■ 2023年 11 月 14 日（火）

		部屋名	会場	8	9	10	11	12	13
2号館	1階	211 展示室	A会場		1SAA AIと実験のコンチェルトで奏でる生命科学のパラダイムシフト（井上 圭一、田端 和仁）		企業展示ブース訪問推奨時間		
		212 展示室	B会場		1SBA クロマチンとSMCタンパク質の動態から理解するゲノムモダリティ（前島 一博、山本 哲也）				
	2階	221 会議室	C会場		1SCA 界面における細胞骨格のダイナミクス（島本 勇太、宮崎 牧人）			キャリア支援説明会（-12:50）	
		222＋223 会議室	D会場		1SDA ようこそ、ボーダーレスなロドプシンの世界へ（山下 高廣、角田 聡）			BPセミナー1 カールツァイス株式会社	
		224 会議室	E会場		1SEA 高速AFMの生体分子計測と情報の融合（高田 彰二、古寺 哲幸）			BPセミナー2 浜松ホトニクス株式会社	
	3階	231 会議室	F会場		1SFA 生体ー環境相互作用をトランススケール解析する学際的アプローチ（鈴木 団、大山 廣太郎、山澤 徳志子）				
		232＋233 会議室	G会場		1SGA 生物物理学のための一分子ナノポア計測の基礎と応用（山崎 洋人、庄司 観、彭 祖奕）				
		234 会議室	H会場		1SHA 台湾-日本二国間シンポジウム（Shang-Te Danny Hsu、Daisuke Nakane）				
3号館	3階	国際会議室	I会場		1YI 若手招待講演シンポジウム				
1号館	4階	141＋142 会議室	J会場		1SJA 生体秩序を生み出す力の計測と操作（吉村 成弘、谷本 博一）				
	3階	131＋132 会議室	K会場			ピッチコンテスト		理事会	
		133＋134 会議室	L会場		1SLA 植物細胞のロジックとケミカルAI（井上 大介、水内 良、松林 英明）				BPPB論文賞受賞講演
4号館	3階	431＋432 会議室	M会場		1SMA 多階層からなる高次構造体ダイナミクス: 分子からルガネラまでの動態を探る（中村 秀樹、松尾 芳隆）				
		437 会議室	諸会議室						
1号館	1階	イベントホール	ポスター会場		貼付	ポスター掲示			
			企業展示会場			機器・試薬展示			

※ 「企業展示ブース訪問推奨時間」は、特に企業展示ブースの訪問を積極的に行っていただきたい時間帯です。
年会運営には企業等からの支援をいただいております。
これ以外の時間帯にも積極的に企業ブース等へ訪問いただき、製品情報等のご収集にお役立てください。

14	15	16	17	18	19	20
学生発表賞対象講演 1GA タンパク質：構造、物性、機能						
学生発表賞対象講演 1GB タンパク質：構造機能相関						
学生発表賞対象講演 1GC タンパク質：計測・解析、タンパク質工学／進化工学						
学生発表賞対象講演 1GD 天然変性、ヘム、膜タンパク質、神経・感覚						
学生発表賞対象講演 1GE DNA・DNA結合タンパク質、RNA・RNA結合タンパク質、DNA／RNAナノテクノロジー、クロマチン・染色体						
学生発表賞対象講演 1GF 分子モーター						
学生発表賞対象講演 1GG 細胞生物学的課題						
学生発表賞対象講演 1GH 生体膜・人工膜、化学受容						
学生発表賞対象講演 1GI 生命の起源・進化、合成生物学・人工細胞、ゲノム生物学、非平衡・生体リズム						
学生発表賞対象講演 1GJ 光生物：視覚・光受容、光遺伝学・光制御						
学生発表賞対象講演 1GK 水・水和／電解質、計算生物学、数理生物学・理論生物学						
学生発表賞対象講演 1GL 光合成、計測、バイオエンジニアリング						
学生発表賞対象講演 1GM バイオイメージング						
			若手奨励賞選考委員会			
			ポスター発表（奇数）	ポスター発表（偶数）	撤去	

■ 2023年 11 月 15日（水）

		部屋名	会場	8	9	10	11	12	13
2号館	1階	211 展示室	A会場		2SAA 動的溶液環境が駆動する生体内液液相分離とアミロイド線維化（菅瀬 謙治、吉田 紀生）		企業展示ブース訪問推奨時間		
		212 展示室	B会場		2SBA トア複合体による細胞応答の仕組みを理解する（小杉 貴洋、中津海 洋一）				
	2階	221 会議室	C会場		2SCA 多彩なアプローチによるイオンチャネル研究（川鍋 陽、細島 頌子）			BPセミナー3 株式会社 堀場製作所	
		222+223 会議室	D会場		2SDA 生物運動研究の最前線（南野 徹、宮田 真人）			BPセミナー4 日本蛋白質構造データバンク	
		224 会議室	E会場		2SEA 生物物理化学が拓く生命現象の観察と操作（須藤 雄気、柴田 幹大）			BPセミナー5 レフェイン・ジャパン 株式会社	（株）エビデント
	3階	231 会議室	F会場		2SFA 生命と物質の境界探査（村田 和義、荒川 和晴）				
		232+233 会議室	G会場		2SGA 生命機能の制御を可能にする圧力バイオロジーの開拓（森松 賢順、西山 雅祥）				
		234 会議室	H会場		2SHA シミュレーションで迫る膜輸送体の新知見（炭竈 享司、岡崎 圭一）				
3号館	3階	国際 会議室	I会場		2SIA The third Japan-U.S. symposium on motor proteins and associated single-molecule biophysics（Tomohiro Shima, Kumiko Hayashi）				
1号館	4階	141+142 会議室	J会場		2SJA 時間タンパク質学（吉種 光、大出 晃士）			BPセミナー6 日本カンタムデザイン 株式会社	
	3階	131+132 会議室	K会場		2SKA 基礎生物科学からベンチャーを起こそう！（永井 健治、渡邉 朋信）				
		133+134 会議室	L会場		2SLA “タンパク質ファイバー“が生み出す自主・自発の階層と適応：生物物理学からの“健康創発科学“（跡見 順子、岩城 光宏）				
4号館	3階	431+432 会議室	M会場		2SMA 定量的な細胞力学解析による動的な生命システムの理解（新宅 博文、牧 功一郎）			分野別専門 委員会	会員総会・総会 シンポジウム
		437 会議室	諸会議室	横河電機（株）				BPPB 編集委員会	
	1階	白鳥 ホール	懇親会 会場						
1号館	1階	イベント ホール	ポスター 会場	貼付	ポスター掲示				
			企業展示 会場		機器・試薬展示				

※ 「企業展示ブース訪問推奨時間」は、特に企業展示ブースの訪問を積極的に行っていただきたい時間帯です。
年会運営には企業等からの支援をいただいております。
これ以外の時間帯にも積極的に企業ブース等へ訪問いただき、製品情報等のご収集にお役立てください。

14	15	16	17	18	19	20
2SAP 分子の集合からシステムへ、そして生命へ：高解像な生命の起源研究（Tony Z. Jia、車 兪澈）		企業展示ブース訪問推奨時間	理事会シンポジウム 次の時代の生物学と、サステナブルなデータベース維持に向けて			
2SBP 高次ゲノム構造揺らぎとその機能（落合 博、新海 創也）						
2SCP シン・合成生物学：既存生命のみに依拠しないシステム創成に向けた化学者からの提案（岸村 顕広、金原 数）						
2SDP 分子イメージングが切り拓く細胞外微粒子研究（鈴木 健一、末次 志郎）						
2SEP 構造・計算・分光研究から解明する光受容性タンパク質の非平衡状態ダイナミクス（山元 淳平、片山 哲郎）						
2SFP 多様なリズム現象から探る概日時計研究の行方（秋山 修志、寺内 一姫）						
2SGP GPCRダイナミクスの全体像（片山 耕大、寿野 良二）						
2SHP クライオ電顕を用いたユニークな生体分子構造決定の試み（山本 直樹、バートン–スミス レイモンド）						
2SIP 液液相分離の生物物理学的研究の最前線（亀田 倫史、鎌形 清人）						
2SJP 高解像度な細胞・微粒子解析テクノロジーの最前線（太田 禎生、渡邊 力也）						
2SKP 超越分子シンポジウム：基礎研究を超越し社会実装へつなげる（川野 竜司、川村 出）						
2SLP 細胞システムの複雑なメカニクス（出口 真次、平田 宏聡 ）						
2SMP 微小環境で行動する単細胞生物の生存戦略（鹿毛 あずさ、野村 真未、柴 小菊）						
					懇親会	
			ポスター発表（奇数）	ポスター発表（偶数）	撤去	

■ 2023年 11 月 16日（木）

		部屋名	会場	8	9	10	11	12	13
2号館	1階	211 展示室	A会場		3SAA 構造生物学的アプローチに基づく液液相分離（LLPS）の機能解明（西田 紀貴、池谷 鉄兵）		企業展示ブース訪問推奨時間		
		212 展示室	B会場		3SBA 天然変性タンパク質を含む創薬標的に対する生物物理学的アプローチ（廣明 秀一、白井 剛）				
	2階	221 会議室	C会場		3SCA 自発と応答の情報物理学（青木 一洋、松岡 里実）				
		222＋223 会議室	D会場		企業との意見交換会 9:40-11:00				
		224 会議室	E会場		3SEA 細胞のメゾ構造体の形成と機能の機構：先端イメジング法による解明（下林 俊典、楠見 明弘）			11:40-13:10 男女共同参画・若手支援委員会企画シンポジウム	
	3階	231 会議室	F会場		3SFA 水和による水運動の不均一性から考える生物分子機能（今清水 正彦、菱田 真史）				
		232＋233 会議室	G会場						
		234 会議室	H会場		3SHA 生体膜の生物物理呼応～生命活動における形と動き～（中瀬 生彦、川口 祥正）			11:50-12:50 科研費説明会	
3号館	3階	国際会議室	I会場						
1号館	4階	141＋142 会議室	J会場		3SJA 光合成の多様な環境への適応原理（広瀬 侑、栗栖 源嗣）			BPセミナー7 日本カンタムデザイン株式会社	
	3階	131＋132 会議室	K会場		3SKA 我ら地球生物の可能性～極限微生物から人工細胞まで～（市橋 伯一、鈴木 志野）				
		133＋134 会議室	L会場		高校生・高専生発表				
4号館	3階	431＋432 会議室	M会場						
		437 会議室	諸会議室						
1号館	1階	イベントホール	ポスター会場	貼付	ポスター掲示				ポスター発表（奇数）
			企業展示会場		機器・試薬展示				

※ 「企業展示ブース訪問推奨時間」は、特に企業展示ブースの訪問を積極的に行っていただきたい時間帯です。
年会運営には企業等からの支援をいただいております。
これ以外の時間帯にも積極的に企業ブース等へ訪問いただき、製品情報等のご収集にお役立てください。

14	15	16	17	18	19	20
ポスター発表（偶数）	撤去					
		閉会式				

第 10 回会員総会シンポジウム：Rocking out Biophysics! IUPAB2024 がやってくる

オーガナイザー：日本生物物理学会　理事会
日　時：11 月 15 日（水）12:40 〜 13:50
場　所：4 号館 3 階 M 会場
演　者：野地博行，西坂崇之，高橋　聡 他
司　会：田端和仁（東大院・工）
※このイベントは日本語で開催します。
* This event will be presented in Japanese language.

概　要：皆さん，あと半年ちょっとで IUPAB2024 が京都で開催されます！ IUPAB は国際純粋・応用生物物理学連合（International Union for Pure and Applied Biophysics）の略称で，世界中の生物物理関係者が一堂に集う，3 年に一度の大会です。日本で開催されるのも実に 1976 年以来 56 年ぶり。半世紀ぶりにやってきた IUPAB を皆さんと大いに盛り上げたいと思っています。今回の IUPAB2024 のテーマは ‘Rocking out Biophysics’ そこで，本シンポジウムでは IUPAB2024 に向けて，野地大会長をはじめ，高橋会長など多くの参加者に Rock なバトルを繰り広げてもらう予定です。皆さんにもこの勢いを感じてもらい IUPAB2024 に流れ込みましょう！

一般社団法人日本生物物理学会　第 12 回 Biophysics and Physicobiology 論文賞受賞講演会
The 12th Award Seminar for outstanding Biophysics and Physicobiology paper

オーガナイザー：日本生物物理学会 Biophysics and Physicobiology 論文賞選考委員会
Organizers: Award committee for outstanding Biophysics and Physicobiology paper
日　時：11 月 14 日（火）12:50 〜 13:50 ／ Nov. 14 Tue.
場　所：1 号館 3 階 L 会場／ Bldg1 Room L
形　式：講演会／ Lecture

第 12 回 Biophysics and Physicobiology 論文賞受賞者

角田　聡
Satoshi Tsunoda
名古屋工業大学　大学院生命応用化学専攻，オプトバイオテクノロジー研究センター
Department of Life Science and Applied Chemistry, Nagoya Institute of Technology

クリプト藻由来チャネルロドプシンの発見から創薬ベンチャー創出へ
GtCCR4, a channelrhodopsin with high light sensitivity

Genetic delivery of photoreceptor genes to cells and tissues originally light insensitive turns into light-sensitive. This technique, optogenetics, has been applied in the manipulation of biological function with unprecedented spatio-temporal precision. Channelrhodopsins (ChRs) found in chlorophyte and cryptophyte alga are directly light-gated ion channels and have been widely applied to optogenetics tools for manipulating neuronal excitability. Furthermore, the optogenetics approach has great potential for the restoration of visual function from an inherited disease, retinitis pigmentosa, in which the patient loses light response of the retina.

In 2017, we identified phylogenetically distinct cation-conducting ChR (GtCCR4) from the cryptophyte algae *Guillardia theta* and investigated its molecular property by spectroscopy and electrophysiology (1).

One of the striking features of GtCCR4 is its high photo-sensitivity, ~25 folds higher than a widely known ChR2, without losing fast time response. Thus, GtCCR4 is able to trigger action potentials in high temporal resolution, similar to ChR2, but requires lower light power when expressed in neurons (2, 3). Inspired by such marked properties of GtCCR4, we launched a start-up company aiming for developing an effective gene therapy for curing retinitis pigmentosa.

(1) Yamauchi et al. “Molecular properties of a DTD channelrhodopsin from *Guillardia theta*” Biophys. Physicobiol. 14, 57–66, 2017
(2) Hososhima et al. “A light-gated cation channel with high reactivity to weak light” *Sci. Rep.* 13(1): 7625. 2023
(3) Hagio et al. “Optogenetic manipulation of neuronal and cardiomyocyte functions in zebrafish using microbial rhodopsins and adenylyl cyclases” *Elife* 12:e83975. doi: 10.7554/eLife.83975. 2023

一般社団法人日本生物物理学会　第 12 回 Biophysics and Physicobiology 論文賞受賞講演会
The 12th Award Seminar for outstanding Biophysics and Physicobiology paper

オーガナイザー：日本生物物理学会 Biophysics and Physicobiology 論文賞選考委員会
Organizers: Award committee for outstanding Biophysics and Physicobiology paper
日　時：11 月 14 日（火）12:50 〜 13:50 ／ Nov. 14 Tue.
場　所：1 号館 3 階 L 会場／ Bldg1 Room L
形　式：講演会／ Lecture

第 12 回 Biophysics and Physicobiology 論文賞受賞者

高田彰二
Shoji Takada
京都大学大学院理学研究科
Graduate School of Science, Kyoto University

郷モデルの過去と現在
Go models: Past and the current status

Since the first paper by Nobuhiro Go, the so-called Go models have been broadly applied to computational studies on proteins and others. I start the talk with reviewing history of Go models, followed by some latest studies that are, to some extent, related to Go models.

