口頭発表　Oral Presentation

第１日目（９月22日（土））／ Day1(Sep. 22, Sat.)

14:00～16:22　A 会場　理学南館１階 坂田・平田ホール／ Room A: Sci. south bldg. 1F Sakata Hirata Hall
分子モーターⅠ
Molecular Motors I

1A1400　コイルドコイル ミオシンの脆弱部位と屈曲性の保存
Prediction of fragile points and conservation of bending ability of coiled coil myosin
Mieko Taniguchi[1], Hideki Tanizawa[2], Sigeki Mitaku[1] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Inst. Wister, USA*)

1A1412　カーボンナノチューブ上におけるミオシン運動の温度応答
Thermal response of myosin motors on single carbon nanotubes
Mitsunori Nagata[1], Hiroshi Matsutaka[1], Takeru Okada[3], Akihiko Ishijima[2], Yuichi Inoue[2] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*IMRAM, Tohoku Univ.*, [3]*Institute of Fluid Science, Tohoku University*)

1A1424　生体分子モーターのためのステップ解析アルゴリズム
Powerful Algorithm for analyzing Stepping Motion of Biological Melecular Motors
Takeshi Nakagawa, Kazuo Sasaki (*Dept. of Applied Physics, Tohoku Univ.*)

1A1436　高時間分解能暗視野顕微鏡を用いたキネシン頭部の前方へのステップの観察
Direct observation of the forward stepping motion of kinesin-1 using dark-field microscopy with 50-μs temporal resolution
Hiroshi Isojima[1], Ryota Iino[2], Hiroyuki Noji[2], Michio Tomishige[1] ([1]*Dept. Appl. Phys., Sch. Eng., Univ. Tokyo*, [2]*Dept. Appl. Chem., Sch. Eng., Univ. Tokyo*)

1A1448　Front-head gating mechanism of kinesin-1 as studied by single molecule FRET observation of ATP binding
Yamato Niitani, Michio Tomishige (*Department of Applied Physics, School of Engineering, The University of Tokyo*)

休憩 15:00-15:10

1A1510　キネシン様モータータンパク質 Ncd の Power-stroke モデルの検証
The test on the power stroke model of Ncd
Masahiko Yamagishi, Yoko Toyoshima, Junichiro Yajima (*Dept. Life Sciences, Grad. Sch. Arts and Sciences, Univ. Tokyo*)

1A1522　細菌べん毛モーター固定子複合体 MotA/B チャネルの選択的透過メカニズム
Selective permeation mechanism through the channel of the stator complex MotA/B in the flagellar motor
Yasutaka Nishihara, Akio Kitao (*IMCB, Univ. of Tokyo*)

1A1534　Sodium Dynamics of the Bacterial Flagellar Motor
Chien-Jung Lo[1], Yoshiyuki Sowa[2], Teuta Pilizota[2], Richard Berry[2] ([1]*Department of Physics, Natioinal Central University, Taiwan*, [2]*Clarendon Laboratory, Department of Physics, University of Oxford*)

1A1546　Engineered disulfide crosslink in the the periplasmic region of PomB impaired function of the Na+-driven flagellar stator complex
Shiwei Zhu, Na Li, Seiji Kojima, Michio Homma (*Division of Biology Science, Graduate School of Science, Nagoya University*)

1A1558　高圧力が引き起こすべん毛繊維のダイナミック構造変化
Dynamic conformational changes of flagellar filament observed by high-pressure microscopy
Masayoshi Nishiyama[1], Yoshiyuki Sowa[2] ([1]*The Hakubi Center, Kyoto Univ.*, [2]*Hosei Univ.*)

1A1610　c-di-GMP 結合タンパク質 YcgR のホモログ PlzD の大量発現による *Vibrio alginolyticus* でのべん毛運動阻害
Flagellar motility inhibition by overexpression of PlzD, a YcgR homolog of c-di-GMP binding protein, in *Vibrio alginolyticus*
Takuro Yoneda, Wakako Morimoto, Seiji Kojima, Michio Homma (*Grad. Sci., Univ. Nagoya*)

14:00～16:22　B 会場　多元数理科学棟５階 509 ／ Room B: Mathematics bldg. 5F 509
蛋白質-構造機能相関Ⅰ
Proteins: Structure & Function I

1B1400　"空隙"ー機能構造創出のための自然の戦略
Cavityーa Nature's strategy for functional sub states in proteins
Kazuyuki Akasaka (*Kinki UNIV., Inst. Adv. Tech.*)

1B1412　HD-exchange motion of free heptameric GroES studied by the use of TROSY and DMSO quenching followed by 2D NMR
Mahesh Chandak[1], Takashi Nakamura[1], Koki Makabe[2], Toshio Takenaka[1], Jin Chen[1], Koichi Kato[1], Kunihiro Kuwajima[1] ([1]*Okazaki Institute of Integrative Bioscience, National Institutes of Natural Sciences, The Graduate University for Advanced Studies (Sokendai)*, [2]*Graduate School of Science and Engineering, Yamagata University*)

1B1424　溶液 NMR を用いた Na^+駆動型べん毛モーターの固定子タンパク質 FliG の C 末端領域構造解析
Solution NMR analysis of FliG C-terminal domain derived from Na^+-driven motor of *Vibrio*
Mizuki Gohara[1], Rei Abe-Yoshizumi[1,2], Shiori Kobayashi[1], Yohei Miyanoiri[3], Yoshikazu Hattori[4], Chojiro Kojima[4], Masatsune Kainosho[3,5], Michio Homma[1] ([1]*Div. Bio. Sci., Grad. Sch. Sci., Nagoya Univ.*, [2]*Department of Frontier Materials, Nagoya Institute of Technology*, [3]*Structural Biology Research Center, Grad. Sch. Sci., Nagoya Univ.*, [4]*Institute for Protein Research, Osaka Univ.*, [5]*Center for Priority Areas, Tokyo Metropolitan Univ.*)

1B1436　酸化還元状態に依存してプロテインジスルフィドイソメラーゼの基質結合部位ドメインの空間配置が変化する仕組み

Molecular mechanism of redox-dependent domain rearrangement of the substrate-binding region of protein disulfide isomerase

Kouya Inagaki[1,2], Yoshinori Uekusa[1,2], Yukiko Kamiya[1,2], Tadashi Satoh[1], Koichi Kato[1,2] ([1]*Grad. Sch. Phar. Sci., Nagoya City Univ.*, [2]*Natl. Inst. Nat. Sci.*)

1B1448 Transferred cross-saturation 法を用いた EB1 の CH ドメインの微小管との結合界面の特定

Microtubule-binding sites of EB1 CH domain revealed by transferred cross-saturation experiments

Teppei Kanaba[1], Ryoko Maesaki[2], Tomoyuki Mori[2], Yutaka Ito[1], Toshio Hakoshima[2], Masaki Mishima[1] ([1]*Grad. Sch. of Sci. and Tech., TMU*, [2]*Grad. Sch.l of Biol. Sci., NAIST*)

休憩 15:00-15:10

1B1510 再構築型生体外タンパク質合成系を用いた分子シャペロンによる凝集抑制効果の大規模解析

Global analysis of aggregation-inhibotion effects of molecular chaperones using a reconstituted cell-free translation system

Tatsuya Niwa[1], Takuya Ueda[2], Hideki Taguchi[1] ([1]*Grad. Sch. of Biosci&Bioteh, Tokyo Institute of Technology*, [2]*Grad. Sch. of Frontier Sciences, The university of Tokyo*)

1B1522 DNA 界面での蛋白質の局所的構造変化

Local conformational changes of proteins in DNA interfaces

Tomoko Sunami, Hidetoshi Kono (*JAEA*)

1B1534 天然変性タンパク質の構造ゆらぎを生かした密度変化誘起型シグナル伝達過程

The possible advantage of structural disorder of intrinsically disordered pr oteins in the new type of signaling mechanism

Nobu C. Shirai[1,2], Macoto Kikuchi[1,2,3] ([1]*Graduate School of Science, Osaka University*, [2]*Cybermedia Center, Osaka University*, [3]*Graduate School of Frontier Biosciences, Osaka University*)

1B1546 分子動力学法による capping protein（CP）の動的構造の解析

Structural fluctuations of capping proteins analyzed by molecular dynamics simulations

Ryotaro Koike[1], Shuichi Takeda[2], Yuichiro Maeda[2], Motonori Ota[1] ([1]*Grad. Sch. Info. Sci., Nagoya Univ.*, [2]*Struct. Biol. Res. Center, Grad. Sch. of Sci., Nagoya Univ.*)

1B1558 シトクローム c 酸化酵素のプロトンポンプ機構に関する分子動力学シミュレーションによる研究

A Molecular Dynamics Study on Proton Pump Function of Cytochrome c Oxidase

Takefumi Yamashita (*Research Center for Advanced Science and Technology, University of Tokyo*)

1B1610 Substrate transport mechanisms in GatCAB: the smallest unidirectional valve in subnano scale

Jiyoung Kang[2], Shigehide Kuroyanagi[2], Yohsuke Hagiwara[2], Masaru Tateno[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Grad. Sch. Pure and Appl. Sci., Univ. Tsukuba*)

14:00～16:22 C 会場 多元数理科学棟 4 階 409 ／ Room C: Mathematics bldg. 4F 409
蛋白質-計測，解析，エンジニアリング
Proteins: Measurement, Analysis, Engineering

1C1400 抗菌ペプチドを利用した病原体検出サンドイッチ発色検出技術の開発

New colorimetric sandwich assay for detection of pathogens by using antimicrobial peptides as detection probes

Chihiro Sakai[1], Eri Hojo[2], Taichi Nakazumi[1], Satoshi Tomisawa[1], Takashi Kikukawa[1], Yasuhiro Kumaki[1], Masakatsu Kamiya[1], Makoto Demura[1], Keiichi Kawano[1], Ryuji Ohtsuki[2], Taro Yonekita[2], Naoki Morishita[2], Takashi Matsumoto[2], Fumiki Morimatsu[2], **Tomoyasu Aizawa**[1] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*R&D Center, Nippon Meat Packers Inc.*)

1C1412 VanX の溶菌活性を用いたルシフェラーゼのスクリーニングの簡略化

Toward a simplified screening method using a novel VanX cell lysis activity

Nan Wu[1], Tetsuya Kamioka[1], Shihori Sohya[1], Tomoki Matsuda[2], Takahisa Ikegami[3], Haruki Nakamura[3], Yutaka Kuroda[1] ([1]*Biotechnology and Department Life Science, Graduate School of Engineering, Tokyo University of Agriculture and Technology*, [2]*Research Institute for Electronic Science, Hokkaido University*, [3]*Institute for Protein Research, Osaka University*)

1C1424 Fluorescent Probe for the Direct Detection of Histone Deacetylase Activity

Koushik Dhara[1], Yuichiro Hori[1], Reisuke Baba[1], Kazuya Kikuchi[1,2] ([1]*Graduate School of Engineering, Osaka University*, [2]*Immunology Frontier Research Center, Osaka University*)

1C1436 RaPID システムによる Akt2 選択的環状ペプチド阻害剤の探索とその阻害ペプチドの生化学的活性の評価

Exploring cyclic peptide inhibitors against the Akt2 kinase by the RaPID system and evaluation of their biochemical properties

Yuuki Hayashi[1], Jumpei Morimoto[2], Hiroaki Suga[2] ([1]*Dept. Life Sci., Grad Sch. Arts and Life Sci., The Univ. Tokyo*, [2]*Dept. Chem., Grad Sch. Sci., The Univ. Tokyo*)

1C1448 低分子抗体の多機能化を可能とするピンポイント化学接合デザイン

Protein engineering for site-specific bioconjugation chemistry: Construction of multiple functional low-molecular antibodies

Mitsuo Umetsu, Asami Ueda, Takeshi Nakanishi, Kentaro Hashikami, Ryutaro Asano, Izumi Kumagai (*Department of Biomolecular Engineering, Graduate School of Engineering, Tohoku University*)

休憩 15:00-15:10

1C1510 ハイブリッドナノセルロームの構成要素としての CBM の機能解析

Hybrid nano-cellulosome: functional analysis of various cellulose binding module as component of artificial cellulosome

Hikaru Nakazawa[1], Do-myoung Kim[1], Takashi Matuyama[2], Nobuhiro Ishida[2], Akinori Ikeuchi[2], Izumi Kumagai[1], Mitsuo Umetsu[1] ([1]*Tohoku univ. tech.*, [2]*Toyota Central R&D lab*)

1C1522 エンド-1,3-β グルカナーゼの糖結合モジュール α-リピートに存在する Trp273 のラミナリン結合への寄与

Contribution of Trp273 in the α-repeat of the carbohydrate-binding module of endo-1,3-β-glucanase to laminarin binding

Tomonari Tamashiro[1], Yoichi Tanabe[1], Kenji Kanaori[2], Teikichi Ikura[3], Nobutoshi Ito[3], Masayuki Oda[1] ([1]*Grad. Sch. of Life and Environ. Sci., Kyoto Pref. Univ.*, [2]*Grad. Sch. of Sci. and Technol., Kyoto Inst. of Technol.*, [3]*Med. Res. Inst., Tokyo Med. and Dent. Univ.*)

1C1534 Construction of an in vitro gene screening system for membrane proteins

Haruka Soga[1], Satoshi Fujii[3], Tetsuya Yomo[2,3], Hajime

Watanabe[1], Tomoaki Matsuura[1,3] ([1]*Dept. Biotech., Grad. Sch. Eng., Osaka Univ.*, [2]*Dept. Bioinfo. Eng., Grad. Sch. IST, Osaka Univ.*, [3]*ERATO, JST.*)

1C1546 Orientation-controlled immobilization of pharaonis halorhodopsin onto gold revealed by SEIRAS

Hao Guo[1,2], Tetsunari Kimura[1,2,3], Yuji Furutani[1,2,4] ([1]*Department of Structural Molecular Science, the Graduate University for Advanced Studies*, [2]*Department of Life and Coordination-Complex Molecular Science, Institute for Molecular Science*, [3]*JST CREST*, [4]*JST PRESTO*)

1C1558 低収量生体分子の時間分解分光計測を目指した新規溶液交換・混合装置の開発

Development of novel rapid buffer-exchange system and microfluidic mixer for time-resolved spectroscopic study of low-yield biomolecules

Tetsunari Kimura[1,2,3], Yuji Furutani[1,2,4] ([1]*Inst. Mol. Sci.*, [2]*Dept. Struct. Mol. Sci., Sokendai*, [3]*CREST/JST*, [4]*PRESTO/JST*)

1C1610 溶液中の金属タンパク質の共鳴 X 線散乱法の開発

Development of resonant X-ray scattering method of metalloproteins in solutions

Mitsuhiro Hirai[1], Kazuki Takeuchi[1], Ryota Kimura[1], Noboru Ohta[2] ([1]*Grad. Sch. Eng., Gunma Univ.*, [2]*SPring-8*)

14:00～16:22 D 会場 多元数理科学棟 3 階 309 ／ Room D: Mathematics bldg. 3F 309
発生，分化，神経
Development, Differentiation, Neuroscience

1D1400 マウス ES 細胞分化の単 1 細胞解析

Single-cell-based analysis of differentiation of mouse ES cells

Atsushi Maruyama[1], Yuichi Wakamoto[2,3], Shogo Nakamura[1], Tatsuo Michiue[2], Shin-ichi Sakai[4], Bayar Hexig[4], Toshihiro Akaike[4], **Kiyoshi Ohnuma**[1] ([1]*TRI, Nagaoka Univ of Tech*, [2]*Grad. Sch. Arts. & Sci., Univ. Tokyo*, [3]*Sakigake, JST*, [4]*Grad. Sch. Biosci. & Biotech., Tokyo Inst of Tech*)

1D1412 顕微ラマン分光法による分化因子刺激後の単一細胞ダイナミクスの計測

Measurements of Single Cell Dynamics upon Stimulation with a Differentiation Factor Using Raman Micro-Spectroscopy

