1 日目（9 月 24 日（水））／Day 1（Sep. 24 Wed.）

1MSF　ベシクルダイナミクスの最前線：先端イメージング，AI，メディカル応用
Unlocking Vesicle Dynamics: Advanced Imaging, AI, and Biomedical Applications

オーガナイザー：Seohyun Lee（東京大学），樋口 秀男（東北大学）
Organizers: Seohyun Lee (The Univ. of Tokyo), Hideo Higuchi (Tohoku Univ.)

18:50〜20:30
F 会場（会議室 202）／Room F（Meeting Room 202）

This symposium introduces advanced analytical methods and imaging techniques to explore vesicle dynamics and their broad implications in biology and disease. Topics include cutting-edge approaches to vesicle transport analysis using advanced imaging techniques and artificial intelligence, comprehensive studies on microbial vesicles with potential applications in vaccine development, and pioneering efforts to understand molecular machinery through exosome engineering as well as synthetic vesicle membrane research. Notably, the symposium will highlight MINFLUX, a revolutionary super-resolution imaging technique recently published in Science, which enables nanometer-scale insights into molecular mechanisms within live cells. By integrating diverse biophysical perspectives with the latest techniques, this session seeks to enhance our understanding of vesicle dynamics and their implications in the biomedical field.

1MSF-1　AI 技術を活用した生細胞内小胞輸送の理解に向けて
AI-Powered Characterization of Vesicle Transport in Live-Cell Systems
○イ ソヒョン（東京大学）
Seohyun Lee (*The University of Tokyo*)

1MSF-2　High-precision tracking of kinesin-1 stepping inside cells using single- and dual-color MINFLUX nanoscopy
Takahiro Deguchi[1], Tobias Engelhardt[2], Nikolay Sergeev[3], Malina Iwanski[4], Roman Schmidt[2], Christopher Heidebrecht[5], Savannah Cattarius[5], Lukas Kapitein[4], Timo Zimmermann[1], Jonas Ries[3] ([1]*European Molecular Biology Laboratory*, [2]*Abberior Instruments GmbH*, [3]*Max Perutz Labs, University of Vienna*, [4]*Utrecht University*, [5]*University of Heidelberg*)

1MSF-3　Structural analysis and advanced live imaging reveal vesicle dynamics of SID1-mediated uptake of large dsRNA molecules
Akira Takai[1,2], Kaoru Kumazaki[3], Toshikuni Awazu[2,4], Taketoshi Kambara[2], Shunya Murakoshi[3], Takafumi Kato[5], Masahiro Hiraizumi[6], Yoshiaki Kise[3], Tsukasa Kusakizako[3], Tomohiro Nishizawa[7], Yasushi Okada[1,2,4,8,9,10], Osamu Nureki[3] ([1]*Grad. Sch. Med., Univ. Tokyo*, [2]*BDR, RIKEN*, [3]*Dept. Bio. Sci., Grad. Sch. Sci., Univ. Tokyo*, [4]*Grad. Sch. Front. Biosci., Osaka Univ.*, [5]*Dept. Biochem., Univ. Oxford*, [6]*Grad. Sch. Eng., Univ. Tokyo*, [7]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [8]*Dept. Phys., Grad. Sch. Sci., Univ Tokyo*, [9]*UBI, Grad. Sch. Sci., Univ. Tokyo*, [10]*WPI-IRCN, IAS, Univ. Tokyo*)

1MSF-4　Bacterial Membrane Vesicles: Biology, Functions, and Medical Applications
Ryoma Nakao, Takehiro Yamaguchi, Kimihiro Abe, Yukihiro Akeda (*Dept Bacteriol. I, Natl. Inst. Infect. Dis., JIHS*)

1MSF-5　Creation of biological phenomena using asymmetric vesicles
Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

1MSG　若手の会が紡いだ生物物理学のフロンティア
Frontiers in Biophysics Spun by the Society of Young Scientists

オーガナイザー：柴垣 光希（北海道大学），藤井 真子（神戸大学）
Organizers: Mitsuki Shibagaki (Hokkaido Univ.), Masako Fujii (Kobe Univ.)

18:50〜20:30
G 会場（会議室 203）／Room G（Meeting Room 203）

The Society of Young Scientists has played an important role in training future generations in scientific research. In biophysics, the Society of Young Scientists in Biophysics started its activities before the foundation of the Biophysical Society of Japan and has produced many prominent researchers. This symposium aims to present the latest development of the Society of Young Scientists in Biophysics and the state-of-the-art science of young researchers who have been involved in the recent advances of this Society.