男女共同参画・若手支援委員会企画シンポジウム
ハイブリッドイベントのベストプラクティスを考える

オーガナイザー：日本生物物理学会　男女共同参画・若手支援委員会
Organizers: Promotion of Gender Equality and Young Researchers Committee
日　時：11 月 16 日（木）11:40 〜 13:10
会　場：2 号館 2 階 E 会場
言　語：日本語
昼　食：お弁当とお茶を無料で提供いたします。ただし，数に限りがあります。
形　式：パネルディスカッション
司　会：西坂崇之（学習院大学）
発表者：南後恵理子（東北大学），大上雅史（東京工業大学），坂内博子（早稲田大学），相沢智康（北海道大学），亘　詩織（株式会社アトラス）

概　要：過去 3 年間，新型コロナウィルスの影響で，対面での年会やその他のイベントの開催が困難でした。一方で，オンラインや，対面・オンラインのハイブリッドなど，様々な開催方式が模索された 3 年間でもありました。その中で，オンライン開催のメリット・デメリットを感じてきたことと思います。年会のハイブリッド化が男女共同参画や若手支援につながるという声もあります。コロナ禍の経験を未来に活かすために，それぞれの経験を共有し，ハイブリッドイベントのベストプラクティスを考察してみるタイミングではないでしょうか。
本シンポジウムでは，ハイブリッド開催の主催経験者，様々な世代・性別の参加経験者に情報を提供していただき，パネルディスカッションを行います。発表・聴講の形式やそれを支えるテクノロジーについてだけでなくコスト面を含めた総括的な意見交換を行い，学会員にとって理想的な未来のハイブリッドイベントを心に描きましょう。具体的には，ハイブリッド開催の意義，メリット・デメリットについて，大きく以下の 3 つの観点から議論を繰り広げたいと考えています。

[1] ワークライフバランス　〜家族・育児・介護と私〜
[2] ハイブリッド開催を支えるテクノロジー　〜ツール開発と利用の観点から〜
[3] ハイブリッド開催におけるコスト　〜参加者と開催者から見た時間と費用〜

本シンポジウムでは，上記 3 項目を主軸として，様々な立場や経験をお持ちの生物物理学会に所属する研究者 4 名，およびシステム開発を基盤として学術分野に貢献する IT 企業 1 名に登壇していただき，パネルディスカッション形式で今後のハイブリッドイベントの在り方について皆さんと一緒に考えていけたら思っています。リアルとオンラインの特徴をうまく活かすことで，生物物理学会年会をさらに盛り上げていける，アイデアをお持ちの学生や若手研究者の方の参加も大変歓迎いたします。一緒にハイブリッドイベントのベストプラクティスを考えましょう。

キャリア支援説明会

オーガナイザー：日本生物物理学会 男女共同参画・若手支援委員会
日　時：11 月 14 日（火）11:50 〜 12:50
会　場：2 号館 2 階 C 会場
形　式：ランチョンセミナーと個別キャリア相談会
※このイベントは日本語で開催します。
* This event will be presented in Japanese language.

概　要：若手研究者や学生の今後のキャリア構築の一助となるように，今年度も「キャリア支援説明会」を開催します。昨年の反響を受けて本年会は，（株）アカリクから講師を迎えて大学院生やポストドクター向けの就職支援活動セミナーを実施します。また，昨年度と同様に今年度も個別キャリア相談会を実施いたしますので，是非ご活用ください。博士課程出身のアカリク社員が何でも質問に答えます！

講師プロフィール

神中 俊明（かみなか としあき）

東京理科大学大学院理学研究科物理学専攻で博士（理学）を取得後，博士研究員を経て 2018 年 10 月より株式会社アカリクに所属しています。博士課程 2 年秋に所属研究室が解散した経験や博士研究員としての活動を元に現在，大学院生を始めとする研究に接する人のキャリア支援，キャリアガイダンス，ワークショップを行っています。研究を志すキャリアの見通しを良くし，研究環境をより良くすることが目標です。

アカリクについて

株式会社アカリクは「知恵の流通の最適化」を目指している企業です。大学院を修了・中退され企業へ就職を希望される方，ポスドクや助教の方のキャリア支援や，専門職転職をされる方のサポートをしています。また，Cloud LaTeX の開発運営や，ジョブ型研究インターンシップの運営，博士人材データベース（JGRAD）の運営補助，セミナー，キャリアマガジン発行を通じて大学院生を始めとする研究者のキャリアがより良いものとなることを目指し，各種事業を展開しております。事業を通して研究者，大学院の環境，企業との関係をより良いものにしていきたいと考えています。

プログラム：理系大学院生や研究者の就活･転職について,「専門外就職」や「博士人材向け」の情報も交えてお話しいたします。

【Part 1】11:50 〜 12:10　大学院生の日頃の時間の使い方
「大学院生は時間がない」「博士課程になると更に忙しい」とはよく耳にすることですが，実際にどれくらい忙しいのかはあまり明らかではありません。そこで，修士課程，博士課程それぞれの時間の使い方についてアカリクで独自に行った調査をご紹介します。

【Part 2】12:10 〜 12:30　最近の就職市場の変化と大学院生の就活スケジュール
最近の就職市場の変化は著しく，大学院生も例外ではありません。2022 年に三省合意により改正された「インターンシップの推進に当たっての基本的考え方」の影響や，2021 年 9 月から博士課程向けに長期・有給で行われている「ジョブ型研究インターンシップ」の制度詳細を踏まえ，現在の産業界･アカデミアの就活スケジュールについてご説明します。

【Part 3】12:30 〜 12:50　企業が求める高度専門人材
企業の採用対象として存在感を増している大学院生を始めとする高度専門人材ですが，実際に企業が何を求めているか，それに対してどのような準備をするのが適切かはあまり知られていません。そこで，企業はどのような高度専門人材を求めているかについて，調査を元にご紹介します。さらに（1）PD のキャリアの考え方，（2）博士課程を中退・単位取得退学する場合の就職活動についてご紹介します。

個別キャリア相談会
就職活動・キャリアに関する悩みや不安を気軽にご相談ください。本大会では，現地（メインアリーナ・ポスター・企業展示会場）での相談会を開催いたします。就活ノウハウや企業での待遇面など，分からないことがあれば遠慮なくお尋ねください。

【ブースオープン時間】
11/14（火）　14:00–18:00
11/15（水）　10:00–12:00, 14:00–19:00
11/16（木）　10:00–15:00
※直接ブースにお越し下さい。空いている場合はすぐご案内できますが，混み合っている場合は，お手数ですが時間を空けて再度お越し下さい。

オンラインでの参加を希望される方は受付フォーム [https://forms.gle/6r5FdJcevQEP285B6] より事前の登録をお願いいたします。

科学研究費助成事業について
Reorganization of KAKENHI: Current Activities of JSPS

世話人：秋山修志（自然科学研究機構　分子科学研究所，日本学術振興会学術システム研究センター専門研究員）

Organizer: Shuji Akiyama (Institute for Molecular Science, NINS; Program Officer, Research Center for Science Systems, JSPS)

日　時：11 月 16 日（木）11:50 〜 12:50

会　場：2 号館 3 階 H 会場

形　式：プレゼンテーション

※このイベントは日本語で開催します。

* This event will be presented in Japanese language.

概　要：今，日本が将来にわたって卓越した研究成果を持続的に生み出し続け，世界の中で存在感を保持できるかが問われています。こうした中，科学技術･学術審議会において，学術研究への現代的要請として，「挑戦性・総合性・融合性・国際性」の四つを挙げ，科研費制度の抜本的改革が提言されました。これを踏まえ，文部科学省では「科研費改革の実施方針」を策定し，科研費の研究種目・枠組みの見直しや審査システムの見直し（「審査システム改革 2018」）が行われ，平成 30 年度科研費（平成 29 年 9 月公募）において，新たな審査システムによる審査を実施しました。今回は，科研費制度の最近の主な変更点を中心に，制度の改善や充実を図った点等について，ご説明をいただきます。

企業参画型ピッチコンテスト

主　催：株式会社リバネス
共　催：日本生物物理学会
日　時：11 月 14 日（火）10:00 〜 11:30
会　場：1 号館 3 階 K 会場

本企画は，研究成果を何かの形で社会還元したいという想いをもつ研究者が自らの研究とアイデアを協賛企業に向けてプレゼンし，産学間でディスカッションや連携を創出するための接点を多く生み出すことを目指すものです。

概　要：
・ピッチコンテストにて，研究者が産業界に向けて自身の研究アピールを 3 分でピッチ（ショートプレゼンテーション）する（50 名程度，事前募集制）。
・事前に応募のあった企業参加者が，ピッチとともに各発表者のポスター発表を聞きに行き，その場でディスカッションを行う。両方の結果に基づき，各参加企業が自身の企業賞を授与する研究者を決定する。
・年会最終日の閉会式にて，各企業賞を発表・授与するピッチコンテストの審査は，この企画に賛同をいただいている協賛企業各社にお願いした方に行っていただき，優秀発表者には協賛企業からの賞金が出ます。

Details of the special project, Company-involved Pitch Contest, are as follows:
Date and Time: November 14th (Tue), 10:00–11:30
Venue: Room K
Hosted by: Leave a Nest Co., Ltd.
Co-sponsored by: Biophysical Society of Japan

The flow of the pitch contest (scheduled) is as follows:
- Researchers will pitch their research appeal to the industrial sector in a short presentation format lasting 3 minutes (approximately 50 people, by advance registration)
- Participating companies who have applied in advance will attend the poster presentations of the presenters along with their pitch, and discussions will be held on the spot. Based on the results of both, each participating company will decide which researcher to award their company prizes to.
- Each company prize will be announced and presented at the closing ceremony of the annual meeting.

9:00〜11:30
I 会場（国際会議室（3 号館 3F））／Room I（International Conference Room (Bldg. 3, 3F)）
1YI　日本生物物理学会若手奨励賞選考会
Early Research in Biophysics Award Candidate Presentations

オーガナイザー：男女共同参画・若手支援委員会
Organizer: Promotion of Gender Equality and Young Researchers Committee

Biophysical Society of Japan (BSJ) grants “Early Career Award in Biophysics” and “Early Career Presentation Award” to young BSJ members for their excellent presentations that show great potential to contribute to the progress of biophysics. In this 19th year, we received 41 highly qualified applications. After the first round of competitive screening based on submitted documents, the following ten applicants were selected as candidates for Early Career Award in Biophysics. In this symposium, each speaker will give a 10-minute presentation followed by a 3-minute discussion as the second round of screening. Up to five awardees of the Early Career Award in Biophysics will be selected. The best presenter will also be awarded IUPAB award from International Union of Pure and Applied Biophysics. The Early Career Presentation Award will be given to the rest of the excellent invited speakers. We welcome all the BSJ members to attend this symposium to foresee the future of biophysics in Japan through the speakers and their research.

09:00　Sakura Takada　1Pos182
1YI0900　**動的な静止構造：人工細胞内に創られたチューリングパターン**
Creation of Turing pattern in artificial cells by PAR system-like mutual inhibition network
○髙田 咲良 [1], 義永 那津人 [2,3], 土居 信英 [1], 藤原 慶 [1]（[1] 慶應大・理工, [2] 東北大 ・AIMR, [3] 産総研・MathAM-OIL）
Sakura Takada[1], Natsuhiko Yoshinaga[2,3], Nobuhide Doi[1], Kei Fujiwara[1] ([1]*Dept. Biosci. and Info., Keio Univ.*, [2]*AIMR, Tohoku Univ.*, [3]*MathAM-OIL, AIST*)

09:15　Hironori Takeda　1Pos030
1YI0915　**ミトコンドリアにおけるタンパク質膜挿入の構造基盤**
Structural basis of the protein membrane insertion by the mitochondrial protein assembly gate
○竹田 弘法（神戸大・科学イノベ）
Hironori Takeda (*Grad. Sch. Sci. Tech. Inno., Kobe Univ.*)

09:30　Takashi Kanadome　3Pos247
1YI0930　**クラスター型プロトカドヘリンの同種親和性相互作用を可視化する蛍光指示薬の開発**
Development of fluorescent indicators for visualizing homophilic interaction of clustered protocadherin
○京 卓志 [1,2], 星野 七海 [3], 永井 健治 [2], 八木 健 [3], 松田 知己 [2]（[1]JST さきがけ, [2] 阪大・産研, [3] 阪大・院生命機能）
Takashi Kanadome[1,2], Nanami Hoshino[3], Takeharu Nagai[2], Takeshi Yagi[3], Tomoki Matsuda[2] ([1]*PRESTO, JST*, [2]*SANKEN, Osaka Univ.*, [3]*FBS, Osaka Univ.*)

09:45　Benjamin Clifton　3Pos019
1YI0945　Ultrahigh-affinity transport proteins from ubiquitous marine bacteria: structure, function, and environmental significance
Benjamin Clifton[1], Uria Alcolombri[2], Colin Jackson[3], Paola Laurino[1] ([1]*Protein Eng. Evol. Unit, Okinawa Inst. Sci. Tech. (OIST)*, [2]*Inst. Environ. Eng., ETH Zurich*, [3]*Research School of Chem., Aust. Nat. Univ. (ANU)*)

10:00 Ryohei Kobayashi 3Pos093

1YI1000 **ミトコンドリア型 ATP 合成酵素の阻害因子 IF_1 が示す回転方向依存的な制御機構: 1 分子操作実験と分子動力学シミュレーション**

Direction-dependent regulation of IF_1 in the mitochondrial ATP synthase by single-molecule manipulation and molecular dynamics simulation

○小林 稜平, 岡崎 圭一（分子研）

Ryohei Kobayashi, Kei-ichi Okazaki (*Inst. for Mol. Sci.*)

10:15 Shiori Iida 1Pos073

1YI1015 **クロマチンの高次構造はクロマチンの局所的な動きとクロマチンのかたさを制御する**

Higher order structure of chromatin regulates local chromatin motion and chromatin stiffness

○飯田 史織 [1,2], 田中 真仁 [3], 田村 佐知子 [1], 鐘巻 将人 [2,4], 島本 勇太 [2,3], 前島 一博 [1,2]（[1] 遺伝研・ゲノムダイナミクス, [2] 総研大・遺伝学, [3] 遺伝研・物理細胞生物学, [4] 遺伝研・分子細胞工学）

Shiori Iida[1,2], Masahito Tanaka[3], Sachiko Tamura[1], Masato Kanemaki[2,4], Yuta Shimamoto[2,3], Kazuhiro Maeshima[1,2] ([1]*Genome Dynamics Lab., Natl. Inst. of Genetics*, [2]*Graduate Institute for Advanced Studies, SOKENDAI*, [3]*Physics and Cell Biology Lab., Natl. Inst. of Genetics*, [4]*Molecular Cell Engineering Lab., Natl. Inst. of Genetics*)

10:30 Minoru Kurisu 2Pos170

1YI1030 **自己生産する細胞のコンセプトを人工系で単純に再設計する：モデル実験系で繋ぐ物質と生命**

Reproduction of a synthetic minimal cell: An experimental approach connecting matter and cell

○栗栖 実 [1], Walde Peter[2], 今井 正幸 [1]（[1] 東北大・院理・物理, [2]ETH・材料）

Minoru Kurisu[1], Peter Walde[2], Masayuki Imai[1] ([1]*Dept. Phys., Grad. Sch. Sci., Tohoku Univ.*, [2]*Dept. Materials, ETH Zürich*)

10:45 Shingo Fukuda 2Pos233

1YI1045 **超低侵襲高速原子間力顕微鏡の開発**

Ultra-low-invasive high-speed atomic force microscopy for visualization of fragile molecular complexes

○福田 真悟, 安藤 敏夫（金沢大学 ナノ生命科学研究所）

Shingo Fukuda, Toshio Ando (*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

11:00 Satoshi Omura 3Pos018

1YI1100 **小型 AsCas12f 酵素のクライオ電子顕微鏡を用いた構造解析およびその改変**

An AsCas12f-based compact genome editing tool derived by deep mutational scanning and structural analysis

Satoshi Omura[1], Tomohiro Hino[2], Ryoya Nakagawa[1], Tomoki Togashi[3], Tsukasa Ohmori[3], Atsushi Hoshino[2], Osamu Nureki[1] ([1]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo.*, [2]*Department of Cardiovascular Medicine, Graduate School of Medical Science, Kyoto Prefectural University of Medicine.*, [3]*Department of Biochemistry, Jichi Medical University School of Medicine.*)

11:15 Ryo Mizuuchi 2Pos159

1YI1115 **原始的な RNA 集団の調査から見つかった自己複製する最小の RNA**

Minimal RNA self-reproduction discovered from a random pool of oligomers

○水内 良 [1,2], 市橋 伯一 [3,4,5]（[1] 早稲田・理工, [2]JST・創発, [3] 東大・総合文化, [4] 東大・先進科学, [5] 東大・普遍性）

Ryo Mizuuchi[1,2], Norikazu Ichihashi[3,4,5] ([1]*Fac. Sci. Eng., Waseda Univ.*, [2]*JST, FOREST*, [3]*Grad. Sch. Arts and Sci., Univ. Tokyo*, [4]*Komaba Inst. Sci., Univ. Tokyo*, [5]*UBI, Univ. Tokyo*)

1 日目（11 月 14 日（火））／Day 1（Nov. 14 Tue.）

1SAA　AI と実験のコンチェルトで奏でる生命科学のパラダイムシフト

The paradigm shift of biological science played by AI–experiment concerti

共催 JST/CREST「バイオ DX」

オーガナイザー：井上 圭一（東京大学），田端 和仁（東京大学）

Organizers: Keiichi Inoue (The Univ. of Tokyo), Kazuhito Tabata (The Univ. of Tokyo)

09:00〜11:30

A 会場（展示室 211（2 号館 1F））／Room A（Exhibition Room 211 (Bldg. 2, 1F)）

The applications of AI in biological and medical fields have been rapidly progressing in these decades. In particular, the structural prediction by Alphafold2 drastically changed the situation of structural biology. The application of AI, however, in other fields is not so established, and many drastic developments are still being demanded. In this symposium, we will present cutting-edge studies incorporating both AI and experiments in a complementary manner for biological and chemical applications. Given the current situation in each discipline, we will discuss the future perspective of biological discovery and paradigm shift by integrating AI and experimental approaches.