Sota Takanezawa[1,2], Shin-ichi Morita[1], Yukihiro Ozaki[2], Yasushi Sako[1] ([1]*Cellular informatics Lab., RIKEN*, [2]*Grad. Sch. Sci. and Tech., Kwansei Gakuin Univ.*)

1D1424 1 分子定量計測技術を用いた *C. elegans* 受精卵における細胞極性のモデル化

Quantitative measurement and mathematical modeling of polarity-protein PAR-2 in *C. elegans* embryos

Yukinobu Arata[1], Tetsuya Kobayashi[2], Michio Hiroshima[1], Chan-gi Pack[1], Masashi Tachikawa[3], Kenichi Nakazato[3], Tatsuo Shibata[4], Yasushi Sako[1] ([1]*Cell. Info., ASI, Riken*, [2]*Inst. Ind. Sci., Univ. Tokyo*, [3]*Theo. Biol., ASI, Riken*, [4]*CDB, Riken*)

1D1436 形態形成中の組織の力学場を推定する

Estimating forces in the growing epithelial tissues

Shuji Ishihara[1,2], Kaoru Sugimura[3,4] ([1]*Grad. Sch. Arts & Sciences, Univ. Tokyo*, [2]*JST PRESTO*, [3]*iCeMS, Kyoto Univ.*, [4]*RIKEN BSI*)

1D1448 ショウジョウバエ形態形成におけるアポトーシスの能動的力学的寄与

Active Mechanical Role of Apoptosis in Tissue Dynamics during Drosophila Morphogenesis

Yusuke Toyama[1,2,3] ([1]*Dep. of Biol. Sci., National University of Singapore*, [2]*Mechanobiology Inst., National University of Singapore*, [3]*Temasek Life Sciences Lab.*)

休憩 15:00-15:10

1D1510 A model of cell-division stop for the limb regeneration

Hiroshi Yoshida (*Faculty of Math. Kyushu Univ.*)

1D1522 ラット培養神経回路網の長期発達過程における同期活動に関わる機能的分子の探索

Analysis of functional molecules underlying synchronous activity during long-term development of rat cultured neuronal networks

Daisuke Ito[1], Keiko Yokoyama[2], Kazutoshi Gohara[2] ([1]*Fac. Adv. Life Sci., Hokkaido Univ.*, [2]*Fac. Eng., Hokkaido Univ.*)

1D1534 モノアラガイの長期記憶におけるインスリンとグルコースの役割

Insulin and glucose for memory in a snail

Etsuro Ito[1], Ryuichi Okada[1], Mika Morikawa[1], Satoshi Takigami[2], Akiko Okuta[3], Manabu Sakakibara[2] ([1]*Kagawa School of Pharmaceutical Sciences, Tokushima Bunri University*, [2]*School of High-Technology for Human Welfare, Tokai University*, [3]*Graduate School of Science, Kyoto University*)

1D1546 光捕捉された神経細胞内シナプス小胞群の集合ダイナミクス

Assembling dynamics of optically trapped synaptic vesicles in neuronal cell

Yusuke Ueda[1,2], Suguru N. Kudoh[2], Takahisa Taguchi[1], Chie Hosokawa[1,2] ([1]*Health Res. Inst., AIST*, [2]*Grad. Sci. Eng., Kwansei Gakuin Univ.*)

1D1558 膜電位感受性色素・カルシウムイメージングに使える新しい超高速共焦点顕微鏡の開発

A new class of confocal microscope for a fast voltage-sensitive dye (VSD) and Ca^{2+} imaging

Takashi Tominaga, Yoko Tominaga (*Dept. Neurophysiol., Kagawa Sch Pharm Sci, Tokushima Buniri Univ*)

1D1610 De novo アセンブルによる軟体動物脳の全トランスクリプトーム解析

***De novo* sequencing and transcriptome analysis of the molluscan brain by deep RNA sequencing**

Hisayo Sadamoto[1], Hironobu Takahashi[2], Taketo Okada[1], Hiromichi Kenmoku[2], Yoshinori Asakawa[2] ([1]*Facul. Pharmaceut. Sci. Kagawa Camp, Univ. Tokushima Bunri*, [2]*Inst. Pharmacognosy, Univ. Tokushima Bunri*)

14:00～16:10 E 会場 多元数理科学棟 1 階 109 ／ Room E: Mathematics bldg. 1F 109
蛋白質-物性 I
Proteins: Property I

1E1400 分子動力学シミュレーションによる Hsp90 と ADP の結合自由エネルギープロファイル

Free energy profile for binding of ADP to Hsp90 with molecular dynamics simulation

Kazutomo Kawaguchi, Hiroyuki Takagi, Masashi Iwayama, Megumi Nishimura, Hiroaki Saito, Hidemi Nagao (*Inst. Sci.*

Eng., Kanazawa Univ.)

1E1412 シャペロニン空洞内の変性タンパク質が受けるコンフォメーション制限

The conformational restriction of denatured protein encapsulated in the chaperonin cage

Fumihiro Motojima, Yuko Motojima-Miyazaki, Masasuke Yoshida (*Kyoto Sangyo Univ.*)

1E1424 小角 X 線散乱によるアミロイド線維形成の初期会合プロセスの解析

Investigation of initial assembling process of fibrillation by small angle X-ray scattering

Eri Chatani[1], Rintaro Inoue[2], Koji Nishida[2], Toshiji Kanaya[2], Masahide Yamamoto[3] ([1]*Dept. Chem., Grad. Sch. Sci., Kobe Univ.*, [2]*Inst. Chem. Res., Kyoto Univ.*, [3]*Kyoto Univ.*)

1E1436 Distinguishing crystal-like amyloid fibrils and glass-like amorphous aggregates from their kinetics of formation

Yuichi Yoshimura[1], Yuxi Lin[1], Hisashi Yagi[1], Young-Ho Lee[1], Hiroki Kitayama[1], Kazumasa Sakurai[1], Masatomo So[1], Hirotsugu Ogi[2], Hironobu Naiki[3], Yuji Goto[1] ([1]*Inst. Protein Res., Osaka Univ.*, [2]*Grad. Sch. Eng. Sci., Osaka Univ.*, [3]*Fac. Med. Sci., Univ. Fukui*)

1E1448 細胞濃度に近い無添加細胞抽出液の調製

A method to prepare cell extract near intracellular concentration without additional salts and buffers

Kei Fujiwara, Shin-ichiro M. Nomura (*Dept. Biorobot., Tohoku Univ.*)

休憩 15:00-15:10

1E1510 TMAO による分子クラウディング環境への蛋白質移相自由エネルギーの三次元描像

Three-Dimensional Imaging of the Protein Transfer Free Energy into the Molecular Crowding Condition with TMAO

Isseki Yu[1], Kyoko Nakada[1], Masataka Nagaoka[2] ([1]*Dep. of Cem. and Biol. Sci. Aoyama Gakuin Univ.*, [2]*Grad. School of Info. Sci., Nagoya Univ.*)

1E1522 シトクロム *c* に対する尿素効果の自由エネルギー解析

Free-energy analysis of urea effect on cytochrome *c*

Yasuhito Karino, Nobuyuki Matubayasi (*Inst. Chem. Res., Kyoto Univ.*)

1E1534 タンパク質の水和水の水素結合ダイナミクスとタンパク質ダイナミクスとの動的カップリング

Kinetics of hydrogen-bonding of protein hydration water and its dynamical coupling with protein dynamics

Hiroshi Nakagawa[1], Mikio Kataoka[1,2] ([1]*Japan Atomic Energy Agency, Quantum Beam Science Directorate*, [2]*Nara Institute of Science and Technology, Graduate School of Materials Science*)

1E1546 テラヘルツ時間領域分光を用いた天然および変性状態タンパク質における低振動スペクトルの水和および温度依存性の観測

Temperature and hydration effects of low-frequency spectra of native and denatured proteins studied by terahertz time-domain spectroscopy

Naoki Yamamoto[1], Atsuo Tamura[2], Keisuke Tominaga[1,2] ([1]*Molecular Photoscience Research Center, Kobe University*, [2]*Graduate School of Science, Kobe University*)

1E1558 誘電緩和分光法によるアルキルカルボン酸の水和特性

Hydration Properties of Alkyl Carboxylate Series by Dielectric Relaxation Spectroscopy

Yangtian Wang, George Mogami, Tetsuichi Wazawa, Nobuyuki Morimoto, Makoto Suzuki (*Grad. Sch. Eng., Tohoku. Univ*)

14:00～16:10 F 会場　理学 B 館 5 階 501 ／ Room F: Sci. Bldg. B 5F 501
光生物-視覚，光受容 I
Photobiology: Vision & Photoreception I

1F1400 サル緑感受性視物質の全反射赤外分光解析

ATR-FTIR study of monkey green-sensitive visual pigment

Kota Katayama[1], Yuji Furutani[1,2], 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*)

1F1412 精製したタコロドプシンの SAXS 測定

SAXS measurements of purified octopus rhodopsin

Shingo Watanabe[1], Mitsuhiro Hirai[2], Tatsuo Iwasa[1,3] ([1]*CEDAR, Muroran IT*, [2]*Grad. Sch. Eng., Gunma Univ.*, [3]*Grad. Sch. Eng., Muroran IT*)

1F1424 ナノディスク試料を用いたロドプシンと錐体視物質によるトランスデューシン活性化効率の比較解析

Comparative analysis of transducin activation by rhodopsin and cone pigments in nanodiscs

Keiichi Kojima, Ryo Maeda, Yasushi Imamoto, Takahiro Yamashita, Yoshinori Shichida (*Dept. Biophys., Grad. Sch. Sci., Kyoto Univ.*)

1F1436 脊椎動物非視覚オプシン Opn5 とその類似光受容タンパク質の分子的性質の解析

Analysis of the molecular properties of vertebrate non-visual opsins, Opn5 and Opn5-like protein

Takahiro Yamashita[1], Hideyo Ohuchi[2], Sayuri Tomonari[3], Sari Fujita-Yanagibayashi[1], Kazumi Sakai[1], Sumihare Noji[3], Yoshinori Shichida[1] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Grad. Sch. Med. Dent. Pharm. Sci., Okayama Univ.*, [3]*Inst. Technol. Sci., Univ. Tokushima Grad.Sch.*)

1F1448 グロイオバクターロドプシンの光反応ダイナミクスの分光研究

Spectroscopic study of photoreaction dynamics of *Groeobacter* rhodopsin

Kumiko Nagata, Keiichi Inoue, Hideki Kandori (*Nagoya Inst. Of Technol.*)

休憩 15:00-15:10

1F1510 ASR の Pro206 はレチナール構造と光反応を制御する

Pro206 of Anabaena sensory rhodopsin is responsible for the isomeric composition of retinal and photochromism

Yoshitaka Kato[1], Akira Kawanabe[2], Kwang-Hwan Jung[3], Hideki Kandori[1] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Grad. Sch. Med., Osaka Univ.*, [3]*Sogang Univ. Korea*)

1F1522 Large deformation of helix F upon formation of the M intermediate of the azide-bound purple form of pharaonis halorhodopsin

Taichi Nakanishi[1], Soun Kanada[1], Midori Murakami[1], Kunio Ihara[2], Tsutomu Kouyama[1] ([1]*Grad. Sch, Sci., Univ. Nagoya*, [2]*Center for Gene Research., Univ. Nagoya*)

1F1534 センサリーロドプシン II-トランスデューサー複合体の比較シミュレーションにより明らかにされた基底状態と M 中間体の差異

Differences between the ground state and the M-intermediate of Sensory Rhodopsin II-Transducer complex revealed by comparative simulations

Koro Nishikata[1,3], Mitsunori Ikeguchi[1], Akinori Kidera[1,2]

(1*Grad. Sch. of Nanobioscience, Yokohama City Univ.*, 2*Research Program for Computational Science, RIKEN*, 3*Bioinformatics And Systems Engineering division (BASE), RIKEN*)

1F1546 **Effect of potential on the photo reaction of Sensory rhodopsin II monolayer studied by Surface Enhanced IR absorption Spectroscopy**
Kenichi Ataka, Joachim Heberle (*Freie Universitaet Berlin, Fachbereich Physik*)

1F1558 **In-situ 光照射固体 NMR による光受容膜蛋白質の光活性状態の解明**
Light activated states of photoreceptor membrane proteins as revealed by in-situ photo-irradiated solid-state NMR
Akira Naito[1], Yuya Tomonaga[1], Tetsurou Hidaka[1], Yusuke Shibafuji[1], Yoshiteru Makino[1], Izuru Kawamura[1], Yuki Sudo[2], Akimori Wada[3], Takashi Okitsu[3], Naoki Kamo[4] (1*Graduate School of Engineering, Yokohama National University*, 2*Graduate School of Science, Nagoya University*, 3*Kobe Pharmaceutical University*, 4*Matsuyama University*)

14:00～16:22 G 会場 理学 B 館 2 階 212 ／ Room G: Sci. bldg. B 2F 212
細胞生物的課題 I
Cell Biology I

1G1400 **Larger Intercellular Adhesion Strength Generates More Coherent and Directional Multicellular Movement - Measurement and Simulation**
Tsuyoshi Hirashima[1], Takanori Iino[2], Yoichiroh Hosokawa[2], Masaharu Nagayama[3,4] (1*Anatomy and Developmental Biology, Faculty of Medicine, Kyoto University*, 2*Graduate School of Materials Science, Nara Institute of Science and Technology*, 3*Research Institute for Electronic Science, Hokkaido University*, 4*CREST, Japan Science and Technology Agency*)

1G1412 **GPI アンカー型タンパク質の短寿命ホモダイマーはラフト組織化・機能のための最小単位である**
Transient GPI-anchored protein homodimers are units for raft organization and function
Kenichi G. N. Suzuki[1], Rinshi S. Kasai[1], Koichiro M. Hirosawa[1], Yuri L. Nemoto[1], Munenori Ishibashi[1], Yoshihiro Miwa[2], Takahiro K. Fujiwara[1], Akihiro Kusumi[1] (1*iCeMS, Kyoto Univ.*, 2*Dept. Pharmacol., Univ. Tsukuba*)

1G1424 **ナノ秒パルス高電界は新規細胞ストレスとして作用して翻訳抑制を引き起こす**
Nanosecond pulsed electric fields act as a novel cellular stress that induces translational suppression
Ken-ichi Yano, Keiko Morotomi-Yano (*Bioelectrics Res. Center, Kumamoto Univ.*)

1G1436 **弾性膜モデルを用いたゴルジ再集合過程シミュレーション**
Simulation study on Golgi reassembly process based on elastic membrane model
Masashi Tachikawa, Atsushi Mochizuki (*Theoretical Biology Laboratory, ASI, RIKEN*)

1G1448 **Analysis of cell behavior near silicon based micro-scale pore**
Yo Otsuka[1], Shinya Murakami[1], Manabu Sugimoto[1], Toshiyuki Mitsui[2] (1*Grad. Sch. Sci., Aogaku Univ*, 2*Assoc. Sci., Aogaku Univ*)

休憩 15:00-15:10

1G1510 **重イオンマイクロビーム照射によるバイスタンダー応答で誘導されるシグナル伝達機構の解明**
Mechanisms of signal transduction activated by heavy-ion microbeam induced bystander responses
Masanori Tomita[1], Hideki Matsumoto[2], Tomoo Funayama[3], Yuichiro Yokota[3], Kensuke Otsuka[1], Munetoshi Maeda[1,4], Yasuhiko Kobayashi[3] (1*Radiat. Safety Res. Cent., CRIEPI*, 2*Biomed. Imaging Res. Cent., Univ. Fukui*, 3*QuBS, JAEA*, 4*R&D, WERC*)

1G1522 **出芽酵母の遺伝子発現パターンの変化における染色体揺らぎの影響**
Effects of conformational fluctuation of chromosomes in budding yeast on the pattern of gene expression
Naoko Tokuda, Masaki Sasai (*Grad. Sch. Eng., Univ. Nagoya*)

