hallym University)

1SA2-07 鳥、ブタ、そしてパンデミックインフルエンザ
Avian, swine, and pandemic influenza
○喜田 宏 (北海道大学大学院獣医学研究科人獣共通感染症リサーチセンター)
Hiroshi Kida (Hokkaido Univ.)

1SA2-08 Avian influenza virus: from migratory bird infection to peptide inhibitor discovery
○George Gao (Virus, IMCAS, China)

1SA2-09 ウイルスベクターと非ウイルスベクターの遺伝子発現効率の定量的比較解析：細胞取込から転写・発現まで
Quantitative analysis of transfection efficiency between viral and non-viral vector: From cellular uptake to transcription/translation
○原島 秀吉 (北海道大学大学院薬学研究院薬剤分子設計学研究室)
Hideyoshi Harashima (Hokkaido Univ.)

1SA2-10 プリオン病　－感染メカニズムとダイナミクスに基づく創薬
Prion diseases - Biophysical approach to the infection mechanism and the structure based drug design
○桑田 一夫 (岐阜大学・人獣感染防御研究センター)
Kazuo Kuwata (Gifu Univ.)

1SA2-11 Closing Remarks
○曽我部 正博 (名古屋大学)
Masahiro Sokabe (Nagoya Univ.)

9:00～11:30　S2 会場/ Room S2

1SA3　インフルエンザ・ウイルス RNA ポリメラーゼ研究の新展開
Novel findings of influenza A virus RNA dependent RNA polymerase

オーガナイザー：朴 三用 (横浜市大), 葛原 隆(徳島文理大)
Organizer: Park Sam-Yong (Yokohama City University), Takashi Kuzuhara (Tokushima Bunri University)

In 1918, a pandemic of influenza A virus resulted in over ten million deaths worldwide, and strategies to prevent any such future pandemic are therefore extremely important. Although inhibitors of neuraminidase and the M2 ion channel are widely used as anti-influenza A virus drugs, adverse effects of these agents and the emergence of drug-resistant viruses have been reported. Since the influenza A virus has an RNA genome, its RNA-dependent RNA polymerase, comprising three subunits,the PA, PB1 and PB2 subunits, is essential for viral transcription and replication. Therefore this enzyme represents a very promising target for anti-viral drug development. The determination of the structure of a target protein is a valuable tool in the development of new drugs.

1SA3-01 インフルエンザウイルスの RNA ポリメラーゼにおけるサブユニット間相互作用

Structural insight into essential subunit contacts of the influenza virus RNA polymerase

○尾林 栄治 (1), 杉山 佳奈子 (1), 吉田 尚史 (1), 河合 文啓 (1), 川口 敦史 (2), 鈴木 由佳理 (2), Jeremy Tame (1), 永田 恭介 (2), 朴 三用 (1) ((1) 横浜市大院・生命ナノシステム: (2) 筑波大・院・人間総合科学)

Eiji Obayashi (1), Kanako Sugiyama (1), Hisashi Yoshida (1), Fumihiro Kawai (1), Atsushi Kawaguchi (2), Yukari Suzuki (2), Jeremy Tame (1), Kyosuke Nagata (2), Sam-Yong Park (1) ((1) Protein Design Laboratory, Yokohama City University: (2) Grad. Sch. of Comprehensive Human Sci., Univ. of Tsukuba)

1SA3-02 インフルエンザ RNA ポリメラーゼ PB2 サブユニット病原性関与ドメインの構造と機能の解析

Structural basis of the influenza A virus RNA polymerase PB2 RNA-binding domain containing the pathogenicity-determinant lysine 627 residue

○葛原 隆, 津下 英明, 宇都宮 敬子, 越後 典子, 木瀬 大輔 (徳島文理大学)

Takashi Kuzuhara, Hideaki Tsuge, Hiroko Utsunomiya, Noriko Echigo, Daisuke Kise (Tokushima Bunri University)

1SA3-03 光ピンセットを用いたインフルエンザウイルス感染による細胞変化の解析

Analysis of the changing of cell by influenza virus infection using the optical tweezers

○本田 文江 (法政大学)

Ayae Honda (Housei University)

1SA3-04 インフルエンザウイルス RNA ゲノムータンパク質複合体輸送の生細胞観察

Live cell imaging of the trafficking of influenza viral ribonucleoprotein complexes

○百瀬 文隆 (北里大学北里生命科学研究所)

Fumitaka Momose (Kitasato Institute for Life Sciences, Kitasato Univ.)

1SA3-05 インフルエンザウイルスゲノム機能発現のウイルスおよび宿主基盤

The molecular mechanism of viral and host factor-dependent replication of the influenza virus genome

○永田 恭介 (筑波大学大学院人間総合科学研究科)

Kyosuke Nagata (Graduate School of Comprehensive Human Sciences, University of Tsukuba)

9:00～11:30　C6 会場/ Room C6

1SA4　生体π空間：その特異性解明と新機能の開拓

Bio-π-space: Mechanistic investigation and creation of new functions

オーガナイザー：神取 秀樹 (名古屋工業大), 安藤 耕司 (京都大)

Organizer: Hideki Kandori (Nagoya Institute of Technology), Koji Ando (Kyoto University)

Unique characteristics of π-electrons are important in biomolecular functions. For example, photoactive proteins contain π-electron-rich chromophore molecules such as retinal, chlorophyll and oxyruciferin, which control light-dependent specific events in biological systems. Enzymes often utilize π-electron-rich molecules such as heme and flavin in the active centers. On the otehr hand, people are recently worried about influence of nano-carbons on our health. In this symposium, young researchers from various fields will present their challenges to "bio-π-space", and mechanism in the highly elaborated π-spaces and creation of new functions will be discussed.

1SA4-01 光受容蛋白質におけるπ空間制御

Bio-π-space in photoreceptive proteins

○神取 秀樹 (名古屋工業大学)

Hideki Kandori (Nagoya Institute of Technology)

1SA4-02 クリプトクローム蛋白質群のπ空間による制御

Unique tuning of the π spaces in a cryptochrome framework

○人見 研一, Elizabeth D. Getzoff (スクリプス研究所)

Kenichi Hitomi, Elizabeth D. Getzoff (Dept of Molecular Biology and the Skaggs Institute for Chemical Biology The Scripps Research Institute)

1SA4-03 ホタル・ルシフェラーゼによるπ空間制御機構

π-space control in firefly luciferase
○中津 亨 (京都大学大学院薬学研究科)
Toru Nakatsu (Graduate School of Pharmaceutical Sciences Kyoto University)

1SA4-04 青色銅タンパク質の電子移動機構における金属配位子間 d-π相互作用に関する理論的研究
Metal-ligand d-π interaction in electron transfer mechanism of blue copper protein: A theoretical study
○安藤 耕司 (京都大学大学院理学研究科)
Koji Ando (Department of Chemistry, Faculty of Science, Kyoto University)

1SA4-05 π電子系からみる分子
Peeping molecules through π-electron systems
○磯部 寛之 (東北大学)
Hiroyuki Isobe (Tohoku University)

13:00～15:30 FL 会場/ Room FL

1SP5 若手研究者による生体金属分子分光学の新展開
New Developments on Molecular Spectroscopy of Biometals by Young Researchers

オーガナイザー：廣田 俊 (奈良先端科学技術大学院大学), 石森 浩一郎 (北海道大学)
Organizer: Shun Hirota (Graduate School of Materials Sceince, Nara Inst. of Sci. and Tech.), Koichiro Ishimori (Hokkaido Univ.)

Metal ions play important roles in many key reactions in life. Understanding of life at the molecular level, therefore, requires detailed biophysical and biochemical characterization of metal ions in biological systems. The unique spectroscopic properties of metal ions have provided clues to reveal their functional and structural significance in our life, and a number of the elegant spectroscopic studies on metal ions have offered various kinds of sophisticated molecular mechanisms in biological systems. Recent progress in molecular spectroscopies has enabled us to examine more complicated and more essential biological systems including DNA-metal ion interactions, dynamics of metalloprotein complexes, membrane-bound metalloproteins, and metal-catalyzed reactions. In this symposium, young active researchers developing their original idea with cutting-edge techniques will give overviews and perspectives of the molecular spectroscopic researches of metal ions in life.

1SP5-01 はじめに
Introduction
○廣田 俊 (奈良先端科学技術大学院大学・物質創成科学研究科)
Shun Hirota (Graduate School of Materials Sceince, Nara Inst. of Sci. and Tech.)

1SP5-02 短寿命な気体分子・金属酵素複合体の分子科学の展開を目指して
Structure and chemistry of short-lived mtalloenzyme-gas molecule complex
○永野 真吾 (理化学研究所・播磨研究所)
Shingo Nagano (RIKEN SPring-8 Center)

1SP5-03 核酸－金属相互作用の NMR 分光法による検出
Detection of metal ion-interaction with DNA/RNA with NMR spectroscopy
○田中 好幸 (東北大学大学院薬学研究科)
Yoshiyuki Tanaka (Graduate School of Pharmaceutical Sciences, Tohoku University)

1SP5-04 電子伝達系におけるタンパク質間相互作用の構造生物学的研究
Structural study of interactions between electron transfer proteins
○野本 直子 (北大・院理)
Naoko Nomoto (Fac.Sci., Hokkaido Univ.)

1SP5-05 [NiFe] ヒドロゲナーゼのＸ線結晶構造解析と赤外分光測定
X-ray crystallographic and FT-IR studies on [NiFe] hydrogenase
○大須賀 久織 (1), 寺脇 慎一 (1), 庄村 康人 (1), 小森 博文 (1), 柴田 直樹 (1), 廣田 俊 (2), 樋口 芳樹 (1) ((1) 兵庫県立大学・大学院生命理学研究科: (2) 奈良先端科学技術大学院大学・物質創成科学研究科)
Hisao Osuka (1), Shin-ich Terawaki (1), Yasuhito Shomura (1), Hirofumi Komori (1), Naoki Shibata (1), Shun Hirota (2), Yoshiki Higuchi (1) ((1) Graduate School of Life Science, Hyogo Univ.: (2) Graduate School of Materials Sceince, Nara Inst. of Sci. and Tech.)

1SP5-06 フォトン・フォースで蛋白質分子を捕まえる
Optical Trapping of Proteins in Aqueous Solution
○坪井 泰之 (北海道大学理学院)

Yasuyuki Tsuboi (Div. Che,., Hokkaido University)

1SP5-07 希土類金属錯体を用いた in vivo イメージング用プローブの開発
Development of lanthanide complex-based probes for in vivo imaging
○水上 進 (大阪大学大学院工学研究科)
Shin Mizukami (Graduate School of Engineering, Osaka University)

1SP5-08 まとめ
Summary
○石森 浩一郎 (北海道大学・大学院理学研究院)
Koichiro Ishimori (Faculty of Science, Hokkaido Univ.)

13:00～15:30　S2 会場/ Room S2

1SP6 メンブラントランスフォーマー！！～生体膜の形を変えるための合体と解離～
Membrane transformers!! ~The combine and the dissociation to change the shape of biomembrane~

オーガナイザー：田端 和仁 (大阪大学産業科学研究所), 滝口 金吾 (名古屋大学)
Organizer: Kazuhito Tabata (ISIR), Kingo Takiguchi (Nagoya University)

Many cellular phenomena, such as vesicle formation, cell division and reconstitution of subcellular organelles, involve deformations of the biomembrane that is closely associated with life activity. These deformations are induced by the dynamic interaction between deforming proteins and biomembrane. With membrane-deforming protein reconstitution and membrane-deforming dynamics as the keyword, this session will host lectures by researchers who aim to elucidate the function and dynamics of membrane-deforming protein.

1SP6-01 人工脂質二重膜上に再構成した COPII 小胞形成過程のイメージング
Visualization of COPII vesicle formation process reconstituted in the artifical lipid bilayer.
○田端 和仁 (1), 佐藤 健 (2), 井出 徹 (3), 西坂 崇之 (4), 中野 明彦 (5), 野地 博行 (1) ((1) 大阪大学産業科学研究所: (2) 東京大学大学院総合文化研究科: (3) 大阪大学大学院生命機能研究科: (4) 学習院大学理学部物理学科: (5) 理化学研究所生体膜研究室)
Kazuhito Tabata (1), Ken Sato (2), Toru Ide (3), Takayuki Nshizaka (4), Akihiko Nakano (5), Hiroyuki Noji (1) ((1) ISIR: (2) Department of Life Sciences, Graduate School of Arts and Sciences, University of Tokyo: (3) Graduate School of Frontier Biosciences, Osaka University: (4) Department of Physics, Gakushuin University: (5) Molecular Membrane Biology Laboratory, RIKEN Advanced Science Institute)

1SP6-02 EFC/F-BAR ドメインタンパク質の構造，機能と制御
Structure, function and regulation of the EFC/F-BAR domain proteins
○嶋田 睦 (1), 寺田 貴帆 (2), 白水 美香子 (2), 山本 雅貴, 永山 國昭 (3), 末次 志郎 (4), 竹縄 忠臣 (5), 横山 茂之 (6) ((1) 理化学研究所放射光科学総合研究センター: (2) 理化学研究所生命分子システム基盤研究領域: (3) 自然科学研究機構岡崎統合バイオサイエンスセンター: (4) 東京大学分子細胞生物学研究所；科学技術振興機構さきがけ: (5) 神戸大学大学院医学研究科: (6) 理化学研究所生命分子システム基盤研究領域；東京大学大学院理学系研究科生物化学専攻)
Atsushi Shimada (1), Takaho Terada (2), Mikako Shirouzu (2), Masaki Yamamoto, Kuniaki Nagayama (3), Shiro Suetsugu (4), Tadaomi Takenawa (5), Shigeyuki Yokoyama (6) ((1) RIKEN SPring-8 Center: (2) RIKEN Systems and Structural Biology Center: (3) Okazaki Institute for Integrative Bioscience, National Institutes of Natural Sciences: (4) Institute of Molecular and Cellular Biosciences, the University of Tokyo; PRESTO, JST: (5) Kobe University Graduate School of Medicine: (6) RIKEN Systems and Structural Biology Center; Department of Biophysics and Biochemistry Graduate School of Science, the University of Tokyo)

1SP6-03 セミインタクト細胞を用いたメンブレンダイナミクスに関わる分子機能解析
Mechanistic insights into membrane dynamics using semi-intact cell system
○加納 ふみ (東京大学大学院総合文化研究科)
Fumi Kano (Graduate School of Arts and Sciences, The University of Tokyo)

1SP6-04 巨大リポソームを用いて明らかにされた第４の細胞骨格セプチンの機能
Septin-induced robust membrane tubulation
○滝口 金吾, 滝口 陽子, 木下 専 (名古屋大学理学研究科生命理学)
Kingo Takiguchi, Yohko Tanaka-Takiguchi, Makoto Kinoshita (Division of Biological Science, Graduate School of Science, Nagoya University)

1SP6-05 細菌のチューブリン “FtsZ” によるリポソームの屈曲と収縮
FtsZ (bacterial tubulin) bending and constricting liposomes
○大澤 正輝, アンダーソン デビッド, エリクソン ハロルド (デューク大学メディカルセンター 細胞生物)

Masaki Osawa, David E. Anderson, Harold P. Erickson (Department of Cell Biology, Duke University Medical Center)

13:00～15:30　C6 会場/ Room C6

1SP7　タンパク質機能の原子レベルの解明　ーＸ線構造、振動分光、分子生物学、理論解析による挑戦ー
Elucidation of Protein Functions at the Atomic Level with X-ray structural, Vibrational spectroscopic, Molecular biological and Theoretical analyses

オーガナイザー：館野 賢 (筑波大学), 吉川 信也 (兵庫県立大学)

Organizers: Masaru Tateno (Tsukuba University), Shinya Yoshikawa (University of Hyogo)

Any life phenomenon is comprised of a set of chemical reactions driven by various proteins. Thus, elucidation of the mechanism of protein functions is equivalent to understanding the mechanism of life process. The function of any protein is facilitated by anisotropies produced inside the protein, not by a simple linear combination of the chemical properties of amino acids composing the protein. In this symposium, possibilities of X-ray structural, vibrational, molecular biological and theoretical analyses for elucidation of the anisotropies will be discussed, referring the recent progresses in two intriguing proteins systems, cytochrome *c* oxidase and RNA-binding proteins.

1SP7-01　タンパク質機能の原子レベルの解明ー序論ー

Elucidation of Protein Functions at Atomic Level with X-ray, Vibrational, Molecular biological and Theoretical analyses, Introduction.

○吉川 信也 (兵庫県立大学大学院生命理学研究科)
Shinya Yoshikawa (University of Hyogo)

1SP7-02　ウシ心筋チトクロム酸化酵素の水素原子レベルのＸ線構造解析

The X-ray structural analysis of bovine heart cytochrome c oxidase at the hydrogen atom level

○月原 冨武 (兵庫県立大学)
Tomitake Tsukihara (University of Hyogo)

1SP7-03　GatCAB の tRNA 認識特異性と分子進化

tRNA recognition and molecular evolution of GatCAB

○中村 彰良 (1), Kelly Sheppard (2), 山根 潤二 (1), 姚 閔 (3), Dieter Söll (2), 田中 勲 (3) ((1) 北海道大学大学院生命科学院: (2) Yale 大学: (3) 北海道大学大学院先端生命科学研究院)
Akiyoshi Nakamura (1), Kelly Sheppard (2), Junji Yamane (1), Yao Min (3), Dieter Söll (2), Isao Tanaka (3) ((1) Division of Life Sciences, Graduate School of Life Science, Hokkaido University: (2) Department of Molecular Biophysics and Biochemistry, Yale University: (3) Faculty of Advanced Life Science, Hokkaido University)

1SP7-04　水溶液中の蛋白質の時間分解赤外分光法

Time-resolved infrared spectroscopy for proteins functioning in aqueous solution

○中島 聡 (兵庫県立大学 生命理学研究科)
Satoru Nakashima (Graduate School of Life Science, University of Hyogo)

1SP7-05　蛋白質の紫外共鳴ラマン分光法

Ultraviolet resonance Raman spectroscopy for functioning proteins

○小倉 尚志 (兵庫県立大学)
Takashi Ogura (University of Hyogo)

1SP7-06　チトクロム酸化酵素の部位特異的同位体標識

Site-directed isotope labeling of cytochrome c oxidase

○島田 秀夫, 片山 幸江, 小倉 尚志, 月原 冨武, 吉川 信也 (兵庫県立大学・大学院生命理学研究科, ピコバイオロジー研究所)
Hideo Shimada, Yukie Katayama, Takashi Ogura, Tomitake Tsukihara, Shinya Yoshikawa (Picobiology Institute, Graduate School of Life Science, University of Hyogo)

1SP7-07　シトクローム酸化酵素におけるプロトン移動機構の第一原理計算による解析

First principles studies on the proton transfer mechanism in cytochrome /c/ oxidase

○白石 賢二 (1), 神谷 克政 (2), 舘野 賢 (1), ボエロ マウロ (1), 押山 淳 (3) ((1) 筑波大学: (2) 兵庫県立大学: (3) 東京大学)
Kenji Shiraishi (1), Katsumasa Kamiya (2), Masaru Tateno (1), Mauro Boero (1), Atsushi Oshiyama (3) ((1) University of Tsukuba: (2) University of Hyogo: (3) University of Tokyo)

1SP7-08　RNA 結合タンパク質の酵素反応機構に関する計算科学的解析

Computational investigations of mechanisms of enzymatic reactions of RNA-binding proteins

○舘野 賢 (1), 畔柳 成秀 (2), 萩原 陽介 (2) ((1) 筑波大学・計算科学研究センタ；筑波大学大学院数理物質科学研究科: (2) 筑波大学大学院)
Masaru Tateno (1), Shigehide Kuroyanagi (2), Yohsuke Hagiwara (2) ((1) Center for Computational Sciences, University of Tsukuba; Graduate School of Pure and Applied Sciences, University of Tsukuba: (2) University of Tsukuba)

第 2 日目 (10 月 31 日 (土)) / Day 2 (Oct. 31, Sat.)

9:00～11:30　FL 会場/ Room FL

2SA1　生物物理と新世代の ESR
Electron Spin Resonance on Biophysics -The Next Generation-

オーガナイザー：三野 広幸 (名古屋大学), 荒田 敏招 (大阪大学)
Organizer: Hiroyuki Mino (Nagoya University), Toshiaki Arata (Osaka University)

Although NMR has been widely applied to biophysical studies for protein structural analysis, ESR had been performed limitedly for the first generation of biophysics. Recently, a great development has achieved for ESR techniques, called 'advanced ESR', which has provided many new concepts for electron spin, and new applications. This gives not only the highly precise determination of the protein structure during enzymatic reaction, but also the detection of the interaction between proteins in action or the new methodologies in vivo. In this symposium, we will introduce recent advancement of the ESR techniques and discuss applications for biological systems today and in future. (Supported by Osaka University Global COE program "System Dynamics of Biological Function")

2SA1-01　はじめに
Presentation of keynote
○三野 広幸 (名古屋大学大学院理学研究科物質理学専攻)
Hiroyuki Mino (Graduate School of Science, Nagoya university)

2SA1-02　時間分解 EPR 法による反応中間体－タンパク質相互作用の解析
Analysis of reaction intermadiate-protein interaction by time-resolved EPR
○小堀 康博 (静岡大学)
Yasuhiro Kobori (Shizuoka University)

2SA1-03　非クラマースイオンを持つ金属タンパク質の強磁場多周波 EPR
High-field and Multi-frequency EPR study of metalloproteins with non-Kramers ions
○八代 晴彦 (1), 二宮 謙太 (2), 堀谷 正樹 (3), 堀 洋 (2), 萩原 政幸 (2) ((1) 科学技術振興機構さきがけ；大阪大学極限量子科学研究センター: (2) 大阪大学極限量子科学研究センター: (3) 理研スプリング８生体金属科学研究室)
Haruhiko Yashiro (1), Kenta Ninomiya (2), Masaki Horitani (3), Hiroshi Hori (2), Masayuki Hagiwara (2) ((1) JST PRESTO; KYOKUGEN Osaka University: (2) KYOKUGEN Osaka University: (3) Riken Spring-8 Center, Biometal Science Laboratory)

2SA1-04　パルス ESR を用いた距離測定によるモーター、スイッチタンパク質の動的解析
Conformational dynamics of motor and switch proteins by distance measurements using pulsed ESR
○荒田 敏昭 (大阪大学大学院理学研究科生物科学専攻)
Toshiaki Arata (Department of Biological Sciences, Graduate School of Science, Osaka University)

2SA1-05　時間分解 EPR によるミオシンの動的構造解析
Structural Dynamics of Myosin by Time-resolved EPR
○Thomas David D. (Department of Biochemistry, Molecular Biology, and Biophysics, University of Minnesota, USA)

2SA1-06　高磁場オーバーハウザーMRI の開発と酸化ストレス疾患への応用
Development of High-Field Overhauser-MRI and Its Application to Oxidative Diseases
○内海 英雄 (九州大学先端融合医療レドックスナビ研究拠点，大学院薬学研究院)
Hideo Utsumi (Depnnovation Center for Medical Redox Navigation, Graduate School of Pharmaceutical Sciences, Kyushu University)

2SA1-07　渡り鳥は地磁気を見ているのか？
Does a migrating bird watch the earth magnetic field?
○前田 公憲 (オックスフォード大学)
Kiminori Maeda (University of Oxford)

9:00～11:30　S1 会場/ Room S1

2SA2　タンパク質の膜透過輸送の最前線
Research frontiers of protein transport across the membrane

オーガナイザー：難波 啓一 (大阪大学), 南野 徹 (大阪大学)

Organizer: Keiichi Namba (Osaka University), Tohru Minamino (Osaka University)

Proteins are transported to their specific places inside and outside of the cell across cytoplasmic or inner-cellular membranes by a wide variety of mechanisms for the formation of cellular structures and organelles. In bacteria such mechanisms include the Sec system for general protein transport across the cytoplasmic membrane of bacteria, the Lol proteins for lipoprotein transport, and the type III protein export system for virulence effector secretion and flagellar formation. In eukaryote, there are many different protein translocator systems in cell organelle such as mitochondria, endoplasmic reticula and peroxisomes. How much is known about the mechanisms of these protein translocation systems and their energetics? The forefront of the field will be overviewed and discussed in the symposium.

2SA2-01　1000 種類のタンパク質を仕分けるミトコンドリアトランスロケータの実体

Mitochondrial translocators that mediate sorting of 1000 different mitochondrial proteins

○山野 晃史, 遠藤 斗志也 (名古屋大学大学院理学研究科物質理学専攻化学系)

Koji Yamano, Toshiya Endo (Department of Chemistry, Graduate School of Science, Nagoya University)

2SA2-02　細菌型リポ蛋白質の選別・輸送・膜局在化を司る Lol システムの構造と機能

Structure and function of the Lol system catalyzing the membrane sorting of bacterial lipoproteins

○徳田 元 (東京大学分子細胞生物学研究所)

Hajime Tokuda (Institute of Molecular and Cellular Biosciences, University of Tokyo)

2SA2-03　ペルオキシソームの形成：膜アセンブリーとタンパク質の膜透過輸送機構

Peroxisome Biogenesis: Mechanistic insights into the import of matrix and membrane proteins

○藤木 幸夫 (九州大学大学院理学研究院生物科学部門: (2) JST, CREST)

Yukio Fujiki (Department of Biology, Faculty of Sciences, Kyushu University: (2) JST, CREST)

2SA2-04　バクテリアのタンパク質膜透過装置の構造と機能

Structure and function of bacterial protein translocation machinery

○森 博幸 (1), 塚崎 智也 (2), 越前 友香 (2), 濡木 理 (2), 伊藤 維昭 (3) ((1) 京都大学、ウイルス研究所: (2) 東京大学、医科学研究所: (3) 京都産業大学)

Hiroyuki Mori (1), Tomoya Tsukazaki (2), Yuka Echizen (2), Osamu Nureki (2), Koreaki Ito (3) ((1) Institute for Virus Research, Kyoto University: (2) The Institute of Medical Science, The University of Tokyo: (3) Kyoto Sangyo University)

2SA2-05　水素イオンで動く細菌べん毛蛋白質輸送装置の動作機構

Dynamic Mechanisms of Proton-Driven Bacterial Flagellar Protein Export

○南野 徹 (大阪大学大学院生命機能研究科)

Tohru Minamino (Graduate School of Frontier Biosciences, Osaka University)

9:00～11:30　S2 会場/ Room S2

2SA3　細胞骨格アクチンの動的制御の生物物理
Structural and functional analysis of actin filament dynamics

オーガナイザー：辰巳 仁史 (名古屋大学), 佐藤 正明 (東北大学)

Organizer: Hitoshi Tatsumi (Nagoya Univ.), Masaaki Sato (Tohoku Univ.)

Actin filaments are two-stranded helical polymers of the protein actin. They appear as flexible structures, and organized into a variety of linear bundles, two dimensional networks, and three dimensional gels. The regulation of the dynamic behavior and assembly and disassembly of actin filaments allows cells to construct an enormous range of structures and cells to migrate on substrate. The aims of this symposium are to introduce recent research progresses made by X-ray diffraction analyses, single molecule imaging, MD-simulations, and electron microscopy, 1) the structure of F-actin, 2) tensile properties of single stress fibers and actin filaments, 3) tension dependent disassembly of actin filaments by cofilin, and 4) cellular responses to force mediated via actin filament dynamics, and to prodive a platform on which we can discuss the future prospects of this field of science.

2SA3-01　重合にともなうアクチン分子の構造変化

Conformational changes in the actin molecule induced by actin polymerization

○小田 俊郎 (理化学研究所 放射光科学総合研究センター)

Toshiro Oda (RIKEN SPring-8 Center)

2SA3-02 アクチンは張力センサーである

F-actin as a stress-sensor

○辰巳 仁史 (1), 早川 公英 (2), 曾我部 正博 (1) ((1)名古屋大学大学院医学系研究科: (2) 科学技術振興機構 ICORP/SORST 細胞力覚)

Hitoshi Tatsumi (1), Kimihide Hayakawa (2), Masahiro Sokabe (1) ((1) Dept Physiol, Nagoya Univ Sch Med: (2) Cell Mechanosensing Project, ICORP/SORST, JST)

2SA3-03 アクチンフィラメントの力学的ふるまい：分子動力学シミュレーション

Mechanical Behavior of Actin Filaments: Molecular Dynamics Simulation Study

○安達 泰治 (1), 松下 慎二 (1), 井上 康博 (1), 北條 正樹 (2), 曽我部 正博 (3) ((1) 京都大学; 理研: (2) 京都大学: (3) 名古屋大学; 科学技術振興機構)

Taiji Adachi (1), Shinji Matsushita (1), Yasuhiro Inoue (1), Masaki Hojo (2), Masahiro Sokabe (3) ((1) Kyoto University; RIKEN: (2) Kyoto University: (3) Nagoya University; JST)

2SA3-04 ストレスファイバの力学特性と細胞内力学環境

Mechanical Property and Intracellular States of Stress Fiber

○佐藤 正明 (東北大学)

Masaaki Sato (Tohoku University)

2SA3-05 細胞認識シグナルとしてのＦアクチンを介した張力

Tension transmitted through F-actin works as a signal for cell-cell communication

○米村 重信 (1), 永渕 昭良 (2), 柴田 真依 (1) ((1) 独立法人理化学研究所　発生・再生科学総合研究センター: (2) 熊本大学発生医学研究所)

Shigenobu Yonemura (1), Akira Nagafuchi (2), Mai Shibata (1) ((1) Riken Center for Developmental Biology: (2) Inst. Molecular Embryology and Genetics, Kumamoto University)

14:30～17:00　FL 会場/ Room FL

2SP4　希少エレメント「希少糖」が拓く新世界

Rare glyco-elements "RARE SUGARS" pioneer a new world

オーガナイザー：何森 健 (香川大学), 深田和宏 (香川大学)

Organizer: Ken Izumori (Kagawa University), Kazuhiro Fukada (Kagawa University)

協賛；松谷化学工業（株），合同会社　希少糖生産技術研究所

Sponsored by Matsutani Chemical Industry Co., Ltd. and Ｉzumoring ＬＬＣ

“RARE SUGARS" are monosaccharides (minimal functional unit of sugars) which occur only rarely in nature, and they come in about 50 types. Most of them have been hardly used for research purposes so far because of their limited availability. Recently, production of rare sugars are becoming possible by using "Izumoring", a newly discovered structural framework of all monosaccharides, and research works on their properties and functions in a wide range of organisms from molecules (micro level) to higher animals (macro level) are growing. This symposium features the accomplishments of current rare sugar studies reaped in Kagawa area where the only industry-academia-government collaboration studies are in progress in the world.

2SP4-01 全希少糖合成戦略：イズモリング

Izumoring; A strategy for total production of rare sugars

○何森 健 (香川大学)

Ken Izumori (Kagawa University)

2SP4-02 希少糖生産方法～バイオリアクターと分離精製技術～

Rare sugar production by bioreactor and separation system

○森本 兼司 (1), 何森 健 (2) ((1) 香川大学研究推進機構希少糖研究センター: (2) 香川大学農学部)

Kenji Morimoto (1), Ken Izumori (2) ((1) Rare Sugar Research Center, Kagawa University: (2) Faculty of Agriculture, Kagawa University)

2SP4-03 希少糖生産酵素の立体構造と触媒反応機構

X-ray structures of the enzymes producing rare sugars and their catalytic reaction mechanisms

○神鳥 成弘, 吉田 裕美 (香川大学)

Shigehiro Kamitori, Hiromi Yoshida (Kagawa University)

2SP4-04 希少糖類の水溶液中における熱力学的安定性

Evaluation of thermodynamic stability of rare sugars in aqueous solution

○深田 和宏 (香川大学)
Kazuhiro Fukada (Kagawa University)

2SP4-05 希少糖の医薬品及び食品への利用
Applicability of rare sugars for medicines and foods
徳田 雅明, ○塚本 郁子 (香川大学医学部)
Masaaki Tokuda, **Ikuko Tsukamoto** (Kagawa University, Faculty of Medicine)

2SP4-06 農業分野への希少糖の利用
Application of rare sugars for agriculture
○秋光 和也, 五味 剣二, 多田 安臣, 田島 茂行, 何森 健 (香川大学)
Kazuya Akimitsu, Kenji Gomi, Yasuomi Tada, Shigeyuki Tajima, Ken Izumori (Kagawa University)

14:30～17:00　S1 会場/ Room S1

2SP5 生体分子の揺らぎをはかる
How are biological molecules fluctuating?

オーガナイザー：寺嶋 正秀 (京都大学), 片岡 幹雄 (奈良先端科学技術大学院大学)
Organizer: Masahide Terazima (Kyoto University), Mikio Kataoka (Nara Institute of Science and Technology)

One of key factors in chemical reactions for biological functions is "fluctuation". Biological molecules are always fluctuating by the thermal energy even during their functions. Studies from a view point of fluctuation and reaction dynamics should be essential for understanding efficient and selective reactions of biomolecules. However, information on fluctuation of biological molecules has not been enough to answer how the fluctuation is related with the function, because techniques to detect fluctuation have not been well developed. In this symposium, we focus on methods to detect the fluctuation experimentally and theoretically, and on showing connections between the fluctuations and functions.

2SP5-01 熱力学で反応中のタンパク質の揺らぎを測る
Detection of protein fluctuations during reactions by the time-resolved thermodynamics
○寺嶋 正秀 (京都大学)
Masahide Terazima (Kyoto University)

2SP5-02 AFM を用いたタンパク質の内部揺らぎの定量的検出
Quantitative detection of the internal fluctuation of proteins by AFM
○川上 勝 (1), 谷口 幸範 (1), BROCKWELL DAVID (2) ((1) 北陸先端科学技術大学院大学: (2) 英国リーズ大学)
Masaru Kawakami (1), Yukinori Taniguchi (1), David Brockwell (2) ((1) Japan Advanced Institute of Science and Technology: (2) University of Leeds)

2SP5-03 蛍光寿命の揺らぎを観る新しい蛍光相関分光法
New fluorescence correlation spectroscopy observing lifetime fluctuation
○石井 邦彦, 田原 太平 (独立行政法人 理化学研究所 田原分子分光研究室)
Kunihiko Ishii, Tahei Tahara (Molecular Spectroscopy Laboratory, RIKEN)

2SP5-04 蛋白質の大振幅ゆらぎと機能の分子シミュレーション研究
Large-amplitude fluctuation and function of proteins studied by molecular simulations
○高田 彰二 (京都大学)
Shoji Takada (Kyoto University)

2SP5-05 チャネル蛋白質の構造揺らぎと機能揺らぎの 1 分子測定
Single-molecular measurements for structural and functional fluctuations of KcsA potassium channel.
○老木 成稔, 清水 啓史, 岩本 真幸, 今野 卓 (福井大学医学部)
Shigetoshi Oiki, Hirofumi Shimizu, Masayuki Iwamoto, Takashi Konno (University of Fukui)

2SP5-06 がん細胞膜の揺らぎをターゲットとする制がん効果
Membrane Targeted Chemotherapy with Hybrid Liposomes for Tumor Cells
○上岡 龍一, 松本 陽子, 古水 雄志 (崇城大学大学院 工学研究科応用生命科学専攻)
Ryuichi Ueoka, Yoko Matsumoto, Yuji Komizu (Division of Applied Life Science, Graduate School of Engineering, Sojo University)

2SP5-07 中性子非弾性散乱で蛋白質の熱揺らぎを測る
Detection of thermal fluctuations of protein by neutron inelastic scattering
○片岡 幹雄 (奈良先端科学技術大学院大学)

Mikio Kataoka (Nara Institute of Science and Technology)

14:30～17:00　S2 会場/ Room S2

2SP6　生体高分子の電子構造解析　スーパーコンピューティングへ向けて
Towards Supercomputing for Electronic Structures of Biological Macromolecules

オーガナイザー：中村 春木 (阪大蛋白研), 佐藤 文俊 (東大生産研), 木寺 詔紀 (横浜市大)

Organizer: Haruki Nakamura (Inst Protein Res, Osaka Univ), Fumitoshi Sato (Inst Indust Sci, The Univ Tokyo), Akinori Kidera (Int Grad School Arts Sci, Yokohama City Univ)

Understanding the mechanisms of enzymatic reaction and electron transfer has so far been a crucial theme in the biophysics field. However, biological macromolecues are too large and too complicated for conventional computational approaches to directly analyze their precise electronic structures. Consequently, the previous analyses for the electronic structures were only made for some small systems by extracting the very local sites in the macromolecules, or by ignoring the dynamic effects of solvent and membrane molecules surrounding the macromolecules. However, the recent rapid progress of the ultra-fast supercomputers and the development of the corresponding software programs are expected to open a new era, where the precise electronic structures are able to be revealed by ab-initio quantum chemical calculations based on the dynamic structures of the macromolecules with the precise solvent effects. Thus, the free energy analysis including the entropy effect could be also possible, even for a huge macromolecular system by using the next-generation supercomputer, which will appear soon and will be available for biophysics researchers.

2SP6-01　序：原子構造から電子構造の解析へ
Introduction: From atomic structures to electronic structures of biological macromolecules
○中村 春木 (阪大蛋白研)
Haruki Nakamura (Institute for Protein Research, Osaka University)

2SP6-02　タンパク質の全電子波動関数計算
All-electron wavefunction calculation on proteins
○平野 敏行, 佐藤 文俊 (東大生研)
Toshiyuki Hirano, Fumitoshi Sato (Institute of Industrial Science, the University of Tokyo)

2SP6-03　スーパーコンピューティングによる蛋白質電子状態及び反応機構の解明に向けて。
Towards Understanding of Protein Electronic Structures and their Biochemical Reactions by Supercomputing
○米澤 康滋, 鷹野 優, 山崎 秀樹, 山中 秀介 (大阪大学蛋白質研究所)
Yasushige Yonezawa, Yu Takano, Hideki Yamasaki, Syusuke Yamanaka (IPR)

2SP6-04　金属蛋白質の触媒反応の理論解析
First principle analyses on reaction mechanism of metalloenzyme
○重田 育照, 神谷 克政 (兵庫県立大学大学院生命理学研究科)
Yasuteru Shigeta, Katsumasa Kamiya (Department Lifecience, University of Hyogo)

2SP6-05　The role of H-doping in the electronic structure, spin localization and electron transfer of iron-sulfur [2Fe-2S] proteins
○Wayne Kenneth Dawson (1), Tohru Terada (2), Kentaro Shimizu (1) ((1) University of Tokyo, Dept of Biotechnology, Bioinformation Lab: (2) Riken, Comp. Sci. Prog., Molecular Scale Team)

2SP6-06　キサントロドプシンの励起エネルギー移動：遷移電子密度を用いた擬クーロン相互作用の計算法の開発
Transition-Density-Fragment Interaction Approach for Excitation-Energy Transfer in Xanthorhodopsin
○藤本 和宏, 林 重彦 (京都大学)
Kazuhiro Fujimoto, Shigehiko Hayashi (Kyoto University)

2SP6-07
3P-063　赤血球凝集反応実験とフラグメント分子軌道法計算に基づくインフルエンザヘマグルチニンの変異予測
Possibility of Mutation Prediction of Influenza Hemagglutinin by Combination of Hemadsorption Experiment and Quantum Chemical Calculation for Antibody Binding
○竹松 和友 (1), 福澤 薫 (2), 尾曲 克己 (3), 中島 捷久 (3), 中島 節子 (3), 望月 祐志 (4), 中野 達也 (5), 渡邉 博文 (6), 田中 成典 (6) ((1) 神戸大学大学院人間発達環境学研究科人間環境学専攻: (2) みずほ情報総研: (3) 名古屋市立大学医学部: (4) 立教大学理学部化学科; JST－CREST: (5) 国立医薬品食品衛生研究所; JST－CREST: (6) 神戸大学大学院工学研究科知能情報学専攻;JST/CREST)
Kazutomo Takematsu (1), Kaori Fukuzawa (2), Katsumi Omagari (3), Katsuhisa Nakajima (3), Setsuko Nakajima (3), Yuji Mochizuki (4), Tatsuya Nakano (5), Hirofumi Watanabe (6), Shigenori Tanaka (6) ((1) Division of Human Environmental Science Graduate School of Human Development and Environment, Kobe University: (2) Mizuho Information & Research Institute, Inc.: (3) Department of Virology, Medical School, Nagoya City University: (4) Department of Chemistry and Research Center for Smart Molecules, Faculty of Science, Rikkyo University;CREST, Japan Science and Technology Agency (JST): (5) Division of

Medicinal Safety Science, National Institute of Health Sciences;CREST, Japan Science and Technology Agency (JST): (6) Graduate School of Engineering Department of Computer Science and Systems Engineering, Kobe University;CREST, Japan Science and Technology Agency (JST))

14:30～17:00　C6 会場/ Room C6

2SP7　フラビン型青色光受容体の多様な光反応と機能
Variety in the photoreactions and functions of flavin-type blue light receptors

オーガナイザー：徳富 哲 (大阪府大), 増田 真二 (東工大)

Organizer: Satoru Tokutomi (Osaka Prefecture University), Shinji MASUDA (Tokyo Institute of Technology)

Well-known photoreceptors, such as rhodopsin, bacteriorhodopsin or phytochrome, bind chromophores with double bond -conjugating systems and show a common photoreaction mechanism, i.e. photoisomerization around a double bond. Recently, another types of photoreceptors absorbing blue light have been found and studied. Cryptochrome was found at first as a blue light receptor mediating photomorphogenetic responses in plants and was turned out to be a regulator or a part of biological clock in animals. Phototropin regulates phototropism, chroloplast relocation and stomata opening of plants. BLUF families show a variety of light regulations. All these photoreceptors carry a flavin chromophore that cannot be photoisomerizable. This symposium aims to introduce and discuss how these non-photoisomerizable chromophores react and conduct signals to the downstream and what is the common and diverse mechanism among them.

2SP7-01　はじめに
Introduction
○徳富 哲 (大阪府立大学・院・理)
Satoru Tokutomi (Osaka Prefecture University, Graduate School of Sceince)

2SP7-02　リン酸化を介したフラビン型青色光シグナル伝達
Blue light signaling through phosphorylation in flavin photoreceptor
○岡島 公司 (大阪府大・理)
Koji Okajima (Grad. Sch. of Sci., Osaka Pref. Univ.)

2SP7-03　タンパク質相互作用を介したフラビン型青色光シグナル伝達
Blue-light dependent cell signaling through protein-to-protein interaction
○増田 真二 (東京工業大学; バイオ研究基盤支援総合センター)
Shinji Masuda (Center for Biological Resources and Informatics, Tokyo Institute of Technology)

2SP7-04　ラマン分光法で迫るフラビンタンパク質の光反応機構の解明
Photocycle mechanisms of flavin-containing blue-light photoreceptors revealed by Raman spectroscopy
○海野 雅司 (佐賀大学理工学部)
Masashi Unno (Department of Chemistry and Applied Chemistry, Saga University)

2SP7-05　FTIR で迫るフラビンタンパク質の光反応機構の解明
Analysis of the photoreactions of flavin-binding proteins by FTIR spectroscopy
○岩田 達也 (名古屋工業大学大学院工学研究科未来材料創成工学専攻)
Tatsuya Iwata (Department of Frontier Materials, Nagoya Institute of Technology)

2SP7-06　計算機シミュレーションで迫るフラビンタンパク質のダイナミクスと機能発現機構
Dynamics and functional mechanism of flavin-containing blue-light photoreceptors as studied by computer simulation
○櫻井 実 (東京工業大学)
Minoru Sakurai (Tokyo Institute of Technology)

2SP7-07　総合討論
General discussion
司会；増田 真二 (東京工業大学; バイオ研究基盤支援総合センター)
Discussion leader**;** Shinji Masuda (Center for Biological Resources and Informatics, Tokyo Institute of Technology)

9:00～11:30　FL 会場/ Room FL

3SA1　モータータンパク質から細胞運動へ：高次機能への組織化
From protein motors to cell motility: regulation, coordination and integration

オーガナイザー：大岩 和弘 (情報通信研究機構), 豊島 陽子 (東京大学)
Organizer: Kazuhiro Oiwa (National Institute of Information and Communications Technology), Yoko Y. Toyoshima (University of Tokyo)

Motor proteins are elaborate molecular machines and their molecular mechanism has been studied in detail especially by single molecule measurement in vitro. In cells, multiple numbers of and multiple species of motor proteins are working together based on the organized structure of the cytoskeleton, and yield highly sophisticated functions. To understand the progression of functional hierarchy, we will discuss about the regulation, coordination and integration of multiple motor proteins.

3SA1-01　高次システムにおけるダイニンの振る舞い
Dynein in the coordinated system
○豊島 陽子 (東京大学総合文化研究科　生命環境科学系)
Yoko Toyoshima (Dept. of Life Sciences, Grad. School of Arts and Sciences, The University of Tokyo)

3SA1-02　LIS1 による細胞質ダイニン順行性運搬のメカニズム
LIS1 and NDEL1 coordinate the plus-end directed transport of cytoplasmic dynein.
○広常 真治 (大阪市立大学・大学院医学研究科)
Shinji Hirotsune (Osaka City University Graduate School of Medicine)

3SA1-03　Modeling Cytoskeletal and Motor Dynamics In Vitro: Insights into Motor Function in a Complex Cellular Environment
○エリカ ホルツバウアー (ペンシルベニア大学)
Erika L.F. Holzbaur (University of Pennsylvania School of Medicine)

3SA1-04　成体脳上衣繊毛の発生・運動・機能
Ependymal Cilia in the Adult Brain: Development, Movement and Function
○澤本 和延 (名古屋市立大学大学院医学研究科再生医学分野)
Kazunobu Sawamoto (Department of Developmental and Regenerative Biology, Nagoya City University Graduate School of Medical Sciences)

3SA1-05　生体運動系の自励振動：変動するナノ機能空間
Self-Oscillation in Motile Biosystems: Variable Functional Nanospace
○石渡 信一 (早稲田大学・理工学術院)
Shin'ichi Ishiwata (Waseda University, Faculty of Science and Engineering)

9:00～11:30　S1 会場/ Room S1

3SA2　麻酔作用の分子機構：生物物理から明らかにされる生体分子と麻酔薬の相互作用
Molecular mechanism of anesthetic action: interactions between biomolecules and anesthetics revealed from biophysics

オーガナイザー：松木 均 (徳島大学), 瀬戸 倫義 (滋賀医科大学)
Organizer: Hitoshi Matsuki (The Univ. of Tokushima), Tomoyoshi Seto (Shiga Univ. of Med. Sci.)

Various theories of anesthesia have been proposed up to now since a Meyer-Overton rule that anesthetic potency is well correlated to a partition coefficient between water and olive oil of the anesthetic at the beginning of 20th century. However, there has been still no theory that can comprehensively explain anesthetic phenomena such as enhancement of anesthetic potency at a low temperature, pressure reversal of anesthesia and cut off phenomenon, etc. When considering that action of an anesthetic first appears in biological membranes, the essence of anesthetic action results in interactions of biomolecules such as membrane proteins and lipid membranes with the anesthetic in special solvent environments produced by water. In the present symposium, the role of water that is closely related to the stabilization of biomolecules is presented, and subsequently latest researches for anesthetic mechanisms by biophysical approaches are introduced.

3SA2-01　全身麻酔の生物物理学

Biophysics of General Anesthesia
○瀬戸 倫義 (滋賀医科大学)
Tomoyoshi Seto (Shiga University of Medical Science)

3SA2-02 分子認識と麻酔に関する統計力学的研究
A Statistical Mechanics Study of Molecular Recognition and Anesthesia
○平田 文男 (分子科学研究所)
Fumio Hirata (Institute for Molecular Science)

3SA2-03 分子液体論に基づく新しいリガンドマッピング法
A Novel Ligand-Mapping Method Based on Molecular Liquid Theory
○今井 隆志 (理研・次世代計算科学)
Takashi Imai (RIKEN CSRP)

3SA2-04 イオンチャンネルにおける麻酔薬の結合部位
Anesthetic Binding Site of Ion-channel
○瀬戸 倫義 (滋賀医科大学)
Tomoyoshi Seto (Shiga University of Medical Science)

3SA2-05 生体分子への麻酔薬の本質的な結合様式：リガンド相互作用の比較研究
Intrinsic binding modes of anesthetics to biomolecules: comparative studies on ligand interactions
○松木 均 (徳島大学大学院ソシオテクノサイエンス研究部)
Hitoshi Matsuki (Institute of Technology and Science, The University of Tokushima)

3SA2-06 生体コロイドにおよぼす麻酔薬の影響の体積測定による研究
Volumetric study of anesthetic effect on biocolloids
○山中 美智男 (九州大学大学院理学研究院)
Michio Yamanaka (Department of Chemistry, Faculty of Sciences, Kyushu University)

3SA2-07 高分解能溶液 NMR による薬物の膜への結合と運動状態の研究
Drug binding and mobility in membranes by high-resolution solution NMR
○岡村 恵美子 (姫路獨協大学薬学部)
Emiko Okamura (Himeji Dokkyo University, Faculty of Pharmaceutical Sciences)

3SA2-08 物理化学的手法によるリン脂質単分子膜への揮発性麻酔薬の作用機構
Action Mechanism of Volatile Anesthetics on the Phospholipid Monolayers using Physicochemical Methods
○山本 靖 (名古屋工業大学大学院　工学研究科　物質工学専攻)
Yasushi Yamamoto (Department of Materials Science and Engineering, Graduate School of Engineering, Nagoya Institute of Technology)

9:00～11:30　S2 会場/ Room S2

3SA3　学習機能を支える記憶とシナプス可塑性の多重メカニズム
Multiple mechanisms of memory and synaptic plasticity underlying learning

オーガナイザー：川原 茂敬 (富山大学), 小西 史朗 (徳島文理大学・香川薬学部)
Organizer: Shigenori Kawahara (University of Toyama), Shiro Konishi (Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University)

協賛；塩野義製薬（株）
Sponsored by Shionogi & Co., Ltd.

Flexibility is one of the characteristics of information processing in biological systems. To accomplish the flexible information processing, there are multiplicity and diversity of mechanisms functioned at molecular and cellular levels as well as at circuit and systems levels, which are integrated in a hierarchical fashion by higher nervous systems. In this symposium, we review the multiplicity and diversity of neural functions characteristic to each level, from molecular to behavioral levels, and will discuss how they could be controlled and modulated to contribute to the flexibility of brain functions and behaviors.

3SA3-01 G-substrate 遺伝子欠損マウスにより解明された小脳依存性運動学習機能
Dual involvement of G-substrate in motor learning revealed by gene deletion
○遠藤 昌吾 (沖縄科学技術研究基盤整備機構)
Shogo Endo (Okinawa Institute of Science and Technology)

3SA3-02 瞬目反射条件づけの記憶成立と発現にかかわるシナプス・分子基盤

Neural mechanisms responsible for eyeblink conditioning evidenced by gene-manipulation studies in mice
○岸本 泰司 (徳島文理大学・香川薬学部)
Yasushi Kishimoto (Kagawa School of Pharamaceutical Sciences, Tokushima Bunri University)

3SA3-03 GABA 作動性伝達に関連したシナプス可塑性の多様性とその役割
Multiple forms of synaptic plasticity around inhibitory GABAergic synapses
○小西 史朗 (徳島文理大学・香川薬学部)
Shiro Konishi (Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University)

3SA3-04 Ｇタンパク共役型受容体群によるシナプス可塑性の調整
Interaction between G protein-coupled receptors (GPCRs) regulates synaptic plasticity
○田端 俊英 (1), 藤田 洋介 (1), 下村 岳司 (1), 白井 義啓 (1), 上窪 裕二 (2), 櫻井 隆 (2), 袋谷 賢吉 (1), 狩野 方伸 (3) ((1) 富山大学大学院理工学研究部神経情報工学研究室: (2) 順天堂大学大学院医学研究科細胞・分子薬理学講座: (3) 東京大学大学院医学系研究科神経生理学講座)
Toshihide Tabata (1), Yosuke Fujita (1), Takeshi Shimomura (1), Yoshihiro Shirai (1), Yuji Kamikubo (2), Takashi Sakurai (2), Kenkichi Fukurotani (1), Masanobu Kano (3) ((1) Lab. for Neural Info. Tech., Grad. Sch. of Sci. & Eng., Univ. of Toyama: (2) Dept.of Cell. & Mol. Pharmacol., Grad. Sch. of Med., Juntendo Univ.: (3) Dept. of Neurophysiol., Grad. Sch. of Med., Univ. of Tokyo)

3SA3-05 マウス瞬目反射条件付けにおける前頭前野と小脳の役割
Roles of the prefrontal cortex and the cerebellum in mice eyeblink conditioning
○川原 茂敬 (富山大学)
Shigenori Kawahara (University of Toyama)

3SA3-06 Roles of the prefrontal cortex and the amygdala in fear conditioning
○June-Seek Choi (Korea University, Department of Psychology)

9:00～11:30　C6 会場/ Room C6

3SA4　ヘモグロビンはいま
Hemoglobin revisited

オーガナイザー：今井 清博 (法政大学), 柴山 修哉 (自治医科大学)
Organizer: Imai Kiyohiro (Hosei University), Shibayama Naoya (Jichi Medical University)

More than one century has passed since hemoglobin began to be fully studied. It is now described in many text books as the normative protein that shows a typical allosteric property. There is a tendency that most students and investigators regard it as already fully solved. From the point of view by hemoglobin experts, however, hemoglobin still carries unsolved subjects, far from full clarification. It can be pointed out that even adequacy of the well-known allosteric model, which is described in the text book, may break down. Nevertheless, not only students and graduate students, but also many investigators in cell biology, biophysics and biochemistry fields scarcely know what should be solved, considering that hemoglobin is the subject in the past. Now, under this subject specific to the old but new protein, hemoglobin, we intend to rearrange and discuss the current problems for young researchers to understand easily and to contribute to further progress in protein science.

3SA4-01 規範蛋白質としてのヘモグロビン
Hemoglobin as the normative protein
○今井 清博 (法政大学生命科学部)
Kiyohiro Imai (Faculty of Bioscience and Applied Chemistry, Hosei University)

3SA4-02 ルート効果を持つ魚ヘモグロビンの構造と機能
Structure and function of Root effect fish hemoglobins
○雲財 悟 (1), 今井 清博 (2), 横山 武司 (1), 朴 三用 (1), 長井 潔 (3), ジェレミー テイム (1) ((1) 横浜市立大学　大学院生命ナノシステム科学研究科: (2) 法政大・生命機能: (3) ＭＲＣ分子生物学研究所)
Satoru Unzai (1), Kiyohiro Imai (2), Takeshi Yokoyama (1), Sam-Yong Park (1), Kiyoshi Nagai (3), Jeremy Tame (1) ((1) Graduate School of Nanobioscience, Yokohama City University: (2) Dept. of Frontier Biosci., Hosei Univ. : (3) MRC Laboratory of Molecular Biology, Cambridge, UK)

3SA4-03 デオキシヘモグロビンの中性子結晶構造解析
Neutron crystallographic analysis of human deoxyhemoglobin
○茶竹 俊行, 森本 幸生 (京都大学原子炉実験所)
Toshiyuki Chatake, Yukio Morimoto (Research Reactor Institute, Kyoto University)

3SA4-04 ヘモグロビン協同現象の構造化学
Structural Chemistry Involved in Hemoglobin Cooperativity

○北川 禎三 (1), 長井 雅子 (2) ((1) (財)豊田理化学研究所: (2) 法政大学)
Teizo Kitagawa (1), Masako Nagai (2) ((1) Toyota Physical and Chemical Research Institute: (2) Hosei University)

3SA4-05 ヘモグロビンのアロステリック平衡の実体
The true nature of the allosteric equilibrium of hemoglobin
○柴山 修哉 (自治医科大学)
Naoya Shibayama (Jichi Medical University)

3SA4-06 蛋白質ダイナミクスはヘモグロビンのアロステリック挙動を説明する：構造変化を伴わないエントロピー・アロステリー
Protein dynamics explain the allosteric behaviors of hemoglobin: Entrpic allostery without conformation changes
○米谷 隆 (ペンシルバニア大、生化学生物物理学科・ジョンソン研)
Takashi Yonetani (Univ. of Pennsylvania, Dept. of Biochem. & Biophys. and Johnson Res. Fdn.)

12:00～14:30　FL 会場/ Room FL

3SP5 生物らしさを実感する動的分子システムの構築～超分子デバイスから生体マシンまでを包括する融合科学～
Development of dynamic molecular systems sharing the characteristics with living systems: from supra-molecular devices to bio-reorganizing machines

オーガナイザー：瀧ノ上 正浩 (東京大学)，豊田 太郎 (千葉大学大学)，小宮 健 (東京工業大学)
Organizer: Masahiro Takinoue (The University of Tokyo), Taro Toyota (Chiba University), Ken Komiya (Tokyo Institute of Technology)

In recent years, bio-inspired molecular and/or mechanical systems, e.g., supramolecular devices, cellular machines etc., have been developed. However, these artificial notable systems are independently studied in each research field because of some limitation of engineering on hierarchical systems. Hence it is quite important to consider them as an integrative science for overcoming the limitation and accelerating such research themes. In this symposium, we take up multiscale molecular systems from nm- to cm-size, and intend to extract universal idea as an integrative science, and discuss its role in biophysics in the future.

3SP5-01 DNA プログラムナノ構造による大平面のセルフアセンブリ
Self-assembly of large planar DNA crystal
○村田 智 (東京工業大学)
Satoshi Murata (Tokyo Institute of Technology)

3SP5-02 マイクロスケール物体の自己組み立て
Self-assembly of Micro-scale Objects
○尾上 弘晃 (東京大学生産技術研究所)
Hiroaki Onoe (Institute of Industrial Science, The University of Tokyo)

3SP5-03 バイオミネラリゼーション機構に基づいた機能性ナノビーズの開発
Development of functionalized magnetic nanobeads based on fundamental biomineralization studies
○松永 是 (東京農工大学)
Tadashi Matsunaga (Tokyo University of Agriculture and Technology)

3SP5-04 BZ 反応で駆動する化学ロボットの創製
Development of a novel autonomous chemical robot
○原 雄介 (早大院理工)
Yusuke Hara (Graduate School of Science and Engineering, Waseda Univ.)

3SP5-05 昆虫－機械融合システムで探る適応能
Insect-Machine Hybrid System for Understanding an Adaptive Behavior
○神崎 亮平 (東京大学 先端科学技術研究センター)
Ryohei Kanzaki (Research Center for Advanced Science and Technology, The University of Tokyo)

12:00～14:30　S1 会場/ Room S1

3SP6 膜タンパク質の立体構造ダイナミクス解析の最前線
Frontiers in analysis of three-dimnsional dynamic structures of membrane proteins

オーガナイザー：内藤 晶 (横浜国立大学), 藤原 敏道 (大阪大学蛋白質研究所)

Organizer: Akira Naito (Yokohama National University), Toshimichi Fujiwara (Institute for Protein Research, Osaka University)

Membrane proteins play an important role in the cell membrane as receptors and as transporters of ions and molecules in the living systems. A complete understanding of protein function can be accomplished with knowledge of not only three-dimensional structure but also local dynamic feature of membrane proteins as they posse various kinds of motions in the molecules. This kind of three-dimensional dynamic structure is not easy to obtain, because membrane proteins are difficult to crystallize for X-ray diffraction studies. In this symposium, it is stressed that three-dimensional dynamic structure in the native state is essential to elucidate the functional insight of the membrane proteins. The three dimensional dynamic structures of membrane proteins obtained from challenging methods such as solid state NMR, neutron diffraction study, FT-IR spectroscopy and X-ray crystallographic study, are discussed in relation to the functional insights of them.

3SP6-01 固体 NMR による膜タンパク質の構造、ダイナミクス、相互作用と活性相関の解明
Structure, dynamics and interaction of membrane proteins in relation to the function as revealed by solid-state NMR
○内藤 晶 (横浜国立大学)
Akira Naito (Yokohama National University)

3SP6-02 Dynamical NMR Structures and Functional Insights of Cytochrome-b5 and Amyloid Peptides
○Ayyalusamy Ramamoorthy (University of Michigan)

3SP6-03 分子シミュレーションと中性子散乱で探る蛋白質の立体構造ダイナミクス
Molecular simulation and neutron scattering studies of protein dynamics
○城地 保昌 (東京大学分子細胞生物学研究所)
Yasumasa Joti (Institute of Molecular and Cellular Biosciences, University of Tokyo)

3SP6-04 HAMP ドメインの構造変化ダイナミクス：センサリーロドプシン II－トランスデューサータンパク質
Dynamics of conformational change of HAMP domain upon photoexcitation of Sensory rhodopsin II -transducer complex
○井上 圭一 (1), 寺嶋 正秀 (2) ((1) 東京工業大学資源化学研究所: (2) 京都大学大学院理学研究科化学専攻)
Keiichi Inoue (1), Masahide Terazima (2) ((1) Chemical Resources Laboratory, Tokyo Institute of Technology: (2) Department of Chemistry, Graduate School of Science, Kyoto University)

3SP6-05 全反射赤外分光法で膜タンパク質–イオン間相互作用を観る
Interaction between membrane protein and ions characterized by ATR-FTIR spectroscopy
○古谷 祐詞 (分子科学研究所; 名古屋工業大学)
Yuji Furutani (Institute for Molecular Science; Nagoya Institute of Technology)

3SP6-06 膜タンパク質結晶化の難しさとその解決策
Strategies for crystallization of membrane proteins
○村田 武士 (千葉大学理学研究科；JST ERATO；理研 SSBC)
Takeshi Murata (Chiba University/Science; JST/ERATO; Riken/SSBC)

3SP6-07 NMR に基づく膜蛋白質の動的構造解析法
Method for the dynamic structural analysis of membrane proteins based on NMR
○藤原 敏道 (大阪大学蛋白質研究所)
Toshimichi Fujiwara (Institute for Protein Research, Osaka University)

12:00～14:30　S2 会場/ Room S2

3SP7　新たな切り口で神経回路を紐解く
Cutting-edge approach to studying neural circuits

オーガナイザー：井上 剛 (岡山大), 小泉 周 (自然科学研究機構生理学研究所)
Organizer: Tsuyoshi Inoue (Okayama Univ), Amane Koizumi (National Institute for Physiological Sciences)

協賛；大塚製薬（株）
Sponsored by Otsuka Pharmaceutical Co., Ltd.

Because of limits of traditional techniques, novel techniques are required to achieve break-through in neuroscience, especially to study synapses and neural circuits. In this view, biophysical approach is an attractive candidate for providing such novel techniques. The purpose of this symposium is a fusion of two research fields, biophysics and neuroscience. Our talks are presented by young

scientists in these fields, who use optical, electrophysiological and computational approaches. We will talk about how biophysical approaches contribute to neuroscience researches, and would like to explore a future perspective of "neurobiophysics".

3SP7-01 人工シナプスを用いたハイブリッド神経回路
Hybrid neuronal circuit using artificial synapses
○井上 剛 (1), 勝 孝 (1), 井本 敬二 (2) ((1) 岡山大院・医歯薬: (2) 生理研・神経シグナル)
Tsuyoshi Inoue (1), Takashi Katsu (1), Keiji Imoto (2) ((1) Lab of Biophys Chem, Grad Sch of Med, Dent and Pharm Sci, Okayama Univ: (2) Dept of Information Physiol, Natl Inst for Physiol Sci (NIPS))

3SP7-02 １分子イメージングによるシナプス可塑性の研究
Approach to synaptic plasticity by single molecule imaging
○坂内 博子 (理化学研究所　脳科学総合研究センター)
Hiroko Bannai (RIKEN, Brain Science Institute)

3SP7-03 メラノプシン遺伝子導入による網膜視機能の回復
Overview of melanopsin research : Restoration of vision by overexpressing melanopsin in blind retina
○小泉 周 (自然科学研究機構生理学研究所)
Amane Koizumi (National Institute for Physiological Sciences)

3SP7-04 覚醒個体脳におけるホールセル記録と２光子イメージング
Whole-cell recording and two-photon imaging in awake animals
○喜多村 和郎 (東京大学)
Kazuo Kitamura (The University of Tokyo)

3SP7-05 光刺激によるシナプス・ニューロン活動の誘発
Optical stimulation of synapses and neurons
○松崎 政紀 (東京大学)
Masanori Matsuzaki (University of Tokyo)

12:00～14:30　C6 会場/ Room C6

3SP8 放射線を利用した生命科学研究の最前線―マイクロビーム照射からフィールド照射まで―
Frontier in Biological Research Using Various Irradiation Systems: from microbeam to field irradiation

オーガナイザー：中島 徹夫 (放射線医学総合研究所)，冨田 雅典 ((財)電力中央研究所)，前田 宗利 ((財)電力中央研究所)
Organizer: Tetsuo Nakajima (National Institute of Radiological Sciences), Masanori Tomita (Central Research Institute of Electric Power Industry), Munetoshi Maeda (Central Research Institute of Electric Power Industry)

Ionizing radiation is recognized as a tool for cancer radiotherapy or X-ray crystallography etc. On the other hand, since Roentgen's discovery of X-rays, we have noticed the existence of ionizing radiation around us environmentally, and have been concerned about the effects on our health. Additionally, recent active exploration to the space brings us new concerns about the effects of cosmic rays. To date, many biological responses to ionizing radiation have been discovered, and particularly, repair systems of radiation-induced DNA damage have been investigated a lot. These days, using the advanced irradiation techniques and developed facilities, various biological phenomena including DNA repair systems have been uncovered. Even the effects of long-term, low-dose-rates irradiation has been analyzed under well-controlled conditions, which was previously dependent on epidemiological data. In this symposium, new discoveries in radiation biology will be showed and discussed with introduction of techniques or facilities used in experiments.