はじめに
Opening Remarks

1SAA-1　**高機能性タンパク質のデザインのための機械学習法の開発およびロドプシンの吸収波長制御への応用**
Development of a new machine-learning method to design high functional proteins and an application for the color tuning of rhodopsins
○井上 圭一（東大・物性研）
Keiichi Inoue (*Inst. Solid State Phys.*)

1SAA-2　**機械学習を用いた微生物ロドプシンのデータ駆動型吸収波長予測**
Data-Driven Prediction for Absorption Wavelengths of Microbial Rhodopsins by using Machine Learning Approaches
○烏山 昌幸（名古屋工業大学）
Masayuki Karasuyama (*Nagoya Institute of Technology*)

1SAA-3　**環状ペプチドの構造と膜透過性に関する大規模データ取得のための方法論の開発**
Development of methodologies for obtaining a large dataset of structures and membrane permeability of cyclic peptides
○森本 淳平（東京大・院工）
Jumpei Morimoto (*Grad. Sch. Eng., Univ. Tokyo*)

1SAA-4　**構造安定性のメガスケール解析**
Mega-scale experimental analysis of protein folding stability in biology and protein design
○坪山 幸太郎 [1,2], ロックリン ガブリエル [2]（[1] 東京大学　生産技術研究所, [2] ノースウェスタン大学）
Kotaro Tsuboyama[1,2], Gabriel Rocklin[2] ([1]*IIS UTokyo*, [2]*Northwestern Univ.*)

1SAA-5 BioDOS: 遺伝子ネットワークの自動デザインを行う論理推論 AI
BioDOS: AI Inference engine for Bio-design automation of genetic network
○木賀 大介 [1], 奥田 宗太 [1], 宮崎 和光 [2], 小玉 直樹 [3], 山村 雅幸 [4]（[1] 早大・電気情報生命, [2] 大学改革支援・学位授与機構, [3] 明大・理工, [4] 東工大・情報院理工院）
Daisuke Kiga[1], Sota Okuda[1], Kazuteru Miyazaki[2], Naoki Kodama[3], Masayuki Yamamura[4] ([1]*Dept Elect Eng and Biosci, Waseda Univ*, [2]*Nation. Inst. for Acad. Deg. & Quality Enhance. of High. Edu.*, [3]*Sch. Sci. and Tech., Meiji Univ.*, [4]*Sch. Comput., Tokyo tech*)

おわりに
Closing Remarks

1SBA クロマチンと SMC タンパク質の動態から理解するゲノムモダリティ
Understanding genome modality of the dynamics of chromatin and SMC proteins

共催 学術変革領域研究（A）「ゲノムモダリティ」

オーガナイザー：前島 一博（国立遺伝学研究所），山本 哲也（北海道大学）
Organizers: Kazuhiro Maeshima (NIG), Tetsuya Yamamoto (Hokkaido Univ.)

09:00〜11:30
B 会場（展示室 212（2 号館 1F））／Room B（Exhibition Room 212 (Bldg. 2, 1F)）

Recent advances of experiments have revealed the multiscale structure and dynamics of eukaryotic genome. Genome forms domains, such as topologically associated domains and compartments, in the mesoscopic length scale (100k-10Mbps) and the dynamics of SMC proteins plays a key role in assembling such domains. In this symposium, we invite experts of the dynamics of chromatin and SMC proteins and the self-assembly of DNA to discuss the biophysical principle behind the structural formation and dynamics of genome.

はじめに
Opening Remarks

1SBA-1 SMC 複合体 DNA セグメントキャプチャーモデルの粗視化シミュレーション
DNA-segment Capture by SMC Complex –A Coarse-grained Simulation Study–
○山内 仁喬, 寺川 剛, ブランダーニ ジョバンニ ブルーノ, 高田 彰二（京都大学・理・生物物理）
Masataka Yamauchi, Tsuyoshi Terakawa, Giovanni Bruno Brandani, Shoji Takada (*Dept. of Biophysics, Grad. of Sci., Kyoto Univ.*)

1SBA-2 Direct visualization of DNA-bound cohesin by HS-AFM
Yumiko Kurokawa[1,2], Kenichi Umeda[3], Noriyuki Kodera[3], Yasuto Murayama[1,2] ([1]*Dept. of Chrom. Sci., Nat. Inst. of Genetics*, [2]*Dept. of Genetics, SOKENDAI*, [3]*WPI-NanoLSI, Kanazawa Univ.*)

1SBA-3 コヒーシン二量化による分子障壁を越えたクロマチンループ形成
Formation of chromatin loops by cohesin dimerization over molecular obstacles
○藤城 新（京都大学 福井謙一記念研究センター）
Shin Fujishiro (*Fukui Institute for Fundamental Chemistry, Kyoto University*)

1SBA-4 Replication-dependent histone (Repli-Histo) labeling revealed that chromatin motion can determine DNA replication timing
Katsuhiko Minami[1,2], Satoru Ide[1,2], Sachiko Tamura[1], Masato T. Kanemaki[1,2], Kazuhiro Maeshima[1,2] ([1]*National Institute of Genetics*, [2]*Graduate Institute for Advanced Studies, SOKENDAI*)

1SBA-5 ゲノムサイズの核酸集合体の液-液相分離のデザイン・制御と応用
Design, control, and application of liquid-liquid phase separation of genome-sized nucleic-acid assembly
○瀧ノ上 正浩 [1,2,3]（[1] 東工大・情報理工, [2] 東工大・生命理工, [3] 東工大・リビングシステムズ材料学研究拠点）
Masahiro Takinoue[1,2,3] ([1]*Dept. Compt. Sci., Tokyo Tech*, [2]*Dept. Life Sci. Tech., Tokyo Tech*, [3]*LiSM, IRFI, Tokyo Tech*)

1SBA-6 A loop extrusion-independent mechanism contributes to chromosome shaping by the condensin complexes
Kazuhisa Kinoshita (*Chromosome Dynamics Lab., RIKEN*)

1SBA-7 Elasticity control of entangled chromosomes: crosstalk between condensin complexes and nucleosomes
Yamamoto Tetsuya[1], Kinoshita Kazuhisa[2], Hirano Tatsuya[2] ([1]*ICReDD, Hokkaido Univ.*, [2]*Riken*)

1SCA 界面における細胞骨格のダイナミクス
Cytoskeletal dynamics at the boundaries

オーガナイザー：島本 勇太（国立遺伝学研究所），宮﨑 牧人（京都大学）
Organizers: Yuta Shimamoto (NIG), Makito Miyazaki (Kyoto Univ.)

09:00〜11:30
C 会場（会議室 221（2 号館 2F））／Room C（Conference Room 221 (Bldg. 2, 2F)）

Cells are compartmentalized by various planer boundaries. At each boundary (e.g., the plasma membrane, the nuclear envelope, and organelle surfaces), cytoskeletal proteins form filamentous meshworks and act dynamically to control cell physiology. Whereas the propensities of individual cytoskeleton and membrane components have been extensively studied, how they work together remains a mystery. This symposium gathers early-career researchers from diverse disciplines, aiming to illuminate the fascinating interplay at these biological boundaries. We envision that the symposium provides an opportunity to foster new ideas and questions that encourage young scientists and promotes exciting biophysics by crossing the interdisciplinary boundaries.

はじめに
Opening Remarks

1SCA-1 アクトミオシンの収縮による膜変形プロセスの再構成
Morphological transitions of lipid vesicles driven by the contraction of cortical actomyosin networks
○宮﨑 牧人 [1,2,3]（[1] 京大・院理, [2] 理研 BDR, [3]JST さきがけ）
Makito Miyazaki[1,2,3] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*RIKEN BDR*, [3]*PRESTO, JST*)

1SCA-2 Spatial organization of cytoplasm directed by the cytoskeleton in human cell extracts
Shohei Yamamoto, Daiju Kitagawa (*Grad. Sch. Pharma. Sci., Univ. Tokyo*)

1SCA-3 カドヘリン/アクトミオシンを介した細胞間張力がモルフォゲン勾配の頑強性を支える
Intercellular tension generated by cadherin-actomyosin interaction ensures robust morphogen gradient formation
○青木 佳南, 樋口 大樹, 石谷 太（阪大・微研・生体統御）
Kana Aoki, Taiki Higuchi, Tohru Ishitani (*Dept. of Homeostatic regulation, RIMD, Osaka Univ.*)

1SCA-4 **オルガネラを支配する力の指輪：オルガネラ分裂リングの分子動作機構**
The rings of power to rule organelles: mechanism of force generation by the organelle division ring
○吉田 大和 [1,2]（[1] 東京大・院・理・生物科学, [2]JST・さきがけ）
Yamato Yoshida[1,2] ([1]*Dept. of Biol. Sci., Grad. Sch. Sci., Univ. of Tokyo*, [2]*JST PRESTO*)

1SCA-5 Plant cytoskeletal dynamics at the nuclear periphery
Kentaro Tamura (*Sch. Food Nutr., Univ. Shizuoka*)

1SCA-6 **初期胚発生における核膜ラミンの時空間動態**
Dynamics of nuclear lamins during early embryonic development
○島本 勇太 [1,2]（[1] 遺伝研, [2] 総研大）
Yuta Shimamoto[1,2] ([1]*Nat'l Inst Genetics*, [2]*SOKENDAI*)

おわりに
Closing Remarks

1SDA ようこそ、ボーダーレスなロドプシンの世界へ
Welcome to the borderless rhodopsin world

共催 JST/CREST「オプトバイオ」

オーガナイザー：山下 高廣（京都大学），角田 聡（名古屋工業大学）
Organizers: Takahiro Yamashita (Kyoto Univ.), Satoshi Tsunoda (Nagoya Inst. of Tech.)

09:00〜11:30
D 会場（会議室 222+223（2 号館 2F））／Room D（Conference Room 222+223 (Bldg. 2, 2F)）

Rhodopsin is a general term for photoreceptive proteins which bind retinal as a chromophore. Rhodopsins are classically classified into two types, animal-type and microbial-type. These two types show no sequence similarities with each other, which leads to the diversity of their molecular functions. However, recent accumulation of the molecular properties of rhodopsins has crossed the border between animal-type and microbial-type. Moreover, the application of various rhodopsins to optogenetics not only contributes to the understanding of the molecular mechanisms underlying the physiological functions in animals but also opens a new field in the treatments of diseases. In this symposium, we would like to introduce the “borderless” rhodopsin world.

はじめに
Opening Remarks

1SDA-1 **動物オプシンと微生物オプシンの境界を超える光サイクル型動物オプシン**
Photocyclic animal opsins break the boundary between animal and microbial opsins
○山下 高廣（京都大・院理）
Takahiro Yamashita (*Grad. Sch. of Sci., Kyoto Univ.*)

1SDA-2 **ベストロドプシン：ユニークな光反応を示す新奇光開閉式陰イオンチャネル**
Bestrhodopsin: a novel light-gated anion channel with unique photoreaction
○今野 雅恵（東大・物性研）
Masae Konno (*ISSP, Univ. Tokyo*)

1SDA-3 **プロトンポンプ型ロドプシンを用いたアポトーシスの光制御**
Optical control of apoptotic cell death by a proton pump rhodopsin
○小島 慧一, 須藤 雄気（岡山大・学術研究院医歯薬）
Keiichi Kojima, Yuki Sudo (*Fac. Med. Dent. Pharm. Sci. Okayama Univ.*)

1SDA-4　**動物ロドプシンの多様性と双安定型の動物ロドプシンを用いた GPCR シグナル伝達の分子特性依存的な光操作**
Diversity of animal rhodopsin and optical control of GPCR signaling by bistable animal rhodopsins in a molecular property-dependent manner
○小柳 光正 [1,2]（[1] 大阪公大・院理, [2] 大阪公大・複合先端機構）
Mitsumasa Koyanagi[1,2] ([1]*Grad. Sch. Sci., Osaka Met. Univ.*, [2]*OMU Adv. Res. Ins. Nat. Sci. Tech., Osaka Met. Univ.*)

1SDA-5　**ようこそ、視覚再生遺伝子治療開発の世界へ**
Welcome to the Visual Restoration Gene Therapy Development World
○堅田 侑作 [1,2]（[1] 慶應大・医学部, [2] ㈱レストアビジョン）
Yusaku Katada[1,2] ([1]*Med., Keio Univ.*, [2]*Restore Vision Inc.*)

1SDA-6　**高感度チャネルロドプシンを利用した視覚疾患遺伝子治薬療開発へ向けて**
Development of gene therapy for vision restoration by using a channelrhodopsin with high light sensitivity
○角田 聡 [1,2]（[1] 名古屋工業大学　生命応用化学専攻, [2] 名古屋工業大学　オプトバイオテクノロジー研究センター）
Satoshi Tsunoda[1,2] ([1]*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology*, [2]*OptoBioTechnology Research Center, Nagoya Institute of Technology*)

おわりに
Closing Remarks

1SEA　高速 AFM の生体分子計測と情報の融合
Integrating biomolecular measurements and IT in high-speed AFM

オーガナイザー：高田 彰二（京都大学），古寺 哲幸（金沢大学）
Organizers: Shoji Takada (Kyoto Univ.), Noriyuki Kodera (Kanazawa Univ.)

09:00〜11:30
E 会場（会議室 224（2 号館 2F））／Room E（Conference Room 224 (Bldg. 2, 2F)）

High-speed AFM has been a unique experimental method that can observe single biomolecular structural dynamics at near physiological condition. However, AFM data directly provide information of the surface envelope of the specimen at intermediate resolution both in time and space so that the underlying three-dimensional structures and their movements need to be inferred from some computations for quantitative analysis. The workshop focuses on recent efforts towards integration of high-speed AFM measurements and information technology (IT)-based methods that are expected to make high-speed AFM methods more powerful in the coming years.

はじめに
Opening Remarks

1SEA-1　**ミオシン V の歩行運動のデータ同化解析：高速原子間力顕微鏡データと分子シミュレーション**
Data assimilation analysis of myosin V walking: High-speed atomic force microscopy data and molecular simulations
○渕上 壮太郎 [1], 松永 康佑 [2], 高田 彰二 [3]（[1] 静県大・薬, [2] 埼大院・理工, [3] 京大院・理）
Sotaro Fuchigami[1], Yasuhiro Matsunaga[2], Shoji Takada[3] ([1]*Sch. Pharm. Sci., Univ. Shizuoka*, [2]*Grad. Sch. Sci. Eng., Saitama Univ.*, [3]*Grad. Sch. Science, Kyoto Univ.*)

1SEA-2 ノイズを含む原子間力顕微鏡画像のためのエンド・ツー・エンド微分可能な探針形状再構成法
End-to-end differentiable blind tip reconstruction for noisy atomic force microscopy images
○松永 康佑（埼大院・理工）
Yasuhiro Matsunaga (*Grad. Sch. Sci. Eng., Saitama Univ.*)

1SEA-3 Protein dynamics by the combination of high-speed AFM and computational modeling
Holger Flechsig (*Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

1SEA-4 微小管切断酵素カタニンの高速 AFM による可視化
Visulalization of microtubule severing by High-speed AFM
大野 麻莉菜 [1], 渋谷 颯人 [1], 古寺 哲幸 [2], ○林 郁子 [1] ([1] 横浜市立大学大学院生命医科学研究科, [2] 金沢大学ナノ生命科学研究所)
Marina Ohno[1], Hayato Shibuya[1], Noriyuki Kodera[2], **Ikuko Hayashi[1]** ([1]*Grad. Sch. Med. Lif. Sci., Yokohama City Univ.*, [2]*NanoLSI, Kanazawa Univ.*)

1SEA-5 Structure and dynamics of oligomers of the TIR domain of MyD88
Hidehito Tochio (*Grad. Sch. Sci., Kyoto Univ.*)

1SEA-6 Sub-molecular-scale observation of Structural Maintenance of Chromosomes complexes by high-speed AFM
Kenichi Umeda[1,2], Yumiko Kurokawa[3], Yasuto Murayama[2,3], Noriyuki Kodera[1] ([1]*WPI-NanoLSI, Kanazawa Univ.*, [2]*JST-PRESTO*, [3]*Nat. Inst. Genetics*)

おわりに
Closing Remarks

1SFA 生体ー環境相互作用をトランススケール解析する学際的アプローチ
Interdisciplinary approaches for trans-scale analysis of organism-environment interactions

共催 学術変革領域研究（B）「筋熱シグナリング」

オーガナイザー：鈴木 団（大阪大学），大山 廣太郎（量子科学技術研究開発機構），
山澤 徳志子（東京慈恵会医科大学）
Organizers: Madoka Suzuki (Osaka Univ.), Kotaro Oyama (QST),
Toshiko Yamazawa (The Jikei Univ.)