1G1534 **人工自己複製システムのダーウィン進化**
Darwinian Evolution of artificial self-replication system
Norikazu Ichihashi[1,2], Tetsuya Yomo[1,2,3] (1*JST ERATO*, 2*Graduate School of Information Science and Technology, Osaka University*, 3*Graduate School of Frontier Bioscience, Osaka University*)

1G1546 **多点蛍光相関分光を用いた時空間解析によるグルココルチコイド受容体の核移行解析**
Nuclear translocation analysis of glucocorticoid receptor by spatiotemporal analysis with multipoint fluorescence correlation spectroscopy
Johtaro Yamamoto, Masataka Kinjo (*Fuc. Adv. Life Sci., Hokkaido Univ.*)

1G1558 **細胞内 FRET イメージングによる情報処理タンパク質 RAF の構造と EGF 応答の相関解析**
Correlation between the molecular conformation and EGF response of RAF by FRET imaging in individual cells
Kayo Hibino[1], Masahiro Ueda[1], Yasushi Sako[2] (1*RIKEN, QBiC*, 2*RIKEN, ASI*)

1G1610 **1 分子キネティクス解析により示された、ヘレギュリンと ErbB タンパク質のダイナミックに変化する相互作用**
Interaction between heregulin and ErbB proteins varies dynamically shown by single-molecule kinetic analysis in living cells
Michio Hiroshima[1,2], Yuko Saeki[3], Mariko Okada-Hatakeyama[3], Yasushi Sako[1] (1*RIKEN ASI*, 2*RIKEN QBiC*, 3*RIKEN RCAI*)

14:00～16:22 H 会場 理学 C 館 5 階 517 ／ Room H: Sci. bldg. C 5F 517
バイオイメージング
Bioimaging

1H1400 **ラスター画像相互相関分光法（ccRICS）を用いた外来 DNA に対する細胞内防御機構の可視化**
Visualization of intracellular defense system against exogenous DNAs by using cross-correlation raster image correlation spectroscopy
Akira Sasaki, Masataka Kinjo (*Fac. Adv. Life Sci., Hokkaido Univ.*)

1H1412 **Non-invasive in vivo imaging of vesicle movement in neutrophils in mouse ear**
Kenji Kikushima, Sayaka Kita, Hideo Higuchi (*Dept of Phys,*

School of Science, The Univ. of Tokyo)

1H1424 脂質二重膜を用いた T 細胞活性化の 1 分子イメージング解析
Single molecule analysis of T cell activation with stimulatory lipid bilayers by live cell imaging
Yuma Ito[1,2], Hirofumi Oyama[1,2], Kumiko Sakata-Sogawa[1,2], Makio Tokunaga[1,2] ([1]*Grad. Sch. Biosci. Biotech., Tokyo Inst. Tech.*, [2]*RCAI, RIKEN*)

1H1436 GTP 交換促進因子 Sos の生細胞一分子計測
Single molecule imaging of guanine nucleotide exchange factor Sos in living cells
Yuki Nakamura[1,2] ([1]*RIKEN sako celluar informatics laboratory*, [2]*Osaka university Yanagida lab*)

1H1448 リガンド結合したβ 2 アドレナリン受容体の短寿命ダイマーは三量体 G タンパク質のターンオーバーを加速する：2 色同時 1 分子観察による測定
Single-molecule imaging revealed acceleration of trimeric G-protein turnover by transient dimerization of liganded β2adrenergic receptor
Rinshi Kasai[1], Takahiro Fujiwara[2], Akihiro Kusumi[1,2] ([1]*Inst. For Frontier Med. Sci., Kyoto Univ.*, [2]*WPI-iCeMS, Kyoto Univ.*)

休憩 15:00-15:10

1H1510 光学顕微鏡と同時観察可能な高速 AFM
High-speed AFM combined with optical microscopy
Shingo Fukuda, Takayuki Uchihashi, Toshio Ando (*Depertment of Mathmatics and Physics, Grad School of Natural Science and Technology Kanazawa Univ*)

1H1522 High-speed AFM observation of intrinsically disordered proteins (NTAIL-GFP, PNT-GFP and SIC1-GFP)
Sujit Kumar Dora[1], Kodera Noriyuki[1], David Bloquel[2], Johnny Habchi[2], Antoine Gruet[2], Sonia Longhi[2], Toshio Ando[1] ([1]*Bio AFM frontier research center, Institute of physics and mathematics, Kanazawa University*, [2]*AFMB Laboratory, University of Aix-Marseille*)

1H1534 位相差電子顕微鏡用の帯電防止位相板
Anti-charging Phase Plates for Phase Contrast Electron Microscopy
Kuniaki Nagayama[1], Toshiyuki Itoh[2], Yoko Kayama[2], Zenpei Saitoh[2], Yukinori Nagatani[1], Yoshihiro Arai[2], Masahiro Ohara[1], Noriko Kai[2], Kazuyoshi Murata[1] ([1]*National Institute for Physiological Sciences*, [2]*Terabase Inc.*)

1H1546 500kV LinacTEM の開発
Development of the 500kV Linac TEM
Yukinori Nagatani[1], Yoshihiro Arai[2], Takumi Sannomiya[3], Tadao Shirai[4], Ryuzo Aihara[2], Giichi Iijima[2], Kuniaki Nagayama[1] ([1]*National Inst. Physiological Sci.*, [2]*Terabase Inc.*, [3]*Tokyo Inst. Tech.*, [4]*RTS*)

1H1558 光学顕微鏡とカソードルミネッセンス顕微鏡を用いたマルチモーダル細胞イメージング
Multimodal cellular imaging with light microscopy and cathodoluminescence microscopy
Hirohiko Niioka[1], Taichi Furukawa[2], Masayoshi Ichimiya[3], Tomohiro Nagata[4], Masaaki Ashida[2], Tsutomu Araki[2], Mamoru Hashimoto[2] ([1]*Inst. for NanoSci. Design, Osaka Univ.*, [2]*Eng. Sci., Osaka Univ.*, [3]*Osaka Dental Univ.*, [4]*Tsukuba Institute for Super Materials, ULVAC Inc.*)

1H1610 精製タンパク質の構造から in situ の構造まで：電顕を使用して
From purified protein structures to in situ structures using EM
Naoyuli Miyazaki[1,2], Mineo Iseki[3], Koji Hasegawa[4], Akihiro Narita[5], Shinichi Adachi[6], Masakatsu Watanabe[7], **Kenji Iwasaki**[1] ([1]*Institute for Protein Research, Osaka University*, [2]*National Institute for Physiological Sciences*, [3]*Pharmaceutical sciences, Toho University*, [4]*AdvanceSoft Corp.*, [5]*Structural Biology Research Center, Nagoya University*, [6]*Institute of Materials Structure Science, High Energy Accelerator Research Organization (KEK)*, [7]*The Graduate School for the Creation of New Photonics Industries*)

14:00～16:22 I 会場　理学 E 館 1 階 131 ／ Room I: Sci. bldg. E 1F 131
生命情報科学，バイオエンジニアリング
Bioinformatics & Bioengineering

1I1400 Analyzing the conservation of the folding nucleuses among the Ferredoxin-like fold in their amino acids sequence
Masanari Matsuoka, Takeshi Kikuchi (*Dept. Bioinf., Coll. Life Sci., Ritsumeikan Univ.*)

1I1412 RNA とタンパク質の相互作用におけるタンパク質構造変化のデータベース解析
Database analysis of the degree of protein conformational changes in RNA-protein interactions
Chihiro Kubota[1], Kei Yura[1,2,3] ([1]*Graduate School of Humanities and Sciences, Ochanomizu University*, [2]*Center for Informational Biology, Ochanomizu University*, [3]*Center of Simulation Sciences, Ochanomizu University*)

1I1424 天然変性タンパク質のデータベース IDEAL の構築
Construction of IDEAL database for the investigation of intrinsically disordered proteins
Takayuki Amemiya[1], Shigetaka Sakamoto[2], Yukiko Nobe[1], Seiko D. Murakami[1], Kazuo Hosoda[3], Ryotaro Koike[1], Hidekazu Hiroaki[4], Motonori Ota[1], Satoshi Fukuchi[3] ([1]*Grad. Schl of Info. Sci.*, [2]*HOLONICS Co., Ltd.*, [3]*Fac. Engr., Maebashi Ins. Tech.*, [4]*Grad. Schl of Pharm. Sci., Nagoya Univ.*)

1I1436 Computational analysis of protean segments (ProSs) in intrinsically disordered proteins (IDPs)
Divya Shaji[1], Takayuki Amemiya[1], Satoshi Fukuchi[2], Motonori Ota[1] ([1]*Graduate school of information science, Nagoya University, Japan*, [2]*Faculty of Engineering, Maebashi Institute of Technology, Japan*)

1I1448 MODIC: a novel ab inito identification system of transcription factor binding motifs in genome DNA sequences
Masaru Tateno[1], Ryo Nakaki[2], Jiyoung Kang[2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Grad. Sch. Pure and Appl. Sci., Univ. Tsukuba*)

休憩 15:00-15:10

1I1510 Interaction of DNA molecules with nanopore studied by fluorescence microscopy
Genki Ando[1], Kazuteru Yamada[2], Toshiyuki Mitsui[1,2] ([1]*Grad. Mat.Sci., Univ. Aoyama*, [2]*Phys., Univ. Aoyama*)

1I1522 診断用 DNA 計算に向けた核酸応答型 DNA 合成システムの構築
Construction of a nucleic-acid-responsive DNA synthesis system for diagnostic DNA-based computing
Ken Komiya, Asako Kobayashi, Masayuki Yamamura (*Interdis. Grad. Sch. of Sci. and Engi., Tokyo Tech.*)

1I1534 DNA scaffold logic: logic operation on molecular inputs using

FRET cascades

Takahiro Nishimura[1], Yusuke Ogura[1], Hirotsugu Yamamoto[2], Kenji Yamada[3], Jun Tanida[3] ([1]*Osaka University*, [2]*The University of Tokushima*, [3]*Osaka University*)

1I1546 寄生虫による接着性宿主細胞への侵入過程観察のためのマイクロ加工デバイスの作製

Observation of parasite invasion with the micro-fabricated device

Tetsuhiko Teshima[1], Hiroaki Onoe[1], Kaori Kuribayashi-Shigetomi[1], Hiroka Aonuma[2], Hirotaka Kanuka[2], Shoji Takeuchi[1] ([1]*The Institue of Industrial Science*, [2]*Jikei University School of Medicine*)

1I1558 金属還元菌 *Shewanella* における微生物呼吸代謝の電気化学的制御

Electrochemical regulation of bacterial respiratory activity of *Shewanella*, a dissimilatory metal reducing bacteria

Shoichi Matsuda[1], Huan Liu[3], Shuji Nakanishi[2], Kazuhito Hashimoto[1,2,3] ([1]*Grad. Sch. Engr., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*, [3]*ERATO/JST*)

1I1610 Spatiotemporal control of cell motility in nano- to micro-scale topographical environment

Hiromi Miyoshi[1], Hiroyoshi Aoki[1], Jungmyoung Ju[1], Sang Min Lee[2], Jong Soo Ko[2], Yutaka Yamagata[1] ([1]*ASI, RIKEN*, [2]*Grad. Sch. Mech. Eng., Pusan National Univ.*)

14:00～16:10　A会場　理学南館１階 坂田・平田ホール／Room A: Sci. south bldg. 1F Sakata Hirata Hall
分子モーターII：ダイニン
Molecular Motors II: Dynein

2A1400　クライオ電子線トモグラフィーを用いた細胞中骨格タンパク質およびモータータンパク質の非侵襲的構造解析
Observation of intracellular cytoskeleton and motor protein in the non-invasive cells with electron cryo-tomography
Shinji Aramaki[1], Kazuhiro Aoyama[2,3], Kota Mayanagi[4], Takuo Yasunaga[1] ([1]*Dept. of Bioscience and Bioinformatics, Grad. School of Computer Sci. and Sys. Eng., Kyushu Inst. of Tech.*, [2]*FEI Company Japan Ltd., Application Lab.*, [3]*Grad. School of Frontier Biosciences, Osaka Univ.*, [4]*Medical Inst. of Bioregulation, Kyushu Univ.*)

2A1412　クライオ電子線トモグラフィーを用いたクラミドモナス軸糸外腕ダイニンにおけるメタロチオネイン標識 LC2 の検出
Detection of metallothionein-tagged LC2 on *chlamydomonas* axonemal ODA by electron cryo-tomography
Mingyue Jin[1,4], Haru-aki Yanagisawa[2], Kotaro Koyasako[1,4], Ritsu Kamiya[2], Kota Mayanagi[3,4], Takuo Yasunaga[1,4] ([1]*Dep. Biosci. Bioinf., Inst. Tech. Kyushu*, [2]*Dep. Biol. Sci., Grad. Sch. Sci., Univ. Tokyo*, [3]*Div. Struct. Biol., Med. Inst. Bioreg., Univ. Kyushu*, [4]*JST*)

2A1424　クライオ電子顕微鏡法とメタロチオネインラベルを用いた軸糸構造の解明
Elucidation of Axoneme architecture by cryo-electron microscopy and metallothionein labeling
Reiko Chijimatsu[1], Mingyue Jin[1,2], Takuo Yasunaga[1,2] ([1]*Kyushu Institute of Technology*, [2]*JST*)

2A1436　電子線トモグラフィー法により明らかになった、LIS1 による細胞質ダイニンの運動活性制御メカニズム
Regulation of cytoplasmic dynein-motility on microtubules by LIS1 revealed by electron-computed tomography
Shiori Toba[1], **Kotaro Koyasako**[2,3], Shinji Hirotsune[1], Takuo Yasunaga[2,3,4] ([1]*Dept. Genetic Disease Research, Osaka City Univ. Grad. Sch. of Medicine*, [2]*Dept. Bioscience & Bioinformatics, Faculty of Computer Science and Systems Engineering, Kyushu Inst. Tech.*, [3]*JST-SENTAN*, [4]*JST-CREST*)

2A1448　ヌクレオチド状態に依存したダイニン分子の形態変化
Nucleotide-dependent morphological change of cytoplasmic dynein
Muneyoshi Ichikawa, Kei Saito, Takayuki Torisawa, Keitaro Shibata, Yuta Watanabe, Tomonori Hata, Yoko Toyoshima (*Grad. Sch. of Arts & Sci., Univ. of Tokyo*)

休憩 15:00-15:10

2A1510　頭部間の直接的相互作用は細胞質ダイニンの連続的な運動に必要ない
A direct interaction between dynein two heads is not necessary for processive movements of dynein
Keitaro Shibata, Yui Utsumi, Takayuki Torisawa, Yoko Toyoshima (*Dept. Life Sci., Grad. Sch. Arts and Sci., Univ. Tokyo*)

2A1522　外部負荷存在下でのヒト細胞質ダイニンのメカノケミカルサイクル
The mechanochemical cycle of human cytoplasmic dynein under external force
Taketoshi Kambara[1], Yoshiaki Tani[1], Motoshi Kaya[1], Tomohiro Shima[2], Hideo Higuchi[1] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*QBiC, Riken*)

2A1534　Rotation of microtubules driven by *Tetrahymena* 22S outer arm dynein and its sub-particles
Shin Yamaguchi, Yoko Toyoshima, Junichiro Yajima (*Dept Life Sciences, Graduate School of Arts and Sciences, Univ. of Tokyo.*)

2A1546　哺乳類細胞質ダイニンが一方向性を獲得する機構について
The mechanism of the transition from diffusion to directed movement in mammalian cytoplasmic dynein
Takayuki Torisawa[1], Furuta Ken'ya[2], Muneyoshi Ichikawa[1], Yoko Toyoshima[1] ([1]*Dept Life Sciences, Graduate School of Arts and Sciences, the Univ of Tokyo*, [2]*Bio ICT lab, NICT*)

2A1558　骨格筋形成過程における細胞質ダイニンの分布変化
The dynamic change of the distribution of cytoplasmic dynein during skeletal muscle differentiation process
Takuya Kobayashi, Motoshi Kaya, Hideo Higuchi (*Department of physics, Graduate school of science, The university of Tokyo*)