はじめに
Opening Remarks

1MSG-1　凝集傾向のある抗菌ペプチドの溶解化戦略およびその多様な多量体化特性の評価
Solubilization strategy of aggregation-prone antimicrobial peptides and evaluation of their diverse multimerization properties
Mitsuki Shibagaki, Jeremia Oktavian Chrisnanto, Kosuke Maeda, Tatsuya Arai, Dessalegn Abeje Tefera, Hiroyuki Kumeta, Fumi Hirai, Tomoyasu Aizawa (*Grad. Sch. Life Sci., Hokkaido Univ.*)

1MSG-2　分光研究から見えてきたウイルスヘリオロドプシンの多様性
Diversity of Viral Heliorhodopsins Uncovered through Spectroscopic Analysis
○水鳥 律（名工大・院工）
Ritsu Mizutori (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

1MSG-3　細菌アクチンの微小管化
Microtubulation of the bacterial actin
○高橋 大地 [1,2], 沼本 修孝 [1], 宮田 真人 [2,3], 沈 建仁 [1,4], Robert C. Robinson[1,5]（[1] 岡山大・異分野基礎, [2] 大阪公大・院理, [3] 大阪公大・複合先端, [4] 岡山大・環境生命自然科学, [5] ウィタヤシリメティ技大・生物工学）
Daichi Takahashi[1,2], Nobutaka Numoto[1], Makoto Miyata[2,3], Jian-Ren Shen[1,4], Robert C. Robinson[1,5] ([1]*RIIS, Okayama Univ.*, [2]*Grad. Sch. Sci., Osaka Met. Univ.*, [3]*OCARINA, Osaka Met. Univ.*, [4]*Grad. Sch. Environ. Life. Nat. Sci. Tech., Okayama Univ.*, [5]*Sch. Biol. Sci. Eng., Vidyasirimedhi Inst. Sci. Tech.*)

1MSG-4　葉緑体 ATP 合成酵素に特有の部位によるレドックス制御機構
Mechanism of redox regulation by region specific to chloroplast F_oF_1-ATP synthase
○秋山 健太郎 [1], 若林 憲一 [2], 久堀 徹 [3]（[1] 産業技術総合研究所, [2] 京都産業大学, [3] 総合研究大学院大学）
Kentaro Akiyama[1], Ken-ichi Wakabayashi[2], Toru Hisabori[3] ([1]*The National Institute of Advanced Industrial Science and Technology*, [2]*Kyoto Sangyo University*, [3]*The Graduate University for Advanced Studies*)

1MSG-5　構造解析および反応速度論を用いたアセト酢酸脱炭酸酵素 AAD の触媒機構の解明
Structural and kinetic insights into the catalytic mechanism of acetoacetate decarboxylase AAD
○石坂 優人 [1,2], Rindfleisch Sören[1,2], Auer Florian[1,2], Gingeleit Lukas[1,2], 鄭 達翔 [3], Bielecki Michael[4], Rabe von Pappenheim Fabian[1,2], Penka Elke[1,2], Kluger Ronald[4], 坂田 絵理 [3], Tittmann Kai[1,2]（[1] ゲッティンゲン大・分子酵素学, [2]MPI・複合科学, [3] ゲッティンゲン大・聴覚神経科学, [4] トロント大・化学）
Masato Ishizaka[1,2], Sören Rindfleisch[1,2], Florian Auer[1,2], Lukas Gingeleit[1,2], Tat Cheung Cheng[3], Michael Bielecki[4], Fabian Rabe von Pappenheim[1,2], Elke Penka[1,2], Ronald Kluger[4], Eri Sakata[3], Kai Tittmann[1,2] ([1]*Dept. Mol. Enzymol., Univ. Göttingen*, [2]*Multidisciplinary Sci., MPI*, [3]*Inst. Auditory Neurosci., Univ. Med. Center Göttingen*, [4]*Dept. Chem., Univ. Toronto*)

1MSG-6 古細菌 SMC 複合体は DNA セグメント捕捉機構によって DNA 上を一方向にトランスロケーションする
DNA Segment Capture Drives Unidirectional DNA Translocation of a Prokaryotic SMC Complex: A Multiscale Simulation Study
○山内 仁喬, ブランダーニ ジョバンニ, 寺川 剛, 高田 彰二（京都大学・理学）
Masataka Yamauchi, Giovanni Brandani, Tsuyoshi Terakawa, Shoji Takada (*Dept. of Biophys., Kyoto Univ.*)

1MSG-7 データベース探索とドッキングシミュレーションを活用した，中鎖アルカン合成酵素の創出と機能解析
Creation of the medium-chain alkane producing enzyme by using the enzyme database search and the docking simulation
○工藤 恒, 近藤 昭彦, 蓮沼 誠久（神戸大・先端バイオ）
Hisashi Kudo, Akihiko Kondo, Tomohisa Hasunuma (*Engineering Biology Research Center., Kobe Univ.*)