09:00〜11:30
F 会場（会議室 231（2 号館 3F））／Room F（Conference Room 231 (Bldg. 2, 3F)）

Response of an organism to external stimuli is an essential step for adaptation to external environment. The response relies on that of cells, biomolecules, and their network. In this symposium, we explore the interactions between organisms and environment throughout the spatial scales. We begin with speakers who examine heat and thermal responses at the scales of atoms, molecules and cells. Their interdisciplinary approaches span over biophysics, computational chemistry, and material science. Next, quantitative fluorescence imaging of kinase activities will be introduced as a representative intracellular signaling that can be perturbed quickly by thermal stimulus. Lastly, we will learn how the organism-environment interactions have been examined successfully by state-of-the-art robots as a constructive approach. This symposium is suitable for those who are interested in interdisciplinary approaches to examine the interaction of biological systems with environment at any spatial scales of biological systems.

はじめに
Opening Remarks

1SFA-1　ミオシン ATP 加水分解初期過程における力学的仕事生成
Mechanical Work Generation at Early Stage of ATP Hydrolysis in Myosin
○栗崎 以久男 [1], 鈴木 団 [2]（[1] 早稲田大学理工学術院総合研究所, [2] 大阪大学蛋白質研究所）
Ikuo Kurisaki[1], Madoka Suzuki[2] ([1]*Waseda Research Institute for Science and Engineering*, [2]*Institute for Protein Research, Osaka University*)

1SFA-2　タンパク質分子中における振動エネルギーフロー時空間マップ
Spaciotemporal mapping of vibrational energy flow in proteins
○水野 操（京大・院理）
Misao Mizuno (*Grad. Sch. Sci., Kyoto Univ.*)

1SFA-3　合成色素を用いた脂質膜のナノ温度計測と局所加熱
Nanothermometry and local heating of lipid membranes using synthetic dyes
○新井 敏, 山崎 健, コン・クァン ブー（金沢大　ナノ研）
Satoshi Arai, Takeru Yamazaki, Vu Cong Quang (*WPI-NanoLSI, Kanazawa univ.*)

1SFA-4　ストレス応答 MAPK シグナルの動的制御とその細胞運命決定への寄与
Dynamics and function of stress-activated MAPK signaling in determining cell fates
○冨田 太一郎, 三上 義礼, 大島 大輔, 鄭 有人, 赤羽 悟美（東邦大・医・統合生理）
Taichiro Tomida, Yoshinori Mikami, Daisuke Ohshima, Yuuto Tei, Satomi Adachi-Akahane (*Dept. Physiology, Fac. Med., Toho Univ.*)

1SFA-5　身体と環境の相互作用から生まれる多様で適応的な運動解明に向けた工学的アプローチ
An engineering approach to investigate the various adaptive behavior derived from the interaction between the body and the environment
○杉本 靖博（大阪大学・工学研究科）
Yasuhiro Sugimoto (*Grad. Sch. of Eng., Osaka Univ.*)

おわりに
Closing Remarks

1SGA　生物物理学のための一分子ナノポア計測の基礎と応用
The fundamental and applications of single-molecule nanopore sensing for biophysical studies

オーガナイザー：山崎 洋人（長岡技術科学大学），庄司 観（長岡技術科学大学），
彭 祖癸（東京農工大学）
Organizers: Hirohito Yamazaki (Nagaoka Univ. of Tech.), Kan Shoji (Nagaoka Univ. of Tech.), Peng Zugui (Tokyo Univ. of Agric. and Tech.)

09:00〜11:30
G 会場（会議室 232+233（2 号館 3F））／Room G（Conference Room 232+233 (Bldg. 2, 3F)）

Life at the molecular levels is modulated by the dynamics and interactions of biological molecules. To understand them, single molecule techniques is straight-forward way to investigate in details. Among the techniques, nanopore sensing is a label-free/high through-put apprach, which measure a modulation of ionic current passing through a nanopore.In this symposium, we will organize the session to boost adoption of nanopore sensing and co-develop advanced solutions in biophysical community. To provide deep-understanding of the sensing, the symposium consists of two parts: how the nanopore sensing work fundamentally and how this sensing can be used for applications.

1SGA-1　Single Molecule Biophysical Studies Using Nanopore Sensing: History and Basic Principles
Hirohito Yamazaki (*TRI, Nagaoka Univ. Tech.*)

1SGA-2 Engineered Nanostructures for Single-Protein Characterisation
Cuifeng Ying (*Dept. of Eng., Sch. of Sci. & Tech., Nottingham Trent Univ., UK*)

1SGA-3 Physically insertion of DNA nanopores into liposomes using nanopore-modified microelectrodes
Hiroki Koiwa[1], Shin-ichiro Nomura[2], Satoshi Murata[2], Kan Shoji[1] ([1]*Graduate School of Engineering, Nagaoka University of Technology*, [2]*Graduate School of engineering, Tohoku University*)

1SGA-4 Molecular Dynamics Study of Ion Transport Through Membrane-Spanning DNA Nanopores
Takuya Mabuchi (*Tohoku University*)

1SGA-5 Scanning Ion Conductance Microscopy Using Biological Nanopore Probes
Kan Shoji (*Nagaoka Univ. Tech.*)

1SGA-6 Theoretical prediction of the nanoparticle size by the resistive-pulse technique with cylindrical and conical nanopores
Yinghua Qiu[1,2], Zihao Gao[1,2], Long Ma[1,2], Chuanzhen Huang[1,3] ([1]*Sch. of Mech. Eng., Shandong Univ.*, [2]*Shenzhen Res. Inst. of Shandong Univ.*, [3]*Sch. of Mech. Eng., Yanshan Univ.*)

1SGA-7 Electric field perturbation on protein structural dynamics and its correlation with protein translocation
Prabhat Tripathi (*Dept. of Chem., Indian Inst. of Tech. (Banaras Hindu Univ.) Varanasi*)

1SGA-8 脂質二分子膜内で会合するβシートペプチドが構築するナノポアの均一化手法の検討
Study on β-sheet peptides in lipid bilayers for preparation of monodisperse-size nanopores
○彭 祖癸 [1], 山地 未紗 [1], 藤田 祥子 [1], 栢森 史浩 [2], 臼井 健二 [2], 川野 竜司 [1] ([1] 東京農工大学・生命工学科, [2] 甲南大学・フロンティアサイエンス学部)
Zugui Peng[1], Misa Yamaji[1], Shoko Fujita[1], Fumihiro Kayamori[2], Kenji Usui[2], Ryuji Kawano[1]
([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, [2]*Faculty of Frontiers of Innovative Research in Science and Technology, Konan University*)

1SHA 台湾-日本二国間シンポジウム
Taiwan-Japan Bilateral Symposium

オーガナイザー：Shang-Te Danny Hsu（Academia Sinica），中根 大介（電気通信大学）
Organizers: Shang-Te Danny Hsu (Academia Sinica), Daisuke Nakane (The Univ. of Electro-Comm.)

09:00〜11:30
H 会場（会議室 234（2 号館 3F））／Room H（Conference Room 234 (Bldg. 2, 3F)）

This symposium aims to highlight the current mainstream topics in biophysics and also explore the collaboration and development in the field of biophysics in the Taiwan-Japan region. The symposium includes young and upcoming researchers from the Biophysical Society of Taiwan and the Biophysical Society of Japan. We hope that the close in-person interaction and constructive discussions at this symposium will keep the scientific activity, and to have a significant impact on the community.

1SHA-1 原生生物の運動と行動
Movement and behavior of protists
○西上 幸範（北海道大学電子科学研究所）
Yukinori Nishigami (*Research Institute for Electronic Science, Hokkaido University*)

1SHA-2 Structural basis of a K11/K48-branched ubiquitin chain recognition by the human 26S proteasome
Shang-Te Danny Hsu[1,2,3], Piotr Draczkoswki[1], Yong-Sheng Wang[1,2], Ting Chen[1], Szu-Ni Chen[1], Kuen-Phon Wu[1,2] ([1]*Inst. of Biological Chemistry, Academia Sinica, Taiwan*, [2]*Inst. of Biochemical Sciences, National Taiwan Univ., Taiwan*, [3]*International Inst. for Sustainability with Knotted Chiral Meta Matter, Hiroshima Univ. Higashihiroshima, Japan*)

1SHA-3 How does alcohol stress trigger cell death in *E. coli*?
Setsu Kato (*Graduate School of Integrated Sciences for Life, Hiroshima University*)

1SHA-4 Structural insights into the molecular basis of recognition mechanism between linear polyubiquitin and the UBAN family
Yu-Chih Lo (*Department of Biotechnology and Bioindustry Sciences, National Cheng Kung University, Tainan / Taiwanese*)

1SHA-5 Cryo-EM Observation of wide range of soft-materials
Tasuku Hamaguchi[1], Keisuke Kawakami[2], Daisuke Unabara[1], Koji Yonekura[1,2,3] ([1]*Tohoku Univ., IMRAM*, [2]*RIKEN SPring-8*, [3]*RIKEN-JEOL Collaboration Center*)

1SHA-6 Structural Insights into the P, D, N-Triloop Interaction of Dual-Specificity Phosphatases (DUSPs)
Chih-Hsuan Lai[1], I-Chen Hu[1], Huai-Chia Chuang[2], Tse-Hua Tan[2], **Ping-Chiang Lyu[1]** ([1]*Institute of Bioinformatics and Structural Biology, National Tsing Hua University, Taiwan*, [2]*Immunology Research Center, National Health Research Institutes, Taiwan*)

1SJA 生体秩序を生み出す力の計測と操作
Measurement and manipulation of mechanical forces working in self-transformation of living systems

共催 学術変革領域研究（A）「生体秩序力学」

オーガナイザー：吉村 成弘（京都大学），谷本 博一（横浜市立大学）
Organizers: Shige H. Yoshimura (Kyoto Univ.), Hirokazu Tanimoto (Yokohama City Univ.)

09:00〜11:30
J 会場（会議室 141+142（1 号館 4F））／Room J（Conference Room 141+142 (Bldg. 1, 4F)）

An embryo produces cells with specific fates, forms, and functions during development. These cells are self-organized into an ordered pattern through collective interactions of biomolecules and mechanical forces at various spatio-temporal scales. We aim at developing new paradigms of the fundamental design principles of biological systems through holistic understanding of how mechanical forces elicit self-organizing feedback leading to progressive self-tuning transformation of multicellular systems. In this symposium, cutting-edge technologies needed to interrogate the mechanical processes and establish a unique model for multi-disciplinary research that harnesses expertise from biomedical sciences, engineering, mathematics, physics, and chemistry will be focused.

1SJA-1 細胞内における構造と構造の力学的関係
A physical relationship between intracellular structures
○谷本 博一（横浜市立大学理学部）
Hirokazu Tanimoto (*Department of Science, Yokohama City University*)

1SJA-2 Mechano-chemical control of directed cell migration through microtubule-focal adhesion crosstalk
Yukako Nishimura[1], Thasaneeya Kuboki[2], Satoru Kidoaki[2], Fumio Motegi[1] ([1]*IGM, Hokkaido Univ.*, [2]*IMCE, Kyushu Univ.*)

1SJA-3 アクチン細胞骨格動態の光操作
Optogenetic control of actin cytoskeletal dynamics
○山本 啓 [1], 山崎 陽祐 [1], 青木 一洋 [2,3,4], 宮﨑 牧人 [1,5]（[1] 理化学研究所 生命機能科学研究センター, [2] 基礎生物学研究所, [3] 生命創成探究センター, [4] 総合研究大学院大学, [5] キュリー研究所）
Kei Yamamoto[1], Yosuke Yamazaki[1], Kazuhiro Aoki[2,3,4], Makito Miyazaki[1,5] ([1]*RIKEN BDR*, [2]*National Institute for Basic Biology (NIBB)*, [3]*Exploratory Research Center on Life and Living Systems (ExCELLS)*, [4]*SOKENDAI*, [5]*Institut Curie*)

1SJA-4 Subcellular shuttling of ZO-1 coordinates collective cell migration
Sayuki Hirano[1,2], Kazuhiro Aoki[1,3], Naoto Ueno[2,3] ([1]*Explor. Res. Cent. on Life and Liv. Systs., Natl. Insts. of Nat. Scis.*, [2]*Intl. Res. Collab. Cent., Natl. Insts. of Nat. Scis.*, [3]*Natl. Inst. for Bas. Biol., Natl. Insts. of Nat. Scis.*)

1SJA-5 Hybrid scaffolds elucidate distinct roles of extracellular matrix in age-related cardiac fibroblast activation
Sun Avery Rui, **Jennifer L Young** (*Mechanobiology Institute, Biomedical Engineering Dept., National University of Singapore*)

1SJA-6 細胞力学と遺伝子発現の複合解析
Combined analysis of mechanical properties and transcriptome in thousands of single cells
○塩見 晃史 [1], 金子 泰洸ポール [1], 西川 香里 [1], 新宅 博文 [1,2]（[1] 理研・開拓, [2] 京都大・医生研）
Akifumi Shiomi[1], Taikopaul Kaneko[1], Kaori Nishikawa[1], Hirofumi Shintaku[1,2] ([1]*CPR, RIKEN*, [2]*LiMe, Kyoto Univ*)

1SJA-7 Stem Cell Differentiation in Confining Microenvironments
Andrew W. Holle[1,2] ([1]*Mechanobiology Institute*, [2]*National University of Singapore*)

1SLA 植物細胞のロジックとケミカル AI
Plant Cell Logic and Chemical AI

共催 学術変革領域研究（A）「分子サイバネティクス」

オーガナイザー：井上 大介（九州大学），水内 良（早稲田大学），松林 英明（東北大学）
Organizers: Daisuke Inoue (Kyushu Univ.), Ryo Mizuuchi (Waseda Univ.), Hideaki Matsubayashi (Tohoku Univ.)

09:00〜11:30
L 会場（会議室 133+134（1 号館 3F））／Room L（Conference Room 133+134 (Bldg. 1, 3F)）

Molecular cybernetics aims to develop artificial molecular information processing systems (Chemical AI) by connecting multiple molecular units that package functional molecules acting as sensors, processors, and actuators. On the other hand, plant cells have simple information processing systems without a central nervous system that may provide inspiration for the design of Chemical AI. In this symposium, molecular cybernetics researchers and plant cell biologists will discuss and explore ideas for designing chemical AI inspired by plant cells, and for applying the fundamental techniques of molecular cybernetics to plant cell research ranging from imaging to reconstruction experiments.

はじめに
Opening Remarks

1SLA-1 植物の道管に見る細胞内パターン形成のロジック
Intracellular patterning in plant xylem vessels
○小田 祥久（名古屋大学大学院理学研究科生命理学）
Yoshihisa Oda (*Bio Sci, Sci, Nagoya Univ*)

1SLA-2 Cell polarity linked to gravity sensing in plant gravitropism
Miyo Terao Morita[1], Takeshi Nishimura[1], Hiromasa Shikata[1], Shogo Mori[1], Yoshinori Abe[2], Takuma Hagihara[2], Masatsugu Toyota[2], Hiroshi Y. Yoshikawa[3], Takumi Higaki[4] ([1]*NIBB, NINS*, [2]*Dept. Biochem. Mol. Biol., Saitama Univ.*, [3]*Dept. Applied Physics, Osaka Univ.*, [4]*FAST, Kumamoto Univ.*)

1SLA-3 Real-time visualization of intra- and inter-plant communication
Masatsugu Toyota[1,2,3] ([1]*Dept. Biochem. Mol. Biol., Saitama Univ.*, [2]*SunRiSE, Suntory Fdn. Life Sci.*, [3]*Dept. Bot., UW-Madison*)

1SLA-4 マイクロ流体デバイスにおける細胞サイズのリポソームの多数同時整列
Simultaneous and Multiple Alignment of Cell-sized Liposomes in a Microfluidic Device
○豊田 太郎 [1,2], 章 逸汀 [1,3], 小淵 晴仁 [1], 浜田 省吾 [4], 杉山 博紀 [5], 安部 桂太 [6], 稲田 晃大 [7], 礒川 悌次郎 [7], 村田 智 [6] ([1] 東大・院総合文化, [2] 東大・生物普遍性連携研究機構, [3] 立教大・理, [4] 東工大・情報理工学院, [5] 自然科学研究機構・生命創成探究セ, [6] 東北大・院工, [7] 兵庫県立大・院工)
Taro Toyota[1,2], Yiting Zhang[1,3], Haruto Obuchi[1], Shogo Hamada[4], Hironori Sugiyama[5], Keita Abe[6], Akihiro Inada[7], Teijiro Isokawa[7], Satoshi Murata[6] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*Univ. Biol. Inst., Univ. Tokyo*, [3]*Coll. Sci, Rikkyo Univ.*, [4]*Int. Grad. Sch. Sci. Eng., Tokyo Inst. Tech.*, [5]*ExCELLS, NINS*, [6]*Grad. Sch. Eng., Tohoku Univ.*, [7]*Grad. Sch. Eng., Univ. Hyogo*)

1SLA-5 生物発光を DNA で自在に操る
Manipulation of Bioluminescence with DNA
○葛谷 明紀（関西大・化学生命工）
Akinori Kuzuya (*Dept. Chem. Mater. Eng., Kansai Univ.*)

1SLA-6 Development of totally synthetic membrane transporters and channels
Kohei Sato (*Sch. Sci. Kwansei Gakuin Univ.*)

おわりに
Closing Remarks

1SMA 多階層からなる高次構造体ダイナミクス: 分子からオルガネラまでの動態を探る
Dynamics of multi-layered supramolecular assemblies : from molecular complexes to organelles

共催 JST/さきがけ「高次構造体」

オーガナイザー：中村 秀樹（京都大学），松尾 芳隆（東京大学）
Organizers: Hideki Nakamura (Kyoto Univ.), Yoshitaka Matsuoka (The Univ. of Tokyo)

09:00〜11:30
M 会場（会議室 431+432（4 号館 3F））／Room M（Conference Room 431+432 (Bldg. 4, 3F)）

Cells contain multi-layered supramolecular assemblies ranging from nanometer- to micrometer-scale structures such as protein complexes, RNA-protein complexes, liquid droplets, and organelles. These ordered and dynamic structures orchestrated by tons of molecules convey complex biological information to regulate various key functions in diverse biological processes. Insights into spatiotemporal dynamics of each supramolecular assembly must thus be getting important to understand the rich behaviors of cells. Accordingly, technologies to approach the dynamics of supramolecular assemblies have been explosively diversified in recent biology. In this symposium, we will invite talented early-career researchers from various relevant research fields and discuss the dynamic function of multi-layered supramolecular assemblies.