2A1610　ダイニンアダプター Bicaudal-D2 の細胞周期依存的核膜局在の分子機構
Molecular mechanism of cell-cycle dependent nuclear envelope localization of Bicaudal-D2
Takashi Murayama, Hiroki Ota, Takashi Sakurai (*Dept. Pharmacol., Juntendo Univ. Sch. Med.*)

14:00～16:22　B会場　多元数理科学棟５階 509／Room B: Mathematics bldg. 5F 509
蛋白質-構造機能相関II：理論，凝集
Proteins: Structure & Function II: Theory, Aggregation

2B1400　単一アミノ酸ポテンシャル力場の改良と短鎖ペプチドの構造予測への応用
Improvement of the Single Amino Acid Potential Force Field and the Application to Structure Prediction of Short Peptides
Michio Iwaoka, Kenichi Dedachi, Taku Shimosato, Toshiya Minezaki (*Tokai Univ*)

2B1412　オンサーガー・マハラップ作用を用いたペプチド系のパスサンプリング
Path sampling for small peptide systems using the Onsager-Machlup action method
Hiroshi Fujisaki[1,2], Yasuhiro Matsunaga[2], Akinori Kidera[2,3] ([1]*Nippon Medical School*, [2]*RIKEN*, [3]*Yokohama City University*)

2B1424　蛋白質系のシミュレーションの緩和モード解析
Relaxation mode analysis for simulations of protein systems
Ayori Mitsutake, Toshiki Nagai, Hiroshi Takano (*Keio Univ.*)

2B1436　A multi-body potential for normal mode analysis of protein structure
Bhaskar Dasgupta, Narutoshi Kamiya, Haruki Nakamura, Akira Kinjo (*Institute for Protein Research, Osaka University*)

2B1448　アクチン線維へのコフィリンの協同的結合の統計力学モデルの作成
A theoretical model of cooperative binding of cofilin to actin filaments
Shotaro Sakakibara[2], Kimihide Hayakawa[1], Hitoshi Tatsumi[2], Masahiro Sokabe[1,2] ([1]*FIRST Research Center for Innovative*

Nanobiodevice, Univ. Nagoya, [2]*Grad. Sch. Med., Univ. Nagoya*)

休憩 15:00-15:10

2B1510 リゾチーム分子中のアミロド性ペプチド
Amyloidogenic Peptides from Hen Lysozyme
Hideki Tachibana[1,3], Masao Fujisawa[1,3], Ryohei Kono[2,3], Minoru Kato[4] ([1]*Sch Biol-Oriented Sci Tech, Kinki Univ*, [2]*Wakayama Med Univ*, [3]*High Press Prot Res Center, Kinki Univ*, [4]*Coll Pharm Sci, Ritsumeikan Univ*)

2B1522 Effects of raft components on the membrane-mediated aggregation of IAPP
Kenji Sasahara (*Kobe University*)

2B1534 タンパク質が生体内レドックス環境に依存して異なる凝集体を形成するメカニズムとその病理学的意義
Redox environment is an intracellular factor to operate distinct pathways for protein aggregation
Yoshiaki Furukawa (*Dept. of Chemistry, Keio Univ.*)

2B1546 銅シャペロンに依存しない SOD1 酵素の活性化制御メカニズム
A copper chaperone-independent mechanism for activation of Cu, Zn-superoxide dismutase
Yasuyuki Sakurai, Yoshiaki Furukawa (*Dept. of Chem, Keio Univ.*)

2B1558 タンパク質凝集体の形態を制御する「凝集後修飾」のメカニズム
A mechanism controlling the morphologies of protein aggregates by "post-aggregation oxidation"
Yasushi Mitomi[1], Takao Nomura[1], Masaru Kurosawa[2], Nobuyuki Nukina[2], Yoshiaki Furukawa[1] ([1]*Dept. of Chem, Keio Univ.*, [2]*RIKEN Brain Science Institute*)

2B1610 ジスルフィド結合の組換えによる不溶性 SOD1 オリゴマーの新たな形成メカニズム－筋萎縮性側索硬化症における分子病理変化
Destabilization of SOD1 facilitates abnormal scrambling of its disulfide bond in the familial form of amyotrophic lateral sclerosis
Keisuke Toichi, Yoshiaki Furukawa (*Dept. of Chem, Keio Univ.*)

14:00～16:22 C 会場　多元数理科学棟 4 階 409 ／ Room C: Mathematics bldg. 4F 409
数理生物学
Mathematical Biology

2C1400 A Brownian particle undergoing reversible binding in a surface: exact theoretical results and an application in single molecule biophysics
Ziya Kalay (*Institute for Integrated Cell-Material Sciences, Kyoto University*)

2C1412 Single-particle-level simulation reveals effects of molecular crowding on biochemical signaling response
Kazunari Kaizu, Koichi Takahashi (*Laboratory for Biochemical Simulation, RIKEN Quantitative Biology Center (QBiC)*)

2C1424 2 つのヒートショック反応系における反応機構の比較
Conflicted dissociation constant in two reaction mechanisms for heat shock response
Masayo Inoue[1], Ala Trusina[2], Namiko Mitarai[2], Kim Sneppen[2] ([1]*CMC, Osaka Univ.*, [2]*CMOL, NBI*)

2C1436 Mathematical analysis for vascular and spot patterns by auxin and PIN dynamics in plant development
Yoshinori Hayakawa[1,2], Atsushi Mochizuki[1,2] ([1]*Tokyo Institute of Technology*, [2]*Wako Inst., Riken*)

2C1448 Modeling wave propagation dynamics in MDCK wound healing assay
Yusuke Sawabu[1], Masaharu Nagayama[2], Takashi Miura[3], Hiroyuki Kitahata[4] ([1]*Inst. of Nat. Sci. and Tech., Kanazawa Univ.*, [2]*Res. Inst. for Elect. Sci. Hokkaido Univ.*, [3]*Kyoto Univ. Grad. Sch. Of Med.*, [4]*Dept. of Phys., Chiba Univ., Grad. Sch. of Sci.*)

休憩 15:00-15:10

2C1510 CA モデルによる多細胞性シアノバクテリアの形態形成ダイナミクスの解析
Analysis of the internal dynamics for pattern formation in multi cellular cyanobacteria by CA model
Jun-ichi Ishihara[1,2], Masashi Tachikawa[2], Hideo Iwasaki[1], Atsushi Mochizuki[2] ([1]*Grad.Sci.Eng., Waseda Univ.*, [2]*Wako Inst., RIKEN*)

2C1522 Modeling the mammalian circadian clock
Craig Jolley, Hiroki Ueda (*RIKEN Center for Developmental Biology, Laboratory for Systems Biology*)

2C1534 Determining the ratio of longitudinal to transverse conductivity in a cardiac tissue culture through application of FFP
Marcel Hoerning[1], Seiji Tagaki[2], Kenichi Yoshikawa[3,4] ([1]*RIKEN, Center for Developmental Biology, Physical Biology Unit*, [2]*Hokkaido University, Research Institute for Electronic Science*, [3]*Doshisha University, Life and Medical Sciences*, [4]*Kyoto University, Department of Physics*)

2C1546 気道上皮細胞における Cl^- 分泌の数理モデル
Mathematical model of Cl^- secretion in airway epithelial cells
Kouhei Sasamoto[1], Naomi Niisato[2,3], Yoshinori Marunaka[2,3] ([1]*Undergraduate Student, Kyoto Prefectural Univ. Med.*, [2]*Molecular Cell Physiology, Kyoto Prefectural Univ. Med.*, [3]*Japan Institute for Food Education and Health, Heian Jogakuin (St. Agnes') Univ.*)

2C1558 エラーカタストロフィーによる HIV-1 擬種集団の自壊過程に関する研究
A Study on a Self-Destruction Process of a HIV-1 Quasispecies Population through the Error Catastrophe
Kouji Harada (*Toyohashi Univ. of Tech. Dept. of Comp. Sci. and Eng.*)

2C1610 Characterization of Death and Division Process in Synthetic Bacterial Population with Antibiotic Treatment
Takashi Nozoe[1], Reiko Okura[1], Yuichi Wakamoto[2,3] ([1]*Grad. Sch. Arts and Sci., Univ. Tokyo*, [2]*Research Center for Complex Systems Biology, Univ of Tokyo*, [3]*JST PRESTO*)

14:12～16:10 D 会場　多元数理科学棟 3 階 309 ／ Room D: Mathematics bldg. 3F 309
計測
Measurements

2D1412 クライオ電子線トモグラフィーに対する超分解能技術
Super-resolution cryo-electron tomography
Ryuzo Azuma[1,2], Takuo Yasunaga[1,2] ([1]*Grad. Sch. of Comp. Sc. & Eng., Dept. of Biosc. & Bioinfo., Kyushu Inst. of Tech.*, [2]*JST*)

2D1424 定量位相顕微鏡による生細胞におけるナノスケールの形状変化の非染色ビデオレートイメージング

Label-free and video-rate imaging of live cell membrane motion in the nanometer-scale by quantitative phase microscope

Toyohiko Yamauchi[1], Takashi Sakurai[2], Hidenao Iwai[1], Yutaka Yamashita[1] ([1]*Hamamatsu Photonics*, [2]*EIIRIS, Toyohashi Univ. of Tech.*)

2D1436 ラマン分光を用いた超音波照射による細胞への影響の評価

Evaluation of Ultrasound Irradiation effects on Cells by using Raman Spectroscopy

Manabu Sugimoto[1], Yo Otsuka[1], Shinya Murakami[1], Toshiyuki Mitsui[2] ([1]*Grad. Sci Eng., Aogaku Univ*, [2]*Assoc Prof, Aogaku Univ*)

2D1448 脂肪酸と 7-ヒドロキシ-4-メチルクマリンを用いた質量と蛍光測定によるアンモニアの二次元検出

Two dimensional ammonia sensing by measurement of mass and fluorescence using 7-hydroxy-4-methylcoumarin film and fatty acid

Yuta Ando, Masahiro Terashita, **Ryohei Matsueda**, Yutaka Tsujiuchi (*Department of Material Science and Engineering, Akita University*)

休憩 15:00-15:10

2D1510 インビトロ心毒性予測のための心筋細胞ネットワークの時間的細胞外電位ゆらぎと空間的伝達速度ゆらぎの評価

Evaluation of temporal fluctuation and spatial fluctuation on cardiomyocyte network for *in vitro* predictive cardiotoxicity measurement

Tomoyo Hamada, Fumimasa Nomura, Tomoyuki Kaneko, Kenji Yasuda (*Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University*)

2D1522 SACLA における非結晶粒子の低温 X 線回折イメージング実験

Cryogenic Coherent X-ray Diffraction Imaging of non-crystalline particles at SACLA

Masayoshi Nakasako[1,2], Yuki Takayama[1,2], Tomotaka Oroguchi[1,2], Yuki Sekiguchi[1,2], Masaki Yamamoto[2], Koji Yonekura[2], Takaaki Hikima[2], Saori Maki-Yonekura[2], Yukio Takahashi[3], Akihiro Suzuki[3], Sachihiro Matsunaga[4], Shoichi Kato[4], Takahiko Hoshi[5] ([1]*Department of Physics, Keio University*, [2]*RIKEN SPring-8 Center, RIKEN Harima Institute*, [3]*Department of Precision Science and Technology, Graduate School of Engineering, Osaka University*, [4]*Department of Applied Biological Science, Faculty of Science and Technology, Tokyo University of Science*, [5]*Kohzu Precision Co.,Ltd.*)

2D1534 A protocol for structure analysis of non-crystalline particles with X-ray free electron laser

Tomotaka Oroguchi, Masayoshi Nakasako (*Department of Physics, Faculty of Science and Technology, Keio University*)

2D1546 イオンコンダクタンス顕微鏡による細胞膜揺らぎの測定

Fluctuation of cell membrane investigated by ion conductance microscopy

Yusuke Mizutani[2], Satoshi Ichikawa[1], Zen Ishikura[1], **Takaharu Okajima**[1] ([1]*Grad. Sch. Inform. Sci. Tech., Hokkaido Univ.*, [2]*Grad. Sch. Life Sci., Hokkaido Univ.*)

2D1558 Relationship between Intercellular Adhesion Strength and Communication Detected by Femtosecond Laser-induced Impulsive Force

Takanori Iino[1], Man Hagiyama[2], Tadahide Furuno[3], Akihiko Ito[2], Yoichiroh Hosokawa[1] ([1]*Nara Institute of Science and Technology*, [2]*Kinki University*, [3]*Aichi Gakuin University*)

14:00～16:22 E 会場 多元数理科学棟 1 階 109 ／ Room E: Mathematics bldg. 1F 109
蛋白質-物性 II
Proteins: Property II

2E1400 AFM を用いたホロミオグロビンの一分子力学計測によるアンフォールディング経路の探索

Mechanical unfolding pathways of holo-myoglobin explored by AFM-based single molecule force spectroscopy

Aya Yoshida, Masaru Kawakami (*Materials Sci, JAIST*)

2E1412 走査型プローブ顕微鏡を用いた癌抑制因子 p53 の一分子構造解析

Single-molecule structural analysis of tumor suppressor p53 using scanning probe microscopes

Seiya Takahashi[1], Yasuyuki Sainoo[1], Risa Kashima[2], Takashi Tokino[3], Tadahiro Komeda[1], Satoshi Takahashi[1], **Kiyoto Kamagata**[1] ([1]*IMRAM, Tohoku Univ.*, [2]*Univ. California*, [3]*Res. Inst. Front. Med., Sapporo Med. Univ. Sch. Med.*)

2E1424 塩基性条件下でのヒトガレクチン 1 のβガラクトシド結合能力

β-Galactoside-binding activity of human galectin-1 at basic pH

Hirotsugu Hiramatsu, Tomohide Nishino, Hideo Takeuchi (*Graduate School of Pharmaceutical Sciences, Tohoku University*)

2E1436 A Molecular Mechanism of Induced-fit of U1A Protein

Ikuo Kurisaki[1,2], Masayoshi Takayanagi[1,2], Masataka Nagaoka[1,2] ([1]*Grad. Sch. Info. Sci. Univ. Nagoya*, [2]*CREST, JST*)

2E1448 Single mutation on a loop alters the key dynamics of the core, but not the average structure

Akihiro Maeno[1], Sunilkumar P.N.[1], Yuji Wada[2], Eiji Ohmae[2], Shin-ichi Tate[2], Kazuyuki Akasaka[1] ([1]*HPPRC, Kinki Univ.*, [2]*Grad. Sch. Sci., Univ. Hiroshima*)

休憩 15:00-15:10

2E1510 ヒト主要組織適合複合体の安定化に置ける揺らぎの重要性について

The effect of flexibility on the stability of Human Leucocyte Antigen

Saeko Yanaka[1], Kenjji Sugase[2], Takamasa Ueno[3], Kouhei Tsumoto[1] ([1]*Med. Genome Sci., Grad. Sch. Frontier Sci., the Univ. of Tokyo*, [2]*Suntory Institue for Bioorganic research*, [3]*Center for AIDS Research, Kumamoto Univ.*)

2E1522 Cavity-dependent dynamics of c-Myb R2R3 revealed by high-pressure fluorescence and NMR spectroscopy

Satomi Inaba[1], Akihiro Maeno[2], Hisayuki Morii[3], Harumi Fukada[4], Kazuyuki Akasaka[2], Masayuki Oda[1] ([1]*Grad. Sch. of Life and Environ. Sci., Kyoto Pref. Univ.*, [2]*High Pressure Protein Res. Center, Kinki Univ.*, [3]*Biomed. Res. Inst., Natl. Inst. Adv. Ind. Sci. Technol.*, [4]*Grad. Sch. of Life and Environ. Sci., Osaka Pref. Univ.*)

2E1534 単純化 BPTI に融合したペプチド系タグ配列を用いたアミノ酸溶解性の測定

Analysis of amino acid contributions to protein solubility using short peptide tags fused to a simplified BPTI variant