3SP8-01 低線量率放射線照射マウス、植物体を用いた長期被ばく生物影響研究
Effects of long-term irradiation on mice or plants using low-dose rates
○中島 徹夫 (放射線医学総合研究所)
Tetsuo Nakajima (National Institute of Radiological Sciences)

3SP8-02 線虫の神経機能に対する放射線影響とマイクロビーム照射実験の構想
Effects of ionizing radiation on the function of the nervous system in *C. elegans* and an attempt to locally targeted microbeam irradiation
○坂下 哲哉 (日本原子力研究開発機構)
Tetsuya Sakashita (Japan Atomic Energy Agency)

3SP8-03 プロトンマイクロビーム細胞照射装置 SPICE を用いた放射線影響研究

Biological studies using proton microbeam irradiation system, SPICE
○小西 輝昭 (1), 及川 将一 (1), 磯 浩之 (1), 石川 剛弘 (1), 樋口 有一 (1), 児玉 久美子 (1), 磯野 真由 (2), 安田 仲宏 (1), 酢屋 徳啓 (1), 今関 等 (1) ((1) (独)放射線医学総合研究所: (2) 首都大学東京)
Teruaki Konishi (1), Masakazu Oikawa (1), Hiroyuki Iso (1), Takahiro Ishikawa (1), Yuichi Higuchi (1), Kumiko Kodama (1), Mayu Isono (2), Nakahiro Yasuda (1), Noriyoshi Suya (1), Hitoshi Imaseki (1) ((1) National Institute of Radiological Sciences: (2) Tokyo Metropolitan University)

3SP8-04 X線マイクロビームを用いた放射線誘発 DNA 損傷修復機構の解析
Repair process of radiation-induced DNA damage induced by X-ray microbeam
○冨田 雅典 (1), 前田 宗利 (1), 宇佐美 徳子 (2), 小林 克己 (2) ((1) (財)電力中央研究所: (2) 高エネルギー加速器研究機構)
Masanori Tomita (1), Munetoshi Maeda (1), Noriko Usami (2), Katsumi Kobayashi (2) ((1) Central Research Institute of Electric Power Industry: (2) High Energy Accelerator Research Organization)

3SP8-05 放射光 X 線を利用した最先端照射技術と放射線生物研究への応用
The latest irradiation technique of synchrotron X-ray and its application to radiation biology
○小林 克己 (1), 宇佐美 徳子 (1), 前田 宗利 (2), 冨田 雅典 (2) ((1) 高エネルギー加速器研究機構，物質構造科学研究所，放射光科学研究施設: (2) (財)電力中央研究所　原子力技術研究所　放射線安全研究センター)
Katsumi Kobayashi (1), Noriko Usami (1), Munetoshi Maeda (2), Masanori Tomita (2) ((1) Photon Factory, IMSS, KEK: (2) Radiation Safety Research Center, Central Research Institute of Electric Power Industry)

サテライトミーティング　Satellite Meeting

第 2 日目(10 月 31 日（土）) / Day 2 (Oct. 31, Sat.)

10:00～11:30　C6 会場/ Room C6

2MA1　「科研費制度を知る：とくに若手研究者に向けて」

オーガナイザー：学術システム研究センターPO　石渡信一 (早稲田大学)
講師：日本学術振興会　審議役　宮嶌和男 (みやじまかずお) 氏

変化しつつある科研費制度の具体的な中身を，生物物理学会の皆さん，とくに若手の研究者たちにわかっていただき，この分野の活性化に資したいと思います．昨年の年会でも，「科研費制度の現状：審査の現場から」と題したサテライトミーティングを開き，参加者にアンケートを行いました(その集計結果は学会誌で報告します)．今回は，宮嶌和男氏に「科研費をはじめとする日本学術振興会事業について－競争的資金を獲得するチャンスを見逃していませんか？－」と題した講演をしていただき，十分な時間をかけて質疑・応答を行います．並行して幾つかのサイエンス・シンポジウムが開かれますが，多くの方々のご参加をお待ちしています．

口頭発表　Oral Presentations

In this program, the speaker is shown by bold characters.

The presentation is for 12 min; the discussion for 2 min; and the computer replacement for 1 min.

第 1 日目 9:00～11:30（10 月 30 日（金））/ Day 1 (Oct. 30, Fri.)

蛋白質-Ｂ) 構造機能相関　1TA1-01～09　C1 会場/ Room C1

1TA1-01
1P-019
Conformation and Activity from Saturation Adsorptions of Lysozyme on the Surfaces of Nanosilica and Nanodiamond

Victor Wei-Keh Wu (1) ((*1) Department of Chemical and Materials Engineering, National Kaohsiung University of Applied Sciences: Victor Basic Research Laboratory*)

1TA1-02
1P-022
藍色細菌 *Synechococcus* sp. PCC 7942 の細胞内亜鉛イオン濃度センサー機能を持つ転写因子 SmtB の亜鉛イオン結合に伴う構造変化に関する多次元 NMR 分光法による解析

Multidimensional NMR spectroscopic analysis with the structural changes of cyanobacterial transcription factor, SmtB, functioning as the sensor for zinc-ion concentration in the cell, following zinc-ion binding

Hayato Morita (1), Hidenori Hayashi (2), Syunnosuke Abe (1), Takahisa Ikegami (3) ((*1) Faculty of Agriculture, Ehime University: (2) Faculty of Science, Ehime University: (3) Institute for Protein Research, Osaka University*)

1TA1-03
1P-028
ビスフェノールＡとの相互作用はカルモジュリンのカルシウム結合能を弱める

Bisphenol A weakens Calcium Binding Affinity of Calmodulin

Koichi Murayama (1), Tomoyoshi Terada (1), Masashi Sonoyama (2), Yasunori Yokoyama (3), Masayuki Nara (4), Yasuo Asami (5), Sadayuki Matsuda (6) ((*1) Graduate School of Medicine, Gifu University : (2) Graduate School of Engineering, Gunma University: (3) Graduate School of Engineering, Nagoya University: (4) College of Liberal Arts and Sciences, Tokyo Medical & Dental University: (5) TA Instruments Japan Inc.: (6) School of Natural Science, Engineering and Agriculture, Hokkaido University of Education at Asahikawa*)

1TA1-04
1P-030
細胞内アクチンの SS 結合による二量体の研究

A study on cytoplasmic actin SS dimers.

Daisuke Fukuhara (1), Hiroaki Kubota (1), Takashi Ohki (2), Shin'Ichi Ishiwata (2) ((*1) Major in Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda Univ.: (2) Dept. of Physics, Faculty of Advanced Science and Engineering, Waseda Univ.*)

1TA1-05
1P-031
Gads の精製と CD28 細胞質内ドメインとの相互作用

Purification of Gads and its interaction with CD28 cytoplasmic domains

Kunitake Higo (1), Jun Takahashi (1), Masayuki Oda (2), Hisayuki Morii (3), Teikichi Ikura (4), Nobutoshi Ito (4), Takachika Azuma (1), Ryo Abe (1) ((*1) Res. Inst. for Biol. Sci., Tokyo Univ. of Sci.: (2) Grad. Sch. of Environ. Sci., Kyoto Pref. Univ.: (3) Natl. Inst. of Adv. Indust. Sci. and Technol.: (4) Grad. Sch. of Biomed Sci., Tokyo Medical and Dental Univ.*)

1TA1-06
1P-033
非機械感受性イオンチャネルは本当に機械刺激によって開かないか？　– 粗視化分子動力学シミュレーション研究

Does a non-mechanosensitive ion channel really not open by mechanical force? – A coarse grained molecular dynamics simulation study

Ken Takahashi (1), Masahiro Sokabe (1) ((*1) Nagoya University Graduate School of Medicine, Dept. of Cellular Biophysiology*)

1TA1-07
1P-029
時間領域テラヘルツ分光法でみる低振動領域におけるタンパク質の動力学転移

Low-frequency dynamical transition of proteins monitored by terahertz time-domain spectroscopy

Ohki Kambara (1), Keisuke Tominaga (1) ((*1) Molecular Photoscience Research Center, Kobe University*)

1TA1-08
βラクタマーゼによるセファロスポリンの加水分解活性と、そのアシル中間体の熱安定性との相関

The correlation between the catalytic susceptibility of cephalosporins and the thermal stabilities of their beta-lactamase acyl intermediates.

Yasushi Nitanai (1), Tatsuro Shimamura (1), Takuro Uchiyama (1), Yoshikazu Ishii (2), Michiyo Takehira (1), Katsuhide Yutani (1), Hiroshi Matsuzawa (3), Masashi Miyano (1) ((*1) RIKEN: (2) Faculty of Medicine, Toho University: (3) Faculty of Pharmaceutical Sciences, Aomori University*)

1TA1-09
1P-032
新規デフェンシンの膜構造と抗菌活性

A new strategy of defensin against Gram-positive bacteria

Keiichi Kawano (1), Takahide Kouno (2), Naoki Fujitani (5), Mineyuki Mizuguchi (4), Tsukasa Osaki (3), Shun-Ichiro Kawabata (3), Tomoyasu Aizawa (1), Makoto Demura (5) ((*1) Grad Sch Sci, Hokkaido Univ: (2) Fac Pharm Sci, Toyama Univ; Dep Biochem Mol Biol & Biophys,Minnesota Univ: (3) Dep Biol, Kyushu Univ: (4) Fac Pharm Sci, Toyama Univ: (5) Grad Sch Life Sci, Hokkaido Univ*)

筋肉 (筋蛋白質・収縮) 1TA2-01～09　C2 会場/ Room C2

1TA2-01
成熟した横紋筋における微小管と適応における役割：チューブリンの分子シャペロンαB-クリスタリンの細胞内機能から

Significant roles of microtubules in mature striated muscle: Insight from correlative expression of tubulin and its molecular chaperone alphaB-crystallin

Yoriko Atomi (1), Hyunseok Jee (1), Takashi Sakurai (1), **Eri Fujita-Ohto** (2) ((*1) The University of Tokyo, Radioisotope Center: (2) The University of Tokyo, The Department of Information and Communication Engineering, Graduate School of Information and Science Technology*)

1TA2-02
平滑筋ミオシン I によるＦアクチン束化のメカニズム

Mechanism of F-actin bundling by smooth muscle myosin I

Yoh Okamoto (1), Tatsuya Kawai (1), Kohei Morimoto (1), Masahiro Kuragano (1) ((*1) Division of Applied Science and Engineering, Muroran Institute of Technology*)

1TA2-03 骨格筋ミオシンの尾部の脆弱部位の予測

Prediction of fragile points of skeletal myosin rods

Mieko Taniguchi (1), Hideki Tanizawa (2), Ghimire Ganga D. (3), Sigeki Mitaku (2) ((*1) Depertment oBiotechnology and Biomaterial Chemistry, Nagoya University: (2) Dpartment of Aplied Physics, School of Engineering, Nagoya Unversity: (3) Reseach Centre Juelich, Institute of Neuroscience and Biophysics, Molecular Biophysics*)

1TA2-04 非同期型昆虫飛翔筋のカルシウムによる張力発生と伸張による張力発生は異なる温度依存性をもつ

Calcium-activated and stretch-activated forces have different temperature dependence in asynchronous flight muscle of insect

Hiroyuki Iwamoto (1) ((*1) SPring-8, JASRI*)

1TA2-05 中性子スピンエコー法によるアクチン分子の運動の測定

Measurements of motions of actin by neutron spin-echo spectroscopy

Satoru Fujiwara (1), Fumiko Matsumoto (1), Hiroshi Nakagawa (1), Hitoshi Endo (2), Toshiro Oda (3) ((*1) Quantum Beam Science Directorate, Japan Atomic Energy Agency: (2) Inst. Solid State Phys., Univ. Tokyo: (3) RIKENSPring-8 center, RIKEN Harima Inst.*)

1TA2-06 格子間隔に依存した２状態モデルにおける筋肉の状態相図

1P-120 Lattice spacing-dependent two state model of striated muscle contraction: Phase diagram and dynamic behavior

Katsuhiko Sato (1), **Masako Ohtaki** (2), Yuta Shimamoto (3), Ishiwata Shin'Ichi (2) ((*1) Dept of Physics, Tohoku Univ.: (2) Dept of Physics, Faculty of Science & Engineering, Waseda Univ.: (3) Laboratory of Chemistry and Cell Biology, Rockefeller Univ.*)

1TA2-07 心筋症発症の分子メカニズム：分子動力学・Ｘ線回折法による変異トロポニン導入心筋の構造解析

Molecular mechanism of hypertrophic cariomyopathycaused by troponin mutation: Molecular dynamics and X-ray diffraction study

Maki Yamaguchi (1), Masako Kimura (1), Shigeru Takemori (1), Tetsuo Ohno (1), Nobutake Akiyama (5), Masaru Watanabe (2), Masatoshi Yumoto (2), Yumiko Otsuka (3), Tsuyoshi Takamura (1), Naoto Yagi (4) ((*1) The Jikei university school of medicine, Dept Physiology: (2) Tokyo medical university, Dept Physiology: (3) Teine keijinkai hospital: (4) SPring-8/JASRI: (5) The Jikei university school of medicine, Dept Molecular immunology*)

1TA2-08 アクチン除去筋における筋節伸展に伴うミオシン頭部配列の変化

Protrusion of myosin heads from their backbone in actin removed striated muscle with sarcomere elongation

Masako Kimura (1), Shigeru Takemori (2), Maki Yamaguchi (2), Tetsuo Ohno (2), Naoto Yagi (3) ((*1) The Jikei University School of Medicine, Department of Molecular Physiology; Tokyo Dental College Ichikawa General Hospital: (2) The Jikei University School of Medicine, Department of Molecular Physiology: (3) Spring8*)

1TA2-09 骨格筋フィラメント格子内の水の状態：ラマン分光法による分子振動観察

Water states in myofilament lattice of skeletal muscle: observation of molecular vibration with Raman spectroscopy

Shigeru Takemori (1), Masako Kimura (2), Tetsuo Ohno (1), Maki Yamaguchi (1) ((*1) The Jikei University School of Medicine: (2) Tokyo Dental College; The Jikei University School of Medicine*)

化学受容　1TA3-01，神経・感覚 (細胞・膜蛋白質・分子) 1TA3-02
神経回路・脳の情報処理　1TA3-03～06，生体膜・人工膜-情報伝達　1TA3-07～09　C3 会場/ Room C3

1TA3-01 霊長類苦味受容体の多型解析

Polymorphisms in the bitter taste receptors of primates.

Nami Suzuki (1), Tohru Sugawara (1), Yasuhiro Go (2), Atsushi Matsui (1), Hirohisa Hirai (1), **Hiroo Imai** (1) ((*1) Primate Research Institute, Kyoto University: (2) Biodiversity Global COE program, Graduate School of Science, Kyoto University*)

1TA3-02 PSD タンパク質 Homer と Shank が形成するネットワーク構造

The Postsynaptic Density Proteins Homer and Shank Form a Polymeric Network Structure

Mariko Hayashi (1), Chunyan Tang (4), Chiara Verpelli (5), Radhakrishnan Narayanan (2), Marissa Stearns (2), Rui-Ming Xu (6), Huilin Li (4), Carlo Sala (5), Yasunori Hayashi (2) ((*1) Department of Pharmacology, School of Medicine, Keio University: (2) RIKEN-MIT Neuroscience Research Center, The Picower Institute for Learning and Memory, Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology: (3) Brain Science Institute, RIKEN: (4) Biology Department, Brookhaven National Laboratory: (5) Consiglio Nazionale delle Ricerche, Institute of Neuroscience and Department of Pharmacology, University of Milan: (6) Structural Biology Program, The Helen L. and Martin S. Kimmel Center for Biology and Medicine at the Skirball Institute of Biomolecular Medicine and Department of Pharmacology, New York University School of Medicine*)

1TA3-03 海洋深層水は海馬のインスリン様成長因子_Ｉ産生を促進してマウスの認知機能を改善する

Deep-sea water improves cognitive function in mice by increasing the production of insulin-like growth factor-I in the hippocampus

Naoaki Harada (1), Minoru Yoshizawa (2), Yoshizumi Asakawa (2), Kenji Okajima (1) ((*1) Department of Translational Medical Science Research, Nagoya City University Graduate School of Medical Sciences: (2) MARINE GOLD Co., Ltd.*)

1TA3-04 培養神経回路網の長期間発達過程における免疫蛍光染色像と電気活動

1P-214 Immunofluorescence imaging and electrical activity during long term development of cultured neuronal networks

Takumi Komatsu (1), Daisuke Ito (1), Naohiro Yamada (1), Hiroki Tamate (1), Kazutoshi Gohara (1) ((*1) Division of Applied Physics, Graduate School of Engineering, Hokkaido University*)

1TA3-05 構成論的アプローチによる昆虫匂い識別機構の分析

A Synthetic Approach for Understanding Olfactory Information Processing in the Moth Brain

Shigehiro Namiki (1), Ryohei Kanzaki (1) ((*1) Research Center for Advanced Science and Technology, The University of Tokyo*)

1TA3-06 資源競合振動子ネットワーク：粘菌ニューロコンピュータのモデル

Resource-competing oscillator network: A model of amoeba-based neurocomputer

Masashi Aono (1), Masahiko Hara (1) ((*1) RIKEN*)

1TA3-07 コントラスト変調と異常分散を用いた膜蛋白質結晶中の脂質二重膜の可視化
1P-199 Visualization of lipid bilayer in the crystal of the membrane protein using x-ray contrast variation and anomalous scattering
Yoshiyuki Norimatsu (1), Junko Tsueda (1), Ayami Hirata (1), Shiho Iwasawa (1), Chikashi Toyoshima (1) ((*1) Institute of Molecular and Cellular Biosciences*)

1TA3-08 Ｔ細胞認識における PUFAs の影響
1P-195 Effects of disruption of lipid rafts by PUFAs on T cell recognition
Keiko Udaka (1), Satoshi Komaniwa (1), Arisa Yano (1), Toshihiro Komatsu (1), Akifumi Hagi (2) ((*1) Department of Immunology, Kochi Medical School: (2) Otsuka Pharmaceutical Factory, Inc.*)

1TA3-09 １分子イメジングによる GPCR ダイマーの解離定数の決定
First determination of the dimer dissociation constant of GPCR in the living cell membrane by single-molecule imaging
Rinshi Kasai (1), Eric Prossnitz (2), Akihiro Kusumi (1) ((*1) Membrane Mechanisms Project, ICORP-JST, Institute for Integrated Cell-Material Sciences (iCeMS), Institute for Frontier Medical Sciences, Kyoto University, Kyoto, Japan: (2) Department of Cell Biology and Physiology, University of New Mexico, Albuquerque, New Mexico, USA*)

分子モーター　1TA4-01～10　C4 会場/ Room C4

1TA4-01 微小管のチロシン付加とグルタミン酸付加によるモータータンパク質の交通ナビゲーション
MTs tyrosination and polyglutamylation for the traffic navigation of motor proteins
Mitsutoshi Setou (1), Koji Ikegami (1), Yoshiyuki Konishi (1) ((*1) Hamamatsu University School of Medicine*)

1TA4-02 KIF1A 分子モーターの一方向性の運動発現機構のシミュレーション研究
1P-129 Mechanism of unidirectional move of KIF1A motor studied by coarse-grained simulations
Ryo Kanada (1), Takeshi Kuwata (2), Kei-Ichi Okazaki (3), Hiroo Kenzaki (1), Shoji Takada (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University: (2) Graduate School of Science, Kobe University: (3) School of Advanced Science and Engineering, Waseda University*)

1TA4-03 滑走するバクテリア、*Mycoplasma mobile* のステップ検出
1P-142 Step detection of gliding bacterium, *Mycoplasma mobile*
Daisuke Nakane (1), Takayuki Nishizaka (2), Makoto Miyata (1) ((*1) Graduate School of Science, Osaka City University: (2) Faculty of Science, Gakushuin University*)

1TA4-04 *Mycoplasma mobile* の滑走運動を阻害するモノクローナル抗体の標的部位
1P-141 Target sites of monoclonal antibody inhibiting *Mycoplasma mobile* gliding
Chie Kawaguchi (1), Shuhei Yoshii (1), Makoto Miyata (1) ((*1) Osaka City University*)

1TA4-05 高速 AFM によるクラミドモナス　ダイニンＣ破壊過程の観察
1P-130 The observation of disintegration processes of *Chlamydomonas* dynein-c by using high-speed AFM
Daisuke Yamamoto (1), Atsushi Miyagi (1), Toshio Ando (1), **Hitoshi Sakakibara** (2) ((*1) Physics, School of Science, Kanazawa University: (2) Biological ICT Group, National Institute of Information and Communications Technology*)

1TA4-06 ミオシンＶの頭部間協調性におけるレバーアームの役割
1P-138 Role of the lever arm in the subunit coordination in myosin V
Yusuke Oguchi (1), Sergey V. Mikhailenko (2), Takashi Ohki (1), Adrian O. Olivares (3), Enrique M. De La Cruz (4), Shin'Ichi Ishiwata (1) ((*1) Department of Physics, Faculty of Science and Engineering, Waseda University: (2) Department of Physics, Gakushuin University: (3) Department of Biology, Massachusetts Institute of Technology: (4) Department of Molecular Biophysics and Biochemistry, Yale University*)

1TA4-07 張力のかかったアクチンフィラメント上でのミオシンＶ一分子運動
1P-139 Single-molecule myosin V movement on a tense actin filament
Hiroaki Kubota (1), Yusuke Oguchi (2), Takashi Ohki (2), Shin'Ichi Ishiwata (2) ((*1) Major in Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda Univ.: (2) Dept. of Physics, Faculty of Advanced Science and Engineering, Waseda Univ.*)

1TA4-08 リバースジャイレースの反応速度の温度依存性
1P-140 Temperature Dependence of Positive Supercoiling by Reverse Gyrase
Taisaku Ogawa (1), Katsunori Yogo (2), Shou Furuike (3), Akihiko Kikuchi (4), Kazuhiko Kinosita (1) ((*1) Dept. of Phys., Grad. School of Science and Engineering, Waseda Univ.: (2) Dept. of Phys., Gakushuin Univ.: (3) Dept. of Phys., Osaka Med. Coll.: (4) Nagoya Univ.*)

1TA4-09 揺らぎの定理を用いた F_1－ATPase のトルク測定
1P-135 Torque measurements of F1-ATPase by using the fluctuation theorem
Kumiko Hayashi (1), Hiroshi Ueno (1), Ryota Iino (1), Hiroyuki Noji (1) ((*1) ISIR, Osaka Univ.*)

1TA4-10 F1-ATPase の温度高感受性待ち時間の一分子速度論解析
1P-143 Single molecule kinetic analysis of the temperature sensitive dwell of F1-ATPase
Tetsuaki Okamoto (1), Shouich Toyabe (1), Eiro Muneyuki (1) ((*1) Department of Physics, Faculty of Science and Engineering, Chuo University*)

細胞生物的課題 (接着，運動，骨格，伝達，膜)　1TA5-01～09　C5 会場/ Room C5

1TA5-01 分裂期の Hela 細胞への局所温度勾配の効果
1P-171 Effect of local temperature gradient on HeLa cells in mitotic phase
Masahiro Motoyoshi (1), Madoka Suzuki (2), Kotaro Oyama (1), Takeshi Itabashi (1), Shin'Ichi Ishiwata (1) ((*1) Department of Physics, Faculty of Science and Engineering, Waseda University: (2) COBRI, Comprehensive Research Organization, Waseda University*)

1TA5-02 分裂中期にある紡錘体形状の左右相称制御

1P-172 Bilateral regulation of spindle shape at metaphase

Kazuya Suzuki (1), Jun Takagi (1), Takeshi Itabashi (1), Shin'Ichi Ishiwata (1) ((*1) Depertment of Physics, Faculty of science and engineering, Waseda University*)

1TA5-03 二光子蛍光寿命イメージング法による Rho GTPase 活性化の単一シナプスレベル可視化解析

Imaging Rho GTPases activation in single dendritic spines by 2-photon fluorescence lifetime imaging microscopy

Hideji Murakoshi (1), Ryohei Yasuda (1) ((*1) Duke University Medical Center*)

1TA5-04 クローディン－３を発現したＬ細胞に形成されたタイトジャンクション様構造の急速凍結レプリカおよび HAADF-STEM による観察

1P-170 Tight junction-like structures in L cells expressing claudin-3 protein observed by quick-freeze-replica and HAADF-STEM.

Kazunori Kawasaki (1), Tomoki Kato (1), Mikio Furuse (2) ((*1) National Institute of Advanced Industrial Science and Technology: (2) Kobe University Graduate School of Medicine*)

1TA5-05 刺激前細胞でのラフト分子のラフト滞在時間は１ミリ秒よりはるかに短い

Molecular trapped time in metastable raft domains in steady-state cells is much shorter than 1 ms

Kenichi G. N. Suzuki (1), Takahiro K. Fujiwara (2), Akihiro Kusumi (2) ((*1) PRESTO-JST; iCeMS, Kyoto University: (2) ICORP-JST; iCeMS, Kyoto University*)

1TA5-06 マイクロ流体中の運動精子における細胞内カルシウムイオンが果たす一役割

A role of $[Ca^{2+}]_i$ in motile sperms in microfluidic environments

Koji Matsuura (1), Yuka Kuroda (1), Toru Hyakutake (2), Shinichiro Yanase (2), Keiji Naruse (3) ((*1) Research Core for Interdiciplinary Sciences, Okayama University: (2) Graduate School of Natural Science and Technology, Okayama University: (3) Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University*)

1TA5-07 異なる接着強度の基質上における細胞の形・運動・力

1P-174 Cellular Shape, motion and forces on various adhesive surfaces

Hirokazu Tanimoto (1), Miki Matsuo (1), Masaki Sano (1) ((*1) Department of Physics, Graduate School of Science, the University of Tokyo*)

1TA5-08 線虫初期胚の細胞質流動の力学的基盤の解明のための、流速分布の測定と 3D シミュレーションによる再構築

1P-173 quantification and 3D simulation reconstruction of the cytoplasmic streaming in *C. elegans* embryo to elucidate its mechanical basis

Ritsuya Niwayama (1), Kyousuke Shinohara (2), Akatusuki Kimura (1) ((*1) SOKENDAI;National Instutute of Genetics, Center for Frontier Research, Cell Architecture Laboratory: (2) Osaka University, Graduate School of Frontier Biosciences, Developmental Genetics Group*)

1TA5-09 ストカスティックシミュレーションの新理論と F-actin 形成への応用

A new theory of stochastic simulation and its application to F-actin dynamics

Kazuhisa Ichikawa (1), Koji Yamada (1), Kensuke Tsuda (1) ((*1) Kanazawa Institute of Technology*)

第１日目 13:00～15:30（10 月 30 日（金））/ Day 1 (Oct. 30, Fri.)

光生物-視覚・光受容　1TP2-01～09　C2 会場/ Room C2

1TP2-01 固体 NMR による光受容タンパク質 *p*pR とその変異体 T204A の局所構造変化の解析

1P-217 Analysis of local protein conformations in photoreceptor *p*pR and its mutant T204A by solid-state NMR

Tetsurou Hidaka (1), Izuru Kawamura (1), Takudo Nishio (1), Kazuhiro Osawa (1), Naoki Kamo (2), Akira Naito (1) ((*1) Graduated School of Engineering, Yokohama National University: (2) College of Pharmaceutical Sciences, Matsuyama University*)

1TP2-02 HAMP ドメインの分子動力学解析：電子スピン常磁性共鳴のデータを満足する４－helix　bundle 構造

1P-219 Molecular dynamical analysis of a HAMP domain: A four-helix bundle structure satisfies the data of electron paramagnetic resonance

Koro Nishikata (1), Sotaro Fuchigami (2), Mitsunori Ikeguchi (2), Akinori Kidera (3) ((*1) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University: (2) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University: (3) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University; Research Program for Computational Science, RIKEN*)

1TP2-03 桿体・錐体視物質における活性中間体の pH 依存性の比較研究

1P-221 Comparative studies on the pH-dependency of the active intermediate between rod and cone visual pigments.

Keita Sato (1), Takahiro Yamashita (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1TP2-04 対イオンの位置を変えたロドプシン変異体におけるレチナール発色団光異性化効率

1P-223 Photoisomerization efficiency of the retinal chromophore in rhodopsin mutants with displaced counterion

Kei Tsutsui (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1TP2-05 代謝型グルタミン酸受容体のリガンド結合に伴う二量体配置転換の比較解析

1P-224 Comparative analyses of ligand-induced dimeric rearrangements of metabotropic glutamate receptors

Masataka Yanagawa (1), Takahiro Yamashita (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1TP2-06 パリエトプシンの分子機能の探索

1P-225 Exploring Molecular Functions of Parietopsin

Kazumi Sakai (1), Yasushi Imamoto (1), Takahiro Yamashita (1), King-Wai Yau (2), Chih-Ying Su (2), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University: (2) Department of Neuroscience, Johns Hopkins University School of Medicine*)

1TP2-07 プロトンポンプを目指したバクテリアのセンサーロドプシンの変異体研究

1P-227 The mutation study to create proton pumps from a bacterial sensor rhodopsin

Akira Kawanabe (1), Jung Kwang-Hwan (2), Hideki Kandori (1) (*(1) Nagoya Institute of Technology: (2) Sogang University*)

1TP2-08 古細菌型ロドプシンのカーボンナノチューブへの内包

1P-228 Encapsulation of ion-pumping rhodopsins into multi-wall carbon nanotubes

Takayoshi Kawashima (1), Kazuhiro Yanagi (3), Zheng Liu (4), Yuji Furutani (5), Kazutomo Suenaga (4), Hiromichi Kataura (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Nanotechnology Research Institute (NRI), National Institute of Advanced Industrial Science and Technology (AIST): (3) Nanotechnology Research Institute (NRI), National Institute of Advanced Industrial Science and Technology (AIST);Department of Physics, Tokyo Metropolitan University: (4) Nanotube Research Center, National Institute of Advanced Industrial Science and Technology (AIST): (5) Department of Frontier Materials, Nagoya Institute of Technology;Institute for Molecular Science*)

1TP2-09 霊長類色覚視物質の赤外分光解析

1P-229 Low-temperature FTIR study of primate color pigments

Kota Katayama (1), Yuji Furutani (2), Hiroo Imai (3), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Life and Coordination-Complex Molecular Science, Institute for Molecular Science: (3) Primate Research Institute, Kyoto University*)

蛋白質-物性（安定性，折れたたみなど） 1TP3-01～08 C3 会場/ Room C3

1TP3-01 ウシβラクトグロブリン非天然中間体による折り畳み速度の促進機構

A channeling role of the non-native intermediate in the folding of β-lactoglobulin

Shunsuke Fujioka (1), **Kazumasa Sakurai** (1), Tsuyoshi Konuma (1), Masanori Yagi (1), Yuji Goto (1) (*(1) Inst. Protein Res., Osaka Univ.*)

1TP3-02 免疫グロブリン軽鎖可変ドメインのフォールディング、アンフォールディング、ミスフォールディング

Folding, unfolding and misfolding behaviours of immunoglobulin light chain variable domain

Daizo Hamada (1) (*(1) Division of Structural Biology (G-COE), Department of Biochemistry and Molecular Biology, Graduate School of Medicine, Kobe University*)

1TP3-03 シアノバクテリア DnaK/DnaJ/GrpE 系の確立と HtpG によるリフォールディング活性の調節

Cyanobacterial DnaK/DnaJ/GrpE system and the modulation of its refolding activity by HtpG

Kensaku Fujita (1), **Hitoshi Nakamoto** (1) (*(1) Department of Biochemistry and Molecular Biology, Saitama University*)

1TP3-04 新規発光共役高分子による新規インスリンフィラメントの細胞毒性と内部構造解明

1P-056 Cell toxicity and inner structure analysis of novel insulin filaments using novel luminescent conjugate polymers

Takahiro Kobayashi (1), **Tamotsu Zako** (2), Masafumi Sakono (2), Mikael Lindgren (3), Peter Nilsson (4), Per Hammarstrom (4), Mizuo Maeda (1) (*(1) Front.Sci., Univ. Tokyo: (2) RIKEN: (3) Dept. Phys., The Norwegian Univ.: (4) Dept. Chem., Linkoping Univ.*)

1TP3-05 レプリカ交換分子動力学法による単量体ポリグルタミンタンパクの特性研究

1P-055 Characterization of monomeric polyglutamine peptides by replica exchange molecular dynamics simulation

Miki Nakano (1), Hirofumi Watanabe (3), Shigenori Tanaka (2) (*(1) Kobe University Graduate School of Human Development and Environment: (2) Kobe University Graduate School of Engineering : (3) CREST, Japan Science and Technology Agency*)

1TP3-06 蛋白質の体積揺らぎ動力学に対する圧力効果

1P-059 Effects of Pressure on Volume-Fluctuation Dynamics of Proteins

Kunitsugu Soda (1), Yudai Shimbo (2), Yasutaka Seki (2), Makoto Taiji (1) (*(1) Computational Systems Biology Group, RIKEN: (2) Dept. Bioeng., Nagaoka Univ. Technol.*)

1TP3-07 移相自由エネルギー計算による異なる溶媒中のペプチドの構造安定性の解析

Peptide conformational preferences in different solutions analyzed by transfer free energy calculations

Hironori Kokubo (1), Char Hu (1), B. Montgomery Pettitt (1) (*(1) Department of Chemistry, University of Houston*)

1TP3-08 固体 NMR によるバイセル存在下でのヒトカルシトニンのアミロイド様線維構造と線維形成機構の解析

1P-035 Amyloidogenic fibrils and the structure of human calcitonin in the presence of phospholipidbilayers as studied by ^{13}C solid-state NMR

Yuki Abe (1), Miya Kamihira (2), Hikari Watanabe (1), Atsushi Kira (1), Izumi Yamane (1), Izuru Kawamura (1), Akira Naito (1) (*(1) Graduate school of Engineering, Yokohama National University: (2) Institute of Multidisciplinary Research, Tohoku University*)

分子モーター 1TP4-01～10 C4 会場/ Room C4

1TP4-01 クラミドモナスを動力源としたマイクロ構造体の駆動

1P-144 Micro-objects driven by *Chlamydomonas*

Taishi Tonooka (1), Kaori Kuribayashi (1), Hiroaki Onoe (1), Masahiro Takinoue (1), Shoji Takeuchi (1) (*(1) Institute of Industrial Science, The University of Tokyo*)

1TP4-02 細胞質ダイニンは細胞周期依存的に微小管系により輸送される

Cell cycle-dependent microtubule-based dynamic transport of cytoplasmic dynein in mammalian cells

Takuya Kobayashi (1), Yoshitaka Kimori (2), Nobuhiro Morone (2), **Takashi Murayama** (1) (*(1) Dept. Pharmacol., Juntendo Univ. Sch. Med.: (2) Nat. Inst. Neurosci., NCNP*)

1TP4-03 キネシンと細胞質ダイニンが混在する微小管上における各分子モーターの一分子運動解析

1P-147 Motility of single molecules of kinesin and cytoplasmic dynein in the presence of many molecules of motor proteins on microtubules

Keitaro Shibata (1), Ken'Ya Furuta (1), Masaki Edamatsu (1), Yoko Toyoshima (1) (*(1) Dept Life Sciences, Graduate School of Arts and Sciences, Univ. of Tokyo*)

1TP4-04 多分子ミオシンの協調的運動の解析

1P-148 Model analysis of cooperative behavior in multiple myosin system

Takeshi Nakagawa (1), Hiroto Tanaka (2), Kazuo Sasaki (1) ((*1) Dept. of Applied Physics, Tohoku Univ.: (2) KARC, NICT; PRESTO, JST*)

1TP4-05 ネックリンカーによるキネシンの ATP 加水分解反応制御

1P-145 Role of the neck linker in controlling the ATP hydrolysis reaction of kinesin

Xiao Ling (1), Teppei Mori (1), Michiko Nakajima (1), Michio Tomishige (1) ((*1) Department of Applied Physics, school of engineering, the University of Tokyo*)

1TP4-06 キネシン１モータードメインのヌクレオチドフリー状態での結晶構造解析

1P-146 Crystal Structure of Nucleotide-free Kinesin-1 Motor Domain Explains Coordinated Walking Mechanism

Tsukasa Makino (1), Teppei Mori (1), Ken-Ichi Miyazono (2), Masaru Tanokura (2), Michio Tomishige (1) ((*1) Department of Applied Physics, University of Tokyo: (2) Department of Applied Biological Chemistry, University of Tokyo*)

1TP4-07 キネシン分子による微小管の滑り運動に内在するトルク成分に関する研究

Characterisation of a torque component present in the kinesins-driven microtubule movement

Junichiro Yajima (1) ((*1) Department of Physics, Gakushuin University*)

1TP4-08 クラス VIII ミオシンは超 high duty ratio である

Class VIII myosin is an extremely highly duty ratio

Kohji Ito (1), Rie Matsumoto (1), Keiichi Yamamoto (1) ((*1) Dept.of Biology, Chiba University*)

1TP4-09 Dynamics of zipping the kinesin neck linker and an RNA hairpin

Dynamics of zipping the kinesin neck linker and an RNA hairpin

Yasuhiro Imafuku (1), Neil Thomas (2) ((*1) Department of Biology, Kyushu University: (2) Physics Department, Birmingham University*)

1TP4-10 Angle Dependency of ATP binding event in V_1－ATPase

Naciye Esma Uner (1), Masahiro Nakano (1), Daichi Okuno (1), Ken Yokoyama (2), Hiroyuki Noji (1) ((*1) The Institute of Scientific and Industrial Research, Osaka University: (2) ATP Synthesis Regulation Project, International Cooperative Research Project (ICORP), Japan Science and Technology Agency, Tokyo*)

核酸-構造・物性　1TP5-01～03，核酸-相互作用・複合体　1TP5-04～07，核酸結合蛋白質　1TP5-08～10
C5 会場/ Room C5

1TP5-01 分子動力学による DNA コンフォーメーション変化における周辺環境の影響

The effect of environment on the conformational transition of DNA studied by molecular dynamics simulations

Satoshi Fujii (1), Hidetoshi Kono (3), Nobuhiro Go (2), Akinori Sarai (1) ((*1) Kyushu Institute of Technology: (2) JAEA: (3) PRESTO, JST*)

1TP5-02 一本鎖 DNA の両末端接触速度における長さ及び溶液の粘度依存性

1P-097 The Length and Viscosity Dependence of End-to-end Collision Rates in Single-stranded DNA

Takanori Uzawa (1), Ryan Cheng (2), Dmitrii Makarov (2), Kevin Plaxco (3) ((*1) Hokkaido University: (2) The University of Texas: (3) University of California Santa Barbara*)

1TP5-03 ２'－O,４'－C-aminomethylene bridged nucleic acid(２',４'－BNANC)修飾による生理的 pH におけるピリミジン型３本鎖核酸形成の

1P-094 促進

Promotion of pyrimidine motif triplex formation at physiological pH by 2'-*O*,4'-*C*-aminomethylene bridged nucleic acid modification

Kiyomi Sasaki (1), Norihiro Sato (1), Satoshi Obika (2), Takeshi Imanishi (2), Hidetaka Torigoe (1) ((*1) Faculty of Science, Tokyo University of Science: (2) Graduate School of Pharmaceutical Sciences, Osaka University*)

1TP5-04 マウステロメア DNA の４本鎖 DNA 構造とマウステロメア結合蛋白質 Pot1 のテロメア DNA 結合ドメインとの相互作用

1P-102 Interaction between tetraplex structure of mouse telomeric DNA and telomeric DNA binding domains of mouse telomere binding protein Pot1

Kaoru Kaneda (1), Hidetaka Torigoe (1) ((*1) Faculty of Science, Tokyo University of Science*)

1TP5-05 RNA 結合タンパク質における疎水表面を用いた塩基認識機構の検証: NOVA-RNA 複合体系での研究

1P-100 Study of RNA base recognition mechanism by aliphatic surface of RNA-binding protein: Case study of NOVA-RNA complex system

Ikuo Kurisaki (1), Atsushi Matsumoto (2), Kei Yura (3), Shigenori Tanaka (4) ((*1) Graduate School of Engineering, Kobe Univ.: (2) Center for Computational Science and Engineering, Japan Atomic Energy Agency: (3) Graduate School of Humanities and Sciences, Ochanomizu Univ.: (4) Graduate School of Engineering, Kobe Univ.; CREST*)

1TP5-06 タンパク質翻訳開始複合体における 30S-mRNA 結合力の１分子顕微解析

1P-101 Single-molecule force measurement for 30S-mRNA interaction in translation initiation

Tomoaki Masuda (1), Ryo Iizuka (1), Takashi Funatsu (1), Sotaro Uemura (3) ((*1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) Center for Nano Bio Integration, The University of Tokyo: (3) Department of Structural Biology, Stanford University School of Medicine: (4) Precursory Research for Embryonic Science and Technology (PRESTO)*)

1TP5-07 タンパク質－DNA 複合体の粗視化シミュレーション：ヌクレオソームのダイナミクス

1P-099 Coarse-grained simulation of protein-DNA complex: dynamics of nucleosome

Hiroo Kenzaki (1), Shoji Takada (2) ((*1) Deptartment of Biophysics, Graduate School of Science, Kyoto University: (2) Deptartment of Biophysics, Graduate School of Science, Kyoto University; JST-CREST*)

1TP5-08 ヌクレオソームコア・パーティクルの分子動力学計算による自由エネルギー・プロファイル

The free energy profile of a nucleosome core particle through the molecular dynamics simulation

Naoko Kanaeda (1), Hisashi Ishida (1), Hidetoshi Kono (1) ((*1) Japan Atomic Energy Agency*)

1TP5-09 機能未知ヒト蛋白質の 23 アミノ酸繰返しドメインの DNA 結合性について

DNA-binding function of the score and three amino acid peptide repeat domain in a human unknown protein

Yasuhiro Nonaka (1), Shohei Myoba (1), Etsuro Okabe (1), Hideki Muto (2), Masakatsu Kamiya (1), Takashi Kikukawa (1), Tomoyasu Aizawa (1), Masataka Kinjo (2), Shigeharu Takiya (3), Makoto Demura (1), Keiichi Kawano (1) (*(1) Department of Biological Sciences, Graduate School of Science, Hokkaido University: (2) Laboratory of Molecular Cell Dynamics, Faculty of Advanced Life Science, Hokkaido University: (3) Center for Genome Dynamics, Graduate School of Science, Hokkaido University*)

1TP5-10 Rad51 の重合による DNA ねじり運動の実時間計測

Real-time imaging of DNA twisting during Rad51 polymerization

Hideyuki Arata (1), Aurelie Dupont (2), Judith Mine-Hattab (2), Axelle Renodon-Corniere (3), Masayuki Takahashi (3), Jean-Louis Viovy (2), Giovanni Cappello (2) (*(1) Curie Institute; JSPS: (2) Curie Institute: (3) Nantes University*)

第 2 日目 9:00～11:30（10 月 31 日（土））/ Day 2 (Oct. 31, Sat.)

蛋白質-機能（反応機構，生物活性など） 2TA1-01～03
蛋白質-物性（安定性，折れたたみなど） 2TA1-04～08，ヘム蛋白質 2TA1-09 C1 会場/ Room C1

2TA1-01 脳脊髄液中アルブミンの SH 基の酸化還元状態解析

Redox state of human lumbar cerebrospinal fluid examined by the sulfhydryl titer of albumin molecules

Seiichi Era (1), Yukie Matsuyama (1), Tomoyoshi Terada (1), Takeshi Minami (1) (*(1) Department of Physiology and Biophysics, Gifu University Graduate School of Medicine*)

2TA1-02 Kinase Inhibition modeling by Proteometrics and docking analysis

Michael Fernandez (1), Akinori Sarai (1), Ahmad Shandar (2) (*(1) Kyushu Institute of Technology. Department of Bioscience and Bioinformatics: (2) National Institute of Biomedical Innovation. Osaka*)

2TA1-03 プロテアソームによる蛋白質分解における最適なユビキチンシグナルと分解開始部位の距離

Optimal spacing between ubiquitin modification and unstructured initiation site for efficient proteasome-mediated degradation

Tomonao Inobe (1), Susan Fishbain (2), Sumit Prakash (2), Andreas Matouschek (2) (*(1) RIKEN: (2) Northwestern University*)

2TA1-04 高圧力 NMR による di-ubiquitin の構造揺らぎ

Conformational fluctuation of di-ubiquitin studied by variable pressure NMR spectroscopy

Ryo Kitahara (1), Takashi Hirano (2), Maho Yagi (3), Tsunehiro Mizushima (2), Kzumi Hata (4), Kazuyuki Akasaka (4), Koichi Kato (5) (*(1) Ritsumeikan University; RIKEN Harima: (2) Nagoya City University: (3) Nagoya City University; Institute for Molecular Science: (4) Kinki University; RIKEN Harima: (5) Institute for Molecular Science; Nagoya City University*)

2TA1-05 シャペロニンは変性タンパク質の一部に結合しつつフォールディングを援助する

Chaperonin assists the folding of denatured polypeptide partly tethered on GroEL

Fumihiro Motojima (1), Masasuke Yoshida (2) (*(1) Tokyo Institute of Technology: (2) Kyoto Sangyo Univ.*)

2TA1-06 タウ由来ペプチドの繊維性凝集におけるリン酸化の部位的効果

Positional effects of phosphorylation upon fibrillation of tau derived peptide

Takashi Konno (1), Masafumi Inoue (2), Kazuki Tainaka (2), Takashi Morii (2) (*(1) University of Fukui: (2) Kyoto University*)

2TA1-07 変性剤が水分子の分極におよぼす効果を考慮した,タンパク質フォールディングのシナリオ: 低濃度の HDO をプローブとする IR 法による研究

A scenario for folding of proteins in terms of the changes in the polarization of the water induced by denaturants; β-Lactoglobulin in aqueous 2,2,2-trifluoroethanol

Kazuko Mizuno (1), Sachie Nakajima (1), Yasuhiro Fujituka (1) (*(1) University of Fukui*)

2TA1-08 膵島アミロイドポリペプチドの脂質二分子膜への結合とアミロイド沈着

Binding of islet amyloid polypeptide to lipid bilayer and amyloid deposition

Kenji Sasahara (1), Kenichi Morigaki (2), Daizo Hamada (1) (*(1) Kobe University, Graduate School of Medicine: (2) Research Institute for Cell Engineering, National Institute of Advanced Industrial Science and technology*)

2TA1-09
2P-072 チトクロム酸化酵素の構造に基づく酸素の一段階 4 電子還元機構とプロトンの高効率ポンプ機構

Cytochrome *c* Oxidase Structures Facilitating the Four-Electron Reduction of Oxygen in One-Step and the High Proton Pump Efficiency

Kazuhiro Ohta (1), Kazumasa Muramoto (2), Kyoko Shinzawa-Itoh (2), Masao Mochizuki (2), Katsumasa Kanda (2), Maki Taniguchi (2), Eiki Yamashita (1), Tomitake Tsukihara (1), Shinya Yoshikawa (2) (*(1) Institute for Protein Research, Osaka University, Japan: (2) Department of Life Science, University of Hyogo, Japan*)

光生物-視覚・光受容 2TA2-01～08 C2 会場/ Room C2

2TA2-01 蛍光共鳴エネルギー移動（FRET）を利用した活性化ロドプシンとトランスデューシンの結合過程の解析

Detection of the binding of activated rhodopsin and transducin by using fluorescence resonance energy transfer (FRET)

Ryo Maeda (1), Ichirouta Seki (1), Yasushi Imamoto (1), Takahiro Yamashita (1), Yoshinori Shichida (1) (*(1) Department of Biophysics, Graduate School of Science, Kyoto University*)

2TA2-02 Ｇタンパク質の GDP-GTP 交換反応におけるアルファサブユニットＣ末端部位の役割

The role of C terminus of alpha subunit in the GDP-GTP exchange reaction on G protein.

Naoki Kimata (1), Takahiro Yamashita (1), Yasushi Imamoto (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

2TA2-03 アーキロドプシンからのプロトン放出に関する分光研究
2P-217 Spectroscopic study of proton release group of archaerhodopsins

Junya Yamada (1), Kunio Ihara (2), Hideki Kandori (1) ((*1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Center for Gene Research, Nagoya University*)

2TA2-04 ロドプシンの細胞質側ループを組み込んだ古細菌ロドプシンの研究
2P-216 Study on chimeric archaeal-rhodopsin containing cytoplasmic loops of bovine rhodopsin

Aya Nakatsuma (1), Takahiro Yamashita (2), Akira Kawanabe (1), Yuji Furutani (3), Yoshinori Shichida (2), Hideki Kandori (1) ((*1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Biophysics, Kyoto University: (3) Institute for Molecular Science;Department of Frontier Materials, Nagoya Institute of Technology*)

2TA2-05 Proteorhodopsin の色を変える E-F ループの変異体
Mechanism of color-tuning mutation in the E-F loop of proteorhodopsin

Keisuke Yamada (1), Akira Kawanabe (1), Maiko Yoshitsugu (1), Hideki Kandori (1) ((*1) Frontier Materials, Nagoya Institute of Technology*)

2TA2-06 ロドプシンにおける相乗的な長距離相互作用による吸収波長制御機構
2P-218 Molecular mechanism of long-range synergetic color tuning between multiple amino acid residues in rhodopsin

Hiroshi Watanabe (1), Yoshiharu Mori (2), Takahisa Yamato (3) ((*1) Graduate School of Science, Nagoya University; Research Fellow of the Japan Society for the Promotion of Science: (2) Graduate School of Science, Nagoya University; CREST,JST: (3) Graduate School of Science, Nagoya University; CREST,JST*)

2TA2-07 イカロドプシンバソ中間体のＸ線結晶構造解析
X-ray crystallographic study of the batho intermediate of squid rhodopsin

Midori Murakami (1), Tsutomu Kouyama (1) ((*1) Department of Physics, Graduate School of Science, Nagoya University*)

2TA2-08 バクテリオロドプシンのＭ中間体の結晶構造の pH 依存性
Crystal structures of Bacteriorhodopsin's M intermediate at various pH levels

Tsutomu Kouyama (1), Masataka Yamamoto (1), Naoki Hayakawa (1), Midori Murakami (1) ((*1) Nagoya University, Graduate School of Science*)

水・水和／電解質　2TA3-01,02，分子遺伝・遺伝情報制御　2TA3-03，生命の起源・進化　2TA3-04～07 計測　2TA3-08,09　C3 会場/ Room C3

2TA3-01 ATP 加水分解における周囲の水のダイナミクスと分極電荷の計算
Calculations of dynamics and polarized charges of water molecules in ATP hydrolysis

Takuya Takahashi (1), Hiromu Ishio (1), Tomoki Shiomi (1), Makoto Suzuki (2) ((*1) Ritsumeikan University: (2) Tohoku University*)

2TA3-02 タンパク質体積パラドックスとその分子的描像：
2P-095 表面カークウッド - バフ積分法による考察
Protein Volume Paradox and its Molecular Picture:
A Study by Surficial Kirkwood-Buff Integral Method

Isseki Yu (1), Masataka Nagaoka (2) ((*1) Department of Chemistry and Biological Science, College of Science and Engineering, Aoyama Gakuin University: (2) Graduate School of Information Science, Nagoya University*)

2TA3-03 Global protein expression profiling with single molecule sensitivity reveals the architecture of biological noise
2P-096 **Yuichi Taniguchi** (1), Paul J Choi (1), Huiyi Chen (1), Mohan Babu (2), Andrew Emili (2), Xiaoliang Sunney Xie (1) ((*1) Harvard University: (2) University of Toronto*)

2TA3-04 発表取り消し (Retracted)

2TA3-05 蛋白質合成システムの適応度地形解析
Exploring the fitness landscape of the protein translation system

Tomoaki Matsuura (1), Yasuaki Kazuta (1), Takuyo Aita (2), Jiro Adachi (1), Tetsuya Yomo (1) ((*1) Department of Bioinformatic Engineering, Osaka Univeristy: (2) Graduate School of Science and Engineering, Saitama University: (3) ERATO, JST*)

2TA3-06 可塑性、進化可能性、安定性:　表現型揺らぎによるマクロ理論
2P-230 Plasticity,　Evolvability and Robustess: A Macroscopic Theory in terms of Phenotypic Fluctuations

Kunihiko Kaneko (1) ((*1) University of Tokyo and　ERATO Complex Systems Biology*)

2TA3-07 DNA 増幅系を内封した自己生産ベシクル
2P-231 DNA replication system in self-reproducing vesicles

Kensuke Kurihara (1), Mieko Tamura (1), Kentaro Suzuki (1), Tadashi Sugawara (1) ((*1) The Univ. of Tokyo*)

2TA3-08 走査型電子顕微鏡における「多色」標識法
"Multi-Color" Labeling in Scanning Electron Microscopy

Hyonchol Kim (1), Hiroyuki Takei (2), Kenji Yasuda (3) ((*1) Kanagawa Academy of Science and Technology: (2) Kanagawa Academy of Science and Technology; Department of Life Sciences, Faculty of Life Sciences, Toyo University: (3) Kanagawa Academy of Science and Technology; Department of Biomedical Information, Division of Biosystems, Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University*)

2TA3-09 細胞内の局所的な温度変化の測定とその解析
2P-258 Measurement and analysis of local temperature change inside living cells.

Kotaro Oyama (1), Madoka Suzuki (2), Vadim Tseeb (3), Fumichika Ono (4), Yusuke Seto (4), Masahiro Motoyoshi (1), Kaoru Iwai (5), Shin'Ichi

Ishiwata (3) (*(1) Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda University: (2) COBRI, Comprehensive Research Organization, Waseda University: (3) Department of Physics, Faculty of Science and Engineering, Waseda University: (4) Bioscience and Biomedical Engineering, Graduate School of Advanced Science and Engineering, Waseda University: (5) Department of Chemistry, Faculty of Science, Nara Women's University*)

分子モーター　2TA4-01～08，細胞生物的課題 (接着，運動，骨格，伝達，膜) 2TA4-09,10　C4 会場/ Room C4

2TA4-01　機能的細菌べん毛モーターにおけるモーター構成素子の交換割合の見積り

Turnover of subunit-exchange in functioning bacterial flagellar motor

Hajime Fukuoka (1), Shun Terasawa (2), Hiroto Takahashi (1), Yuichi Inoue (1), Akihiko Ishijima (1) (*(1) Tohoku Univ.; IMRAM: (2) Tohoku Univ.;Grad. Sch. Life Sci.*)

2TA4-02　高温におけるキメラべん毛モーターの回転トルク応答

2P-132　Torque response of bacterial flagellar motor induced by transient heating.

Yuichi Inoue (1), Hajime Fukuoka (1), Akihiko Ishijima (1) (*(1) Tohoku University*)

2TA4-03　F_1－ATPase のストールトルク

Stall torque of F_1-ATPase

Shoichi Toyabe (1), Takahiro Watanabe-Nakayama (2), Tetsuaki Okamoto (1), Seishi Kudo (3), Eiro Muneyuki (1) (*(1) Faculty of Engineering, Chuo University: (2) Grad. School of Bioscience and Biotechnology, Tokyo Institute of Technology: (3) Faculty of Engineering, Toin University of Yokohama*)

2TA4-04　チューブリンＣ末端の伸長した構造が弱結合に果たす役割

2P-134　The role of extended C-terminal tail of tubulin on weak-binding interaction between motor proteins and microtubules

Itsushi Minoura (1), Seiichi Uchimura (1), Masashi Degawa (1), Etsuko Muto (1) (*(1) RIKEN Brain Science Institute*)

2TA4-05　KIF1A の１次元ブラウン運動にチューブリンＣ末端は必要か？

2P-135　Is the tubulin C-terminus tail necessary for the 1D Brownian motion of KIF1A?

Masashi Degawa (1), Itsushi Minoura (1), Seiichi Uchimura (1), Etsuko Muto (1) (*(1) RIKEN BSI*)

2TA4-06　細胞質ダイニンのステップ機構

Walking mechanism of cytoplasmic dynein

Tomohiro Shima (1), Reiko Okura (2), Motoshi Kaya (1), Takahide Kon (2), Hideo Higuchi (1), Kazuo Sutoh (2) (*(1) Graduate School of Science, University of Tokyo: (2) Graduate School of Arts and Sciences, University of Tokyo*)

2TA4-07　ダイニンの力発生に伴う構造変化

Structural changes in dynein molecules accompanying force generation

Hironori Ueno (1), Takuo Yasunaga (2), Chikako Shingyouji (3), Takami Yamaguchi (4), Keiko Hirose (5) (*(1) Institute for International Advanced Interdisciplinary Research, Tohoku University International Advanced Research and Education Organization : (2) Department of Biochemical Engineering and Science, Kyushu Institute of Technology: (3) Department of Biological Sciences, Graduate School of Science, University of Tokyo: (4) Department of Biomedical Engineering, Tohoku University: (5) Research Institute for Cell Engineering, AIST*)

2TA4-08　in vitro 滑り運動中のミオシン頭部の構造と SH1-SH2 架橋ミオシン頭部の３次元再構成像との比較

Reconstructed 3-D structure of SH1-SH2 crosslinked myosin head and its comparison with intermediate crossbridge configuration during in vitro motility

Eisaku Katayama (1), Yoshitaka Kimori (2), Norio Baba (3) (*(1) Division of Biomolecular Imaging, Institute of Mecical Science, The University of Tokyo: (2) National Center of Neurology and Psychiatry, National Institute of Neuroscience: (3) Department of Information Science, Kogakuin University*)

2TA4-09　細胞内の特定のアクチンフィラメントは、ミオシンⅡの S1 と結合しやすい

Specific subsets of actin filaments in cells have a high affinity for S1 of myosin II.

Taro Uyeda (1), Akira Nagasaki (1), Akira Ichihara (1), Takashi Hirano (1) (*(1) National Institute of Advanced Industrial Science and Technology*)

2TA4-10　アメーバ様細胞の走化性運動の戦略

Strategies for chemotaxis of amoeboid cells

Shin-Ichiro Nishimura (1), Masaki Sasai (2), Masahiro Ueda (3) (*(1) Department of Mathematical and Life Sciences, Hiroshima University: (2) Graduate School of Engineering, Nagoya University: (3) Graduate School of Frontier Biosciences, Osaka University; CREST, JST*)

蛋白質-計測・解析の方法論　2TA5-01～04，バイオエンジニアリング　2TA5-05～10　C5 会場/ Room C5

2TA5-01　タンパク質平衡揺らぎの独立成分分析

2P-064　Independent Component Analysis of Equilibrium Fluctuations in Proteins

Yusuke Naritomi (1), Sotaro Fuchigami (1), Mitsunori Ikeguchi (1), Akinori Kidera (2) (*(1) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University: (2) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University;Research Program for Computational Science, RIKEN*)

2TA5-02　ベイズ法によるタンパク質の内部構造の推定

2P-065　Uncovering the hidden structure of the protein using Bayesian inference

Makito Miyazaki (1), Takahiro Harada (2) (*(1) Department of Physics, Graduate School of Science, Kyoto University: (2) Department of Physics, Graduate School of Science, The University of Tokyo*)

2TA5-03　低温電子顕微鏡法における生体超分子複合体に対する電子線照射損傷の定量的評価

2P-070　Electron dose effect on 3D image reconstruction of a biological macromolecular structure by electron cryomicroscopy

Masamichi Ashihara (1), Takayuki Kato (1), Takashi Fujii (1), Hideyuki Matsunami (2), Tomoko Miyata (1), Kenji Iwasaki (3), Keiichi Namba (1)

((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Okinawa Institute of Science and Technology: (3) Institute for Protein Research, Osaka University*)

2TA5-04 誘電緩和分光による酸性から中性 pH 領域における Pseudomonas aeruginosa シトクロム c の水和解析

Hydration study of *Pseudomonas aeruginosa* cytochrome *c*551 in the range of acidic to neutral pH by dielectric relaxation spectroscopy

Tetsuichi Wazawa (1), Takashi Miyazaki (2), Takafumi Sonoyama (3), Yoshihiro Sambongi (3), Makoto Suzuki (2) ((*1) CREST, JST: (2) Tohoku University Graduate School of Engineering: (3) Graduate School of Biosphere Science, Hiroshima University*)

2TA5-05 微細加工基板上でのマイコプラズマ・モービレ運動についての改良されたシミュレーション

An improved simulation of *Mycoplasma mobile* movements on micropatterned surfaces

Takahiro Nitta (1), Shogo Asano (1), Yuichi Hiratsuka (2), Makoto Miyata (3), Motohisa Hirano (1) ((*1) Gifu University: (2) JAIST: (3) Osaka City University*)

2TA5-06 相同組換えタンパク質 RecA を用いた新規オプティカルマッピング法の開発

2P-276 Development of novel DNA optical mapping method using homologous recombination protein, RecA

Yuya Goto (1), **Yuji Kimura** (2), Hidehiro Oana (3), Masao Washizu (4) ((*1) Department of Mechanical engineering, the University of Tokyo: (2) Deparment of Bioengineering, the University of Tokyo;JST CREST: (3) Department of Mechanical engineering, the University of Tokyo; JST CREST: (4) Department of Bioengineering and Mechanical engineering, the University of Tokyo; JST CREST*)

2TA5-07 マイクロ流体デバイスを用いた 8 並列型ソーター

8-Parallel Bioparticle Sorter with 3-Dimensional PDMS Chip

Hirokazu Sugino (1), Kazuto Ozaki (2), Takahiro Arakawa (3), Yoshitaka Shirasaki (4), Yuki Nara (2), Shuichi Shoji (2), Takashi Funatsu (1) ((*1) The University of Tokyo: (2) Waseda University: (3) Tokyo Medical and Dental University: (4) RIKEN*)

2TA5-08 異種ビーズを隣接させた状態で観察可能なダイナミックマイクロアレイ

2P-277 Dynamic Microarray Technology for observation of adjacent different beads

Tetsuhiko Teshima (1), Kosuke Iwai (1), Hirotaka Ishihara (1), Shoji Takeuchi (1) ((*1) Institute of Industrial Science (IIS), The University of Tokyo*)

2TA5-09 細胞ビルドアップ型ウエットナノロボティクスの構築と機能発現―長期間室温で駆動する昆虫細胞シートの開発―

Construction and Function Emergence of Cellular Wet NanoRobotics-Development of Long-term and Room Temperature Operable Insect Cell Sheet-

Keisuke Morishima (1), Yui Sakuma (1), Kikuo Iwabuchi (1), Yoshikatsu Akiyama (2), Masayuki Yamato (2), Teruo Okano (2) ((*1) Tokyo University of Agriculture and Technology: (2) Tokyo Women's Medical University*)

2TA5-10 bistable な DNA で実装する温度バンドパスフィルタ

2P-278 Thermal band pass filter implemented with a bistable DNA

Ken Komiya (1), Masayuki Yamamura (1), John A. Rose (2) ((*1) Tokyo Institute of Technology: (2) Ritsumeikan APU*)

第 2 日目 14:30～16:00（10 月 31 日（土））/ Day 2 (Oct. 31, Sat.)