おわりに
Closing Remarks

1MSH 日本のタンパク質水素可視化最近の動き
Recent developments in protein hydrogen visualization in Japan

オーガナイザー：田中 伊知朗（茨城大学），栗原 和夫（QST）
Organizers: Ichiro Tanaka (Ibaraki Univ.), Kazuo Kurihara (QST)

18:50〜20:30
H 会場（会議室 204）／Room H（Meeting Room 204）

Determining the positions of hydrogen atoms in biomolecules is an essential theme in life science. A groundbreaking neutron detector developed in Japan about 30 years ago has spread to research reactors around the world and has been of great help in determining hydrogen positions. Nowadays, neutron analysis technology is steadily improving thanks to the next generation of accelerator-based neutron sources in Japan and US. On the other hand, cryo-EM has also been attracting attention for its ability to obtain hydrogen position information, and we are now in an era where AI can predict the structure of biomolecules one after another. In addition to classical neutrons, we will consider future directions, including recent efforts to visualize hydrogen position information.

1MSH-1 導入と中性子回折装置を中心とした世界的現状
Introduction and current status of neutron diffractometers worldwide
○田中 伊知朗（茨城大学）
Ichiro Tanaka (*Ibaraki University*)

1MSH-2 TOF 型単結晶中性子回折装置 iBIX の現状と将来計画
Current status and future prospects for TOF type single crystal neutron diffractometer iBIX
Katsuhiro Kusaka, Terutoshi Sakakura, Haruki Sugiyama (*NIAPC, CROSS*)

1MSH-3 Measurement of hydrogen properties using cryo-EM and ED
Koji Yonekura[1,2] ([1]*RIKEN SPring-8/*, [2]*IMRAM, Tohoku University*)

1MSH-4 中性子 D/H コントラスト結晶解析による鶏卵白リゾチームの水和構造の研究
Neutron D/H contrast crystallographic study of hydration structure of hen-egg-white lysozyme
○茶竹 俊行 [1], 角南 智子 [2], 藤原 悟 [2], 田中 伊知朗 [3], 日下 勝弘 [4]（[1] 京大・複合研, [2]QST, [3] 茨大・院理工, [4]CROSS）
Toshiyuki Chatake[1], Tomoko Sunami[2], Satoru Fujiwara[2], Ichiro Tanaka[3], Katsuhiro Kusaka[4] ([1]*KURNS*, [2]*QST*, [3]*Grad. Sch. Sci. Eng., Ibaraki Univ.*, [4]*CROSS*)

1MSH-5 タンパク質の主鎖のやわらかさをデザインする。-中性子と ^{15}N NMR が示唆する主鎖ペプチド結合の部位特異的緩和の原理とその利用-
Designing main-chain flexibility of proteins. Principle of site-specific relaxation of peptide bonds and an application in protein design
○千葉 かおり（茨城高専）
Kaori Chiba (*National Institute of Technology, Ibaraki College*)

1MSH-6 単色法を用いたタンパク質用中性子回折装置の日本における現状と将来
Monochromatic Neutron Diffractometers for Protein Crystallography at Present and in the Future in Japan
○栗原 和男 [1], 河野 史明 [1], 清水 瑠美 [1], 田村 格良 [2], 大原 高志 [3], 茶竹 俊行 [4], 井上 倫太郎 [4], 平野 優 [1,5], 玉田 太郎 [1,5]（[1]QST・量生研, [2] 原子力機構・新試験研究炉, [3] 原子力機構・J-PARC セ, [4] 京大・複合研, [5] 千葉大・cQUEST）
Kazuo Kurihara[1], Fumiaki Kono[1], Rumi Shimizu[1], Itaru Tamura[2], Takashi Ohhara[3], Toshiyuki Chatake[4], Rintaro Inoue[4], Yu Hirano[1,5], Taro Tamada[1,5] ([1]*iQLS, QST*, [2]*New Res. Reactor Promo. Office, JAEA*, [3]*J-PARC Center, JAEA*, [4]*KURNS, Kyoto Univ.*, [5]*cQUEST, Chiba Univ.*)

1MSI タンパク質デザインへの誘い
Invitation to Protein Design

オーガナイザー：小杉 貴洋（分子科学研究所），新津 藍（理化学研究所）
Organizers: Takahiro Kosugi (IMS), Ai Niitsu (RIKEN)

18:50〜20:30
I 会場（会議室 205）／Room I（Meeting Room 205）

The field of protein design has been honored with the 2024 Nobel Prize in Chemistry, highlighting its transformative potential and the promising future. Now, the technology is expected to be of interest to many researchers and to be applied across a broad range of research fields. In this symposium, talented early-career researchers introduce their cutting-edge technologies, the latest advancements, and forthcoming challenges in protein design and its applied fields. We aim to provide useful information for researchers in diverse fields, enabling them to incorporate protein design technologies into their own research. Furthermore, we hope this symposium serves as a catalyst for innovations and increased excitement in protein design.