Yutaka Kuroda[1], Alam, M. Khan[1], Mohammad, M. Islam[1,2] ([1]*Dept of Biotech and Life Sci, TUAT*, [2]*Dept of Mol Biol and Biochem, Chittagon University*)

2E1546 Protein Aggregation Kinetics Using Short Amino acid

Peptide Tags
Monsur A. Khan[1], Mohammad M. Islam[1,2], Yutaka Kuroda[1] ([1]*Tokyo University of Agriculture and Technology*, [2]*University of Chittagong, Bangladesh*)

2E1558 **Protein specific partial charges by Ab-initio fragment molecular orbital method for more accurate protein simulations**
Le Chang, Shoji Takada (*Grad. Sch. Sci., Kyoto Univ.*)

2E1610 **Regulatory Mechanism of the fluorescence emission from Green Fluorescent Protein Chromophore**
Jumpei Torii, Shoji Yamashita, Etsuko Nishimoto (*Institute of Biophysics, Faculty of Agriculture, Graduate school of Kyushu University*)

14:00〜16:10 F 会場 理学 B 館 5 階 501 ／ Room F: Sci. bldg. B 5F 501
光生物-視覚，光受容 II
Photobiology: Vision & Photoreception II

2F1400 **全原子量子化学計算によるレチナールタンパク質の吸収波長制御機構の解析**
Full-Quantum Chemical Calculations of the Absorption Maxima of Retinal Proteins
Tomohiko Hayashi[1], Azuma Matsuura[2], Hiroyuki Sato[2], Minoru Sakurai[1] ([1]*Center for Biological Resources and Informatics, Tokyo Institute of Technology*, [2]*Fujitsu Laboratories, Ltd.*)

2F1412 **プロテオロドプシンにおける細胞質側ループの変異がもたらす遠隔的波長制御メカニズム**
Mechanism of color change of proteorhodopsin by mutations at distant cytoplasmic loop
Yuya Ozaki[1], Rei Abe-Yoshizumi[1], Susumu Yoshizawa[2], Kazuhiro Kogure[2], Hideki Kandori[1] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech*, [2]*AORI, Univ. Tokyo*)

2F1424 **キメラタンパク質を用いた Rhodobacter capsulatus 由来 Photoactive Yellow Protein の相互作用部位の解明**
Analysis of interaction sites on the Photoactive Yellow Protein of Rhodobacter capsulatus with chimeric proteins
Mayu Shimad, Yoichi Yamazaki, Hironari Kamikubo, Mariko Yamaguchi, Mikio Kataoka (*Grad. Sch. Mat. Sci., NAIST*)

2F1436 **FTIR study of Aureochrome that possesses LOV domain at the C-terminus**
Shota Ito[1], You Zhang[1], Tatsuya Iwata[2], Osamu Hisatomi[3], Fumio Takahashi[4], Hironao Kataoka[5], Hideki Kandori[1] ([1]*Nagoya Inst. Tech*, [2]*Ctr. Fost. Yng. Innov., Nagoya Inst. Tech*, [3]*Grad. Sch. Sci., Osaka Univ*, [4]*PRESTO, JST*, [5]*Botanical Gardens, Tohoku Univ*)

2F1448 **LOV ドメインを鋳型としたレドックス感受性蛍光タンパク質の開発**
Construction of LOV-based redox-sensitive fluorescent proteins
Yukiko Ono[1], Tatsuya Iwata[2], Hideki Kandori[1] ([1]*Nagoya Inst. Of Technol.*, [2]*Ctr. Fost. Yng. Innov. Res., Nagoya Inst. Tech.,*)

休憩 15:00-15:10

2F1510 **クラミドモナス由来の全長フォトトロピンが示す光反応ダイナミクスの時間分解検出**
Time-resolved study on photoreaction dynamics of full-length phototropin from Chlamydomonas reinhardtii
Yusuke Nakasone[1], Koji Okajima[2], Yusuke Aihara[3], Akira Nagatani[3], Satoru Tokutomi[2], Masahide Terazima[1] ([1]*Grad. Chem. Sci, Kyoto Univ.*, [2]*Grad. Sci, Osaka Prefecture Univ.*, [3]*Grad. Biol. Sci, Kyoto Univ.*)

2F1522 **N 末アミノ酸残基の有無は AppA BLUF ドメインの保存されたトリプトファン残基の位置に影響しない**
N-Terminal Truncation Does Not Affect the Location of a Conserved Tryptophan in the BLUF Domain of AppA from *Rhodobacter sphaeroide*
Masashi Unno[1], Yuuki Tsukiji[1], Kenshuke Kubota[1], Shinji Masuda[2,3] ([1]*Depart. Chem. Appl. Chem., Saga University*, [2]*Center for BioRes. & Inform., Tokyo Inst. Tech.*, [3]*PRSTO, JST*)

2F1534 **Substrate-Dependent Measurement Revealed Different Protein Conformations on Photoactivation and DNA Repair of E. coli CPD Photolyase**
I Made Mahaputra Wijaya[1], Yu Zhang[1], Junpei Yamamoto[2], Kenichi Hitomi[3], Shigenori Iwai[2], Elizabeth D. Getzoff[3], Hideki Kandori[1] ([1]*Nagoya Institute of Technology*, [2]*Osaka University*, [3]*The Scripps Research Institute, La Jolla, USA*)

2F1546 **アニオンラジカル型の(6-4)光回復酵素による DNA 修復**
Repair of damaged DNA by the anion radical form of (6-4) photolyase
Daichi Yamada[1], Yu Zhang[1], Tatsuya Iwata[2], Junpei Yamamoto[3], Kenichi Hitomi[4], Shigenori Iwai[3], Elizabeth Getzoff[4], Hideki Kandori[1] ([1]*Nagoya Inst. Tech.*, [2]*Ctr. Fost. Yng. Innov. Res., Nagoya Inst. Tech.*, [3]*Grad. Sch. Eng. Sci., Osaka Univ.*, [4]*The Scripps Res. Inst. USA*)

2F1558 **光センサータンパク質 UVR8 の解離・回復反応カイネティックスの測定**
The study of the dissociation and recovery reaction kinetics for photo-sensor protein UVR8
Takaaki Miyamori[1], Yusuke Nakasone[1], Kenichi Hitomi[2], John M. Christie[3], Elizabeth D. Getzoff[2], Masahide Terazima[1] ([1]*Grad. Sci. Chem., Univ. Kyoto*, [2]*Scripps Research Inst.*, [3]*Univ. Glasgow*)

14:00〜16:22 G 会場 理学 B 館 2 階 212 ／ Room G: Sci. bldg. B 2F 212
生体膜・人工膜
Biological & Artificial Membranes

2G1400 **膜融合におけるストーク構造からの変形：分子動力学シミュレーション**
Morphology change of fusion stalk studied by molecular dynamics simulation
Shuhei Kawamoto, Wataru Shinoda (*Nano. AIST*)

2G1412 **蛍光検出と電気計測による膜タンパク質計測に向けた脂質膜チャンバアレイ**
Lipid bilayer chamber array toward fluorescent and electrophysiological measurement of membrane proteins
Taishi Tonooka[1], Ryuji Kawano[2], Koji Sato[1], Toshihisa Osaki[2], Shoji Takeuchi[1] ([1]*Institute of Industrial Science, The University of Tokyo*, [2]*Kanagawa Academy of Science and Technology*)

2G1424 **蛋白質毒素ライセニンがスフィンゴミエリンを含む脂質膜中に誘起するポア形成： 単一 GUV 法による研究**
Single Giant Unilamellar Vesicle Method Reveals Lysenin-Induced Pore Formation in Lipid Membranes Containing

Sphingomyelin
Jahangir Md. Alam[1], Toshihide Kobayashi[2], Masahito Yamazaki[1] ([1]*Int. Biosci. Sec., Grad. Sch. Sci. Tech., Shizuoka University*, [2]*Lipid Bio. Lab., RIKEN*)

2G1436 人工細胞ベシクルにおける脂質ドメインへの化合物局在を介したドメインサイズと膜崩壊率の制御
Localization of bulky-molecules in raft-like domains on phase-separated liposomes: Control of domain size and bursting rate of liposome
Miho Yanagisawa[1], Damien Baigl[2], Kenichi Yoshikawa[3] ([1]*Grad. Sch. Sci., Kyushu Univ.*, [2]*Depart. Chem., Ecole Normale Superieure*, [3]*Depart. Biomed. Info., Doshisya Univ.*)

2G1448 PI4P と脂質膜曲率による Kes1 ステロール輸送活性の制御
Regulation of Kes1 sterol transport activity by PI4P and lipid membrane curvature
Hirokazu Yokoyama[1], Masaki Wakabayashi[1], Yasushi Ishihama[1], Minoru Nakano[2] ([1]*Graduate School of Pharmaceutical Sciences, Kyoto University*, [2]*Graduate School of Medicine and Pharmaceutical Sciences, University of Toyama*)

休憩 15:00-15:10

2G1510 リン脂質輸送タンパク質 Sec14 の脂質輸送メカニズムの解明
Elucidation of lipid transfer mechanism of phospholipid transfer protein Sec14
Chisato Takahashi[1], Makiko Yamada[1], Masaki Wakabayashi[1], Yasushi Ishihama[1], Minoru Nakano[2] ([1]*Grad. Sch. Pharm., Kyoto Univ.*, [2]*Grad.Sch.Pharm., Toyama Univ.*)

2G1522 ゲル、アミノ酸、水素化アモルファスシリコンを用いた光制御イオン伝導整流素子
Photo-controlled ion conductive rectification element using gel, amino acids and hydrogenated amorphous silicon film
Takaaki Ichikawa[1], **Hiroki Suzuki**[1], Ryohei Matsueda[1], Hiroshi Masumoto[2], Takashi Goto[3], Yutaka Tsujiuchi[1] ([1]*Department of Material Science and Engineering, Akita University*, [2]*Center for Interdisciplinary Research, Tohoku University*, [3]*Institute for Materials Research, Tohoku University*)

2G1534 高速 AFM による CFTR チャネルの動態観察
Single molecular observation of CFTR channels by high speed AFM
Hayato Yamashita[1], Kazuhiro Mio[2], Muneyo Mio[2], Takayuki Uchihashi[3], Masato Yasui[1], Toshio Ando[3], Yoshiro Sohma[1,4] ([1]*Pharmacol., Keio Univ. Med. Sch.*, [2]*AIST*, [3]*Dept of Physics, Kanazawa Univ.*, [4]*Dalton Cardiovas. Res. Cen., Univ. Missouri-Columbia*)

2G1546 KcsA チャネルの細胞内ドメインは不活性化に影響を与える
The KcsA channel cytoplasmic domain effects on the inactivation gating
Minako Hirano[1,2], Yukiko Onishi[2], Daichi Okuno[2], Toru Ide[1,2] ([1]*GPI*, [2]*RIKEN*)

2G1558 原子間力顕微鏡によるカリウムイオンチャネル KcsA の脂質膜中でのゲート開閉構造の直接観察
Direct Observation of Ion Entryway of Potassium Channel KcsA in Lipid Bilayer by Atomic Force Microscopy
Ayumi Sumino[1], Takashi Sumikama[2], Masayuki Iwamoto[2], Takahisa Dewa[1,3], Shigetoshi Oiki[2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Deprt. of Mol. Physiol. and Biophys., Univ. of Fukui Fac. Med. Sci.*, [3]*JST-PRESTO*)

2G1610 全反射赤外分光法による KcsA のイオン選択フィルターの振動解析
The Vibrational Analysis of the Selectivity Filter of KcsA by using ATR-FTIR Spectroscopy
Yuji Furutani[1,2], Hirofumi Shimizu[3], Yusuke Asai[1], Tetsuya Fukuda[1], Shigetoshi Oiki[3], Hideki Kandori[1] ([1]*Grad. Sch. Tech., Nagoya Inst. Tech.*, [2]*Inst. Mol. Sci.*, [3]*Facul. Med. Sci., Univ. Fukui*)

14:00～16:22 H 会場 理学 C 館 5 階 517 ／ Room H: Sci. bldg. C 5F 517
筋肉
Muscle

2H1400 中性子散乱による心筋症関連トロポニン変異体のダイナミクス測定
Dynamics of cardiomyopathy-causing mutant of troponin observed by neutron scattering
Tatsuhito Matsuo[1], Francesca Natali[3], Giuseppe Zaccai[2,3], Satoru Fujiwara[1] ([1]*QuBS, JAEA*, [2]*CNRS*, [3]*ILL*)

2H1412 スピンラベル ESR 距離測定による細いフィラメントのアクチン、トロポミオシン、トロポニンの動的構造解析
Structural dynamics of actin, tropomyosin, and troponin in the thin filament as studied by distance measurements using spin-labeling ESR
Keisuke Ueda[1,2], Chenchao Zhao[1], Akie Yamamoto[1], Takayasu Somiya[1], Tomoki Aihara[1,3], Shoji Ueki[4], Masao Miki[5], **Toshiaki Arata**[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Inst. Prot. Res., Osaka Univ.*, [3]*Harima Inst., Riken*, [4]*Tokushima-Bunri Univ.*, [5]*Univ. Fukui*)

2H1424 アクチン周りのハイパーモバイル水の形成とその熱力学的考察
Formation of hyper-mobile water around actin and its thermodunamic considerations
Makoto Suzuki, George Mogami, Tetsuichi Wazawa, Asato Imao, Noriyoshi Ishida (*Tohoku Univ. Grad. Sch. Eng.*)

2H1436 アクチン様トレッドミリングモータが満たすべき最小条件
Minimum requirements for the actin-like treadmilling motor system
Akihiro Narita (*Grad. Sch. Sci., Nagoya Univ.*)

2H1448 3 次元トラッキングによる *in vitro* アクチンフィラメントモーティリティーアッセイ
Three-dimensional tracking of gliding actin filament in an *in vitro* motility assay
Tatsuya Naganawa, Togo Shimozawa, Tomoko Masaike, Takayuki Nishizaka (*Gakushuin Univ.*)

休憩 15:00-15:10

2H1510 Ca^{2+}に依存しない熱パルスによる心筋細胞の On-Off 制御
Ca^{2+}-independent on-off regulation of a cardiomyocyte by microscopic heat pulses
Kotaro Oyama[1], Akari Mizuno[1], Seine Shintani[1], Hideki Itoh[1], Takahiro Serizawa[1], Norio Fukuda[2], Madoka Suzuki[3,4], Shin'ichi Ishiwata[1,3,4] ([1]*Sch. Adv. Sci. Eng., Waseda Univ.*, [2]*Dept. Cell Physiol., Jikei Univ. Sch. Med.*, [3]*Org. Univ. Res. Initiatives, Waseda Univ.*, [4]*WABIOS, Waseda Univ.*)

2H1522 ミオシン分子の非線形弾性とフィラメントの弾性変形を考慮した筋収縮のシミュレーション
The Effects of Nonlinear Elasticity of Myosin Molecules on Muscle Contraction Studied by Numerical Simulation
Keita Miyamoto, Kazuo Sasaki (*Dept. Appl. Phys., Sch. Eng., Tohoku Univ.*)

2H1534 高塩濃度溶液中における熱変性したミオシン分子のミオシンフィラ

メントへの付着

Adhesion of heat-denatured myosin molecules to myosin filament at high salt concentration

Masato Shimada[1], Eisuke Takai[1], Daisuke Ejima[2], Kentaro Shiraki[1] ([1]*Facul. of Pure and Appl. Sci., Univ. of Tsukuba.*, [2]*Institute for Innovation, Ajinomoto Co. Inc.*)

2H1546 ラット幼若心筋細胞内サルコメア集団の自励振動(SPOC)特性

Auto-oscillation (SPOC) properties of sarcomeres in rat neonetal cardiomyocytes

Seine Shintani[1], Kotaro Oyama[1,2], Norio Fukuda[2], Shin'ichi Ishiwata[1,3] ([1]*Sch. Adv. Sci. Eng., Waseda Univ.*, [2]*Dept. Cell Physiol., Jikei Univ. Sch. Med.*, [3]*WABIOS, Waseda Univ.*)