1SMA-1 **翻訳停滞を解消する共翻訳的な品質管理機構**
Co-translational quality control induced by translational arrest
○松尾 芳隆, 稲田 利文（東京大学医科学研究所）
Yoshitaka Matsuo, Toshifumi Inada (*Institute of Medical Science, The University of Tokyo*)

1SMA-2 **1 分子イメージングで探る細胞分裂と細胞死のクロマチン動態**
Chromatin dynamics in mitosis and apoptosis
○日比野 佳代 [1,2,3], 境 祐二 [4], 鐘巻 将人 [1,2], 前島 一博 [1,2]（[1] 遺伝研, [2] 総研大, [3]JST・さきがけ, [4] 京大）
Kayo Hibino[1,2,3], Yuji Sakai[4], Masato Kanemaki[1,2], Kazuhiro Maeshima[1,2] ([1]*Natl. Inst. Genet.*, [2]*SOKENDAI*, [3]*PRESTO, JST*, [4]*Kyoto Univ.*)

1SMA-3 Efficient information usage by cells – and cell biologists
Keita Kamino[1,2] ([1]*Institute of Molecular Biology, Academia Sinica*, [2]*Institute of Physics, Academia Sinica*)

1SMA-4 Activity-dependent extension of smooth endoplasmic reticulum (sER) into dendritic spines as a synaptic basis of memory consolidation
Natsumi Ageta-Ishihara[1,2], Makoto Kinoshita[3] ([1]*Dept Biomol Sci, Facul Sci, Toho Univ*, [2]*JST, PRESTO*, [3]*Grad Sch Sci, Nagoya Univ*)

1SMA-5 **極微抽出—イオン化法による組織・細胞の多次元化学分布情報**
Measurement of Multidimensional Chemical Distribution Information in Tissues and Cells by Ultrafine Extraction-Ionization Technique
○大塚 洋一（阪大・院理）
Yoichi Otsuka (*Grad. Sch. Sci., Osaka Univ.*)

1SMA-6 Understanding molecular behavior within membraneless organelles using molecular dynamics simulation
Eiji Yamamoto (*Dept. Sys. Des. Eng., Keio Univ.*)

2 日目（11 月 15 日（水））／Day 2（Nov. 15 Wed.）

2SAA **動的溶液環境が駆動する生体内液液相分離とアミロイド線維化**
Liquid-liquid phase separation and amyloid formation driven by dynamic solution environments
共催 学術変革領域研究（B）「動的溶液環境」

オーガナイザー：菅瀬 謙治（京都大学），吉田 紀生（名古屋大学）
Organizers: Kenji Sugase (Kyoto Univ.), Norio Yoshida (Nagoya Univ.)

08:50〜11:20
A 会場（展示室 211（2 号館 1F））／Room A（Exhibition Room 211 (Bldg. 2, 1F)）

In cells, the solution environment is constantly changing due to varying concentrations of chemicals, mechanical stimuli, and electric fields. In recent years, it has become evident that intrinsically disordered proteins, which do not have specific conformations, undergo liquid-liquid phase separation and amyloid fibrillization in response to the ‘dynamic’ solution environment. In this workshop, we invite researchers who are taking various approaches to the effect of dynamic solution environment on protein structure, function, and aggregation and discuss future developments.

はじめに
Opening Remarks

2SAA-1　生体分子系のための溶媒和理論の開発
Development of molecular theory of solvation for biomolecular systems
○吉田 紀生（名古屋大・情報）
Norio Yoshida (*Grad. Sch. Info., Nagoya Univ*)

2SAA-2　アミロイド β 凝集体の形成と解離の全原子分子動力学シミュレーション
All-atom molecular dynamics simulations for the formation and dissociation of amyloid-β aggregates
○奥村 久士 [1,2,3]（[1] 生命創成探究センター, [2] 分子研, [3] 総研大）
Hisashi Okumura[1,2,3] ([1]*ExCELLS*, [2]*Inst. Mol. Sci.*, [3]*SOKENDAI*)

2SAA-3　レドックス応答する人工アミロイド繊維
Redox-responsive artificial amyloid fibers
○池田 将 [1,2,3]（[1] 岐阜大・工, [2] 岐阜大・iGCORE, [3] 岐阜大・COMIT）
Masato Ikeda[1,2,3] ([1]*Faculty of Eng., Gifu Univ.*, [2]*iGCORE, Gifu Univ.*, [3]*COMIT, Gifu Univ.*)

2SAA-4　RNA グアニン四重鎖は α-シヌクレインの液-固相転移を誘導する
RNA G-quadruplexes provide a scaffold for the liquid–solid phase transition of α-synuclein
○松尾 和哉 [1], 矢吹 悌 [1,2], 塩田 倫史 [1,2]（[1] 熊本大・発生研・ゲノム神経, [2] 熊本大・薬学部）
Kazuya Matsuo[1], Yasushi Yabuki[1,2], Norifumi Shioda[1,2] ([1]*Dept. Genomic Neurology, Inst. Molecular Embryology and Genetics, Kumamoto Univ.*, [2]*Grad. Sch. Pharmaceut. Sci., Kumamoto Univ.*)

2SAA-5　Sup35NM 濃縮相からのアミロイド核生成の速度論的解析
Kinetic analysis of amyloid nucleation in Sup35NM condensates
○福山 真央（東北大・多元研）
Mao Fukuyama (*IMRAM, Tohoku Univ,*)

2SAA-6　Evaluation of intrinsically-disordered protein self-condensation inside living cells
Hideki Nakamura[1,2], Kaori Farnè[2] ([1]*Hakubi Center, Kyoto Univ.*, [2]*Grad. Sch. Eng., Kyoto Univ.*)

2SAA-7　ハイドロトロープとしての ATP の作用機序
Mechanism of ATP function as a hydrotrope
西澤 茉由 [2], ヴァリンダ エリック [3], 森本 大智 [2], コーン ベンジャミン [4],
シェーラー ウルリッヒ [4], 白川 昌宏 [2], ○菅瀬 謙治 [1,2]（[1] 京大・農学, [2] 京大・工学, [3] 京大・医学, [4]IPF Dresden）
Mayu Nishizawa[2], Erik Walinda[3], Daichi Morimoto[2], Benjamin Kohn[4], Ulrich Scheler[4],
Masahiro Shirakawa[2], **Kenji Sugase[1,2]** ([1]*Grad. Sch. Ag., Kyoto Univ.*, [2]*Grad. Sch. Eng., Kyoto Univ.*, [3]*Grad. Sch. Med., Kyoto Univ.*, [4]*IPF Dresden*)

おわりに
Closing Remarks

2SBA　トア複合体による細胞応答の仕組みを理解する
Uncovering the mechanisms of cell response by TOR complexes

オーガナイザー：小杉 貴洋（分子科学研究所），中津海 洋一（名古屋市立大学）
Organizers: Takahiro Kosugi (IMS), Hirokazu Nakatsumi (Nagoya City Univ.)

08:50〜11:20
B 会場（展示室 212（2 号館 1F））／Room B（Exhibition Room 212 (Bldg. 2, 1F)）

Response of cells for environments is one of the interesting topics in biology. Target of Rapamycin (TOR) complexes play central roles on signaling pathways for cells to appropriately respond to change in their environment, such as nutritional status, and also known to be associated with various diseases. To uncover the mechanisms, a variety of approach for cells of various species will be of crucial importance. In this symposium, by inviting talented early-career researchers in various research fields who are developing cutting-edge approaches to research the function of TOR complexes, we would like to introduce new attractive target to the Biophysical Society of Japan.

はじめに
Opening Remarks

2SBA-1 mTOR による液ー液相分離制御と翻訳調節
mTOR-dependent Regulation of Liquid-Liquid Phase Separation and Translation
○中津海 洋一 [1], 白根 道子 [1], 中山 敬一 [2]（[1] 名古屋立大・院薬学, [2] 九大・生医研）
Hirokazu Nakatsumi[1], Michiko Shirane[1], Keiichi I. Nakayama[2] ([1]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [2]*Med. Inst. Bioreg., Kyushu Univ.*)

2SBA-2 Making TOP mRNA a Top Priority: Unraveling the Regulation of Protein Synthesis Machinery through Poly(A) Tail Dynamics
Koichi Ogami[1,2], Shin-ichi Hoshino[2] ([1]*Grad. Sch. Med., Nagoya University*, [2]*Grad. Sch. Pharm. Sci., Nagoya City University*)

2SBA-3 Analysis of TOR pathways regulating the initiation of sexual differentiation in fission yeast
Yoko Otsubo, Akira Yamashita (*Nat. Inst. Basic Biology*)

2SBA-4 TOR 活性と PKA 活性測定センサーの開発による分裂酵母の栄養源感知システムの解明
Development of biosensors for measuring TOR and PKA activity to elucidate the nutrition sensing system in fission yeast
○後藤 祐平 [1,2], 酒井 啓一朗 [2], 鎌田 芳彰 [1], 大坪 瑶子 [1], 山下 朗 [1], 青木 一洋 [1,2]（[1] 基生研, [2] 生命創成探究センター）
Yuhei Goto[1,2], Keiichiro Sakai[2], Yoshiaki Kamada[1], Yoko Otsubo[1], Akira Yamashita[1], Kazuhiro Aoki[1,2] ([1]*NIBB*, [2]*ExCELLs*)

2SBA-5 細胞周期依存的な mTORC1/S6K 活性化の可視化
Visualization of cell cycle-dependent mTORC1/S6K activation
○小松 直貴, 宮脇 敦史（理研・脳センター）
Naoki Komatsu, Atsushi Miyawaki (*RIKEN CBS*)

2SBA-6 Pib2 はシステインを直接感知し TORC1 活性を制御する
Pib2 is a cysteine sensor for the regulation of TORC1 activity
○荒木 保弘, 曽 慶忠, 野田 健治（大阪大学・院歯学）
Yasuhiro Araki, Qingzhong Zeng, Takeshi Noda (*Grad. Sch. Dent., Osaka Univ.*)

2SBA-7 構造モデルに基づいて酵母トア複合体を改造し、その役割を明らかにすることを目指して
Toward understanding role of yeast Tor complexes by structure-based engineering approach
○小杉 貴洋 [1,2,3,4]（[1] 自然科学・分子研・協奏分子, [2] 自然科学・生命創成, [3] 総研大, [4]JST・さきがけ）
Takahiro Kosugi[1,2,3,4] ([1]*CIMoS, IMS, NINS*, [2]*ExCELLS, NINS*, [3]*SOKENDAI*, [4]*PRESTO, JST*)

おわりに
Closing Remarks

2SCA　多彩なアプローチによるイオンチャネル研究
Invitation to Ion Channel Research

オーガナイザー：川鍋 陽（香川大学），細島 頌子（名古屋工業大学）
Organizers: Akira Kawanabe (Kagawa Univ.), Shoko Hososhima (Nagoya Inst. of Tech.)

08:50〜11:20
C 会場（会議室 221（2 号館 2F））／Room C（Conference Room 221 (Bldg. 2, 2F)）

Ion channels are a large and diverse group of membrane proteins that can open and close in response to various stimuli such as membrane potential, ligand, pH and light. Thus, ion channels play an essential role in signal transduction in nerve, muscle and brain by regulating the electrical activity of cells. Recently, many types of ion channels including channelrhodopsins, have been used to manipulate biological phenomena. However, many important questions about ion channels such as gating, ion selectivity and transport mechanisms, remain unresolved. In this symposium, we would like to introduce the latest and most interesting ion channel research.

はじめに
Opening Remarks

2SCA-1　円石藻ウイルスが持つヘリオロドプシンのイオン輸送メカニズム
Light-induced proton-transporting heliorhodopsins from marine giant viruses
○細島 頌子（名工大・院工）
Shoko Hososhima (*Grad. Sch. Eng., Nagoya Inst. Tech.*)

2SCA-2　アニオンチャネルロドプシンの細胞内ドメインの知られざる役割
Unknown role of the extended cytoplasmic domain of anion channelrhodopsin
○大木 優也 [1], 篠根 司 [1], 猪子 咲陽 [2], 須藤 未羽 [2], 出村 誠 [1,2,3], 菊川 峰志 [1,2,3], 塚本 卓 [1,2,3] ([1] 北海道大学大学院生命科学院, [2] 北海道大学理学部生物科学科高分子機能学, [3] 北海道大学大学院先端生命科学研究院）
Yuya Ohki[1], Tsukasa Shinone[1], Sayo Inoko[2], Miu Sudo[2], Makoto Demura[1,2,3], Takashi Kikukawa[1,2,3], Takashi Tsukamoto[1,2,3] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Division of Macromolecular Functions, Department of Biological Science, School of Science, Hokkaido University*, [3]*Faculty of Advanced Life Science, Hokkaido University*)

2SCA-3　イオン透過性のアクアポリン 6 は大きな単位コンダクタンスをもち、酸性溶液と中性溶液でアニオンとカチオンに対する選択性が変化する
Ion-permeable Aquaporin 6 has a large unitary conductance and changes selectivity for anion and cation in acidic and neutral solutions
○真木 孝尚 [1], 老木 成稔 [2], 岩本 真幸 [1]（[1] 福井大・医・分子神経科学, [2] 福井大・高エネ研）
Takahisa Maki[1], Shigetoshi Oiki[2], Masayuki Iwamoto[1] ([1]*Dept. Mol. Neurosci., Facul. Med. Sci., Univ. Fukui*, [2]*Biomed. Imaging Res. Center, Univ. Fukui*)

2SCA-4　電位依存性プロトンチャネルの機能制御
Functional regulation of the voltage-gated proton channel
○川鍋 陽, 藤原 祐一郎（香川大・医）
Akira Kawanabe, Yuichiro Fujiwara (*Fac. Med., Kagawa Univ.*)

2SCA-5　非天然蛍光アミノ酸 Anap をプローブとして用いた電位感受性酵素 VSP の分子機構解明
Analysis of molecular mechanism of voltage-sensing phosphatase (VSP) probed by a fluorescent unnatural amino acid
○水谷 夏希, 岡村 康司（阪大・院医・統合生理）
Natsuki Mizutani, Yasushi Okamura (*Integrative Physiol., Grad. Sch. Med., Osaka Univ.*)

2SCA-6　電位依存性カリウムチャネル複合体の相互作用面に導入されたアミノ酸残基のサイズが機能修飾に及ぼす影響
Functional impact of the size of introduced amino acid residues at the interaction face of voltage-gated K^+ channel complexes
○糟谷 豪, 中條 浩一（自治医科大学医学部生理学講座統合生理学部門）
Go Kasuya, Koichi Nakajo (*Division of Integrative Physiology, Department of Physiology, Jichi Medical University*)

2SDA　微生物運動研究の最前線
Frontiers of Microbial Movement Research

オーガナイザー：南野 徹（大阪大学），宮田 真人（大阪公立大学）
Organizers: Tohru Minamino (Osaka Univ.), Makoto Miyata (Osaka Metro. Univ.)