ヘム蛋白質　2TP1-01～06　C1 会場/ Room C1

2TP1-01 アジ化物イオン結合酸化型チトクロム酸化酵素の精密構造解析

2P-073 Refined structural analysis of azide ion bound cytochrome *c* oxidase in the oxidized state

Kazumasa Muramoto (1), Rika Inaoka (1), Tomoko Maeda (1), Kyoko Shinzawa-Itoh (1), Eiki Yamashita (2), Tomitake Tsukihara (3), Shinya Yoshikawa (1) ((*1) Dept. of Life Sci., Univ. of Hyogo; Picobio. Inst., Univ. of Hyogo: (2) Inst. for Protein Res., Osaka Univ.: (3) Picobio. Inst., Univ. of Hyogo; Inst. for Protein Res., Osaka Univ.*)

2TP1-02 チトクロム酸化酵素結晶 F 型中間体の再酸化反応による生成

2P-074 Cytochrome *c* oxidase crystal in the F intermediate state produced by reoxidation

Kazumasa Muramoto (1), Rie Harada (1), Tomoko Maeda (1), Kyoko Shinzawa-Itoh (1), Eiki Yamashita (2), Tomitake Tsukihara (3), **Shinya Yoshikawa** (1) ((*1) Dept. of Life Sci., Univ. of Hyogo; Picobio. Inst., Univ. of Hyogo: (2) Inst. for Protein Res., Osaka Univ.: (3) Picobio. Inst., Univ. of Hyogo; Inst. for Protein Res., Osaka Univ.*)

2TP1-03 アミノ酸置換によるウシ心筋チトクロム *c* 酸化酵素の水素結合ネットワークの機能解析

2P-076 The functional analysis of hydrogen bond network in bovine heart cytochrome *c* oxidase by mutagenesis

Ryohta Aminaka (1), Kunitoshi Shimokata (2), Mai Itoh (1), Yukie Katayama (1), Tomitake Tsukihara (1), Shinya Yoshikawa (1), Hideo Shimada (1) ((*1) Graduate School of Life Science, University of Hyogo: (2) WORLD INTEC CO., LTD.*)

2TP1-04 チトクロム c 酸化酵素におけるヒドロキシファルネシルエチル基の共鳴ラマンマーカーバンド

2P-075 Resonance Raman Marker Bands of Hydroxyfarnesylethyl Substituent of Cytochrome c Oxidase

Miyuki Sakaguchi (1), Kyoko Shinzawa-Itoh (1), Shinya Yoshikawa (1), Hiroshi Fujii (2), Takashi Ogura (1) ((*1) University of Hyogo: (2) Okazaki Institute for Integrative Bioscience*)

2TP1-05 チトクロム *c* 酸化酵素の CO 光解離後の構造緩和過程の追跡

2P-077 Structural Relaxation Process of Cytochrome *c* Oxidase Following Photolysis of Carbonmonoxide

Izumi Ishigami (1), Satoru Nakasima (2), Kyoko Shinzawa-Itoh (1), Shinya Yoshikawa (1), Takashi Ogura (1) ((*1) University of Hyogo, Grad.Sch. Life Sci.: (2) Picobiology Inst., Grad.Sch. Life Sci., University of Hyogo*)

2TP1-06 水生動物トラフグヘムオキシゲナーゼによるヘム分解の特徴

Characterization of the heme degradation by heme oxygenase from aquatic animal, *Takifugu rubripes*

Taiko Migita (1), Xuhong Zhang (2) ((*1) Yamaguchi　University: (2) Yamagata University*)

膜蛋白質　2TP2-01～03，生体膜・人工膜-興奮・チャネル　2TP2-04，生体膜・人工膜-輸送　2TP2-05　C2 会場/ Room C2

2TP2-01
2P-084
ハロロドプシン NpHR の三量体構造は F150 残基の対称配置によって安定化される
Stabilization of trimeric assembly of halorhodopsin, NpHR by C_3-symmetric geometry among F150 aromatic rings
Takashi Tsukamoto (1), Takanori Sasaki (2), Kazuhiro Fujimoto (3), Takashi Kikukawa (4), Masakatsu Kamiya (2), Tomoyasu Aizawa (1), Keiichi Kawano (4), Makoto Demura (1) (*(1) Faculty of Advanced Life Science, Hokkaido University.: (2) School of Science and Technology, Meiji University.: (3) Graduate School of Science, Kyoto University.: (4) Faculty of Science, Hokkaido University.*)

2TP2-02
2P-085
DMPC、DPPC 二重層に再構成したバクテリオロドプシンの可視領域における円二色性測定
Circular dichroism measurement of bacteriorhodopsin reconstituted in DMPC and DPPC bilayer in visible region
Lumi Negishi (1), Taku Kitoh (1), Yasunori Yokoyama (1), Masashi Sonoyama (2), Shigeki Mitaku (1) (*(1) Depertment of Applied Physics, Graduate School of Engineering, Nagoya University: (2) Depertment of Applied Chemistry and Chemical Biology, Graduate School of Engineering, Gunma University*)

2TP2-03
2P-079
細胞溶解毒素の自発的なαヘリックスーβバレル変換におけるαヘリックスのアンフォールディングとβストランドの整列化の解析
The Spontaneous α-Helix to β-Barrel Transition of a Pore-Forming Protein: Timing of Helix Unfolding and β-Strand Alignment
Takehiro Sato (1), Tweten Rodney K. (2), Johnson Arthur E. (1) (*(1) Texas A&M Health Science Center: (2) University of Oklahoma Health Sciences Center*)

2TP2-04
2P-179
KCNQ1 チャネル複合体ストイキオメトリーの密度依存的変化
Density-dependent changes in stoichiometry of KCNQ1 complex
Koichi Nakajo (1), Maximilian Ulbrich (2), Yoshihiro Kubo (1), Isacoff Ehud (2) (*(1) National Institute for Physiological Sciences: (2) University of California, Berkeley*)

2TP2-05
Trans-membrane delivery of semiconductor quantum dots in living cells
Vasudevanpillai Biju (1), Abdulaziz Anas (1), Tetsuya Okuda (1), Tamitake Itoh (1), Mitsuru Ishikawa (1) (*(1) Health Technology Research Center, National Institute of Advanced Industrial Science and Technology (AIST)*)

非平衡・生体リズム　2TP3-01～05　C3 会場/ Room C3

2TP3-01
2P-254
集団ダイナミクスにおけるノイズ強度のシステムサイズ依存性はネットワーク構造が決定する
Structure of networks determines the system size dependency of noise intensity in collective dynamics
Naoki Masuda (1), Yoji Kawamura (2), **Hiroshi Kori** (3) (*(1) University of Tokyo: (2) JAMSTEC: (3) Ochanomizu University*)

2TP3-02
2P-255
クラミドモナスにおける光誘導倒立生物対流の細胞ダイナミクス
Cellular dynamics of light-induced inverted bioconvection in *Chlamydomonas reinhardtii*
Naoki Sato (1) (*(1) University of Tokyo, Graduate School of Arts and Sciences*)

2TP3-03
遺伝的に均質な線虫 *C. elegans* 集団の生存曲線に現れる多成分性の定量的解析
Biophysical approach on heterogeneity revealed in an isogenic *C. elegans* cohort
Hitoshi Suda (1), Tetsuji Shoyama (1), Yuka Shimizu (1) (*(1) Tokai University: (2) Tokai University: (3) Tokai University*)

2TP3-04
KaiC による藍色細菌時計出力蛋白質 SasA のリン酸化レベルの制御
Modulation by KaiC of the phosphorylation level of SasA in the main output pathway of the cyanobacterial clock
Jonathan Valencia Swain (1), Kyouhei Bitou (1), Reiko Murakami (1), Katsumi Imada (2), Masahiro Ishiura (1) (*(1) Center for Gene Research, Nagoya University: (2) Graduate School of Frontier Biosciences, Osaka University*)

2TP3-05
スピンラベル法による藍色細菌時計タンパク質の解析
Novel interaction sites on cyanobacterial circadian clock proteins revealed by ESR
Risa Mutoh (1), Hiroyuki Mino (2), Reiko Murakami (3), Tatsuya Uzumaki (2), Kentaro Ishii (3), Masahiro Ishiura (3) (*(1) Center for Gene Research, Nagoya University; Graduate School of Science, Nagoya University: (2) Graduate School of Science, Nagoya University: (3) Center for Gene Research, Nagoya University*)

生命情報科学-構造ゲノミクス　2TP4-01～05，生命情報科学-機能ゲノミクス　2TP4-06　C4 会場/ Room C4

2TP4-01
2P-236
最適化された記述子群を用いたドメインリンカー予測法の開発
An SVM-Domain Linker Prediction Trained with Optimized Features Selected by Random Forest
Teppei Ebina (1), Hiroyuki Toh (2), Yutaka Kuroda (1) (*(1) Dept of Biotech and Life Sci, Tokyo Univ of A & T (TUAT): (2) Div. Bioinf, Med. Inst. of Bioreg, Kyushu Univ*)

2TP4-02
2P-237
会合状態変化を伴うタンパク質間相互作用面上の挿入および欠失
Insertion and/or deletion regions on protein-protein interface to alter oligomeric states.
Hafumi Nishi (1), Motonori Ota (1) (*(1) Grad. Sch. of Inform. Sci., Nagoya Univ.*)

2TP4-03
相互作用プロファイルを用いた　揺らぎをもつタンパク質の相互作用予測解析
Post-docking process for flexible protein docking problems by using interaction fingerprints
Nobuyuki Uchikoga (1), Takatsugu Hirokawa (2) (*(1) JBIC: CBRC: (2) CBRC*)

2TP4-04
GPCR 立体構造情報とGタンパク質結合選択性の相関性
Relation between GPCR structure and G protein coupling selectivity.
Makiko Suwa (1), Yukiteru Ono (2), Minoru Sugihara (1) (*(1) National Institute of Advanced Industrial Science and Technology: (2) Information and Mathematical Science Laboratory Inc.*)

2TP4-05 NMR による天然変性タンパク質配列の網羅的検証法

A method for systematic assessment of intrinsically unstructured proteins and protein regions by NMR

Natsuko Goda (1), Kana Shimizu (3), Yohta Kuwahara (1), Tamotsu Noguchi (3), Takahisa Ikegami (4), Motonori Ota (5), **Hidekazu Hiroaki** (1) (*(1) Graduate School of Medicine, Kobe University: (2) 2. Institute for Bioinformatics Research and Development, Japan Science and Technology Agency (BIRD-JST): (3) 3. Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology: (4) Institute for Protein Research, Osaka University: (5) 5. Graduate School of Information Sciences, Nagoya University*)

2TP4-06 大規模データマイニングから明らかになったタンパク質リン酸化と複合体形成の関係

2P-239 Macroscopic Relationships between Protein Phosphorylation and Physical Interaction

Nozomu Yachie (1), Rintaro Saito (1), Naoyuki Sugiyama (2), Masaru Tomita (1), Yasushi Ishihama (3) (*(1) Inst. Adv. Biosci., Keio Univ.; Syst. Biol. Prog., Grad. Sch. Media & Gov., Keio Univ.: (2) Inst. Adv. Biosci., Keio Univ.: (3) Inst. Adv. Biosci., Keio Univ.; PRESTO, JST*)

蛋白質-構造　2TP5-01～05　C5 会場/ Room C5

2TP5-01 TEM と SEM によるタンパク質複合体の構造解析

2P-018 Structure analysis of membrane protein complexes using TEM and SEM

Chikara Sato (1), Kazuhiro Mio (1), Toshihiko Ogura (1), Yuusuke Maruyama (1), Hidetoshi Nishiyama (2), Mitsuo Suga (2) (*(1) National Institute of Advanced Industrial Science and Technology (AIST): (2) JEOL*)

2TP5-02 Folding simulations of chignolin by self-learning multiscale method

2P-002 **Wenfei Li** (1), Shoji Takada (1) (*(1) Kyoto University, Department of Biophysics: (2) CREST, Japan Science and Technology Inc.*)

2TP5-03 CFTR チャネルの単粒子構造解析

2P-017 Three-dimensional reconstruction of human CFTR chloride channel

Kazuhiro Mio (1), Toshihiko Ogura (1), Muneyo Mio (1), Tzyh-Chang Hwang (2), Yoshiro Sohma (3), Chikara Sato (1) (*(1) National Institute of Advanced Industrial Science and Technology: (2) John M. Dalton Cardiovascular Research Center: (3) Keio University School of Medicine*)

2TP5-04 Real-time observation of model-membrane morphological transformations induced by different amyloid beta molecular assemblies

Mun'Delanji Vestergaard (1), Masamune Morita (1), Tsutomu Hamada (1), Masahiro Takagi (1) (*(1) Japan Advanced Institute of Science and Technology*)

2TP5-05 ラット肝臓由来ボルトの３．５Å 分解能での構造解析

The structure of rat liver vault at 3.5 Å resolution

Koji Kato (1), Hideaki Tanaka (1), Eiki Yamashita (1), Tomoyuki Sumizawa (2), Yong Zhou (3), Min Yao (3), Kenji Iwasaki (1), Masato Yoshimura (4), Tomitake Tsukihara (5) (*(1) Institute for Protein Research Osaka University: (2) University of Occupational and Environmental Health: (3) Faculty of Advanced Life Science Hokkaido University: (4) National Synchrotron Radiation Research Center: (5) Department of Life Science University of Hyogo*)

第 3 日目 9:00～11:30（11 月 1 日（日））/ Day 3 (Nov. 1, Sun.)

蛋白質-蛋白質工学／進化工学　3TA1-01,02，蛋白質-構造機能相関　3TA1-03～08　C1 会場/ Room C1

3TA1-01 無機材料特異的抗体の界面結合機構に関する物理化学的アプローチ

How high affinity material binding antibody can recognize inorganic surface

Takamitsu Hattori (1), Mitsuo Umetsu (2), Takeshi Nakanishi (1), Satoshi Ohara (3), Hiroya Abe (3), Izumi Kumagai (1) (*(1) Dept. of Biomol. Eng., Grad. Sch. of Eng., Tohoku Univ.: (2) Dept. of Biomol. Eng., Grad. Sch. of Eng., Tohoku Univ.; Center for Interdiscipl. Res., Tohoku Univ.; PRESTO, JST.: (3) Joining and Welding Res. Inst., Osaka Univ.*)

3TA1-02 モチーフプログラム化人工タンパク質によるアモルファスーリン酸カルシウム結晶直接転移の誘導

Direct transformation from amorphous to crystalline calcium phosphate facilitated by motif-programmed artificial proteins

Toru Tsuji (1), Kazuo Onuma (2), Akira Yamamoto (3), Mayumi Iijima (4), Kiyotaka Shiba (5) (*(1) Keio University Advanced Research Center: (2) Institute for Human Science and Biomedical Engineering, National Institute of Advanced Industrial Science & Technology: (3) Incubation Center, PENTAX Coropration: (4) Dental Materials and Technology,Asahi University: (5) Division of Protein Engineering, Cancer Institute, Japanese Foundation for Cancer Research*)

3TA1-03 蛋白質構造ゆらぎの二面角系主成分分析

Principal Component Analysis of Proteins in Dihedral Angle Space

Satoshi Omori (1), Sotaro Fuchigami (1), Mitsunori Ikeguchi (1), Akinori Kidera (1) (*(1) Graduate School of Nanobioscience, Yokohama City : (2) Research Program for Computational Science*)

3TA1-04 *Streptococcus sobrinus* グルコシルトランスフェラーゼ－Ｉのグルカン結合特異性

Glucan binding specificity of *Streptococcus sobrinus* glucosyltransferase-I

Hideyuki Komatsu (1) (*(1) Dept Bioscience & Bioinformatics, Graduate School of Computer Science & Systems Engineering, Kyushu Institute of Technology*)

3TA1-05 リガンド結合に伴うタンパク質の構造変化の解析

Investigation of Protein Domain Motions by Molecular Dynamics Simulations

Hiroko Kondo (1), Noriaki Okimoto (2), Gentaro Morimoto (2), Makoto Taiji (1) (*(1) The University of Tokyo; RIKEN: (2) RIKEN*)

3TA1-06 Ｘ線小角散乱で観察した KaiC のリン酸化依存的構造変化

Assembly and Disassembly of Cyanobacterial Clock Proteins Orchestrated by the Phosphorylation-Dependent Conformational Changes of Pacemaking KaiC

Shuji Akiyama (1), Atsushi Nohara (2), Tatsuro Ishida (2), Kazuki Ito (3), Yuichiro Maeda (4), Taeko Nishiwaki (5), Takao Kondo (5) ((*1) Graduate School of Science, Nagoya University; JST PREST; JST CREST; RIKEN SPring-8 Center: (2) Graduate School of Science, Nagoya University: (3) RIKEN SPring-8 Center: (4) The Structural Biology Research Center, Graduate School of Sciences, Nagoya University: (5) Graduate School of Science, Nagoya University; JST CREST*)

3TA1-07 タンパク質構造の内部運動変調により誘導される酵素活性変化機構の解明

Protein structural dynamics and function relationships revealed by NMR spectroscopy

Shin-Ichi Tate (1), Chiho Murakami (1), Yuji Horiuchi (1), Eiji Ohmae (1), Kunihiko Gekko (1) ((*1) Hiroshima University*)

3TA1-08 極低温電子顕微鏡を用いた 100S リボソームの立体構造解析

Structural analysis of 100S ribosome by cryo-EM

Takayuki Kato (1), Hideji Yoshida (2), Yasushi Maki (2), Shou Furuike (2), Masami Ueta (3), Akiko Sakai (4), Akira Wada (3), Keiichi Namba (4) ((*1) Grad. Sch. of Frontier Biosci., Osaka Univ.: (2) Dept. Phys., Osaka Med. Coll.: (3) Yoshida Biol. Lab.: (4) Dept. Chem., Osaka Med. Coll.*)

光生物-視覚・光受容　3TA2-01～09　C2 会場/ Room C2

3TA2-01 ２種類の BLUF ドメイン、AppA と PAC の赤外分光解析
3P-212 FTIR study of two BLUF domains, AppA and PAC

Tatsuya Iwata (1), Akihide Watanabe (1), Mineo Iseki (2), Masakatsu Watanabe (2), Hideki Kandori (1) ((*1) Department of Frontier Materials, Nagoya Institute of Technology: (2) School of Advanced Sciences, The Graduate University for Advanced Studies*)

3TA2-02 フォトトロピンの温度依存的反応効率と温度センサーとしての機能の実験的証拠

Temperature-dependent reaction efficiency of phototropin and possible function of temperature sensor

Yusuke Nakasone (1), Kazunori Zikihara (2), Daisuke Matsuoka (3), Satoru Tokutomi (2), Tomomi Suzuki (1), Akira Nagatani (1), **Masahide Terazima** (1) ((*1) Kyoto University: (2) Osaka Prefecture University: (3) Kobe University*)

3TA2-03 赤感受性錐体視物質における塩化物イオン依存的な吸収波長シフトに関わるアミノ酸残基

Amino acid residues responsible for Cl^--dependent shift of absorption maximum in red-sensitive cone pigments

Takahiro Yamashita (1), Shuhei Nakamura (1), Kei Tsutsui (1), Takefumi Morizumi (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

3TA2-04 オールトランスレチナールを発色団とするオプシン、ペロプシンの分子機能解析

Functional analysis of all-*trans*-retinal-containing opsin peropsin

Sari Fujita (1), Takahiro Yamashita (1), Yasushi Imamoto (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

3TA2-05 脂質膜におけるアレスチンのロドプシンへの結合の解析

Analysis of arrestin binding to rhodopsin in lipid bilayer.

Hisao Tsukamoto (1), Abhinav Sinha (2), David Farrens (2) ((*1) Osaka City University; Oregon Health & Science University: (2) Oregon Health & Science University*)

3TA2-06 PYP のＮ末端領域の構造変化についての理論研究

Structural change on the N-terminal domain of PYP

Motoshi Kamiya (1), Shinji Saito (2), Iwao Ohmine (3) ((*1) Chem. Dept., Nagoya Univ.: (2) IMS: (3) Fukui Inst.*)

3TA2-07 タンパク質における光化学反応の磁場効果

Magnetic Field Effects on the photochemical reactions in protein systems

Kiminori Maeda (1), Ema Dell (1), Alexander Robinson (1), Kevin Henbest (1), Adelbert Bacher (2), Monika Joshi (2), Erik Schleicher (4), Stefan Weber (4), Robert Bittl (3), Peter Hore (1), Chris Timmel (1) ((*1) University of Oxford: (2) Technische Universitat Munchen,: (3) Freie Universitat Berlin: (4) Albert-Ludwigs-Universitat Freiburg*)

3TA2-08 PELDOR 測定による青色光センサータンパク質 SyPixD 重合体のタンパク間相互作用の解析

PELDOR analysis of the protein-protein interaction in the blue light sensor BLUF protein SyPixD

Toru Kondo (1), Kazuhiko Tsutsui (1), Shinji Masuda (2), Hiroyuki Mino (1) ((*1) nagoya university: (2) tokyo institute of technology*)

3TA2-09 時間分解 ESR 法を用いた青色光センサータンパク質 SyPixD の光反応過程の研究

Time resolved EPR study of light reaction processes in blue light sensing protein SyPixD

Kazuhiko Tsutsui (1), Tooru Kondou (1), Shinji Masuda (2), Hiroyuki Mino (1) ((*1) Nagoya University Graduate School of Science Division of Material Science: (2) Tokyo Institute of Technology*)

生体膜・人工膜-ダイナミクス　3TA3-01～04，生体膜・人工膜-構造・物性　3TA3-05～09　C3 会場/ Room C3

3TA3-01 自己組織化における転写の時空間制御
3P-181 Spatio-temporal regulation of transcriptional pulses during self-organization in Dictyostelium

Noritaka Masaki (1), Satoshi Sawai (2) ((*1) JST-ERATO Complex Systems Biology: (2) Graduate School of Arts andSciences, University of Tokyo; JST-ERATO Comlex Systems Biology*)

3TA3-02 Functionally rotating mechanism of a multidrug transporter studied by coarse-grained simulation
3P-182 **Xin-Qiu Yao** (1), Hiroo Kenzaki (1), Shoji Takada (1) ((*1) Kyoto University, Department of Biophysics: (2) CREST, Japan Science and Technology Corporation*)

3TA3-03 I-BAR ドメインの膜結合分子ダイナミクス
3P-186 Molecular Dynamics of the Membrane Binding by I-BAR Domain

Kazuhiro Takemura (1), Shiro Suetsugu (2), Akio Kitao (3) (*(1) IMCB, Univ. of Tokyo;IMS: (2) IMCB, Univ of Tokyo;PRESTO, JST: (3) IMCB, Univ of Tokyo;CREST, JST*)

3TA3-04 筒状ベシクルにおける周期的ドメイン構造
Periodic domain strucuture on ternary tubular veiscles

Miho Yanagisawa (1), Masayuki Imai (2), Takashi Taniguchi (1) (*(1) Kyoto University: (2) Ochanomizu university*)

3TA3-05 非ラメラ構造の脂質２分子膜に対する重水置換効果
Heavy water effect on the molecular shape of lipid in non-bilayer structures

Hiroshi Takahashi (1) (*(1) Biophysics Laboratory, Department of Chemistry and Chemical Biology, Gunma University, Japan*)

3TA3-06 酸化ストレスによる細胞サイズリポソームの動的構造変化
Dynamic shape transitions of cell-sized liposomes upon oxidative stress

Tsuyoshi Yoda (1), Mun'Delanji Vestergaad (1), Tsutomu Hamada (1), Yoko Ogawa (2), Yasukazu Yoshida (2), Masahiro Takagi (1) (*(1) School of Materials Science.JAIST: (2) Health Technology Research Center AIST*)

3TA3-07 脂質・界面活性剤混合系を用いた固体基板表面への脂質二分子膜固定化手法の開発
3P-180 Detergent assisted formation of substrate supported phospholipid membranes

Kenichi Morigaki (1), Shigeki Kimura (1), Takehiko Inaba (1), Takashi Okazaki (1), Takashi Kawasaki (1), Hiromasa Imaishi (2) (*(1) National Insitute of Advanced Industrial Science and Technology: (2) Research Center for Environmental Genomics, Kobe University*)

3TA3-08 化学架橋による脂質膜の強化
Faculty of Science and Technology, SEIKEI University

Yuuta Kawashima (1), Tsutomu Takahashi (1), Seiichi Suzuki (1) (*(1) Faculty of Science and Technology, SEIKEI University*)

3TA3-09 Ｔジャンクション型マイクロ流路を用いた均一直径ベシクルの形成
FORMATION OF MONODISPERSE VESICLES WITH A MICROFLUIDIC T-JUNCTION

Tomoaki Kurakazu (1), Shoji Takeuchi (1) (*(1) Center for International Research on Micromechatronics, Institute of Industrial Science, The University of Tokyo*)

細胞生物的課題 (接着，運動，骨格，伝達，膜) 3TA4-01～10 C4 会場/ Room C4

3TA4-01 拡散係数の異なる２状態を遷移する分子の拡散と細胞膜からの解離に関する解析
State transition and dissociation kinetics of membrane-bound molecules revealed by single-molecule imaging

Satomi Matsuoka (1), Tatsuo Shibata (2), Masahiro Ueda (1) (*(1) Graduate School of Frontier Biosciences, Osaka University;JST, CREST: (2) Department of Mathematical and Life Science, Hiroshima University;PREST, JST*)

3TA4-02 Ｘ線繊維回折による微小管構造動態の解析
X-ray diffraction analysis of the dynamic features of microtubule structure

Shinji Kamimura (1), Hiroyuki Iwamoto (2), Daisuke Miyashiro (3) (*(1) Department of Biological Sciences, Faculty of Science and Engineering, Chuo University: (2) Life and Environmental Division, SPring-8, JASRI: (3) Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo*)

3TA4-03 単一接着斑形成ダイナミクスの可視化
Visualization for dynamics of single focal adhesion formation

Hideaki Miyoshi (1), Tadao Sugiura (1), Kotaro Minato (1) (*(1) Nara institute of science and technology*)

3TA4-04 マスト細胞のヒスタミン分泌の研究
Histamine and exocytosis in mast cells studied with ^{1}H-NMR

Kazuo Yoshizaki (1), Takashi Hayano (2), Mitsuo Kitamura (1), Naoki Arizono (3) (*(1) Univ Tokushima Grad Sch, Inst HBS, Dpt Physiol.: (2) Otsu Municipal Hospital; Univ Tokushima, Sch Med, Dpt Physiol: (3) Kyoto Pref Univ Med, Dpt Med Zool*)

3TA4-05 ナトリウムイオン駆動型モーター固定子タンパク質 PomB のペリプラズム側ドメインの構造と機能の解析
Structural and functional analysis of the periplasmic domain of PomB, a stator component of the sodium-driven bacterial flagellar motor

Seiji Kojima (1), Katsumi Imada (2), Mayuko Sakuma (1), Keiichi Namba (2), Michio Homma (1) (*(1) Division of Biological Science, Graduate School of Science, Nagoya University: (2) Graduate School of Frontier Biosciences, Osaka University*)

3TA4-06 ATR-FTIR により明らかとなったべん毛モーター回転トルク発生のために必須な固定子と Na イオン結合の検出
Assignment of the essential Na+ binding of a stator unit for torque generation of bacterial flagellar motor by ATR-FTIR spectroscopy

Yuki Sudo (1), Yuya Kitade (2), Yuji Furutani (2), Masaru Kojima (3), Seiji Kojima (3), Michio Homma (3), Hideki Kandori (2) (*(1) Division of Science, Nagoya University; JST, PRESTO: (2) Department of Frontier Materials, Nagoya Institute of Technology: (3) Division of Science, Nagoya University*)

3TA4-07 なぜアクチンフィラメントＰ端は“遅い”のか
Why actin pointed end is the slow end?

Akihiro Narita (1), Yuichiro Maeda (1) (*(1) Structural Biology Research Center, Nagoya Univ.*)

3TA4-08 抗体修飾ナノ針を用いた細胞内繊維状タンパク質の力学検出による細胞選別法の開発
A novel method of cell discrimination by mechanical detection between cytoskeletal marker protein and antibody immobilized on nanoneedle

Shingo Mieda (1), Chikashi Nakamura (2), Takanori Kihara (3), Noriyuki Nakamura (2), Jun Miyake (2) (*(1) Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology: (2) Research Institute for Cell Engineering, Institute of Advanced Industrial Science and*

Technology: (3) Center for NanoBio Integration, The University of Tokyo)

3TA4-09 浸潤する単球への内皮細胞 PECAM-1 の局所集積

Role of dynamic recruitment of Endothelial PECAM-1 to Transmigrating Monocytes

Noriyuki Kataoka (1), Ken Hashimoto (2), Satoshi Mohri (2), Fumihiko Kajiya (1) (*(1) Kawasaki University of Medical Welfare: (2) Kawasaki Medical School*)

3TA4-10 表現型ゆらぎによる環境適応

Phenotypic fluctuation induced biological adaptation

Bei-Wen Ying (1), Yoichiro Ito (3), Yoshihiro Shimizu (1), Yuki Matsumoto (1), Junya Ichinose (3), Saburo Tsuru (1), Tetsuya Yomo (4) (*(1) Grad. Sch. Information Sci. & Tech., Osaka Univ.: (2) Grad. Sch. Frontier Biosci.: (3) ERATO, JST: (4) Grad. Sch. Information Sci. & Tech., Osaka Univ.; Grad. Sch. Frontier Biosci., Osaka Univ.; ERATO, JST*)

蛋白質-構造　3TA5-01～05，膜蛋白質　3TA5-06～08　C5 会場/ Room C5

3TA5-01 点変異によって 13 度熱安定化した BPTI 変異体の構造及び熱安定性の解析

THERMODYNAMIC AND STRUCTURAL ANALYSIS OF A 13-DEGREE STABILIZATION IN BPTI VARIANTS

Mohammad Islam (1), Shihori Sohya (1), Keiichi Noguchi (1), Shun-Ichi Kidokoro (2), Masafumi Yohda (1), Yutaka Kuroda (1) (*(1) Tokyo University of Agriculture and Technology (TUAT): (2) Nagaoka University of Technology*)

3TA5-02 温度・圧力によるペプチドの構造変化：マルチバーリック・マルチサーマル分子動力学シミュレーション

Conformational changes of a peptide induced by temperature and pressure: multibaric-multithermal molecular dynamics simulations

Hisashi Okumura (1) (*(1) Institute for Molecular Science, The Graduate University for Advanced Studies*)

3TA5-03 中性子とＸ線の高分解能結晶解析によるブタ膵臓エラスターゼ一阻害剤複合体の全原子構造

Structure of Porcine Pancreatic Elastase in Complex with Peptidic Inhibitor Determined by High Resolution Neutron and X-ray Crystallography

Taro Tamada (1), Takayoshi Kinoshita (2), Kazuo Kurihara (1), Motoyasu Adachi (1), Takashi Oohara (1), Toshiji Tada (2), Ryota Kuroki (1) (*(1) Japan AtomicEnergy Agency: (2) Osaka Prefecture University*)

3TA5-04 筋収縮制御タンパク質トロポニンの二量子コヒーレンス ESR による構造解析

Structural Analysis of Troponin in Regulation of Muscle Contraction by Double Quantum Coherence ESR

Jun Abe (1), Yasunori Ohba (1), Shoji Ueki (2), Toshiaki Arata (3), Seigo Yamauchi (1) (*(1) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University: (2) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University: (3) Department of Biological Sciences, Graduate School of Science, Osaka University*)

3TA5-05 黄色ブドウ球菌の２成分性毒素γヘモリジンが形成するヘテロヘプタマー膜孔複合体の立体構造解析

Three-dimentional structure analysis of staphylococcal γ-hemolysin heteroheptameric transmembrane pore complex

Noriko Tomita (1), Hitomi Anzai (2), Jun Kaneko (3), Yoshiyuki Kamio (4), Makoto Ohta (1) (*(1) Institute of Fluid Science, Tohoku University: (2) Graduate School of Engineering, Tohoku University: (3) Graduate School of Agricultural Science, Tohoku University: (4) Department of Human Health and Nutrition, Shokei Gakuin College*)

3TA5-06 電子線結晶解析によって明らかになったヒト赤血球膜蛋白質バンド３膜貫通ドメインの立体構造

The three-dimensional structure of human erythrocyte band 3 membrane domain determined by electron crystallography

Tomohiro Yamaguchi (1), Yoko Hiroaki (2), Yohei Ikeda (1), Yoshito Abe (3), Hiroyuki Kuma (5), Dongchon Kang (4), Naotaka Hamasaki (5), Yoshinori Fujiyoshi (2), Teruhisa Hirai (1) (*(1) RIKEN Harima Institute: (2) Faculty of Science, Kyoto Univ: (3) Graduate School of Pharmaceutical Sciences, Kyushu Univ: (4) Graduate School of Medical Sciences, Kyushu Univ: (5) Faculty of Pharmaceutical Sciences, Nagasaki International Univ*)

3TA5-07 分子動力学的手法を用いたアクアポリンに関する研究

Molecular Dynamics Simulations of Aquaporin

Yoshinori Hirano (1), Kenji Yasuoka (2), Makoto Suematsu (1), Masato Yasui (1) (*(1) School of Medicine Keio University : (2) Keio University Science and Technology*)

3TA5-08 膜タンパク質アクアポリンの構造と進化

The Structure and Evolution of Aquaporin

Michiko Nosaka (1), Kei Yamasita (2) (*(1) Sasebo National College of Technology: (2) Tyugai Pharmaceutical Co. Ltd./ Kurume National College of Technology*)

第３日目 12:00～13:30（11 月 1 日（日））/ Day 3 (Nov. 1, Sun.)

生命情報科学-分子進化　3TP1-01，数理生物学　3TP1-02～06　C1 会場/ Room C1

3TP1-01 GPCR のオリゴマー化研究のためのウェブサービス

Web services to investigate GPCR oligomerization

Wataru Nemoto (1), Kazuhiko Fukui (1), Hiroyuki Toh (2) (*(1) Advanced Industrial Science and Technology, Computational Biology Research Center: (2) Kyushu University, Medical Institute of Bioregulation*)

3TP1-02 Akt 経路のローパスフィルタ特性による EGF 受容体と下流のリン酸化シグナル強度の逆転

3P-241 Decoupling of receptor and downstream phosphorylation in Akt pathway by its low-pass filter characteristics

Yu Toyoshima (1), Kazuhiro Fujita (2), Shinsuke Uda (1), Yu-Ichi Ozaki (1), Hiroyuki Kubota (1), Shinya Kuroda (1) (*(1) Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo: (2) Department of Computational Biology, Graduate School of Frontier Sciences,*

University of Tokyo)

3TP1-03 高性能粒子反応拡散シミュレーションが明らかにする信号伝達経路における時空間相関の役割: MAP キナーゼを例に

High-performance particle reaction-diffusion simulations reveal roles of spatio-temporal correlations in signaling pathways: a study on the MAP kinase system

Koichi Takahashi (1), Sorin Tanase-Nicola (2), Pieter Rein Ten Wolde (2) (*(1) RIKEN: (2) AMOLF*)

3TP1-04 真性粘菌変形体のチューブ構造に保存される細胞運動の履歴

3P-240 Locomotive history of *Physarum* plasmodium recorded in its tubular structure

Tomohiro Shirakawa (1), Yukio-Pegio Gunji (2), Yoshihiro Miyake (1) (*(1) Department of Computational Intelligence and Systems Science, Interdisplinary Graduate School of Science and Engineering, Tokyo Institute of Technology: (2) Department of Earth and Planetary Sciences, Graduate School of Science, Tokyo Institute of Technology*)

3TP1-05 バクテリアのセンシングノイズと走化性

Bacterial chemotaxis is enhanced by nonadaptive fluctuation in sensory system

Masatoshi Nishikawa (1), Tatsuo Shibata (2) (*(1) Hiroshima University, CREST: (2) Hiroshima University, CREST, PREST*)

3TP1-06 生体分子のパタン表面での挙動をシミュレートする

Computational Simulation of the Behaviors of Bilogical Macromolecules on Patterned Surfaces

Dan Zhu (1), Bo Zhao (1), Chun Mao (1), Xiaohua Huang (1), Masaru Matsuo (2) (*(1) Jiangsu Key Laboratory of Biofunctional Materials, College of Chemistry and Environmental Science, Nanjing Normal University: (2) Nara Women's University*)

光生物-光合成　3TP2-01～05　C2 会場/ Room C2

3TP2-01 金属置換した紅色光合成細菌反応中心の赤外分光研究

3P-225 FTIR study of metal-replaced bacterial photosynthetic reaction center.

Akihide Watanabe (1), Tastuya Iwata (1), Mark L Paddock (2), Melvin Y Okamura (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Physics, University of California, San Diego*.)

3TP2-02 好熱性ラン藻の D1:3 は恒常的に発現している D1:1 よりも構造的に安定な光化学系 II 複合体を構成する

The substitution of D1:3 for D1:1 in Photosystem II of *Thermosychenococcus elongatus* results in a structurally more stable complex.

Miwa Sugiura (1), Sayo Harada (2), Eri Iwai (2), Takashi Manabe (2), Hidenori Hayashi (1), Alain Boussac (3) (*(1) Cell-Free Science and Technology Research Center, Ehime University: (2) Department of Chemistry, Ehime University: (3) iBiTec-S, CEA Saclay, France*)

3TP2-03 シリカメソ多孔体細孔中に導入した好熱性シアノバクテリア光化学系 II コア複合体の機能

Function of photosystem II core complexes of a thermophilic cyanobacterium introduced into silica mesoporous materials

Tomoyasu Noji (1), Chihiro Kamidaki (1), Keisuke Kawakami (2), Jian-Ren Shen (2), Tsutomu Kajino (3), Yoshiaki Fukushima (3), Takeshi Sekitoh (4), Shigeru Itoh (1) (*(1) Division of Material Science, Graduate School of Science, Nagoya University: (2) Graduate School of Natural Science and Technology, Okayama University: (3) Toyota Central R&D Labs. Inc.: (4) TOYOTA MOTOR CORPORATION*)

3TP2-04 Ca^{2+}を除去した Mn クラスターの S_0 および高酸化状態の ESR

Modified S_0-state and higher oxidized state EPR signal in Ca^{2+}-depleted Mn-cluster.

Momoko Kuriyaki (1), Hiroyuki Mino (1) (*(1) Graduate School of Science, Nagoya University*)

3TP2-05 Photosystem II の蛋白質環境がどのようにしてクロロフィルペア P680 の強力な酸化力を引き出しているか

How photosynthetic reaction centers control oxidation power in chlorophyll pairs P680 in Photosystem II

Hiroshi Ishikita (1) (*(1) Kyoto University, Career-Path Promotion Unit for Young Life Scientists*)

バイオイメージング　3TP3-01～06　C3 会場/ Room C3

3TP3-01 DNA—ヘリカーゼ相互作用の 1 分子観察

3P-253 Single—molecule observation of DNA-helicase interaction

Hiroaki Yokota (1), Yuko Chujo (2), Emi Nishimoto (3), Yoshie Harada (3) (*(1) iCeMS, Kyoto Univ.; PRESTO, JST: (2) Dept. of Frontier Sci., Univ. of Tokyo: (3) iCeMS, Kyoto Univ*.)

3TP3-02 II 型 DNA トポイソメラーゼの手品のような反応を直接みる

3P-261 Direct Observation of DNA Unlinking Magic by a Type-II DNA Topoisomerase.

Katsunori Yogo (1), Taisaku Ogawa (1), Saki Obata (1), Gen Nakajima (1), Junpei Suzuki (1), Kazuhiko, Jr. Kinosita (1) (*(1) Department of Physics, Waseda University*)

3TP3-03 細胞内 mRNA の長時間観察を可能にする蛍光核酸プローブ

3P-262 Long-term monitoring of intracellular mRNA by hybridization-sensitive fluorescent nucleotide probe

Takeshi Kubota (1), Shuji Ikeda (1), Hiroyuki Yanagisawa (1), Mizue Yuki (1), Akimitsu Okamoto (1) (*(1) ASI, RIKEN*)

3TP3-04 軸対称偏光素子を用いた GFP1 分子発光双極子モーメントの 3 次元計測

Three dimensional measurement of emission dipole orientation of single GFP molecules by the use of axisymmetric polarizers

Tomomi Tani (1), Mami Nomura (4), Kenta Saito (2), Takeharu Nagai (1) (*(1) Resarch Institute for Electronic Science: (2) Nikon Imaging Center, Hokkaido University: (3) JST: (4) Graduate School of Frontier Sciences, University of Tokyo*)

3TP3-05 光学顕微鏡（対物外アポダイズド位相差）と電子顕微鏡のインタラクティブ観察による、細胞核内部を運動する構造の同定

3P-260 Interactive observation of optical and electron microscopy revealed moving particles in the nucleus.

Kaoru Katoh (1), Ayako Kojima (1), Emiko Kobayashi (2), Kazunori Kawasaki (2) (*(1) Neurosci. Res. Inst, AIST: (2) Cell Eng. Res. Inst,, AIST*)

3TP3-06　ストレプトアビジン二次元結晶基板の高速 AFM 観察への適用

Streptavidin 2D crystals as solid supports for the visualization of biomolecular processes by high-speed AFM

Daisuke Yamamoto (1), Naoki Nagura (2), Saeko Omote (2), Masaaki Taniguchi (2), Toshio Ando (1) (*(1) College of Science and Engineering, Kanazawa University;CREST/JST: (2) College of Science and Engineering, Kanazawa University*)

その他　3TP4-01，発生・分化　3TP4-02～04，ゲノム生物学-ゲノム構造　3TP4-05　C4 会場/ Room C4

3TP4-01　フォトンフォースによる水溶液中のアミノ酸の分子捕捉

Optical Trapping of Amino Acids in Aqueous Solution by Photon Force

Tatsuya Shoji (1), Yasuyuki Tsuboi (1), Noboru Kitamura (1) (*(1) Hokkaido Univ.*)

3TP4-02　一周一細胞の上皮性チューブの形成

Formation of an epithelial tube of single cell-size circumference

Hisao Honda (1), Tatsuzo Nagai (2), Housei Wada (3), Kagayaki Kato (3), Shigeo Hayashi (3) (*(1) Hyogo University: (2) Kyushu-Kyoritsu University RC: (3) RIKEN CDB*)

3TP4-03　枯葉に擬態した蛾の翅模様にみられる揺らぎ構造とモジュールデザイン

Variational and Modular Design of Moth Wing Pattern Mimicking a ‘Dead Leaf’

Takao Suzuki (1), **Shigeru Kuratani** (1) (*(1) RIKEN CDB Lab. for Evol. Morph.*)

3TP4-04　ニワトリ砂胃の平滑筋は cSWiP-1 によって間充織細胞から分化する

Differentiation of smooth muscle in chiclen gizzard is induced by cSWiP-1 protein

Akio Inoue (1), Kazuki Mori (1), Takefumi Kofuji (1) (*(1) Department of Biology, Graduate School of Science, Osaka University*)

3TP4-05　遺伝子間距離構造から見える海洋性シアノバクテリアのゲノム構造進化

Evolution of isoapostatic genome structure in marine cyanobacteria.

Naobumi Sasaki (1), Naoki Sato (1) (*(1) University of Tokyo*)

ポスター発表　Poster Presentations

In this program, the speaker is shown by bold characters.
Place your poster on the board which is 90 cm (width) x 210 cm (height). You should present your poster in a whole day that is assigned. The first digit of your poster number is the assigned day (1, Oct. 30; 2, Oct. 31; 3, Nov. 1). The final three digits indicate the poster panel number. Place your poster at 9:00-10:00 in the morning, and discuss with the participators according to the following table. Remove it after the discussion time.

final digit	Day 1, Oct. 30	Day 2, Oct. 31	Day 3, Nov. 1
odd number	16:00-17:00	16:15-17:15	13:30-14:30
even number	17:00-18:00	17:15-18:15	14:30-15:30

第１日目（10 月 30 日（金））/ Day 1 (Oct. 30, Fri.)

1P-001　異方性スピン相互作用を用いた新規 NMR 法によるマルトース結合タンパク質の基質依存的な構造変化解析

Ligand-induced molecular morphological change of maltose binding protein revealed by a novel NMR approach using anisotropic spin interactions

Noriaki Hiroguchi (1), Aiko Imada (1), Shin-Ichi Tate (2) (*(1) Dept. Mathematical and Life Sciences, Hiroshima Univ.: (2) Dept. Mathematical and Life Sciences, Hiroshima Univ.;PRESTO/JST*)

1P-002　Bovine 由来グリシン開裂酵素系 H-protein の微小重力環境下での結晶化と高分解能Ｘ線結晶構造解析

Crystallization in microgravity conditions and high-resolution X-ray crystallography of bovine H-protein of the glycine cleavage system

Akifumi Higashiura (1), Takeshi Kurakane (1), Makoto Matsuda (1), Mamoru Suzuki (1), Kazuko Fujiwara (2), Koji Inaka (3), Masaru Sato (4), Tomoyuki Kobayashi (4), Tetsuo Tanaka (4), Hiroaki Tanaka (5), Atsushi Nakagawa (1) (*(1) Institute for Protein Research: (2) Institute for Enzyme Research: (3) Maruwa Foods and Biosciences, Inc.: (4) Japan Aerospace Exploration Agency: (5) Confocal Science, Inc.*)

1P-003　EM Navigaor で見る３次元電子顕微鏡による構造データ

Viewing 3D electron microscopy data by EM Navigator

Hirofumi Suzuki (1), Kenji Iwasaki (1), Haruki Nakamura (1) (*(1) IPR, Osaka-univ.: (2) Protein Data Bank Japan*)

1P-004　In-cell NMR による細胞内蛋白質の分子動態解析

Structural and dynamical studies of proteins in living cells by in-cell NMR spectroscopy

Junpei Hamatsu (1), Tomomi Hanashima (1), Masaki Mishima (1), Yutaka Ito (1) (*(1) Department of Chemistry Tokyo Metropolitan University; CREST/JST*)

1P-005　In-cell NMR 法を用いた生細胞内におけるプロテインＧ B1 ドメインの高次構造解析

Structure determination of protein G B1 domain in living *E. coli* cells by in-cell NMR spectroscopy

Tomomi Hanashima (1), Junpei Hamatsu (1), Masahiro Shirakawa (2), Masaki Mishima (1), Yutaka Ito (1) (*(1) Dept. of Chem., Tokyo Metropolitan Univ.; CREST/JST: (2) Dept. of Eng., Univ. of Kyoto; CREST/JST*)

1P-006　異常Ｘ線小角散乱法によるネイティブおよび再構成ウマ脾臓フェリチン内の鉄イオンコアの構造研究

Evaluation of iron core size in native and reconstituted horse spleen ferritin molecules using anomalous small-angle X-ray scattering technique

Yoji Inoko (1), **Yoshitsugu Kataoka** (1), Akira Ogata (1), Yasushi Watanabe (2) (*(1) Graduate School of Engineering Science, Osaka Univ. : (2) National Food Research Institute*)

1P-007　細菌べん毛フック繊維連結部の極低温電子顕微鏡による構造解析

Structural analysis of the flagellar hook-filament junction by electron cryomicroscopy

Fumiaki Makino (1), Takayuki Kato (1), Tomoko Miyata (1), Keiichi Namba (1) (*(1) Graduate School of Frontier Bioscience, Osaka University*)

1P-008　らせん対称性を持つ生体超分子の極低温電子顕微鏡による高速・高分解能構造解析：原子分解能を目指して

High-throughput, high-resolution cryoEM structural analysis of helical assemblies of biological macromolecules toward atomic resolution

Takashi Fujii (1), Takayuki Kato (1), Keiichi Namba (1) (*(1) Graduate School of Frontier Biosciences, Osaka University*)

1P-009　構造情報を含めた蛋白質ファミリーを表現するプロファイル条件付確率場モデルの開発

Development of Profile Conditional Random Fields for Modeling Protein Families with Structural Information

Akira Kinjo (1) (*(1) Institute for Protein Research, Osaka University*)

1P-010　ギャップジャンクションヘテロチャネル形成の適合性に関する構造的考察

Structural insight into docking compatibility of heterotyic gap junction channel

So Nakagawa (1), Shoji Maeda (1), Michihiro Suga (1), Eiki Yamashita (1), Tomitake Tsukihara (1) (*(1) Institute fot Protein Research, Osaka University: (2) Department of Life Science, University of Hyogo*)

1P-011　Ｘ線小角散乱法による CELーIII の多量体化機構及びその構造解析

ANALYSIS OF THE OLIGOMERIZATION MECHANISM AND STRUCTURE OF CEL-III BY SMALL-ANGLE X-RAY SCATTERING

Shuichiro Goda (1), Hitoshi Sadakata (1), Keigo Hisamatsu (1), Yuzuru Hiragi (2), Tomomitsu Hatakeyama (1) (*(1) Nagasaki University: (2) Kansai Medical University*)

1P-012 ヒト MTH1 活性部位の二つの Asp 残基のプロトネーション状態が異なる分子動力学シミュレーション

Molecular dynamics simulations of human MTH1 under different protonation states for two Asp residues in its active site

Ken-Ichiro Sawada (1), Shin-Ichi Fujiwara (1), **Takashi Amisaki** (1), Yuriko Yamagata (2) (*(1) Department of Biological Regulation, Faculty of Medicine, Tottori University: (2) Graduate School of Pharmaceutical Sciences, Kumamoto University*)

1P-013 複数のサポートベクタマシンの組み合わせによるタンパク質局所構造予測法の開発

Development of protein local structure prediction method based on combination of multiple support vector machines

Shugo Nakamura (1), Masanori Kakuta (1), Kentaro Shimizu (1) (*(1) The University of Tokyo*)

1P-014 アミノ酸側鎖のペプチド立体構造に及ぼす影響

The side chain effects on the conformation of the peptides

Ryota Jono (1), Kentaro Shimizu (1), Tohru Terada (2) (*(1) The university of Tokyo: (2) Molecular Scale Team, Computational Science Research Program, RIKEN*)

1P-015 バイオロジカルユニットを考慮したリガンド結合タンパク質データベースの構築

Development of protein-ligand complex's database considering biological units

Hiroki Ikezawa (1), Mizuki Morita (2), Kentaro Shimizu (1) (*(1) Graduate School of Agricultural and Life Sciences, The University of Tokyo: (2) National Institute of Biomedical Innovations*)

1P-016 計算的手法を用いた酵素設計：部位特異的変異によるパラ水酸化安息香酸水酸化酵素の基質特異性の改変

Computationally assisted enzyme design: Converting substrate specificity of p-hydroxybenzoate hydroxylase by site directed mutation

Kohsuke Hida (1), Seiji Saito (2), Tatsunari Nishi (3), Kentaro Shimizu (1) (*(1) Department of Biotechnolgy, Graduate School of Agricultural and Life Science, The University of Tokyo: (2) Graduate School of Agricultural and Life Science, The University of Tokyo; Genaris, Inc.: (3) Agricultural Bioinfomatics Research Unit, Graduate School of Agricultural and Life Science, The University of Tokyo;Genaris, Inc.*)

1P-017 ボツリヌス毒素構造の in silico 解析

In silico approaches for predicting botulinum toxin structure

Tomonori Suzuki (1), Tohru Ohyama (2), Toshihiro Watanabe (2), Koichi Niwa (2), Satoru Miyazaki (1) (*(1) Fac. of Pharmaceutical Sciences, Tokyo University of Science: (2) Fac. of Bioindustry, Tokyo University of Agriculture*)

1P-018 蛋白質立体構造予測のためのメタスコアの開発

Development of a meta-score for protein structure prediction

Matsuyuki Shirota (1), Takashi Ishida (2), Kengo Kinoshita (1) (*(1) Inst. Med. Sci., Univ. of Tokyo; BIRD JST: (2) Inst. Med. Sci., Univ. of Tokyo*)

1P-019 Conformation and Activity from Saturation Adsorptions of Lysozyme on the Surfaces of Nanosilica and Nanodiamond

1TA1-01 **Victor Wei-Keh Wu** (1) (*(1) Department of Chemical and Materials Engineering, National Kaohsiung University of Applied Sciences: (2) Victor Basic Research*)

1P-020 Mechanism of Interfacial Activation of a Family Ⅰ.3 Lipase with Two Lid Structures Revealed by X-ray Crystallography and Molecular Dynamics Simulation

Clement Angkawidjaja (1), Hiroyoshi Matsumura (2), Yuichi Koga (1), Kazufumi Takano (1), Shigenori Kanaya (1) (*(1) Osaka University, Department of Material and Life Science: (2) Osaka University, Department of Applied Chemistry*)

1P-021 The effect of bound water molecules on binding orientations in CDK2 inhibitors

Raghunadha Reddy Burri (1), Akio Kitao (1) (*(1) University of Tokyo, Laboratory of Molecular Design center for Bioinformatics*)

1P-022 藍色細菌 *Synechococcus* sp. PCC 7942 の細胞内亜鉛イオン濃度センサー機能を持つ転写因子 SmtB の亜鉛イオン結合に伴う構造変化に関する多次元 NMR 分光法による解析

1TA1-02

Multidimensional NMR spectroscopic analysis with the structural changes of cyanobacterial transcription factor, SmtB, functioning as the sensor for zinc-ion concentration in the cell, following zinc-ion binding

Hayato Morita (1), Hidenori Hayashi (2), Syunnosuke Abe (1), Takahisa Ikegami (3) (*(1) Faculty of Agriculture, Ehime University: (2) Faculty of Science, Ehime University: (3) Institute for Protein Research, Osaka University*)

1P-023 異なる結合様式をもつジユビキチンの分子動力学シミュレーション

Molecular Dynamics Simulation Study of Diubiquitins with Different Linkages

Sotaro Fuchigami (1), Mitsunori Ikeguchi (1), Akinori Kidera (2) (*(1) Grad. Sch. of Nanobioscience, Yokohama City Univ.: (2) Grad. Sch. of Nanobioscience, Yokohama City Univ.; RPCS, RIKEN*)

1P-024 抗 HIV 活性を有する天然型 APOBEC3G タンパク質の構造、１本鎖 DNA との相互作用及び酵素反応のリアルタイムモニタリング

1YP1-07

Structure, interaction with single-stranded DNA, and real-time monitoring of the enzymatic reaction of wild-type APOBEC3G possessing anti-HIV activity

Ayako Furukawa (1), Takashi Nagata (1), Ryuichi Sugiyama (2), Hiroshi Takaku (2), Masato Katahira (1) (*(1) Yokohama City University: (2) Chiba Institute of Technology*)

1P-025 翻訳後修飾を受けるタンパク質の立体構造変化データベース解析

Database analysis of protein structural changes with post-translational modifications

Takayuki Amemiya (1), Sotaro Fuchigami (1), Mitsunori Ikeguchi (1), Akinori Kidera (2) (*(1) Graduate school of nanobioscience, Yokohama city university: (2) Graduate school of nanobioscience, Yokohama city university;Computational Science Research Program, RIKEN*)

1P-026 α－ラクトアルブミンの MG 状態と生物機能

The molten globule state and the biological function of α-lactalbumin

Takashi Nakamura (1), Koki Makabe (2), Tomoyasu Aizawa (3), Keiichi Kawano (4), Makoto Demura (3), Kunihiro Kuwajima (2) (*(1) Okazaki Institute for Integrative Bioscience: (2) Okazaki Institute for Integrative Bioscience; Department of Functional Molecular Science, The Graduate University for Advanced Studies: (3) Division of Life Science, Graduate School of Life Science, Hokkaido University: (4) Department of Biological Sciences, Graduate School of Science, Hokkaido University*)

1P-027 全反射赤外分光法によるマルチ銅酸化酵素のカルボン酸の機能解析

Carboxyl group functions in the multicopper oxidase CueO studied by ATR-FTIR

Masayo Iwaki (1), Tsutomu Kajino (1), Kunishige Kataoka (2), Takeshi Sakurai (2) (*(1) Toyota Central R&D Labs., Inc.: (2) Graduate School of Natural Science and Technology, Kanazawa University*)

1P-028 ビスフェノールＡとの相互作用はカルモジュリンのカルシウム結合能を弱める

1TA1-03 Bisphenol A weakens Calcium Binding Affinity of Calmodulin

Koichi Murayama (1), Tomoyoshi Terada (1), Masashi Sonoyama (2), Yasunori Yokoyama (3), Masayuki Nara (4), Yasuo Asami (5), Sadayuki Matsuda (6) (*(1) Graduate School of Medicine, Gifu University : (2) Graduate School of Engineering, Gunma University: (3) Graduate School of Engineering, Nagoya University: (4) College of Liberal Arts and Sciences, Tokyo Medical & Dental University: (5) TA Instruments Japan Inc.: (6) School of Natural Science, Engineering and Agriculture, Hokkaido University of Education at Asahikawa*)

1P-029 時間領域テラヘルツ分光法でみる低振動領域におけるタンパク質の動力学転移

1TA1-07 Low-frequency dynamical transition of proteins monitored by terahertz time-domain spectroscopy

Ohki Kambara (1), Keisuke Tominaga (1) (*(1) Molecular Photoscience Research Center, Kobe University*)

1P-030 細胞内アクチンの SS 結合による二量体の研究

1TA1-04 A study on cytoplasmic actin SS dimers.

Daisuke Fukuhara (1), Hiroaki Kubota (1), Takashi Ohki (2), Shin'Ichi Ishiwata (2) (*(1) Major in Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda Univ.: (2) Dept. of Physics, Faculty of Advanced Science and Engineering, Waseda Univ.*)

1P-031 Gads の精製と CD28 細胞質内ドメインとの相互作用

1TA1-05 Purification of Gads and its interaction with CD28 cytoplasmic domains

Kunitake Higo (1), Jun Takahashi (1), Masayuki Oda (2), Hisayuki Morii (3), Teikichi Ikura (4), Nobutoshi Ito (4), Takachika Azuma (1), Ryo Abe (1) (*(1) Res. Inst. for Biol. Sci., Tokyo Univ. of Sci.: (2) Grad. Sch. of Environ. Sci., Kyoto Pref. Univ.: (3) Natl. Inst. of Adv. Indust. Sci. and Technol.: (4) Grad. Sch. of Biomed Sci., Tokyo Medical and Dental Univ.*)

1P-032 新規デフェンシンの膜構造と抗菌活性

1TA1-09 A new strategy of defensin against Gram-positive bacteria

Keiichi Kawano (1), Takahide Kouno (2), Naoki Fujitani (5), Mineyuki Mizuguchi (4), Tsukasa Osaki (3), Shun-Ichiro Kawabata (3), Tomoyasu Aizawa (1), Makoto Demura (5) (*(1) Grad Sch Sci, Hokkaido Univ: (2) Fac Pharm Sci, Toyama Univ; Dep Biochem Mol Biol & Biophys,Minnesota Univ: (3) Dep Biol, Kyushu Univ: (4) Fac Pharm Sci, Toyama Univ: (5) Grad Sch Life Sci, Hokkaido Univ*)

1P-033 非機械感受性イオンチャネルは本当に機械刺激によって開かないか？ – 粗視化分子動力学シミュレーション研究

1TA1-06 Does a non-mechanosensitive ion channel really not open by mechanical force? – A coarse grained molecular dynamics simulation study

Ken Takahashi (1), Masahiro Sokabe (1) (*(1) Nagoya University Graduate School of Medicine, Dept. of Cellular Biophysiology*)

1P-034 ヒトカルシトニンのアミロイド様線維形成機構の解析と初期過程の観察

Analyses of amyloid fibrillation mechanism of hCT and observation of the initial fibrillation process as studied by ^{13}C solid-state NMR and TEM

Hikari Watanabe (1), Miya Kamihira (2), Masasi Konndou (3), Michio Sato (3), Masamichi Nakakoshi (3), Akira Naito (1) (*(1) Grad. Sch. Eng, Yokohama Natl. Univ. : (2) Institute of Multidisciplinary Research, Tohoku Univ. : (3) Instrumental Analysis Center, Grad. Sch. Eng, Yokohama Natl. Univ.*)

1P-035 固体 NMR によるバイセル存在下でのヒトカルシトニンのアミロイド様線維構造と線維形成機構の解析

1TP3-08 Amyloidogenic fibrils and the structure of human calcitonin in the presence of phospholipidbilayers as studied by ^{13}C solid-state NMR

Yuki Abe (1), Miya Kamihira (2), Hikari Watanabe (1), Atsushi Kira (1), Izumi Yamane (1), Izuru Kawamura (1), Akira Naito (1) (*(1) Graduate school of Engineering, Yokohama National University: (2) Institute of Multidisciplinary Research, Tohoku University*)

1P-036 Ｈ/Ｄ交換を用いたシャペロニン複合体の構造機能解析

Structure and function of GroEL-GroES-nucleotide complexes studied by H/D exchange technique

Atsushi Mukaiyama (1), Takashi Nakamura (1), Tapan. K. Chaudhuri (1), Koki Makabe (1), Kunihiro Kuwajima (2) (*(1) Okazaki Institute for Integrative Bioscience: (2) Okazaki Institute for Integrative Bioscience; Department of Functional Molecular Science, School of Physical Sciences, Graduate University for Advanced Studies*)

1P-037 βラクトグロブリンと src SH3 ドメイン蛋白質が高濃度 EGOH と TFE の中で取るαヘリックスの多い状態は，コンパクトでも完全変性状態でもない

α-helix-rich-states of β-lactoglobulin and src SH3, formed in high concentration of ethelene glycol and trifluoroethanol, are not either fully unfolded or compact

Masaji Shinjo (1), Yoshitaka Matsumura (1), Xianju Jin (1), Hiroshi Kihara (1) (*(1) Kansai Medical University*)

1P-038 Structural change of PI3K SH3 domain at acidic pH

Yoshitaka Matsumura (1), Masaji Shinjo (1), Nobuyuki Okishio (2), **Hiroshi Kihara** (1) (*(1) Kansai Medical University: (2) Hokkaido Red Cross Blood Center*)

1P-039 Rad53 FHA1 ドメインのフォールディング経路に現れるαヘリカルバースト

An observed α-helical burst of FHA1 domain of Rad53 in the folding pathway

Yoshitaka Matsumura (1), Masaji Shinjo (1), Anjali Mahajan (2), Ming-Daw Tsai (3), Hiroshi Kihara (1) (*(1) Department of Physics, Kansai Medical*

University: (2) Center for Pharmaceutical Biotechnology, University of Illinois at Chicago: (3) Departments of Chemistry and Biochemistry, The Ohio State University)

1P-040 リゾチームのＳ－Ｓ結合欠損変異体における残留非ランダム構造

Residual Nonrandom Structures in Disulfide-Deficient Variants of Lysozyme

Kenichi Kasai (1), Kuniaki Narama (1), Yasuo Noda (1), Hideki Tachibana (2), Shin-Ichi Segawa (1) (*(1) Sch. Sci.&Tech.,Kwansei Gakuin Univ: (2) Sch. Biology-Oriented Sci.&Tech.,Kinki Univ*)

1P-041 モルテングロビュール段階で見出される PCP（ピロリドンカルボキシルペプチダーゼ）の逐次折れたたみ経路とそれに続く天然構造への転移

Sequential folding pathway of PCP (pyrrolidone carboxyl peptidase) found in the molten-globule-like stage and the following folding transition.

Yohei Yokota (1), Christopher Kinnman (1), Kazuyoshi Yabumoto (1), Yasuo Noda (1), Katsuhide Yutani (2), Shin-Ici Segawa (1) (*(1) Sch. Sci. & Tec., Kwansei Gakuin Univ.: (2) RIKEN SPring-8 Center., Harima Inst.*)

1P-042 新規創製した人工タンパク質におけるプロ領域の役割

Characterization of a propeptide region in prouroguanylin using de novo designed Disulfide Hybrid Protein

Masaki Okumura (1), Hironori Konishi (2), Yuhei Yamazaki (1), Hiroshi Yamaguchi (1), Yuji Hidaka (2) (*(1) Graduate school of science and technology, Kwansei Gakuin Univ.: (2) Graduate school of science and engineering, Kinki univ.*)

1P-043 ケミカルシャペロンとして働く抗プリオン化合物 GN8

Anti-prion Compound GN8 Acts as a Chemical Chaperon for Prion Protein

Norifumi Yamamoto (1), Kazuo Kuwata (1) (*(1) Center for Emerging Infectious Diseases, Gifu University*)

1P-044 シーディングによる２種類のプリオンアミロイド線維の伝播

Propagation of two types of prion amyloid fibrils by seeding

Keiichi Yamaguchi (1), Tomoharu Matsumoto (1), Junji Hosokawa-Muto (1), Kazuo Kuwata (1) (*(1) Center for Emerging Infectious Diseases, Gifu University*)

1P-045 蛋白質の低温変性構造に関する理論解析

A Theoretical Analysis on Characteristics of Protein Structures Induced by Cold Denaturation

Hiraku Oshima (1), Takashi Yoshidome (2), Ken-Ichi Amano (2), Masahiro Kinoshita (2) (*(1) Pioneering Research Unit for Next Generation, Kyoto University: (2) Institute of Advanced Energy, Kyoto University*)

1P-046 アラニンベースペプチドのヘリックスーコイル転移に及ぼす圧力効果：統計力学理論解析

Pressure effect on helix-coil transition of an alanine -based peptide: Statistical-mechanical analysis

Takashi Yoshidome (1), Masahiro Kinoshita (1) (*(1) Institute of Advanced Energy, Kyoto University*)

1P-047 蛋白質の二次構造形成における側鎖のパッキングの役割

Roles of side-chain packing in the formation of secondary structures of a protein

Satoshi Yasuda (1), Ryota Kodama (1), Takashi Yoshidome (1), Yuichi Harano (2), Masahiro Kinoshita (1) (*(1) Institute of Advanced Energy, Kyoto University: (2) Institute for Protein Research, Osaka University*)

1P-048 蛋白質熱安定性における水のエントロピー効果

Crucial importance of water-entropy effect in thermal stability of proteins.