2H1558 横紋筋サルコメアのフィラメント格子の安定性

Stability of Myofilament Lattice in Striated Muscle Sarcomere

Shigeru Takemori[1], Masako Kimura[2], Maki Yamaguchi[1], Tetsuo Ohno[1], Naoya Nakahara[1], Shunnya Yokomizo[3] ([1]*Jikei Univ. Sch. Med.*, [2]*Kagawa Nutrition Univ.*, [3]*Tokai Univ. Graduate Sch. Physical Education*)

2H1610 羽ばたくマルハナバチ中で拮抗する 2 種の飛翔筋の超高速 X 線回折像同時記録

Simultaneous ultrafast X-ray recordings of actions of two antagonistic flight muscles during wingbeat of live bumblebee

Hiroyuki Iwamoto, Naoto Yagi (*SPring-8, JASRI*)

14:00～16:22 I 会場　理学 E 館 1 階 131 ／ Room I: Sci. bldg. E 1F 131
細胞生物的課題 II：Prokaryotes
Cell Biology II: Prokaryotes

2I1400 海洋性ビブリオ菌の周毛性べん毛形成の抑制に関与する DnaJ モチーフを持った新規遺伝子の解析

A novel gene of dnaJ family plays a role in the suppression of flagellation in Vibrio alginolyticus

Takehiko Nishigaki[1], Maya Kitaoka[1], Kunio Ihara[2], Noriko Nishioka[1], Seiji Kojima[1], Michio Honma[1] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Gene., Univ. Nagoya*)

2I1412 バクテリアⅣ型線毛の粘着脱離動力学

Unbinding Dynamics of Type IV Pili

Tomonari Sumi[1,2], Rahul Marathe[2], Stefan Klumpp[2] ([1]*Dept. Comp. Sci. Eng., Toyohashi Univ. Tech.*, [2]*Dept. Theo. & Bio-syst., Max Planck Inst. Colloids & Interfaces*)

2I1424 細菌べん毛特異的シャペロン FliT の C 末αヘリックの役割

Role of the C-terminal α-helix of FliT chaperone in the export of its cognate substrate FliD

Tohru Minamino[1], Miki Kinoshita[1,2], Noritaka Hara[1], Katsumi Imada[2], Keiichi Namba[1,3] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*Grad. Sch. Sci., Osaka Univ.*, [3]*QBiC RIKEN*)

2I1436 べん毛輸送装置近傍の局所 pH に対する FliI ATPase の効果

Effect of FliI ATPase on local pH around the bacterial flagellar protein export apparatus

Yusuke V. Morimoto[1,2], Nobunori Kami-ike[1], Tomoko Miyata[1], Keiichi Namba[1,2], Tohru Minamino[1] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*QBiC, RIKEN*)

2I1448 Na^+駆動型べん毛モーター固定子タンパク質 PomA の細胞質ループ領域の示差走査熱量測定を用いた性質検討

Characterization of cytoplasmic loop of PomA, Na^+-driven flagellar stator protein, using differential scanning calorimetry

Shiori Kobayashi[1], Rei Abe-Yoshizumi[1,2], Mizuki Gohara[1], Seiji Kojima[1], Michio Homma[1] ([1]*Division of Biological Science, Graduate School of Science, Nagoya University*, [2]*Department of Frontier Materials, Nagoya Institute of Technology*)

休憩 15:00-15:10

2I1510 プラグを欠失した Na^+駆動型べん毛モーター固定子複合体の精製・再構成系の構築

Purification and reconstitution of the plug-deleted Na^+-driven stator complex from *Vibrio alginolyticus*

Tetsuya Oba, Seiji Kojima, Michio Homma (*Division of Biological Science, Graduate school of science, Nagoya University*)

2I1522 蛍光相関分光法（FCS）を用いたべん毛モーターを構成するタンパク質間の相互作用解析

Analysis of interactions between rotor proteins of flagellar motor using Fluorescence Correlation Spectroscopy

Takaaki Kishi, Seiji Kojima, Michio Homma (*Division of Biological Science, Graduate School of Science, Nagoya University, Chikusa-ku, Nagoya, Japan.*)

2I1534 Na^+駆動型べん毛モーターの固定子と回転子間における荷電残基変異による協調作用の解析

Synergetic effects of the mutations of charged residues between the rotor and the stator in the Na^+-driven flagellar motor

Norihiro Takekawa, Seiji Kojima, Michio Homma (*Div. of Biol. Sci., Grad. Sch. of Sci., Nagoya Univ.*)

2I1546 光分解されたセリンへの大腸菌の応答計測

Measurement of cellular response of single *E. coli* to the photoreleased serine

Takashi Sagawa[1], Hajime Fukuoka[2], Yuichi Inoue[2], Hiroto Takahashi[2], Takahiro Muraoka[2], Kazushi Kinbara[2], Akihiko Isjijima[2] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*IMRAM, Tohoku Univ.*)

2I1558 CheZ 極局在の有無における大腸菌細胞内シグナル伝達の計測

Propagation of intracellular signaling molecule in the presence and absence of polar localization of CheZ in a single *E. coli* cell

Hajime Fukuoka[1], Takashi Sagawa[2], Yuichi Inoue[1], Hiroto Takahashi[1], Akihiko Ishijima[1] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. life Sci., Tohoku Univ.*)

2I1610 大腸菌の遊泳速度に及ぼすγ線照射の効果

Effect of gamma ray irradiation on the swimming speed of *Escherichia coli*

Eriko Fujimoto[1], Masakazu Furuta[2], Tatsuo Atsumi[3], **Mikio Kato**[2] ([1]*Osaka Prefecture University School of Science*, [2]*Osaka Prefecture University Graduate School of Science*, [3]*Gifu University of Medical Science*)

9:12～11:10　A 会場　理学南館 坂田・平田ホール／ Room A: Sci. south bldg. 1F Sakata Hirata Hall
分子モーター III：F1-ATPase, マイコプラズマ
Molecular Motors III: F1 ATPase and Mycoplasma

3A0912 **F_1-ATPase と繊毛軸糸の機能に関わる構造変化**
Motions in F_1-ATPase and ciliary axonemes that drive functions
Tomoko Masaike[1], Koji Ikegami[2], Rinako Nakayama[1], Mitsutoshi Setou[2], Takayuki Nishizaka[1] ([1]*Department of Physics, Gakushuin University*, [2]*Department of Cell Biology and Anatomy, Hamamatsu University School of Medicine*)

3A0924 **高速暗視野照明による金ナノロッドの方向検出システムを用いた F1-ATPase の回転の検出**
Detection of rotation of F1-ATPase using high-speed orientational detection of gold nanorod
Sawako Enoki[1,2], Ryota Iino[1,2], Hiroyuki Noji[1,2] ([1]*Grad. Sch. Engineering., Univ. Tokyo*, [2]*CREST*)

3A0936 **UTP を基質とした時の F1-ATPase の回転運動**
Characterization of UTP driven rotation of F1-ATPase
Hidenobu Arai, Rikiya Watanabe, Hiroyuki Noji (*Grad. applchem., Univ. Tokyo*)

3A0948 **Single Molecule Analysis of Inhibitory Pausing States of V_1-ATPase**
Naciye Esma Tirtom[1], Yoshihiro Nishikawa[2], Daichi Okuno[3], Masahiro Nakano[4], Ken Yokoyama[5], Hiroyuki Noji[1] ([1]*Department of Applied Chemistry, School of Engineering, University of Tokyo,* [2]*Dept. of Biotechnology, Osaka University,* [3]*RIKEN, Osaka, Japan*, [4]*The Institute of Scientific and Industrial Research,* [5]*Dept. of Biolmolecular Sciences, Kyoto Sangyo University*)

休憩 10:00-10:10

3A1010 **F_1-ATPase のトルク伝達における DELSEED ループの役割**
The role of DELSEED loop in torque-transmission of F_1-ATPase
Kazuma Koyasu[1], Rikiya Watanabe[1], Mizue Tanigawara[2], Hiroyuki Noji[1] ([1]*Department of Applied Chemistry, School of Engineering, The University of Tokyo*, [2]*Graduate School of Frontier Biosciences, Osaka University*)

3A1022 **F_1-ATPase の回転子γサブユニットに有限のトルク発生に必要な残基はない**
None of the rotor residues of F_1-ATPase are essential for torque generation
Ryohei Chiwata[1], Tomoya Kawakami[1], Ayako Kohori[1], Shou Furuike[2], Katsuyuki Shiroguchi[3], Kazuo Sutoh[1], Masasuke Yoshida[4], Kazuhiko Jr. Kinosita[1] ([1]*Dept. Physics, Fac. Sci. Eng., Waseda Univ.*, [2]*Fac. Physics, Osaka Med. Col.*, [3]*Dept. Chem. and Chem. Biol., Harvard Univ.*, [4]*Dept. of Mol. Biosci., Kyoto Sangyo Univ.*)

3A1034 **F1-ATPase のシリンダーから中心軸を引き抜く力の測定**
UNBINDING FORCE MEASUREMENTS OF THE SHAFT FROM THE CYLINDER OF F1-ATPase
Tatsuya Naito, Kaoru Okada, Tomoko Masaike, Takayuki Nishizaka (*Dept Phys, Gakushuin Univ.*)

3A1046 **リポソーム膜中に再構成した好熱菌由来 F_oF_1- ATP 合成酵素による ATP 駆動 H^+輸送の定量**
Quantification of ATP-driven H^+ transport by thermophilic *Bacillus* PS3 F_oF_1-ATP synthase reconstituted in a liposomal membrane
Yuzo Kasuya[1], Naoki Soga[1], Toshiharu Suzuki[2], Masasuke Yoshida[2], Kazuhiko Kinosita[1] ([1]*Dept. Phys., Facl. Sci. Eng., Waseda Univ.*, [2]*Dept. Mol. Bio., Facl. Life Sci., Kyoto Sangyo Univ.*)

3A1058 **マイコプラズマモービレゴーストのステップ検出**
Detection of steps of *Mycoplasma mobile* gliding ghost
Yoshiaki Kinosita[1], Daisuke Nakane[2,3], Kana Mizutani[1], Makoto Miyata[2], Takayuki Nishizaka[1] ([1]*Dept.phys., Gakushuin Univ*, [2]*Dept. Biol., Osaka City Univ*, [3]*Present address: Mol. Microbiol. and Immunol., Grad. Sch. Biomed. Sci., Nagasaki Univ*)

9:00～11:22　B 会場　多元数理科学棟 5 階 509 ／ Room B: Mathematics bldg. 5F 509
蛋白質-構造機能相関 III：動態，生体リズム
Proteins: Structure & Function III: Dynamics and Circadian Rhythm

3B0900 **原核生物由来ナトリウムチャネルにおける C 末端 4 ヘリックスバンドルを用いたゲーティング制御**
The cytosolic C-terminal four-helix bundle regulates the gating of prokaryotic sodium channel
Katsumasa Irie, Takushi Shimomura, Yoshinori Fujiyoshi (*CeSPI., Univ. Nagoya*)

3B0912 **[NiFe]ヒドロゲナーゼ成熟化因子 HypE，HypF の X 線結晶構造解析**
X-ray structural analysis of HypE and HypF, maturation factors for [NiFe]-hydrogenases
Yasuhito Shomura[1,2], Yoshiki Higuchi[1,2] ([1]*Grad. Sch. Life Sci., Univ. Hyogo*, [2]*RIKEN/SPring-8 Center*)

3B0924 **Dynamic structural and antigen binding analyses of antibody single-chain Fvs**
Yusuke Tanaka[1], Hiroshi Sekiguchi[2], Yuji C. Sasaki[3], Takachika Azuma[4], Masayuki Oda[1] ([1]*Grad. Sch. of Life and Environ. Sci., Kyoto Pref. Univ.*, [2]*Jpn. Syn. Rad. Res. Inst.*, [3]*Grad. Sch. of Fron. and Sci., Univ. of Tokyo.*, [4]*Res. Ins. for Biol. Sci., Tokyo Univ. of Sci.*)

3B0936 **PYP の光構造変化の機械的な制御**
Mechanical control of light-induced protein conformational change of photoactive yellow protein
Yasushi Imamoto, Take Matsuyama, Yoshinori Shichida (*Grad. Sch. Sci., Kyoto Univ.*)

3B0948 **αカテニンによるアクトミオシン収縮の阻害**
Inhibition of actomyosin contractility by α-catenin, a component of adherens junctions
Shuya Ishii[1], Takashi Ohki[1], Hiroaki Kubota[1], Shin'ichi Ishiwata[1,2,3] ([1]*Dept. of Phys., Faculty of Sci. and Eng., Waseda Univ.*, [2]*Adv. Res. Inst. for Scie. and Eng., Waseda Univ.*, [3]*WABIOS, Waseda Univ.*)

休憩 10:00-10:10

3B1010 ダイニンモータードメインの溶液中の分子動力学シミュレーション
Molecular dynamics simulations of dynein motor domain in explicit water
Narutoshi Kamiya[1], Tadaaki Mashimo[2], Yu Takano[1], Takahide Kon[1], Genji Kurisu[1], Haruki Nakamura[1] ([1]*Institute for Protein Research, Osaka Univ.*, [2]*BIRC, AIST*)

3B1022 A computational Investigation into the MHC-I Recognition Mechanism of MIR2 from Kaposi's Sarcoma-Associated Herpesvirus
Pai-Chi Li[1,2], Naoyuki Miyashita[3], Satoshi Ishido[1], Yuji Sugita[2] ([1]*RIKEN Research Center for Allergy and Immunology*, [2]*RIKEN Advanced Science Institute*, [3]*RIKEN Quantitative Biology Center*)

3B1034 タンパク質構造変化経路予測法の新規開発
A Novel Method to simulate protein conformational change upon ligand binding
Koichi Tamura, Shigehiko Hayashi (*Grad. Sch. Sci., Univ. Kyoto*)

3B1046 時計タンパク質 KaiA-KaiC 相互作用の ESR 解析
Interactions between cyanobacterial clock proteins KaiA and KaiC revealed by ESR analysis
Kentaro Ishii[1], Toshiaki Arata[2], Masahiro Ishiura[1] ([1]*Center for gene research Nagoya Univ.*, [2]*Grad. Sch. of Science, Osaka Univ.*)

3B1058 ATP を中間体とするシアノバクテリア概日時計蛋白質 KaiC の新規脱リン酸化機構
Autodephosphorylation of cyanobacterial circadian clock protein KaiC occurs via formation of ATP as an intermediate
Taeko Ohkawa-Nishiwaki, Takao Kondo (*Div.Biol.Sci., Grad. Schl. Sci., Nagoya Univ.*)

3B1110 シアノバクテリアの時計タンパク質 KaiC の ATPase に備わる分子内フィードバック制御
Intramolecular feedback regulation of cyanobacterial KaiC ATPase
Atsushi Mukaiyama[1,2], Yasuhiro Onoue[1,2], Masato Osako[1,2], Takao Kondo[1,2], Shuji Akiyama[3] ([1]*Grad. Sch. of Sci., Nagoya Univ.*, [2]*CREST/JST*, [3]*IMS, SOKENDAI*)

9:00〜11:22 C 会場 多元数理科学棟 4 階 409 ／ Room C: Mathematics bldg. 4F 409
核酸
Nucleic Acids

3C0900 DNA/RNA 結合タンパク質 TDP-43 が特異的な塩基配列を認識するメカニズム
Tandem-like fusion of two heterologous RNA-recognition motifs in TDP-43 enhances the specificity to its target nucleotide sequence
Yo Suzuki, Yoshiaki Furukawa (*Dept. of Chem, Keio Univ.*)

3C0912 不安定な二次構造をつくる DNA のハイブリダイゼーション速度
Hybridization Rates of DNA Strands with Unstable Self-folded Secondary Structures
Hiroaki Hata[1], Akira Suyama[1,2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Arts and Sci., Univ. Tokyo*)