08:50〜11:20
D 会場（会議室 222+223（2 号館 2F））／Room D（Conference Room 222+223 (Bldg. 2, 2F)）

Microorganisms use their own motility apparatus to move in a variety of environments. The motility apparatus is a highly dynamic and robust protein complex containing motor proteins that convert electrochemical or chemical energy to mechanical action for movement. Because motor-protein complexes are under the control of complex sensory signal transduction networks, microorganisms can migrate towards environments favourable for survival and away from unfavourable environments. Furthermore, motor-protein complexes autonomously adjust their mechanical functions in response to environmental changes. In this symposium, we would like to discuss the molecular mechanisms behind these processes and to clarify the design principles common to seemingly diverse motility.

はじめに
Opening Remarks

2SDA-1　細菌べん毛の III 型分泌システムにおけるプロトン-タンパク質アンチポーター機構
Proton-protein antiporter mechanism in the type III secretion system of the bacterial flagellum
○南野 徹 [1], 木下 実紀 [1], 難波 啓一 [1,2,3]（[1] 阪大・生命機能, [2] 阪大・日本電子 YOKOGUSHI 協働研究所, [3] 理研・SPring-8）
Tohru Minamino[1], Miki Kinoshita[1], Keiichi Namba[1,2,3] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*JEOL YOKOGUSHI, Osaka Univ.*, [3]*RIKEN SPring-8*)

2SDA-2　細菌の行動展示
Behavioral exhibition of bacteria
○中根 大介（電通大・院情報理工）
Daisuke Nakane (*Grad. Sch. Info. Eng., UEC*)

2SDA-3　らせん形細菌スピロヘータの生物物理学
Biophysics of spirochetes
○中村 修一（東北大・院工・応物）
Shuichi Nakamura (*Dept. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*)

2SDA-4　ミニマル細菌に構築された細菌アクチン MreB による最小の細胞運動メカニズム
Mechanism of minimal cell motility by bacterial actin MreBs reconstructed in a minimal bacterium
○木山 花 [1], 柿澤 茂行 [2], 高橋 大地 [1], 宮田 真人 [1,3]（[1] 大阪公大・院理, [2] 産総研・生物プロセス, [3] 大阪公大・複合先端）
Hana Kiyama[1], Shigeyuki Kakizawa[2], Daichi Takahashi[1], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Osaka Metropolitan Univ.*, [2]*Bioproduction Res. Inst., AIST*, [3]*OCARINA, Osaka Metropolitan Univ.*)

2SDA-5　**細胞性粘菌の単細胞と多細胞体におけるシグナル伝達の可視化**
Visualization of signal transduction in unicellular and multicellular stages of *Dictyostelium*
○森本 雄祐 [1,2]（[1] 九工大・院情工, [2]JST さきがけ）
Yusuke V. Morimoto[1,2] ([1]*Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*PRESTO, JST*)

おわりに
Closing Remarks

2SEA　生物物理化学が拓く生命現象の観察と操作
Biophysicochemical methods and techniques drive the observation and manipulation of the biological phenomena

オーガナイザー：須藤 雄気（岡山大学），柴田 幹大（金沢大学）
Organizers: Yuki Sudo (Okayama Univ.), Mikihiro Shibata (Kanazawa Univ.)

08:50〜11:20
E 会場（会議室 224（2 号館 2F））／Room E（Conference Room 224 (Bldg. 2, 2F)）

This symposium will focus on the observation and manipulation of biological phenomena using biophysicochemical methods and technologies. Several researchers who analyze both multiple spatial scales from molecules to organisms and multiple time scales from photoreaction to biological responses and molecular evolution will provide and discuss from various biological points of view. Specifically, high-speed atomic force microscopy (HS-AFM) (Shibata), optogenetics (Sudo), single molecule imaging (Iino), radiation imaging (Osakada), cryogenic electron microscopy (Nozawa) will be presented with the selected talk(s) from young researcher(s).

2SEA-1　**高速原子間力顕微鏡により可視化された活性化状態依存的な CaMKII の構造ダイナミクス**
High-speed atomic force microscopy reveals the activity-dependent structural dynamics of CaMKII
○柴田 幹大（金沢大・NanoLSI）
Mikihiro Shibata (*WPI-NanoLSI, Kanazawa Univ.*)

2SEA-2　**ヒストン H2A と H2B を含まないヌクレオソーム様複合体の構造機能解析**
Functional and structural analysis reveal a nucleosome-like particle without histones H2A and H2B
○野澤 佳世 [1], 胡桃坂 仁志 [2]（[1] 東京工業大学・生命理工学院, [2] 東京大学・定量生命科学研究所）
Kayo Nozawa[1], Hitoshi Kurumizaka[2] ([1]*Tokyo Institute of Technology, School of Life Science and Technology*, [2]*The University of Tokyo, Institute for Quantitative Biosciences*)

2SEA-3　**生物発光を用いて植物体内の温度をオルガネラレベルで高感度に可視化する温度センサーの開発**
A highly sensitive bioluminescent thermosensor to capture the plant temperature at the organelle level
○福島 俊一 [1], 佐藤 智亮 [1], 長部 謙二 [2], 永井 健治 [1]（[1] 大阪大・産業科学研究所, [2] 沖縄科学技術大学院大学）
Shun-ichi Fukushima[1], Tomoaki Sato[1], Kenji Osabe[2], Takeharu Nagai[1] ([1]*SANKEN, Univ. Osaka*, [2]*OIST*)

2SEA-4　**バイオサイエンスへの応用を目指した高機能性光・放射線応答性有機ナノ材料の開発**
Development of functional light- and radiation-responsive organic nanomaterials for bioscience applications
○小阪田 泰子 [1,2]（[1] 大阪大学高等共創研究院, [2] 大阪大学産業科学研究所）
Yasuko Osakada[1,2] ([1]*Osaka university, IACS*, [2]*Osaka university, SANKEN*)

2SEA-5　分子モーターの 1 分子イメージングとエンジニアリング
Single-molecule imaging and engineering of molecular motors
○飯野 亮太 [1,2]（[1] 自然科学研究機構 分子科学研究所, [2] 総研大）
Ryota Iino[1,2] ([1]*Institute for Molecular Science, NINS*, [2]*SOKENDAI*)

2SEA-6　微生物ロドプシンの多機能性と光遺伝学ツール
Multifunctional microbial rhodopsins and their applications in optogenetics
○須藤 雄気（岡山大院医歯薬）
Yuki Sudo (*Okayama Univ.*)

2SFA　生命と物質の境界探査
Exploring the boundary between life and matter

共催 生命創成探究センター「先端共創プラットフォーム」

オーガナイザー：村田 和義（生命創成探究センター），
荒川 和晴（慶應義塾大学/生命創成探究センター）
Organizers: Kazuyoshi Murata (ExCELLS), Kazuharu Arakawa (Keio Univ./ExCELLS)

08:50〜11:20
F 会場（会議室 231（2 号館 3F））／Room F（Conference Room 231 (Bldg. 2, 3F)）

Understanding the morphology, function, and dynamics of genomes and molecular complexes of individual extremophiles is progressing as survival strategies in various extreme environments. On the other hand, a metagenomic-based exploration of more extreme environments reveals the importance not only of independent survival strategies of individual organisms but also of cooperative survival strategies through interactions between coexisting heterologous organisms. This project will observe the molecular complexes of morphology, function, dynamics, and their associated biological interactions of viruses, prokaryotes, and eukaryotes living in extreme environments, and elucidate the simple or minimal mechanisms and principles. We will connect these to a systematic understanding of the boundary between matter and life.

はじめに
Opening Remarks

2SFA-1　リボソーム自己複製プロセスの構成的理解による物質と生命の境界探査
Exploring the boundary between matter and life through a constitutive understanding of the ribosomal self-replication process
○青木 航（阪大・工）
Wataru Aoki (*Grad. Sch. Eng*)

2SFA-2　Construction of model catalytic proteins to investigate the origin of prebiological catalyses
Koki Makabe[1,2] ([1]*Yamagata Univ.*, [2]*PRESTO*)

2SFA-3　Life-without-water -Shining tardigrades illuminate the way to exploring the mechanism of dehydrated ametabolic state-
Sae Tanaka[1,2], Kazuharu Arakawa[1,2] ([1]*ExCELLS, NINS*, [2]*IAB, Keio Univ.*)

2SFA-4　メドゥーサウイルスにコードされるヒストンの宿主細胞内でのウイルス複製における役割について
Role of medusavirus-encoded histones in viral replication in host cells
○武村 政春 [1], 東浦 彰史 [2], 村田 和義 [3]（[1] 東京理科大・院理, [2] 広島大・院医, [3] 自然科学研究機構・ExCELLS）
Masaharu Takemura[1], Akifumi Higashiura[2], Kazuyoshi Murata[3] ([1]*Grad. Sch. Sci., Tokyo Univ. Sci.*, [2]*Grad. Sch. Med., Hiroshima Univ.*, [3]*Res. Inst. Nat. Sci., ExCELLS*)

2SFA-5 Dynamic change of mechanical properties of bacteria investigated by high-speed AFM based force mapping
Christian Ganser[1], Shigetaka Nishiguchi[1,2], Takayuki Uchihashi[1,3] ([1]*National Institutes of Natural Sciences, ExCELLS*, [2]*Osaka University, Department of Biotechnology (present affiliation)*, [3]*Nagoya University, Department of Physics*)

2SFA-6 Unraveling the Mechanisms of Desiccation Tolerance: Insights from Anhydrobiotic Tardigrade CAHS1 Fibrous Condensates
Maho Yagi-Utsumi[1,2], Koichi Kato[1,2] ([1]*ExCELLS, NINS*, [2]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*)

2SFA-7 微生物ダークマターを通じて生命—物質の境界を明らかにするために
Unveiling the boundary between life and matter via the exploration of microbial dark matter
○武藤 久（自然科学研究機構・生命創成探究センター）
Hisashi Muto (*ExCELLS, NINS*)

おわりに
Closing Remarks

2SGA 生命機能の制御を可能にする圧力バイオロジーの開拓
Pressure stimuli regulate the biological functions

オーガナイザー：森松 賢順（岡山大学），西山 雅祥（近畿大学）
Organizers: Masatoshi Morimatsu (Okayama Univ.), Masayoshi Nishiyama (Kindai Univ.)

08:50〜11:20
G 会場（会議室 232+233（2 号館 3F））／Room G（Conference Room 232+233 (Bldg. 2, 3F)）

Various "pressure stimuli" such as hydrostatic pressure, osmotic pressure, and compressive force regulate a variety of biological functions from the molecular system to the tissue level. Recent studies have shown that pressure stimulus signaling elicits a wide range of cellular responses, providing new insights into biological and biomedical research areas. In this symposium, we will present and discuss recent studies on how pressure stimuli regulate biological function. We will also introduce the emerging field of Pressure Biology.

はじめに
Opening Remarks

2SGA-1 Comparison of Pressure Responses Among Piezo-sensitive and Piezophilic Bacteria
Douglas H. Bartlett (*Scripps Inst. Oceanography, UCSD / USA*)

2SGA-2 酵母のメカノセンシングと高水圧ストレス応答
Mechanosensing and Cellular Responses to High Hydrostatic Pressure in Yeast
○阿部 文快（青山学院大・理工）
Fumiyoshi Abe (*Coll. Sci. Eng., Aoyama Gakuin Univ.*)

2SGA-3 Hydrostatic pressure stimuli regulate the pattern of the intracellular calcium concentration
Masatoshi Morimatsu (*Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University*)

2SGA-4 減圧力顕微鏡法
Depressurization microscopy
○西山 雅祥（近大理工）
Masayoshi Nishiyama (*KINDAI Univ.*)

2SGA-5 Hypotonic Pressure Induced Osmotic Calcium Response States
Zidan Gao, Masatoshi Morimatsu (*Cardiovascular Phsiology,Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University*)

2SGA-6 **表皮癌細胞の増殖の機械的調節における細胞—細胞間接着と細胞—基質間接着の異なる役割**
Distinct roles of cell-cell and cell-ECM adhesions in mechanical regulation of epidermal cancer cell proliferation
Hiroaki Hirata[1,2], Oleg Dobrokhotov[2,3], Masahiro Sokabe[2,4] ([1]*Dep. Appl. Biosci., Kanazawa Inst. Tech.*, [2]*Mechanobiol., Grad. Sch. Med., Nagoya Univ.*, [3]*Randall Centre Cell Mol. Biophys., King's College London*, [4]*Human Info. Sys. Lab., Kanazawa Inst. Tech.*)

おわりに
Closing Remarks

2SHA シミュレーションで迫る膜輸送体の新知見
New insight into membrane transport proteins by simulation studies

オーガナイザー：炭竈 享司（JST さきがけ），岡崎 圭一（分子科学研究所）
Organizers: Takashi Sumikama (PRESTO, JST), Kei-ichi Okazaki (IMS)

08:50〜11:20
H 会場（会議室 234（2 号館 3F））／Room H（Conference Room 234 (Bldg. 2, 3F)）

Membrane transport proteins play essential roles in many physiological functions, such as maintenance of concentration gradients, nerve conductions, and synthesis of ATP. In principle, molecular motion should be involved in these functions, and observation of such molecular motion is necessary to fully understand their mechanisms. Recent computational simulations using high-performance computers have made it possible to fundamentally explain such functions at the molecular level. In this symposium, we will present recent advances in this field that help us understand (1) ion conduction and selectivity mechanism through the ion channels, (2) those through the ion pumps, (3) alternating-access conformational dynamics of transporters.

2SHA-1 **K^+チャネルでの選択的イオン透過と Na^+チャネルのゲーティングの新機構**
Selective ion permeation through the K^+ channels and novel gating mechanism of the Na^+ channel
○炭竈 享司 [1,2]（[1] さきがけ, JST, [2] 金沢大学）
Takashi Sumikama[1,2] ([1]*PRESTO, JST*, [2]*Kanazawa University*)

2SHA-2 Principles of selective transport in ion channels and nanopores
Ben Corry (*Research School of Biology, Australian National University*)

2SHA-3 **量子分子動力学シミュレーションによるロドプシンにおける化学反応の理論的解析**
Quantum molecular dynamics simulation studies for reactions in rhodopsin proteins
○小野 純一（早稲田大学 理工学術院総合研究所）
Junichi Ono (*Waseda Research Institute for Science and Engineering (WISE), Waseda University*)

2SHA-4 **分子動力学（MD）法による SR-Ca^{2+}-ATPase の E1P-E2P 転移での構造変化解析**
Molecular dynamics (MD) simulations of structural changes in the E1P-E2P transition of SR-Ca^{2+}-ATPase
○小林 千草 [1], 稲葉 謙次 [2], 杉田 有治 [1,3,4]（[1] 理研・R-CCS, [2] 東北大・院多元物質科学, [3] 理研・CPR, [4] 理研・BDR）
Chigusa Kobayashi[1], Kenji Inaba[2], Yuji Sugita[1,3,4] ([1]*RIKEN R-CCS*, [2]*IMRAM, Tohoku Univ.*, [3]*RIKEN CPR*, [4]*RIKEN BDR*)

2SHA-5 **分子シミュレーションと AlphaFold2 によるトランスポータータンパク質の構造ダイナミクス解明**
Conformational dynamics of transporter proteins revealed by molecular simulation and AlphaFold2
○岡崎 圭一（分子科学研究所）
Kei-ichi Okazaki (*Institute for Molecular Science*)

2SIA The third Japan-U.S. symposium on motor proteins and associated single-molecule biophysics

オーガナイザー：島 知弘（東京大学），林 久美子（東京大学）
Organizers: Tomohiro Shima (The Univ. of Tokyo), Kumiko Hayashi (The Univ. of Tokyo)

08:50〜11:20
I 会場（国際会議室（3 号館 3F））／Room I（International Conference Room (Bldg. 3, 3F)）

This is a series of motor protein symposia, starting in 2021, that will bring together researchers from Japan and the U.S.-two leading countries in the field- to foster the exchange of ideas and promote cutting-edge collaborative research. With a lineup of renowned experts in the field, this symposium provides an exceptional opportunity to present the latest advances in our understanding of motor protein movement and regulation. This time, we are especially featuring international young scientists as speakers who are also willing to contribute to the educational programs of IUPAB2024. In addition, the symposium will promote gender equality by providing an opportunity for discussion as part of the introduction of the speakers.