Ryota Kodama (1), Takashi Yoshidome (1), Ken-Ichi Amano (1), Yuichi Harano (2), Masahiro Kinoshita (1) (*(1) Institute of Advanced Energy, Kyoto University: (2) Institute for Protein Research, Osaka University*)

1P-049 可溶性モノマーとの化学交換を介したアミロイドβタンパク質オリゴマーの検出

Transient formation of amyloid β-protein oligomer characterized by chemical exchange with soluble monomer

Takahiro Yamaguchi (1), Katsumi Matsuzaki (1), Masaru Hosino (1) (*(1) Graduate School of Pharmaceutical Sciences, Kyoto University*)

1P-050 金属イオン結合により誘起されるデノボデザイン３本鎖ヘリックスバンドルタンパク質の物性解析

Properties of a *de novo* designed three-helix bundle protein induced by metal-ion-binding

Nobutaka Komichi (1), Toshiki Tanaka (2), Yuji Sasaki (3), Masayuki Oda (1) (*(1) Graduate School of Life and Environmental Sciences, Kyoto Prefectural University: (2) Graduate School of Engineering, Nagoya Institute of Technology: (3) Graduate School of Frontier Sciences, The University of Tokyo*)

1P-051 エンドー１,3-βグルカナーゼの糖結合モジュールによるラミナリン結合アフィニティとアビディティ

Laminarin binding affinity and avidity by carbohydrate-binding module of endo-1,3-β-glucanase

Tomonari Tamashiro (1), Yoichi Tanabe (2), Masayuki Oda (2) (*(1) Faculty of Agriculture, Kyoto Prefectual University: (2) Graduate School of Life and Environmental Sciences, Kyoto Prefectural University*)

1P-052 ３α－hydroxysteroid dehydrogenase Ｃ端残基の二量体形成や触媒活性に及ぼす影響

Effects of C-terminal residues of 3α-hydroxysteroid dehydrogenase on its dimer formation and catalytic activity

Kotaro Hara (1), Yuichiro Takagi (2), Shigeru Ueda (3), Masayuki Oda (2) (*(1) Faculty of Agriculture, Kyoto Prefectural University: (2) Graduate School of Life and Environmental Sciences, Kyoto Prefectural University: (3) Asahi Kasei Pharma Co.*)

1P-053 深海微生物 *Moritella profunda* 由来ジヒドロ葉酸還元酵素の立体構造解析

Structure and stability of dihydrofolate reductase from deep-sea bacterium *Moritella profunda*

Kazumi Hata (1), Tomoyuki Tanaka (2), Chiho Murakami (3), Eiji Ohomae (3), Kunihiko Gekko (3), Yoshitsugu Shiro (2), Kazuyuki Akasaka (1) (*(1) Kinki University; RIKEN SPring-8 Center: (2) RIKEN SPring-8 Center: (3) Hiroshima University*)

1P-054 タンパク質の熱力学的性質に及ぼすシクロデキストリンの添加効果

Effects of cyclodextrine on thermodynamic properties of protein

Tadashi Kamiyama (1), Megumi Satoh (1), Eri Aoki (1), Daisuke Takeuchi (1), Takahiro Tateishi (1), Takayoshi Kimura (1) (*(1) Kinki Univ. Fac. Sci. and Eng.*)

1P-055 レプリカ交換分子動力学法による単量体ポリグルタミンタンパクの特性研究

1TP3-05 Characterization of monomeric polyglutamine peptides by replica exchange molecular dynamics simulation

Miki Nakano (1), Hirofumi Watanabe (3), Shigenori Tanaka (2) (*(1) Kobe University Graduate School of Human Development and Environment: (2) Kobe University Graduate School of Engineering : (3) CREST, Japan Science and Technology Agency*)

1P-056 新規発光共役高分子による新規インスリンフィラメントの細胞毒性と内部構造解明

1TP3-04 Cell toxicity and inner structure analysis of novel insulin filaments using novel luminescent conjugate polymers

Takahiro Kobayashi (1), Tamotsu Zako (2), Masafumi Sakono (2), Mikael Lindgren (3), Peter Nilsson (4), Per Hammarstrom (4), Mizuo Maeda (1) (*(1) Front.Sci., Univ. Tokyo: (2) RIKEN: (3) Dept. Phys., The Norwegian Univ.: (4) Dept. Chem., Linkoping Univ.*)

1P-057 キャピラリー内トラップによる一分子の長時間観察：蛋白質の折り畳みへの応用

1YP1-02 Long-time observation of a single molecule trapped in a capillary cell: application for protein folding

Kiyoto Kamagata (1), Yuji Goto (2), Satoshi Takahashi (3) (*(1) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University: (2) Institute for Protein Research, Osaka University: (3) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University;CREST, JST*)

1P-058 ポリグルタミン病の新たな分子病理メカニズム_タンパク質線維の構造伝播による発症制御の可能性

1YP1-08 Cross-seeding fibrillation of Q/N-rich proteins offers new pathomechanism of polyglutamine diseases

Yoshiaki Furukawa (1), Kumi Kaneko (1), Masaru Kurosawa (1), Gen Matsumoto (1), Nobuyuki Nukina (1) (*(1) RIKEN, Brain Science Institute*)

1P-059 蛋白質の体積揺らぎ動力学に対する圧力効果

1TP3-06 Effects of Pressure on Volume-Fluctuation Dynamics of Proteins

Kunitsugu Soda (1), Yudai Shimbo (2), Yasutaka Seki (2), Makoto Taiji (1) (*(1) Computational Systems Biology Group, RIKEN: (2) Dept. Bioeng., Nagaoka Univ. Technol.*)

1P-060 青色光センサータンパク質フォトトロピンの光反応に対する Crowding 効果

The effect of macromolecular crowding on photoreaction of a blue light sensor protein; phototropin

Tsuguyoshi Toyooka (1), Yuusuke Nakasone (1), Kazunori Zikihara (2), Tooru Tokutomi (2), Masahide Terazima (1) (*(1) Department of Chemistry, Graduate School of Science, Kyoto University.: (2) Research Institute for Advanced Science and Technology, Department of Biological Science, Graduate School of Science, Osaka Prefecture University.*)

1P-061 光センサータンパク質 TePixD の反応ダイナミクスへの圧力効果

Pressure effects on reaction dynamics of a photosensor protein TePixD

Kunisato Kuroi (1), Keisuke Tanaka (1), Yusuke Nakasone (1), Kouji Okajima (2), Masahiko Ikeuchi (3), Satoru Tokutomi (4), Masahide Terazima (1) (*(1) Department of Chemistry, Graduate School of Science, Kyoto University: (2) Department of Life Sciences (Biology), Graduate School of Arts and Sciences, The University of Tokyo;Research Institute for Advanced Science and Technology, Department of Biological Science, Graduate School of Science, Osaka Prefecture University: (3) Department of Life Sciences (Biology), Graduate School of Arts and Sciences, The University of Tokyo: (4) Research Institute for Advanced Science and Technology, Department of Biological Science, Graduate School of Science, Osaka Prefecture University*)

1P-062 線形応答自由エネルギー法を用いた Chalcone Isomerase による触媒反応の理論的研究

Theoretical Analysis of Chalcone Isomerase Catalyzed Reaction Using Linear Response Free Energy Method

Ryoichi Kida (1), Masahiro Higashi (2), Shigehiko Hayashi (1), Shigeki Kato (1) (*(1) Graduate School of Science Kyoto University: (2) Institute of Molecular Science*)

1P-063 フラビン依存性オキシダーゼが示す非ミカエリス - メンテン型反応機構の理論的解析

Theoretical analysis of the reaction mechanism of non-Michaelis kinetics of flavin-dependent oxidases

Tetsuo Ishida (1), Atsushi Yamamoto (1), Hiroyuki Tanaka (1), Kihachiro Horiike (1) (*(1) Shiga University of Medical Science*)

1P-064 二重標識したマルトース結合蛋白質の基質結合と折りたたみの一分子観測

Single molecule observation of the ligand binding and folding dynamics of maltose binding protein doubly labeled by a cell free system

Akihiro Yamamori (1), Kiyoto Kamagata (2), Issei Iijima (3), Takahiro Hohsaka (3), Yuji Goto (4), Satoshi Takahashi (5) (*(1) Graduate School of Science, Osaka University: (2) Institute of Multidisciplinary Reserch for Advanced Materials, Tohoku University: (3) School of Materials Science., Japan Advanced Institute of Science and Technology: (4) Institute for Protein Research, Osaka University: (5) Institute of Multidisciplinary Reserch for Advanced Materials, Tohoku University;CREST, JST*)

1P-065 X 線結晶解析における水分子位置評価および蛋白質水和構造予測プログラムの開発

Development of programs to check the hydration sites identified by X-ray crystallography and to predict protein hydration structures

Daisuke Matsuoka (1), Masayoshi Nakasako (1) (*(1) Graduate School of Science and Technology, Keio University*)

1P-066 分子動力学法を用いた生体高分子系の緩和モード解析

Relaxation Mode Analysis of a Biopolymer System by Molecular Dynamics

Toshiki Nagai (1), Ayori Mitsutake (1), Hiroshi Takano (1) (*(1) Graduate School of Science and Technology, Keio University*)

1P-067 単純並列化によるマルチカノニカル分子動力学法のサンプリング効率の向上

Improvement of Sampling Efficiency of Multicanonical Molecular Dynamics by Trivial Parallelization

Jinzen Ikebe (1), Koji Umezawa (1), Junichi Higo (2), Narutoshi Kamiya (2), Takanori Sugihara (3), Yasushige Yonezawa (4), Haruki Nakamura (4) (*(1) Graduate School of Frontier Biosciences, Osaka University : (2) The Center for Advanced Medical Engineering and informatics, Osaka University: (3) RIKEN Next-Generation Supercomputer R&D Center: (4) Institute for Protein Research, Osaka University*)

1P-068 全反射赤外分光法による V 型 ATPase の Na^+結合構造に関する研究

Sodium ion binding sites of V-ATPase studied by ATR-FTIR spectroscopy

Yuji Furutani (1), Hideki Kandori (2), Takeshi Murata (3) ((*1) Institute for Molecular Science; Nagoya Institute of Technology: (2) Nagoya Institute of Technology: (3) Chiba University*)

1P-069 分子モデリング法と溶液Ｘ線散乱法による天然解鎖蛋白質の構造解析

Structural Analysis of a Natively Unfolded Protein by Combining Molecular Modeling and Solution X-ray Scattering

Yasutaka Seki (1), Tomoyasu Aizawa (2), Yudai Shimbo (1), Kunitsugu Soda (3) ((*1) Department of Bioengineering, Nagaoka University of Technology: (2) Department of Biological Sciences, Graduate School of Science, Hokkaido University: (3) Computational Systems Biology Research Group, RIKEN*)

1P-070 飛行時間型二次イオン質量分析法による固定化ポリペプチドの評価におけるクラスター一次イオン源の影響

Effect of time-of-flight secondary ion mass spectrometry with cluster primary ion source on detection of immobilized-polypeptide

Kohei Yamamoto (1), Nobuhiko Kato (2), Masahiro Kudo (2), Satoka Aoyagi (1) ((*1) Faculty of Life and Environmental Science, Shimane University: (2) Department of Materials and Life Science, Seikei University*)

1P-071 Zero-mode waveguides を利用した GroEL-GroES 相互作用の１分子蛍光イメージング

Single molecule fluorescence imaging of GroEL-GroES interaction in zero-mode waveguides

Tomoya Sameshima (1), Taro Ueno (1), Jun-Ichi Wada (2), Mutsuko Aoki (2), Ryo Iizuka (1), Naonobu Shimamoto (2), Iwao Ohdomari (2), Takashi Tanii (2), Takashi Funatsu (1) ((*1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) Faculty of Science and Engineering, Waseda University*)

1P-072 高速に系統的な進化を行うためにたんぱく質ハミングライブラリーを作製する諸技術

Versatile techniques in making of a protein Hamming library for the fast systematic directed evolution

Yosuke Miyazawa (1), Takuyo Aita (3), Yuzuru Husimi (2) ((*1) Saitama University: (2) Saitama University Research Management Bureau: (3) Saitama University*)

1P-073 RNA 複製酵素を提示した自己言及型 in　vitro　virus の自律進化に向けてⅡ

Twards in vitro autonomous evolution of self-referring *in vitro* virus displaying an RNA replicase, Ⅱ

Hidenao Arai (1), Tomoya Kinoshita (1), Biyani Manish (2), Yuzuru Husimi (1) ((*1) Dept. of Functional Materials Sci, Saitama Univ.: (2) Inst. of Engineering Innovation, Graduate School of Engineering, Univ. of Tokyo*)

1P-074 ２種類の異なる代謝経路で機能する TIM バレル酵素によるキメラ酵素の作製

Chimeric enzymes between two TIM barrel enzymes involved in different metabolic pathway

Yuriya Abe (1), Tomoko Mase (1), Satoshi Akanuma (1), Akihiko Yamagishi (1) ((*1) Tokyo Univ. of Pharm. Life Sci.*)

1P-075 古細菌祖先型と真正細菌祖先型ヌクレオシド二リン酸キナーゼの耐熱性の違い

Stability difference between resurrected Archaeal and Bacterial ancestors of nucleoside diphosphate kinase

Ami Kobayashi (1), Satoshi Akanuma (1), Naoki Nemoto (1), Mitsuo Kimura (1), Shin-Ichi Yokobor (1), Akihiko Yamagishi (1) ((*1) Dept. of Mol. Biol., Tokyo Univ. of Pharm. Life Sci.*)

1P-076 共発現によるペプチド封入体化発現法におけるパートナータンパク質の検討

Effect of aggregation-prone protein on inclusion body formation in coexpression system for peptide

Satoshi Tomisawa (1), Tomoyasu Aizawa (1), Masakatsu Kamiya (1), Takashi Kikukawa (1), Makoto Demura (1), Keiichi Kawano (1) ((*1) Grad. Sch. of Sci.,Hokkaido Univ*)

1P-077 共鳴ラマン分光法によるヘモグロビンMの近位または遠位チロシン残基の配位状態と四次構造の解明

Coordination states of proximal or distal tyrosine residue in Hemoglobins M and their quaternary structures probed by resonance Raman spectroscopy

Yayoi Aki (1), Masako Nagai (2), Kiyohiro Imai (3), Michihiko Aki (4), Teizo Kitagawa (5) ((*1) Grad. Sch. of Med. Sci.,Kanazawa Univ.: (2) Res. Center for Micro-Nano Tech., Hosei Univ.: (3) Dept. of Frontier Biosci., Hosei Univ.: (4) Graduate Univ. for Advanced Studies: (5) Toyota Phys. and Chem. Inst.*)

1P-078 ナノ構造を有する電極を電子供給基質としたシトクロム P450 反応の駆動と計測

Electrochemically-driven Cytochrome P450 Reactions at Nanostructured Electrode Surfaces

Yasuhiro Mie (1), Mashiki Ikegami (1), Yasuo Komatsu (1) ((*1) National Institute of Advanced Industrial Science and Technology (AIST)*)

1P-079 急速混合凍結 EPR 法によるシトクロム P450cam 反応中間体の捕捉と動的解析

Cryotrapped reaction intermediates in cytochrome P450cam and kinetics analyses by newly developed rapid freeze-quench EPR method

Hiroshi Hori (1), Riki Kitano (1), Naoki Inoue (1), Koji Takemoto (1) ((*1) Osaka Univ.*)

1P-080 デオキシヘモグロビンの電子状態解明に向けた連続可変多周波 EPR 共振器の開発

Development of a continuously frequency-variable EPR resonator to elucidate the electronic structures of deoxy-hemoglobin

Kenta Ninomiya (1), Haruhiko Yashiro (2), Hiroshi Hori (1), Masayuki Hagiwara (1) ((*1) KYOKUGEN Osaka University: (2) Japan Science and Technology Agency*)

1P-081 ポルフィリン側鎖のヘムの電子構造への影響に関する理論的研究

Density Functional Study of Roles of Porphyrin Ring in Electronic Structures of Heme

Yu Takano (1), Haruki Nakamura (1) ((*1) Institute for Protein Research, Osaka University*)

1P-082 ヒト由来インドールアミン２,3-ジオキシゲナーゼにおけるヘム近傍アミノ酸残基の役割と基質阻害機構

Role of the Heme Environmental Amino Acid Residues and Mechanism of the Substrate Inhibition in Human Indoleamine 2,3-Dioxygenase

Masaki Horitani (1), Hiroshi Sugimoto (1), Erisa Kometani (2), Tatsuya Yamamoto (1), Yoshitsugu Shiro (1) ((*1) RIKEN SPring8 Center: (2) Graduate School of Life Science, University of Hyogo*)

1P-083 チトクロム酸化酵素休止酸化型の１.４ Å 分解能Ｘ線構造解析

X-ray structural analysis of cytochrome c oxidase in the resting oxidized state at 1.4 Å resolution

Kazunori Maeda (1), Kazumasa Muramoto (1), Masao Mochizuki (1), Tomoko Maeda (1), Kyoko Shinzawa-Itoh (1), Michihiro Suga (2), Kazuhiro Ohta (2), Eiki Yamashita (2), Tomitake Tsukihara (2), Shinya Yoshikawa (1) (*(1) Department of Life Science, University of Hyogo, Japan: (2) Institute for Protein Research, Osaka University, Japan*)

1P-084 多剤排出トランスポーターAcrB の分子動力学シミュレーション

All-atom molecular dynamics simulation of bacterial multidrug efflux transporter AcrB

Tsutomu Yamane (1), Mitsunori Ikeguchi (1) (*(1) Yokohama City University Graduate School of Nanobioscience Department of Supramolecular Biology*)

1P-085 膜活性タンパク質の新規設計

De novo design of membrane-active proteins

Naoki Yamamoto (1), Atsuo Tamura (1) (*(1) Department of chemistry, Graduate school of science, Kobe university*)

1P-086 多次元固体 NMR 法による膜蛋白質 *p*HtrII の主鎖構造解析

Mainchain structural analysis of transmembrane halobacterial tranceducer *p*HtrII by multi-dimensional magic-angle-spinning solid-state NMR

Ayako Egawa (1), Kokoro Hayashi (2), Chojiro Kojima (2), Hideo Akutsu (1), Toshimichi Fujiwara (1) (*(1) Institute for Protein Research, Osaka University: (2) Graduate School of Biological Sciences, Nara Institute for Science and Technology*)

1P-087 ウシ心筋 NADH-ユビキノン酸化還元酵素 2 次元結晶の極低温電子顕微鏡試料の調製

The specimen preparation of 2-D crystals of bovine heart NADH-ubiquinone oxidoreductase for cryo-electron microscopy.

Satoko Amano (1), Satoru Shimada (1), Masahide Hikita (1), Kyoko Shinzawa-Itoh (1), Christoph Gerle (2), Kazutoshi Tani (2), Yoshinori Fujiyoshi (2), Atsuo Miyazawa (3), Shinya Yoshikawa (1) (*(1) Department of Life Science, University of Hyogo : (2) Kyoto University., Science, Biophysics: (3) Structural Physiology Research Group, RIKEN SPring-8 Center*)

1P-088 共鳴ラマン分光法によるウシ心筋ミトコンドリア呼吸鎖 NADHーユビキノン酸化還元酵素の FMN と鉄ー硫黄クラスターの構造解析

Structural analysis of FMN and iron-sulfer clusters of tje bovine heart NADH-ubiquinone oxidoreductase by resonance Raman spectra

Masahide Hikita (1), Masakazu Moriyama (1), Takashi Ogura (1), Kyoko Shinzawa-Itoh (1), Shinya Yoshikawa (1) (*(1) Department of Life Science,Graduate School of Life Science,University of Hyogo*)

1P-089 ウシ心筋 NADHーユビキノン酸化還元酵素の二次元結晶化

2-D crystallization of bovine heart NADH-ubiquinone oxidoreductase.

Satoru Shimada (1), Satoko Amano (1), Masahide Hikita (1), Kyoko Shinzawa-Itoh (1), Christoph Gerle (2), Kazutoshi Tani (2), Yoshinori Fujiyoshi (2), Atsuo Miyazawa (1), Shinya Yoshikawa (1) (*(1) Department of Life Science, University of Hyogo: (2) Department of Life Science, Kyoto University*)

1P-090 ヒト由来 2 回膜貫通型タンパク質 Ifitm5 の構造研究;NMR 法を用いた立体構造解析のためのサンプル調製

Structural study of Ifitm5, a human double transmembrane protein; sample preparation for NMR analysis

Takashi Tsukamoto (1), Xiang Lan Li (2), Masakatsu Kamiya (1), Nobutaka Hanagata (2), **Makoto Demura** (1) (*(1) Faculty of Advanced Life Science, Hokkaido University: (2) Nanotechnology Innovation Center, National Institute for Materials Science*)

1P-091 バクテリオロドプシンのフォースカーブのシミュレーション

Simulation of force-distance curve of bacteriorhodopsin

Tatsuya Yamada (1), Shigeki Mitaku (1) (*(1) Department of Applied Physics, Nagoya University.*)

1P-092 核酸塩基の 1 電子酸化に由来するラジカル種の検出と DFT 計算による同定

Detection of a radical species originated from the one-electron oxidation of nucleic-acid bases and the DFT calculation for identification

Kouto Migita (1), Catharina T. Migita (1), Ryo Miyamoto (2) (*(1) Yamaguchi University: (2) Hirosaki University*)

1P-093 1 分子計測と MD シミュレーションによる DNA1 塩基対機械的伸張におけるエネルギー地形と確率的経路

Stochastic and dynamic pathways detected by quasi-static mechanical unzipping of single-base pair of DNA and MD simulations

Akihiro Fukagawa (1), Michio Hiroshima (2), Makio Tokunaga (3) (*(1) Department of Biological Information, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology: (2) Advanced Science Institute, RIKEN: (3) Department of Biological Information, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology; Research Center for Allergy and Immunology, RIKEN*)

1P-094
1TP5-03 2'－O,4'－C-aminomethylene bridged nucleic acid(2',4'－BNANC)修飾による生理的 pH におけるピリミジン型 3 本鎖核酸形成の促進

Promotion of pyrimidine motif triplex formation at physiological pH by 2'-*O*,4'-*C*-aminomethylene bridged nucleic acid modification

Kiyomi Sasaki (1), Norihiro Sato (1), Satoshi Obika (2), Takeshi Imanishi (2), Hidetaka Torigoe (1) (*(1) Faculty of Science, Tokyo University of Science: (2) Graduate School of Pharmaceutical Sciences, Osaka University*)

1P-095 誘電緩和分光法による DNA オリゴマーの水和状態解析

Hydration property analysis of DNA oligomer by dielectric relaxation spectroscopry

Akira Tsuchiko (1), Yoshiyuki Tanaka (2), Tetsuichi Wazawa (1), Nobuyuki Morimoto (1), Makoto Suzuki (1) (*(1) Tohoku Univ. Grad. Sch.of Eng.: (2) Tohoku Univ. Grad. Sch.of Pharm.: (3) CREST JST*)

1P-096 DNA の B-Z 転移における溶媒効果

Solvation effect on B-Z DNA transition

Yutaka Maruyama (1), Norio Yoshida (1), Fumio Hirata (1) (*(1) Institute for Molecular Science*)

1P-097 一本鎖 DNA の両末端接触速度における長さ及び溶液の粘度依存性
1TP5-02 The Length and Viscosity Dependence of End-to-end Collision Rates in Single-stranded DNA

Takanori Uzawa (1), Ryan Cheng (2), Dmitrii Makarov (2), Kevin Plaxco (3) (*(1) Hokkaido University: (2) The University of Texas: (3) University of California Santa Barbara*)

1P-098 レプリカ交換法による巨大タンパク質－核酸複合系の粗視化シミュレーション研究

Replica exchange simulations applied for coarse-grained models of giant protein-nucleic acid complex

Naoto Hori (1), Hiroo Kenzaki (1), Shoji Takada (2) ((*1) Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.: (2) Dept. Biophysics, Grad. Sch. Sci., Kyoto Univ.; CREST, JST*)

1P-099 タンパク質－DNA 複合体の粗視化シミュレーション：ヌクレオソームのダイナミクス

1TP5-07 Coarse-grained simulation of protein-DNA complex: dynamics of nucleosome

Hiroo Kenzaki (1), Shoji Takada (2) ((*1) Deptartment of Biophysics, Graduate School of Science, Kyoto University: (2) Deptartment of Biophysics, Graduate School of Science, Kyoto University; JST-CREST*)

1P-100 RNA 結合タンパク質における疎水表面を用いた塩基認識機構の検証: NOVA-RNA 複合体系での研究

1TP5-05 Study of RNA base recognition mechanism by aliphatic surface of RNA-binding protein: Case study of NOVA-RNA complex system

Ikuo Kurisaki (1), Atsushi Matsumoto (2), Kei Yura (3), Shigenori Tanaka (4) ((*1) Graduate School of Engineering, Kobe Univ.: (2) Center for Computational Science and Engineering, Japan Atomic Energy Agency: (3) Graduate School of Humanities and Sciences, Ochanomizu Univ.: (4) Graduate School of Engineering, Kobe Univ.; CREST*)

1P-101 タンパク質翻訳開始複合体における 30S-mRNA 結合力の 1 分子顕微解析

1TP5-06 Single-molecule force measurement for 30S-mRNA interaction in translation initiation

Tomoaki Masuda (1), Ryo Iizuka (1), Takashi Funatsu (1), Sotaro Uemura (3) ((*1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) Center for Nano Bio Integration, The University of Tokyo: (3) Department of Structural Biology, Stanford University School of Medicine: (4) Precursory Research for Embryonic Science and Technology (PRESTO)*)

1P-102 マウステロメア DNA の 4 本鎖 DNA 構造とマウステロメア結合蛋白質 Pot1 のテロメア DNA 結合ドメインとの相互作用

1TP5-04 Interaction between tetraplex structure of mouse telomeric DNA and telomeric DNA binding domains of mouse telomere binding protein Pot1

Kaoru Kaneda (1), Hidetaka Torigoe (1) ((*1) Faculty of Science, Tokyo University of Science*)

1P-103 タンパク質・DNA 間相互作用の予測のための疎視化に関する研究

Study of coarse graining for prediction of interaction between protein and DNA

Shunsuke Mieda (1), Misako Aida (1) ((*1) Hiroshima University*)

1P-104 Rhodobacter sphaeroides 活性中心の Ab initio QM/MM による研究

Ab initio QM/MM study of photosynthesis reaction center of Rhodobacter sphaeroides

Kazuto Nakata (1), Yasushige Yonezawa (2), **Shusuke Yamanaka** (2), Toshikazu Takada (3), Haruki Nakamura (2) ((*1) NEC Corporation: (2) Protein Institute, Osaka University: (3) RIKEN Next-Generation Supercomputer R&D Center*)

1P-105 ウシ由来シトクロム酸化酵素のヘム *a* およびヘム a_3 の電子構造に関する理論的研究：その酸化および還元状態の解析

Computational analysis of electronic structures of hemes a / a_3 of the bovine cytochrome *c* oxidase in the reduced and oxidized states

Mauro Boero (1), **Jiyoung Kang** (1), Masaru Tateno (1) ((*1) University of Tsukuba*)

1P-106 軟Ｘ線発光分光法による水溶液中の酢酸の分子軌道対称性の直接観測

Direct observation of orbital symmetry of acetic acid in aqueous solution by soft x-ray emission spectroscopy

Yuka Horikawa (1), Takashi Tokushima (2), Atsunari Hiraya (3), Shik Shin (4) ((*1) RIKEN/SPring-8; Dep. of Physical Science, Hiroshima Univ.: (2) RIKEN/SPring-8: (3) Dep. of Physical Science, Hiroshima Univ.: (4) RIKEN/SPring-8; ISSP University of Tokyo*)

1P-107 電解質中の同符号マクロイオン間の実効相互作用

Effective Interaction between Like-Charged Macroions Immersed in Electrolyte Solution

Ryo Akiyama (1) ((*1) Dep. of Chem., Kyushu Univ*)

1P-108 トレハロースの水和構造と抗酸化作用に関する計算機シミュレーション

Computer Simulation on the Interactions between Trehalose and Diene in aqueous solution. Implication for the Antioxidant Function of Trehalose

Kota Sakakura (1), Minoru Sakurai (1) ((*1) Center for Biological Resources and Informatics Tokyo Institute of Technology*)

1P-109 ポリビニルスルホン酸およびそのアルカリ金属塩水溶液の水和特性

Hydration properties of Aqueous solutions of Poly (vinyl sulfonic acid) and its alkali metal salts

Norihiko Tanno (1), Takashi Miyazaki (1), Tetsuichi Wazawa (1), Makoto Suzuki (1) ((*1) Tohoku Univ. Grad.Sch.of Eng: (2) JST-CREST*)

1P-110 高分子電解質ハイドロゲルの膨潤に及ぼすハイパーモバイル水の効果

Effect of hyper-mobile water on the swelling of polyelectrolyte hydrogels

Ayumi Dohi (1), Takashi Miyazaki (2), Nobuyuki Morimoto (1), Makoto Suzuki (1) ((*1) Graduate School of Engineering, Tohoku University: (2) Industrial Technology Center of Wakayama prefecture*)

1P-111 ハイパーモバイル水を形成する高分子水溶液におけるプロトン拡散係数

Enhancement of Proton Diffusion Coefficients in Highly Charged Polymer (PAMPS) Aqueous Solutions

Tsubasa Ogawa (1), Takashi Miyazaki (1), Makoto Suzuki (1) ((*1) Graduate School of Engineering, Tohoku Univ: (2) JST-CREST*)

1P-112 リン酸中和反応のエントロピー変化に対する誘電水和解析および ATP 加水分解系への応用

Dielectric hydration analysis of the negative entropy change for the neutralization of sodium dihydrogenphosphate solutions and application for ATP hydrolysis system

George Mogami (1), Takashi Miyazaki (2), Makoto Suzuki (1) ((*1) Dept. of Materials Processing, Graduate School of Engineering, Tohoku University: (2) Industrial Technology Center of Wakayama Prefecture: (3) CREST, Japan Science and Technology Agency*)

1P-113 Brownian motor in muscle mechanics

Lorenzo Marcucci (1), Tetsuya Shimokawa (1), Mitsuhiro Iwaki (1), Toshio Yanagida (1) ((*1) Osaka University, Graduate school of Frontier Biosciences, Soft Biosystem Group*)

1P-114 アクチン－ミオシン硬直複合体の高分解能３次元像の獲得

Obtainment of high resolution 3D map of actin-myosin rigor complex

Yoshihiro Tsukada (1), Takeyuki Wakabayashi (2), Takuo Yasunaga (1) ((*1) Dept Bioscience and Bioinformatics, Computer Science and Systems Engineering, Kyushu Institute of Technology Graduate School: (2) Dept Biosciences, School of Schience and Engineering, Teikyo University*)

1P-115 アクチンフィラメントの滑り運動と形態の歪みの関係

Relationship between the sliding movement of actin filaments and their morphological distortions

Kouji Oota (1), Shigeru Sakurazawa (1) ((*1) Graduate School of Systems Information Science, Future University-Hakodate*)

1P-116 骨格筋活性化におけるトロポニン構造変化と細胞内カルシウム濃度の同時測定

Simultaneous measurements of the troponin structural change and the intracellular Ca^{2+} concentration during skeletal muscle activation

Tatsuhito Matsuo (1), Naoto Yagi (1) ((*1) SPring-8/JASRI: (2) Department of Engineering Science, Osaka University*)

1P-117 アクチンのヌクレオチド結合領域のゆらぎ

Conformational fluctuation in the nucleotide binding region of actin

Atsushi Ooi (1), Tsuyoshi Okagaki (1) ((*1) Graduate School of Bioresources, Mie University*)

1P-118 Cy3 蛍光標識されたアクチン繊維の運動の光感受性阻害

Photosensitive inhibition of motility of actin filaments covalently conjugated with Cy3 dyes

Kuniyuki Hatori (1), Syunsuke Matsushita (1), Hirotsugu Kimijima (1) ((*1) Department of Bio-System Engineering, Yamagata University*)

1P-119 デスミンはアクトミオシンの滑り運動に影響を与える

Desmin affects the sliding movement of actomyosins

Asami Matsuda (1), Kuniyuki Hatori (1) ((*1) Department of Bio-System engineering, Yamagata University*)

1P-120 格子間隔に依存した２状態モデルにおける筋肉の状態相図

1TA2-06 Lattice spacing-dependent two state model of striated muscle contraction: Phase diagram and dynamic behavior

Katsuhiko Sato (1), **Masako Ohtaki** (2), Yuta Shimamoto (3), Ishiwata Shin'Ichi (2) ((*1) Dept of Physics, Tohoku Univ.: (2) Dept of Physics, Faculty of Science & Engineering, Waseda Univ.: (3) Laboratory of Chemistry and Cell Biology, Rockefeller Univ.*)

1P-121 分子動力学による理論的研究：分子の揺らぎからわかる F1-ATPase のサブユニット協調性

Structural fluctuation and cooperativity in F_1-ATPase: a molecular dynamics study

Yuko Ito (1), Mitsunori Ikeguchi (1) ((*1) Graduate School of Nanobioscience, Yokohama City University*)

1P-122 ゼルニケ位相差法によるビブリオ菌べん毛フック基部体の低温電子線トモグラフィー

Zernike phase contrast cryo-electron tomography of *Vibrio* flagellar hook-basal body

Naoki Hosogi (1), Hideki Shigematsu (1), Hiroyuki Terashima (2), Michio Homma (2), Kuniaki Nagayama (1) ((*1) Laboratory of Nano-Structure Physiology, Okazaki Institute for Integrative Bioscience: (2) Graduate School of Science, Nagoya University*)

1P-123 回転分子モーター F_1－ATPase の触媒部位へ結合したヌクレオチドの高精度位置検出

High-Accuracy Localization of Single Nucleotides Bound to the Catalytic Sites in Rotary Motor F_1-ATPase

Kengo Adachi (1), Tomoko Masaike (1), Kazuhiro Oiwa (2), Takayuki Nishizaka (1) ((*1) Gakushuin Univ: (2) Kobe Adv ITC Res Ctr*)

1P-124 １分子破断力測定系の様々な分子モーターへの応用

Versatility of the unbinding force measurements at the single-molecule level adapted to different molecular motors

Sergey Mikhailenko (1), Yusuke Oguchi (2), Takashi Ohki (2), Adrian O. Olivares (3), Enrique M. De La Cruz (3), Shin'Ichi Ishiwata (2), Tomoko Masaike (1), Takayuki Nishizaka (1) ((*1) Department of Physics, Faculty of Science, Gakushuin University: (2) Department of Physics, Faculty of Science and Engineering, Waseda University: (3) Molecular Biophysics & Biochemistry Department, Yale University, USA*)

1P-125 １分子 FRET 計測による F_1－ATPase の β サブユニットの構造変化の検出

Conformational changes of the β subunits in F_1-ATPase revealed by single molecule FRET measurement

Mitsuhiro Sugawa (1), Masaru Kobayashi (1), Takayuki Nishizaka (1), Tomoko Masaike (1) ((*1) Gakushuin University*)

1P-126 バクテリアべん毛モーターの熱力学的コントロール

1YP1-05 Thermodynamic control of bacterial flagellar motors

Masayoshi Nishiyama (1), Yoshiyuki Sowa (2), Shigeichi Kumazaki (3), Yoshifumi Kimura (3), Michio Homma (4), Akihiko Ishijima (5), Masahide Terazima (3) ((*1) Kyoto Univ. & JST: (2) Hosei Univ.: (3) Kyoto Univ.: (4) Nagoya Univ.: (5) Tohoku Univ.*)

1P-127 フィラメント近傍で形成されるリニアーモータータンパク質のエントロピックポテンシャル場：単純化モデル計算 I

Entropic potential field formed for a linear-motor protein near a filament: Simple model calculation I.

Ken-Ichi Amano (1), Takashi Yoshidome (2), Masahiro Kinoshita (2) ((*1) Graduated School of Energy Science, Kyoto University: (2) Institute of Advanced Energy, Kyoto University*)

1P-128 細菌べん毛モーターの圧力依存性

Pressure dependence of the bacterial flagellar motors.

Manabu Hasumi (1), Yoshihumi Kimura (1), Masahide Terazima (1), Masayoshi Nishiyama (1) ((*1) Department of Chemistry, Graduate School of Science, Kyoto University*)

1P-129 KIF1A 分子モーターの一方向性の運動発現機構のシミュレーション研究

1TA4-02 Mechanism of unidirectional move of KIF1A motor studied by coarse-grained simulations

Ryo Kanada (1), Takeshi Kuwata (2), Kei-Ichi Okazaki (3), Hiroo Kenzaki (1), Shoji Takada (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University: (2) Graduate School of Science, Kobe University: (3) School of Advanced Science and Engineering, Waseda University*)

1P-130 高速 AFM によるクラミドモナス　ダイニンＣ破壊過程の観察

1TA4-05 The observation of disintegration processes of *Chlamydomonas* dynein-c by using high-speed AFM

Daisuke Yamamoto (1), Atsushi Miyagi (1), Toshio Ando (1), **Hitoshi Sakakibara** (2) ((*1) Physics, School of Science, Kanazawa University: (2) Biological ICT Group, National Institute of Information and Communications Technology*)

1P-131 ミオシンＶのカルシウム調節

Calcium regulation of myosin V

Yuri Koyama (1), Hiroshi Koide (1), Shin'Ichiro Tanaka (1), Saeko Omote (1), Toshio Ando (2) ((*1) Department of Mathematics and physics, Grad school of natural science and technology, Kanazawa univ,: (2) JST/CREST*)

1P-132 アクトミオシンⅡの高速 AFM 観察

Observation of actomyosin II dynamics by high-speed atomic force microscopy

Masayuki Imai (1), Toshio Ando (2) ((*1) Dept of Mathematics and Physics, Graduate School of Natural Science and Technology, Kanazawa Univ.: (2) School of Mathematics and Physics, College of Science and Engineering, Kanazawa Univ; CREST/JST*)

1P-133 軸糸外腕ダイニンの構造及び微小管と複合体を形成する際のメカニズム

Structure of flagellar outer dynein arm and the structural mechanism in formation of the outer dynein arm-microtubule complexes

Mingyue Jin (1), Hiroko Takazaki (1), Takuo Yasunaga (1) ((*1) Department of bioscience and bioinformatics, Kyushu institute of technology*)

1P-134 ATP 合成酵素の結晶化

Crystallization of ATPsynthase

Yasuo Shirakihara (1), Hiromi Tanikawa (1), Kazuaki Yoshimune (2), Satoshi Murakami (3), Toshiharu Suzuki (3), Masasuke Yoshida (3) ((*1) National Inst of Genetics: (2) National Inst of Adv. Industrial and Technology: (3) Tokyo Inst of Technology*)

1P-135 揺らぎの定理を用いたＦ$_1$－ATPase のトルク測定

1TA4-09 Torque measurements of F1-ATPase by using the fluctuation theorem

Kumiko Hayashi (1), Hiroshi Ueno (1), Ryota Iino (1), Hiroyuki Noji (1) ((*1) ISIR, Osaka Univ.*)

1P-136 カタユウレイボヤ軸糸外腕ダイニンの構造解析

Structural analysis of Outer Arm Dynein molecules purified from *Ciona intestinalis*

Jun Harano (1), Hironori Ueno (2), Katsutoshi Mizuno (3), Takuo Yasunaga (4), Kazuo Inaba (3), Keiko Hirose (1) ((*1) A.I.S.T / Univ. of Tsukuba: (2) Tohoku Univ.: (3) Univ. of Tsukuba: (4) Kyushu Institute of Technology*)

1P-137 DNA を鋳型としたモータータンパク質複合体の構築

DNA-templated assembly of multiple motor protein complexes

Ken'Ya Furuta (1), Yoko Toyoshima (2), Hiroaki Kojima (1) ((*1) NICT, Biological ICTG: (2) Dept Life Sciences, Graduate School of Arts and Sciences, Univ. of Tokyo*)

1P-138 ミオシンＶの頭部間協調性におけるレバーアームの役割

1TA4-06 Role of the lever arm in the subunit coordination in myosin V

Yusuke Oguchi (1), Sergey V. Mikhailenko (2), Takashi Ohki (1), Adrian O. Olivares (3), Enrique M. De La Cruz (4), Shin'Ichi Ishiwata (1) ((*1) Department of Physics, Faculty of Science and Engineering, Waseda University: (2) Department of Physics, Gakushuin University: (3) Department of Biology, Massachusetts Institute of Technology: (4) Department of Molecular Biophysics and Biochemistry, Yale University*)

1P-139 張力のかかったアクチンフィラメント上でのミオシンＶ一分子運動

1TA4-07 Single-molecule myosin V movement on a tense actin filament

Hiroaki Kubota (1), Yusuke Oguchi (2), Takashi Ohki (2), Shin'Ichi Ishiwata (2) ((*1) Major in Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda Univ.: (2) Dept. of Physics, Faculty of Advanced Science and Engineering, Waseda Univ.*)

1P-140 リバースジャイレースの反応速度の温度依存性

1TA4-08 Temperature Dependence of Positive Supercoiling by Reverse Gyrase

Taisaku Ogawa (1), Katsunori Yogo (2), Shou Furuike (3), Akihiko Kikuchi (4), Kazuhiko Kinosita (1) ((*1) Dept. of Phys., Grad. School of Science and Engineering, Waseda Univ.: (2) Dept. of Phys., Gakushuin Univ.: (3) Dept. of Phys., Osaka Med. Coll.: (4) Nagoya Univ.*)

1P-141 *Mycoplasma mobile* の滑走運動を阻害するモノクローナル抗体の標的部位

1TA4-04 Target sites of monoclonal antibody inhibiting *Mycoplasma mobile* gliding

Chie Kawaguchi (1), Shuhei Yoshii (1), Makoto Miyata (1) ((*1) Osaka City University*)

1P-142 滑走するバクテリア、*Mycoplasma mobile* のステップ検出

1TA4-03 Step detection of gliding bacterium, *Mycoplasma mobile*

Daisuke Nakane (1), Takayuki Nishizaka (2), Makoto Miyata (1) ((*1) Graduate School of Science, Osaka City University: (2) Faculty of Science, Gakushuin University*)

1P-143 F1-ATPase の温度高感受性待ち時間の一分子速度論解析

1TA4-10 Single molecule kinetic analysis of the temperature sensitive dwell of F1-ATPase

Tetsuaki Okamoto (1), Shouich Toyabe (1), Eiro Muneyuki (1) ((*1) Department of Physics, Faculty of Science and Engineering, Chuo University*)

1P-144 クラミドモナスを動力源としたマイクロ構造体の駆動

1TP4-01 Micro-objects driven by *Chlamydomonas*

Taishi Tonooka (1), Kaori Kuribayashi (1), Hiroaki Onoe (1), Masahiro Takinoue (1), Shoji Takeuchi (1) ((*1) Institute of Industrial Science, The University of Tokyo*)

1P-145 ネックリンカーによるキネシンの ATP 加水分解反応制御

1TP4-05 Role of the neck linker in controlling the ATP hydrolysis reaction of kinesin

Xiao Ling (1), Teppei Mori (1), Michiko Nakajima (1), Michio Tomishige (1) ((*1) Department of Applied Physics, school of engineering, the University of Tokyo*)

1P-146 キネシン１モータードメインのヌクレオチドフリー状態での結晶構造解析

1TP4-06 Crystal Structure of Nucleotide-free Kinesin-1 Motor Domain Explains Coordinated Walking Mechanism

Tsukasa Makino (1), Teppei Mori (1), Ken-Ichi Miyazono (2), Masaru Tanokura (2), Michio Tomishige (1) ((*1) Department of Applied Physics, University of Tokyo: (2) Department of Applied Biological Chemistry, University of Tokyo*)

1P-147 キネシンと細胞質ダイニンが混在する微小管上における各分子モーターの一分子運動解析

1TP4-03 Motility of single molecules of kinesin and cytoplasmic dynein in the presence of many molecules of motor proteins on microtubules

Keitaro Shibata (1), Ken'Ya Furuta (1), Masaki Edamatsu (1), Yoko Toyoshima (1) ((*1) Dept Life Sciences, Graduate School of Arts and Sciences, Univ. of Tokyo*)

1P-148 多分子ミオシンの協調的運動の解析

1TP4-04 Model analysis of cooperative behavior in multiple myosin system

Takeshi Nakagawa (1), Hiroto Tanaka (2), Kazuo Sasaki (1) ((*1) Dept. of Applied Physics, Tohoku Univ.: (2) KARC, NICT; PRESTO, JST*)

1P-149 シナプスの NMDA 受容体のリサイクル：エンドサイトシス／エクソサイトシスと膜内並進拡散との協働機構

Synaptic NMDA receptor recycling by the concerted actions of endocytosis/exocytosis and lateral diffusion in the plasma membrane

Chieko Nakada (1), Yuri Nemoto (2), Hiroko Hijikata (1), Hiroto Yoshida (2), Shigeo Okabe (3), Takahiro Fujiwara (1), Akihiro Kusumi (1) ((*1) ICORP-JST;Institute for Frontier Medical Sciences, Kyoto University-iCeMS: (2) Institute for Frontier Medical Sciences, Kyoto University-Institute for Integrated Cell-Material Sciences (iCeMS): (3) Graduate School of Medicine, University of Tokyo*)

1P-150 細胞の化学固定後にも残存するラフト分子の拡散運動：細胞膜上での拡散運動の１分子追跡による研究

Persisting diffusion of raft-associated molecules even after chemical fixation of the cell: a single-molecule tracking study

Kenji Tanaka (1), Manami Miyahara (2), Kenichi Suzuki (3), Miyako Yahara (1), Hisae Tsuboi (1), Koichiro Hirosawa (1), Takahiro Fujiwara (1), Akihiro Kusumi (1) ((*1) Membrane Mechanisms Project, ICORP-JST, Institute for Integrated Cell-Material Science (iCeMS), Institute for Frontier Medical Sciences, Kyoto University. : (2) Tottori University Medical School: (3) PRESTO-JST, Institute for Integrated Cell-Material Science (iCeMS), Kyoto University*)

1P-151 神経_免疫相互作用における接着分子 CADM1 の機能解析

Cell Adhesion Molecule 1 (CADM1) Works in Two Ways in Neuro-Immune Interaction

Tadahide Furuno (1), Keisuke Okamoto (2), Miho Sekimura (2), Akihiko Ito (3), Naohide Hirashima (2), Mamoru Nakanishi (1) ((*1) School of Pharmacy, Aichi Gakuin University: (2) Graduate School of Pharmaceutical Sciences, Nagoya City University: (3) Institute of Medical Science, The University of Tokyo*)

1P-152 アクチン調節タンパク質 zyxin のストレスファイバーへの張力依存的会合

Tension-dependent association of the actin-regulatory protein zyxin with stress fibers

Hiroaki Hirata (1), Hitoshi Tatsumi (2), Masahiro Sokabe (3) ((*1) Cell Mechanosensing Project, SORST, Japan Science and Technology Agency: (2) Dept. of Physiology, Graduate School of Medicine, Nagoya Univ.: (3) Cell Mechanosensing Project, SORST, Japan Science and Technology Agency; Dept. of Physiology, Graduate School of Medicine, Nagoya Univ.*)

1P-153 アクチンフィラメントの運動自由度の制限はコフィリンの結合頻度を低下させる

Restricted motion of actin filament reduces binding of cofilin to the filament

Kimihide Hayakawa (1), Yusuke Hunato (2), Hitoshi Tatsumi (2), Masahiro Sokabe (2) ((*1) Cell Mechnosensing Project, SORST, JST: (2) Dept. of Physiology, Nagoya University Graduate School of Medicine*)

1P-154 異なったキネティクスを持った経路が乳腺における ATP 放出に関わっている

Multi Pathways with Different Kinetics Contribute to ATP Releases in Mammary Epithelial Cells

Kishio Furuya (1), Kyoko Harada (1), Masahiro Sokabe (2) ((*1) JST, Cell Mechanosensing: (2) Graduate School of Medicine, Nagoya University*)

1P-155 細胞骨格に作用する力が細胞骨格の調節タンパクの結合性に与える影響の熱力学的検討

Thermodynamic investigation of modulation of binding affinity between cytoskeleton and its regulatory proteins in response to mechanical stresses

Yasuhiro Inoue (1), Taiji Adachi (1), Masaki Hojo (2) ((*1) Kyoto University; RIKEN: (2) Kyoto University*)

1P-156 移動性細胞におけるアクトミオシン相互作用の摂動に伴うアクチン構造ダイナミクスの変化

Perturbation of Actomyosin Interaction Modulates Actin Network Dynamics in Migrating Cells

Kennedy Omondi Okeyo (1), Taiji Adachi (2), Masaki Hojo (1) ((*1) Kyoto University: (2) Kyoto University; Computational Cell Biomechanics Team, VCAD System Research Program, RIKEN*)

1P-157 バクテリア模型のバイアストランダムウォーク

Biased random walk of a model bacterium

Seishi Kudo (1), Toshiki Sasaki (1), Takeshi Morishita (1) ((*1) Toin University of Yokohama*)

1P-158 細胞外基質から剥れた MDCK 細胞の凝集と細胞死

Cellular aggregation and death in MDCK cells detached from matrix.

Yumiko Emoto (1) ((*1) Kyushu University*)

1P-159 細胞のメカノタクシスを誘起する弾性勾配条件の決定とフラストレーション運動誘導への応用

Determination of the elasticity-gradient condition to induce cell mechanotaxis and its application for induction of the frustration movement

Takahito Kawano (1), Satoru Kidoaki (1) ((*1) Kyushu University, Institute for Materials Chemistry and Engineering*)

1P-160 非対称弾性勾配ゲルを用いた細胞運動の長距離整流化

Long-ranged rectification of cell movement on the asymmetric elastic-gradient gels

Hiroyuki Sakashita (1), Satoru Kidoaki (1) ((*1) Institute for Materials Chemistry and Engeening, Kyushu University*)

1P-161 異種間のバクテリアにおけるべん毛構成蛋白質 FliC/FliD 交換の影響

Exchanges of FliC/FliD between different species

Satoshi Inaba (1), Manami Hashimoto (1), Shin-Ichi Aizawa (1) (*(1) Prefectural Hiroshima of University*)

1P-162 *Paenibacillus alvei* のスウォーム運動におけるべん毛の役割について

The roles of flagella in swarming motility of *Paenibacillus alvei*

Kyouhei Miyauchi (1), **Yoshika Nosaka** (1), Masatoshi Fujihara (2), Ryou Harasawa (2), Shin-Ichi Aizawa (1) (*(1) Prefectural University of Hiroshima: (2) Iwate University*)

1P-163 FliK の機能と構造の関係について

The relation between function and structure of FliK

Shino Mizuno (1), Shin-Ichi Aizawa (1), Shin-Ichi Tate (2) (*(1) Prefectural University of Hiroshima: (2) Hiroshima University*)

1P-164 *Actinoplanes missouriensis* における胞子べん毛の構造解析

Structural analysis of spore flagella in *Actinoplanes missouriensis*

Kaoru Uchida (1), Moon Sun Jang (2), Azusa Fujita (2), Yasuo Ohnishi (2), Sueharu Horinouchi (2), Masayuki Hayakawa (3), Shin-Ichi Aizawa (1) (*(1) Prefectural University of Hiroshima: (2) University of Tokyo: (3) University of Yamanashi*)

1P-165 腸内細菌 *Selenomonas ruminantium* の側毛べん毛と運動性

Lateral flagelle of *Selenomonas ruminantium* and its roles in cell motility.

Shohei Haya (1), Takao Miyazaki (2), Naoki Abe (2), Shin-Ichi Aizawa (1) (*(1) Prefectural University of Hiroshima: (2) Tohoku University*)

1P-166 べん毛モーターの熱反応性

Thermal effects on the flagellar motor

Kazuya Monma (1), Manami Hashimoto (1), Nobuyuki Uchikoga (2), Shin-Ichi Aizawa (1) (*(1) Prefectural University of Hiroshima: (2) Japan Biological Informatics Consortium*)

1P-167 細菌の走化性精度を決定付けるものは何か？

What determines the accuracy of bacterial chemotaxis?

Toshinori Namba (1), Masatoshi Nishikawa (2), Tatsuo Shibata (3) (*(1) Hiroshima University: (2) Hiroshima University; JST, CREST: (3) Hiroshima University; JST, CREST; PREST, JST*)

1P-168 細胞性粘菌の仮足生成の統計解析

Statistical analysis of time series of psudopodia formation in Dictyostelium cells

Tatsuo Shibata (1), Naohiro Akuzawa (2), Satoshi Fujise (2), Akihiro Nagamatsu (2), Masatoshi Nishikawa (3) (*(1) Hiroshima University; PREST, JST; JST CREST: (2) Hiroshima University: (3) Hiroshima University; JST CREST*)

1P-169 lac オペロンの二重安定性における環境応答

Adaptive response to environmental changes utilizing the bistability of the lactose operon

Yoshihiro Shimizu (1), Bei-Wen Ying (1), Junya Ichinose (2), Yoichiro Ito (2), Tetsuya Yomo (3) (*(1) Grad. Sch. Information Sci. & Tech., Osaka Univ.: (2) ERATO, JST: (3) ERATO, JST; Grad. Sch. Information Sci. & Tech., Osaka Univ.; Grad. Sch. Frontier Biosci., Osaka Univ.*)

1P-170 クローディン－３を発現したＬ細胞に形成されたタイトジャンクション様構造の急速凍結レプリカおよび HAADF-STEM による観察

1TA5-04 Tight junction-like structures in L cells expressing claudin-3 protein observed by quick-freeze-replica and HAADF-STEM.

Kazunori Kawasaki (1), Tomoki Kato (1), Mikio Furuse (2) (*(1) National Institute of Advanced Industrial Science and Technology: (2) Kobe University Graduate School of Medicine*)

1P-171 分裂期の Hela 細胞への局所温度勾配の効果

1TA5-01 Effect of local temperature gradient on HeLa cells in mitotic phase

Masahiro Motoyoshi (1), Madoka Suzuki (2), Kotaro Oyama (1), Takeshi Itabashi (1), Shin'Ichi Ishiwata (1) (*(1) Department of Physics, Faculty of Science and Engineering, Waseda University: (2) COBRI, Comprehensive Research Organization, Waseda University*)

1P-172 分裂中期にある紡錘体形状の左右相称制御

1TA5-02 Bilateral regulation of spindle shape at metaphase

Kazuya Suzuki (1), Jun Takagi (1), Takeshi Itabashi (1), Shin'Ichi Ishiwata (1) (*(1) Depertment of Physics, Faculty of science and engineering, Waseda University*)

1P-173 線虫初期胚の細胞質流動の力学的基盤の解明のための、流速分布の測定と 3D シミュレーションによる再構築

1TA5-08 quantification and 3D simulation reconstruction of the cytoplasmic streaming in *C. elegans* embryo to elucidate its mechanical basis

Ritsuya Niwayama (1), Kyousuke Shinohara (2), Akatusuki Kimura (1) (*(1) SOKENDAI;National Instutute of Genetics, Center for Frontier Research, Cell Architecture Laboratory: (2) Osaka University, Graduate School of Frontier Biosciences, Developmental Genetics Group*)

1P-174 異なる接着強度の基質上における細胞の形・運動・力

1TA5-07 Cellular Shape, motion and forces on various adhesive surfaces

Hirokazu Tanimoto (1), Miki Matsuo (1), Masaki Sano (1) (*(1) Department of Physics, Graduate School of Science, the University of Tokyo*)

1P-175 異なる試料調製条件下におけるタンパク質内包リポソームの構造特性

Structural Characteristics of Liposome Occluding Proteins Under Different Preparation Conditions

Yoshihiko Hagiwara (1), Mitsuhiro Hirai (1) (*(1) Graduate School of Engineering, Gunma-University*)

1P-176 浸透圧下における糖脂質を含んだベシクル構造の pH 依存性について：広角Ｘ線散乱による研究

Wide-angle X-ray scattering study of pH dependence on the structure of the vesicle containing glycosphingolipid under osmotic pressure

Teruaki Onai (1), Mitsuhiro Hirai (1) (*(1) Dept. of Engineering, Gunma-Univ.*)

1P-177　アガロースゲルに埋め込まれた GUV のマイクロリアクター利用

Embedment of GUVs in agarose gels and their application as microreactors

Kanta Tsumoto (1), Masahiro Oohashi (1), Masahiro Tomita (1) ((*1) Mie University Graduate School of Engineering*)

1P-178　パターン化モデル生体膜における脂質二分子膜の側方収縮

Lateral contraction of phospholipid bilayers in micropatterned model membranes

Takashi Okazaki (1), Kenichi Morigaki (1) ((*1) AIST*)

1P-179　リン脂質／コレステロールの 3 成分系からなるベシクルにおけるドメイン構造の共焦点蛍光顕微鏡観察

Domain Formation in Ternary Vesicles of Phospholipids and Cholesterol by Observed Confocal Fluorescence Microscopy

Masahiro Hibino (1), Tsuyoshi Shimada (1) ((*1) Muroran Institute of Technology*)

1P-180　遠心沈降によるジャイアントベシクル融合

Fusion of Giant Vesicles Induced by Centrifugation

Mariko Matsunaga (1), Taro Toyota (1), Masanori Fujinami (1) ((*1) Department of Applied Chemistry and Biotechnology, Graduate School of Engineering, Chiba University*)

1P-181　遠心沈降法によりジャイアントベシクルに内包されたカタラーゼの振動反応

Oscillatory Reaction of Catalase Encapsulated in Giant Vesicles Prepared by W/O Emulsion Centrifugation Method

Taro Toyota (1), Takafumi Kikuchi (1), Masanori Fujinami (1) ((*1) Department of Applied Chemistry and Biotechnology, Graduate School of Engineering, Chiba University*)

1P-182　AFM 観察のための平坦化親水基板上での脂質膜の安定化

Lipid membrane stabilized on a flat hydrogel substrate for atomic force microscopy

Akihiko Takagi (1), Hitomi Hokonohara (2), Tomoij Kawai (2) ((*1) ISIR, Osaka Univ; Riken: (2) ISIR, Osaka University*)

1P-183　マイクロ流路を用いた一枚膜リポソームのサイズ制御方法の検討

Size control of uniamellar giantvesicle using microfluidics

Kazuya Nishimura (1), Taro Toyota (2), Hiroaki Suzuki (1), Tetsuya Yomo (1) ((*1) Graduate School of Information Science and Technology, Osaka University: (2) Graduate School of Engineering, Chiba University*)

1P-184　一枚膜巨大リポソーム内生化学反応の定量的評価

Quantitative evaluation of biochemical reactions encapsulated in giant unilamellar liposomes

Koji Nishimura (1), Takeshi Sunami (2), Hiroaki Suzuki (1), Tomoaki Matsuura (1), Tetsuya Yomo (3) ((*1) Osaka University: (2) ERATO, JST: (3) Osaka University;ERATO, JST*)

1P-185　コネキシン巨大プロテオリポソームの構築と機能

Preparation and function of connexin giant proteoliposomes

Koki Kamiya (1), Kanta Tsumoto (2), Tetsuro Yoshimura (2), Kazunari Akiyoshi (1) ((*1) Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University: (2) Graduate School of Engineering, Mie University*)

1P-186　抗菌ペプチド・マガイニン 2 が脂質膜中に形成するポアの大きさ

The Size of the Pore in Lipid Membranes Induced by Antimicrobial Peptide Magainin 2

Yukihiro Tamba (1), **Hirotaka Ariyama** (1), Victor Levadny (2), Masahito Yamazaki (1) ((*1) Shizuoka University, Integrated Bioscience: (2) Russian Academy of Science*)

1P-187　毒性タンパク質ライセニンが誘起する秩序液体相の脂質膜中のポア形成：単一 GUV 法による研究

Lysenin-Induced Pore Formation in Lipid Membranes in Liquid-Ordered Phase: the Single GUV Method Study

Yuko Saga (1), Toshihide Kobayashi (2), **Masahito Yamazaki** (3) ((*1) Shizuoka University: (2) Riken: (3) Shizuoka University*)

1P-188　抗菌ペプチドが誘起する脂質膜中のポア形成のメカニズムー理論的解析

Mechanism of Subcritical Pore Formation in Charged Lipid Vesicles Induced by Antimicrobial Peptides

Victor Levadny (1), Yukihiro Tamba (2), Masahito Yamazaki (2) ((*1) Shizuoka University, Russian Acadmy of Science: (2) Shizuoka University*)

1P-189　エタノールインジェクション法を利用したリポソーム融合

Liposome fusion induced by charged lipids incorporated in the preformed liposomes using the ethanol injection method

Takeshi Sunami (1), Filippo Caschera (2), Yuki Morita (3), Kazuya Nishimura (3), Taro Toyota (4), Martin Hanczyc (2), Tomoaki Matsuura (3), Hiroaki Suzuki (3), Tetsuya Yomo (5) ((*1) ERATO, JST: (2) University of Southern Denmark: (3) Osaka University: (4) Chiba University: (5) Osaka University; ERATO, JST*)

1P-190　高頻度に分裂するベシクル自己複製系の構築とマイクロチャンバーを用いたその形態変化ダイナミクス計測

Constructing highly self-reproducible giant vesicles and measurement of the morphological dynamics in microchambers

Takuya Tomita (1), Tadashi Sugawara (3), Yuichi Wakamoto (2) ((*1) Department of Basic Science, Graduate School of Arts and Sciences, The University of Tokyo : (2) Research Center for Complex Systems Biology, The University of Tokyo: (3) Department of Basic Science, Graduate School of Arts and Sciences, The University of Tokyo ;Research Center for Complex Systems Biology, The University of Tokyo*)

1P-191　KcsA チャネルの開閉に伴う構造変化

Rearrangements in the KcsA cytoplasmic domain underlie its gating

Minako Hirano (1), Yuko Takeuchi (1), Takaaki Aoki (1), Toshio Yanagida (1), Toru Ide (1) ((*1) Graduate School of Frontier Biosciences, Osaka University*)

1P-192　OmpF ポリンの陽イオン透過シミュレーション

Molecular dynamics simulation of cation permeation through OmpF porin

Yasuhiro Matsuura (1), Atsushi Suenaga (2), Tadashi Ando (1), Ichiro Yamato (1) ((*1) Department of Biological Science and Technology, Tokyo

University of Science: (2) High-performance Mol Simul Team, Comput Sys Biol Res Group, Adv Comput Sci Dept, RIKEN Adv Sci Inst)

1P-193 不活性化しない変異体である E71A を用いた KcsA カリウムチャネルの pH 依存性

pH-dependent gating of KcsA potassium channel examined by using an "inactivation-free" mutant, E71A.

Yuka Matsuki (1), Masayuki Iwamoto (1), Hirofumi Shimizu (1), Shigetoshi Oiki (1) (*(1) Department of Molecular Physiology and Biophysics, University of Fukui Faculty of Medical Sciences*)

1P-194 サブミリセカンド時間分解能での KcsA カリウムイオンチャネル開閉構造変化計測

Conformational Changes of Single-Molecular KcsA Potassium Channels during Gating Recorded in a Sub-Millisecond Time Resolution

Hirofumi Shimizu (1), Masayuki Iwamoto (1), Takashi Konno (1), Reo Sakakura (2), Yoshimitsu Aoki (2), Shigetoshi Oiki (1) (*(1) Department of Molecular Physiology and Biophysics, University of Fukui Faculty of Medical Sciences: (2) Department of Electronics and Electrical Engineering, Faculty of Science and Technology, Keio University*)

1P-195 T 細胞認識における PUFAs の影響

1TA3-08 Effects of disruption of lipid rafts by PUFAs on T cell recognition

Keiko Udaka (1), Satoshi Komaniwa (1), Arisa Yano (1), Toshihiro Komatsu (1), Akifumi Hagi (2) (*(1) Department of Immunology, Kochi Medical School: (2) Otsuka Pharmaceutical Factory, Inc.*)

1P-196 FPGA を用いた 1 分子生体シミュレーター

Single Molecule Bio-Simulator on FPGA

Michihiro Hori (1), Masahiro Ueda (1) (*(1) Osaka University*)

1P-197 細胞内 1 分子解析に基づいた走化性応答における受容体－G 蛋白質間相互作用のモデル

Two state model of G protein-coupled chemoattractant receptors for directional sensing in chemotaxis

Yukihiro Miyanaga (1), Michihiro Hori (1), Tatsuo Shibata (2), Mashahiro Ueda (1) (*(1) Graduate School of Frontier Biosciences, Osaka University,: (2) Department of mathematical and life science, Hiroshima university*)

1P-198 トロンボポエチンシグナルの初期段階は脂質ラフトによって制御されている

Initial thrombopoietin signaling is regulated by lipid rafts

Akihiko Sakamoto (1), Takashi Kato (2), Takashi Funatsu (3) (*(1) Graduate School of Pharmaceutical Sciences, The University of Tokyo; Center for Medical System Innovation, The University of Tokyo: (2) Faculty of Education and Integrated Arts and Sciences, Waseda University: (3) Graduate School of Pharmaceutical Sciences, The University of Tokyo; Center for NanoBio Integration, The University of Tokyo; CREST, Japan Science and Technology Agency*)

1P-199 コントラスト変調と異常分散を用いた膜蛋白質結晶中の脂質二重膜の可視化

1TA3-07 Visualization of lipid bilayer in the crystal of the membrane protein using x-ray contrast variation and anomalous scattering

Yoshiyuki Norimatsu (1), Junko Tsueda (1), Ayami Hirata (1), Shiho Iwasawa (1), Chikashi Toyoshima (1) (*(1) Institute of Molecular and Cellular Biosciences*)

1P-200 小脳核グルタミン酸作動性シナプスにおけるモノアミンを介した修飾作用

Monoaminergic cross-talk action at the mossy fiber-deep cerebellar nuclei synapses

Fumihito Saitow (1), Hidenori Suzuki (1) (*(1) Dept. Pharmacology, Nippon Medical School*)

1P-201 固体 NMR 分光法による SWAP-70 PH ドメインの脂質膜界面における構造転移および機能の解析

A solid state NMR study of the structure and function of the SWAP-70 PH domain induced at the membrane interface.