3C0924 長鎖 DNA の 1 分子内折り畳みはカチオン性ポリマー凝縮剤の長さによってモードが変わる
Folding of a Single Giant Duplex DNA Chain Expresses Contrastive Behaviors depending on the Length of Cationic Polymer
Tatsuo Akitaya[1], Norio Hazemoto[2], Toshio Kanbe[3], Makoto Demura[4], Hideaki Yamaguchi[1], Koji Kubo[5], Anatoly Zinchenko[5], Shizuaki Murata[5], Kenichi Yoshikawa[6] ([1]*Fac. Pharm., Meijo Univ.*, [2]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [3]*Sch. Med., Nagoya Univ.*, [4]*Grad. Sch. Life Sci., Hokkaido Univ.*, [5]*Grad. Sch. Env. Study, Nagoya Univ.*, [6]*Grad. Sch. Life Med. Sci., Doshisha Univ.*)

3C0936 カリウムイオン依存的な四重鎖構造形成によって活性がオンになるインテリジェントリボザイムの創製
Development of intelligent ribozyme whose activity switches on in response to K^+ via quadruplex formation
Yudai Yamaoki[1,2], Tsukasa Mashima[1,2], Yu Sakurai[3], Yukari Hara[3], Takashi Nagata[1,2], Masato Katahira[1,2] ([1]*Inst. Adv. Energy, Kyoto Univ.*, [2]*Grad. Sch. Energy Sci., Kyoto Univ.*, [3]*Grad. Sch. Nanobio., Yokohama City Univ.*)

3C0948 翻訳伸長におけるリボソームと tRNA の挙動－粗視化分子シミュレーションによる解析
Dynamical motions of tRNA and ribosome complex during translation elongation studied by coarse-grained molecular simulations
Naoto Hori, Shoji Takada (*Grad. Sch. Sci., Kyoto Univ.*)

休憩 10:00-10:10

3C1010 A structural basis for the antibiotic resistance conferred by an A1408G mutation in 16S rRNA
Jiro Kondo (*Fac. Sci. Tech., Sophia University*)

3C1022 Q β replicase を構成する翻訳因子の RNA 合成における役割
Non-canonical functions of translational factors as RNA replication cofactors
Daijiro Takeshita, Kozo Tomita (*Biomed. Res. Inst., AIST*)

3C1034 抗 HIV 宿主因子 APOBEC3G の位置依存的デアミネーション反応機構の解明
Elucidation of the location-dependent deamination reaction mechanism of an anti-HIV factor, APOBEC3G
Ayako Furukawa[1,2], Kenji Sugase[2], Ryo Morishita[3], Taashi Nagata[1], Akifumi Takaori[4], Akihide Ryo[5], Masato Katahira[1] ([1]*Inst. of Adv. Energy, Kyoto Univ.*, [2]*Bioorg. Res. Inst., Suntory Found. Life Sci.*, [3]*CellFree Sci.*, [4]*Grad. Sch. Med., Kyoto Univ.*, [5]*Grad. Sch. Med., Yokohama City Univ.*)

3C1046 大腸菌非六量体型 DNA ヘリカーゼ UvrD は多量体で DNA を巻き戻す
Single-molecule visualization of a non-hexameric helicase reveals active roles of its oligomeric forms in DNA unwinding
Hiroaki Yokota, Yoshie Harada (*iCeMS, Kyoto Univ.*)

3C1058 リボソーム-SecM 翻訳アレスト配列間相互作用の 1 分子顕微解析
Single-molecule force measurement for the interaction between ribosome and SecM arrest sequence
Zhuohao Yang, Ryo Iizuka, Takashi Funatsu (*Grad. Sch. of Pharm. Sci., The Univ. of Tokyo*)

3C1110 The probability of double-strand breaks in genome-sized DNA decreases markedly as the DNA concentration increases
Shunsuke Shimobayashi[1], Takafumi Iwaki[2], Toshiaki Mori[3], Kenichi Yoshikawa[1,4] ([1]*Grad. Sch. of Sci., kyoto Univ.*, [2]*Fukui Inst., Kyoto Univ.*, [3]*Rad. Res. Cent., Osaka Pref. Univ.*, [4]*Grad. Sch. of Life and Med. Sci., Doshisha Univ.*)

9:00～11:10　D 会場　多元数理科学棟 3 階 309 ／ Room D: Mathematics bldg. 3F 309
光生物-光合成
Photobiology: Photosynthesis

3D0900　膜配向した PS II の ENDOR 法による Mn クラスター周辺のプロトンの位置の決定
Determine the location of protons surrounding Mn cluster of PS II by proton matrix ENDOR using oriented PS II membrane
Hiroki Nagashima, Hiroyuki Mino (*Division of Material Science, Graduate School of Science, Nagoya University*)

3D0912　Factors that differentiate the H-bond strengths of water near the Schiff bases in bacteriorhodopsin and *Anabaena* sensory rhodopsin
Hiroshi Ishikita[1,2], Keisuke Saito[1], Hideki Kandori[3] ([1]*Career-Path, Kyoto U*, [2]*JST PRESTO*, [3]*Nagoya Inst Tech*)

3D0924　BLUF ドメインの光反応における水素結合環境の変化
Structural changes of hydrogen-bonding environment upon the photoreaction of the BLUF domains
Tatsuya Iwata[1], Shota Ito[2], Mineo Iseki[3], Masakatsu Watanabe[4], Hideki Kandori[2] ([1]*Cent. Fost. Young Innov. Res., NITech*, [2]*Dept. Front. Mater., NITech*, [3]*Faculty Pharm. Sci., Toho Univ.*, [4]*Grad. Sch. Creat. New Photo. Ind.*)

3D0936　励起移動を記述する変分マスター方程式の改良および PSII への適用
Improvement of variational master equation describing excitation energy transfer, and its application to PSII
Yuta Fujihashi, Akihiro Kimura (*Department of Physics, Graduate School of Science, Nagoya University*)

3D0948　光化学系 II コア複合体での非光化学的消光の可能性
Possible non-photochemical quenching mechanism within pohotosystem II core complex
Yutaka Shibata[1], Shunsuke Nishi[2], Keisuke Kawakami[3], Jian-Ren Shen[4], Thomas Renger[5] ([1]*Grad. Sch. Sci., Tohoku Univ.*, [2]*Grad. Sch. Sci., Nagoya Univ.*, [3]*Adv. Res. Inst., Osaka City Univ.*, [4]*Grad. Sch. Sci., Okayama Univ.*, [5]*JKU Linz*)

休憩 10:00-10:10

3D1010　低温光化学系 II における多重光還元 $Mn_4CaO_5H_x$クラスター分布: 時間平均 XRD 構造の照射 X 線量依存性
X-ray dose dependence of time-averaged XRD structure of multi-photoreduced $Mn_4CaO_5H_x$ clusters in photosystem II at low temperature
Masami Kusunoki (*Department of Physics, School of Science Technology, Meiji University*)

3D1022　光化学系 II 酸素発生系 S_2状態における Mn 間磁気的相互作用の解明
Determination of magnetic couplings of S_2 state Mn-cluster in Photosystem II studied by PELDOR measurement
Mizue Asada[1], Hiroki Nagashima[1], Faisal Hammad Mekky Koua[2], Jian-Ren Shen[2], Hiroyuki Mino[1] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Grad. Sch. Natl. Sci. & Tech., Univ. Okayama*)

3D1034　光化学系 II におけるキノン電子受容体の酸化還元電位制御機構
Mechanism of controlling the redox potentials of the quinone electron acceptors in photosystem II
Ryota Ashizawa[1], Takuya Iwasa[1], Miwa Sugiura[2], Takumi Noguchi[1] ([1]*Division of Material Science, Graduate School of Science, Nagoya University*, [2]*Division of Material Science, Graduate School of Science, Nagoya University*)

3D1046　光合成バクテリア反応中心の電子移動経路解析
Electron Transfer Pathway Analysis in Bacterial Photosynthetic Reaction Center
Hirotaka Kitoh-Nishioka, Koji Ando (*Grad. Sch. Sci. Kyoto Univ.*)

3D1058　光合成細菌 Rhodopseudomonas の遺伝子発現パターンの電気化学制御
Electrochemical regulation of gene expression profiles of Rhodopseudomonas, a photosynthesis bacterium
Yue Lu[1], Syoichi Matsuda[1], Shuji Nakanishi[2], Kazuhito Hashimoto[1] ([1]*The Univesity of Tokyo, School of Engineering, Department of Applied Chemistry*, [2]*Research Center for Advanced Science and Technology*)

9:00～11:22　E 会場　多元数理科学棟 1 階 109 ／ Room E: Mathematics bldg. 1F 109
蛋白質-構造
Proteins: Structure

3E0900　核膜孔複合体構造変化による核移行制御機構の構造基盤
Structural basis for nuclear import regulated by molecular rearrangements in the nuclear pore complex
Junya Kobayashi[1], Yoshiyuki Matsuura[1,2] ([1]*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, [2]*Strl. Biol. R. Ctr., Grad., Nagoya Univ.*)

3E0912　NADH シトクロム b_5還元酵素超高分解能結晶構造解析による水素と外殻電子の観察
Visualizing hydrogens and outer-shell electrons of NADH cytochrome b_5 reductase by ultra-high resolution crystallography
Kiyofumi Takaba[1], Kazuki Takeda[1], Masayuki Kosugi[1], Taro Tamada[2], Ryota Kuroki[2], Kunio Miki[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*JAEA*)

3E0924　最新の各種固体 NMR 法を用いた絹の構造解析
Silk Structure studied by Newly-developed Solid-state NMR
Keiko Okushita, Koji Yazawa, Akihiro Aoki, Tetsuo Asakura (*Grad. Sch. of Eng., Tokyo Univ. Agr. Tech.*)

3E0936　Interaction of human calcitonin with curcumin as an inhibitor of fibrillation as revealed by NMR and docking simulation
Ken Takeuchi[1], Hikari Watanabe[1], Javkhlantugs Namsrai[1], Hiroshi Hirota[2], Akira Naito[1] ([1]*Yokohama National University Graduate School of Engineering*, [2]*Riken*)

3E0948　単粒子クライオ電子顕微鏡解析によるサポウイルスキャプシドの 8-Å 構造
8-Å structure of sapovirus capsid by single particle electron cryomicroscopy
Naoyuki Miyazaki[1], David Taylor[1], Grant Houseman[2], Kosuke Murakami[2], Kuniaki Nagayama[1], Kazuhiko Katayama[2], Kazuyoshi Murata[1] ([1]*National Institute for Physiological Sciences*, [2]*National Institute of Infectious Diseases*)

休憩 10:00-10:10

3E1010　Structural analysis of the 26S proteasome by cryo-electron microscopy and Single-Particle Analysis

Zhuo Wang[1], Yasuo Okuma[1], Daisuke Kasuya[2], Kaoru Mitsuoka[3], Yasushi Saeki[4], Yasunaga Takuo[1] ([1]*Department of Bioscience and Bioinformatics, Faculty of Computer Science and Systems Engineering, Kyushu Institute of Technology*, [2]*Biomedicinal Information Research Center, Japan Biologycal Information Consortium (JBIC)*, [3]*Biomedicinal Information Research Center, National Institute of Advanced Industrial Science and Technology*, [4]*Laboratory of Protein Metabolism, Tokyo Metropolitan Institute of Medical Science*)

3E1022 大気圧電子顕微鏡（ASEM）によるタンパク質微結晶とマイコプラズマの液中観察

Direct electron microscopy of protein crystals and Mycoplasma cells in solution using the Atmospheric SEM

Yuusuke Maruyama[1], Tatsuhiko Ebihara[1], Daisuke Nakane[2], Hidetoshi Nishiyama[3], Takayuki Nishizaka[4], Miki Senda[5], Kazuhiro Mio[1], Mitsuo Suga[3], Toshiya Senda[1], Makoto Miyata[2], **Chikara Sato**[1] ([1]*AIST*, [2]*Univ. Osaka City*, [3]*JEOL*, [4]*Univ. Gakushuin*, [5]*JBIC*)

3E1034 粗視化 Go モデルを用いた Ferredoxine-like fold タンパクのフォールディング機構の解析

Analyses of folding processes on the Ferredokin-like fold proteins by means of a coarse grained Go model

Masatake Sugita, Takeshi Kikuchi (*Dept. Bioinf., Coll. Life Sci., Ritsumeikan Univ.*)

3E1046 異なる参照状態を用いた統計ポテンシャルによるタンパク質モデル構造の最適化

Optimization of protein model structures according to statistical potentials with different reference states

Matsuyuki Shirota[1,2], Kengo Kinoshita[1,2,3] ([1]*GSIS, Tohoku Univ.*, [2]*ToMMo, Tohoku Univ.*, [3]*IDAC, Tohoku Univ.*)

3E1058 クーロンレプリカ交換法を用いた A β フラグメントに関する研究

Studies on a Aβ fragment by the Coulomb replica-exchange method

Satoru Itoh[1,2], Hisashi Okumura[1,2] ([1]*Institute for Molecular Science*, [2]*The Graduate University for Advanced Studies*)

3E1110 レプリカ交換インターフェースプログラム(REIN)

Replica-exchange interface program (REIN)

Naoyuki Miyashita[1,2,3], Suyong Re[4], Yuji Sugita[1,2,3,4] ([1]*RIKEN QBiC*, [2]*RIKEN CSRC*, [3]*RIKEN AICS*, [4]*RIKEN ASI*)

9:00～11:10　F 会場　理学 B 館 5 階 501 ／ Room F: Sci. bldg. B 5F 501
膜蛋白質
Membrane Proteins

3F0900 サポーテット膜を用いた膜タンパク質の顕微鏡下でのイオン輸送活性計測

Evaluation of ion-pump activity of membrane proteins reconstituted on supported membrane under optical microscope

Jyunan Ki, Rikiya Watanabe, Kazuhito Tabata, Hiroyuki Noji (*Department of Applied Chem., Univ. Tokyo*)

3F0912 Catalytic activity of MsbA reconstituted in nanodisc particles is modulated by remote interactions with the bilayer

Takeaki Kawai[1], Jose Caaveiro[1,2], Toyomasa Katagiri[3], Hisashi Tadakuma[1], Takuya Ueda[1], Kouhei Tsumoto[1,2,4] ([1]*Grad. Sch. of Front. Sci., Univ. of Tokyo*, [2]*Inst. Med. Sci., Univ. of Tokyo*, [3]*Inst. Gen. Res., Univ. of Tokushima*, [4]*Dep. Chem. Bio., Univ. of Tokyo*)

3F0924 線虫イネキシン 6 ギャップ結合チャネルの単離と機能特性

Isolation and characterization of C. elegans innexin-6 gap junction channels

Atsunori Oshima[1], Tomohiro Matsuzawa[2], Kouki Nishikawa[1], Yoshinori Fujiyoshi[1] ([1]*CeSPI, Nagoya Univ.*, [2]*Grad. Sch. of Sci., Kyoto Univ.*)

3F0936 ATR-FTIR 法を用いた KcsA 野生型と不活化しない変異体に対するカチオン誘起構造変化の赤外分光分析

Cation-induced structural changes in the WT and non-inactivating mutant KcsA studied by ATR-FTIR

Chikako Muramatsu[1], Masayo Iwaki[1], Tetsuya Fukuda[1], Yusuke Asai[1], Yuji Furutani[1,2], Hideki Kandori[1] ([1]*Grad. Sch. Tech., Nagoya Inst. Tech.*, [2]*Inst. Mol. Sci.,*)

3F0948 黄色ブドウ球菌の 2 成分性膜孔形成毒素の分子機構

Molecular basis of staphylococcal bi-component pore forming toxin

Yoshikazu Tanaka[1], Daichi Yamashita[2], Keitaro Yamashita[2], Yuka Kawai[2], Jun Kaneko[3], Noriko Tomita[4], Makoto Ohta[4], Yoshiyuki Kamio[5], Min Yao[1], Isao Tanaka[1] ([1]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [2]*Grad. Schl. of Life Sci., Hokkaido Univ.*, [3]*Grad. Schl. of Agri. Sci., Tohoku Univ.*, [4]*Inst. of Fluid Sci., Tohoku Univ.*, [5]*Grad. Schl. of Life Sci., Tohoku Univ.*)