はじめに
Opening Remarks

1MSI-1 AI が導くバイオ分子デザイン：タンパク質と，その先へ
AI-guided biomolecule design: protein and beyond
○齋藤 裕（北里大学・未来工）
Yutaka Saito (*Dept. Front. Eng., Kitasato Univ.*)

1MSI-2 進化的アルゴリズムとネットワーク理論を融合した酵素リデザイン法の開発
Development of enzyme redesign strategy combining evolutionary algorithm and network theory
○中野 祥吾（静岡県大・食栄）
Shogo Nakano (*Grad. Div. Nut. Sci., Univ. Shizuoka*)

1MSI-3 Molecular Programming Using De Novo Designed Proteins
Zibo Chen (*School of Life Sciences, Westlake University*)

1MSI-4 A Rapid and Universal Pipeline for GPCR Structure Determination through In Silico Construct Optimization and de novo Protein Design
Hideaki Kato (*The University of Tokyo*)

おわりに
Closing Remarks

1MSJ　ゲノム構造の原理を紐解く：理論と実験の融合
Elucidating the Principles of Genome Organization: Bringing Together Theory and Experiments

オーガナイザー：Giovanni Brandani（京都大学），河野 秀俊（QST）
Organizers: Giovanni Brandani (Kyoto Univ.), Hidetoshi Kono (QST)

18:50〜20:30
J 会場（会議室 206）／Room J（Meeting Room 206）

Functional genome organization emerges from a complex interplay of structural and dynamic factors across multiple scales. This symposium will bring together experimentalists and theoreticians to discuss key aspects of genome organization, including the action of SMC complexes, chromatin structure and dynamics, and 3D genome compartmentalization. By fostering interactions between theory and experiments, we aim to stimulate new insights, where experimental observations inspire theoretical models and computational predictions guide new experiments. This symposium includes contributions from diverse perspectives to advance our understanding of genome organization and create a dynamic exchange of ideas within this rapidly evolving field.

はじめに
Opening Remarks

1MSJ-1　生きたヒト細胞内の分裂期染色体の化学的・物理的性質
Chemical and physical properties of human mitotic chromosomes in living cells
○日比野 佳代（阪大・蛋白研）
Kayo Hibino (*Inst. Protein Res., Univ. Osaka*)

1MSJ-2　DNA 複製動態から染色体の振る舞いを明らかにする
Deciphering the behavior of chromosomes through DNA replication dynamics
○平谷 伊智朗（理化学研究所　生命機能科学研究センター）
Ichiro Hiratani (*RIKEN Center for Biosystems Dynamics Research*)

1MSJ-3　ヒトゲノムのデータ駆動的アノテーションを目指した大規模立体構造比較解析
Large-scale comparative analysis of the 3D genome structure for data-driven annotation of the human genome
○中戸 隆一郎（東京大学定量生命科学研究所）
Ryuichiro Nakato (*Institute for Quantitative Biosciences, the University of Tokyo*)

1MSJ-4　Enhanced A/B Compartment Assignment: Improved Consistency, Orientation, and Resolution with HiC-SCA
○ジャスティン チャン スオン [1], 河野 秀俊 [1,2]（[1]QST, [2] 千葉大学）
Justin Chan[1], Hidetoshi Kono[1,2] ([1]*iQLS, QST*, [2]*Center of Quantum Life Science for Structural Therapeutics (cQUEST), Chiba University*)

1MSJ-5　コヒーシンサブユニット Scc1 ヘリックス領域の構造機能解析
Structural and Functional Analysis of Conserved Helical Regions in the Cohesin Subunit Scc1
○木下 慶美, 西山 朋子（京都大・院生物）
Yoshimi Kinoshita, Tomoko Nishiyama (*Grad. Sch. Sci., Kyoto University*)

1MSJ-6　Phase diagram approach to elucidate the organization principle of mitotic chromosome
Tetsuya Yamamoto (*ICReDD, Hokkaido Univ.*)

1MSJ-7　クロマチンドメインの生物種間サイズ分布を説明する普遍的な理論
A universal theory describes chromatin domain size distributions across species
○藤城 新（京大・福井謙一）
Shin Fujishiro (*FIFC, Kyoto Univ.*)

おわりに
Closing Remarks