Naomi Tokuda (1), Hitoshi Yagisawa (1), Yasuhisa Fukui (2), Satoru Tuzi (1) (*(1) Grad. Schl. Life Sci., Univ. Hyogo.: (2) Hoshi. Univ.*)

1P-202 サリニバクターSRI シグナル伝達系を用いた、走光性大腸菌作成に向けた試み

Towards engineering of phototactic *Escherichia coli* by using sensory rhodopsin I and Che proteins from *Salinibacter ruber*

Daisuke Suzuki (1), Michio Homma (1), Yuki Sudo (1) (*(1) Division of Biological Science, Graduate School of Science, Nagoya University*)

1P-203 蛙坐骨神経の複合活動電位に及ぼすビスフェノールＡの抑制作用

Inhibitory action of bisphenol A on compound action potentials in frog sciatic nerves

Kotaro Mizuta (1), Tsugumi Fujita (1), Hiroki Yamagata (1), Eiichi Kumamoto (1) (*(1) Department of Physiology, Faculty of Medicine, Saga University*)

1P-204 ラット脊髄後角における TRPA1 チャネルの局所麻酔薬によるシナプス前性の活性化

Presynaptic activation by local anesthetics of TRPA1 channels in the rat spinal dorsal horn

Lian-Hua Piao (1), Tsugumi Fujita (1), Chang-Yu Jiang (1), Kotaro Mizuta (1), Hai-Yuan Yue (1), Masanari Inoue (1), **Eiichi Kumamoto** (1) (*(1) Dept. Physiol., Fac. Med., Saga Univ.*)

1P-205 フルボキサミンの光異性化の理論的研究

Theoretical study of photoisomerization of fluvoxamine

Kei Odai (1), Tohru Sugimoto (2), Etsuro Ito (3) (*(1) Dept. of informatics and Media Technology, Shohoku Coll., Japan: (2) Dept. of Humanities, Coll. of Engin., Kanto Gakuin Univ., Japan.: (3) Lab. of Functional Bio., Kagawa School of Pharmaceutical Sci., Tokushima Bunri Univ. Japan.*)

1P-206 モルモット盲腸筋層間神経叢培養グリア細胞の受容体、イオンチャネル及び膜電位に対する神経伝達物質の作用

Neurotransmitters act on receptors, ion channels, and membrane potentials in cultured glial cells from the myenteric plexus of the guinea-pig cecum

Kazuo Suzuki (1), Kazunori Ohta (1), Tomoharu Kimura (1), Syoichi Siga (1), Tomo Inoue (1), Daisuke Matsumoto (1), Mitsuyoshi Iwata (1), Masashi Sato (1), Katsuhiko Ikeda (1) (*(1) Department of Biomedical Engineering, Tokai University*)

1P-207 束ニューラルネットワークによる追加学習

Incremental learning by lattice neural networks

Daisuke Uragami (1), Hiroyuki Ohta (2) (*(1) Gakushuin University: (2) National Defense Medical College*)

1P-208 アオリイカが表出する模様の中の動的変化

Dynamic changes of chromatic pattern in squid, *Sepioteuthis lessoniana*

Mamiko Suzuki (1), Tetsuya Kimura (2), Hiroto Ogawa (3), Kohji Hotta (1), Kotaro Oka (1) ((*1) Graduate School of Science & Technology, Keio Univ.: (2) Lab. for Alzheimer's Disease, RIKEN BSI: (3) Graduate School of Science, Hokkaido Univ.*)

1P-209 光活性化 GFP を用いたシナプス分子の追跡

Tracking of synaptic proteins at synapse by photoactivatable GFP in hippocampal neurons

Kazuyuki Kiyosue (1), Kimihiko Kameyama (1) ((*1) National Institute of Advanced Industrial Science and Technology (AIST)*)

1P-210 図と地の認識とラティスによる表現

Figure and background recognition and expression with lattice theory

Yujin Kitamura (1), Pegio-Yukio Gunji (1) ((*1) Kobe University*)

1P-211 主観色認識と色再認における嗅覚刺激の影響性；嗅覚と色覚の異種感覚間連合

Olfactory effect in subjective colors and color recognition ; crossmodal association between odors and colors

Tomoaki Nakamura (1), Yukio Gunnji (1) ((*1) Graduate school of sciences of Kobe university*)

1P-212 機能的 MRI を用いたベンハムコマによる主観色生起の神経基盤の解明

Neural basis of subjective color perception during Benham's top illusion: a functional magnetic resonance imaging study

Hiroki Tanabe (1), Yusuke Morito (1), Tomoko Sakai (1), Norihiro Sadato (1) ((*1) National Institute for Physiological Sciences*)

1P-213 神経回路網における自律活動調整の分子機構

The molecular mechanism of the modulation of the spontaneous activity in a neuronal network

Ai Kiyohara (1), Takahisa Taguchi (2), Suguru Kudoh (3) ((*1) School of Science, Osaka University: (2) National Institute of Advanced Industrial Science and Technology (AIST): (3) Division of Human System Interaction, School of Science*)

1P-214 培養神経回路網の長期間発達過程における免疫蛍光染色像と電気活動

1TA3-04 Immunofluorescence imaging and electrical activity during long term development of cultured neuronal networks

Takumi Komatsu (1), Daisuke Ito (1), Naohiro Yamada (1), Hiroki Tamate (1), Kazutoshi Gohara (1) ((*1) Division of Applied Physics, Graduate School of Engineering, Hokkaido University*)

1P-215 固体 NMR によるバクテリオロドプシンの圧力によって誘起されるレチナール異性化機構の解析

Pressure induced retinal isomerization in bacteriorhodopsin as studied by solid-state NMR

Hirohide Nishikawa (1), Kana Tajima (1), Izuru Kawamura (1), Akimori Wada (2), Satoru Tuzi (3), Akira Naitou (1) ((*1) Graduate School of Engineering, Yokohama National University: (2) Kobe Pharmaceutical University: (3) Department of Life Science, University of Hyogo*)

1P-216 ^{13}C 固体 NMR によるバクテリオロドプシンの Tyr コンフォメーション変化の解析

Conformational changes at Tyr residues in Bacteriorhodopsin as studied by high-resolution ^{13}C solid state NMR

Izuru Kawamura (1), Moyako Horigome (1), Junko Tanabe (1), Masato Omine (1), Satoru Tuzi (2), Akira Naito (1) ((*1) Yokohama National University: (2) University of Hyogo*)

1P-217 固体 NMR による光受容タンパク質 *p*pR とその変異体 T204A の局所構造変化の解析

1TP2-01 Analysis of local protein conformations in photoreceptor *p*pR and its mutant T204A by solid-state NMR

Tetsurou Hidaka (1), Izuru Kawamura (1), Takudo Nishio (1), Kazuhiro Osawa (1), Naoki Kamo (2), Akira Naito (1) ((*1) Graduated School of Engineering, Yokohama National University: (2) College of Pharmaceutical Sciences, Matsuyama University*)

1P-218 固体 ^{13}C NMR による ppR の細胞質表面部位の相互作用変化の観測

Change of interaction in cytoplasmic surface region of ppR with pHtrII in the complex formation as studied by solid-state NMR

Takahiro Kondo (1), Izuru Kawamura (1), Takudo Nisio (1), Naoki Kamo (2), Akira Naito (1) ((*1) Graduate School of Engineering , Yokohama National University: (2) Graduate School of Pharmaceutical Sciences, Hokkaido University ; College of Pharmaceutical Sciences, Matsuyama University*)

1P-219 HAMP ドメインの分子動力学解析：電子スピン常磁性共鳴のデータを満足する 4 —helix bundle 構造

1TP2-02 Molecular dynamical analysis of a HAMP domain: A four-helix bundle structure satisfies the data of electron paramagnetic resonance

Koro Nishikata (1), Sotaro Fuchigami (2), Mitsunori Ikeguchi (2), Akinori Kidera (3) ((*1) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University: (2) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University: (3) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University; Research Program for Computational Science, RIKEN*)

1P-220 ロドプシンの構造を安定化する分子内相互作用

Intramolecular interaction of rhodopsin stabilizing the native structure

Yasushi Imamoto (1), Kazumi Sakai (1), Takahiro Yamashita (1), Yoshinori Shichida (1) ((*1) Kyoto University*)

1P-221 桿体・錐体視物質における活性中間体の pH 依存性の比較研究

1TP2-03 Comparative studies on the pH-dependency of the active intermediate between rod and cone visual pigments.

Keita Sato (1), Takahiro Yamashita (1), Yoshinori Shichida (1) ((*1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1P-222 青色光センサータンパク質 PixD の光誘起構造変化および分子間相互作用変化の研究

Study on light-induced conformational change and intermolecular interaction change of a blue light sensor protein PixD

Keisuke Tanaka (1), Yusuke Nakasone (2), Koji Okajima (3), Masahiko Ikeuchi (4), Satoru Tokutomi (5), Masahide Terazima (6) ((*1) Department of Chenistry, Graduate School of Science, Kyoto University: (2) Department of Chenistry, Graduate School of Science, Kyoto University: (3) Department of Life Sciences (Biology), Graduate School of Arts and Sciences, The University of Tokyo; Research Institute for Advanced Science and Technology, Department of Biological Science, Graduate School of Science, Osaka Prefecture University: (4) Department of Life Sciences (Biology), Graduate School of Arts and Sciences, The University of Tokyo: (5) Research Institute for Advanced Science and Technology, Department of Biological Science,*

Graduate School of Science, Osaka Prefecture University: (6) Department of Chenistry, Graduate School of Science, Kyoto University)

1P-223 対イオンの位置を変えたロドプシン変異体におけるレチナール発色団光異性化効率
1TP2-04 Photoisomerization efficiency of the retinal chromophore in rhodopsin mutants with displaced counterion

Kei Tsutsui (1), Yoshinori Shichida (1) (*(1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1P-224 代謝型グルタミン酸受容体のリガンド結合に伴う二量体配置転換の比較解析
1TP2-05 Comparative analyses of ligand-induced dimeric rearrangements of metabotropic glutamate receptors

Masataka Yanagawa (1), Takahiro Yamashita (1), Yoshinori Shichida (1) (*(1) Department of Biophysics, Graduate School of Science, Kyoto University*)

1P-225 パリエトプシンの分子機能の探索
1TP2-06 Exploring Molecular Functions of Parietopsin

Kazumi Sakai (1), Yasushi Imamoto (1), Takahiro Yamashita (1), King-Wai Yau (2), Chih-Ying Su (2), Yoshinori Shichida (1) (*(1) Department of Biophysics, Graduate School of Science, Kyoto University: (2) Department of Neuroscience, Johns Hopkins University School of Medicine*)

1P-226 高速原子間力顕微鏡（AFM）を用いたバクテリオロドプシンの光励起に伴う動態観察
1YP1-03 High-speed atomic force microscopy visualization reveals dynamic molecular processes in photo-activated bacteriorhodopsin

Mikihiro Shibata (1), Hayato Yamashita (1), Takayuki Uchihashi (2), Hideki Kandori (3), Toshio Ando (2) (*(1) Kanazawa University: (2) Kanazawa University;JST/CREST: (3) Nagoya Institute of Technology*)

1P-227 プロトンポンプを目指したバクテリアのセンサーロドプシンの変異体研究
1TP2-07 The mutation study to create proton pumps from a bacterial sensor rhodopsin

Akira Kawanabe (1), Jung Kwang-Hwan (2), Hideki Kandori (1) (*(1) Nagoya Institute of Technology: (2) Sogang University*)

1P-228 古細菌型ロドプシンのカーボンナノチューブへの内包
1TP2-08 Encapsulation of ion-pumping rhodopsins into multi-wall carbon nanotubes

Takayoshi Kawashima (1), Kazuhiro Yanagi (3), Zheng Liu (4), Yuji Furutani (5), Kazutomo Suenaga (4), Hiromichi Kataura (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Nanotechnology Research Institute (NRI), National Institute of Advanced Industrial Science and Technology (AIST): (3) Nanotechnology Research Institute (NRI), National Institute of Advanced Industrial Science and Technology (AIST);Department of Physics, Tokyo Metropolitan University: (4) Nanotube Research Center, National Institute of Advanced Industrial Science and Technology (AIST): (5) Department of Frontier Materials, Nagoya Institute of Technology;Institute for Molecular Science*)

1P-229 霊長類色覚視物質の赤外分光解析
1TP2-09 Low-temperature FTIR study of primate color pigments

Kota Katayama (1), Yuji Furutani (2), Hiroo Imai (3), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Life and Coordination-Complex Molecular Science, Institute for Molecular Science: (3) Primate Research Institute, Kyoto University*)

1P-230 光合成酸素発生反応における CP43-354 位グルタミン酸の FTIR による構造解析
FTIR study on the structure of CP43-E354 in the photosynthetic oxygen-evolving center

Hiroyuki Suzuki (1), Yuichiro Shimada (2), Tohru Tsuchiya (2), Tatsuya Tomo (2), Mamoru Mimuro (2), Takumi Noguchi (1) (*(1) Institute of Materials Science, University of Tsukuba: (2) Graduate School of Human and Environmental Studies, Kyoto University*)

1P-231 光化学系 II における除草剤の Q_B 結合部位への相互作用
Interactions of herbicides in the Q_B binding site in photosystem II: Analysis by Fourier transform infrared spectroscopy

Ryouta Takahashi (1), Takumi Noguchi (1) (*(1) Inst. of Mater. Sci., Univ. of Tsukuba*)

1P-232 QA 再構成と FTIR 解析による PSII における第一電子受容体 QA の分子間相互作用の解明
Molecular interaction of the primary quinone electron acceptor QA in photosystem II as studied by QA reconstitution and FTIR analysis

Yuta Kozue (1), Akira Takano (1), Ikuyo Sugimoto (2), Hiroyuki Suzuki (1), Miwa Sugiura (3), Yuichiro Takahashi (2), Takumi Noguchi (1) (*(1) Institute of Materials Science, University of Tsukuba: (2) The Graduate School of Natural Science and technology, Okayama University: (3) Cell-Free Science and Technology Research Center, Ehime University*)

1P-233 除草剤効果を使用した植物の光傷害メカニズムの解明
The mechanism of photodamage of phososystem II as revealed by herbicide effects and FTIR difference spectroscopy

Issei Idedan (1), Yuichi Shibuya (1), Takumi Noguchi (1) (*(1) Graguate School of Pure and Applied Sciences University of Tsukuba*)

1P-234 分光電気化学的手法により計測した光化学系 II フェオフィチン *a* の酸化還元電位
Redox potential of pheophytin *a* in photosystem II measured by spectroelectrochemistry

Yuki Kato (1), Miwa Sugiura (2), Tadashi Watanabe (1) (*(1) Institute of Industrial Science, the University of Tokyo: (2) Cell-Free Science and Technology Research Center, Ehime University*)

1P-235 統計的四面体ポテンシャルを用いたペプチド_タンパク質の高速ブラインドドッキング法の開発
Toward the fast blind docking of a peptide to a target protein by using a four-body statistical pseudo-potential

Takuyo Aita (1), Koichi Nisigaki (1), Yuzuru Husimi (1) (*(1) Saitama University*)

1P-236 MD シミュレーションとタンパク質のコンキャビティ形状比較を用いたバーチャルスクリーニング
Virtual screening to separate active ligands from decoys using MD simulation and concavity shape comparing

Chie Motono (1), Takatsugu Hirokawa (1) (*(1) Computational Biology Research Center, The National Institute of Advanced Industrial Science and Technology*)

1P-237 アミノ酸配列からのタンパク質揺らぎ領域予測とタンパク質間相互作用への適用
Prediction of protein motion from amino acid sequence and its application to protein-protein interaction

Shuichi Hirose (1), Kiyonobu Yokota (2), Hiroshi Wako (3), Shigeru Endo (4), Satoru Kanai (5), Tamotsu Noguchi (1) (*(1) AIST, CBRC; Research Institute of IT Biology/Faculty of Science and Engineering, Waseda University: (2) AIST, CBRC: (3) School of Social Sciences, Waseda University;*

Research Institute of IT Biology/Faculty of Science and Engineering, Waseda University: (4) Department of Physics, School of Science, Kitasato University: (5) PharmaDesign, Inc.)

1P-238 構造生物学と計算機科学に基づいたタイトジャンクションを制御する化合物の探索

Search for compounds that modulate tight-junction activity : structural biology and computational approaches.

Shogo Mase (1), Kaori Satomura (2), Natsuko Goda (1), Yukari Akiyoshi (3), Takeshi Tenno (4), Mikio Furuse (2), Hidekazu Hiroaki (4) (*(1) Graduate School of Medicine, Kobe University ; Institute for Bioinformatics Research and Development, Japan Science and Technology Agency (BIRD-JST): (2) Graduate School of Medicine, Kobe University ; Target Proteins Research Program (TPRP): (3) Graduate School of Medicine, Kobe University: (4) Graduate School of Medicine, Kobe University ; Institute for Bioinformatics Research and Development, Japan Science and Technology Agency (BIRD-JST) ; Target Proteins Research Program (TPRP)*)

1P-239 相互作用傾向値とホモログにおける既知相互作用部位の情報を用いたドメイン間相互作用部位予測

Prediction of domain-domain interaction sites from interface propensity and known interface positions of homologs

Masafumi Shionyu (1), Satoru Hirako (2), Hideaki Ishikawa (2) (*(1) Facalty of Bioscience, Nagahama Institute of Bio-Science and Technology: (2) Graduate School of Bioscience, Nagahama Institute of Bio-Science and Technology*)

1P-240 タンパク質間相互作用およびドメイン間相互作用ネットワークの構築と比較

Construction and comparison of PPI and DDI network

Akihiro Okuno (1), Kengo Kinoshita (2), Motonori Ota (3) (*(1) Graduate School of Biosci. & Biotech., Tokyo Institute of Technology: (2) Institute of Medical Science, University of Tokyo: (3) Graduate School of Information Science, Nagoya University*)

1P-241 ２種の栄養要求性大腸菌からなる人工相利共生系において観察される協力的な適応的表現型可塑性

Cooperative and adaptive phenotypic plasticity observed in a synthetic mutualism composed of two auxotrophs of *Escherichia coli*

Kazufumi Hosoda (1), Kotaro Mori (1), Akiko Kashiwagi (2), Shingo Suzuki (1), Tetsuya Yomo (1) (*(1) Osaka university: (2) Hirosaki university*)

1P-242 一細胞培養系を用いた中心珪藻の殻形態の表現型多様性の測定

Phenotypic plasticity of the cell morphology of the centric diatom (*Cyclotella meneghiniana*) by the on-chip single-cell cultivation system.

Yuka Shirokawa (1), Kenji Karino (2), Shigeki Mayama (2), Yuichi Wakamoto (3), Masakazu Shimada (4) (*(1) Department of Biological Sciences, the University of Tokyo: (2) Department of Biology, Tokyo Gakugei University: (3) Research Center for Complex Systems Biology, the University of Tokyo: (4) Department of Systems Sciences, the University of Tokyo*)

1P-243 圏論におけるゆるいカテゴリー同値をもちいた学習システムへの応用

Applying weak equivalence of categories between partial maps and pointed sets to the 2-arm bandit problem with changing conditions

Takayuki Niizato (1), Yukio Gunji (1) (*(1) Kobe University: (2) Kobe University*)

1P-244 真性粘菌変形体における形態発展パターンの自発的切り替え

Spontaneous switching of morphology development pattern in the plasmodium of *Physarum polycephalum*

Masaki Yamachiyo (1), Tomohiro Shirakawa (2), Yukio-Pegio Gunji (1) (*(1) Dept. of Earth and Planetary Sciences, Graduate School of Sciences, Kobe University: (2) Dept. of Computational Intelligence and Systems Science, Interdisciplinary Graduate School of Science and Engineering, Tokyo Institute of Technology*)

1P-245 二つの同値関係から構成される束と行動の論理（真性粘菌変形体の行動に関する束論的解析）

Analysis for the behavior of *Physarum* plasmodium using lattice

Iori Tani (1), Tomohiro Shirakawa (2), Yukio-Pegio Gunji (1) (*(1) Graduate School of Science, Department of Earth and Planetary Sciences, Kobe University: (2) Department of Computational Intelligence and Systems Science, Interdisplinary Graduate School of Science and Engineering, Tokyo Institute of Technology*)

1P-246 混雑した細胞内環境における分子機械システムの振舞い

Reaction-Diffusion Behavior of a Molecular Machinery in the Crowded Environment of the Cell

Yuichi Togashi (1) (*(1) Osaka University*)

1P-247 生体に学ぶゆらぎ制御について：時間遅れとノイズを含む倒立振子の安定性

Biologically inspired stochastic feedback control: the stochastic stability in an inverted pendulum system with delay and noise.

Michihito Takami (1), Tetsuya Shimokawa (1), Yuichi Togashi (1), Toshio Yanagida (1) (*(1) Osaka University Graduate School of Frontier Biosciences*)

1P-248 適応素子結合系モデルによる環境変化に対する多様な応答過程

Various response processes against the environmental change by coupled adaptive elements model

Masayo Inoue (1), Kunihiko Kaneko (1) (*(1) University of Tokyo*)

1P-249 細胞選別のドメイン成長過程の解析

Kinetics of domain growth in cell sorting process

Akihiko Nakajima (1), Shuji Ishihara (2) (*(1) Department of Basic Science, University of Tokyo: (2) Department of Basic Science, University of Tokyo; PRESTO, JST*)

1P-250 ESR 法を用いたシアノバクテリア時計タンパク質 KaiA － KaiC 相互作用の解析

ESR analysis of the interaction between cyanobacterial clock proteins KaiA and KaiC

Kentarou Isii (1), Reiko Murakami (2), Risa Mutou (2), Zyonatan Barensia Suwan (2), Masahiro Isiura (2), Tosiaki Arata (1) (*(1) Department of Biological Science, Graduate School of Science, Osaka university : (2) Center for Gene Research, Nagoya University*)

1P-251 BZ 反応の三次元模様への磁界の影響に関する基礎検討

Evaluation of the magnetic field influence on three-dimensional patterns of BZ reaction

Tadasuke Hamamura (1), Ayae Oda (1), Akira Yano (1), Satoka Aoyagi (1) (*(1) Faculty of Life and Environmental Science, Shimane University*)

1P-252 Briggs-Rauscher（BR）反応の半回分式反応器間における周期の振動現象

Evaluation of oscillation between the semi-batch reactors of Briggs-Rauscher reaction

Mituko Majima (1), Yuuki Sugihara (1), Satoka Aoyagi (1) (*(1) Faculty of Life and Environmental Science, Shimane University*)

1P-253 反応複製系のエネルギー論

Energetics of a reproducing protocell with chemical reaction process

Yohei Kondo (1), Kunihiko Kaneko (1) (*(1) The University of Tokyo*)

1P-254 フラクタル様マイクロ流路を用いた生化学反応計測システム

Fractal-shaped micro channel system for kinetic analysis of biochemical reaction

Katsuki Hirata (1), Tetsuo Ichii (2), Hiroaki Suzuki (1), Tomoaki Matsuura (1), Tetsuya Yomo (1) (*(1) Osaka university : (2) ERATO, JST*)

1P-255 蛍光偏光法を用いる新規 SNP 検出法の開発

Development of a Novel SNP Detection Method Using Fluorescence Polarization

Masafumi Shimizu (1), Hiromi Arai (1), Makoto Tsuruoka (1) (*(1) School of Bioscience and Biotechnology, Tokyo University of Technology*)

1P-256 → 3P-275 へ変更 定常流中の大腸菌速度の大腸菌サイズ依存性の理論的導出

The theoretical evaluation of the dependency of the velocity of *Escherichia coli* on their size in the stationary flow

Takeshi Miyakawa (1), Kitao Fujiwara (1), Kyouhei Takahashi (1), Ryota Morikawa (1), Masako Takasu (1) (*(1) Tokyo University of Pharmacy and Life Sciences*)

1P-257 原子間力顕微鏡によるβラクトグロブリン一抗βラクトグロブリン抗体に対する温度の影響の計測

Evaluation of temperature effect on interaction between beta-lactoglobulin and anti-beta-lactoglobulin antibody by AFM

Jun'Ichi Wakayama (1), Shigeru Sugiyama (1) (*(1) National Food Researh Institute, NARO*)

1P-258 リン脂質膜で囲まれたマイクロメートルスケールの空間に閉じ込められた長鎖 DNA 分子の高次構造変化

Conformational transition on a long DNA molecule confined in a micrometer-scale space surrounded by a phospholipid membrane

Ayako Kato (1), Takahiro Sakaue (2), Akihiko Tsuji (3), Kenichi Yoshikawa (4) (*(1) Grad. Sch. Pharm. Sci., Josai Univ: (2) Dept. Phys., Grad. Sch. Sci., Kyushu Univ: (3) Spatio-Temporal Order ICORP, JST: (4) Dept. Phys., Grad. Sch. Sci., Kyoto Univ;Spatio-Temporal Order ICORP, JST*)

1P-259 バクテリアー細胞レベルでの細胞内 ATP イメージング

Single cell imaging of ATP level inside bacteria

Keisuke Tomiyama (1), Masahiro Nakano (1), Hiromi Imamura (2), Hiroyuki Noji (1) (*(1) the institute scientific and industrial research, osaka university: (2) Japan Science and Technology Agency*)

1P-260 ナノ蛍光金クラスターの開発と生体 1 分子計測への応用

Preparation of Highly Fluorescent Au Nanoclusters and Application for Biomolecular Imaging

Shin-Ichi Tanaka (1), Dhermendra Tiwari (2), Takashi Jin (2), Yasushi Inouye (1) (*(1) Graduate school of Frontier Biosciences, Osaka University: (2) Immunology Frontier Research Center, Osaka University*)

1P-261 蛍光蛋白質を用いた張力感受性プローブの開発

Developments of the force sensitive fluorescent probe using fluorescent proteins.

Watanabe Tomonobu (1), Keiko Yoshizawa (1), Yanagida Toshio (1) (*(1) WPI, Immunology Frontier Research Center, Osaka University*)

1P-262 バイオロジカルシステムに最適化した三次元ナノスコピー

3D nanoscopy optimized for biological systems

Singo Fukui (1), Keiko Yosizawa (2), Tomonobu Watanabe (2), Tosio Yanagida (1) (*(1) Graduate School of Frontier Biosciences, Osaka University: (2) Immunology Frontier Research Center, Osaka University*)

1P-263 量子ドットを用いたベータアミロイドペプチド凝集のイメージング

Imaging of amyloid-beta peptide aggregation in vitro and in vivo by a quantum dot-based nanoprobe

Kiyotaka Tokuraku (1), Meg Marquardt (2), Tsuneya Ikezu (2) (*(1) Miyakonojo National College of Technology: (2) University of Nebraska Medical Center*)

1P-264 VSFG 検出赤外超解像顕微鏡を用いた生きた細胞の赤外イメージング

IR imaging of living cell by VSFG detected IR super-resolution microscopy

Satoshi Kogure (1), Keiichi Inoue (1), Katuya Kikuchi (1), Masaaki Fujii (1), Makoto Sakai (1) (*(1) Tokyo Institute of Technology*)

1P-265 振動和周波発生赤外超解像顕微鏡の開発と細胞への応用

Development of vibrational sum-frequency generation IR super-resolution microscope and its application to cells

Keiichi Inoue (1), Satoshi Kogure (1), Katsuya Kikuchi (1), Masaaki Fujii (1), Makoto Sakai (1) (*(1) Chemical Resources Laboratory, Tokyo Institute of Technology*)

1P-266 アストロサイトにおけるカルシウムシグナルの空間的制御機構の解明

Spatial Regulation of Calcium Signals in Astrocytes

Misa Arizono (1) (*(1) The Institute of Medical Science ,University of Tokyo*)

1P-267 神経成長因子による細胞内軸索輸送の促進機構

Augmentation of retrograde axonal transport velocity after the application of nerve growth factor

Mami Nomura (1), Takeharu Nagai (2), Tomomi Tani (2) (*(1) Graduate School of Fronteir Science, University of Tokyo, Dpt. Medical Genome Science: (2) RIES, University of Hokkaido*)

1P-268 新規ローダミン骨格に基づいた近赤外蛍光イメージングプローブの開発

Evolution of Group 14 Rhodamines as a Platform for Far-red to Near-infrared Emitting Fluorescence Probes

Yuichiro Koide (1), Yasuteru Urano (2), Tetsuo Nagano (1) (*(1) Graduate School of Pharmaceutical Sciences, The University of Tokyo, JST CREST: (2) Graduate School of Pharmaceutical Sciences, The University of Tokyo*)

1P-269 線形アンチセンスプローブを用いた生細胞の内在性 mRNA のリアルタイム追跡

Real time monitoring of endogenous mRNA in living cells using linear antisense probe

Kohki Okabe (1), Yoshie Harada (2), Takashi Funatsu (1) (*(1) Graduate School of Pharmaceutical Sciences, University of Tokyo: (2) Institute for Integrated Cell-Material Sciences, Kyoto University*)

1P-270 ストレス環境における生きた細胞の内在性 mRNA のリアルタイムイメージング

Real-time imaging of endogenous mRNAs in living cells during stress

Junwei Zhang (1), Kohki Okabe (1), Takashi Funatsu (1) (*(1) Laboratory of Bio-Analytical Chemistry, Graduate School of Pharmaceutical Sciences, University of Tokyo*)

1P-271 キネシン－カルモジュリン融合蛋白質を用いた分子シャトルの開発

Kinesin Calmodulin Fusion Protein as a Molecular Shuttle

Hideki Shishido (1), Kiyoshi Nakazato (1), Eisaku Katayama (2), Shigeru Chaen (3), Shinsaku Maruta (1) (*(1) Div. of Bioinfo., Grad. Sch. of Eng., Soka Univ.: (2) Div. of Biomolecular Imaging, Inst. of Med. Sci., Univ. of Tokyo.: (3) Dept. of Int. Sci. in Phys. and Biol., Coll. of Humanity and Sci., Nihon Univ.*)

1P-272 プログラム死する大腸菌の開発

The development of *E.coli* programmed death system

Kumiko Arata (1), Kazauhito Tabata (1), Hirohuki Noji (1) (*(1) Department of Biomolecular Energetics, The Institute of Scientific and Industrial Research, Osaka University*)

1P-273 編むことで構成された 3 次元マイクロハイドロゲル構造

Three-dimensional Hydrogel Microstructures Fabricated by Knitting

Hiroaki Onoe (1), Shoji Takeuchi (1) (*(1) Institute of Industrial Science, The University of Tokyo*)

1P-274 生物物理学のための細胞サイズ半透膜チャンバー

A cell-sized semipermeable chamber for biophysics

Masahiro Takinoue (1), Shoji Takeuchi (1) (*(1) Institute of Industrial Science, The University of Tokyo*)

1P-275 蛍光性 BODIPY ケージド化合物を用いた生体分子の時空間光制御

Spatial and temporal control of biomolecules by green light irradiation with use of fluorescent BODIPY-caged compounds

Nobuhiro Umeda (1), Yasuteru Urano (1), Tetsuo Nagano (1) (*(1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) CREST, JST: (3) JSPS*)

1P-276 Rc-PYP と相互作用タンパク質を用いた酵素活性の光制御系の作製

Light dependent enzyme activity control by use of interaction of the Rc-PYP

Harumasa Kubo (1), Yoichi Yamazaki (1), Hironari Kamikubo (1), Mikio Kataoka (1) (*(1) NARA INSTITUTE of SCIENCE and TECHNOLOGY*)

第 2 日目（10 月 31 日（土））/ Day 2 (Oct. 31, Sat.)

2P-001 電子線結晶構造解析による水チャネル AQP1 の高分解能構造解析

High-resolution structural analysis of a water channel, AQP1, by electron crystallography

Kaoru Mitsuoka (1), Hiroko Endou (1), Daisuke Kasuya (2), Nobuhiko Gyobu (2) (*(1) BIRC, AIST: (2) BIRC, JBIC*)

2P-002 Folding simulations of chignolin by self-learning multiscale method

2TP5-02 **Wenfei Li** (1), Shoji Takada (1) (*(1) Kyoto University, Department of Biophysics: (2) CREST, Japan Science and Technology Inc.*)

2P-003 アミロイドーシス原因タンパク質トランスサイレチンの中性子結晶構造解析に向けて

Towards the Neutron Crystallographic Analysis of Amyloid Protein, Transthyretin

Takeshi Yokoyama (1), Yuko Nabeshima (2), Mineyuki Mizuguchi (2), Ichiro Tanaka (1), Nobuo Niimura (1) (*(1) Frontier Research Center for Applied Atomic Sciences, University of Ibaraki, : (2) Graduate School of Medicine and Pharmacuetical Science, University of Toyama*)

2P-004 X 線小角散乱による DNA 相同組換えのメディエータである分裂酵母 Swi5 と Sfr1 の溶液構造解析

Solution structures of DNA recombination mediators Swi5 and Sfr1 in fission yeast studied by small-angle x-ray scattering

Yuichi Kokabu (1), Tomotaka Oroguchi (1), Yasuto Murayama (1), Naoyuki Kuwabara (1), Tsutomu Yamane (1), Hiroshi Hashimoto (1), Satoru Unzai (1), Toshiyuki Shimizu (1), Hiroshi Iwasaki (1), Mitsunori Ikeguchi (1) (*(1) Yokohama City University*)

2P-005 ニンジンレグインスリン結合タンパク質の結晶構造

Crystal structure of leginsulin binding protein from carrot

Takuya Yoshizawa (1), Hiroshi Hashimoto (1), Toshiyuki Shimizu (1), Satoru Unzai (1), Yuji Nishiuchi (2), Hisashi Hirano (1), Mamoru Sato (1) (*(1) Yokohama City University: (2) PEPTIDE INSTITUTE, INC.*)

2P-006 ヒト由来 REV7－REV3 複合体の X 線結晶構造解析

Crystal structure of human REV7 in complex with REV3 fragment

Kodai Hara (1), Toshiyuki Shimizu (1), Yoshiki Murakumo (2), Tomo Hanafusa (3), Haruo Ohmori (3), Mamoru Sato (1), Hiroshi Hashimoto (1) (*(1) Yokohama City University: (2) Nagoya University Graduate School of Medicine: (3) Institute for Virus research, Kyoto University*)

2P-007 130℃までの熱変性における牛血清アルブミンの構造に対するジェミニ型界面活性剤の保護効果

Protective Effect of Gemini Surfactant on Secondary Structural Change of Bovine Serum Albumin in Thermal Denaturation up to 130 ℃

Yoshiko Moriyama (1), Yuu Tanizaki (1), Hironori Harano (1), Kunio Takeda (1) (*(1) Okayama University of Science*)

2P-008 超好熱始原菌由来 Type III Rubisco の構造を基にした活性最適化

Structure-based optimization for catalytic activity of a Type III Rubisco from a hyperthermophile

Yuichi Nishitani (1), Masahiro Fujihashi (1), Takashi Doi (1), Shosuke Yoshida (2), Haruyuki Atomi (2), Tadayuki Imanaka (3), Kunio Miki (1) ((*1) Graduate School of Science, Kyoto Univ.: (2) Graduate School of Engineering, Kyoto Univ.: (3) College of Life Sciences, Ritsumeikan Univ.*)

2P-009 張力がアクチンフィラメントの力学特性に及ぼす影響

Effects of tensile force on mechanical properties of actin filament

Shinji Matsushita (1), Taiji Adachi (1), Yasuhiro Inoue (1), Masaki Hojo (2), Masahiro Sokabe (3) ((*1) Department of Mechanical Engineering and Science, Kyoto University; Computational Cell Biomechanics Team, RIKEN: (2) Department of Mechanical Engineering and Science, Kyoto University: (3) Department of Physiology, Nagoya University ; ICORP/SORST Cell Mechanosensing, JST*)

2P-010 高電位鉄イオウタンパク質(HiPIP)の０.５ Å 分解能における結晶構造解析

Crystal structure of a high-potential iron sulfur protein (HiPIP) at 0.5 Å resolution

Kazuki Takeda (1), Yu Hirano (1), Zheng-Yu Wang (2), Kunio Miki (1) ((*1) Kyoto University: (2) Ibaraki University*)

2P-011 サツマハオリムシ V2 巨大ヘモグロビン（分子量 40 万）の結晶構造

Crystal structure of a 400 kDa hemoglobin (V2Hb) from *Lamellibrachia satsuma*

Nobutaka Numoto (1), Taro Nakagawa (2), Yoshihiro Fukumori (3), Kunio Miki (4) ((*1) Department of Chemistry, Graduate School of Science, Kyoto University; School of Natural System, College of Science and Engineering, Kanazawa University: (2) School of Natural System, College of Science and Engineering, Kanazawa University; Research Center for Micro-Nano Technology, Hosei University: (3) School of Natural System, College of Science and Engineering, Kanazawa University: (4) Department of Chemistry, Graduate School of Science, Kyoto University*)

2P-012 DFT 計算を用いた Pseudomonas sp. B-0831.由来３α－HSD の補酵素 NAD/NADH の結合性に対する pH 依存性

DFT Studies on the pH dependency of coenzyme NAD/NADH binding to 3α-HSD from *Pseudomonas* sp. B-0831

Aki Kokami (1), Kazuya Iwata (1), Masayuki Oda (1), Masami Lintuluoto (1) *((1) Graduate School of life and environmental science, Kyoto prefectural university)*

2P-013 電子顕微鏡法・単粒子解析法によるアセチルコリン受容体の構造解析

Structure of acetylcholine receptor by electron cryo-microscopy and single particle analysis

Hiroaki Fukuchi (1), Yuri Nishino (2), Atsuo Miyazawa (2), Takuo Yasunaga (1) ((*1) Kyushu Institute of Technology: (2) RIKEN*)

2P-014 ３つのクラミドモナス外腕ダイニン重鎖の立体配置とその相互作用

Configurational Interactions of *Chlamydomonas* Three Outer Arm Dynein Heavy Chains

Hiroko Takazaki (1), Mingyue Jin (1), Takuo Yasunaga (1) ((*1) Kyushu Institute of Technology*)

2P-015 β2-Microglobulin フラグメントが形成するアミロイド線維の真空紫外 CD スペクトルの理論的解析

Theoretical Analysis of Vacuum-Ultraviolet CD spectrum of Amyloid Fibril Formed by β2-Microglobulin Fragment

Koichi Matsuo (1), Hirotsugu Hiramatsu (3), Kunihiko Gekko (4), Robert.W Woody (2) ((*1) Synchrotron Radiation Center, Hiroshima University; Biochemistry and Molecular Biology, Colorado State University, USA: (2) Biochemistry and Molecular Biology, Colorado State University, USA: (3) Okazaki Institute for Integrative Bioscience : (4) Graduate School of Science, Hiroshima University*)

2P-016 HMGB2 タンパク質に含まれる２つのドメインの溶液中における相対配向の決定

Preferential domain orientation of a full length HMGB2 protein determined by a novel NMR technique

Jun-Ichi Uewaki (1), Hiroshi Moriuchi (2), Naoko Tate (2), Shin-Ichi Tate (3) ((*1) Dept.Mathematical and Life Sciences, Hiroshima University: (2) Research Institute of Pharmaceutical Sciences Musashino University: (3) Dept.Mathematical and Life Sciences, Hiroshima University;PRESTO/JST*)

2P-017 CFTR チャネルの単粒子構造解析

2TP5-03 Three-dimensional reconstruction of human CFTR chloride channel

Kazuhiro Mio (1), Toshihiko Ogura (1), Muneyo Mio (1), Tzyh-Chang Hwang (2), Yoshiro Sohma (3), Chikara Sato (1) ((*1) National Institute of Advanced Industrial Science and Technology: (2) John M. Dalton Cardiovascular Research Center: (3) Keio University School of Medicine*)

2P-018 TEM と SEM によるタンパク質複合体の構造解析

2TP5-01 Structure analysis of membrane protein complexes using TEM and SEM

Chikara Sato (1), Kazuhiro Mio (1), Toshihiko Ogura (1), Yuusuke Maruyama (1), Hidetoshi Nishiyama (2), Mitsuo Suga (2) ((*1) National Institute of Advanced Industrial Science and Technology (AIST): (2) JEOL*)

2P-019 M－フィコリンのＣ反応性タンパク質結合部位

Binding site of C-reactive protein on M-ficolin

Michikazu Tanio (1), Toshiyuki Kohno (1) ((*1) Mitsubishi Kagaku Institute of Life Sciences (MITILS)*)

2P-020 複製開始制御因子 Sld2 のリン酸化による機能スイッチの構造学的研究

Structural study on molecular switching mechanism by phosphorylation of Sld2

Shogo Abe (1), Mariko Ariyoshi (1), Hidehito Tochio (1), Hiroyuki Araki (2), Masahiro Shirakawa (1) ((*1) Department of Engeneering, Kyoto university: (2) National Institute of Genetics*)

2P-021 好冷性酵素と中温性酵素における触媒活性の理論的研究

Theoretical study of catalytic activity in psychrophilic and mesophilic enzymes

Takahiro Kosugi (1), Shigehiko Hayashi (1) ((*1) Graduate School of Science, Kyoto University*)

2P-022 pH 一定 MD 法を用いた melittin の膜挿入過程の理論的研究

Membrane insertion of melittin using constant pH molecular dynamics

Akira Sai (1), Shigehiko Hayashi (1) ((*1) Department of Chemistry Graduate School of Science Kyoto University*)

2P-023　２種類の３α－hydroxysteroid　dehydrogenase のヌクレオチド補因子特異性の相違

Difference in nucleotide cofactor specificity between the two 3α-hydroxysteroid dehydrogenases

Yuichiro Takagi (1), Shigeru Ueda (2), Masayuki Oda (1) ((*1) Graduate School of Life and Environmental Sciences, Kyoto Prefectural Univ.: (2) Asahi Kasei Pharma Co.*)

2P-024　SH3 ドメイン欠損変異体を用いた Grb2 及び Gads と CD28 細胞質内ドメインとの分子間相互作用

Molecular interactions of CD28 cytoplasmic domains with Grb2 and Gads using their SH3-deficient mutants

Kuniomi Nakamura (1), Masayuki Oda (1), Hisayuki Morii (2), Ryo Abe (3) ((*1) Graduate School of Life and Environmental Sciences , Kyoto Prefectural University: (2) National Institute of Advanced Industrial Science and Technology: (3) Research Institute for Biological Sciences, Tokyo University of Science*)

2P-025　高速 AFM による GroEL-基質タンパク質複合体の直接観察

Direct observation of GroEL-substrate complexes by high-speed atomic force microscopy

Masaaki Taniguchi (1), Daisuke Yamamoto (2), Noriyuki Kodera (2), Toshio Ando (2) ((*1) School of Mathematics and Physics, College of Science and Engineering, Kanazawa University: (2) School of Mathematics and Physics, College of Scie nce and Engineering, Kanazawa University; CREST/JST*)

2P-026　分子機構における力学ネットワーク内に生じる揺らぎの伝達

Transduction of fluctuations along internal mechanical network in molecular machines

Daiki Kaita (1), Hiraku Nishimori (1), Akinori Awazu (1) ((*1) Hiroshima University science research course*)

2P-027　コンピュータシミュレーションによる HIV－１プロテアーゼの薬剤耐性度予測

Drug Susceptibility Estimation of HIV-1 Protease with Computational Methods

Hirotaka Ode (1), Masaru Yokoyama (1), Hironori Sato (1), Shiro Ibe (2), Seiishiro Fujisaki (2), Naoto Mamiya (2), Motohiro Hamaguti (2), Wataru Sugiura (2), Yoshiyuki Yokomaku (2) ((*1) National Institute of Infectious Diseases, Pathogen Genomics Center: (2) National Hospital Organization Nagoya Medical Center*)

2P-028　サルモネラ菌べん毛ロッドキャップ蛋白質 FlgJ の結晶構造と変異体解析

Structure-based mutational analyses of FlgJ, a putative flagellar rod cap protein from *Salmonella*

Yuki Kikuchi (1), Hideyuki Matsunami (2), Midori Yamane (3), Katsumi Imada (1), Keiichi Namba (1) ((*1) Grad. Sch. of Front. Biosci., Osaka Univ. ; Dynamic NanoMachine Project, ICORP, JST: (2) Grad. Sch. of Front. Biosci., Osaka Univ. ; Okinawa Inst. Sci. Tech.: (3) Grad. Sch. of Front. Biosci., Osaka Univ.*)

2P-029　FliI と FliJ の構造より明らかとなったべん毛輸送装置と F1-ATPase における共通の構造

Common architecture between the flagellar export apparatus and F_1-ATPase revealed by the structure of FliI and FliJ.

Tatsuya Ibuki (1), Tohru Minamino (3), Tomoko Miyata (1), Takayuki Kato (1), Keiichi Namba (2), Katumi Imada (2) ((*1) Grad. Sch. of Frontier Biosci., Osaka Univ. : (2) Grad. Sch. of Frontier Biosci., Osaka Univ;Dynamic NanoMachine Project, ICORP, JST: (3) Grad. Sch. of Frontier Biosci., Osaka Univ;Dynamic NanoMachine Project, ICORP, JST;PRESTO, JST*)

2P-030　藍色細菌 *T. elongatus* の時計蛋白質 KaiB における機能と動的構造との相関の解析

Analysis of the correlation between the function and structural dynamics on the clock protein KaiB from a cyanobacterium *T. elongatus*

Hiroaki Tanaka (1), Masahiro Ishiura (2), Takahisa Ikegami (1) ((*1) Institute for Protein Research, Osaka University: (2) The Center for Gene Research, Nagoya University*)

2P-031　分子動力学/結合自由エネルギー計算によるヒト血清アルブミン－warfarin 結合に及ぼす脂肪酸の影響解析

Analysis of the effect of fatty acids on HSA-warfarin binding using molecular dymamics/binding free energy calculations

Shin-Ichi Fujiwara (1), Takashi Amisaki (1) ((*1) Department of Biological Regulation, Faculty of Medicine, Tottori University*)

2P-032　基準振動に基づく蛋白質 - 蛋白質相互作用の動的特徴の解析

Analysis of dynamic characteristics of protein-protein interactions derived from normal modes

Yuko Tsuchiya (1), Shigeru Endo (2), Hiroshi Wako (3), Kengo Kinoshita (1) ((*1) Inst. of Med. Sci., Univ. of Tokyo: (2) School of Sci., Kitasato Univ.: (3) School of Social Sci., Wasada Univ.*)

2P-033　タンパク質立体構造上でのリガンド構造アセンブルによるリガンド結合部位の予測

Ligand fragment assembly to predict ligand binding sites on protein three-dimensional structures.

Kota Kasahara (1), Kengo Kinoshita (2), Toshihisa Takagi (3) ((*1) The University of Tokyo, Graduate School of Frontier Sciences.: (2) Institute of Medicinal Science, The University of Tokyo: (3) Database Center for Life Science;Graduate School of Frontier Sciences, The University of Tokyo;National Institute of Genetics*)

2P-034　分子動力学法を用いた酸化型アズリン_還元型シトクロム c_{551} 複合体の熱力学的安定性

Molecular dynamics study on thermodynamical stability of Oxidized Azurin – Reduced Cytochromec_{551} complex

Keisuke Matsumoto (1), Riki Nakamura (1), Taku Mizukami (2), Hiroaki Saitou (1), Masaru Tateno (3), Kiyoshi Nishikawa (1), Hidemi Nagao (1) ((*1) Faculty of Mathematics and Physics, Institute of Science and Engineering, Kanazawa University: (2) School of Materials Science, Japan Advanced Institute Science and Technology: (3) Graduate School of Pure and Applied Sciences University of Tsukuba*)

2P-035　GFP 融合蛋白質 GFP-GST のナノ秒回転ダイナミクス

Nano-second rotational dynamics of GFP-fused protein, GFP-GST

Eishirou Suzui (1), Yuuki Mizoe (1), Etsuko Nishimoto (1), Shoji Yamashita (1) ((*1) Faculty of Agriculture, Graduate School of Kyushu University*)

2P-036　ニガウリトリプシンインヒビターにおける Trp-Trp 間エネルギー移動

Tryptophan-tryptophan energy transfer in bitter gourd trypsin inhibitor

Hironori Soejima (1), Shuzo Matsumoto (1), Etsuko Nishimoto (1), Shoji Yamashita (1) ((*1) Faculty of Agriculture, Graduate school of Kyushu University*)

2P-037　ペプチド系の多変数シミュレーティッド・テンパリングレプリカ交換シミュレーション

Multi-dimensional simulated-tempering replica-exchange simulations of a peptide

Ayori Mitsutake (1) ((*1) Keio University*)

2P-038 β２ミクログロブリンが形成するアミロイド線維の溶液 NMR による直接観察

Direct Observation of β_2-microglubulin amyloid fibrils using solution NMR

Yuichi Yoshimura (1), Kazumasa Sakurai (1), Eri Chatani (2), Young-Ho Lee (1), Takahisa Ikegami (1), Atsushi Kameda (1), Hironobu Naiki (3), Yuji Goto (1) ((*1) Inst. Prot. Res., Osaka Univ.: (2) Fac. Pharm. Sci., Ritsumeikan Univ.: (3) Fac. Med. Sci., Univ. of Fukui*)

2P-039 粗視化モデルを用いた全原子シミュレーションの効率化

Sampling enhancement for all-atom simulation using coarse-grained model

Hiromitsu Shimoyama (1), Yasushige Yonezawa (1), Haruki Nakamura (1) ((*1) Institute for Protein Research, Osaka University*)

2P-040 カーボンナノチューブと蛋白質の MD シミュレーション

MD simulation of carbon nanotube and protein

Tomoshi Kameda (1) ((*1) CBRC AIST*)

2P-041 フォールディングのキネティクスにおけるアミノ酸残基の役割_格子タンパク質に統計力学モデルを適用して_

Roles of individual amino acid residues in folding/unfolding kinetics of lattice proteins studied with a simple statistical mechanical model

Haruo Abe (1), Hiroshi Wako (2) ((*1) Nishinippon Institute of Technology : (2) Waseda University*)

2P-042 スモールヒートショックプロテイン StHsp14.0 の変性蛋白質鎖保護機構

Aggregation inhibition mechanism of Small heat shock protein, StHsp14.0

Toshihiko Oka (1), Tetsuya Abe (2), Atsushi Nkagome (2), Msafumi Yohda (2) ((*1) Department of Physics, Faculty of Science, Shizuoka University: (2) Department of Biotechnology and Life Science, Tokyo University of Agriculture & Technology*)

2P-043 Stopped-Flow 法によるウマβラクログロブリンのフォールディング反応解析

A stopped-flow analysis of beta-lactoglobulin folding

Toshiaki Miyajima (1), Seiichi Tsukamoto (1), Kanako Nakagawa (1), Kazuo Fujiwara (1), Masamichi Ikeguchi (1) ((*1) Department of Bioinformatics, Soka University*)

2P-044 β－lactoglobulin の二量体形成のためのキー配列

Key residues for β-lactoglobulin dimerization

Hideaki Ohtomo (1), Kanako Nakagawa (1), Kazuo Fujiwara (1), Masamichi Ikeguchi (1) ((*1) Department of Bioinformatics, soka university.*)

2P-045 異種核 NMR を用いたウマβ－ラクトグロブリンフォールディングコアの構造解析

Structural analysis of equine β-lactoglobulin folding core using heteronuclear NMR

Mio Yamamoto (1), Kanako Nakagawa (1), Kazuo Fujiwara (1), Masamichi Ikeguchi (1) ((*1) Department of Bioinformatics, Soka University*)

2P-046 水素/重水素交換法によるβ－ラクトグロブリンの構造揺らぎの解析

CONFORMATIONAL FLUCTUATION OF β-LACTOGLOBULIN MONITORED BY HYDROGEN EXCHANGE

Masatoshi Ito (1), Yoshiteru Yamada (2), Kanako Nakagawa (1), Kazuo Fujiwara (1), Masamichi Ikeguchi (1) ((*1) Department of Bioinformatics, Soka University: (2) SPring8*)

2P-047 基準振動解析データベース PDBη および ProMode－oligomer の開発

Development of normal mode analysis databases PDBη and *P*roMode-oligomer

Hiroshi Wako (1), Shigeru Endo (2) ((*1) School of Social Sciences, Waseda University: (2) Kitasato University*)

2P-048 重水素交換法を用いたアミロイド線維伸長機構の解析

Analysis of the mechanism of the amyloid fiber extension using H/D exchange

Kotaro Yanagi (1), Kazumasa Sakurai (1), Young-Ho Lee (1), Takahisa Ikegami (1), Hironobu Naiki (2), Yuji Goto (1) ((*1) Institute for Protein Research, Osaka University: (2) Faculty of Medical Sciences, Fukui University: (3) CREST/JST*)

2P-049 天然変性蛋白質 pKID と KIX ドメイン複合体形成における結合と折り畳みが共役した相互作用の計算科学による解析

Computational approach to the coupled folding and binding in the interaction between pKID and the KIX domain

Koji Umezawa (1), Jinzen Ikebe (1), Haruki Nakamura (2), Junichi Higo (3) ((*1) Graduate School of Frontier Biosciences, Osaka University.: (2) Institute for Protein Research, Osaka University.: (3) The Center for Advanced Medical Engineering and Informatics, Osaka University.*)

2P-050 一分子測定法による乳性蛋白質β－ラクトグロブリンの折り畳み過程の観測

Single molecule observation of the folding of bovine β-lactoglobulin

Takayuki Kadota (1), Kiyoto Kamagata (2), Hiroyuki Oikawa (2), Kazumasa Sakurai (1), Yuji Goto (1), Satoshi Takahashi (2) ((*1) Institute for Protein Research, Osaka University: (2) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*)

2P-051 GM1 ガングリオシドクラスターを介したアミロイドβタンパク質の凝集機構

Mechanism of amyloid β-protein aggregation mediated by GM1 ganglioside cluster

Keisuke Ikeda (1), Masaru Hoshino (2), Katsumi Matsuzaki (2) ((*1) institute for protein research, Osaka university: (2) graduate school of pharmaceutical sciences, Kyoto university*)

2P-052 SDSL-ESR を用いたアミロイド線維構造に関する研究

Site directed spin labeling - electron spin resonance analysis of the structure of amyloid fibrils

Masatomo So (1), Hisashi Yagi (1), Kazumasa Sakurai (1), Hironobu Naiki (2), Toshiaki Arata (3), Yuji Goto (1) ((*1) Institute for Protein Research, Osaka University: (2) Faculty of Medical Science, University of Fukui: (3) Graduate School of Science, Osaka University*)

2P-053 設計したジスルフィド結合が低温ショック蛋白質の安定性や一本鎖 DNA との分子間相互作用に及ぼす影響

Effect of a designed disulfide bond on the stability of cold shock protein and its molecular interaction with single-stranded DNA molecules single-stranded DNA molecules

Naoto Hirose (1), Aoi Hasegawa (1), Shun-Ichi Kidokoro (1) ((*1) Dept. of Bioengineering, Nagaoka Univ. of Technol.*)

2P-054 GroES の変性状態におけるコンフォメーション変化とダイナミクスの特性

Characteristics of conformational changes and dynamics in unfolded state of GroES

Hisanori Iwasa (1), Shunsuke Meshitsuka (2), Kunihiro Hongo (3), Tomohiro Mizobata (3), Yasushi Kawata (3) ((*1) Dept. of Chem. and Biotech., Grad. Sch. of Eng., Tottori Univ.: (2) Dept. of Biomed. Sci., Grad. Sch. of Med. Sci., Tottori Univ.: (3) Dept. of Chem. and Biotech., Grad. Sch. of Eng., Tottori Univ.; Dept. of Biomed. Sci., Grad. Sch. of Med. Sci., Tottori Univ.*)

2P-055 水のエントロピーに焦点を置いたタンパク質－リガンド間結合能の新規計算手法

New computational method for protein-ligand binding affinities focused on water entropy

Shuntaro Chiba (1), Junma Nomura (1), Yuichi Harano (2), Masahiro Kinoshita (3), Minoru Sakurai (1) ((*1) Center for Biological Resources and Infomatics, Tokyo Inst. Tech.: (2) Department of Biological Science, Graduate School of Science, Osaka univ.: (3) Institute of Advanced Energy, Kyoto Univ.*)

2P-056 タンパク質 2 量体形成と空間サイズ効果: 粒子モデルとの比較

Confinement effect on protein dimerization: Explicit chain and particle approximation

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2P-057 GroEL/ES をフォールディングに必要とするタンパク質群の同定から見えた特徴

Identification of the absolutely GroEL/ES-dependent substrates and their properties

Kei Fujiwara (1), Hideki Taguchi (1) ((*1) Graduate School of Frontier sciences, The University of Tokyo*)

2P-058 ヒト主要組織適合複合体の安定性が細胞障害性Ｔ細胞活性に及ぼす影響

The impact of the stability of Human Leukocyte Antigen (HLA) on the activity of Cytotoxic T Lymphocyte (CTL)

Saeko Yanaka (1), Chihiro Motozono (2), Motonori Kudou (1), Takamasa Ueno (2), Kouhei Tsumoto (1) ((*1) the Graduate School of Frontier Sciences Medical Genome Sciences: (2) Division of Viral Immunology Center for AIDS Research Kumamoto University*)

2P-059 P450 の QM／MM シミュレーション

QM/MM Simulation of P450

Jiro Shimada (1), Hiroaki Fukunishi (1), Ken'Ichi Kamijo (1) ((*1) NEC Nanoelectronics Research Laboratories*)

2P-060 相補的高分子電解質を用いた酵素活性制御

Regulation of enzymatic activity using complementary polyelectrolyte pair

Shunsuke Tomita (1), Len Ito (2), Hiroshi Yamaguchi (3), Gen-Ichi Konishi (4), Yukio Nagasaki (1), Kentaro Shiraki (1) ((*1) Graduate School of Pure and Applied Sciences, University of Tsukuba: (2) Japan Synchrotron Radiation Research Institute: (3) School of Science and Technology, Kwansei Gakuin University: (4) Graduate School of Science & Engineering, Tokyo Institute of Technology*)

2P-061 GatCAB におけるアンモニア輸送機構の計算科学的解析

Novel channel of glutamine amidotransferase CAB for ammonia transport revealed by molecular dynamics simulations

Shigehide Kuroyanagi (1), Yohsuke Hagiwara (1), Masaru Tateno (2) ((*1) University of Tsukuba: (2) University of Tsukuba: (3) University of Tsukuba*)

2P-062 好熱好酸性古細菌 *Themoplasma acidophilum* 由来グリセロール－1-リン酸デヒドロゲナーゼの発現、精製と解析

Recombinant expression, purification and characterization of G-1-P dehydrogenase from *Thermoplasma acidophilum*

Chihiro Tokunaga (1), Ken Tokuda (1), Satoshi Akanuma (1), Akihiko Yamagishi (1) ((*1) Dept. of Mol. Biol., Tokyo Univ. of Pharm. Life Sci.*)

2P-063 表面力測定によるホスホリレーシグナル伝達系に関与するタンパク質間相互作用の研究

Study of phosphorelay protein interactions by surface force measurement

Motoi Konishi (1), Shin Takaya (1), Miya Kamihira-Ishijima (1), Masaya Fujita (2), **Kazue Kurihara** (1) ((*1) IMRAM, Tohoku Univ.: (2) University of Houston*)

2P-064 タンパク質平衡揺らぎの独立成分分析

2TA5-01 Independent Component Analysis of Equilibrium Fluctuations in Proteins

Yusuke Naritomi (1), Sotaro Fuchigami (1), Mitsunori Ikeguchi (1), Akinori Kidera (2) ((*1) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University: (2) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University;Research Program for Computational Science, RIKEN*)

2P-065 ベイズ法によるタンパク質の内部構造の推定

2TA5-02 Uncovering the hidden structure of the protein using Bayesian inference

Makito Miyazaki (1), Takahiro Harada (2) ((*1) Department of Physics, Graduate School of Science, Kyoto University: (2) Department of Physics, Graduate School of Science, The University of Tokyo*)

2P-066 画像処理ソフトウェア Eos:GPU コンピューティングの導入と普及版立体視システムへの対応

Development of Eos: efficient 3D reconstruction of biomolecules from electron micrographs by enabling GPU computing and use of stereoscopic devices

Ryuzo Azuma (1), Mingyue Jim (1), Hiroko Takazaki (1), Akito Tominaga (1), Hiroaki Fukuchi (1), Koki Ohta (1), Keita Shirakawa (1), Yoshihiro Tsukada (1), Seiya Tsurusaki (1), Junnichi Yoshitake (1), Takuo Yasunaga (1) ((*1) Kyushu Institute of Technology*)

2P-067 少数の傾斜画像による 3 次元像構築と構造分類によるタンパク質ポリモルフィズムの解析

Protein polymorphism detection using subtomographic maps and structural classification.

Kouki Ohta (1), Takuo Yasunaga (1) ((*1) Kyusyu Institute of Technology*)

2P-068 電子顕微鏡を用いたトモグラフィー画像解析システムの検証

Tests of the tomography system using a transmission electron microscope

Seiya Tsurusaki (1) ((*1) Kyushu Institute of Technology*)

2P-069 ランダムコニカルティルト法によるタンパク質構造解析ツールの検証

Semiautomated analysis of protein structure by the random conical tilting method

Junichi Yoshitake (1), Kenji Iwasaki (2), Takuo Yasunaga (1) ((*1) Kyushu Institute of Technology: (2) Institute for Protein Research, Osaka University*)

2P-070 低温電子顕微鏡法における生体超分子複合体に対する電子線照射損傷の定量的評価

2TA5-03 Electron dose effect on 3D image reconstruction of a biological macromolecular structure by electron cryomicroscopy

Masamichi Ashihara (1), Takayuki Kato (1), Takashi Fujii (1), Hideyuki Matsunami (2), Tomoko Miyata (1), Kenji Iwasaki (3), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Okinawa Institute of Science and Technology: (3) Institute for Protein Research, Osaka University*)

2P-071 Surface enhanced resonance raman scattering of HbA and HbA1c: Implications for diabetic diagnosis

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2P-072 チトクロム酸化酵素の構造に基づく酸素の一段階４電子還元機構とプロトンの高効率ポンプ機構

2TA1-09 Cytochrome *c* Oxidase Structures Facilitating the Four-Electron Reduction of Oxygen in One-Step and the High Proton Pump Efficiency

Kazuhiro Ohta (1), Kazumasa Muramoto (2), Kyoko Shinzawa-Itoh (2), Masao Mochizuki (2), Katsumasa Kanda (2), Maki Taniguchi (2), Eiki Yamashita (1), Tomitake Tsukihara (1), Shinya Yoshikawa (2) ((*1) Institute for Protein Research, Osaka University, Japan: (2) Department of Life Science, University of Hyogo, Japan*)

2P-073 アジ化物イオン結合酸化型チトクロム酸化酵素の精密構造解析

2TP1-01 Refined structural analysis of azide ion bound cytochrome *c* oxidase in the oxidized state

Kazumasa Muramoto (1), Rika Inaoka (1), Tomoko Maeda (1), Kyoko Shinzawa-Itoh (1), Eiki Yamashita (2), Tomitake Tsukihara (3), Shinya Yoshikawa (1) ((*1) Dept. of Life Sci., Univ. of Hyogo; Picobio. Inst., Univ. of Hyogo: (2) Inst. for Protein Res., Osaka Univ.: (3) Picobio. Inst., Univ. of Hyogo; Inst. for Protein Res., Osaka Univ.*)

2P-074 チトクロム酸化酵素結晶Ｆ型中間体の再酸化反応による生成

2TP1-02 Cytochrome *c* oxidase crystal in the F intermediate state produced by reoxidation

Kazumasa Muramoto (1), Rie Harada (1), Tomoko Maeda (1), Kyoko Shinzawa-Itoh (1), Eiki Yamashita (2), Tomitake Tsukihara (3), **Shinya Yoshikawa** (1) ((*1) Dept. of Life Sci., Univ. of Hyogo; Picobio. Inst., Univ. of Hyogo: (2) Inst. for Protein Res., Osaka Univ.: (3) Picobio. Inst., Univ. of Hyogo; Inst. for Protein Res., Osaka Univ.*)

2P-075 チトクロムｃ酸化酵素におけるヒドロキシファルネシルエチル基の共鳴ラマンマーカーバンド

2TP1-04 Resonance Raman Marker Bands of Hydroxyfarnesylethyl Substituent of Cytochrome c Oxidase

Miyuki Sakaguchi (1), Kyoko Shinzawa-Itoh (1), Shinya Yoshikawa (1), Hiroshi Fujii (2), Takashi Ogura (1) ((*1) University of Hyogo: (2) Okazaki Institute for Integrative Bioscience*)

2P-076 アミノ酸置換によるウシ心筋チトクロム *c* 酸化酵素の水素結合ネットワークの機能解析

2TP1-03 The functional analysis of hydrogen bond network in bovine heart cytochrome *c* oxidase by mutagenesis

Ryohta Aminaka (1), Kunitoshi Shimokata (2), Mai Itoh (1), Yukie Katayama (1), Tomitake Tsukihara (1), Shinya Yoshikawa (1), Hideo Shimada (1) ((*1) Graduate School of Life Science, University of Hyogo: (2) WORLD INTEC CO., LTD.*)

2P-077 チトクロム *c* 酸化酵素の CO 光解離後の構造緩和過程の追跡

2TP1-05 Structural Relaxation Process of Cytochrome *c* Oxidase Following Photolysis of Carbonmonoxide

Izumi Ishigami (1), Satoru Nakasima (2), Kyoko Shinzawa-Itoh (1), Shinya Yoshikawa (1), Takashi Ogura (1) ((*1) University of Hyogo, Grad.Sch. Life Sci.: (2) Picobiology Inst., Grad.Sch. Life Sci., University of Hyogo*)

2P-078 Prediction of equilibrium and dynamic structural properties of membrane proteins

Shandar Ahmad (1), Hemjit Singh (2), Yogesh Paudel (2), Takaharu Mori (3), Yuji Sugita (3), Kenji Mizuguchi (1) ((*1) National Institute of Biomedical Innovation; Institute of Bioinformatics Research and Development, Japan Science and Technology Agency (JST-BIRD); Graduate School of Frontier Bioscience, Osaka University: (2) National Institute of Biomedical Innovation; Institute of Bioinformatics Research and Development, Japan Science and Technology Agency (JST-BIRD): (3) Advanced Science Institute, RIKEN*)

2P-079 細胞溶解毒素の自発的なαヘリックスーβバレル変換におけるαヘリックスのアンフォールディングとβストランドの整列化の解析

2TP2-03 The Spontaneous α-Helix to β-Barrel Transition of a Pore-Forming Protein: Timing of Helix Unfolding and β-Strand Alignment

Takehiro Sato (1), Tweten Rodney K. (2), Johnson Arthur E. (1) ((*1) Texas A&M Health Science Center: (2) University of Oklahoma Health Sciences Center*)

2P-080 銅イオン輸送性 P-type ATPase の機能解析と低分解能溶液構造

Functional charactarization and low resolution solution structure of copper pumping P-type ATPase from *Thermus thermophilus* HB8

Naoyuki Kuwabara (1), Takadhi Oda (1), Gen Shikauchi (1), Hiroshi Hashimoto (1), Mamoru Sato (1), Toshiyuki Shimizu (1) ((*1) Biol., Grad. Sch. of Nanobio., Yokohama City Univ.*)

2P-081 高親和性 IgE 受容体β鎖Ｃ末端領域の構造解析

Secondary Structure and Conformation Change in mutation of FcεRI β Chain C-terminal Region Investigated by Circular Dichroism Spectroscopy

Tomoyoshi Terada (1), Koichi Murayama (1), Seiichi Era (1), Chisei Ra (2) ((*1) Physiology and Biophysics, Gifu University graduate School of Medicine: (2) Division of Molecular Cell Immunology and Allergy, Advanced Medical Research Center, Nihon University Graduate School of Medical Science*)

2P-082 酢酸菌のセルロース合成酵素複合体における GxCesA と GxCesB との直接相互作用

Direct interaction between GxCesA and GxCesB in cellulose synthase complex of *Gluconacetobacter xylinus*

Ami Sugano (1), Junji Sugiyama (1), Tomoya Imai (1) ((*1) Research Institute for Sustainable Humanosphere, Kyoto University*)

2P-083 SMR 型多剤排出輸送担体と基質の相互作用に伴う熱量変化

Thermodynamic parameters of interaction between SMR-type multidrug transporter and its substrates

Kazumi Shimono (1), Tomomi Someya (2), Mikako Shirouzu (2), Shigeyuki Yokoyama (3), Seiji Miyauchi (4) ((*1) Matsuyama Univ.; RIKEN SSBC: (2) RIKEN SSBC: (3) Dept. Biophys. Biochem., Grad. Sch. of Sci., Univ. of Tokyo: (4) Matsuyama Univ.*)

2P-084 ハロロドプシン NpHR の三量体構造は F150 残基の対称配置によって安定化される

2TP2-01 Stabilization of trimeric assembly of halorhodopsin, NpHR by C_3-symmetric geometry among F150 aromatic rings

Takashi Tsukamoto (1), Takanori Sasaki (2), Kazuhiro Fujimoto (3), Takashi Kikukawa (4), Masakatsu Kamiya (2), Tomoyasu Aizawa (1), Keiichi Kawano (4), Makoto Demura (1) ((*1) Faculty of Advanced Life Science, Hokkaido University.: (2) School of Science and Technology, Meiji University.: (3) Graduate School of Science, Kyoto University.: (4) Faculty of Science, Hokkaido University.*)

2P-085 DMPC、DPPC 二重層に再構成したバクテリオロドプシンの可視領域における円二色性測定

2TP2-02 Circular dichroism measurement of bacteriorhodopsin reconstituted in DMPC and DPPC bilayer in visible region

Lumi Negishi (1), Taku Kitoh (1), Yasunori Yokoyama (1), Masashi Sonoyama (2), Shigeki Mitaku (1) ((*1) Depertment of Applied Physics, Graduate School of Engineering, Nagoya University: (2) Depertment of Applied Chemistry and Chemical Biology, Graduate School of Engineering, Gunma University*)

2P-086 転写因子のゲノムスケールでのターゲット予測：相互作用情報を用いた方法

Genome-wide target prediction of transcriptional factor: a method based on interaction data

Hiroaki Ohba (1), Satoshi Fujii (1), Akinori Sarai (1) ((*1) Kyushu Institute of Technology*)

2P-087 水と核酸塩基間の相互作用自由エネルギーランドスケープ

Interaction free energy landscape between nucleobase and a water

Tomoki Yoshida (1), Misako Aida (1) ((*1) Graduate School of Science, Hiroshima University; Center for Quantum Life Sciences*)

2P-088 ベイズ統計学的解釈によるタンパク質－DNA 認識における indirect readout の評価

Role of indirect readout in protein-DNA recognition assessed by a Bayesian approach

Satoshi Yamasaki (1), Kazuhiko Fukui (1), Hidetoshi Kono (2), Kentaro Shimizu (3), Akinori Sarai (4), Tohru Terada (5) ((*1) Computational Biology Research Center, AIST: (2) Computational Biology Group, Quantum Beam Science Directorate, Japan Atomic Energy Agency: (3) Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo: (4) Department of Bioscience and Bioinformatics, Graduate School of Computer Science and Systems Engineering, Kyushu Institute of Technology: (5) Molecular Scale Team, Computational Science Research Program, RIKEN*)

2P-089 DNA ブランチマイグレーションの反応速度予測に向けて

Towards the prediction of kinetics of DNA branch migration

Fumiaki Tanaka (1), Masami Hagiya (1) ((*1) University of Tokyo*)

2P-090 DNA 分子で作られた二次元結晶の成長メカニズムの解明

Elucidation of growth mechanism of two-dimensional crystal created by DNA molecules

Tadashi Ohtani (1), Miho Tagawa (2), Koh-Ichiroh Shohda (1), Akira Suyama (1) ((*1) Department of Life Sciences, Graduate School of Arts And Sciences, The University of Tokyo: (2) Center for Functional Nanomaterials, Brookhaven National Laboratory*)

2P-091 時間分解蛍光分光を用いた逆ミセルに入れたタンパク質の水和水のダイナミクスの研究

Study of the dynamics of hydrated water of protein in reverse micelle using time-resolved fluorescence spectroscopy

Masato Ono (1), Hiroshi Murakami (2), Nobuyuki Ichinose (1) ((*1) Graduated School of Science and Technology, Kyoto Institute of Technology: (2) Japan Atomic Energy Agency*)

2P-092 塩の溶媒和効果が誘起する水/有機溶媒混合系の階層的秩序

Multi-lamellar structures induced by hydrophilic and hydrophobic ions added to a binary mixture of water and organic solvent

Koichiro Sadakane (1), Akira Onuki (1), Michihiro Nagao (2), Koji Nishida (4), Hitoshi Endo (5), Satoshi Koizumi (6), Hideki Seto (7), Hideki Seto (7) ((*1) Kyoto University: (2) National Institute of Standards and Technology: (3) Cyclotron Facility, Indiana University: (4) Institute for Chemical Research, Kyoto University: (5) Institute for Solid State Physics, The University of Tokyo: (6) Japan Atomic Energy Agency*)

2P-093 αシェイプを用いた蛋白質分子内空洞の探索プログラムの作成

An application program by using alpha-shape method for searching voids of a protein

Masayuki Irisa (1) ((*1) Kyushu Institute of Technology*)

2P-094 蛋白質の熱容量温度依存性と水の状態方程式の関係

Heat capacity changes of protein and the equation of state of water

Junji Yasuniwa (1), Masayuki Irisa (1) ((*1) Kyushu Institute of Technology Graduate School of Computer Science and Systems Engineering*)

2P-095 タンパク質体積パラドックスとその分子的描像：

2TA3-02 表面カークウッド - バフ積分法による考察

Protein Volume Paradox and its Molecular Picture:
A Study by Surficial Kirkwood-Buff Integral Method

Isseki Yu (1), Masataka Nagaoka (2) ((*1) Department of Chemistry and Biological Science, College of Science and Engineering, Aoyama Gakuin University: (2) Graduate School of Information Science, Nagoya University*)

2P-096 Global protein expression profiling with single molecule sensitivity reveals the architecture of biological noise

2TA3-03 **Yuichi Taniguchi** (1), Paul J Choi (1), Huiyi Chen (1), Mohan Babu (2), Andrew Emili (2), Xiaoliang Sunney Xie (1) ((*1) Harvard University: (2) University of Toronto*)

2P-097 青枯病菌の持つ LysR タイプ転写調節因子 PhcA の転写調節機構の解明

The global virulence regulator PhcA negatively controls the *Ralstonia solanacearum hrp* regulatory cascade by repressing expression of the PrhIR signalling proteins

Kouhei Ohnishi (1), Takeshi Yoshimochi (1), Akinori Kiba (1), Yasufumi Hikichi (1) ((*1) Kochi University*)

2P-098 細胞分裂を考慮した分節時計の２次元シミュレーション

Influence of cell cycles to the oscillation of segmentation clock: Simulation with a two-dimensional model

Yoshihiro Sonoda (1), Kazuhito Ito (2), P. Tomoki Terada (2), Masaki Sasai (2) ((*1) Dept. of Computational Science and Engineering, Grad. Sch. of Engineering, Nagoya Univ: (2) Department of Applied Physics,Grad. Sch. of Engineering, Nagoya University*)

2P-099 細胞分化の動的モデル：幹細胞カオス仮説

A Dynamic Model for Irreversible Differentiation in a Stem Cell System: Chaos Hypothesis

Chikara Furusawa (1), Kunihiko Kaneko (2) ((*1) Graduate School of Information Science and Technology, Osaka University; Complex Systems Biology Project, ERATO, JST: (2) Graduate School of Arts and Sciences, University of Tokyo; Complex Systems Biology Project, ERATO, JST*)

2P-100 組織のプロポーション決定の力学的基盤の解析

Elastic Analysis of Tissue Growth in Drosophila

Kaoru Sugimura (1), Shuji Ishihara (2), Tadashi Uemura (3), Atsushi Miyawaki (4) ((*1) RIKEN: (2) Univ. of Tokyo: (3) Kyoto Univ: (4) RIKEN BSI*)

2P-101 環形動物斜紋筋のコネクチン様 4000K 蛋白質の部分配列

Partial sequence of connectin-like 4000K-protein in obliquely striated muscle of a polychaete (Annelida)

Koki Yuasa (1), Shinichirou Hatakeyama (1), Sumiko Kimura (1) ((*1) Department of Biology, Graduate School of Science, Chiba University*)

2P-102 活性化レベルに依存する骨格筋自励振動現象の振舞い

The behavior of spontaneous oscillations of skeletal myofibril depending on the activation levels

Takeshi Konno (1), Yuta Shimamoto (2), Shin'Ichi Ishiwata (1) ((*1) Waseda University: (2) Laboratory of Chemistry and Cell Biology, Rockefeller University*)

2P-103 正常および心筋症ヒト心筋における SPOC の研究

A study of SPOC in failing and non-failing human cardiomyocytes

Mitsunori Yamane (1), Cristobal G. Dos Remedios (2), Satoshi Kurihara (3), Norio Fukuda (3), Shin'Ichi Ishiwata (1) ((*1) Department of Physics, Faculty of Science and Engineering, Waseda University: (2) Bosch Institute, The University of Sydney: (3) Department of Cell Physiology, The Jikei University School of Medicine*)

2P-104 分子動力学計算で探るミオシン構造状態の結合ヌクレオチドに対する応答

Molecular dynamics simulation on the allosteric response of myosin due to bound nucleotide

Takato Sato (1), Mitsunori Takano (1) ((*1) Graduate School of Advanced Science and Engineering, Waseda Univ.*)

2P-105 筋原繊維内におけるミオシン II 動態の１分子直接観察

Direct observation of single myosin II molecule dynamics within a myofibril

Yasunori Komori (1), Atsuko Iwane (3), Toshio Yanagida (1) ((*1) Graduate School of Frontierbioscience, Osaka Univ. : (2) yuragi project, MEXT: (3) Graduate School of Medicine, Osaka Univ.*)

2P-106 同位体スピンラベルを利用した骨格筋アクチン - トロポミオシン間の高精度距離解析

Highly accurate distance analysis between tropomyosin and actin of skeletal muscle using isotopically substituted spin label

Keisuke Ueda (1), Chieko Kimura-Sakiyama (2), Masao Miki (3), Toshiaki Arata (4) ((*1) Institute for Protein Research, Osaka University: (2) ERATO Actin Filament Dynamics Project: (3) Department of Applied Chemistry and Biotechnology, Graduate School of Engineering, University of Fukui: (4) Department of Biological Sciences, Graduate School of Science, Osaka University*)

2P-107 Ｘ線繊維回折法によるフル、ノンオーバーラップ骨格筋のミオシンクロスブリッジの配向解析

Analysis of orientation of myosin crossbridges in full- and non-overlapped skeletal muscles by X-ray fiber diffraction

Kanji Oshima (1), Yasunobu Sugimoto (2), Katsuzo Wakabayashi (3) ((*1) The Center for Advanced Medical Engineering and Informatics, Osaka University: (2) Division of Biophysical Engineering, Graduate School of Engineering Science, Osaka University: (3) Division of Biophysical Engineering, Graduate School of Engineering Science, Osaka University*)

2P-108 ミオシン相互作用による Cys374 の疎水性

From the hydrophobicity of Cys374 of actin molecules to its interactions with myosin.