はじめに
Opening Remarks

2SIA-1 **生体分子モーターからなるアクティブマターを用いた物理リザーバー演算装置の構築**
Construction of a physical reservoir computing device using active matter made from a swarm of biomolecular motors
○龔 逸鳴 [1], 臼杵 義亨 [2], コビル アリフ ムハンマド ラセドウル [3], 佐田 和己 [2,3], 川又 生吹 [4], オベル加藤 ナタナエル [5], 市川 正敏 [1], 角五 彰 [1]（[1] 京大・院理, [2] 北大・院総化, [3] 北大・院理, [4] 東北大・院工, [5] お茶大・情報理）
Yiming Gong[1], Gikyo Usuki[2], Arif Md. Rashedul Kabir[3], Kazuki Sada[2,3], Ibuki Kawamata[4], Nathanael Aubert-Kato[5], Masatoshi Ichikawa[1], Akira Kakugo[1] ([1]*Grad. Sch. Sci., Kyoto. Univ*, [2]*Grad. Sch. Che. Sci. Eng., Hokkaido. Univ*, [3]*Fac. Sci, Hokkaido. Univ*, [4]*Grad. Sch. Eng., Tohoku. Univ*, [5]*Dep. Infor. Sci., Ochanomizu. Univ*)

2SIA-2 Kinesin-1, 2 and 3 motors use family-specific mechanochemical strategies to effectively compete with dynein during bidirectional transport
William Hancock[1,2], Allison Gicking[1], Tzu-Chen Ma[1], Qingzhou Feng[1], Rui Jiang[1], Somayesadat Badieyan[3], Michael Cianfrocco[3] ([1]*Department of Biomedical Engineering, Pennsylvania State University*, [2]*Department of Chemistry, Pennsylvania State University*, [3]*Department of Biological Chemistry and the Life Sciences Institute, University of Michigan*)

2SIA-3 Plant KIF15 functions as a vesicle transporter for the cell plate formation during cytokinesis
Takema Sasaki, Gohta Goshima, **Moe Yamada** (*Grad. Sch. Sci., Nagoya Univ.*)

2SIA-4 TRAK adaptors regulate the recruitment and activation of dynein and kinesin in mitochondrial transport
Merve Aslan[1], John Canty[1], Andrew Hensley[2], Amanda Jack[1], Ahmet Yildiz[1,2,3] ([1]*Biophysics Graduate Group, UC Berkeley*, [2]*Physics Department, UC Berkeley*, [3]*Department of Molecular and Cellular Biology, University of California at Berkeley*)

2SIA-5 Alphaherpesvirus neuroinvasion is achieved by regulation of the kinesin-1 microtubule motor
Gregory Allan Smith (*Northwestern Univ. Feinberg Sch. Med.*)

2SIA-6 Extreme-Value Analysis of Intracellular Cargo Transport by Motor Proteins
Kumiko Hayashi (*ISSP, Univ. Tokyo*)

2SJA 時間タンパク質学
Chronoproteinology

共催 学術変革領域研究（B）「時間タンパク質学」

オーガナイザー：吉種 光（東京都医学総合研究所），大出 晃士（東京大学）
Organizers: Hikari Yoshitane (TMIMS), Koji Ode (The Univ. of Tokyo)

08:50〜11:20
J 会場（会議室 141+142（1 号館 4F））／Room J（Conference Room 141+142 (Bldg. 1, 4F)）

There are various time scales in biology such as longevity, seasonal responses, circadian rhythmicity, developmental processes, cell division cycles, and heartbeats. In other words, living organisms consists of different time scales. What are the mechanisms for measuring “time” that correspond to each event at different time scale? This symposium is co-organized with Transformative Research Areas (B) "Chronoproteinology". We will focus on proteins responsible for molecular mechanisms that directly regulate time information. The physical properties and dynamics of proteins could generate “time” on various time scales as autonomous protein oscillators. The dynamics includes protein-protein interactions, post-translational modifications, enzymatic activities, and conformational changes.

はじめに
Opening Remarks

2SJA-1 時間タンパク質学:時計タンパク質の相互作用リズムと翻訳後修飾コード
Chrono-proteinology: circadian interaction rhythms of clock proteins and chrono-code of their post-translational modifications
○吉種 光（東京都医学総合研究所）
Hikari Yoshitane (*Tokyo Metropolitan Institute of Medical Science*)

2SJA-2 時計タンパク質の翻訳後修飾による概日時計の駆動機構
Timekeepers of the mammalian circadian clock regulate post-translational modifications
○篠原 雄太（北海道大学 遺伝子病制御研究所）
Yuta Shinohara (*Inst. for Genetic Medicine, Hokkaido univ.*)

2SJA-3 温度依存的な時計関連タンパク質の量的制御は周期の温度補償性と関連する
The temperature-dependent quantitative control of the clock proteins is associated with temperature compensation in Arabidopsis thaliana
○前田 明里, 松尾 宏美, 中道 範人（名古屋大学大学院 生命農学研究科）
Akari Maeda, Hiromi Matuo, Norihito Nakamichi (*Grad. Sch. Bio-Agric., Nagoya Univ.*)

2SJA-4 ニワトリクリプトクロム 1 変異体における FAD 結合の増強と光反応サイクル
Enhanced FAD-binding and photocycle in a chicken cryptochrome 1 mutant
○石塚 皓貴, 三浦 宏太, 岡野 恵子, 岡野 俊行（早稲田大・院先進理工・電生）
Koki Ishizuka, Kota Miura, Keiko Okano, Toshiyuki Okano (*Dept. Elec. Eng., Grad. Sch. ASE., Waseda Univ.*)

2SJA-5　細胞の中のリズム：その細胞自律性と非自律性
Circadian rhythms in a cell: cell-autonomous and non-cell-autonomous
○村中 智明 [1], 小山 時隆 [2]（[1] 名古屋大・院生命農学, [2] 京都大・院理学）
Tomoaki Muranaka[1], Tokitaka Oyama[2] ([1]*Grad. Sch. of Bioagri. Sci., Nagoya Univ.*, [2]*Grad. Sch. of Sci., Kyoto Univ.*)

2SJA-6　緑藻から探る非転写概日振動体
Exploring non-transcriptional circadian oscillators from green algae
○松尾 拓哉（北里大・院理学）
Takuya Matsuo (*Grad. Sch. Sci., Univ. Kitasato*)

2SJA-7　概年時計の分子基盤
Molecular basis of the circannual clock
○吉村 崇 [1,2]（[1] 名大・WPI-ITbM, [2] 名大・院生命農学）
Takashi Yoshimura[1,2] ([1]*WPI-ITbM, Nagoya Univ.*, [2]*Grad. Sch. Bioagricult. Sci., Nagoya Univ.*)

おわりに
Closing Remarks

2SKA　基礎生物科学からベンチャーを起こそう！
Venture out of basic bioscience!

オーガナイザー：永井 健治（大阪大学），渡邉 朋信（広島大学）
Organizers: Takeharu Nagai (Osaka Univ.), Tomonobu Watanabe (Hiroshima Univ.)

08:50〜11:20
K 会場（会議室 131+132（1 号館 3F））／Room K（Conference Room 131+132 (Bldg. 1, 3F)）

The social implementation of academic research is expected to not only promote positive-feedback between basic science and industry/society but also provide new career paths for young researchers. Therefore, venture entrepreneurship from basic bioscience including biophysics can be a savior of Japan with a growing concern about the decline of scientific capabilities. In this symposium we would like to discuss the social implementation of basic bioscience from various viewpoints so as to encourage entrepreneurship among biophysicists, especially graduate students and young researchers. We hope audiences will see that basic science also has ample potential to venture out into a successful business/career.

はじめに
Opening Remarks

2SKA-1　DNA 複製純粋研究からのオリシロ起業、売却
A journey of OriCiro from academia research to M&A exit
○末次 正幸 [1,2]（[1] 立教大・理, [2] モデルナ・エンザイマティクス株式会社）
Masayuki Suetsugu[1,2] ([1]*Col. of Sci., Rikkyo Univ.*, [2]*Moderna Enzymatics Co., Ltd.*)

2SKA-2　セツロテックを起業した 3 つの理由
Three reasons I started my business “Setsurotech”
○竹本 龍也 [1,2]（[1] 徳島大学先端酵素学研究所/, [2] 株式会社セツロテック）
Tatsuya Takemoto[1,2] ([1]*Institute of Advanced Medical Sciences, Tokushima University*, [2]*Setsuro tech Inc.*)

2SKA-3　VC から見た基礎生物学スタートアップの最前線
The Forefront of Basic Biology Startups from a VC's Perspective
○山家 創（リアルテックホールディングス（株））
Sou Yanbe (*Real Tech Holdings Co.,Ltd.*)

2SKA-4　生きたままの試料を分子分光するスクリーニング技術：多点同時ラマンプレートリーダー
Screening Technique for Molecular Spectroscopy of Live Samples: Multi-Point Simultaneous Raman Plate Reader
○畔堂 一樹 [1,2]（[1] 大阪大学, [2] 産業技術総合研究所）
Kazuki Bando[1,2] ([1]*Osaka University*, [2]*National Institute of Advanced Industrial Science and Technology (AIST)*)

2SKA-5　アカデミアからベンチャーへー若手生物学研究者に伝えたいこと
From Academia to the Venture Company- A Message to Young Biologists
○髙橋 政代（株式会社ビジョンケア）
Masayo Takahashi (*Vision Care Inc.*)

2SKA-6　若者だけじゃない！ オジサンも起業する！！
Not just the youth! Older men are also becoming entrepreneurs!!
○永井 健治（阪大・産研）
Takeharu Nagai (*SANKEN, Osaka Univ.*)

2SKA-7　「生もの」生物物理学
"Raw foods" biophysics
○渡邉 朋信 [1,2]（[1] 広大・原医研, [2] 理研・神戸）
Tomonobu Watanabe[1,2] ([1]*RIRBM, Hiroshima Univ.*, [2]*BDR, Riken*)

おわりに
Closing Remarks

2SLA　“タンパク質ファイバー”が生み出す自主・自発の階層と適応：生物物理学からの“健康創発科学”
"Protein Fibers" Generate Voluntary and Spontaneous Hierarchies and Adaptations: "Health Emergence Science" from Biophysics

オーガナイザー：跡見 順子（東京農工大学），岩城 光宏（情報通信研究機構）
Organizers: Yoriko Atomi (Tokyo Univ. of Agric. & Tech.), Mitsuhiro Iwaki (NICT)

08:50〜11:20
L 会場（会議室 133+134（1 号館 3F））／Room L（Conference Room 133+134 (Bldg. 1, 3F)）

Fumio Osawa, founder of the Biophysical Society, insightfully observed that the essence of life is "voluntary and spontaneous". The system principle that has evolved is form-dependent dynamics. Although we can raise issues from pathology, we are far from elucidating the "health principle" that allows us to live a 120-year lifespan. This symposium will explore the way to extend the principle of autonomy and spontaneity of life, which is emerged by self-association of protein fibers and led to adaptation by molecular chaperones, from molecules and cells to the physical and mental problems of human beings. We advocate health emergent science from biophysics.

はじめに
Opening Remarks

2SLA-1 微小管におけるチューブリン C 末端の動態
Dynamical state of the C-terminal tail of tubulin on the microtubule
○高野 光則（早稲田大・物理）
Mitsunori Takano (*Dept Phys & Appl Phys, Waseda Univ*)

2SLA-2 DNA メカノテクノロジーの開発と細胞の高解像力学計測
DNA mechanotechnology and high-resolution imaging of cellular mechanical forces
○岩城 光宏 [1,2,3]（[1] 情報通信・未来 ICT 研, [2] 理研・生命機能セ, [3] 阪大・免疫フロンティア）
Mitsuhiro Iwaki[1,2,3] ([1]*Adv. ICT Res. Inst., NICT*, [2]*RIKEN*, [3]*IFReC, Osaka Univ.*)

2SLA-3 サルコメア合成に向けた、細胞骨格と DNA ナノテクノロジーを融合した再構築系の探求
Exploring a Novel Reconstituted System Combining Cytoskeletons and DNA Nanotechnology Toward Sarcomere Synthesis
○井上 大介（九大・院芸工）
Daisuke Inoue (*Fac. Des., Kyushu Univ.*)

2SLA-4 理論解析による細胞の力学的ホメオスタシスのシステム論的メカニズム
Theoretical analysis of the system relation in cellular mechanical homeostasis
○松元 瑛司, 松永 大樹, 出口 真次（大阪大学大学院基礎工学研究科）
Eiji Matsumoto, Daiki Matsunaga, Shinji Deguchi (*Graduate School of Engineering Science, Osaka University*)

2SLA-5 Endothelial plasma membranes and mitochondria act as mechanosensory complexes that mediate sensing and signaling of shear stress
Kimiko Yamamoto (*Grad. Sch. Med., The Univ. Tokyo*)

2SLA-6 ヒトの生物物理学的評価の提案：健康におけるタンパク質線維の冗長性と創発性
Proposal of biophysical evaluation of human as an organism: redundancy and emergency of protein fibers in health
○跡見 順子（帝京大学先端総合研究機構）
Yoriko Atomi (*Teikyo University, ACRO*)

おわりに
Closing Remarks

2SMA 定量的な細胞力学解析による動的な生命システムの理解
Quantitative analysis of cellular mechanics to dissect dynamics of biological systems

共催 JST/JCREST「多細胞」

オーガナイザー：新宅 博文（理化学研究所），牧 功一郎（京都大学）
Organizers: Hirofumi Shintaku (RIKEN), Koichiro Maki (Kyoto Univ.)

08:50〜11:20

M 会場（会議室 232+233（2 号館 3F））／Room M（Conference Room 232+233 (Bldg. 2, 3F)）

The mechanical phenotype of cells is a key biophysical property that arises from the intracellular states at the molecular level and is associated with cellular function. In multiple cellular contexts, the mechanical phenotypes are coordinated for autonomous morphogenesis and functional maturation. In this symposium, we invite researchers from various fields, including engineering, computational biology, and basic biology, and showcase research attempts that focus on the mechanical phenotype for diagnosis purposes and for dissecting the dynamics of biological systems.

2SMA-1　筋細胞の方向を制御する生体力学的なメカニズム
DIRECTIONALITY OF DEVELOPING SKELETAL MUSCLES IS SET BY MECHANICAL FORCES
Kazunori Sunadome[11,12], Alek G Erickson[1], Delf Kah[2], Ben Fabry[2], Csaba Adori[3], Shigeaki Kanatani[4], Polina Kameneva[5], Louis Faure[5], Marketa Kaucka[6], Ivar Dehnisch Ellström[7], Marketa Tesarova[8], Tomas Zikmund[8], Jozef Kaiser[8], Steven Edwards[9], Koichiro Maki[10], Taiji Adachi[10], Takuya Yamomoto[11,12], Kaj Fried[3], Igor Adameyko[1,5] ([1]*Department of Physiology and Pharmacology, Karolinska Institutet*, [2]*Department of Physics, University of Erlangen-Nuremberg*, [3]*Department of Neuroscience, Karolinska Institutet*, [4]*Department of Medical Biochemistry and Biophysics, Division of Molecular Neurobiology, Karolinska Institutet*, [5]*Department of Neuroimmunology, Center for Brain Research, Medical University Vienna*, [6]*Max Planck Institute for Evolutionary Biology*, [7]*Spinalis Foundation*, [8]*Central European Institute of Technology, Brno University of Technology*, [9]*KTH Royal Institute of Technology*, [10]*Department of Biosystems Science, Institute for Life and Medical Sciences, Kyoto University*, [11]*Institute for the Advanced Study of Human Biology (ASHBi), Kyoto University*, [12]*Center for iPS Cell Research and Application, Kyoto University*)

2SMA-2　Mechanical behaviors of nuclear chromatin in chondrocytes under hydrostatic pressure
Koichiro Maki (*Inst. Life Med. Sci., Kyoto University*)

2SMA-3　形態形成を不可逆に進行させる上皮折りたたみの力学的可塑性
Mechanical Plasticity of Epithelial Folding for Irreversible Progression of Morphogenesis
○奥田 覚（金沢大学ナノ生命科学研究所）
Satoru Okuda (*Nano Life Science Institute, Kanazawa University*)

2SMA-4　病気を診断するために細胞を絞る
Squeezing cells to diagnose disease
Dino Di Carlo (*Department of Bioengineering, UCLA*)

2SMA-5　ナノポアエレクトロポレーションを活用した細胞表面張力と遺伝子発現の 1 細胞解析
Nanopore electroporation enables profiling cell surface tension and gene expression at single-cell resolution
○新宅 博文 [1,2], 塩見 晃史 [2], 金子 泰洸ポール [2], 西川 香里 [2]（[1] 京大・医生研, [2] 理研・開拓）
Hirofumi Shintaku[1,2], Akifumi Shiomi[2], Taikopaul Kaneko[2], Kaori Nishikawa[2] ([1]*LiMe, Kyoto Univ*, [2]*CPR, RIKEN*)

2SAP　分子の集合からシステムへ、そして生命へ：高解像な生命の起源研究
From molecules to systems, and eventually to life: high resolution Origins of Life research

オーガナイザー：Tony Z. Jia（Tokyo Tech），車 兪澈（海洋研究開発機構）
Organizers: Tony Z. Jia (Tokyo Tech), Yutetsu Kuruma (JAMSTEC)

14:00〜16:30
A 会場（展示室 211（2 号館 1F））／Room A（Exhibition Room 211 (Bldg. 2, 1F)）

Life began from a mixture of chemicals in the early Earth environment, and eventually resulted in the emergence of functional cells by passing through intermediates such as assemblies and systems. However, nearly every aspect of this historical transition leading to the emergence of life remains unsolved. In this symposium, we will highlight research focusing on each step of the origins of life, with an attempt to develop and increase the resolution of origins of life studies to more accurately reveal the step-wise transition from non-life to life.