休憩 10:00-10:10

3F1010 分子動力学法によるグラミシジン A を含んだ脂質二重層膜の構造と圧力特性

Structure and lateral pressure profile of lipid bilayer containing gramicidin A by molecular dynamics simulation

Hiroaki Saito, Masashi Iwayama, Megumi Nishimura, Hiroyuki Takagi, Kazutomo Kawaguchi, Hidemi Nagao (*Kanazawa University*)

3F1022 代謝型グルタミン酸受容体の膜貫通領域における 1 アミノ酸変異がアゴニストをインバースアゴニストに変える

Single amino acid substitution in the transmembrane domain of metabotropic glutamate receptor changes an agonist into an inverse agonist

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

3F1034 non-detergent sulfobetaine (NDSB)による G 蛋白質共役型受容体 (GPCR)の熱安定化

Thermal stabilization of G protein-coupled receptor by non-detergent sulfobetaines (NDSBs)

Toshihide Yamai, Layla Takahashi, Masato Nakajima, Naoki Yamashita, Takeshi Ishii, Shigeki Takeda, Kaori Wakamatsu (*Gunma Univ.*)

3F1046 固体 NMR を用いた熱および圧力により誘起されるバクテリオロドプシンの構造と運動性変化の解析

Thermal and Pressure induced structural and dynamics changes of bacteriorhodopsin as studied by solid-state NMR

Izuru Kawamura[1], Miyako Horigome[1], Hirohide Nishikawa[1], Kana Tajima[1], Takashi Okitsu[2], Akimori Wada[2], Satoru Tuzi[3], Tatsuo Iwasa[4], Akira Naito[1] ([1]*Grad. Sch. Eng., Yokohama Natl. Univ.*, [2]*Kobe Pharm. Univ.*, [3]*Univ. Hyogo*, [4]*Muroran Inst. Tech.*)

3F1058 OBSERVATION OF TRANSMEMBRANE PROTEIN BY HIGH SPEED ATOMIC FORCE MICROSCOPY: BACTERIORHODOPSIN D85S MUTANT, A CHLORIDE PUMP

Maxime Ewald[1], Mikihiro Shibata[2], Takayuki Uchihashi[1,3], Hideki Kandori[4], Toshio Ando[1,3] ([1]*School of Mathematics & Physics, Institute of Science & Engineering, Kanazawa*

University, [2]Department of Neurobiology, Duke University Medical Center, [3]Bio-AFM Frontier Research Center, College of Science and Engineering, Kanazawa University, [4]Department of Frontier Materials, Nagoya Institute of Technology)

9:00～11:22 G 会場 理学 B 館 2 階 212 ／ Room G: Sci. bldg. B 2F 212
生体膜・人工膜-構造・物性
Biological & Artificial Membranes: Structure & Property

3G0900 **好熱性 *Meiothermus ruber* H328 株が産生放出する高耐性ケラチン分解性プロテアーゼ複合体のフリーズレプリカ電子顕微鏡観察**
Freeze-replica observation of keratinolytic protease complex produced and released from *Meiothermus ruber* H328
Kazunori Kawasaki[1], Maachi Kataoka[2], Keiji Nomura[2], Yasushi Shigeri[1], Kunihiko Watanabe[2] ([1]*AIST*, [2]*Grad. Sch. Kyoto Pref. Univ.*)

3G0912 **Effects of model peptides for late embryogenesis abundant (LEA) proteins on the thermal properties of liposomes**
Takao Furuki, Minoru Sakurai (*Center for Biol. Resources and Informatics, Tokyo Inst. Tech.*)

3G0924 **微細パターン化モデル生体膜における膜結合タンパク質の濃縮の空間的制御**
Spatially controlled accumulation of membrane-bound protein in a micro-patterned model biological membrane
Fumiko Okada[1], Kenichi Morigaki[1,2] ([1]*Grad. Sch. Agr., Univ. Kobe*, [2]*Res. Cent. Env. Genomi., Univ. Kobe*)

3G0936 **圧力摂動熱量法によるジミリストイルホスファチジルコリン二分子膜の緩和挙動の解明への試み**
An attempt to reveal the relaxation behavior of dimyristoylphosphatidylcholine bilayer by pressure perturbation calorimetry
Nobutake Tamai, Sayuri Kakibe, Saeko Tanaka, Masaki Goto, Hitoshi Matsuki (*Dept. Life System, Inst. Technol. & Sci., Univ. of Tokushima*)

3G0948 **リン脂質二重膜の圧力誘起指組み構造形成：疎水鎖長依存性と形成限界**
Pressure-induced interdigitation of phospholipid bilayer membranes: dependence of acyl-chain length and limitation of the formation
Hitoshi Matsuki, Masaki Goto, Nobutake Tamai (*Institute of Technology and Science, The University of Tokushima*)

休憩 10:00-10:10

3G1010 **均一でないリン脂質単分子膜における崩壊現象について**
Collapse of nonuniform phospholipid monolayers
Masahiro Hibino, Ken Hashimoto, Takuya Fujisawa (*Div. Appl. Sci., Muroran Inst. Technol.*)

3G1022 **脂質分子の電荷が引き起こす膜構造変化：2 次元相分離と 3 次元曲率**
Charge-induced transition in membrane mesoscopic structures: lateral domains and vesicular shapes
Hiroki Himeno, Tsutomu Hamada, Masahiro Takagi (*1Shool of Materials Science, Japan Advanced Institute of Science and Technology*)

3G1034 **油中水滴エマルション遠心沈降法を用いたミクロスフェア内包型ジャイアントベシクル**
Microsphere-containing giant vesicles prepared by water-in-oil emulsion centrifugation method
Yuno Natsume[1], Taro Toyota[1,2] ([1]*Grad. Art. Sci., Univ. Tokyo*, [2]*JST PRESTO*)

3G1046 **オイルフリー GUV に封入された分子演算システム RTRACS**
Molecular computing system RTRACS encapsulated in oil-free giant unilamellar vesicle
Koh-ichiroh Shohda, Tadashi Sugawara, Akira Suyama (*Grad. Sch. Arts Sci., Univ. Tokyo*)

3G1058 **低い pH が誘起する DOPS/MO 膜の液晶相からキュービック相への相転移の初期過程**
Initial Step of Low pH-Induced Lamellar to Bicontinuous Cubic Phase Transition in Dioleoylphosphatidylserine/Monoolein
Toshihiko Oka[1], Tomoki Takahashi[1], Taka-aki Tsuboi[1], Masahito Yamazaki[2] ([1]*Fac. Sci., Shizuoka Univ.*, [2]*Grad. Sch. Sci. Tech., Shizuoka Univ.*)

3G1110 **X 線及び電子線回折法を用いた皮膚角層の構造解析**
Breakthrough for Unresolved Structural Problems in Skin Function by Combined Use of X-ray and Electron Diffraction Methods
Hiromitsu Nakazawa[1], Ichiro Hatta[2], Satoru Kato[1] ([1]*Sch. Sci. Tech. kwansei Gakuin Univ.*, [2]*Nagoya Industrial Science Research Inst.*)

9:00～11:22 H 会場 理学 C 館 5 階 517 ／ Room H: Sci. bldg. C 5F 517
細胞生物的課題 III：細胞骨格，細胞運動
Cell Biology III: Cytoskeleton & Motility

3H0900 **GTP 結合状態と GDP 結合状態の微小管分子構造における大きな構造変化**
Large Conformational Changes in Tubulin in the GTP- and GDP-States Microtubules Observed by Cryo Electron Microscopy
Hiroaki Yajima[1], Toshihiko Ogura[2], Ryo Nitta[1], Yasushi Okada[1], Chikara Sato[2], Nobutaka Hirokawa[1] ([1]*Grad. Sch. Med., Univ. Tokyo*, [2]*Biomedical Research Inst., AIST*)

3H0912 **紡錘体は一方の極から他方へ構造変化を伝搬することで対称形状を維持する**
Meiotic spindles maintain the symmetrical shape by propagating structural changes to the opposite side
Kazuya Suzuki[1], Jun Takagi[1], Takeshi Itabashi[1], Shin'ichi Ishiwata[1,2] ([1]*Dept. Phys., Adv Sci. Eng., Waseda Univ.*, [2]*WABIOS*)

3H0924 **高圧負荷によって誘導されるクラミドモナス非運動性変異株鞭毛の屈曲運動**
Resurrection of flagellar bending movements in *chlamydomonas* paralyzed mutants at high pressure
Toshiki Yagi[1], Masayoshi Nishiyama[2] ([1]*Grad. Sch. Medicine, Univ. Tokyo*, [2]*The Hakubi Center, Kyoto Univ.*)

3H0936 **走化性誘因物質の進行パルス刺激によって誘発された一方向細胞運動**
Directed cell migration induced by travelling waves of chemoattractant
Akihiko Nakajima[1], Satoshi Sawai[1,2] ([1]*Grad. Sch. Arts & Sci., Univ. Tokyo*, [2]*Res. Cent. for Complex Systems Biology, Univ. Tokyo*)

3H0948 **極性を持つアメーバ細胞の走化性運動に関する理論**
Theory on the chemotaxis of an amoeboid cell with the cell polarity
Tetsuya Hiraiwa, Tatsuo Shibata (*Kobe, Riken*)

休憩 10:00-10:10

3H1010 **Controlled cell migration with ultrasound**
Shinya Murakami[1], Yo Otsuka[1], Manabu Sugimoto[1], Toshiyuki Mitsui[2] ([1]*Grad. Sci. Eng., Aogaku Univ.*, [2]*Assoc Prof., Aogaku Univ.*)

3H1022 **筋肉と異なるストレスファイバーの収縮特性**
Contractile properties of stress fibers are distinct from those of muscles
Shinji Deguchi, Tsubasa Matsui, Daiki Komatsu, Masaaki Sato (*Tohoku University*)

3H1034 **Smooth muscle differentiation related transcription factor CRP2 directly regulates physical properties of actin filaments**
Takanori Kihara[1], Satoko Shinohara[1], Yasunobu Sugimoto[2], Jun Miyake[1] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*Nagoya Univ. Synchrotron Radiat. Res. Center*)

3H1046 **細胞接着班における p130Cas と Src の動的相互作用を介した遊走制御機構の解明**
A distinct role for the dynamics of p130Cas at focal adhesion via interaction with Src in the regulation of cell migration
Hiroaki Machiyama[1,2], Hiroaki Hirata[1], Yasuhiro Sawada[1,2] ([1]*Mechanobiology Inst., Nat. Univ. Singapore*, [2]*Dept. Biol. Sci., Nat. Univ. Singapore*)

3H1058 **Spatiotemporal regulation of signaling by active cytoskeletal remodeling**
Bhaswati Bhattacharyya[1], Abhishek Chaudhuri[3], Kripa Gowrishankar[4], Satyajit Mayor[5], Madan Rao[4] ([1]*iCeMS, Kyoto University*, [2]*Rudolf Peierls Centre for Theoretical Physics, University of Oxford, UK*, [3]*Raman Research Institute, Bangalore, India*, [4]*NCBS-TIFR, Bangalore, India*)

3H1110 **Arp2/3 とアクチンを内包した油中液滴のフィロポディア様変形**
Filopodia-like protrusions in water-in-oil droplets induced by Arp2/3 and actin polymerization
Masataka Chiba[1], Makito Miyazaki[1], Takashi Ohki[1], Shin'ichi Ishiwata[1,2] ([1]*Dept. of Phys., Waseda Univ.*, [2]*WABIOS, Waseda Univ.*)

9:12～11:10 I 会場 理学 E 館 1 階 131 ／ Room I: Sci. bldg. E 1F 131
ヘム蛋白質
Heme Proteins

3I0912 **ヘモグロビンのアロステリック平衡のリアルな描像**
A realistic picture of allosteric equilibrium of hemoglobin
Naoya Shibayama[1], Sam-Yong Park[2] ([1]*Biophysics, Jichi Med. Univ.*, [2]*Protein Design Lab., Yokohama City Univ.*)

3I0924 **ヘムをヘム垂線のまわりに 90° 回転した時の共鳴ラマンスペクトル変化：ヘムオキシゲネース**
Effects of Heme Rotation around the Heme Normal by 90° on Resonance Raman Spectra of Heme Proteins; Observation for Heme Oxygenase
Sachiko Yanagisawa[1], Hiroshi Fujii[2], Saburo Neya[3], Takashi Ogura[1], Teizo Kitagawa[1] ([1]*University of Hyogo*, [2]*Okazaki Inst. Integrative Biosci.*, [3]*Chiba University*)

3I0936 **ヘムオキシゲナーゼにおける CO 光解離後の構造変化および CO の放出経路**
Protein motions and CO migration following CO photolysis in heme oxygenase
Masakazu Sugishima[1,2], Keith Moffat[2,3], Masato Noguchi[1] ([1]*Dept. Med. Biochem., Kurume Univ. Sch. Med.*, [2]*Dept. Biochem. & Mol. Biol., Univ. Chicago*, [3]*BioCARS, Univ. Chicago*)

3I0948 **多様な生物種によるヘムオキシゲナーゼ反応の微調整戦略：オキシヘムの安定化**
Strategy of a variety of organisms for the fine-tuning of heme oxygenase reactions: Stabilization of the oxyheme intermediate
Sayuri Takada, Taiko Migita (*Dep. Biol. Chem., Fac. Agr., Yamaguchi Univ.*)

休憩 10:00-10:10

3I1010 **Ultraviolet Resonance Raman Study on Indoleamine 2, 3-Dioxygenase**
Masayuki Hara[1], Sachiko Yanagisawa[1], Hiroshi Sugimoto[2], Yoshitsugu Shiro[2], Takashi Ogura[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Harima Inst., Riken*)

3I1022 **An Intermediate Conformation of Cytochrome Oxidase in the Ligand-Free State Identified by Time-Resolved Resonance Raman Spectroscopy**
Izumi Ishigami, Takeshi Nishigaki, Kyoko Shinzawa-Itoh, Shinya Yoshikawa, Satoru Nakashima, **Takashi Ogura** (*Grad. Schl. Life Sci., U. Hyogo*)

3I1034 **ポンプ・プローブレーザーと同期したパルスフローシステムの開発とそれを用いたタンパク質の時間分解赤外分光解析**
Time-Resolved IR Analyses of Proteins Using a Novel Pulse Flow System Synchronized with Pump/Probe Lasers
Minoru Kubo[1], Satoru Nakashima[1], Masao Mochizuki[1], Kyoko Shinzawa-Itoh[2], Shinya Yoshikawa[1,2], Takashi Ogura[1,2] ([1]*Picobiology Inst., Grad. Sch. Life Sci., Univ. Hyogo*, [2]*Dept. Life Sci., Grad. Sch. Life Sci., Univ. Hyogo*)

3I1046 **チトクロム *c* 酸化酵素のヘム *a* 側鎖に由来する共鳴ラマン線の帰属**
The assignment of the resonance Raman bands of heme *a* peripheral substituents in cytochrome *c* oxidase
Miyuki Sakaguchi[1], Yukie Katayama[2], Hiroshi Fujii[3], Hideo Shimada[2], Takashi Ogura[1,2] ([1]*Grad. Sch. Life. Sci., Univ. Hyogo*, [2]*Picobiol. Inst., Grad. Sch. Life. Sci., Univ. Hyogo*, [3]*Okazaki Inst. Integr. Biosci.*)

3I1058 **シアン結合型構造から推察される一酸化窒素還元酵素の反応機構**
Functional Implications from Structural Characterization of CN-bound Nitric Oxide Reductase
Takehiko Tosha, Nozomi Sato, Norihiro Okada, Hiroshi Sugimoto, Yoshitsugu Shiro (*Harima Inst., RIKEN*)