Takahiro Hayashizaki (1), Ryousuke Suzuki (1), Eiichi Imai (1), Hazime Honda (1) ((*1) Department of Bioengineering, Nagaoka University of Technology*)

2P-109 多分子ミオシンシステムの運動モデル（測定プローブの影響を含めたエネルギー効率の視点から）

Mathematical model of multiple myosin system with measurement probes, focusing on energy efficiency.

Hiroto Tanaka (1) ((*1) NICT, PRESTO.JST*)

2P-110 Radial spokes は head-tail-joint のフレキシビリティに方向性を持つ

The head-tail-joint flexibility of radial spokes depends on its direction

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2P-111 CH ドメインを持つ新規イネキネシン O12 とアクチンとの相互作用

Interaction of the novel rice kineisn O12 that has the calponin homology domain with actin.

Nozomi Umezu (1), Kazunori Kondo (2), Toshiaki Mitsui (3), Shinsaku Maruta (1) ((*1) Division of Bioinformatics, Graduate School of Engineering, Soka University: (2) Dept. of Bioinformatics, Faculty of Engineering, Soka University: (3) Graduate School of Science and Technology, Niigata

University)

2P-112 新規イネキネシン K23 の特徴付け

Characterization of the novel rice kinesin K23

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2P-113 Stopped Flow FRET を用いたミオシンクロスブリッチサイクルの構造解析

Analysis of Conformation of Skeletal Muscle Myosin Cross-bridge Cycle using Stopped Flow FRET

Masafumi Yamada (1), **Koichiro Ishiyama** (1), Eisaku Katayama (2), Yoshitaka Kimori (3), Shinsaku Maruta (1) (*(1) Dept. of Bioinfo., Fuc. of Eng., Soka Univ. : (2) Div. of Biomolecular Imaging, Inst. of Med. Sci., The Univ. of Tokyo: (3) Dept. of Ultrastr. Res., Nat'l Inst. of Neurosci., Nat'l Ctr of Neurol. and Psych.*)

2P-114 アゾベンゼン誘導体によるキネシンの機能の光制御

Photo-regulation of kinesin function using azobenzene derivative

Takeshi Itaba (1), Masafumi Yamada (1), Shinsaku Maruta (1) (*(1) Division of Bioengineering, Graduate School of Engineering, Soka University*)

2P-115 キネシンにおける特有のループ L5 の機能的役割

The functional role of the unique loop L5 of kinesin

Kumiko Ishikawa (1), Keiko Tanaka (1), Shinsaku Maruta (1) (*(1) Division of Bioinfomatics, Graduate school of engineering, Soka University*)

2P-116 新規 ATP 誘導体の合成およびモータータンパク質との相互作用

Synthesis of novel fluorescent ATP analogue and interaction with nucleotide dependent motor proteins

Taro Kimura (1), Masafumi D, Yamada (1), Shinsaku Maruta (1) (*(1) Division of Bioinformatics, Graduate School of Engineering, Soka University*)

2P-117 Ｘ線小角散乱を用いたキネシンネックリンカーの構造変化の解析

Analysis of conformational change of kinesin neck-linker using using small angle X-ray solution scattering

Keiko Tanaka (1), Yasunobu Sugimoto (2), Masafumi D. Yamada (1), Katsuzo Wakabayashi (2), Shinsaku Maruta (1) (*(1) Division of Bioinformatics, Graduate school of Engineering, Soka University: (2) Graduate school of Engineering Science, Osaka University*)

2P-118 分子モーターの力発生におけるブラウニアン・ラチェット機構の寄与

Contribution of Brownian ratchet mechanism to the force-generation of molecular motors

Mitsunori Takano (1), Jun Narita (1) (*(1) Dept. Phys, Waseda Univ.*)

2P-119 ゲルゾリンＣ末端部位を使った細胞質アクチンのアフィニティ精製

Purification of Cytoplasmic Actin by the Affinity Chromatography Using C-Terminal Half of Gelsolin

Takashi Ohki (1), Kotaro Oyama (1), Shin'Ichi Ishiwata (1) (*(1) waseda university/Science and Engineering/Physics*)

2P-120 タンパク質間粗視化力場のアクトミオシン結合過程への応用

Application of an inter-protein coarse-grained force field to binding process of actomyosin

Kei-Ichi Okazaki (1), Mitsunori Takano (1) (*(1) School of Advanced Science and Engineering, Waseda University*)

2P-121 ミオシンＶの運動性におけるトロポミオシンの役割

Role of tropomyosin in the motility of myosin V along an actin filament

Junji Ishizuka (1), Yusuke Oguchi (1), Jun-Ichi Yoshimoto (1), Hiroaki Kubota (1), Takashi Ohki (1), Shin'Ichi Ishiwata (1) (*(1) Department of Physics, Faculty of Science and Engineering, Waseda University*)

2P-122 理論的立場から見たミオシン分子モーターにおける歪みセンサの役割

The role of the strain sensor in myosin motor molecules from theoretical point of view

Tetsuya Shimokawa (1) (*(1) Osaka University*)

2P-123 シンプルな光学系で高時間・高空間分解能を実現する暗視野顕微鏡の開発

Simple Total Internal Reflection Dirk-field Microscopy with Nanometer spatial precision and Microsecond Temporal Resolution

Hiroshi Ueno (1), So Nishikawa (2), Ryota Iino (1), Kazuhito Tabata (1), Hiyroyuki Noji (1) (*(1) The Institute of Scientific and Industrial Research, Osaka University: (2) Nikon Corporation*)

2P-124 新規３次元配向計測顕微鏡の開発

Development of new microscopy for determining three dimensional orientations of single molecules

Masashi Ohmachi (1), Yasunori Komori (1), Atsuko H. Iwane (1), Toshio Yanagida (1) (*(1) Frontier Biosciences, Osaka University*)

2P-125 ダブルトラップ系を用いたミオシンⅡのアクチンとの負荷依存的な結合の観察

Strain-dependent bindings of myosin II to actin using double trap system

Tomohisa Ran (1), Mitsuhiro Iwaki (2), Tomotaka Komori (1), Toshio Yanagida (1) (*(1) Graduate School of Frontier Biosciences, Osaka University: (2) Graduate School of Medicine, Osaka University*)

2P-126 F_1－ATPase のγサブユニットの固さ測定

Stiffness of γ subunit of F_1-ATPase

Daichi Okuno (1), Ryota Iino (1), Rie Hasegawa (1), Hiroyuki Noji (1) (*(1) ISIR, Osaka Univ.: (2) ISIR, Osaka Univ.: (3) ISIR, Osaka Univ.: (4) ISIR, Osaka Univ.*)

2P-127 大腸菌由来 F_oF_1－ATP 合成酵素のεサブユニットによる活性阻害機構

Mechanism of inhibition by C-terminal α-helices of the ε subunit of *Escherichia coli* F_oF_1-ATP synthase

Ryota Iino (1), Rie Hasegawa (1), Kazuhito Tabata (1), Hiroyuki Noji (1) (*(1) ISIR, Osaka University*)

2P-128 F_1－ATPase のβサブユニットのＣ末ドメインとγサブユニットの相互作用に関する研究

Interaction between C terminus domain of β subunit and γ subunit of F_1-ATPase

Mizue Tanigawara (1), Kazuhito Tabata V. (1), Hiroyuki Noji (1) ((*1) The Institute of Industrial and Scientific Research, Osaka University*)

2P-129 F1 の加水分解反応に重要な ATP 周辺残基の機能解析

The effect of the critical residues; αR364, βE190, βK164, for ATP hydrolysis on F1-ATPase

Yuki Matsukage (1), Rikiya Watanabe (1), Mizue Tanigawara (1), Kazuhito Tabata (1), Hiroyuki Noji (1) ((*1) ISIR, Osaka University*)

2P-130 F1 の回転運動におけるリン酸解離反応の役割

The completion of chemo-mechanical coupling scheme of F_1-ATPase; The determination of the timing of Pi-release

Rikiya Watanabe (1), Hiroshi Ueno (1), Ryota Iino (1), Hiroyuki Noji (1) ((*1) ISIR, Osaka University*)

2P-131 ミオシン６の SHREC 計測

SHREC measurement of myosin-VI stepping motion

Keigo Ikezaki (1), Mitsuhiro Sugawa (1), So Nishikawa (1), Atsuko Iwane (1), Toshio Yanagida (1) ((*1) Frontier Biosciences, Osaka Univ.*)

2P-132 高温におけるキメラべん毛モーターの回転トルク応答

2TA4-02 Torque response of bacterial flagellar motor induced by transient heating.

Yuichi Inoue (1), Hajime Fukuoka (1), Akihiko Ishijima (1) ((*1) Tohoku University*)

2P-133 ミトコンドリアマトリクスのインポートモータ mtHsp70 の作動機構の解析

Step-size analyses of the mitochondrial Hsp70 import motor reveal the Brownian ratchet in operation

Koji Yamano (1), Mika Kuroyanagi-Hasegawa (1), Masatoshi Esaki (1), Mihiko Yokota (1), Toshiya Endo (1) ((*1) Department of Chemistry, Graduate School of Science, Nagoya University*)

2P-134 チューブリンＣ末端の伸長した構造が弱結合に果たす役割

2TA4-04 The role of extended C-terminal tail of tubulin on weak-binding interaction between motor proteins and microtubules

Itsushi Minoura (1), Seiichi Uchimura (1), Masashi Degawa (1), Etsuko Muto (1) ((*1) RIKEN Brain Science Institute*)

2P-135 KIF1A の１次元ブラウン運動にチューブリンＣ末端は必要か？

2TA4-05 Is the tubulin C-terminus tail necessary for the 1D Brownian motion of KIF1A?

Masashi Degawa (1), Itsushi Minoura (1), Seiichi Uchimura (1), Etsuko Muto (1) ((*1) RIKEN BSI*)

2P-136 *Gluconobacter* 属酢酸菌の酸性条件下でのべん毛運動

Flagellar motility of *Gluconobacter* species under acidic conditions

Toshiharu Yakushi (1), Shin-Ya Kubota (2), Takeshi Hosaka (2), Kikuo Sen (2), Kazunobu Matsushita (1) ((*1) Yamaguchi University: (2) Shinshu University*)

2P-137 基質の周期的伸展・収縮による粘菌アメーバの運動極性形成の機構

A possible mechanism of directional migration in *Dictyostelium* cells induced by the cyclic stretch and shrinkage of the substratum

Yoshiaki Iwadate (1), Shigehiko Yumura (2) ((*1) Dept. Functional Mol. Biol., Grad. Sch. Medicine, Yamaguchi Univ.; PRESTO, JST: (2) Dept. Functional Mol. Biol., Grad. Sch. Medicine, Yamaguchi Univ.*)

2P-138 マクロファージによる逐次貪食過程の観察

Single event observation of sequential phagocytosis by macrophage

Masahito Hayashi (1), Kenji Yasuda (2) ((*1) Kanagawa Academy of Science and Technology: (2) Kanagawa Academy of Science and Technology;Dept Biomedical Information, Inst Biomaterials and Bioengineering, Tokyo Med Dent Univ*)

2P-139 異方的周期構造の微細パターンにおける細胞運動のマイクロ干渉イメージング

Micro-interferometric Imaging on Cell Motion Directed by Anisotropic and Periodic Micropattern

Tomohiro Nakanishi (1), Taro Toyota (1), Kiyoshi Ohnuma (2), Makoto Asashima (3), Masanori Fujinami (1) ((*1) Department of Applied Chemistry and Biotechnology, Graduate School of Engineering, Chiba University: (2) Department of Life Sciences (Biology), Graduate School of Arts and Sciences, The University of Tokyo: (3) Organ Development Research Laboratory, National Institute of Advanced Industrial Science and Technology (AIST)*)

2P-140 インフルエンザウイルス行動の可視化解析技術の開発

Development of quick imaging technique for analyzing influenza virus behavior

Tatsuya Sakai (1) ((*1) Kawasaki Medical School*)

2P-141 肥満細胞の脱顆粒メカニズム：アクチン骨格再構成での活性化タンパク質Ｃの役割

Mechanism of mast cell degranulation: Roles of activated protein C in the rearrangement of actin cytoskeleton

Fumichika Ono (1), Madoka Suzuki (2), Kotaro Oyama (3), Svetlana Strukova (4), Shinichi Ishiwata (3) ((*1) Bioscience and Biomedical Engineering,Graduate Scool of Science and Engineering,Waseda University: (2) Comprehensive Research Organization, Waseda University: (3) Department of Physics, Faculty of Science and Engineering, Waseda University: (4) Department of Human and Animal Physiology, The Lomonosov Moscow State University*)

2P-142 細菌べん毛蛋白質輸送装置構成蛋白質 FlhB のＣ末細胞質ドメインの機能解析

Functional analysis of the C-terminal cytoplasmic domain of the FlhB component of the bacterial flagellar protein export apparatus

Akira Hida (1), Tatsuya Ibuki (1), Nao Moriya (1), Tohru Minamino (2), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Graduate School of Frontier Biosciences, Osaka University;PRESTO, JST*)

2P-143 栄養枯渇に対する適応応答における遺伝子発現の確率性

Stochastic gene expression induced population selection promotes adaptation to nutrient depletion

Saburo Tsuru (1), Bei-Wen Ying (1), Kotaro Mori (2), Junya Ushioda (1), Akiko Kashiwagi (3), Tetsuya Yomo (1) ((*1) Graduate School of Information Science and Technology, Osaka University: (2) Graduate School of Frontier Biosciences, Osaka University: (3) Faculty of Agriculture and Life Science, Hirosaki University*)

2P-144 細菌べん毛モーター・スイッチ複合体の極低温電子顕微鏡による構造解析

Structural analysis of the flagellar hook-basal body with the C ring by electron cryomicroscopy

Tomoko Miyata (1), Takayuki Kato (1), Takashi Fujii (1), Takashi Fujii (2), Hideyuki Matsunami (2), Hideyuki Matsunami (3), Keiichi Namba (1), Keiichi Namba (2) ((*1) Graduate school of Frontier Biosciences, Osaka University: (2) ICORP Dynamic NanoMachine Project, JST: (3) Okinawa Institute of Science and Technology Promotion Corporation*)

2P-145 栄養欠乏に対する適応応答の定量的観測

Quantitative observation of adaptive response to nutrient starvation

Yuki Matsumoto (1), Bei-Wen Ying (1), Yoichiro Ito (2), Junya Ichinose (2), Tetsuya Yomo (3) ((*1) Grad. Sch. Information Sci. and Tech., Osaka Univ.: (2) ERATO, JST: (3) Grad. Sch. Information Sci. and Tech., Osaka Univ.;ERATO, JST;Grad. Sch. Frontier Biosci, Osaka Univ.*)

2P-146 糸状仮足伸長時におけるミオシンＸの動作機構

The mechanism of myosin-X during filopodialprotrusion.

Syugo Nishiyama (1), Tomonobu M Watanabe (3), Toshio Yanagida (1), Mitsuo Ikebe (2) ((*1) Graduate School of Frontier Biosciences,Osaka University: (2) University of Massachusetts medical school, Physiology: (3) Immunology Frontier Research Center, Osaka University*)

2P-147 電位感受性ホスファターゼを用いた細胞内イノシトールリン脂質シグナル経路の電気的操作

Electrical manipulation of phosphatidylinositol lipids signaling by voltage sensitive phosphatase in living cells

Masayuki Sato (1), Yasushi Okamura (2), Masahiro Ueda (1) ((*1) Laboratories for Nanobiology, Graduate School of Frontier Biosciences: (2) Graduate School of Medicine, Faculty of Medicine*)

2P-148 プロトン駆動型細菌べん毛モーターのトルク発生における固定子蛋白質 MotA Pro-173 の機能解析

Role of a Conserved Proline Residue, Pro-173, of MotA in the Mechanochemical Reaction Cycle of Proton-Driven Bacterial Flagellar Motor

Shuichi Nakamura (1), Yusuke Morimoto (1), Nobunori Kami-Ike (1), Tohru Minamino (2), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Graduate School of Frontier Biosciences, Osaka University; PRESTO, JST*)

2P-149 サルモネラ菌べん毛 MS リング構成タンパク質 FliF のペリプラズム領域の発現系構築と精製

Expression and purification of a periplasmic fragment of the flagellar MS-ring protein FliF from *Salmonella*

Shinji Yoshida (1), Hideyuki Matsunami (2), Shigehiro Nagashima (1), Katsumi Imada (1), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Dynamic NanoMachine Project, ICORP, JST: (3) Okinawa Inst. Sci. Tech.*)

2P-150 イノシトールリン脂質系の自己組織化ダイナミクス

Self-organization in phosphatidylinositol lipids signalling pathway for random cell migration and polarization

Yoshiyuki Arai (1), Tatsuo Shibata (2), Satomi Matsuoka (1), J. Masayuki Sato (1), Toshio Yanagida (3), Masahiro Ueda (1) ((*1) Graduate school of Frontier Biosciences, Osaka University; JST, CREST: (2) Department of mathematical and life science, Hiroshima University; JST, CREST; PRESTO, JST: (3) Graduate school of Frontier Biosciences, Osaka University*)

2P-151 精子鞭毛波形調節における NCS ファミリータンパク質カラクシンの機能

Function of NCS family protein calaxin in the regulation of sperm flagellar waveform

Katsutoshi Mizuno (1), Kogiku Shiba (1), Kazuo Inaba (1) ((*1) Shimoda Marine Reserch Center, University of Tsukuba*)

2P-152 細胞内シグナル情報伝達ネットワークにおける刺激・応答関係を直接記述する新規の理論的スキームの開発

A novel theoretical scheme to describe stimulus/response relationships of biochemical reaction networks

Tatsunori Nishimura (1), Masaru Tateno (1) ((*1) Graduate School of Pure and Applied Sciences University of Tsukuba; Center for Computational Sciences*)

2P-153 オンチップ多電極電位計測システムを用いたマウス胎仔心筋細胞における細胞外電位の波形解析

Waveform analysis of the field potential recordings of mouse embryonic cardiomyocytes by using *On-chip* multi electrode array (MEA) system

Fumimasa Nomura (1), Tomoyuki Kaneko (1), Yuki Tomoe (1), Kenji Yasuda (1) ((*1) Inst. of Biomaterials and Bioengineering, Tokyo Medical and Dental Univ.*)

2P-154 多電極チップを用いた心筋細胞小集団による長期的心毒性評価法の開発

Development of long-term assessment method for cardiac toxicity by small cardiomyocyte clusters using MEA chip

Yuki Tomoe (1), Tomoyuki Kaneko (1), Fumimasa Nomura (1), Tamae Takato (1), Kenji Yasuda (1) ((*1) Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University*)

2P-155 多電極計測システムを用いた心筋細胞ネットワークの集団化効果の理解

Understanding the community effects in cardiomyocyte networks using on-chip single-cell measurement system

Tomoyuki Kaneko (1), Fumimasa Nomura (1), Yuki Tomoe (1), Kenji Yasuda (1) ((*1) Department of Biomedical Information, Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University*)

2P-156 ホヤ精子走化性実測データに基づく 精子誘引物質感知機構のシミュレーション解析

Chemoattractant Sensing Mechanisms in Sperm: Experimental and Simulation Study

Daisuke Miyashiro (1), Kogiku Siba (2), Sinji Kamimura (3), Syouji Baba (4), Manabu Yoshida (2) ((*1) University of Tokyo: (2) Misaki Marine Biological Station, Graduate School of Science, The University of Tokyo: (3) Department of Biological Sciences, Faculty of Science and Engineering, Chuo University: (4) Department of Advanced Biosciences, Graduate School of Humanities and Sciences, Ochanomizu University*)

2P-157 生体の動的機能を模した階層的超分子ゲルファイバー

BIOMIMETIC FUNCTIONAL FIBROUS GEL CONSTRUCTED BY HIERARCHICAL SUPRAMOLECULAR ASSEMBLY OF ORGANIC MOLECULES

Daisuke Kiriya (1), Hiroaki Onoe (1), Masato Ikeda (2), Itaru Hamachi (2), Shoji Takeuchi (1) ((*1) Institute of Industrial Science, The University of Tokyo: (2) Graduate School of Engineering, Kyoto University*)

2P-158 細胞間シグナリングの適応現象の１細胞レベル解析

Single-cell level analysis of adaptation in chemoattractant signaling in *Dictyostelium*

Keita Kamino (1), Satoshi Sawai (2) ((*1) Graduate School of Arts and Sciences, University of Tokyo : (2) Graduate School of Arts and Sciences,University of Tokyo;JST-ERATO Complex Systems Biology*)

2P-159 t-BuOOH 誘導性ミトコンドリア膜透過性変化の測定

Measurements of mitochondrial permeability change induced by t-BuOOH

Yoshihiro Matsunomoto (1), Xiaolei Shi (1), Chisako Fujita (1), Yoshihiro Ohta (1) ((*1) Div. of Biotechnology and Life Science, Tokyo University of Agriculture*)

2P-160 ｔ_BuOOH 誘導性細胞死における CypD の役割：ミトコンドリアによる ATP 供給への関与

The role of Cyclophilin D in *t*-BuOOH induced cell death: its involvement in mitochondrial ATP supply

Chisako Fujita (1), Kiyotaka Machida (2), Hiroyuki Osada (2), Yoshihiro Ohta (1) ((*1) Div. of Biotechnology and Liffe Science, Tokyo University of Agriculture and Technology: (2) Antibody Lab, Riken*)

2P-161 高分子溶液中における生物プローブの有効性について

Study on Bio-Probe in Polymer Solutions

Daisuke Maki (1), Zenji Yatabe (2), Masatoshi Yoshimura (2), Chihiro Hashimoto (3), Hideharu Ushiki (4) ((*1) Natural Resources and Ecomaterials, Graduate School of Agriculture, Tokyo University of Agriculture and Technology.: (2) United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology.: (3) Department of Applied Chemistry and Biotechnology, Niihama National College of Technology. : (4) Institute of Symbiotic Science and Technology, Tokyo University of Agriculture and Technology.*)

2P-162 新規細胞モデルとしての分子コンピュータ封入ベシクル

A vesicle encapsulating molecular computer: as a model system of cellular life

Kohichiroh Shohda (1), Tadashi Sugawara (2), Akira Suyama (1) ((*1) Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo: (2) Department of Basic Science, Graduate School of Arts and Sciences, The University of Tokyo*)

2P-163 示差走査熱量測定及び蛍光分光測定によるメリチンと脂質膜の相互作用の研究

The interaction of melittin with phospholipid membranes investigated by differential scanning calorimetry and fluorescent spectrometry

Atsuji Kodama (1), Tetsuhiko Ohba (1), Kazuo Ohki (1) ((*1) Department of Physics, Tohoku University*)

2P-164 Physical Properties of Amphotericin B-containing Liposomes

Li Wu (1), Kazuo Ohki (1), Tetsuhiko Ohba (1) ((*1) Department of Physics, Graduate School of Science, Tohoku University*)

2P-165 ジパルミトオレオイルホスファチジルエタノールアミンの非二分子膜形成

Non-bilayer formation of dipalmitoleoylphosphatidylethanolamine

Yuki Nagi (1), Masaki Goto (2), Nobutake Tamai (2), Hitoshi Matsuki (2), Shoji Kaneshina (2) ((*1) Grad. Sch. of Advan. Tech. & Sci., The Univ. of Tokushima: (2) Inst. Tech. & Sci., The Univ. of Tokushima*)

2P-166 ジアシルホスファチジルコリン二分子膜相挙動に及ぼすアシル鎖長依存性及び非依存性のコレステロール効果

Acyl-Chain Length Dependent and Independent Effects of Cholesterol on Bilayer Phase Behavior of Diacylphosphatidylcholines

Takuya Izumikawa (1), Suguru Fukui (1), Maiko Uemura (1), Masaki Goto (2), Nobutake Tamai (2), Hitoshi Matsuki (2), Shoji Kaneshina (2) ((*1) Grand. Sch. of Advan. Tech.& Sci., The Univ of Tokushima: (2) Inst. Tech. & Sci., The Univ of Tokushima*)

2P-167 不飽和アシル鎖を有する非対称リン脂質の二分子膜相挙動

Bilayer phase behavior of asymmetric phospholipids with an unsaturated acyl chain

Kaori Tada (1), Masaki Goto (1), Nobutake Tamai (1), Hitoshi Matsuki (1), Shoji Kaneshina (1) ((*1) Inst. Tech. & Sci., The Univ. of Tokushima*)

2P-168 圧力摂動熱量法および密度法を用いた脂質二分子膜の体積挙動の解明

Volume behavior of phospholipid bilayer membranes revealed by pressure perturbation calorimetry and densitometry

Nobutake Tamai (1), Yuko Nambu (2), Kazuyo Fujishige (2), Masaki Goto (1), Shoji Kaneshina (1), Hitoshi Matsuki (1) ((*1) Institute of Technology and Science, The University of Tokushima: (2) Graduate School of Advanced Technology and Science, The University of Tokushima*)

2P-169 固体 NMR によるイノシトールリン脂質結合型タンパク質構造解析のための新規バイセル平面膜の開発

Development of Planer Lipid Bilayers System using Bicelle for Structural Characterization of Membrane Bound Proteins by Solid State NMR

Naoko Uekama (1), Katsuhisa Kawai (2), Masashi Okada (2), Hitoshi Yagisawa (2), Satoru Tuzi (2), Katsuyuki Nishimura (1) ((*1) Institute for Molecular Science: (2) Department of Life Science, University of Hyogo*)

2P-170 自発展開脂質二重膜に対する曲率印加の効果

Effect of curvature on the self-spreading behaviour of lipid bilayer

Hideki Nabika (1), Kei Murakoshi (1) ((*1) Graduate School of Science, Hokkaido University*)

2P-171 油中水滴法を用いた、浸透圧ストレスに対するリポソームの挙動観察

Direct observation of the behavior of liposome under the desired osmotic env ironment

Masae Ohno (1), Tsutomu Hamada (2), Michio Homma (1), Kingo Takiguchi (1) ((*1) Division of Biological Science, Graduate School of Science, Nagoya University : (2) School of Materials Science, Japan Advanced Institute of Science and*)

2P-172 生体膜のレプリカ交換分子動力学シミュレーション

Replica-exchange molecular dynamics simulations of membrane systems

Tetsuro Nagai (1), Yuko Okamoto (2) ((*1) Department of Physics School of Science Nagoya University: (2) Department of Physics School of Science Nagoya University*)

2P-173 表面電荷の pH 応答性を利用したベシクル融合と物質輸送

Artificial vesicular transport utilizing pH-induced aggregation ability

Kentaro Suzuki (1), Kensuke Kurihara (1), Tadashi Sugawara (1) (*(1) Grad. School of Arts and Sciences, The Univ. of Tokyo*)

2P-174 静磁場下における人口脂質膜のダイナミクスの光学顕微鏡観察 （２）

Direct microscopic observation of biomembrane dynamics under a static magnetic field (2)

Kouya Tamatsukuri (1), Tetsuhiko Ohba (1), Gen Sazaki (2), Kazuo Ohki (1) (*(1) Department of Physics, Tohoku University: (2) Institute for Materials Research, Tohoku University*)

2P-175 脂質二重膜の動的挙動制御による分子フィルタ効果の発現

Control of self-spreading dynamics of lipid bilayer toward novel molecular filtration

Tomoki Sumida (1), Hideki Nabika (1), Kei Murakoshi (1) (*(1) Division of Chemistry, Graduate School of Science, Hokkaido University*)

2P-176 ブラウニアン・ラチェット機構に基づく二次元分子分別システムの構築

Construction of the two-dimensional molecular separation system based on the Brownian ratchet mechanism

Toshinori Motegi (1), Hideki Nabika (1), Kei Murakoshi (1) (*(1) Hokkaido univ.*)

2P-177 リポソーム再構成 SNARE 系を用いたマスト細胞脱顆粒機構の解析

Effects of synaptotagmin on the membrane fusion between liposomes containing SNARE proteins involved in mast cell exocytosis

Yumiko Nagai (1), Satoshi Tadokoro (1), Naohide Hirashima (1) (*(1) School of Pharmaceutical Sciences, Nagoya City Univ*)

2P-178 大沢モデルにおける大きなスパイク状の揺らぎ生成

Generation of large spike-like fluctuations in the Oosawa model

Shunsuke Ooyama (1), Masatoshi Nishikawa (2), Tatsuo Shibata (3) (*(1) hiroshima univ.: (2) hiroshima univ. ; JST, CREST : (3) hiroshima univ. ; JST, CREST ; PREST,JST*)

2P-179 KCNQ1 チャネル複合体ストイキオメトリーの密度依存的変化

2TP2-04 Density-dependent changes in stoichiometry of KCNQ1 complex

Koichi Nakajo (1), Maximilian Ulbrich (2), Yoshihiro Kubo (1), Isacoff Ehud (2) (*(1) National Institute for Physiological Sciences: (2) University of California, Berkeley*)

2P-180 電位依存性Ｋ$^{+}$チャネルのゲーティング機構解析

Gating mechanism analysis in voltage sensitive potassium channels

Yuko Takeuchi (1), Minako Hirano (1), Takaaki Aoki (1), Toshio Yanagida (1), Toru Ide (1) (*(1) Graduate School of Frontier Bioscience, Osaka University*)

2P-181 抗生物質の単一チャネル電流計測およびバイオセンサーへの応用

Single antibiotics channel current measurement and its application for biosensor

Takaaki Aoki (1), Minako Hirano (1), Yuko Takeuchi (1), Toshihide Kobayashi (2), Toshio Yanagida (1), Toru Ide (1) (*(1) Graduate School of Fronteier Biosciences, Osaka University : (2) Advanced Science Institute, RIKEN*)

2P-182 Ｆ$_{o}$回転モーター内のプロトン経路におよぼす局所誘電率の効果

Effect of local dielectric constants on the proton pathway in F_o rotary motor

Kentaro Fukunaga (1), Mitsunori Takano (1) (*(1) Graduate School of Advanced Science and Engineering, Waseda Univ.*)

2P-183 細菌べん毛タイプ III 輸送装置ゲート構成蛋白質 FlhA に保存された荷電残基の機能解析

Functional analysis of conserved charged residues of FlhA, an export gate component of bacterial flagellar type III protein export appratus

Noritaka Hara (1), Tohru Minamino (2), Keiichi Namba (1) (*(1) Graduate school of Frontier Biosciences, Osaka University: (2) Graduate school of Frontier Biosciences, Osaka University; PRESTO, JST*)

2P-184 KcsA チャネルの全反射赤外分光解析

ATR-FTIR study of KcsA channel

Yusuke Asai (1), Yuji Furutani (2), Hirofumi Simizu (3), Shigetoshi Oiki (3), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Life and Coordination-complex Molecular Science, Institute for Molecular Science: (3) Department of Molecular Physiology and Biophysics, University of Fukui Faculty of Medical Sciences*)

2P-185 細菌化学感覚受容体キメラのフェノール応答能の解析

Phenol-sensing properties of the bacterial chemoreceptor chimeras.

Ken Takeuchi (1), Tomohiro Tokunaga (1), Naoya Yamauchi (1), **Tomonori Iwama** (1), Keiichi Kawai (1) (*(1) Faculty of Applied Biological Sciences, Gifu University*)

2P-186 コレラ菌走化性受容体ホモログのリガンド認識

Ligand recognition of chemoreceptor homologs involved in chemotaxis toward amino acids in *Vibrio cholerae*

Soichiro Nishiyama (1), Hirotaka Tajima (3), Kazuho Suzuki (1), Tomoya Hira (1), Daisuke Suzuki (3), Yasuaki Ito (3), Michio Homma (3), Ikuro Kawagishi (1) (*(1) Dept. Frontier Biosci., Hosei Univ: (2) Res. Cen. Micro-Nano Tech., Hosei Univ.: (3) Div. Biol. Sci., Grad. Sch. Sci. Nagoya Univ.*)

2P-187 テトラシステイン配列結合蛍光試薬 FlAsH を使用した大腸菌走化性受容体の局在観察

Observation of chemoreceptor clusters in *Escherichia coli* by using a small fluorescent probe FlAsH

Takehiko Inaba (1), Kaori Miura (2), Ikuro Kawagishi (3) (*(1) Research Center for Micro-Nano Technology, Hosei University: (2) Dept. Materials Chemistry, Graduate School of Engineering, Hosei Univ.: (3) Dept. Frontier Biosci., Faculty of Bioscience and Applied Chemistry, Hosei Univ.*)

2P-188 コレラ菌走化性関連シグナリングシステム I および III の局在制御

Localization of chemotaxis-related components of systems I and III of *V. cholerae* under aerobic and anaerobic conditions

Geetha Hiremath (1), Tatsuaki Ebisawa (1), Akhiro Hyakutake (2), So-Ichiro Nishiyama (3), Ikuro Kawagishi (3) (*(1) Department. of Materials.*

Chemistry, Graduate School of Engineering, Hosei University: (2) Nikken BioMedical Laboratory Inc.: (3) Department of Frontier Bioscience, Faculty of Bioscience and Applied Chemistry, Hosei University)

2P-189 *Vibrio alginolyticus* の側毛による surface swarming の走化性制御

Characterization of chemotactic control surface swarming by lateral flagella in *Vibrio alginolyticus*

Manabu Konishi (1), Tomoya Hira (2), So-Ichiro Nisiyama (3), Masaru Kojima (4), Ikuro Kawagishi (3) (*(1) Department of Materials Chemistry, Graduate School of Engineering, Hosei University: (2) Department of Frontier Bioscience, Faculty of Engineering, Hosei University: (3) Department of Frontier Bioscience, Faculty of Bioscience and Applied Chemistry, Hosei University: (4) Department of Micro-Nano Systems Engineering, Graduate School of Engineering, Nagoya University*)

2P-190 大腸菌走化性受容体 Tar は忌避物質 Ni2+を直接結合する

The aspartate chemoreceptor Tar of *Escherichia coli* directly binds to the repellent Ni^{2+}

Hirotaka Tajima (1), Eri Iijima (2), Noriko Ohta (1), Yoshiyuki Sowa (3), Ikuro Kawagishi (3) (*(1) Division of Biological Science, Graduate School of Science, Nagoya University: (2) Department of Frontier Bioscience, Faculty of Engineering, Hosei university: (3) Department of Frontier Bioscience, Faculty of Bioscience and Applied Chemistry, Hosei university*)

2P-191 クロスリンカーを用いた大腸菌走化性受容体のクラスター構造の特性解析

Characterization of the structure of the chemoreceptor cluster in *Escherichia coli* using chemical cross-linkers

Noriko Ohta (1), Hiroki Irieda (1), Kousuke Jintori (2), Tsuyoshi Watanabe (2), Michio Homma (1), Ikuro Kawagishi (2) (*(1) Division of Biological Science, Graduate School of Science, Nagoya University: (2) Department of Frontier Bioscience, Faculty of Bioscience and Applied Biochemistry, Hosei University*)

2P-192 記憶・学習中枢海馬に性差はあるか

Is there sex difference in the hippocampus, the center of learning and memory?

Yasushi Hojo (1), Shimpei Higo (6), Toshihiro Komimami (2), Hideo Mukai (1), Takeshi Yamazaki (3), Nobuhiro Harada (4), Seijiro Honma (5), Tetsuya Kimoto (1), Suguru Kawato (1) (*(1) The University of Tokyo; BIRD, JST: (2) The University of Tokyo: (3) Hiroshima University: (4) Fujita Health University: (5) ASKA Pharma Medical: (6) The University of Tokyo; JPSP Research Fellow*)

2P-193 女性ホルモンによる海馬神経スパイン制御機構

Effect of estrogen on spine regulation in hippocampus

Rei Sato (1), Yusuke Hatanaka (1), Suguru Kawato (1) (*(1) University of Tokyo*)

2P-194 ラット海馬神経シナプス可塑性に対するビスフェノールＡの低用量作用

Low dose effects of Bisphenol A on the Synaptic Plasticity in Rat Hippocampal Neurons

Tetsuya Kimoto (1), Yasushi Hojo (1), Rei Sato (1), Suguru Kawato (1) (*(1) Dept. of Biophysics and Life Sciences, Grad. School of Arts and Sciences, University of Tokyo*)

2P-195 男性ホルモンによる海馬 CA1・CA3 スパインの急性的増加とその細胞内情報伝達経路の解析

Androgen rapidly increased the density of dendritic spines in the hippocampus via several kinases

Yusuke Hatanaka (1), Tetsuya Kimoto (1), Suguru Kawato (1) (*(1) Dept Life Sciences, Graduate School of Arts and Sciences., Univ of Tokyo*)

2P-196 女性ホルモンはストレスによる記憶書き込み阻害を回復させる：急性効果

Rapid restoration effect by estradiol on stress-induced suppression of long term potentiation in rat hippocampus

Suguru Kawato (1), Yuuki Ooishi (2) (*(1) Univ of Tokyo: (2) NTT Communication*)

2P-197 多時間スケールをもつ学習モデルとその相空間構造の変化

Learning Model with Multiple timescales and Change in a Structure of Phase Space

Tomoki Kurikawa (1) (*(1) Department of Basic Science, University of Tokyo*)

2P-198 新規な神経スパインの解析手法とその適用

Novel methods and its applications for analysis of spines in neurons

Hideo Mukai (1), Yuusuke Hatanaka (1), Gen Murakami (1), Kenji Mitsuhashi (1), Suguru Kawato (1) (*(1) Dept. Biophys. and Life Sci. Grad. Sch. Arts & Sci., The Univ. of Tokyo; Bioinfomatics Project, JST*)

2P-199 遺伝子改変マウスを利用した摂食調節に関与するニューロンの同定

The use of gene-targeted mice to identify neurons involved in the regulation of feeding behavior

Shuhei Horio (1) (*(1) Department of Molecular Pharmacology, Division of Pharmaceutical Sciences, Institute of Health and Biosciences, The University of Tokushima*)

2P-200 瞬目反射条件付けの記憶獲得および消去に関与する内在性カンナビノイドの同定

The identification of endocannabinoid ligand responsible for memory formation and extinction of classical eyeblink conditioning

Junko Nakayama (1), Yasushi Kishimoto (1), Ikuko Oku (1), Yutaka Kirino (1) (*(1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University*)

2P-201 瞬目条件反射の獲得と発現における代謝型グルタミン酸受容体１型(mGluR1)の役割

The functional role of mGluR1 within cerebellar Purkinje cells in acquisition and expression of conditioned eyeblink response

Yasushi Kishimoto (1), Harumi Nakao (2), Atsu Aiba (2), Yutaka Kirino (1) (*(1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University: (2) Kobe University, Grad. Sch. Medicine*)

2P-202 ナメクジ嗅覚中枢の振動的活動における GABA 受容体を介した調節機構

GABA receptor-mediated modulation of oscillatory neuronal activity in slug olfactory center

Suguru Kobayashi (1), Mariko Hattori (1), Ryota Matsuo (1), Etsuro Ito (1) (*(1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University*)

2P-203 マウス瞬目反射条件づけにおける一酸化窒素（NO）の役割

Physiological role of nitric oxide (NO) in eyeblink conditioning of mice

Yoshiichiro Kitamura (1), Junko Nakayama (1), Yutaka Kirino (1) (*(1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University*)

2P-204 Rhodobacter capsulatus 由来 PYP の相互作用様式の解析

Interaction mechanism of the photoactive yellow protein of Rhodobacter caplsulatus

Yoichi Yamazaki (1), Narihito Ota (1) , Hironari Kamikubo (1), Mikio Kataoka (1) (*(1) Nara Institute Science and Technology*)

2P-205 Rc-PYP の低温分光

The low-temperature spectroscopy of Rc-PYP

Yuya Hamaguchi (1), Yoichi Yamazaki (1), Hironari Kamikubo (1), Mikio Kataoka (1) (*(1) Nara Institute of Science and Technology*)

2P-206 キメラを用いた Photoactive Yellow Protin の研究

Analysis of the different properties in two PYPs by use of chimera proteins.

Keisuke Matsumoto (1), Yoichi Yamazaki (1), Hironari Kamikubo (1), Mikio Kataoka (1) (*(1) Nara Institute of Science and Technology*)

2P-207 Photoactive Yellow Protein の低障壁水素結合

1YP1-10 Low-barrier hydrogen bond in Photoactive Yellow Protein

Shigeo Yamaguchi (1), Hironari Kamikubo (1), Kazuo Kurihara (2), Ryota Kuroki (2), Yoichi Yamazaki (1), Mikio Kataoka (3) (*(1) Nara Institute of Science and Technology: (2) Japan Atomic Energy Agency: (3) Nara Institute of Science and Technology; Japan Atomic Energy Agency*)

2P-208 高速原子間力顕微鏡によるロドプシンの動態観察

Direct observation of rhodopsin dynamics in disc membrane by high-speed AFM

Hayato Yamashita (1), Mikihiro Sibata (1), Takayuki Uchihashi (5), Yuji Hurutani (2), Takahiro Yamashita (3), Hideki Kandori (4), Yoshinori Shichida (3), Toshio Ando (5) (*(1) Faculty of Science, Depertment of Physics, Kanazawa University: (2) Institute for molecular science; Nagoya Institute of Technology: (3) Depertment of Biophysics, Kyoto University: (4) Nagoya Institute of Technology: (5) Faculty of Science, Depertment of Physics, Kanazawa University;CREST-JST*)

2P-209 イカロドプシンとウシオプシンの分子動力学シミュレーション

Molecular Dynamics Simulation of Squid Rhodopsin and Bovine Opsin

Minoru Sugihara (1), Makiko Suwa (1) (*(1) National Institute of Advanced Industrial Science and Technology (AIST), Computational Biology Research Center (CBRC)*)

2P-210 S-modulin 依存的なロドプシンのリン酸化抑制にはマイクロドメインが重要である

Microdomain in Rod Photoreceptor Disk Membrane is Crucial for Ca^{2+} -dependent Suppression of Rhodopsin Kinase by S-modulin

Fumio Hayashi (1), Keiji Seno (2) (*(1) Kobe Univ: (2) Hamamatsu Univ. School of Medicine*)

2P-211 カエル視細胞の cGMP 分解酵素 PDE6 の二つのγサブユニットは機能分担を行っている

Functional differentiation within two γ subunits of cGMP-phosphodiesterase 6 (PDE6) in frog photoreceptor

Natsumi Saito (1), Fumio Hayashi (1) (*(1) Department of Biology, Faculty of Science, Kobe University*)

2P-212 組換えタンパク質を用いたオーレオクロームの解析

Analyses of aureochrome expressed in *E.coli*

Osamu Hisatomi (1), Keigo Furuya (1), Fumio Takahashi (2), Hironao Kataoka (2) (*(1) Osaka University: (2) Tohoku University*)

2P-213 ２種類の視物質キナーゼ（GRK1、GRK7）の活性の違いをもたらす領域の特定

Identification of a region responsible for higher phosphorylation activity of GRK7 than GRK1

Aki Seno (1), Norihiko Takemoto (1), **Shuji Tachibanaki** (1), Satoru Kawamura (1) (*(1) Grad. Sch. of Frontier Biosciences, Osaka University*)

2P-214 低温分光測定によるゼブラフィッシュクリプトクローム DASH 光反応経路の決定

Photoreaction pathway in zebrafish Cryptochrome-DASH determined by low temperature spectroscopy

Reo Fukazawa (1), Kazunori Zikihara (1), Tomoko Ishikawa (2), Takeshi Todo (2), Satoru Tokutomi (1) (*(1) Department of Biological Science, Graduate School of Science, Osaka Prefecture University: (2) Department of Medical Genetics, Graduate School of Medicine, Osaka University.*)

2P-215 シロイヌナズナ青色光受容体・フォトトロピン２の光シグナル伝達に対するアルギニン 427 の関与

Involvement of Arg427 in the light-signal transduction of Arabidopsis phototropin2, a blue-light photoreceptor

Kazunori Zikihara (1), Hitomi Katsura (1), Sho Oyamatsu (2), Minoru Sakurai (2), Satoru Tokutomi (1) (*(1) Department of Biological Science, Graduate School of Science, Osaka Prefecture University: (2) Center for Biological Resources and Informatics, Tokyo Institute of Technology*)

2P-216 ロドプシンの細胞質側ループを組み込んだ古細菌ロドプシンの研究

2TA2-04 Study on chimeric archaeal-rhodopsin containing cytoplasmic loops of bovine rhodopsin

Aya Nakatsuma (1), Takahiro Yamashita (2), Akira Kawanabe (1), Yuji Furutani (3), Yoshinori Shichida (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Biophysics, Kyoto University: (3) Institute for Molecular Science;Department of Frontier Materials, Nagoya Institute of Technology*)

2P-217 アーキロドプシンからのプロトン放出に関する分光研究

2TA2-03 Spectroscopic study of proton release group of archaerhodopsins

Junya Yamada (1), Kunio Ihara (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Center for Gene Research, Nagoya University*)

2P-218 ロドプシンにおける相乗的な長距離相互作用による吸収波長制御機構

2TA2-06 Molecular mechanism of long-range synergetic color tuning between multiple amino acid residues in rhodopsin

Hiroshi Watanabe (1), Yoshiharu Mori (2), Takahisa Yamato (3) (*(1) Graduate School of Science, Nagoya University; Research Fellow of the Japan Society for the Promotion of Science: (2) Graduate School of Science, Nagoya University; CREST,JST: (3) Graduate School of Science, Nagoya University; CREST,JST*)

2P-219 発光キノコ Mycena　Chlorophos の発光分子機構の解明

Molecular mechanism of bioluminescent *Mycena Chlorophos*

Shuhei Hayashi (1), Ryuichi Fukushima (1), Naiohisa Wada (1) ((*1) Toyo Univ.*)

2P-220 ピコ秒時間分解蛍光分光法による黄化葉の緑化途上における光合成系タンパク質複合体構築過程の観測

Assembly process of photosynthetic pigment-protein complexes during greening of etiolated leaves observed by picosecond time-resolved fluorescence spectroscopy

Yutaka Shibata (1), Shinsuke Okui (1), Yoshiaki Nakagawa (1), Yukari Tahara (1), Shigeru Itoh (1) ((*1) Nagoya University*)

2P-221 ラン藻 *Leptolyngbya boryana* における光非依存型プロトクロロフィリド還元酵素欠損株の細胞内色素分布の顕微分光法による解析

Intracellular pigment distribution in a cyanobacterial mutant lacking light-independent protochlorophyllide reductase using confocal microscope

Yukari Tahara (1), Yutaka Shibata (1), Haruki Yamamoto (2), Yuichi Fujita (2), Shigeru Itoh (1) ((*1) Division of Material Science, Graduate School of Science, Nagoya University: (2) Laboratory of Molecular Plant Physiology, Graduate School of Bioagricultural Sciences, Nagoya University*)

2P-222 シリカメソ多孔体内部の細孔への巨大光合成膜タンパク質複合体の導入とその熱耐性向上機構

Introduction of photosynthetic protein-pigment super complex into nanopores inside silica mesoporous materials and the increase of heat stability inside SMM

Chihiro Kamidaki (1), Souji Ishizaka (1), Tomoyasu Noji (1), Daiju Fujita (1), Tsutomu Kajino (2), Yoshiaki Fukushima (2), Takeshi Sekitoh (3), Shigeru Itoh (1) ((*1) Division of Material Science, Graduate School of Science, Nagoya University: (2) Toyota Central R&D Labs. Inc. : (3) Material Engineering Div.3 TOYOTA MOTOR CORPORATION*)

2P-223 極低温時間分解蛍光測定による *Thermosynechococcus vulucanus* の光化学系２の二量体と単量体のエネルギー移動の比較

Comparision of energy-transfer process between photosystem II monomer and dimer from *Thermosynechococcus vulucanus* studied by time-resolved fluorescence measurement at cryogenic temperature.

Shunsuke Nishi (1), Masayuki Komura (1), Tomoyasu Ｎｏｊｉ (1), Keisuke Kawakami (2), Jian-Ren Shen (2), Yutaka Shibata (1), Shigeru Itoh (1) ((*1) Division of Material Science, Graduate School of Science, Nagoya University: (2) Graduate School of Natural Science and Technology, Okayama University*)

2P-224 被照射細胞における照射領域とバイスタンダー細胞死の関係

Relationship between bystander cell death and intracellular energy-deposition sites

Munetoshi Maeda (1), Masanori Tomita (1), Noriko Usami (2), Katsumi Kobayashi (2) ((*1) Central Research Institute of Electric Power Industry (CRIEPI) : (2) High Energy Accelerator Research Organization (KEK)*))

2P-225 MHz 超音波による U937 細胞におけるシグナルトランスダクションの発現

Expression of signal transduction induced by megahertz ultrasound in human myeloid U937 cells

Yusuke Odate (1), Pak-Kon Choi (1), Wakako Hiraoka (1) ((*1) Department of physics, School of Science and Technology, Meiji University*)

2P-226 フィチン酸（IP６）の活性酸素阻害作用と生物学的効果

Phytic acid-induced ROS regulation and its biological effects on human cells

Asuka Kato (1), Yuki Hirakawa (1), Yoshihiko Inomata (2), Mamoru Aizawa (2), Wakako Hiraoka (1) ((*1) Department of Physics, School of Science and Technology, Meiji University: (2) Laboratory of Biomaterials, Department of Applied Chemistry, School of Science and Technology, Meiji University*)

2P-227 分子内力学ネットワークと分子間反応ネットワークのフラストレーションと機能

Frustrations and functions of molecular machines and reaction networks

Akinori Awazu (1) ((*1) Dept. of Mathematical and Life Sciences*)

2P-228 再帰的な遺伝情報の自己複製システムが in vitro で実現する条件を知る

1YP1-01 What is the condition of realizing a self-replication system of genetic information in vitro?

Norikazu Ichihashi (1), Tomoaki Matsuura (3), Tetsuya Yomo (2) ((*1) Graduate School of Information Science and Technology, Osaka University: (2) Graduate School of Information Science and Technology; Graduate School of Frontier Bioscience, Osaka University; ERATO, JST: (3) Graduate School of Information Science and Technology, Osaka University*)

2P-229 熱水環境下における機能性分子の出現

Fluorescent oligomers as a garbage: a product from hydrothermal vents.

Hideaki Takehana (1), Eiichi Imai (1), Hajime Honda (1) ((*1) Department of Bioengineering, Nagaoka University of Technology*)

2P-230 可塑性、進化可能性、安定性:　表現型揺らぎによるマクロ理論

2TA3-06 Plasticity,　Evolvability and Robustess: A Macroscopic Theory in terms of Phenotypic Fluctuations

Kunihiko Kaneko (1) ((*1) University of Tokyo and　ERATO Complex Systems Biology*)

2P-231 DNA 増幅系を内封した自己生産ベシクル

2TA3-07 DNA replication system in self-reproducing vesicles

Kensuke Kurihara (1), Mieko Tamura (1), Kentaro Suzuki (1), Tadashi Sugawara (1) ((*1) The Univ. of Tokyo*)

2P-232 複合体形成に関与するタンパク質複合体界面の絡まり構造

The interwinding nature of protein interfaces and its implication for protein complex formation

Kei Yura (1), Steven Hayward (3) ((*1) Center for Informational Biology, Ochanomizu University: (2) Graduate School of Humanities and Sciences, Ochanomizu University: (3) School of Computing Sciences, University of East Anglia: (4) School of Biological Sciences, University of East Anglia*)

2P-233 ドメイン構造に基づく生体分子ネットワークの構築と解析

Construction and Analysis of Biomolecular Network based on Domain Structures

Yukari Hayashi (1), Akinori Sarai (2), Satoshi Fujii (3) ((*1) Kyushu Institute of Technology: (2) Kyushu Institute of Technology: (3) Kyushu Institute of Technology*)

2P-234 ストラクチュロームにおける分子ネットワークの系統的解析

Systematic Analysis of Biomolecular Network in Structurome

Mitsuaki Ohtsuka (1), Satoshi Fujii (1), Akinori Sarai (1) ((*1) Kyushu Institute of Technology*)

2P-235 タンパク質機能解析のための配列と構造の粗視化の新手法

A method for coarse level description of sequence and structure for the analysis of protein function

Hisako Ichiahra (1), Wataru Nemoto (2), Hiroyuki Toh (1) ((*1) Medical Institute of Bioregulation, Kyushu Univ.: (2) CBRC, AIST*)

2P-236 最適化された記述子群を用いたドメインリンカー予測法の開発

2TP4-01 An SVM-Domain Linker Prediction Trained with Optimized Features Selected by Random Forest

Teppei Ebina (1), Hiroyuki Toh (2), Yutaka Kuroda (1) ((*1) Dept of Biotech and Life Sci, Tokyo Univ of A & T (TUAT): (2) Div. Bioinf, Med. Inst. of Bioreg, Kyushu Univ*)

2P-237 会合状態変化を伴うタンパク質間相互作用面上の挿入および欠失

2TP4-02 Insertion and/or deletion regions on protein-protein interface to alter oligomeric states.

Hafumi Nishi (1), Motonori Ota (1) ((*1) Grad. Sch. of Inform. Sci., Nagoya Univ.*)

2P-238 部分アミノ酸配列のクラスタリングによる酵素の機能予測

Functional classification of enzymes by clustering of subsequences consisting of active sites and ligand interaction sites.

Chioko Nagao (1), Nozomi Nagano (2), Kenji Mizuguchi (1) ((*1) National Institute of Biomedical Innovation (NIBIO): (2) Computational Biology Research Center (CBRC), AIST; Institute for Bioinformatics Research and Development (BIRD), Japan Science and Technology Agency (JST)*))

2P-239 大規模データマイニングから明らかになったタンパク質リン酸化と複合体形成の関係

2TP4-06 Macroscopic Relationships between Protein Phosphorylation and Physical Interaction

Nozomu Yachie (1), Rintaro Saito (1), Naoyuki Sugiyama (2), Masaru Tomita (1), Yasushi Ishihama (3) ((*1) Inst. Adv. Biosci., Keio Univ.; Syst. Biol. Prog., Grad. Sch. Media & Gov., Keio Univ.: (2) Inst. Adv. Biosci., Keio Univ.: (3) Inst. Adv. Biosci., Keio Univ.; PRESTO, JST*)

2P-240 酵母プロテオームにおけるβシグナルを持たない新規ミトコンドリアβバレル型外膜タンパク質の探索

Search for Novel Mitochondrial β-barrel Outer Membrane Proteins without β-signal in Yeast Proteome

Kenichiro Imai (1), Paul Horton (1), Michel Gromiha (1) ((*1) CBRC, AIST*)

2P-241 核外移行シグナルの配列解析

Sequence Analysis of Nuclear Export Signals

Szu-Chin Fu (1), Paul Horton (2) ((*1) Department of Computational biology, Graduate School of Frontier Science, University of Tokyo, Japan: (2) Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST), Japan*)

2P-242 立体構造を用いたタンパク質機能予測法 FCANAL のさまざまなタンパク質への応用

FCANAL, structure-based protein function prediction method, applied to various types of proteins.

Yuuichi Watanabe (1), Kousuke Kaido (1), Takashi Ando (1), Ichiro Yamato (1), Satoru Miyazaki (2) ((*1) Department of Biological Science and Technology,Tokyo University of Science: (2) 2Department of Pharmaceutical Science and Technology,Tokyo University of Science*)

2P-243 カーネル密度推定を用いたベイズ分類器による配列上の蛋白質間相互作用部位予測

The prediction of protein-protein interaction sites in sequences using a naïve bayes classifier with a kernel density estimation

Yoichi Murakami (1), Kenji Mizuguchi (1) ((*1) National Institute of Biomedical Innovation*)

2P-244 ヒトゲノムからの電荷周期性を持つ DNA 結合タンパク質の解析

Analysis of DNA binding proteins with charge periodicity from human genome

Runcong Ke (1), Noriyuki Sakiyama (1), Shigeki Mitaku (1) ((*1) Dept. of Appl. Phys., Grad Sch. of Engi., Nagoya Univ.*)

2P-245 発生過程の細胞上皮系にかかる力の推定

Estimating forces in the growing epithelial cells

Shuji Ishihara (1), Kaoru Sugimura (3), Atsushi Miyawaki (3) ((*1) Graduate School of Arts and Sciences, Univ. of tokyo: (2) PRESTO, JST: (3) RIKEN BSI*)

2P-246 二温度系におけるロバストネスの進化の統計力学的研究

A statistical-mechanical study of evolution of robustness in noisy environment

Ayaka Sakata (1), Koji Hukushima (1), Kunihiko Kaneko (2) ((*1) Graduate School of Arts and Sciences, University of Tokyo: (2) Graduate School of Arts and Sciences, University of Tokyo, Complex Systems Biology Project, ERATO, JST*)

2P-247 細胞性粘菌の細胞運動を支配する位相方程式と最小記述

The phase equation and minimal description for cell locomotion of dictyostelium

Miki Yamamoto (1), Yusuke Maeda (2), Hirokazu Tanimoto (1), Masaki Sano (1) ((*1) Department of Physics, the University of Tokyo: (2) Rockefeller University*)

2P-248 KaiC タンパク質の概日振動シミュレーションにおけるリン酸化サイクルと ATPase 活性の協調

Coordinated dynamics of phosphorylation and ATP hydrolysis in the simulated circadian oscillation of KaiC

Shinsuke Itagaki (1), Tetsuro Nagai (1), Kazuhito Itoh (2), Tomoki P. Terada (2), Masaki Sasai (2) ((*1) Department of Computational Science and Engineering, Nagoya University: (2) Department of Applied Physics, Nagoya University*)

2P-249 KaiC リン酸化概日振動の引き込み現象

Entrainment of Circadian Oscillation of Phospholyration Level of KaiC in vitro

Tetsuro Nagai (1), Tomoki Terada (2), Masaki Sasai (3) (*(1) Department of Computational Science and Engineering, Nagoya University: (2) Department of Applied Physics, Nagoya University: (3) Department of Applied Physics, Nagoya University;Department of Computational Sciences, Korea Institute for Advanced Study*)

2P-250 細胞内アクチンネットワーク構築に関連するタンパク質の動態解析

Numerical analysis of intracellular molecular dynamics related to organization of actin networks

Michiko Sugawara (1), Hideo Yokota (1) (*(1) RIKEN: (2) PRESTO, JST*)

2P-251 ATM タンパク質の自己リン酸化による双安定性を利用した DNA 損傷シグナルの検出と信号増幅機構

Bistability depending on the ATM autophosphorylation as a sensor and amplifier of DNA damage signals

Kazunari Mouri (1), Nacher Jose (2), Tatsuya Akutsu (3) (*(1) RIKEN: (2) Future University-Hakodate: (3) Institute for Chemical research, Kyoto University*)

2P-252 Pacing induced control of spiral waves in heart tissue

Marcel Horning (1), Akihiro Isomura (2), Kenichi Yoshikawa (1) (*(1) Kyoto University, Department of Physics: (2) Kyoto University, Institute for Virus Research*)

2P-253 化学反応系の離散性：時間変動解析

Discreteness of Chemically Reacting Systems: Time Fluctuation Analysis

Taichi Haruna (1) (*(1) Graduate School of Science, Kobe University; PRESTO, JST*)

2P-254 集団ダイナミクスにおけるノイズ強度のシステムサイズ依存性はネットワーク構造が決定する

2TP3-01 Structure of networks determines the system size dependency of noise intensity in collective dynamics

Naoki Masuda (1), Yoji Kawamura (2), **Hiroshi Kori** (3) (*(1) University of Tokyo: (2) JAMSTEC: (3) Ochanomizu University*)

2P-255 クラミドモナスにおける光誘導倒立生物対流の細胞ダイナミクス

2TP3-02 Cellular dynamics of light-induced inverted bioconvection in *Chlamydomonas reinhardtii*

Naoki Sato (1) (*(1) University of Tokyo, Graduate School of Arts and Sciences*)

2P-256 二面偏波式干渉技術を用いた熱応答性高分子の分子ダイナミクス解析

Molecular Dynamics of thermal response polymer using dual polarization interferometry

Kohei Shiba (1), Takeshi Mori (1), Takuro Niidome (1), Yoshiki Katayama (1) (*(1) Kyushu University*)

2P-257 超高速リアルタイム PCR 装置を用いた非特異的 DNA 断片増幅の抑制

Minimized Non-specific Amplification with A Rapid Denaturation to Annealing Temperature Transition Using Novel Ultra Rapid Real-Time PCR system

Hideyuki Terazono (1), Hiroyuki Takei (3), Kenji Yasuda (2) (*(1) Kanagawa Academy of Science and Technology: (2) Kanagawa Academy of Science and Technology; Department of Biomedical Information, Division of Biosystems, Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University: (3) Kanagawa Academy of Science and Technology; Faculty of Life Science, Toyo University*)

2P-258 細胞内の局所的な温度変化の測定とその解析

2TA3-09 Measurement and analysis of local temperature change inside living cells.

Kotaro Oyama (1), Madoka Suzuki (2), Vadim Tseeb (3), Fumichika Ono (4), Yusuke Seto (4), Masahiro Motoyoshi (1), Kaoru Iwai (5), Shin'Ichi Ishiwata (3) (*(1) Pure and Applied Physics, Graduate School of Advanced Science and Engineering, Waseda University: (2) COBRI, Comprehensive Research Organization, Waseda University: (3) Department of Physics, Faculty of Science and Engineering, Waseda University: (4) Bioscience and Biomedical Engineering, Graduate School of Advanced Science and Engineering, Waseda University: (5) Department of Chemistry, Faculty of Science, Nara Women's University*)

2P-259 人口平面膜法と AFM を融合させた膜蛋白質の電流、力同時計測手法の開発

Combined AFM and channel recording system for electrophysiological and dynamic channel function research

Mitsunori Kitta (1), Hiroyuki Tanaka (1), Tomoji Kawai (1) (*(1) the Institute of Science and Industrial Research, Osaka University*)

2P-260 神経突起内ミトコンドリアの光学距離と膜電位

Optical distance and membrane potential of mitochondria in neurites

Keisuke Haseda (1), Kazuhiro Kajiyama (2), Yoshihiro Ohta (3) (*(1) Div. Biotechnology and Lifescience , Tokyo University of Agriculture and Technology: (2) Div. Biotechnology and Lifescience , Tokyo University of Agriculture and Technology: (3) Div. Biotechnology and Lifescience , Tokyo University of Agriculture and Technology*)

2P-261 シグナル伝達活性化におけるＴ細胞受容体分子会合の１分子解析

Single molecule analysis of microclustering of signaling molecules on T cell activation

Makio Tokunaga (1), Kumiko Sakata-Sogawa (2) (*(1) Grad. School of Bioscience & Biotechnology, Tokyo Inst. of Technology: (2) Research Center for Allergy & Immunology, RIKEN*)

2P-262 分子内閉環・開環を制御原理とする新規酵素活性検出蛍光プローブの設計

Novel design strategy for various fluorescence probes to detect activity of protease based on unique intramolecular spirocyclization

Masayo Sakabe (1), Yasuteru Urano (2), Tetsuo Nagano (1) (*(1) Graduate School of Pharmaceutical Sciences, Univ of Tokyo, JST CREST: (2) Graduate School of Pharmaceutical Sciences, Univ of Tokyo*)

2P-263 がん選択的な PDT の実現を目指した activatable 光増感剤の開発

Development of an Activatable Photosensitizing Probe Aimed for Tumor Specific PDT

Yuki Ichikawa (1), Yasuteru Urano (2), Tetsuo Nagano (1) (*(1) Graduate school of Pharmaceutical Sciences, The University of Tokyo; JST CREST: (2) Graduate school of Pharmaceutical Sciences, The University of Tokyo*)

2P-264 ミューラー行列イメージング法の構築２

Construction of Mueller matrix imaging system

Yasuaki Eda (1), Kazuo Ohki (1), Tetsuhiko Ohba (1) (*(1) Dept Physics, Graduate School of Science Tohoku Univ*)

2P-265 有機シリカ粒子技術を用いた新規なマルチモーダルイメージングプローブの開発

Development of novel multimodal imaging probe using organosilica particle technology

Michihiro Nakamura (1), Kazunori Ishimura (1) (*(1) Dep. of Anatomy and Cell Biology, University of Tokushima Graduate School*)

2P-266 新規遠心顕微鏡を用いた重力感受に関わるアミロプラスト動態の解析

Analysis of amyloplast dynamics involved in gravity sensing using a novel centrifuge microscope

Masatsugu Toyota (1), Masao Tasaka (1), Miyo Morita Terao (2) (*(1) Graduate School of Biological Sciences, Nara Institute of Science and Technology: (2) Graduate School of Biological Sciences, Nara Institute of Science and Technology; PRESTO, JST*)

2P-267 蛍光タンパク質の 2 量体界面への変異が FRET インジケータのダイナミックレンジに及ぼす影響

The effect on the dynamic range of FRET indicators by mutation in fluorescent protein dimerization interface

Ippei Kotera (1), Takeharu Nagai (1), Takuya Iwasaki (1) (*(1) Research Institute for Electronic Science, Hokkaido University*)

2P-268 FRET 指示薬における遷移双極子モーメント、FRET 効率、及びダイナミックレンジの相互関係

Correlation among dipole orientation, FRET efficiency and dynamic range of FRET-based indicators

Daisuke Nagai (1), Sanq-Yeob Kim (1), Tomomi Tani (1), Takeharu Nagai (1) (*(1) Research Institute for Electronic Science, Hokkaido*)

2P-269 植物細胞における長時間生理機能イメージングを目指した赤方化指示薬開発

Long time physiological imaging of plant cells with reduced autofluorescence by using a Ca^{2+} indicator composed of a red-shifted FRET pair.

Toshiaki Uematsu (1), Ippei Kotera (1), Kenta Saito (1), Noriyuki Hatsugai (1), Kazuki Horikawa (1), Takeharu Nagai (1) (*(1) Research Institute for Electronic Science, Hokkaido University*)

2P-270 単一細胞エレクトロポレーションによって培養小脳神経細胞に導入された siRNA の効果の長期リアルタイムモニタリング

Long-term and real-time monitoring of effects of small interfering RNA introduced by single-cell electroporation in cultured cerebellar neurons

Masahiko Tanaka (1), Yuchio Yanagawa (2), Naohide Hirashima (1) (*(1) Graduate School of Pharmaceutical Sciences, Nagoya City University: (2) Graduate School of Medicine, Gunma University*)

2P-271 投影型 X 線顕微鏡によるケジラミのマイクロ CT

Micro-CT of *Pthirus pubis* by projection X-ray micosopy

Junichi Moriya (1), Toshiaki Higashikawa (2), Hideyuki Yoshimura (1) (*(1) Meiji university: (2) Higashikawa Dermatology Office*)

2P-272 蛍光タンパク質を用いた核膜透過性の検討

Diffusion of Large Molecules into Assembling Nuclei Revealed Using an Optical Highlighting Technique

Satoshi Shimozono (1), Hidekazu Tsutsui (1), Atsushi Miyawaki (1) (*(1) The Institute of Physical and Chemical Research*)

2P-273 テトラアンミン錯体とアポフェリチンを用いた新規化合物半導体ナノ粒子の作製

Synthesis of new semiconductor nano-particles by a tetraammine complex and cage-shaped protein, apoferritin

Kenji Iwahori (1), Rie Takagi (2), Naoko Kishimoto (2), Midori Yamane (2), Ichiro Yamashita (3) (*(1) PRESTO, Japan Science and Technology Agency; Nara Insitute of Science and Technology: (2) Nara Institute of Science and Technology, Material and Science : (3) Nara Institute of Science and Technology, Material and Science; ATRL, Panasonic*)

2P-274 細胞観察用 tip-scan 型高速原子間力顕微鏡の開発

Development of tip-scan type of high-speed AFM for cell imaging

Yasutaka Okazaki (1), Takayuki Uchihashi (2), Toshio Ando (2) (*(1) Department of Mathematics and Physics, Grad School of Natural Science and Technology, kanazawa Univ.: (2) School of Mathematics and Physics, College of Science and Engineering, Kanazawa Univ.;CREST/JST*)

2P-275 自己集合核酸からなる拡張可能なナノトラス構造体：そのデザインと階層的な構築

Expandable nano-truss-structures made of self-assembled nucleic acids: Their designing and hierarchical construction

Takanobu Tsutsumi (1), Takao Okada (2), Kenshi Hayashi (1) (*(1) Division of Genome Analysis, Research Center for Genetic Information, Medical Institute of Bioregulation, Kyushu University: (2) Reseaarch Institute of Biomolecule Metrology Co., Ltd*)

2P-276 相同組換えタンパク質 RecA を用いた新規オプティカルマッピング法の開発

2TA5-06 Development of novel DNA optical mapping method using homologous recombination protein, RecA

Yuya Goto (1), **Yuji Kimura** (2), Hidehiro Oana (3), Masao Washizu (4) (*(1) Department of Mechanical engineering, the University of Tokyo: (2) Deparment of Bioengineering, the University of Tokyo;JST CREST: (3) Department of Mechanical engineering, the University of Tokyo; JST CREST: (4) Department of Bioengineering and Mechanical engineering, the University of Tokyo; JST CREST*)

2P-277 異種ビーズを隣接させた状態で観察可能なダイナミックマイクロアレイ

2TA5-08 Dynamic Microarray Technology for observation of adjacent different beads

Tetsuhiko Teshima (1), Kosuke Iwai (1), Hirotaka Ishihara (1), Shoji Takeuchi (1) (*(1) Institute of Industrial Science (IIS), The University of Tokyo*)

2P-278 bistable な DNA で実装する温度バンドパスフィルタ

2TA5-10 Thermal band pass filter implemented with a bistable DNA

Ken Komiya (1), Masayuki Yamamura (1), John A. Rose (2) (*(1) Tokyo Institute of Technology: (2) Ritsumeikan APU*)

第 3 日目（11 月 1 日（日））/ Day 3 (Nov. 1, Sun.)

3P-001 PCNA G178S 変異体の構造解析

Structural analysis of PCNA with G178S mutation

Asami Hishiki (1), Toshiyuki Shimizu (1), Satoko Akashi (1), Satoru Unzai (1), Mamoru Sato (1), **Hiroshi Hashimoto** (1) (*(1) Yokohama City University*)

3P-002 時間分割X線結晶構造解析による銅・トパキノン含有アミン酸化酵素反応機構の構造学的研究

X-ray crystal structure analysis of reaction intermediate of Copper and TPQ containing Amine oxidase from *Arthrobacter globiformis*

Misumi Kataoka (1), Ayuko Tominaga (1), Masayuki Ohtsu (1), Toshihide Okajima (2), Katsuyuki Tanizawa (2), Hiroshi Yamaguchi (1) (*(1) School of Science and Technology, Kwansei Gakuin University: (2) Institute of Scientific and Industrial Research, Osaka University*)

3P-003 SDSL EPR による距離測定におけるスピンラベル分子の運動性の影響

The influence of the spin label mobility on the distance measurement of SDSL EPR in protein structure

Shoji Ueki (1), Jun Abe (2), Yasunori Ohba (2), Toshiaki Arata (3) (*(1) Kagawa School of Pharmaceutical Science, Tokushima Bunri Univ.: (2) Tohoku Univ.: (3) Graduate School of Science, Osaka Univ.*)

3P-004 ホスト決定残基 K627 を含むインフルエンザウィルス RNA ポリメラーゼ PB2 のX線結晶構造解析

Crystal structure of influenza virus RNA polymerase PB2 including host determinant residue K627

Hideaki Tsuge (1), Hiroko Utsunomiya (1), Daisuke Kise (2), Noriko Echigo (2), Takashi Kuzuhara (2) (*(1) Institute for Health Sciences, Tokushima Bunri University: (2) Faculty of Pharmaceutical Sciences, Tokushima Bunri University*)

3P-005 四量体 Orai1 分子は細長い細胞質ドメインを持つ水滴形構造である

3D structure of tetrameric Orai1 channel; a teardrop-shaped structure with a long, tapered cytoplasmic domain

Yuusuke Maruyama (1), Toshihiko Ogura (1), Kazuhiro Mio (1), Kenta Kato (2), Takeshi Kaneko (2), Shigeki Kiyonaka (2), Yasuo Mori (2), Chikara Sato (1) (*(1) National Institute of Advanced Industrial Science and Technology (AIST): (2) Department of Synthetic Chemistry and Biological Chemistry, Graduate School of Engineering, Kyoto University*)

3P-006 蛋白質のデコイ構造識別関数 DFMAC の拡張と性能評価

Expansion of decoy-discriminating function DFMAC and its performance in some applications

Yoshihide Makino (1), Nobuya Itoh (1) (*(1) Department of Biotechnology, Faculty of Engineering, Toyama Prefectural University*)

3P-007 アルツハイマー病関連タンパク質に存在する D-アミノ酸に関する解析

D-amino acids are contained in the Alzheimer's disease-related proteins.

Akiko Kasai (1), Naoko Tate (1) (*(1) Faculty of Pharmacy, Reserch Institute of Pharmaceutical Science, Musashino University*)

3P-008 ヒト由来アリルカーボンリセプタダイオキシン結合ドメインの構造モデリングとその動的構造の解析

Structural Modeling and Dynamical Properties of Human Aryl Hydrocarbon Receptor Dioxin Binding domain

Sundaram Arulmozhira (1), Yohsuke Hagiwara (2), Takao Ohno (1), **Masaru Tateno** (2) (*(1) National Institute of Material Science: (2) University of Tsukuba*)

3P-009 蛋白質高次構造会合・解離反応に及ぼす kosmotrope や chaotrope 溶質の影響

Effect of Kosmotropic and Chaotropic Solutes on the Assembly of Protein Macromolecular Structures

Yuki Yashiro (1), Antonio Tsuneshige (2) (*(1) Department of Materials Chemistry, Graduate School of Engineering: (2) Department of Frontier Bioscience, Faculty of Bioscience and Applied Chemistry, Hosei University, Tokyo, JAPAN*)

3P-010 ナトリウム結合部位を標的としたトロンビン阻害剤の設計に関する研究

A study on the design of thrombin inhibitors targeting the Na^+ binding site

Daisuke Iyaguchi (1), Kouichi Uno (1), Eiko Toyota (1) (*(1) Graduate School of Pharmaceutical Sciences, Health Sciences University of Hokkaido*)

3P-011 化合物の自動サーチとフィッティング方の開発

A method of locating and fitting ligands for X-ray crystallography

Yong Zhou (1), Junji Yamane (2), Min Yao (1), Isao Tanaka (1) (*(1) Faculty of Advance Life Science, Hokkaido University: (2) Graduate School of Life Science, Hokkaido University*)

3P-012 新規フォールドに対する立体構造予測に向けてーフラグメントアセンブリ法による予測精度のライブラリ依存性—

Toward the Success of Template-Free Protein Structure Prediction -Dependency of Performance on the Fragment Libraries-

Shintaro Minami (1), George Chikenji (1) (*(1) Department of Computational Science and Engineering, Nagoya University Graduate School of Engineering*)

3P-013 文脈依存スコアによる蛋白質構造予測

Context-specific score for protein structure prediction

Hikmet Cetin (1), Takeshi N Sasaki (2), **Masaki Sasai** (3) (*(1) Nagoya University: (2) Aichi Shukutoku University: (3) Nagoya University; Korea Institute for Advanced Study*)

3P-014 フラグメントアセンブリによる大規模蛋白質構造リファインメント

Large scale protein structure refinement by fragment assembly

Kengo Sawada (1), George Chikenji (2) (*(1) Department of Computational Science and Engineering, Nagoya University: (2) Department of Engineering , Nagoya University*)

3P-015 “ゴーストウォーター”を含む全原子モデルによるタンパク質構造予測

Protein structure prediction by the all atom model that includes “ghost water”

Shumpei Sawato (1), George Chikenji (1) (*(1) Dept. of Compu. Sci. and Eng., Grad. Sch. of Eng., Nagoya Univ.*)

3P-016 マウスプリオンタンパク質ミュータントの線維形成

Fibril formation of mouse prion mutants

Masaki Shibuya (1), Yasuko Watanabe (2), Kazuhisa Kubota (1), Keiko Takahashi (3), Hidehiko Nakagawa (4), Naoki Miyata (4), Osamu Inanami (2), Wakako Hiraoka (1) (*(1) Department of Physics, School of Science and Technology, Meiji University: (2) Laboratory of Radiation Biology, Department of Environmental Veterinary Medical Sciences, Graduate School of Veterinary Medicine, Hokkaido University: (3) Department of*

Nanochemistry, Faculty of Engineering, Tokyo Polytechnic University: (4) Department of Organic and Medicinal Chemistry, Graduate School of Pharmaceutical Sciences, Nagoya City University)

3P-017 アミノ酸対形成傾向がβシート中でのストランド配置順に与える効果

Effect of amino acid pairing propensity on β-strand order in the β-sheets

Hiromi Suzuki (1) ((*1) School of Agriculture, Meiji University*)

3P-018 網羅的比較シミュレーションシステムの開発

Development of an exhaustive comparative simulation system

Tohru Terada (1), Tadaomi Furuta (1), Takayuki Amemiya (2), Akinori Kidera (3) ((*1) Molecular Scale Team, Computational Science Research Program, RIKEN: (2) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University: (3) Molecular Scale Team, Computational Science Research Program, RIKEN;Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University*)

3P-019 Go モデルによるタンパク質のフォールディングシミュレーションと残基間平均距離統計に基づくフォールディング機構予測との比較

Protein folding simulation based on the Go model and comparison with the predictions of folding mechanism based on the interresidue average distance statistics

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3P-020 T4 ファージ尾部基盤を構成するウェッジの in vitro 分子集合

Baseplate Wedge Assembly of Bacteriophage T4 in vitro

Moh Lan Yap (1), Yasunori Monzaki (1), Kazuhiro Mio (2), Leiman Petr (3), Shuji Kanamaru (1), Fumio Arisaka (1) ((*1) Grad. Sch. of Biosci. and Biotech., Tokyo Institute of Technology: (2) National Institute of Advanced Industrial Science and Technology, AIST: (3) École Polytechnique Fédérale de Lausanne, Institut de physique des systèmes biologiques, Cubotron, Switzerland*)

3P-021 ヒトガレクチン１の糖結合活性の pH 依存性

pH dependence of the galactoside-binding activity of human galectin-1

Katsuyuki Takeuchi (1), Hirotsugu Hiramatsu (1), Hideo Takeuchi (1) ((*1) Graduate School of Pharmaceutical Science, Tohoku University*)

3P-022 細菌べん毛ペリプラズムタンパク質 FlgA のＸ線結晶構造と機能解析

X-ray Crystal Structure and Functional Analysis of a Periplasmic Flagellar Protein FlgA

Hideyuki Matsunami (1), Samatey Fadel A. (1), Shigehiro Nagashima (2), Katsumi Imada (2), Keiichi Namba (2) ((*1) Trans-Membrane Trafficking Unit, OIST; Dynamic NanoMachine Project, ICORP, JST: (2) Dynamic NanoMachine Project, ICORP, JST; Grad. Sch. Frontier. Biosci., Osaka Univ.*)

3P-023 Febuxostat とキサンチン脱水素酵素の鍵と鍵穴機構におけるタンパク質の揺らぎの重要性

Significance of enzyme fluctuation in the lock-key mechanism between xanthine oxidoreductase and Febuxostat

Hiroto Kikuchi (1), Hiroshi Fujisaki (2), Tadaomi Furuta (4), Ken Okamoto (3), Takeshi Nishino (3), Silke Leimkuhler (4) ((*1) Dept. of Phys., Nippon Medical School: (2) Molecular Scale Team, Computational Science Research Program, RIKEN: (3) Dept. of Biochem. and Mol. Biol., Nippon Medical School: (4) Inst. of Biochem. and Biol., Univ. of Potsdam, Germany*)

3P-024 インターロイキン 13 受容体α２（IL-13Rα２）の調製とその性質

Expression and Characterization of Interleukin-13 receptor α2 chain (IL-13Rα2)

Fumiko Matsumoto (1), Taro Tamada (1), Eijiro Honjo (1), Shoichiro Ohta (2), Kenji Izuhara (2), Ryota Kuroki (1) ((*1) Molecular Structural Biology Group, Quantum Beam Science Directorate, Japan Atomic Energy Agency: (2) Division of Medical Biochemistry, Department of Biomolecular Sciences, Saga Medical School*)

3P-025 F_oF_1－ATP 合成酵素の非共鳴ラマン研究

Non-Resonance Raman Investigations of Bovine Mitochondrial F_oF_1-ATPsynthase

Kaoru Mieda (1), Minoru Kubo (1), Kyoko Shinzawa-Itoh (1), Takashi Ogura (1), Shinya Yoshikawa (1) ((*1) Department of Life Science, Graduate School of Life Science, University of Hyogo*)

3P-026 新規がん細胞増殖抑制ペプチドの構造 - 活性相関

Structure-activity relationship of a novel peptide with cancer cell growth-inhibitory activity.

Keisuke Oyauchi (1), Masakatsu Kamiya (1), Tomoyasu Aizawa (2), Makoto Demura (1), Koichi Suzuki (3), Keiichi Kawano (2) ((*1) Graduate School of Life Science, Hokkaido University: (2) Graduate School of Science, Hokkaido University: (3) Faculty of Agriculture, Iwate University*)

3P-027 2009 年に流行したブタインフルエンザウイルスはヒト型受容体に結合しやすくなったか？

The binding affinity of swine influenza virus which caused global outbreak in 2009 to human type receptor.

Katsumi Omagari (1) ((*1) Nagoya City University*)

3P-028 ATPase 活性の抑制機構を理解するための KaiC のＮ末端ドメインのＸ線構造解析

X-ray structural analysis of N-terminal domain of KaiC (KaiCI) for understanding of restrained ATPase activity

Se-Young Son (1), Hee-Jin Kang (2), Ken-Ichi Miyazono (2), Masaru Tanokura (2), Nobuhisa Watanabe (3), Takao Kondo (1), Shuji Akiyama (1) ((*1) Graduate School of Science, Nagoya University; JST CREST: (2) Graduate School of Agricultural and Life Sciences, The University of Tokyo: (3) Graduate School of Engineering, Nagoya University*)

3P-029 クラマースの理論とタンパク質機能の分子力学

Kramers theory and molecular mechanism of protein functions

Atumi Yamasita (1), Takahisa Yamato (2) ((*1) Department of Physics School of Science Nagoya University : (2) Department of Physics School of Science Nagoya University;CREST-JST;Baylor College of Medicine*)

3P-030 ミトコンドリア膜間部タンパク質 Tim40 の構造解析

Structural analysis of mitochondrial thiol oxidase Tim40

Shin Kawano (1), Takaki Momose (1), Kayoko Terao (1), Koji Yamano (1), Nobuhisa Watanabe (2), Toshiya Endo (1) ((*1) Department of Chemistry, Nagoya University: (2) Nagoya University Synchrotron radiation Research Center*)

3P-031 分子動力学計算を用いた LILRB1/HLA-G と LILRB2/HLA-G の結合機構の違いに関する研究

Molecular dynamics simulation studies on the differences in the binding mechanism of LILRB1/HLA-G and LILRB2/HLA-G

Naoyuki Miyashita (1), Katsumi Maenaka (2), Yuji Sugita (3) ((*1) RIKEN Computational Science Research Program: (2) Medical Institute of Bioregulation, Kyushu University: (3) RIKEN Advanced Science Institute; JST-BIRD; JST-CREST*)

3P-032 高分解能結晶構造によるフェリチンにおける鉄放出の分子機構の解明

Atomic Resolution Structures Indicate A Molecular Mechanism for Iron Release Through Functional Pore in Ferritin.

Takehiko Tosha (1), Ho-Leung Ng (3), Onita Bhattasali (2), Tom Alber (3), Elizabeth Theil (2) ((*1) RIKEN SPring-8 Center, Harima Institute: (2) Children's Hosp. Oakland Res. Inst.: (3) UC-Berkeley*)

3P-033 オンサーガー・マハラップ作用とレプリカ交換を組み合わせたパスサンプリング：モデル計算

Transition path sampling using the Onsager-Machlup action with replica exchange: Model calculations

Hiroshi Fujisaki (1), Motoyuki Shiga (2), Akinori Kidera (3) ((*1) Molecular Scale Team, Computational Science Research Program, RIKEN: (2) Material Simulation, Center for Computational Science & E-systems, JAEA: (3) Molecular Scale Team, Computational Science Research Program, RIKEN; Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University*)

3P-034 脂肪酸β酸化酵素複合体構造変化の分子動力学シミュレーション

Molecular dynamics simulation of conformational change in a fatty acid β-oxidation multienzyme complex

Tadaomi Furuta (1), Tohru Terada (1), Akinori Kidera (2) ((*1) Molecular Scale Team, Computational Science Research Program, RIKEN: (2) Molecular Scale Team, Computational Science Research Program, RIKEN;Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University*)

3P-035 自由エネルギー変分原理に基づく結合自由エネルギー予測と化学的性質によるリガンドの分類

Prediction of binding free energy based on a free energy variational principle and classification of ligands by chemical property

Yasutomo Mianami (1), Takeshi Kikuchi (1) ((*1) Dept. Bioinfomatics, Col. Life Sci., Ritsumeikan Univ.*)

3P-036 低 pH 条件下のニワトリリゾチームにおける圧力－温度の相図

The pressure-temperature phase diagram of hen lysozyme at low pH

Akihiro Maeno (1), Hiroshi Matsuo (2), Kazuyuki Akasaka (1) ((*1) High Pressure Protein Research Center, Institute of Advanced Technology, Kinki University, Japan: (2) Niigata Industrial Creation Organization, Japan*)

3P-037 酸化還元反応に伴うアズリン－シトクロム複合体の 自由エネルギー変化

Free Energy Change of Azurin-Cytochrome Complex by Redox Reaction: A Molecular Dynamics Study

Hidemi Nagao (1), Hiroaki Saito (1), Keisuke Matsumoto (1), Riki Nakamura (1), Taku Mizukami (2) ((*1) Kanazawa University: (2) JAIST*)

3P-038 エネルギー表示法による球状タンパク質の溶媒和自由エネルギー計算

Solvation free energy of globular protein: an estimation by means of energy representation method

Hiroaki Saito (1), Keisuke Matsumoto (1), Riki Nakamura (1), Taku Mizukami (2), Kiyoshi Nishikawa (1), Hidemi Nagao (1) ((*1) Faculty of mathematics and physics, institute of science and engineering, Kanazawa University: (2) School of Materials Science, Japan Advanced Institute of Science and Technology (JAIST)*)

3P-039 アズリン(II) - シトクロム(II)複合体の水和構造の違いによる安定性の変化

Stability of Azurin(II)-Cytochrome(II) Complex: An effect of Change of Hydration Structure

Riki Nakamura (1), Keisuke Matsumoto (1), Hiroaki Saito (1), Taku Mizukami (2), Masaru Tateno (3), Kiyoshi Nishikawa (1), Hidemi Nagao (1) ((*1) Faculty of Mathematics and physics, institute of science and engineering, Kanazawa University: (2) School of Materials Science, Janan Advanced Institute of Science and Technology (JAIST): (3) Graduate School of Pure and Applied Sciences, Tsukuba University*)

3P-040 分子動力学シミュレーションによる staphylococcal protein A の B domain のフォールディング機構の研究

Folding simulation of the B-domain of staphylococcal protein A

Kenichiro Nishi (1), Tohru Terada (2), Kentaro Shimizu (1) ((*1) Graduate School of Agricultural and Life Sciences, The University of Tokyo: (2) Computational Science Research Program, RIKEN*)

3P-041 all-βタンパク質の二次構造拘束付きマルチカノニカル分子動力学シミュレーション

Multicanonical molecular dynamics simulation of an all-β protein with secondary structure restraints

Asahiko Nishimura (1), Tohru Terada (2), Kentaro Shimizu (1) ((*1) Department of Biotechnology, Graduate School of Agricultural and Life Sciences, University of Tokyo: (2) RIKEN*)

3P-042 ライン共焦点顕微鏡による蛋白質折り畳みのマイクロ秒分解一分子追跡

Microsecond-resolved single-molecule time traces of protein folding by a line-illuminated confocal microscopy

Hiroyuki Oikawa (1), Kiyoto Kamagata (1), Yuji Goto (2), Satoshi Takahashi (1) ((*1) Institute of Multidisciplinary Research for Advanced Materials, Tohoku University; CREST, JST: (2) Institute for Protein Research, Osaka University*)

3P-043 誘電緩和分光法による、シトクロム c の中間変性状態における水和状態の温度依存性

Temperature dependences of hydration properties of intermediately denatured horse heart cytochrome *c*

Yusuke Miyashita (1), Tetsuichi Wazawa (2), Takashi Miyazaki (1), Makoto Suzuki (1) ((*1) Tohoku Univ. Grad. Sch. of Eng.: (2) CREST/JST*)

3P-044 水溶性球状タンパク質への麻酔薬の本質的な結合様式

Intrinsic binding modes of anesthetics to water-soluble globular proteins

Makoto Nishimoto (1), Nobutake Tamai (2), Michio Yamanaka (3), Hitoshi Matsuki (2) ((*1) Grad. Sch. of Advan. Tech. & Sci., The Univ. of Tokushima: (2) Inst. Tech. & Sci., The Univ. of Tokushima: (3) Dept. of Chem. Fac. of Sci., Kyushu Univ.*)

3P-045 Staphylococcal nuclease アラニン挿入変異体の結晶学的研究

Crystallographic study of the alaine insertion mutants of Staphylococcal nuclease

Hiroshi Yoshioka (1), Sigeo Yamaguchi (1), Hironari Kamikubo (1), Yoichi Yamazaki (1), Mariko Yamaguchi (1), Mikio Kataoka (1) (*(1) Nara Institute of Science and Technology*)

3P-046 エレメント置換による蛋白質の機能獲得の試み

Attempt to create an artificial functional protein by exchange of functional elements.

Akihiro Kogasaka (1), Hironari Kamikubo (1), Masayoshi Onitsuka (1), Yoichi Yamazaki (1), Mariko Yamaguchi (1), Mikio Kataoka (1) (*(1) Nara institute of science and technology*)

3P-047 アゾベンゼンを用いた構造エレメントのモジュレーション

Direct structural modulation of the structure element of SNase by using the azobenzene linkage.

Kensuke Saito (1), Hironari Kamikubo (1), Yoichi Yamazaki (1), Mariko Yamaguchi (1), Mikio Kataoka (1) (*(1) Nara Institute of Science and Technology*)

3P-048 誘導折り畳み反応のΦ値解析: スタフィロコッカルヌクレアーゼ変異体の誘導折り畳み反応におけるリガンド結合の役割

Φ-value analysis of induced folding: the role of the ligand binding in induced folding of disordered staphylococcal nuclease mutant

Masayoshi Onitsuka (1), **Hironari Kamikubo** (1), Yoichi Yamazaki (1), Mikio Kataoka (1) (*(1) Nara Institute of Science and Technology*)

3P-049 電子常磁性共鳴分光法による天然変性 Staphylococcal Nuclease 変異体の構造解析

Structural Characterization of the Intrinsically Disordered Mutants of Staphylococcal Nuclease by Electron Paramagnetic Resonance Spectroscopy

Hiroki Sawada (1), S.Budamagunta Madhu (2), Hironari Kamikubo (1), Yoichi Yamazaki (1), Mariko Yamaguchi (1), C. Voss John (2), Mikio Kataoka (1) (*(1) Graduate School of Materials Science, Nara Institute of Science and Technology: (2) Department of Biochemistry and Molecular Medicine, School of Medicine, University of California, Davis*)

3P-050 網羅的アラニン挿入変異解析法を用いたジヒドロ葉酸還元酵素の機能発現及び構造形成領域の抽出

Extraction of the regions encoded foldability and/or functionability from Dihydrofolate reductase by the systematic alanine insertion

Rumi Shiba (1), Hironari Kamikubo (1), Mika Umeyama (1), Sayaka Tsukasa (1), Yoichi Yamazaki (1), Mariko Yamaguchi (1), Masahiro Iwakura (2), Mikio Kataoka (1) (*(1) Nara institute of science and technology: (2) National Institute of Advanced Industrial Science and Technology*)

3P-051 網羅的アラニン挿入変異解析による Human p100 SNase 様ドメインの構造形成に関わる領域の抽出

Extraction of the structural element of SNase-like domain in Human p100 by Alanine Insertion Analysis

Yoko Ogawa (1), Hironari Kamikubo (1), Chikako Komeda (1), Mariko Yamaguchi (1), Yoichi Yamazaki (1), Mikio Kataoka (1) (*(1) NAIST*)

3P-052 HMGB2 タンパク質の構造安定性に関する解析

Analysis of structure stability of HMGB2

Hiroshi Moriuchi (1), Shin-Ichi Tate (2), Naoko Tate (1) (*(1) Research Institute of Pharmaceutical Science, Musashino University: (2) Graduate School of Science, Hiroshima University*)

3P-053 蛋白質アロステリーの統計力学

Statistical Mechanical Theory of Protein Allostery

Kazuhito Itoh (1), Masaki Sasai (1) (*(1) Department of Applied Physics, Nagoya University*)

3P-054 拡張アンサンブル法を用いた生体分子の温度・圧力依存性の研究

Molecular dynamics study of temperature and pressure effects on a biomolecule with generalized-ensemble algorithms

Yoshiharu Mori (1), Yuko Okamoto (1) (*(1) Department of Physics, School of Science, Nagoya University*)

3P-055 異なる蛋白質のアロステリックな構造変化のカメレオン郷モデルによるモデリング

Modeling allosteric conformational changes of different proteins with chameleon Go Model

Syogo Yokota (1), Takahiro Yamashita (1), Tomoki Terada (2) (*(1) Department of Computational Science and Engineering, Nagoya University: (2) Department of Applied Physics,Nagoya University*)

3P-056 遺伝的交叉を用いた徐冷分子動力学シミュレーション

A simulated annealing molecular dynamics simulation with a genetic crossover for protein systems

Yoshitake Sakae (1), Tomoyuki Hiroyasu (2), Mitsunori Miki (3), Yuko Okamoto (1) (*(1) Department of Physics, Nagoya University: (2) Department of Biomedical Information, Doshisha University: (3) Department of Intelligent Information Engineering and Sciences, Doshisha University*)

3P-057 レプリカ交換モンテカルロシミュレーションを用いた膜タンパク質の構造予測シミュレーション

Prediction of membrane protein structures by replica-exchange Monte Carlo simulations

Koichi Sugimoto (1), Hironori Kokubo (2), Yuko Okamoto (1) (*(1) Department of Physics School of Science Nagoya University: (2) Department of Chemistry University of Houston*)

3P-058 新規一分子解析法を用いたアミロイドβ多量体の解析

Amyloid beta oligomer formation studied by newly developed single molecule analysis method

Naofumi Terada (1), Tamotsu Zako (1), Masafumi Sakono (1), Mizuo Maeda (1) (*(1) RIKEN*)

3P-059 生体高分子の MM-CG シミュレーション

Multiscale MM-CG Simulation of Complex Biological Systems

Kei Moritsugu (1), Akinori Kidera (2) (*(1) RIKEN: (2) Yokohama City University; RIKEN*)

3P-060 スクロース溶液内における RNase Aのβ－シートの体積挙動

Volumetric property of β-Sheets of RNase A in Sucrose Solution

Tsubasa Yamamoto (1), Eri Chatani (2), Minoru Kato (1) (*(1) Graduate School of Science and Engineering, Ritsumeikan University: (2) Department of Pharmacy, Ritsumeikan University*)

3P-061 ジスルフィド結合の位置はリゾチームアミロイド様線維の体積特性に違いをもたらす

The position of disulfide cross-linking makes a difference in volumetric properties of the lysozyme amyloid-like fibril

Ryohei Kono (1), Kazuyuki Akasaka (3), Hideki Tachibana (2) ((*1) Second Department of internal medicine, Wakayama Medical Universityy: (2) Graduate School of Biology-Oriented Science and Technology, Kinki University: (3) High Pressure Protein Research Center, Institute of Advanced Technology, Kinki University*)

3P-062 ATP 加水分解中のミオシン内残基間距離の相対変化の PDB データを用いた研究

Relatively Changes of Distances between Each Pair of Amino Acid Residues in Myosin Motor Domain during ATP Hydrolysis

Hiroshi Kagawa (1), Yoshinori Nagai (2), Hiroshi Wako (3) ((*1) Physics Laboratory, Nippon Medical School: (2) Center for Information Science, Kokushikan University: (3) School of Social Sciences, Waseda University*)

3P-063 赤血球凝集反応実験とフラグメント分子軌道法計算に基づくインフルエンザヘマグルチニンの変異予測

2SP6-07 Possibility of Mutation Prediction of Influenza Hemagglutinin by Combination of Hemadsorption Experiment and Quantum Chemical Calculation for Antibody Binding

Kazutomo Takematsu (1), Kaori Fukuzawa (2), Katsumi Omagari (3), Katsuhisa Nakajima (3), Setsuko Nakajima (3), Yuji Mochizuki (4), Tatsuya Nakano (5), Hirofumi Watanabe (6), Shigenori Tanaka (6) ((*1) Division of Human Environmental Science Graduate School of Human Development and Environment, Kobe University: (2) Mizuho Information & Research Institute, Inc.: (3) Department of Virology, Medical School, Nagoya City University: (4) Department of Chemistry and Research Center for Smart Molecules, Faculty of Science, Rikkyo University;CREST, Japan Science and Technology Agency (JST): (5) Division of Medicinal Safety Science, National Institute of Health Sciences;CREST, Japan Science and Technology Agency (JST): (6) Graduate School of Engineering Department of Computer Science and Systems Engineering, Kobe University;CREST, Japan Science and Technology Agency (JST)*))

3P-064 昆虫由来新規ケモカイン HCP の解析

Characterization of a novel peptide which mediates aggregation and migration of hemocytes from an insect

Masakatsu Kamiya (1), Shin-Ichi Nakatogawa (2), Yasunori Oda (3), Tatsuro Kamijima (1), Tomoyasu Aizawa (2), Makoto Demura (1), Yoichi Hayakawa (3), Keiichi Kawano (2) ((*1) Graduate of Life Science, Hokkaido University: (2) Graduate of Science, Hokkaido University: (3) Faculty of Agriculture, Saga University*)

3P-065 プリオンタンパク質可溶性オリゴマーの蛍光相関分光法による解析

Analysis of Soluble Oligomers of Prion Protein by Fluorescence Correlation Spectroscopy

Hiroshi Sakata (1), Motohiro Horiuchi (2), Masataka Kinjo (1) ((*1) Laboratory of Molecular Cell Dynamics, Faculty of Advanced Life Science, Hokkaido University: (2) Laboratory of Prion Diseases, Graduate School of Veterinary Medicine, Hokkaido University*)

3P-066 シアル酸結合免疫グロブリン様レクチン（シグレック）－７によるシアロ糖鎖認識の生化学的および分子ドッキング解析

Docking simulation and biochemical analyses of sialylated glycan recognition of sialic acid binding Ig-like lectin (Siglec)-7

Nao Yamakawa (1), Hitomi Kosaki (2), Paul Crocker (3), Gerard Vergoten (4), Chihiro Sato (2), Ken Kitajima (5) ((*1) Bioscience and Biotechnology center, Global COE systems biology, Nagoya University: (2) Bioscience and Biotechnology center, Graduate School of Bioagricultural Sciences, Nagoya University: (3) College of Life Sciences, University of Dundee: (4) Universite des Sciences et Technologies de Lille, Unite Glycobiologie Structurale et Fonctionnelle: (5) Bioscience and Biotechnology center, Global COE systems biology, Graduate School of Bioagricultural Sciences, Nagoya University*)

3P-067 BIACORE-Ｘから良質な速度論的データを得る手法

GETTING HIGH QUALITY KINETIC DATA FROM A BIACORE-X SPR BIOSENSOR

Mai Nemoto (1), Damien Hall (1) ((*1) Institute of Basic Medical Science University of Tsukuba*)

3P-068 単粒子解析における局所類似性分類に基づく高精度粒子拾い上げ法の開発

Accurate and robust particle pickup method for single particle analysis was developed using local-similarity classification

Masaaki Kawata (1), Chikara Sato (1) ((*1) National Institute of Advanced Industrial Science and Technology (AIST)*)

3P-069 Ｘ線自由電子レーザを用いた単分子イメージングの理論

Theory of single molecule imaging by X-ray free-electron laser

Atsushi Tokuhisa (1), Junichiro Taka (1), Hidetoshi Kono (1), Nobuhiro Go (2) ((*1) Japan Atomic Energy Agency: (2) RIKEN SPring-8 Center*)

3P-070 べん毛タイプⅢ蛋白質輸送装置 FliH/FliI 複合体の構造解析に向けた試料調製

Steps towards structural analysis of the FliH/FliI complex of the flagellar type III protein export apparatus

Akihiro Kawamoto (1), Tohru Minamino (1), Tomoko Miyata (1), Takayuki Kato (1), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University*)

3P-071 重水素標識を利用した中性子小角散乱法によるプロテアソーム構成タンパク PA28 およびα７サブユニットの溶液構造解析

Solution structural analyses of PA28 and α7 subunit of the 20S proteasome by SANS in conjunction with deuterium labeling techniques

Eiji Kurimoto (1), Hiroki Sahashi (2), Eri Sakata (2), Kenta Okamoto (2), Yasufumi Minami (3), Masaaki Sugiyama (4), Koichi Kato (5) ((*1) Facul. Pharm. Meijo Univ.; Grad. Sch. Pharm. Sci. Nagoya City Univ.: (2) Grad. Sch. Pharm. Sci. Nagoya City Univ.: (3) Dept. Biotech. Maebashi Inst. Tech.: (4) Research Reactor Inst., Kyoto Univ. : (5) Okazaki Inst. Integ. Biosci. Natl. Inst. Natl .Sci.; Grad. Sch. Pharm. Sci. Nagoya City Univ.*)

3P-072 バルク脂質膜表面積を再現する膜タンパク質系の分子動力学シミュレーション法

Development of the method reproducing the bulk lipid surface-area in the molecular dynamics simulation of the protein-membrane complex

Takaharu Mori (1), Fumiko Ogushi (2), Yuji Sugita (3) ((*1) RIKEN；JST-BIRD: (2) RIKEN: (3) RIKEN；JST-BIRD；JST-CREST*)

3P-073 逐次モンテカルロ法による FRET 時系列解析

Analysis of single-molecule FRET trajectories by sequential Monte Carlo method

Yasuhiro Matsunaga (1), Akinori Kidera (2) ((*1) Molecular Scale Team, Computational Science Research Program, RIKEN: (2) Molecular Scale Team, Computational Science Research Program, RIKEN; Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University*)

3P-074 *Paracoccus denitrificans* チトクロム *c* 酸化酵素の大腸菌由来無細胞系での合成

Synthesis of *Paracoccus denitrificans* cytochrome *c*oxidase in the *E. coli* cell-free system

Yukie Katayama (1), Tomitake Tsukihara (1), Shinya Yoshikawa (1), Hideo Shimada (1) ((*1) Picobiology Institute, Graduate School of Life Science, University of Hyogo*)

3P-075 基質カンファー結合によるチトクロム P450cam の構造変化

Substrate *d*-camphor binding induces structural change of cytochrome P450cam

Keisuke Sakurai (1), Takashi Hayashi (2), Tomitake Tsukihara (1), **Hideo Shimada** (1) ((*1) Picobiology Institute, Graduate School of Life Science, University of Hyogo: (2) Department of Applied Chemistry, Graduate School of Engineering, Osaka University*)

3P-076 チトクロム P450cam の活性部位からの水クラスター排出機構

Mechanism of the water exclusion from the active site of cytochrome P450cam

Keisuke Sakurai (1), Katsuyoshi Harada (2), Kunitoshi Shimokata (3), Takashi Hayashi (2), Hideo Shimada (1) ((*1) Picobiology Institute, Graduate School of Life Science, University of Hyogo: (2) Department of Applied Chemistry, Graduate School of Engineering, Osaka University: (3) WORLD INTEC*)

3P-077 インドールアミン２、３ジオキシゲナーゼの酸素同位体感受性共鳴ラマンバンドの検出

Detection of Two Oxygen-Isotope Sensitive Resonance Raman Bands for Human Indoleamine 2, 3-Dioxygenase

Sachiko Yanagisawa (1), Keiko Yotsuya (2), Yumi Hashiwaki (1), Masaki Horitani (2), Hiroshi Sugimoto (2), Yoshitsugu Shiro (2), Takashi Ogura (1) ((*1) University of Hyogo: (2) RIKEN HARIMA*)

3P-078 結晶中の完全酸化型ウシ心筋チトクロム酸化酵素の酸素還元中心の解析

Characterization of the O_2 reduction site of crystalline fully oxidized bovine heart cytochrome *c* oxidase.

Masao Mochizuki (1), Kazumasa Muramoto (1), Kyoko Shinzawa-Ito (1), Tomoko Maeda (1), Rika Inaoka (1), Shinya Yoshikawa (1) ((*1) Picobiology Institute, Graduate School of Life Science, University of Hyogo*)

3P-079 化学修飾ヘモグロビン酸素結合機能の蛋白濃度依存性

Tetramer-dimer equilibrium of chemically modified hemoglobin as studied by protein concentration-dependences of the oxygen equilibrium curve

Takanori Inao (1), Sako Kuriyama (1), Kiyohiro Imai (2) ((*1) Dept. of Materials Chem., Grad. Sch. of Eng., Hosei Univ: (2) Dept. of Frontier Biosci., Fac. of Biosci and Aapplied Chem,.Hosei Univ.*)

3P-080 シトクロム *c* におけるシトクロム *c* 酸化酵素との電子伝達反応に重要なアミノ酸残基の検討

Identification of amino acid residues responsible for the electron transfer reaction with cytochrome *c* oxidase in cytochrome *c*.

Kaoru Inoue (1), Koichi Sakamoto (1), Naoko Nomoto (1), Takeshi Uchida (1), Kyoko Shinzawa-Ito (2), Shinya Yoshikawa (2), Koichiro Ishimori (1) ((*1) Hokkaido University: (2) University of Hyogo*)

3P-081 コンピュータシミュレーションによる ABC トランスポーター・Sav1866 の薬剤排出機構の解明

Computer simulation reveals the drug transport mechanism of ABC transporter Sav1866

Kentaro Adachi (1), Minoru Sakurai (1) ((*1) Center for Biological Resources and Informatics, Tokyo Institute of Technology*)

3P-082 機械受容型イオンチャネルダイナミクスの統計的解析

Statistical analysis of the mechanosensitive ion channel's dynamics

Kazuto Sei (1), Chun Biu Li (2), Tamiki Komatsuzaki (2) ((*1) Graduate School of Life Science, Hokkaido University: (2) Research Institute for Electronic Science, Hokkaido University*)

3P-083 バクテリオロドプシンミュータント L93A の長寿命化した光反応中間体の結晶学的研究

Crystallographic study of a long-lived photoreaction intermediate of the L93A mutant of bacteriorhodopsin

Yoshikazu Yamazaki (1), Masanori Hikake (1), Midori Murakami (1), Kunio Ihara (1), Tutomu Kouyama (1) ((*1) nagoya university*)

3P-084 紫膜バクテリオロドプシンの光退色現象におけるタンパク質_脂質間相互作用の影響

Effect of protein-lipid interaction on irreversible photobleaching of bacteriorhodopsin in purple memebrane

Tasuke Narishige (1), **Yasunori Yokoyama** (1), Masashi Sonoyama (1), Shigeki Mitaku (1) ((*1) Department of Applied Physics, Graduate School of Engineering, Nagoya University*)

3P-085 DMPC、DPPC 二層膜に再構成したバクテリオロドプシンの光退色

Photobleaching of bacteriorhodopsin reconstituted in DMPC and DPPC bilayer.

Taku Kitoh (1), Lumi Negishi (1), Yasunori Yokoyama (1), Masashi Sonoyama (1), Shigeki Mitaku (1) ((*1) Department of Applied Physics,Graduate school of engineering, Nagoya University: (2) Department of Applied Chemistry and Chemical Biology, Gunma University*)

3P-086 バクテリオロドプシンに対するフォースカーブ測定のための細胞質側と細胞外側の識別

Identification of cytoplasmic and extracellular side of bacteriorhodopsin for force spectroscopy

Yosuke Higashi (1), Satoshi Ozaki (1), Naoya Watanabe (2), Yasunori Yokoyama (1), Masashi Sonoyama (1), Shigeki Mitaku (1) ((*1) Graduate School of Engineering, Nagoya University: (2) SII NanoTechnology Inc.*)

3P-087 大腸菌機械受容チャネル MscL のメカノゲーティングにおける水の浸潤と透過の役割

Role of Water Penetration and Permeation in Mechano-Gating of the *E-coli* Mechanosensitive Channel MscL

Yasuyuki Sawada (1), Masaki Murase (2), Masahiro Sokabe (1) ((*1) Dept. Physiol. Nagoya Univ. Grad. Sch. Med.: (2) ICORP/SORST Cell Mechanosensing, JST*)

3P-088 FGF23 分泌における ppGalNAc-T3 の役割

Role of Polypeptide GalNAc-transferase T3 in FGF23 secretion

Kentaro Kato (1), Charlotte Jeanneau (2), Imran Dar (2), Mads Agervig Tarp (2), Anna Benet-Pagès (3), Eric Paul Bennett (4), Ulla Mandel (4), Tim M. Strom (3), Henrik Clausen (2) ((*1) Department of Medical Biochemistry and Genetics, University of Copenhagen; Recently moved to Graduate School of Advance Life Science, Hokkaido University: (2) Department of Medical Biochemistry and Genetics, University of Copenhagen: (3) GSF*

National Research Center: (4) Faculty of Health Sciences, School of Dentistry, University of Copenhagen)

3P-089 Visualization of the assembly and disassembly of *S. cerevisiae* Rad51 on duplex DNA in real-time

Ichiro Amitani (1), Amitabh V Nimonkar (1), Ronald J Baskin (1), Stephen C Kowalczykowski (1) (*(1) University of California, Davis*)

3P-090 バクテリオファージ Mu の標的免疫反応の光学顕微鏡下での直接観察

Direct Observation of Bacteriophage Mu Transposition Target Immunity

Yong-Woon Han (1), Kiyoshi Mizuuchi (2) (*(1) Insitute for Integrated Cell-Material Sciences, Kyoto University: (2) National Institute of Diabetes, Digestive and Kidney Diseases, Natinal Institutes of Health, USA*)

3P-091 SUMO 化による転写調節因子 heat shock factor 2 の DNA 結合阻害の分子機構

Molecular basis for SUMOylation-dependent regulation of DNA binding activity of Heat Shock Factor 2

Mariko Ariyoshi (1), Yukihiro Tateishi (1), Ryuji Igarashi (1), Hideyuki Hara (2), Kenji Mizuguchi (3), Hidehito Tochio (1), Masahiro Shirakawa (1) (*(1) Graduate School of Engineering, Kyoto University: (2) ESR Division, Bruker Biospin K.K.: (3) National Institute of Biomedical Innovation*)

3P-092 部位特異的変異体を用いた bHLH 因子の解析

Analyses of a bHLH transcription factor using site-directed mutants

Keigo Furuya (1), Koji Hasegawa (1), Osamu Hisatomi (1) (*(1) Osaka University*)

3P-093 Leucyl-tRNA 合成酵素における酵素機能発現の計算科学的解析

Computational analyses of expression mechanisms of enzymatic functions in leucyl-tRNA synthetase

Yohsuke Hagiwara (1), Osamu Nureki (2), Masaru Tateno (3) (*(1) University of Tsukuba: (2) University of Tokyo: (3) University of Tsukuba*)

3P-094 クラスターDNA 損傷と修復酵素 hOGG1 の分子動力学シミュレーション

Molecular dynamics simulation of cluster damaged DNA and hOGG1

Mariko Higuchi (1), Miroslav Pinak (1) (*(1) Japan Atomic Energy Agency*)

3P-095 分子動力学シミュレーションによる DNA 修復誘導タンパク質 MutS-DNA 複合体の動的解析

Molecular dynamics simulations of DNA repair protein MutS and DNA complexes

Hisashi Ishida (1) (*(1) Japan Atomic Energy Agency*)

3P-096 蛍光相関分光法を用いた FMBP- 1 の生体内分子動態解析

In vivo analysis of the molecular dynamics of FMBP-1 by fluorescence correlation spectroscopy

Shohei Myoba (1), Hideki Muto (2), Mai Kimoto (3), Masakatsu Kamiya (1), Takashi Kikukawa (1), Tomoyasu Aizawa (1), Masataka Kinjo (2), Shigeharu Takiya (3), Makoto Demura (1), Keiichi Kawano (1) (*(1) Department of Biological Sciences, Graduate School of Science, Hokkaido University: (2) Laboratory of Molecular Cell Dynamics, Faculty of Advanced Life Science, Hokkaido University: (3) Center for Genome Dynamics, Graduate School of Science, Hokkaido University*)

3P-097 構造情報に基づく蛋白質・DNA 認識における協同性の解析

Structure-based Analysis of Cooperativity in Protein-DNA Recognition

Akihiro Tanaka (1), Satoshi Fujii (1), Hidetoshi Kono (2), Akinori Sarai (1) (*(1) Dept. Bioscience and Bioinformatics, Kyushu Institute of Technology: (2) Neutron Science Research Center and Center for Promotion of Computational Science and Engineering, Japan Atomic Energy Research Institute*)

3P-098 TPM 法を用いたタンパク質翻訳中における mRNA に沿ったリボソームの運動解析

Analysis of the ribosomal movement along mRNA during translation by tethered particle motion method

Chihoko Arimori (1), Ryo Iizuka (1), Takashi Funatsu (1), Sotaro Uemura (2) (*(1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) Stanford University, School of Medicine*)

3P-099 一分子破断力測定によるリボソームーmRNA 相互作用力の非対称性の検討

Asymmetric ribosome interaction with mRNA in translation initiation

Masatoshi Tachibana (1), Tomoaki Masuda (1), Ryo Iizuka (1), Takashi Funatsu (1), Sotaro Uemura (2) (*(1) Graduate School of Pharmaceutical Science, The University of Tokyo: (2) Department of Structural Biology, Stanford University School of Medicine*)

3P-100 AFM を用いたテロメスタチン誘導体とＧカルテット構造 DNA の結合解析

Analysis of binding of telomestatin derivative to G-quadruplex DNA by using AFM

Yui Furunaga (1), Shingo Mieda (1), Kazunori Ikebukuro (1), Kazuo Nagasawa (1), Noriyuki Nakamura (2), Chikashi Nakamura (2) (*(1) Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology: (2) Research Institute for Cell Engineering, AIST*)

3P-101 分子動力学法による DNA-タンパク質間相互作用のシミュレーション解析

Simulation analysis of interactions between DNA and protein by molecular dynamics

Masahiro Watanabe (1), Tomonori Suzuki (2), Satoru Miyazaki (1) (*(1) Graduate School of Pharmaceutical Sciences, Tokyo University of Science: (2) Fac.of Pharmaceutical Sciences,Tokyo University of Sciences*)

3P-102 逆ミセル中蛋白質のテラヘルツ周波数領域のダイナミクスの水和効果

Hydration effect on dynamics of a protein in a reverse micelle in the terahertz frequency range

Hiroshi Murakami (1), Takaki Nishi (2), Yuji Toyota (3) (*(1) Japan Atomic Energy Agency: (2) JAEA;Kyoto Inst. Tech.: (3) JAEA;Osaka City Univ.*)

3P-103 蛋白質の調和運動と非調和運動に対する水和効果

Hydration affects both harmonic and anharmonic nature of protein dynamics

Hiroshi Nakagawa (1), Yasumasa Joti (2), Akio Kitao (2), Mikio Kataoka (3) (*(1) Japan Atomic Energy Agency: (2) University of Tokyo: (3) Nara Institute of Science and Technology;Japan Atomic Energy Agency*)

3P-104 DNA 周囲の水の分布：分子動力学シミュレーションと 3D—RISM による計算結果の比較

Comparison of DNA hydration patterns obtained from MD simulation and 3D-RISM theory

Yoshiteru Yonetani (1), Yutaka Maruyama (2), Fumio Hirata (2), Hidetoshi Kono (1) (*(1) Japan Atomic Energy Agency: (2) Institute for Molecular Science*)

3P-105 水の集団運動の解析およびそれを通じた溶質分子と水分子の動力学的相互作用の解明

Analysis of cooperative modes of water and understandings of dynamical interaction between water and solute molecules through it

Hiroshi Teramoto (1), Tamiki Komatsuzaki (1) (*(1) Hokkaido University*)

3P-106 蛋白質と水和水の構造変化相関： PYP の分子動力学的研究

Correlation of structural change in protein and hydration water: Molecular dynamic study of PYP

Taku Mizukami (1), Ayumu Sugiyama (2), Riki Nakamura (2), Keisuke Matsumoto (2), Hiroaki Saito (2), Hidemi Nagao (3) (*(1) Japan Advanced Institute od Sience and Technology: (2) Faculty of Mathematics and Physics, Institute of Science and Engineering, Kanazawa University: (3) School of Mathematics and Physics, College of Science and Engineering, Kanazawa University*)

3P-107 アクチンフィラメントへのトロポミオシンの協同的な結合の可視化

Visualizing the cooperative binding of tropomyosin molecules along an actin filament

Ryota Yanai (1), Hajime Honda (1), Eiichi Imai (1) (*(1) Dept. of BioEngineering, Nagaoka Univ. of Technology*)

3P-108 アクチン繊維内のモノマー配置の揺らぎ

Fluctuating configurations of monomers within an actin filament

Hajime Honda (1), Toshiya Haga (1), Kazutaka Mori (1), Yousuke Taguchi (1), Ei-Ichi Imai (1), Koshin Mihashi (2) (*(1) Dep. Bioeng., Nagaoka Univ. Tech.: (2) Nagoya Univ.*)

3P-109 アクトミオシンによる微小検出システム構築の試み

An attempt nano-detection system applying actomyosin motility systems

Naoto Yoshida (1), Tetsuya Seki (1), Eiichi Imai (1), Hajime Honda (1) (*(1) Department of Bioengineering, Nagaoka University of Technology*)

3P-110 蛍光クラスター法によるアクトミオシン単分子相互作用の可視化

Observing the interaction of single actin molecules with myosins in vitro

Yousuke Taguchi (1), **Kyohei Ito** (1), Eiichi Imai (1), Katsuhiko Shimada (2), Hajime Honda (1) (*(1) Department of Bioengineering, Nagaoka University of Technology: (2) School of Design and Architecture, Nagoya City University*)

3P-111 アクチンフィラメント上でのトロポミオシンのコイルドコイルの捻れ

Twisting and Untwisting of Tropomyosin coiled Coil on Actin Filament

Kenji Murakami (1), M. Stewart (2), **Takeyuki Wakabayashi** (1) (*(1) Dept. Biosciences, School of Science and Engineering, Teikyo University: (2) MRC Lab. Mol. Biol.*)

3P-112 筋原線維格子内へのポリエチレングリコールの浸透

whether Ethlene Glycol diffuse into the sarcomere lattice or not.

Tetsuo Ohno (1) (*(1) The Jikei University School of Medicine*)

3P-113 三次元 FRET 解析によるＦアクチンートロポミオシンＮ端領域 (83-104)複合体 のアトミックモデル構築

FRET between Residues on Actin and the N-terminal region (83–111) of Tropomyosin in the Reconstituted Thin Filament.

Masashi Bunya (1), Satoshi Makimura (1), Hidetaka Tobita (2), **Masao Miki** (1) (*(1) Applied Chemistry and Biotechnology, University of Fukui: (2) Material Science and Engineering, University of Fukui*)

3P-114 コラーゲン薄膜を用いた C2C12 筋管細胞による収縮力の測定

Measurement of active tension generated by C2C12 myotubes using thin collagen film

Hideaki Fujita (1), Kazunori Shimizu (1), Eiji Nagamori (1) (*(1) Toyota Central R&D Labs. Inc.*)

3P-115 MYPT1 のＣ末端側フラグメントの構造と機能

Structure and Function of the C-terminal functional fragment of MYPT1

Shinya Ohki (1), Shunsuke Mori (1), Ryou Iwaoka (1), Fumiko Matsuzawa (2), Masumi Eto (3) (*(1) Japan Advanced Institute of Science and Technology: (2) Altif Laboratories Inc.: (3) Thomas Jefferson University*)

3P-116 γサブユニットの部分的切除による F_1– ATPase の回転の研究

Rotation of F_1 - ATPase with truncated γ - subunits

Ryohei Chiwata (1), Tomonari Kawakami (2), Ayako Kohori (3), Shou Furuike (4), Katsuyuki Shiroguchi (4), Masasuke Yoshida (5), Kazuhiko Kinosita Jr. (4) (*(1) Dept. of Bioscience, Grad. School of Science and Engineering, Waseda Univ.: (2) Waseda University: (3) Waseda University: (4) Waseda University: (5) Tokyo Institute of Technology; ATP-synthesis Regulation, ICORP, JST*)

3P-117 アクチン変異体がミオシン５の運動性に与える影響の解析

The influence of mutated actin filament against processive myosin-V motility

Tomotaka Komori (1), Atsuko Iwane (1), Toshio Yanagida (1) (*(1) Graduate school of Frontier Biosciences, Osaka University*)

3P-118 ＧアクチンとＦアクチンに存在する明確な２状態

Two Distinct Forms of Actin in Monomeric and Filamentous states

Masatoshi Morimatsu (1), Yuichi Togashi (1), So Nishikawa (1), Mitsuhiro Sugawa (1), Atsuko Iwane (1), Toshio Yanagida (1) (*(1) Graduate School of Frontier Biosciences, Osaka Unv.*)

3P-119 モータータンパク質の３次元計測

3D tracking of motor proteins

Thomas Martin (1), So Nishikawa (1), Mitsuhiro Sugawa (1), Atsuko Iwane (1), Toshio Yanagida (1) (*(1) Graduate School of Frontier Biosciences, Osaka Unv.*)

3P-120 ミオシン VI のストレインセンサーの定量解析

Quantitative analysis of strain-sensor for myosin-VI

Mitsuhiro Iwaki (1), Atsuko Iwane (2), Tetsuya Shimokawa (2), Toshio Yanagida (2) ((*1) Graduate School of Medicine, Osaka University: (2) Graduate School of Frontier Biosciences, Osaka University*)

3P-121 プロトン駆動型べん毛モーターのプロトン透過活性とトルク発生サイクルとの相関関係

Relationship between proton conductivity and the rate of torque-generation cycle of the proton-driven flagellar motor

Yong-Suk Che (1), Keiichi Namba (1), Tohru Minamino (2) ((*1) Graduate School of Frontier Biosciences, Osaka University: (2) Graduate School of Frontier Biosciences, Osaka University; PRESTO, JST*)

3P-122 歩行運動中のミオシンＶのモータードメイン一個の力学特性

The mechanical properties of a single myosin V motor domain during gait motion

Keisuke Fujita (1), Mitsuhiro Iwaki (2), Atsuko Iwane (1), Masatoshi Morimatsu (1), Toshio Yanagida (1) ((*1) Graduate School of Frontier Bioscience, Osaka University: (2) Graduate School of Medicine, Osaka University*)

3P-123 pH イメージングシステムを用いた細胞内 pH とべん毛モーター回転の同時計測

Simultaneous measurement of intracellular pH and bacterial flagellar motor rotation using a high-resolution pH imaging system

Yusuke Morimoto (1), Nobunori Kami-Ike (1), Tohru Minamino (2), Keiichi Namba (1) ((*1) Graduate School of Frontier Biosciences, Osaka University; ICORP Dynamic NanoMachine P., JST: (2) Graduate School of Frontier Biosciences, Osaka University; ICORP Dynamic NanoMachine P., JST; PRESTO, JST*)

3P-124 自己調節するキネシン運動の可視化

Visualization of self-regulated kinesin motility.

Atsuko Iwane (1), Tomonobu Watanabe (2), Toshio Yanagida (3) ((*1) Laboratories for Nanobiology, Graduate School of Frontier Biosciences Osaka University: (2) WPI immun. Fronti. Res. Center. Osaka University: (3) Laboratories for Nanobiology, Graduate School of Frontier Biosciences Osaka University, WPI immun. Fronti. Res. Center. Osaka University*)

3P-125 アクチンへの G146V 変異は骨格筋ミオシンとの相互作用中の力発生を阻害する。

G146V mutation in actin inhibits force generation during interaction with skeletal myosin.

Taro Noguchi (1), Masatoshi Morimatsu (3), Kohji Ito (4), Atsuko Iwane (3), Toshio Yanagida (3), Taro Uyeda (2) ((*1) Life and Environmental Sciences, Univ. of Tsukuba; Research Institute for Cell Engineering, AIST: (2) Life and Environmental Sciences, Univ. of Tsukuba; Research Institute for Cell Engineering, AIST: (3) Graduate School of Frontier Biosciences, Osaka University: (4) Dept.of Biology, Chiba University*)

3P-126 2mM ATP における DNSO 下での F1-ATPase のステップ運動

Stepping rotation of F1-ATPase at 2 mM ATP in the presence of DMSO (dimethylsulfoxide).

Kazuhiro Nishizuka (1), Shoiti Toyabe (1), Tetsuaki Okamoto (1), Eiro Muneyuki (1) ((*1) Dept,Physics,Chuo Univ*)

3P-127 F1-ATPase のβ－サブユニット(Y341W)単体へのヌクレオチド結合の温度依存性

Temperature dependence of nucleotide binding to β-subunit of F1-ATPase revealed by fluorescence measurement.

Yusuke Naka (1), Eiro Muneyuki (1), Hidemitsu Osakabe (1), Tomoko Masaike (2) ((*1) Dept. Physics, Chuo Univ.: (2) Dept. Physics, Gakushuin Univ.*)

3P-128 レーザー照射による繊維状タンパク質のバイアスブラウン運動

Biased browninan motion of fibrous proteins under laser irradiation.

Chiharu Nagatomi (1), Shusuke Matsuura (2), Eiichi Imai (1), Hajime Honda (1) ((*1) Dept of Bioengineering, Nagaoka University of Technology: (2) Dept of Bioengineering, Yatsushiro National College of Technology*)

3P-129 アクチンフィラメントへのミオシンの協同的結合はアクチン－ミオシン－ADP-Pi 状態で起こる

Cooperative binding of myosin to actin filaments occurs in the actin-myosin-ADP-Pi state

Ryo Toya (1), Rika Kurogi (2), Taro Q.P.Uyeda (3), Kiyotaka Tokuraku (1) ((*1) miyakonojo national collage of technology: (2) University of Miyazaki: (3) National Institute of Advanced Industrial Science and technology*)

3P-130 ミオシン・アクチン系におけるドッキング過程の分子動力学シミュレーション

Molecular dynamics simulation for the docking process of myosin against an actin filament

Tadashi Masuda (1) ((*1) Tokyo Medical and Dental University*)

3P-131 キネシン頭部の選択的な前方着地におけるネックリンカーの役割

Role of the neck linker on the preferential forward stepping of kinesin

Hiroshi Isojima (1), Teppei Mori (1), Michio Tomishige (1) ((*1) The University of Tokyo*)

3P-132 一分子 FRET 法による尾部によるキネシン１の運動制御機構

Regulation of kinesin-1 motility by tail domain as studied by single molecule FRET

Takahiro Aoki (1), Takayuki Ariga (1), Michio Tomishige (1) ((*1) tokyodaigakuinn: (2) Tokyodaigaku: (3) Tokyodaigaku*)

3P-133 蛍光 ATP を用いたキネシンの運動解析

Movement analysis of kinesin on microtubules using fluorescent ATP

Masashi Kondo (1), Makoto Tsunoda (1), Takashi Funatsu (2) ((*1) Graduate School of Pharmaceutical Sciences, The University of Tokyo: (2) Graduate School of Pharmaceutical Sciences, The University of Tokyo; CNBI, The University of Tokyo; CREST, Japan Science and Technology Agency*)

3P-134 腸内連鎖球菌Ｖ型 ATPase の膜内在性サブユニット（NtpI）の発現と精製

Expression and purification of the membrane subunit NtpI of *Enterococcus hirae* V-ATPase

Misaki Yamamoto (1), Kenji Mizutani (2), Yoshimi Kakinuma (3), Ichiro Yamato (1), So Iwata (4), Takeshi Murata (5) ((*1) Grad. Sch. Indus. Sci. Tech., Tokyo Univ. Sci.: (2) Grad. Sch. Med., Kyoto Univ.: (3) Fac. Agri., Ehime Univ.: (4) Grad. Sch. Med., Kyoto Univ.; JST, ERATO, Iwata Project:*

(5) Fac. Sci., Chiba Univ.; Grad. Sch. Med., Kyoto Univ.; JST, ERATO, Iwata Project)

3P-135 LIS1 による dynein の運動制御のメカニズム

LIS1 regulates dynein motility in a dimerization-dependent manner

Takayuki Torisawa (1), Masami Yamada (2), Shinji Hirotsune (2), Yoko Toyoshima (1) (*(1) Dept Life Sciences, Graduate School of Arts and Sciences, Univ. of Tokyo: (2) Dept Genetic Disease Research, Osaka City Univ. Graduate School of Medicine*)

3P-136 同一細胞におけるべん毛モーター回転運動の同時計測

Simultaneous measurement of rotational movment of multiple flagellar motor in a single cell

Shun Terasawa (1), Hajime Fukuoka (2), Hiroto Takahashi (2), Yuichi Inoue (2), Akihiko Ishijima (2) (*(1) Grad. Sch. Life Sci., Tohoku Univ.: (2) IMRAM, Tohoku Univ.*)

3P-137 PFG-SE H-NMR によって明らかにしたアクチン水溶液中のプロトン拡散係数の増大：重合の寄与

Accelerated proton diffusion coefficient in actin aqueous solutions revealed by pulse field gradient spin echo proton NMR: Effect of actin polymerization

Takashi Sagawa (1), Makoto Suzuki (1), Tetsuichi Wazawa (2), Tsubasa Ogawa (1) (*(1) School of Engineering, Tohoku University: (2) CREST, JST*)

3P-138 二つの頭部が非対称な役割を演じる細胞質ダイニンの理論モデル

Kinetic model of cytoplasmic dynein with asymmetric roles of the leading and trailing heads

Hidemi Akiyama (1), Kazuo Sasaki (1) (*(1) Department of Applied Physics, Tohoku University*)

3P-139 誘電緩和分光によるアクトミオシンの水和解析:ADP 型と AMP.PNP 型の比較

Hydration analysis of actomyosin: comparison between ADP type and AMP-PNP type

Tatsuya Osada (1), Takashi Sagawa (1), Masahiro Hirose (1), Tetsuichi Wazawa (2), Makoto Suzuki (1) (*(1) Graduate school of Engineering Tohoku University: (2) CREST, JST*)

3P-140 枯草菌べん毛モーター固定子タンパク MotA、MotP の保存された荷電アミノ酸残基の解析

Analysis of the conserved charged residues in flagellar stator proteins MotA and MotP of *Bacillus subtilis*.

Yuka Takahashi (1), Naoya Terahara (3), Yukiyo Koizumi (2), Masahiro Ito (1) (*(1) Graduate School of Life Sciences, Toyo University: (2) Faculty of Life Sciences, Toyo University: (3) Bio-Nano Electronics Research Centre, Toyo University*)

3P-141 *in vitro* motility assay における微小管の進行方向性

The turning tendency of the microtubule driven by the axonemal dynein subspecies c

Yuji Shitaka (1), Kazuhiro Oiwa (1), Hiroaki Kojima (1) (*(1) National Institute of Information and Communications Technology*)

3P-142 ミオシン線維双極トラックに沿ったアクチン滑り運動速度の温度依存性

Temperature dependence of sliding velocity of actin filaments along bipolar tracks of myosin filament.

Hiroyuki Okubo (1), Masanori Iwai (1), Takahiro Kobatake (1), **Shigeru Chaen** (1) (*(1) Department of Integrated Sciences in Physics and Biology,College of Humanities and Sciences, Nihon University*)

3P-143 べん毛モーター高速回転時のステップ

Steps in fast flagellar rotation

Yoshiyuki Sowa (1), Richard Berry (2) (*(1) Department of Frontier Bioscience, Hosei University; Department of Physics, University of Oxford: (2) Department of Physics, University of Oxford*)

3P-144 滑り運動を可能にするアクチン・ミオシン間相互作用の自由エネルギーランドスケープ

Free energy landscape of the interaction between actin and myosin underlying the sliding movement of the myosin head

Akio Togashi (1), Takeshi N. Sasaki (2), Masaki Sasai (3), Tomoki P. Terada (3) (*(1) Dept. of Computational Science and Engineering, Grad. Sch. of Engineering, Nagoya Univ.: (2) Dept. of Library and Information Science, Faculty of Letters, Aichi Shukutoku Univ.: (3) Dept. of Applied Physics, Grad. Sch. of Engineering, Nagoya Univ.*)

3P-145 ツリガネムシ収縮過程の高速ビデオカメラによる研究

Contraction process of *Vorticella* stalk measured by high-speed camera

Ruri Hidema (1), Zenji Yatabe (1), Chihiro Hashimoto (2), Noriko Tsuchiya (1), Masatoshi Tachibana (1), Bernard Pansu Robert (3), Hideharu Ushiki (4) (*(1) United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology.: (2) Department of Applied Chemistry and Biotechnology, Niihama National College of Technology. : (3) PPSM, ENS de Cachan.: (4) Institute of Symbiotic Science and Technology, Tokyo University of Agriculture and Technology.*)

3P-146 アメーバ運動における温度効果の動画像解析

Study of Temperature Effect on Amoeboid Locomotion by Motion Image Analysis

Masatoshi Yoshimura (1), Chihiro Hashimoto (2), Hideharu Ushiki (3) (*(1) United Graduate School of Agricultural Science, TUAT.: (2) Department of Applied Chemistry and Biotechnology, Niihama National College of Technology. : (3) Institute of Symbiotic Science and Technology, Tokyo University of Agriculture and Technology.*)

3P-147 ５種類の白色腐朽菌を用いたゲーム関係論の構築

Construction of game's relationship theory using five white-rot fungi

Tatsuaki Dohmitsu (1), Zenji Yatabe (2), Masatoshi Yoshimura (2), Chihiro Hashimoto (3), Hideharu Ushiki (4) (*(1) Graduate School of Agriculture, Tokyo University of Agriculture and Technology: (2) United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology.: (3) Department of Applied Chemistry and Biotechnology, Niihama National College of Technology.: (4) Institute of Symbiotic Science and Technology, Tokyo University of Agriculture and Technology.*)

3P-148 形態変化中の粘菌細胞が示す一様刺激への走化性応答

Chemotactic response to a uniform stimulus in Dictyostelium cells undergoing cell shape change

Daisuke Taniguchi (1), Kunihiko Kaneko (2), Satoshi Sawai (2) (*(1) toudaiinsougoubunka: (2) JST-ERATOkanekohukuzatsukeiseimei*)

3P-149 細胞表面における後方輸送の平均二乗変位（MSD）を用いた解析

Backward transport on cell surface: analysis with mean square displacement method

Daisuke Nobezawa (1), **Hidetake Miyata** (1) ((*1) Physics Department, tohoku University*)

3P-150 細菌べん毛フック長制御タンパク質 FliK の構造特性

Structural property of the bacterial flagellar hook length control protein FliK

Yuri Motomochi (1), **Yumiko Saijo-Hamano** (2), Mariko Nukada (3), Yukio Furukawa (2), Keiichi Namba (2), Tohru Minamino (4) ((*1) Department of Food Science and Nutrition, Doshisha Women's College of Liberal Arts : (2) Graduate School of Frontier Biosciences, Osaka University: (3) JST ICORP : (4) Graduate School of Frontier Biosciences, Osaka University; JST, PRESTO*)

3P-151 細菌べん毛ロッドの再構成

In vitro reconstitution of the bacterial flagellar rod

Haruka Hotta (1), Takashi Fujii (2), Yumiko Saijo-Hamano (2), Keiichi Namba (2), **Katsumi Imada** (2) ((*1) Dept. Food Science and Nutrition, Doshisha Women's College of Liberal Arts: (2) Dept. Frontier Biosciences, Osaka Univ.*)

3P-152 情報伝達タンパク質 Ras、RAF 間の分子認識と細胞内信号伝達制御

1YP1-06 Mutual molecular recognition of Ras and RAF for accurate signal transduction

Kayo Hibino (1), Yasushi Sako (1) ((*1) RIKEN*)

3P-153 アクトミオシンリングの収縮による上皮損傷修復の機構とその意義

Mechanism of wound closure by constriction of the actomyosin ring and its significance

Shigenobu Yonemura (1), Mai Shibata (1) ((*1) Riken Center for Developmental Biology*)

3P-154 細胞性粘菌の走電性情報処理で探る細胞運動揺らぎの機能

Functional analysis of cellular migrational fluctuation under electrotaxis in *Dictyostelium* cells

Hiroaki Takagi (1), Masayuki Sato (2), Masahiro Ueda (2) ((*1) Nara Medical University ; JST, CREST: (2) Osaka University ; JST, CREST*)

3P-155 印加する外力の周波数に依存した細胞の生理的応答

Cellular responses to cyclic stretch depending on velocity of the stretch

Takeomi Mizutani (1), Shin Onodera (2), Hisashi Haga (1), Kazushige Kawabata (1) ((*1) Divisions of Biological Sciences, Graduate School of Science, Hokkaido University: (2) Department of Sports Medicine and Joint Reconstruction Surgery, Graduate School of Medicine, Hokkaido University*)

3P-156 蛍光相関分光法を用いた細胞内における外来 DNA の拡散と分解のモニタリング

Monitoring intracellular diffusion and degradation of exogenous DNA using fluorescence correlation spectroscopy.

Akira Sasaki (1), Masataka Kinjo (1) ((*1) Labolatory of Molecular Cell Dynamics,Faculty of Advanced Life Science, Hokkaido University*)

3P-157 周期構造を有する細胞シートを用いた細胞力学

Mechanics of a cell-sheet with periodic structures

Masahiro Tsuchiya (1), Yusuke Mizutani (1), Megumi Tadaki (1), Kouichi Kawahara (1), Takaharu Okajima (1) ((*1) Graduate School of Information Science and Technology, Hokkaido University*)

3P-158 リーディングラメラにおける粒状機械構造のアクチン細胞骨格依存的なダイナミクス：高速生細胞 SPM を用いた研究

Dynamics of Microgranular Mechanical Architecture Regulated by Actin Cytoskeleton in Leading Lamella: A Study Using High-Speed Live-Cell SPM

Kazushi Tamura (1), Takeomi Mizutani (1), Hisashi Haga (1), Kazushige Kawabata (1) ((*1) Division of Biological Sciences, Graduate School of Science, Hokkaido University*)

3P-159 デジタル画像相関法により得られた 局所伸展刺激下における細胞骨格ネットワークの不均一な変形分布

Heterogeneous deformation of cytoskeletal network under external stretch processed by digital image correlation method

Kenichi Doi (1), Takeomi Mizutani (1), Yasuyuki Morita (2), Masakazu Uchino (3), Mitsugu Todo (2), Hisashi Haga (1), Kazushige Kawabata (1) ((*1) Division of Biological Sciences, Graduate School of Science, Hokkaido University: (2) Research Institute for Applied Mechanics, Kyusyu University: (3) Fukuoka Industrial Technology Center*)

3P-160 伸展刺激に対する細胞の硬化応答は細胞が 2 サイクル以上の周期伸展を記憶することで消失する

Effect on cellular stiffness response to external stretch by memorizing more than 2 cycles of stretch in a myoblast

Kenji Takemoto (1), Waka Mitsui (2), Kazushi Tamura (1), Takeomi Mizutani (1), Hisashi Haga (1), Kazushige Kawabata (1) ((*1) Division of Biological Sciences, Graduate School of Science, Hokkaido University: (2) Faculty of Science, Hokkaido University*)

3P-161 IgE 受容体会合体への Lyn キナーゼの動的リクルート：2 色同時蛍光 1 分子追跡法による研究

Dynamic recruitment of Lyn kinase to IgE receptor cluster: Dual color single-molecule tracking study

Koichiro M. Hirosawa (1), Kenichi G. N. Suzuki (2), Takahiro K. Fujiwara (1), Yahara Miyako (1), Akihiro Kusumi (1) ((*1) Membrane Mechanisms Project, ICORP-JST; Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University: (2) PREST-JST*)

3P-162 Na^+駆動型べん毛モーターのＣリング付き基部体精製の試み

ATTEMPT TO PURIFY THE HOOK-BASAL BODY WITH C-RING FROM THE Na^+-DRIVEN FLAGELLAR MOTOR

Masafumi Koike (1), Seiji Kojima (1), Michio Homma (1) ((*1) Division of Biological Science, Graduate school of science, Nagoya Univ.*)

3P-163 試験管再構成モデルを用いた力刺激による接着関連タンパク質の集積

Force-dependent assembly of adhesion-related proteins in an *in vitro* model of adhesive structures

Daisuke Kiyoshima (1), Hiroaki Hirata (1), Hitoshi Tatsumi (1), Masahiro Sokabe (3) ((*1) Nagoya University Graduate School of Medicine: (2) National Institute for Physiological Science;SORST, Cell Mechanosensing Project, Japan Science and Technology Agency: (3) Nagoya University Graduate School of Medicine;SORST, Cell Mechanosensing Project, Japan Science and Technology Agency*)

3P-164 ビブリオ菌べん毛モーターコンポーネントの FCS 解析に向けた FliF の大量発現と精製

Overproduction and purification of *Vibrio* FliF for studying interactions between flagellar rotor proteins by FCS analysis

Ryo Ogawa (1), Rei Yoshizumi (1), Seiji Kojima (1), Michio Homma (1) ((*1) Division of Biological Science, Graduate School of Science, Nagoya University*)

3P-165 べん毛モーター固定子の集合における FliG のＣ末端荷電残基の役割

Role of the conserved charged residues in the C-terminal domain of FliG on the flagellar stator assembly in *Vibrio*

Natsumi Nonoyama (1), Seiji Kojima (1), Michio Homma (1) ((*1) Division of Biological Science, Graduate School of Science, Nagoya University*)

3P-166 好塩性真性細菌 *Salinibacter ruber* の走光性解析

Phototactic behavior of the extremely halophilic eubacterium *Salinibacter ruber*

Tomomi Kitajima (1), Yuki Sudo (1), Michio Homma (1) ((*1) Division of Biological Science, Graduate School of Science, Nagoya University*)

3P-167 １分子技術を用いた、リガンド非結合下での EGF 受容体クラスタリング機構の解析

Clustering of Epidermal Growth Factor Receptor without Ligand Binding Analyzed by Single-Molecule Techniques

Michio Hiroshima (1), Kayo Hibino (1), Yasushi Sako (1) ((*1) RIKEN*)

3P-168 生細胞内蛋白質拡散と相互作用解析から見る ErbB シグナル伝達ネットワーク

Understanding of ErbB signaling network by diffusion and interaction analysis of proteins in living cells

Changi Back (1), Yuko Saeki (1), Yasushi Sako (1), Mariko Hatakeyama (1) ((*1) RIKEN*)

3P-169 非極性ケラトサイトにおける突出と収縮のダイナミクス

Protrusion and retraction dynamics in non-polarized fish epidermal keratocytes

Hiromi Miyoshi (1), Taiji Adachi (1) ((*1) RIKEN VCAD System Research Program*)

3P-170 シミュレーションと再構成系における ERK 二重リン酸化の双安定性

Numerical analysis and reconstitution of the dual-phosphorylation of ERK

Masahiro Takahashi (1), Toshio Yanagida (2), Yasushi Sako (1) ((*1) RIKEN: (2) Graduate School of Frontier Biosciences, Osaka University*)

3P-171 バイオサーファクタントの不飽和脂肪酸組成が正電荷リポソームによる遺伝子導入に及ぼす影響

Composition of unsaturated fatty acids in biosurfactants affects efficiency of gene transfection mediated by cationic liposomes

Yoshikazu Inoh (1), Tadahide Furuno (1), Naohide Hirashima (2), Dai Kitamoto (3), Mamoru Nakanishi (1) ((*1) School of Pharmacy, Aichi Gakuin University: (2) Graduate School of Pharmaceutical Sciences, Nagoya City University: (3) National Institute of Advanced Industrial Science and technology*)

3P-172 固体 NMR による抗菌ペプチド LFampinB の細菌模倣膜との相互作用と運動性に関する研究

Dynamics and interaction of bovine lactoferrampin with mimetic bacterial membrane as studied by solid-state NMR

Atsushi Tsutsumi (1), Atsushi Kira (2), Masako Umeyama (1), Izuru Kwamura (1), Akira Naito (1) ((*1) Graduated School of Engeneering, Yokohama National University: (2) Ulvac, Inc.*)

3P-173 固体 NMR と QCM による Mristoylated Alanine_Rich C Kinase Substrate と Phosphoinositides との相互作用解析

Interaction of Myristoylated Alanine-Rich C Kinase Substrate with Phosphoinositides in Phospholipid Membrenes as studied by QCM and solid-state NMR

Atsushi Nakamura (1), Atsushi Kira (2), Emiko Yamauchi (3), Izuru Kawamura (1), Akira Naito (1) ((*1) Graduate School of Engineering, Yokohama National University : (2) Graduate School of Engineering, Yokohama National University ; ULVAC, Inc.: (3) Eisai, Inc.*)

3P-174 ^{13}C NMR によるオピオイドペプチドダイノルフィンとκ－受容体細胞外第２ループの相互作用解析

Interaction of opioid peptide dynorphin with extracellular loop 2 of κ-opioid receptor as studied by ^{13}C NMR

Yoshiyuki Sasaki (1), Takenori Miyamori (1), Akira Naitou (1), Izuru Kawamura (1), Atsushi Kira (2) ((*1) Graduated School of Yokohama National University: (2) ULVAC, Inc.*)

3P-175 電子線回折法を用いた経皮吸収促進剤のヒト皮膚角層脂質充填構造に対する影響の解析

Electron diffraction study on the effect of transdermal absorption promoters on the lipid packing in human skin stratum corneum

Yoshinao Ban (1), Hiromitsu Nakazawa (1), Satoru Kato (1) ((*1) Kwansei Gakuin University*)

3P-176 ホスファチジルコリン/ステロールから成る単一巨大リポソームの相転移挙動

Phase transition behavior of a single giant unilamellar vesicle composed of phosphatidylcholine and cholesterol analogue

Masao Ihara (1), Satoru Kato (1) ((*1) Kwansei Gakuin University*)

3P-177 浮遊密度法による脂質/コレステロール類似体混合バイレイヤーにおける分子間相互作用の解析

Study on molecular interaction in lipid/cholesterol-analogue mixed bilayers by the neutral floatation method

Tsubasa Miyoshi (1), Satoru Kato (1), Masanao Kinoshita (1), Tatsuma Nakano (1) ((*1) Department of Physics, Graduate School of Science and Technology, Kwansei Gakuin University*)

3P-178 水素化アモルファスシリコン薄膜上のジミリストイルフォスファチジルコリン・バクテリオロドプシン複合薄膜の IRRAS 解析

IRRAS Analysis on Composite Film of Dimyristoyl-Phosphatidylcoline and Bacteriorhodopsin on hydrogenated amorphous silicon film

Yutaka Tsujiuchi (1), Hiroshi Masumoto (2), Takashi Goto (3) ((*1) Dept of Material Sci & Eng, Akita Univ: (2) Center for Interdisciplinary Research, Tohoku Univ: (3) Institute for Materials Research, Tohoku Univ*)

3P-179 水素化アモルファスシリコン薄膜上の単純クーマリン・生体膜構成分子複合薄膜

Composite film of simple coumarin and membrane constituent molecule on hydrogenated amorphous silicon film

Ryogo Ito (1), Hiroshi Masumoto (2), Takashi Goto (3), Yutaka Tsujiuchi (1) ((*1) Dept of Material Sci&Eng, Akita Univ: (2) Center for Interdisciplinary Research, Tohoku Univ: (3) Institute for Materials Research, Tohoku Univ*)

3P-180 脂質・界面活性剤混合系を用いた固体基板表面への脂質二分子膜固定化手法の開発

3TA3-07 Detergent assisted formation of substrate supported phospholipid membranes

Kenichi Morigaki (1), Shigeki Kimura (1), Takehiko Inaba (1), Takashi Okazaki (1), Takashi Kawasaki (1), Hiromasa Imaishi (2) ((*1) National Insitute of Advanced Industrial Science and Technology: (2) Research Center for Environmental Genomics, Kobe University*)

3P-181 自己組織化における転写の時空間制御

3TA3-01 Spatio-temporal regulation of transcriptional pulses during self-organization in Dictyostelium

Noritaka Masaki (1), Satoshi Sawai (2) ((*1) JST-ERATO Complex Systems Biology: (2) Graduate School of Arts andSciences, University of Tokyo; JST-ERATO Comlex Systems Biology*)

3P-182 Functionally rotating mechanism of a multidrug transporter studied by coarse-grained simulation

3TA3-02 **Xin-Qiu Yao** (1), Hiroo Kenzaki (1), Shoji Takada (1) ((*1) Kyoto University, Department of Biophysics: (2) CREST, Japan Science and Technology Corporation*)

3P-183 タンパク質によって誘起される膜形態ダイナミクス：粗視化分子シミュレーション

Membrane morphology dynamics induced by proteins: Coarse-grained molecular simulations

Shinji Fujiwara (1), Hiroo Kenzaki (1), Shoji Takada (2) ((*1) Dept of Biophysics, Grad School of Science Kyoto University: (2) Dept of Biophysics, Grad School of Science Kyoto University;CREST JST*)

3P-184 アルギニンペプチドによる脂質二重膜の変形

Membrane deformation by arginine-rich peptide

Shuhei Kawamoto (1), Masako Takasu (2), Hidemi Nagao (1), Shiroh Futaki (3) ((*1) Department of Computational Science, Faculty of Science, Kanazawa University: (2) Tokyo University of Pharmacy and Life Science: (3) Biofunctional Design Chemistry, Institute for Chemical Research, Kyoto University*)

3P-185 エピガロカテキンガレートの誘起する GUV の破裂のメカニズム

The mechanism of the epigallocatechin gallate-induced burst of giant unilamellar vesicles

Yukihiro Tamba (1), Shinya Ohba (2), Victor Levadny (3), Masahito Yamazaki (2) ((*1) Shizuoka University; Suzuka National College of Technology: (2) Shizuoka University: (3) Russian Academy of Sciences; Shizuoka University*)

3P-186 I-BAR ドメインの膜結合分子ダイナミクス

3TA3-03 Molecular Dynamics of the Membrane Binding by I-BAR Domain

Kazuhiro Takemura (1), Shiro Suetsugu (2), Akio Kitao (3) ((*1) IMCB, Univ. of Tokyo;IMS: (2) IMCB, Univ of Tokyo;PRESTO, JST: (3) IMCB, Univ of Tokyo;CREST, JST*)

3P-187 流動電位から解析した開状態 KcsA カリウムチャネル内のイオンと水の分布

Steady state distribution of ion and water in the open structure of KcsA potassium channel evaluated by the streaming potential

Masayuki Iwamoto (1), Hirofumi Shimizu (1), Shigetoshi Oiki (1) ((*1) Div. Molec. Physiol. Biophys., Univ. Fukui Fac. Med. Sci.*)

3P-188 マスト細胞におけるストア作動性 Ca チャネル Orai の機能解析

Function analysis of store operated Ca channel Orai in mast cells

Naohide Hirashima (1), Miho Ikeya (1), Hirofumi Konishi (1), Satoshi Tadokoro (1) ((*1) Graduate School of Pharmaceutical Sciences, Nagoya City University*)

3P-189 小脳における発火頻度とエネルギー産生能の関係

Action potential frequency and energy production capability are correlated in the cerebellar neuron.

Takeshi Kanda (1), Hajime Hirase (1) ((*1) RIKEN Brain Science Institute*)

3P-190 グルタミン酸トランスポーターによる軟体動物腹足類の咀嚼リズム形成の制御

Roles of glutamate transport systems in feeding rhythm generation of pond snails

Dai Hatakeyama (1), Koichi Mita (1), Suguru Kobayashi (1), Hisayo Sadamoto (1), Etsuro Ito (1) ((*1) Tokushima Bunri University*)

3P-191 ストレスホルモンが後シナプスに及ぼす急性効果

Rapid morphological changes of postsynapses induced by stress hormone in rat hippocampus

Yoshimasa Komatsuzaki (1), Masatoshi Kasuya (2), Yasushi Hojo (2), Suguru Kawato (2) ((*1) Nihon Univ; Univ of Tokyo: (2) Univ of Tokyo; JST Bioinformatics*)

3P-192 末梢神経損傷後に脊髄で増加する P2Y 受容体

Induction of P2Y receptors in the spinal cord following peripheral nerve injury.

Kimiko Kobayashi (1), Hiroki Yamanaka (1), Koichi Noguchi (1) ((*1) Department of Anatomy and Neuroscience, Hyogo College of Medicine*)

3P-193 カエル神経筋接合部シナプスにおける Mg^{2+}を含んだ Ca^{2+}フリー溶液中での連続刺激による自発放出頻度増大現象の主要因は Ca^{2+}チャネルを通じてのシナプス前末端内への Mg^{2+}蓄積である

Accumulation of Mg^{2+} in the frog motor nerve terminals through N-type Ca^{2+} channels causes stimulation-induced enhancement of MEPP frequency under Ca^{2+}-free Mg^{2+}-containing condition

Naoya Suzuki (1) ((*1) Nagoya University, School of Science, Department of Physics*)

3P-194 ナメクジ嗅覚中枢における FMRFamide 陽性ニューロンの役割

The role of FMRFamidergic neurons in the olfactory center of *Limax*

Mariko Hattori (1), Suguru Kobayashi (1), Ryota Matsuo (1), Etsuro Ito (1) ((*1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University*)

3P-195 海馬スライス標本 CA1 野の層依存的なフィードフォワード抑制動員の VSD 光計測法による可視化

Layer dependent recruitment of feed-forward inhibition revealed by fast VSD-imaging in area CA1 of rat hippocampal slice preparation

Yoko Tominaga (1), Takashi Tominaga (2) ((*1) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University: (2) Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University; RIKEN BSI*)

3P-196 コルチコステロンはマウス脳海馬の CA1 領域において AMPA 刺激による Ca^{2+}信号を急性的に調節する

Croticosterone rapidly modulates AMPA receptor-driven Ca^{2+} signals in mouse hippocampal CA1 region.

Akiyoshi Suzuki (1), Wakako Sawada (1), Yoshimasa Komatsuzaki (2), Suguru Kawato (3), Minoru Saito (1) ((*1) Graduated School of Integrated Basic Sciences: (2) College of Sience and Technology, Nihon University: (3) Graduate School of Arts and Sciences, University of Tokyo*)

3P-197 キセノンガスによる大脳皮質由来培養神経回路網の電気活動抑制効果

The effect of Xenon gas inhibition of electrical activities of cortical cultured neuronal networks

Shotaro Suzuki (1), Tsutomu Uchida (1), Masafumi Nagayama (1), Kazutoshi Gohara (1) ((*1) Division of Applied Physics, Graduate School of Engineering, Hokkaido University, Japan*)

3P-198 内在性ノイズを持つ神経細胞モデルのパルス刺激に対する応答

The response of neuron models with intrinsic noise to pulse train inputs

Takanobu Yamanobe (1) ((*1) Dept. Physiology, Graduate School of Medicine, Hokkaido Univ*)

3P-199 コオロギ尾葉感覚系における連続気流刺激に対する方向依存的可塑性

Directional-dependent plasticity induced by successive air-current stimuli in the cricket cercal sensory system

Hiroto Ogawa (1), Momoko Oe (2), Kotaro Oka (3) ((*1) Dept. Biol. Sci., Fac. Sci., Hokkaido Univ.: (2) Dept. Biol. Sci., Sch. Sci., Hokkaido Univ.: (3) Dept. Bioscience and Informatics, Fac. Sci. and Tech., Keio Univ.*)

3P-200 小脳プルキンエ細胞層直下に局在する抑制性介在ニューロンの電気生理学的性質

Physiological distinction of inhibitory interneurons located underneath Purkinje cell layer of mouse cerebellum

Moritoshi Hirono (1), Masahisa Yamada (1), Kunihiko Obata (2) ((*1) RIKEN Brain Science Institute, Yamada Research Unit: (2) RIKEN Brain Science Institute, Obata Research Unit*)

3P-201 薬剤投与マウスの歩行指標の開発

New index for a behavioral differentiation across psychomotor stimulants

Hiroto Shoji (1), Yasuhito Nakatomi (5), Chihiro Yokoyama (3), Daiki Masaki (4), Kenji Fukui (4), Kazumitsu Hanai (6) ((*1) Kyoto Prefectural University of Medicine: (2) RESTO JST: (3) Functional Probe Research Lab, RIKEN Frontier Research System: (4) Dept Life-science, Kyoto Prefectural Univ of Medicine : (5) Dept Psychiatry, Graduate School of Medical Science, Kyoto Prefectural Univ of Medicine: (6) Dept Physics, Graduate School of Medical Science, Kyoto Prefectural Univ of Medicine*)

3P-202 ヨーロッパモノアラガイの中枢神経系で見られる陰影反射の神経基盤

The neuronal substrates of predator induced stress on the shadow response in *Lymnaea*

Hiroshi Sunada (1), Manabu Sakakibara (1), Tetsuro Horikoshi (1) ((*1) Graduate School of Bioscience, Tokai University*)

3P-203 軟体動物腹足類における神経型 NO 合成酵素の同定

Gene Expression of Neuronal Nitric Oxide Synthease in the mollusk, *Lymnaea stagnalis*

Hisayo Sadamoto (1), Etsuro Ito (1) ((*1) Tokushima Bunri University*)

3P-204 老化マウスの瞬目反射条件付け学習におけるニコチン性アセチルコリン受容体の関与

Contribution of nicotinic acetylcholine receptor to the classical eyeblink conditioning in aged mice

Takashi Kubota (1), Yutaka Kirino (1) ((*1) Tokushima Bunri University*)

3P-205 大腸菌発現系を用いた *salinarum* ハロロドプシンの機能的再構成

Functional Reconstitution of *salinarum* Halorhodopsin Expressed in *Escherichia coli*

Yasutaka Yamashita (1), Takashi Kikukawa (1), Kamiya Masakatsu (2), Tomoyasu Aizawa (2), Keiichi Kawano (1), Naoki Kamo (3), Makoto Demura (2) ((*1) Graduate School of Science, Hokkaido University: (2) Graduate School of Life Science, Hokkaido University: (3) College of Pharmaceutical Science, Matsuyama University*)

3P-206 共鳴ラマン分光法によるファラオニスフォボロドプシンＮ中間体の検出

Photointermediates of *Natronomonas pharaonis* phoborhodopsin revealed by resonance Raman spectroscopy

Masashi Unno (1), Yusuke Tateishi (1), Yutaka Nakao (2), Jun Tamogami (2), Naoki Kamo (3) ((*1) Department of Chemistry and Applied Chemistry, Saga University: (2) Faculty of Advanced Life Sciences, Hokkaido University: (3) College of Pharmaceutical Sciences, Matsuyama University*)

3P-207 ファラオニスフォボロドプシンの光反応サイクルに対する pH の影響

pH effect on the photoreaction cycle of pharaonis phoborhodopsin

Gang Dai (1), Kanako Yamagami (2), Yoichi Ikeda (3), Jun Tamogami (4), Naoki Kamo (5), Tatsuo Iwasa (6) ((*1) Division of Engineering for Composite Functions, Muroran institute of technology: (2) Department of Materials Science and Engineering, Muroran Institute of Technology: (3) Graduate School of Pharmaceutical Sciences, Hokkaido University: (4) Faculty of Advanced Life Science, Hokkaido University: (5) College of Pharmaceutical Science, Matsuyama Universit: (6) Division of Engineering for Composite Functions; Department of Materials Science and Engineering, Muroran Institute of Technology*)

3P-208 *Halobacterium salinarum* 由来のフォボロドプシン（センサリーロドプシン II）の光化学反応サイクルとプロトン移動

The photochemical reaction cycle and photo-induced proton transfer of phoborhodopsin from *Halobacterium salinarum* (sensory rhodopsin II)

Jun Tamogami (1), Yoichi Ikeda (2), Ayaka Takemura (2), Takashi Kikukawa (1), Makoto Demura (1), Naoki Kamo (3) ((*1) Faculty of Advanced Life Science, Hokkaido University: (2) Graduate School of Pharmaceutical Sciences, Hokkaido University: (3) College of Pharmaceutical Sciences, Matsuyama University*)

3P-209 ファラオニスハロロドプシンの Cl^-輸送機構における Asp252 の役割

Role of Asp252 in chloride transport by *pharaonis* halorhodopsin

Takashi Kikukawa (1), Seiji Miyauchi (2), Hiroaki Ichio (3), Taku Kitagawa (3), Makoto Demura (3), Naoki Kamo (4) ((*1) Graduate School of Science, Hokkaido Univ: (2) College of Pharmaceutical Sciences, Matsuyama Univ: (3) Graduate School of Life Science, Hokkaido Univ: (4) College of Pharmaceutical Sciences, Matsuyama Univ; Graduate School of Life Science, Hokkaido Univ*)

3P-210 FMN 結合型蛍光タンパク質 iLOV の光反応

Photoreaction of iLOV, an FMN-binding fluorescence protein.

Naoki Hozumi (1), Tatsuya Iwata (1), Kenichi Hitomi (2), Elizabeth D. Getzoff (2), John M. Christie (3), Hideki Kandori (1) (*(1) Nagoya Institute of Technology: (2) The Scripps Research Institute; (3) The Scripps Research Institute; University of Glasgow*)

3P-211 (6-4) 光回復酵素による DNA 修復の赤外分光観測

Direct observation of enzymatic (6-4) photoproduct conversion by FTIR spectroscopy

Yu Zhang (1), Tatsuya Iwata (1), Junpei Yamamoto (2), Kenichi Hitomi (3), Shigenori Iwai (2), Takeshi Todo (4), Elizabeth D Getzoff (3), Hideki Kandori (1) (*(1) Nagoya Institute of Technology: (2) Graduate School of Engineering Science, Osaka University: (3) Department of Molecular Biology and The Skaggs Institute for Chemical Biology, The Scripps Research Institute, USA: (4) Graduate School of Medicine, Osaka University*)

3P-212 ２種類の BLUF ドメイン、AppA と PAC の赤外分光解析

3TA2-01 FTIR study of two BLUF domains, AppA and PAC

Tatsuya Iwata (1), Akihide Watanabe (1), Mineo Iseki (2), Masakatsu Watanabe (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) School of Advanced Sciences, The Graduate University for Advanced Studies*)

3P-213 バクテリオロドプシンとハロロドプシンを発現している大腸菌の比較生理学

Comparative physiologiy between bR and hR expressing *Escherichia coli*

Kunio Ihara (1) (*(1) Nagoya University*)

3P-214 細菌の光センサーSRI とトランスデューサーHtrI の複合体の性質

The properties of eubacterial sensory rhodopsin I in the complex with its cognate transducer protein

Hiroki Irieda (1), Akiko Okada (1), Daisuke Suzuki (1), Yuji Furutani (2), Akira Kawanabe (2), Michio Homma (1), Hideki Kandori (2), Yuki Sudo (3) (*(1) Division of Biological Science, Graduate School of Science, Nagoya University: (2) Department of Frontier Materials, Nagoya Institute of Technology: (3) Division of Biological Science, Graduate School of Science, Nagoya University; PRESTO, JST*)

3P-215 光センサータンパク質 AnPixJ のシリカ多孔体中への吸着

Adsorption of light-sensor protein AnPixJ to the silica nanoporous materials

Yusuke Tomita (1), Syun Aoki (1), Tomoyasu Noji (1), Chihiro Kamidaki (1), Tatsuya Uzumaki (1), Tetsurou Jin (2), Rei Narikawa (3), Masahiko Ikeuchi (3), Shigeru Itoh (1) (*(1) Nagoya university: (2) Research Institute for Innovation in Sustainable Chemistry, National Institute of Advanced Industrial Science and Technology (AIST): (3) Department of Life Science (Biology), Graduate School of Art And Sciences, University of Tokyo*)

3P-216 タコロドプシンの結晶化

Crystallization of octopus rhodopsin

Jin Zhang (1), Soun Kanada (1), Motoyuki Tsuda (2), Tatsuo Iwasa (3), Midori Murakami (1), Tsutomu Kouyama (1) (*(1) Nagoya University, Graduate School of Science: (2) Tokushima Bunri University, Kagawa School of Pharmaceutical Sciences: (3) Muroran Institute of Technology*)

3P-217 Natronomonas pharaonis 由来光駆動塩素イオンポンプハロロドプシンの結晶構造解析

Crystallographic studies of the light-driven chloride pump halorhodopsin from Natronomonas pharaonis

Soun Kanada (1), Yu Takeguchi (1), Midori Murakami (1), Kunio Ihara (2), Tsutomu Kouyama (1) (*(1) Nagoya University, Graduate School of Science: (2) Nagoyauniversity, Center for Gene Research*)

3P-218 網膜変性モデルにおける多点電極アレイによる網膜神経機能の評価

Assessment of neuronal function in retinal degeneration models by using Multi-electrode array system

Kohei Homma (1), Zi-Bing Jin (1), Michiko Mandai (1), Masayo Takahashi (1) (*(1) RIKEN Center for Developmental Biology*)

3P-219 MD 及び MO 計算による PYP のＭ中間体の原子レベル構造

The atomic-level structure of the M intermediate of photoactive yellow protein as explored by MD and MO calculations

Toshifumi Nozawa (1), **Minoru Sakurai** (1) (*(1) Tokyo Institute of Technology*)

3P-220 暗状態及び明状態の LOV2-Ser/Thr キナーゼドッキングモデルに対する MD シミュレーション

Molecular dynamics simulation for LOV2 - Ser/Thr kinase docking models in the dark and light states

Hideyuki Takeda (1), Kohta Nakano (1), Kazunori Zikihara (2), Satoru Tokutomi (2), Minoru Sakurai (2) (*(1) Center for Biol. Res. Info., Tokyo Inst. Tech: (2) Department of Biological Science, Osaka Prefecture University*)

3P-221 光化学系 II の光合成反応中心の励起状態に関する理論的研究

Theoretical Study of Excited States of Photosynthetic Reaction Center in Photosystem II: Structure and Interaction

Yuya Kitagawa (1), Jun-Ya Hasegawa (1), Matsuda Kenji (1) (*(1) Dept. of Synthetic Chemistry and Biological Chemistry, Graduate School of Engineering, Kyoto Univ.*)

3P-222 光合成細菌のバクテリオクロロフィル分子への非天然型側鎖導入法の開発

Development of Introduction of Unnatural Groups into Bacteriochlorophyll Molecules in Photosynthetic Bacteria

Yoshitaka Saga (1), Risato Nishimori (1), Takashi Yoshioka (1) (*(1) Kinki University*)

3P-223 ホモダイマー型光合成反応中心のアフィニティ精製と分光学的性質

Spectroscopic characterization of the His-tagged homodimeric photosynthetic reaction center

Chihiro Azai (1), Toru Kondo (2), Jiro Harada (3), Shigeru Itoh (2), Hirozo Oh-Oka (1) (*(1) Department of Biological Science, Graduate School of Science, Osaka University: (2) Division of Material Science (Physics), Graduate School of Science, Nagoya University: (3) Faculty of Sciences and Engineering, Department of Bioscience and Biotechnology, Ritsumeikan University; Present, Department of Medical Biochemistry, School of Medicine, Kurume University*)

3P-224 クロロフィル側鎖回転異性体の理論解析

Theoretical analysis of the side group rotamers of chlorophyll

Hideki Yamasaki (1), Yu Takano (1), Haruki Nakamura (1) (*(1) Institute for protein research, Osaka university*)

3P-225 金属置換した紅色光合成細菌反応中心の赤外分光研究

3TP2-01 FTIR study of metal-replaced bacterial photosynthetic reaction center.

Akihide Watanabe (1), Tastuya Iwata (1), Mark L Paddock (2), Melvin Y Okamura (2), Hideki Kandori (1) (*(1) Department of Frontier Materials, Nagoya Institute of Technology: (2) Department of Physics, University of California, San Diego.*)

3P-226 転写因子制御領域におけるモチーフ解析

Motif Analysis of Transcription Factors in Regulatory Region

Tmoaki Sakai (1), Satoshi Fujii (1), Akinori Sarai (1) (*(1) Kyusyu Institute of technology*)

3P-227 次世代シーケンサにおけるメイトペアの距離情報を利用した配列解析アルゴリズムの開発

Development of resequcencing algorithm for next generation sequencer based on mate-pair distance

Naoaki Ono (1), Shingo Suzuki (1), Chikara Furusawa (2), Hiroshi Shimizu (1), Tetsuya Yomo (3) (*(1) Dept. Bioinfor. Eng., IST, Osaka Univ.: (2) Dept. Bioinfor. Eng., IST, Osaka Univ.; ERATO, JST : (3) Dept. Bioinfor. Eng., IST, Osaka Univ.; ERATO, JST; Grad. School Frontier Biosci., Osaka Univ.*)

3P-228 化学構造比較プログラム KCOMBU の開発

KCOMBU : a program for matching of chemical structures

Takeshi Kawabata (1) (*(1) Nara Institute of Science and Technology*)

3P-229 相同蛋白質の複合体構造データに基づいた結合リガンドの構造分類

Structural classification of binding ligands using homologous protein-ligand complex structures

Yusuke Miyata (1), Takeshi Kawabata (1) (*(1) NARA Institute of Science and Technology*)

3P-230 物理化学的性質の解析による膜タンパク質のトポロジー予測法の開発

Development of the Prediction Method of Membrane Protein Topology

Toshiyuki Tsuji (1), Shigeki Mitaku (1) (*(1) Department of Applied Physics Graduate School of Engineering Nagoya University: (2) Department of Applied Physics Graduate School of Engineering Nagoya University*)

3P-231 タンパク質中のゆらぎの大きな領域を予測するための新規インデックス(AUF インデックス)

Novel index (AUF index) for predicting dynamical fluctuation of polypeptide segments in proteins

Naoyuki Asakawa (1), **Noriyuki Sakiyama** (2), Reiko Teshima (3), Shigeki Mitaku (1) (*(1) Graduate School of Engineering, Nagoya University: (2) Graduate School of Engineering, Nagoya University; Venture Business Laboratory, Nagoya University: (3) National Institute of Health Sciences*)

3P-232 Motion Tree 法による蛋白質の階層的構造変化の解析

Dissection of hierarchical conformational changes in proteins with the Motion Tree

Ryotaro Koike (1), Motonori Ota (2), Akinori Kidera (3) (*(1) Graduate School of Information Science Nagoya University; BIRD JST: (2) Graduate School of Information Science Nagoya University: (3) Yokohama City University Graduate School of Nanobioscience; RIKEN Computational Science Research Program*)

3P-233 RNA-タンパク質相互作用の共変化の，kink-turn motif における相互情報量計算による同定

Identification of co-variation between RNA and protein in a kink-turn RNP motif

Aya Kitamura (1), Hirohide Saito (2), Eric Westhof (3), Tan Inoue (2) (*(1) ICORP, Japan Science and Technology Corporation (JST): (2) Department of Gene Mechanisms, Graduate School of Biostudies, Kyoto University: (3) Institut de Biologie Moléculaire et Cellulaire, CNRS*)

3P-234 未構造タンパク質の機能的進化的特性：生物種特異的解析

Functional and Evolutionary Characteristics of Disordered Proteins: Species-Specific Analyses

He Huang (1), Akinori Sarai (1) (*(1) Dept Life Bioscience and Bioinformatics, Computer Science and Systems Engineering, Kyushu Institute of Technology*)

3P-235 立体構造情報を利用したインフルエンザゲノムの進化メカニズムの探索

Exploration of the evolutionally mechanism of the influenza virus genome using the three-dimensional structure information

Shingo Yamamoto (1), Tomonori Suzuki (2), Satoru Miyazaki (1) (*(1) Graduate School of Pharmaceutical Sciences, Tokyo University of Science: (2) Fac. of Pharmaceutical Sciences, Tokyo University of Science*)

3P-236 A SUBTLE MODEL OF AMYLOID' S ROLE IN DISEASE BASED ON FIBRIL FRACTURE

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3P-237 経路形成が信号伝播履歴に依存する２体経路系におけるパターン

Pattern formation in a couple of dendritic paths correlated with a history of signal propagation

Ikuko Motoike (1) (*(1) PRSTO JST, iCeMS Kyoto Univ.*)

3P-238 Quantifying the Local Transition Heterogeneity of Multiscale Complex Networks Reconstructed from Single-Molecule Time Series

Chun Biu Li (1) (*(1) Research Institute for Electronic Science, Hokkaido University); JST/CREST*)

3P-239 分子クラウディング効果が細胞内化学反応に及ぼす影響

Effect of molecular crowding on in vivo macromolecular reactions

Kenta Yashima (1), Noriko Hiroi (2), Akira Funahashi (2), Kotaro Oka (2) (*(1) Keio university Advanced Research Centers: (2) Keio university Department of Biosciences and Informatics*)

3P-240 真性粘菌変形体のチューブ構造に保存される細胞運動の履歴

3TP1-04 Locomotive history of *Physarum* plasmodium recorded in its tubular structure

Tomohiro Shirakawa (1), Yukio-Pegio Gunji (2), Yoshihiro Miyake (1) (*(1) Department of Computational Intelligence and Systems Science,*

Interdisplinary Graduate School of Science and Engineering, Tokyo Institute of Technology: (2) Department of Earth and Planetary Sciences, Graduate School of Science, Tokyo Institute of Technology)

3P-241 Akt 経路のローパスフィルタ特性による EGF 受容体と下流のリン酸化シグナル強度の逆転

3TP1-02 Decoupling of receptor and downstream phosphorylation in Akt pathway by its low-pass filter characteristics

Yu Toyoshima (1), Kazuhiro Fujita (2), Shinsuke Uda (1), Yu-Ichi Ozaki (1), Hiroyuki Kubota (1), Shinya Kuroda (1) (*(1) Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo: (2) Department of Computational Biology, Graduate School of Frontier Sciences, University of Tokyo*)

3P-242 バクテリアコロニーにおける細胞の集団運動の解析

Experimental analysis of bacterial collective motion during colony development

Haruka Sugiura (1), Masaki Sano (1) (*(1) Graduate School of Science, University of Tokyo*)

3P-243 モノアラガイの巨大ニューロンに見られる複雑な発火パターンの非線形解析

Nonlinear analysis of firing patterns of the central giant cell of Lymnaea stagnalis

Yu Kumai (1), Yu-Ta Hamasaki (1), Yasusi Konno (2), Minoru Saito (4) (*(1) Graduate School of Integrated Basic Sciences: (2) Graduate School of Integrated Basic Sciences: (3) Graduate School of Integrated Basic Sciences: (4) Graduate School of Integrated Basic Sciences*)

3P-244 培養心室筋細胞の引き込み応答における刺激波形の効果

Effect of waveform on the entrainment of cultured ventricular muscle cells

Akira Ozeki (1), Takahiro Harada (2) (*(1) Graduated School of Engineering, University of Fukui: (2) Graduated School of Science, University of Tokyo*)

3P-245 包埋切片の原子間力顕微鏡観察によるデンプン粒子のナノスケール構造解析

Nanometer-scale structure analyses of food-material by atomic force microscopy combined with resin embedded section.

Shigeru Sugiyama (1), Kazumi Tsukamoto (1), Kimiko Yamamoto (2), Toshio Ohtani (1) (*(1) National Food Research Institute, NARO: (2) National Institute of Agrobiological Sciences*)

3P-246 原子間力顕微鏡を用いた酸化ストレスによる細胞肥大過程の力学特性評価

Mechanics of cardiac cells under hypertrophy induced by oxidative stress measured with an atomic force microscope

Yusuke Mizutani (1), Masahiro Tsuchiya (1), Koichi Kawahara (1), Takaharu Okajima (1) (*(1) Graduate School of Information Science and Technology, Hokkaido University*)

3P-247 AFM 粘弾性測定によるデキストラン伸長時における中間体の検出

Evidence for the existence of an intermediate state upon stretching dextran captured by AFM viscoelasticity measurement

Yukinori Taniguchi (1), Masaru Kawakami (2) (*(1) Japan Advanced Institute of Science and Technology: (2) Japan Advanced Institute of Science and Technology (JAIST); PRESTO of Japan Science and Technology Corporation (JST)*)

3P-248 単一分子ダイナミクスの実時間観察を可能にする 2 チャンネル同時タイムスタンプ計測

Dual time-stamp measurement for realtime observation of single molecular dynamics

Kenji Okamoto (1), Yasushi Sako (1) (*(1) RIKEN*)

3P-249 共焦点観察によるマウス側脳室繊毛の nm 精度運動解析

Motility analysis with nm-accuracy and high temporal resolution of mice ependymal cilia by confocal imaging

Togo Shimozawa (1), Yuki Hirota (2), Kazunobu Sawamoto (2), Hideo Higuchi (1) (*(1) CREST JST; Dept. of Phys. Univ. of Tokyo : (2) School of Medicine, Nagoya City Univ.*)

3P-250 細胞サイズ微小空間に拘束された DNA 分子のコンフォメーション変化と転写活性の可視化解析

Analysis of the conformational transition and transcriptional activity of a DNA molecule confined in a cell-sized microdroplet

Akihiko Tsuji (1), Kenichi Yoshikawa (2) (*(1) Spatio-Temporal Order, ICORP, JST: (2) Spatio-Temporal Order, ICORP, JST; Dep. Phys., Grad. Sch. Sci., Kyoto Univ.*)

3P-251 細胞分裂周期における細胞内 ATP ダイナミクスのイメージング

Imaging of intracellular ATP dynamics during cell division cycle

Hiromi Imamura (1), Hiroyuki Noji (2) (*(1) Japan Science and Technology Agency: (2) ISIR, Osaka University*)

3P-252 Parvovirus B19 の粒子サイズのダイナミズムとウイルス除去膜内での挙動

Size diversity of parvovirus B19 and its behavior on the virus removal filter.

Jun Adan-Kubo (1), Mikihiro Yunoki (1), Kazuyoshi Ikuta (2) (*(1) Infectious Pathogen Research Group, Osaka Research Laboratory, Benesis Corp.: (2) Department of Virology, Research Institute for Microbial Diseases, Osaka University*)

3P-253 DNA—ヘリカーゼ相互作用の 1 分子観察

3TP3-01 Single—molecule observation of DNA-helicase interaction

Hiroaki Yokota (1), Yuko Chujo (2), Emi Nishimoto (3), Yoshie Harada (3) (*(1) iCeMS, Kyoto Univ.; PRESTO, JST: (2) Dept. of Frontier Sci., Univ. of Tokyo: (3) iCeMS, Kyoto Univ.*)

3P-254 高速原子間力顕微鏡による ATP 加水分解反応中の p97 の動態観察

Direct observation of structural changes in p97 during the ATPase cycle using High-speed AFM

Naoya Miyagawa (1), Daisuke Yamamoto (2), Teru Ogura (3), Shingo Nishikori (4), Toshio Ando (2) (*(1) Dept. of Mathematics and Physics, Kanazawa Univ.: (2) Dept. of Mathematics and Physics, Kanazawa Univ.; JST/CREST: (3) Div. of Molecular Cell Biology, Inst. of Molecular Embryology and Genetics, Kumamoto Univ.; JST/CREST (4) Div. of Molecular Cell Biology, Inst. of Molecular Embryology and Genetics, Kumamoto Univ.*)

3P-255 パラメトリック共振モード高速 AFM を用いた低侵襲生体分子イメージング

Low-invasive molecular imaging by high speed AFM based on parametric resonance

Tetsuro Yamamoto (1), Takayuki Uchihashi (2), Toshio Ando (2) ((*1) Department of Mathematics and physics, Grad school of natural science and technology, Kanazawa univ: (2) School of mathematics and physics , College of science and engineering , Kanazawa univ, CREST-JST*)

3P-256 超音波高速原子間力顕微鏡による表面下構造のイメージング

Visualization of subsurface structures by high-speed ultrasonic force microscopy

Hiroki Watanabe (1), Takayuki Uchihashi (2), Toshio Ando (2) ((*1) Department of Mathematics and Physics Sciences, Grad School of Natural Science and Technology, kanazawa Univ.: (2) School of Mathematics and Physics , College of Science and Engineering , kanazawa Univ.;CREST/JST*)

3P-257 高速原子間力顕微鏡による探針試料間の相互作用力の検出感度の向上

Enhancement of detection sensitivity of tip-sample interaction in high-speed AFM

Masato Yoshida (1), Takayuki Uchihashi (2), Toshio Ando (2) ((*1) Department of Mathematics and Physics, Grad School of Natural Science and Technology, kanazawa Univ.: (2) School of Mathematics and Physics, College of Science and Engineering,Kanazawa Univ.CREST/JST*)

3P-258 誤差を含む混合蛍光スペクトルに対するスペクトル分離の有効性の検討

The validity of linear unmixing of spectra containing serially correlated error terms.

Sosuke Iwai (1), Taro Uyeda Qp (2) ((*1) Faculty of Education, Hirosaki University: (2) Research Institute for Cell Engineering, National Institute of Advanced Industrial Science and Technology*)

3P-259 シアノバクテリア細胞周期におけるクロモソーム DNA 形状変化の観察

Observation of bulk structural change of chromosomal DNA during the cell cycle of *Synechococcus elongatus* PCC 7942

Yasuko Kaneko (1), Yukiko Seki (1), Sayuri Hagiwara (1), Koji Nitta (2), Kuniaki Nagayama (3) ((*1) Saitama University: (2) Terabase Inc.: (3) Okazaki Inst. Integrative Biosci., Natl. Inst. Natural Sci.*)

3P-260 光学顕微鏡（対物外アポダイズド位相差）と電子顕微鏡のインタラクティブ観察による、細胞核内部を運動する構造の同定

3TP3-05 Interactive observation of optical and electron microscopy revealed moving particles in the nucleus.

Kaoru Katoh (1), Ayako Kojima (1), Emiko Kobayashi (2), Kazunori Kawasaki (2) ((*1) Neurosci. Res. Inst, AIST: (2) Cell Eng. Res. Inst,, AIST*)

3P-261 II 型 DNA トポイソメラーゼの手品のような反応を直接みる

3TP3-02 Direct Observation of DNA Unlinking Magic by a Type-II DNA Topoisomerase.

Katsunori Yogo (1), Taisaku Ogawa (1), Saki Obata (1), Gen Nakajima (1), Junpei Suzuki (1), Kazuhiko, Jr. Kinosita (1) ((*1) Department of Physics, Waseda University*)

3P-262 細胞内 mRNA の長時間観察を可能にする蛍光核酸プローブ

3TP3-03 Long-term monitoring of intracellular mRNA by hybridization-sensitive fluorescent nucleotide probe

Takeshi Kubota (1), Shuji Ikeda (1), Hiroyuki Yanagisawa (1), Mizue Yuki (1), Akimitsu Okamoto (1) ((*1) ASI, RIKEN*)

3P-263 モーター蛋白質で駆動するディスプレイの開発

Development of a display driven by microtubule motor protein

Susumu Aoyama (1), Masahiko Shimoike (1), Yuichi Hiratsuka (2) ((*1) School of Materials Science, JAIST: (2) School of Materials Science, JAIST; JST PRESTO*)

3P-264 アポフェリチンを使ったカルシウムナノ粒子の合成における二酸化炭素分圧の影響

Effect of carbon dioxide partial pressure in Calcium nanoparticle synthesis using apoferritin

Hiroko Fukano (1), Mamoru Aizawa (1), Hideyuki Yoshimura (1) ((*1) Meiji University*)

3P-265 アポフェリチンを用いた酸化アルミニウムの作製

Aluminum oxide synthesis using apoferritin

Kazuo Tomita (1), Tomoaki Harada (1), Toru Konishi (1), Hideyuki Yoshimura (1) ((*1) Meiji University*)

3P-266 微小管による温度可逆的なハイドロゲルの創製

Thermo-reversible hydrogel formed by microtubules

Ryuzo Kawamura (1), Ken-Ichi Sano (1), Istuki Kunita (1), Taiki Tominaga (1), Naoko Oda (1), Kuniharu Ijiro (2), Yoshihito Osada (1) ((*1) Molecular and System Life Science Unit, RIKEN Advanced Science Institute: (2) Molecular Device Laboratory, Research Institute for Electric Science, Hokkaido University; Molecular and System Life Science Unit, RIKEN Advanced Science Institute*)

3P-267 重合可能なタンパク質の可逆的な“バイオハイドロゲル”の創製

Reversible 3D-crosslinked 'bio-hydrogel' by polymerizable proteins

Itsuki Kunita (1), Taiki Tominaga (1), Ryuzo Kawamura (1), Hiromichi Nakagawa (1), Naoko Oda (1), Rikako Tsukamoto (2), Kuniharu Ijiro (2), Ken-Ichi Sano (1), Yoshihito Osada (1) ((*1) Molecular and System Life Science Unit, RIKEN advanced Science Institute.: (2) Molecular Device Laboratory, Research Institute for Electric Science, Hokkaido University; Molecular and System Life Science Unit, RIKEN advanced Science Institute.*)

3P-268 遺伝的アルゴリズムによるキネシン・微小管を用いたマイクロ輸送機構のためのトラック形状最適化

Module Structural Design for Material Transport System Propelled by Kinesin with Genetic Algorithm

Takuya Sunagawa (1), Akihito Tanahashi (1), Motohisa Hirano (1), Matthew Downs (2), Henry Hess (2), Takahiro Nitta (1) ((*1) Gifu university: (2) University of Florida*)

3P-269 マイクロビームＸ小角散乱を用いた縮毛矯正による人毛の内部構造変化の解析

Analysis of internal structural change of person hair by the arrangement of straight- permed curly hair with microbeam's small angle X-ray scattering

Satoshi Yamaki (1), Minori Kakizawa (1), Tomoyuki Kawasoe (1), Hideki Shimizu (1), Itirou Hatta (2), Noboru Ohta (2) ((*1) SHISEIDO CO.,LTD: (2) Japan Synchrotron Radiation Research Institute (JASRI)*)

3P-270 BMRB 日本サイトにおける低分子量生体高分子の NMR データ登録（SMSDep）受け付け開始

The acceptation of NMR data deposition for biological small molecule structure (SMSDep) have been started at BMRB in Japan

Eiichi Nakatani (1), Yoko Harano (2), Naohiro Kobayashi (2), Steven Mading (3), Takanori Matsuura (1), Hideo Akutsu (2), Eldon L. Ulrich (3),

Haruki Nakamura (2), Toshimichi Fujiwara (2) (*(1) Institute for Protein Research, Osaka University; JST-BIRD PDBj: (2) Institute for Protein Research: (3) University of Wisconsin Madison, BioMagResBank*)

3P-271 細胞への取込を向上させるためのサイズ制御された蛍光ナノ粒子の合成

Synthesis of size-controlled fluorescent nanoparticles to improve cellular uptake

Fumihiko Fujii (1), Hirotoshi Furusho (2), Yutaro Kumagai (3), Takashi Jin (1) (*(1) Immunology Frontier Research Center, Osaka University: (2) Research Center for Ultra-High Voltage Electron Microscopy, Osaka University: (3) Department of Host Defense, Research Institute of Microbial Disease, Osaka University*)

3P-272 カーボンナノチューブ表面でのタンパク質の吸着と構造変化

Adsorption and structure change of protein on carbon nanotube surfaces

Atsushi Hirano (1), Yutaka Maeda (2), Takeshi Akasaka (3), Kentaro Shiraki (1) (*(1) Inst. of Appl. Phys., Univ. of Tsukuba: (2) Dept. of Chem., Tokyo Gakugei Univ.; JST, PRESTO: (3) TARA, Univ. of Tsukuba*)

3P-273 オリゴアルギニンによるウシ胸腺 DNA の凝集体形成のメカニズム

Condensation mechanism of calf thymus DNA by oligoarginines

Jinya Taniguchi (1), Shigeru Negi (2), Koji Kano (1), Yukio Sugiura (2) (*(1) Faculty of science and Engineering, Doshisha University : (2) Faculty of Pharmaceutical Sciences, Doshisha Women's University*)

3P-274 複雑ネットワーク上におけるブーリアンダイナミクスのループ構造

Loop sturucture of Boolean dynamics in complex network

Shu-Ichi Kinoshita (1) (*(1) Organisation for the Strategic Coordination of Research and Intellectual Property, Meiji University*)

3P-275 定常流中の大腸菌速度の大腸菌サイズ依存性の理論的導出

The theoretical evaluation of the dependency of the velocity of *Escherichia coli* on their size in the stationary flow

Takeshi Miyakawa (1), Kitao Fujiwara (1), Kyouhei Takahashi (1), Ryota Morikawa (1), Masako Takasu (1) (*(1) Tokyo University of Pharmacy and Life Sciences*)

3P-276 How large are the contributions to catalysis from conformational motions?

Andrei Pisliakov (1) (*(1) Theoretical Biochemistry Lab, RIKEN Advanced Science Institute)*