はじめに
Opening Remarks

2SAP-1 **相分離液滴の人工細胞としての活用：細胞構造と運動の協奏**
Reproduction of cell structure and motility using cell-sized droplets in an aqueous two-phase system
○柳澤 実穂（東大総合文化・先進）
Miho Yanagisawa (*Komaba Inst., Univ. Tokyo*)

2SAP-2 Spectroscopic and Biophysical Methods to Determine Differential Salt-Uptake by Primitive Membraneless Polyester Microdroplets
Chen Chen[1,2], Ruiqin Yi[2], Motoko Igisu[3], Chie Sakaguchi[4], Rehana Afrin[2], Christian Potiszil[4], Tak Kunihiro[4], Katsura Kobayashi[4], Eizo Nakamura[4], Yuichiro Ueno[2,5], Andre Antunes[6,10], Anna Wang[7], Kuhan Chandru[8], Jihua Hao[9], Tony Z. Jia[2,10] ([1]*RIKEN Center for Sustainable Resource Science*, [2]*Earth-Life Science Institute, Tokyo Institute of Technology*, [3]*Institute for Extra-cutting-edge Science and Technology Avant-garde Research (X-star), JAMSTEC*, [4]*The Pheasant Memorial Laboratory for Geochemistry and Cosmochemistry, Okayama University*, [5]*Department of Earth and Planetary Sciences, Tokyo Institute of Technology*, [6]*State Key Laboratory of Lunar and Planetary Sciences, MUST*, [7]*School of Chemistry, UNSW Sydney*, [8]*Space Science Center (ANGKASA), National University of Malaysia*, [9]*CAS Laboratory of Crust-Mantle Materials and Environments, University of Science and Technology of China*, [10]*Blue Marble Space Institute of Science*)

2SAP-3 **凍結融解サイクルによる DNA 連結反応の効率化と生体情報分子の伸長環境への示唆**
Effective DNA hybridization via freeze-thaw cycles and implication for prebiotic formation of large information molecules
○野田 夏実 [1], 高橋 南帆 [2], 野村 浩平 [2], 橋谷 文貴 [3], 阿部 洋 [2,3,4], 松浦 友亮 [1]（[1] 東京工業大学 地球生命研究所, [2] 名古屋大学 大学院理学研究科, [3] 名古屋大学 物質科学国際研究センター, [4] 名古屋大学 統合糖鎖研究拠点 iGCORE, 糖鎖生命コア研究拠点）
Natsumi Noda[1], Naho Takahashi[2], Kohei Nomura[2], Fumitaka Hashiya[3], Hiroshi Abe[2,3,4], Tomoaki Matsuura[1] ([1]*Earth-Life Science Institute (ELSI), Tokyo Institute of Technology*, [2]*Graduate School of Science, Nagoya University*, [3]*Research Center for Material Science, Nagoya University*, [4]*Institute for Glyco-core Research (iGCORE), Nagoya University*)

2SAP-4 Protocell interaction dynamics: Implications for the survival of the 'fittest'?
Souradeep Das, **Sudha Rajamani** (*Department of Biology, IISER Pune*)

2SAP-5 **分子進化におけるアミノ酸の網羅的な変異分布の冪乗法による解析**
Power-method analysis of the exhaustive distribution of amino acid mutations in molecular evolution
○大森 環, 山中 雅則（日大・理工）
Kan Omori, Masanori Yamanaka (*CST, Nihon Univ.*)

2SAP-6 **複数のサブシステムから構成される人工細胞**
Functional expression in artificial cell system composed of multi-subsystems
○車 兪澈 [1], 江藤 澄江 [2], 松村 るみゑ [1], 嶋根 康弘 [1], ベルハヌ サミュエル [2], 笠間 健嗣 [2], 藤見 麻衣 [2]（[1] 海洋研究開発機構, [2] 東京工業大学）
Yutetsu Kuruma[1], Sumie Eto[2], Rumie Matsumura[1], Yasuhiro Shimane[1], Samuel Berhanu[2], Takeshi Kasama[2], Mai Fujimi[2] ([1]*Japan Agency for Marine-Earth Science and Technology*, [2]*Tokyo Institute of Technology*)

おわりに
Closing Remarks

2SBP　高次ゲノム構造揺らぎとその機能
Higher-order structural fluctuations in the genome and their functions

オーガナイザー：落合 博（九州大学），新海 創也（理化学研究所）
Organizers: Hiroshi Ochiai (Kyushu Univ.), Soya Shinkai (RIKEN)

14:00〜16:30
B 会場（展示室 212（2 号館 1F））／Room B（Exhibition Room 212 (Bldg. 2, 1F)）

Genomic DNA contains the information necessary for the development and maintenance of living organisms, and forms cell-type-specific higher-order structures while exhibiting dynamic behavior. Recent studies, which employ live-cell imaging and mathematical and physical simulations, have revealed that these fluctuations in higher-order genomic structure play biological roles. In this symposium, experts in the field will present their latest research findings and discuss the functions of fluctuations in higher-order genomic structures.

はじめに
Opening Remarks

2SBP-1　細胞内のユークロマチンは本当にオープン構造か？
Is euchromatin really open in the cell ?-Condensed but liquid-like domain organization of active chromatin regions in living human cells
○前島 一博 [1,2]（[1] 国立遺伝学研究所, [2] 総研大）
Kazuhiro Maeshima[1,2] ([1]*National Institute of Genetics*, [2]*SOKENDAI*)

2SBP-2　Histone FRET microscopy of live cell genome architecture
Elizabeth Hinde (*School of Physics, University of Melbourne*)

2SBP-3　Polymer physics of Hi-C data reveals linear viscoelasticity of the 3D genome
Soya Shinkai, Shuichi Onami (*RIKEN BDR*)

2SBP-4　Computer simulations on mechanical influence of molecular actions to chromatin organization and dynamics
Rakesh Das[2], Takahiro Sakaue[3], Gv Shivashankar[4,5], Jacques Prost[2,6], **Tetsuya Hiraiwa[1,2]** ([1]*Institute of Physics, Academia Sinica*, [2]*Mechanobiology Institute, National University of Singapore*, [3]*Department of Physics and Mathematics, Aoyama Gakuin University*, [4]*ETH Zurich, Switzerland*, [5]*Paul Scherrer Institute*, [6]*Laboratoire Physico Chimie Curie, Institut Curie*)

2SBP-5　Meiotic pairing via rapid homolog juxtaposition in budding yeast
Tadasu Nozaki, Beth Weiner, Nancy Kleckner (*Harvard University, MCB*)

2SBP-6　転写バーストサイクル過程で変化する高次ゲノム構造
Higher-order genomic structures transformed during the transcription burst cycle
○落合 博（九大・生医研・遺伝子発現動態）
Hiroshi Ochiai (*Div. of Gene Exp. Dyna., MIB, Kyushu Univ.*)

2SBP-7　Chromatin dynamics and the role of RNA polymerase II
Lea Costes[1], Silvia Kocanova[1], Thomas Mangeat[1], Manoel Manghi[2], **Kerstin Bystricky[1]** ([1]*Molecular Cellular and Developmental biology unit, Center for Integrative Biology (CBI), University of Toulouse, CNRS, Toulouse, France*, [2]*Laboratoire de Physique Théorique (LPT), University of Toulouse, CNRS, Toulouse, France*)

おわりに
Closing Remarks

2SCP　シン・合成生物学：既存生命のみに依拠しないシステム創成に向けた化学者からの提案
Material-driven biomimetic systems for a new paradigm of synthetic biology

オーガナイザー：岸村 顕広（九州大学），金原 数（東京工業大学）
Organizers: Akihiro Kishimura (Kyushu Univ.), Kazushi Kinbara (Tokyo Tech.)

14:00〜16:30
C 会場（会議室 221（2 号館 2F））／Room C（Conference Room 221 (Bldg. 2, 2F)）

Synthetic biology has recently made remarkable progress and is expected to be a discipline that will innovate medicine, agriculture, and industries. From the viewpoint of material sciences, however, the current synthetic biology seems to target systems that can work only under limited conditions within a very limited material framework allowed on our planet. In this symposium, we aim to discuss the synthesis of living creatures and the creation of new systems beyond the framework of existing organisms on Earth. We invite up-and-coming material scientists as speakers to build a new paradigm of synthetic biology and bring a new perspective to biophysics. We are convinced that this symposium will help to enable the evolution of living creatures beyond the framework of conventional biology and for the creation of life as yet unseen.

はじめに
Opening Remarks

2SCP-1　合理的に設計された合成コアセルベートに基づくタンパク質取り込み活性を有する人工非膜オルガネラの開発
Development of artificial membraneless organelle with protein sequestration activity based on rationally designed synthetic coacervates
○岸村 顕広 [1,2,3]（[1] 九州大学大学院工学研究院応用化学部門, [2] 九州大学分子システム科学センター, [3] 九州大学未来化学創造センター）
Akihiro Kishimura[1,2,3] ([1]*Kyushu University, Department of Applied Chemistry, Faculty of Engineering*, [2]*Kyushu University, Center for Molercular Systems*, [3]*Kyushu University, Center for Future Chemistry*)

2SCP-2　化学反応制御の液液相分離：化学者視点から考案した合成低分子ペプチドの合理的設計と機能発現
Chemical design of synthetic short peptides toward reaction-controlled liquid-liquid phase separation
○窪田 亮（京大・院工）
Ryou Kubota (*Grad. Sch. Eng., Kyoto Univ.*)

2SCP-3　脂質ベシクルと金属化合物の融合による生体模倣システムの構築
Construction of biomimetic system by hybridization of lipid vesicles and metal compounds
○越山 友美（立命館大 生命科学）
Tomomi Koshiyama (*Coll. Life Sci., Ritsumeikan Univ.*)

2SCP-4　Phospholipid Bilayer Surrounded by Amphipathic DNA Double-decker Ring as Synthetic Membrane Model for Membrane Proteins Study
Seaim Lwin Aye[1], Thorsten Schmidt[2], Yusuke Sato[1] ([1]*Department of Intelligent and Control Systems, Graduate School of Computer Science and Systems Engineering, Kyushu Institute of Technology, Iizuka, Fukuoka, JAPAN 820-2502*, [2]*Department of Physics, Kent State University, Kent, OH 44242, USA*)

2SCP-5　無機ナノシートを利用した生体模倣システムの構築
Development of biomimetic systems using inorganic nanosheets
○佐野 航季（信州大・繊維学部）
Koki Sano (*Fac. of Textile Sci. and Tech., Shinshu Univ.*)

2SCP-6 Synthesized micro-materials for self-sustainable works: Morphologies of active-molecule assemblies alter the apparent reaction kinetics
○景山 義之（北大・院理）
Yoshiyuki Kageyama (*Fac. Sci., Hokkaido Univ.*)

おわりに
Closing Remarks

2SDP 分子イメージングが切り拓く細胞外微粒子研究
Extracellular Fine Particle Research facilitated by State-of-the-Art Microscopy Techniques

共催 JST/CREST「細胞外微粒子」

オーガナイザー：鈴木 健一（岐阜大学/国立がん研究センター研究所），
末次 志郎（奈良先端科学技術大学院大学）
Organizers: Kenichi Suzuki (Gifu Univ./NCC), Shiro Suetsugu (NIAST)

14:00〜16:30
D 会場（会議室 222+223（2 号館 2F））／Room D（Conference Room 222+223 (Bldg. 2, 2F)）

Extracellular fine particles including exogenous fine particle such as PM2.5 and endogenous fine particles such as extracellular vesicles (EVs) including exosomes, have generated significant attention due to their ability to induce crucial biological responses. For instance, EVs serve as mediators of intercellular communication. However, due to the heterogeneity of extracellular fine particles and the difficulty of separation, the molecular mechanisms underlying biological responses to these particles and their dynamics have been very controversial. To elucidate these mechanisms, it is imperative to characterize individual extracellular fine particles in living cells by microscopy. This symposium aims to focus on studies that uncover the behavior of extracellular fine particles by cutting-edge imaging techniques such as single-molecule/super-resolution imaging, lattice-light sheet microscopy, and scanning electron-assisted dielectric microscopy.

2SDP-1 The BAR domain assembly and the extracellular vesicle formation from cellular protrusions
Shiro Suetsugu (*Grad Sch Sci Tech, NAIST*)

2SDP-2 小胞による細胞間コミュニケーションの新しい様式と役割ー隣接細胞間直接輸送と細胞形質同調ー
Novel mode and roles of vesicle-mediated cellular communication - direct intercellular transfer and phenotypic synchronization -
○山下 潤（東大・院医学）
Jun K. Yamashita (*Grad. Sch. Med., Univ. Tokyo*)

2SDP-3 走査電子誘電率顕微鏡による細胞内のメラニン色素小胞の直接観察と画像解析
Direct observation of intracellular melanosomes using scanning electron dielectric microscopy and the image analysis
○小椋 俊彦, 岡田 知子（産総研・健康医工学研究部門）
Toshihiko Ogura, Tomoko Okada (*Health and Medical Research Institute, Nat. Inst. Adv. Ind. Sci. Tech. (AIST)*)

2SDP-4　細胞外小胞が誘起する接着シグナルが、標的細胞によるそれ自身の取り込みを促進する
Small extracellular vesicles trigger adhesion signaling that facilitates their uptake by the target cells
○廣澤 幸一朗 [1], 佐藤 雄介 [2], 山口 英利子 [1], 河村 奈穂子 [1], 安藤 弘宗 [1], 横田 康成 [3], 鈴木 健一 [1,4,5]（[1] 岐大・糖鎖生命コア研究所, [2] 東北大・院理・化学, [3] 岐大・工・電情, [4]CREST, JST, [5] 国立がん研究センター・研究所）
Koichiro M. Hirosawa[1], Yusuke Sato[2], Eriko Yamaguchi[1], Naoko Komura[1], Hiromune Ando[1], Yasunari Yokota[3], Kenichi G.N. Suzuki[1,4,5] ([1]*iGCORE, Gifu Univ.*, [2]*Dept. Chem. Tohoku Univ.*, [3]*Dept. Eng., Gifu Univ.*, [4]*CREST, JST*, [5]*Natl. Cancer Ctr. Res. Inst.*)

2SDP-5　進化した aifA を用いたエクソソームの不均一性の高精度解明
High-precision elucidation of exosome heterogeneity using advanced aifA
○許 岩 [1,2]（[1] 大阪公立大・院工, [2]JST・CREST）
Yan Xu[1,2] ([1]*Grad. Sch. Eng., Osaka Metropolitan Univ.*, [2]*JST, CREST*)

2SDP-6　両親媒性 α-helix ペプチドによる高曲率性膜認識を利用した細胞外小胞解析プローブの設計と応用
Amphipathic helical peptide-based fluorescent probes with membrane curvature-sensing properties for analysis of extracellular vesicles
○佐藤 雄介（東北大院理）
Yusuke Sato (*Graduate School of Science, Tohoku Univeristy*)

2SEP　構造・計算・分光研究から解明する光受容性タンパク質の非平衡状態ダイナミクス
Unraveling the non-equilibrated dynamics of photoreceptive proteins by structural, theoretical, and spectroscopic investigations

共催 新学術領域研究「高速分子動画」

オーガナイザー：山元 淳平（大阪大学），片山 哲郎（徳島大学）
Organizers: Junpei Yamamoto (Osaka Univ.), Tetsuro Katayama (Tokushima Univ.)

14:00〜16:30
E 会場（会議室 224（2 号館 2F））／Room E（Conference Room 224 (Bldg. 2, 2F)）

Time-resolved serial femtosecond crystallography (TR-SFX) using X-ray free electron laser can capture transient structures of proteins at work and thus is a powerful strategy to make Molecular Movies. However, complementary techniques are also required to interpret the obtained data and decipher the structural dynamics at an atomic resolution. In this symposium, we focus on the nonequilibrated dynamics of photoreceptive proteins revealed by various techniques, such as structural analyses, theoretical calculations, and time-resolved spectroscopy. We will discuss the latest outcomes and the future of time-resolved structural analyses including TR-SFX.

はじめに
Opening Remarks

2SEP-1　光合成タンパク質における励起エネルギー移動の計算機シミュレーション
Computational Simulations of Excitation Energy Transfers in Photosynthetic Proteins
○鬼頭 宏任 [1], 下岡 渉 [2], 伊藤 繁 [2], 木村 明洋 [2]（[1] 近畿大・理工・エネ物, [2] 名大院・理・物理）
Hirotaka Kitoh[1], Wataru Shimooka[2], Shigeru Itoh[2], Akihiro Kimura[2] ([1]*Dept. eMAT, Fac. Sci. Eng., Kindai Univ.*, [2]*Dept. Phys. Grad. Sch. Sci., Nagoya Univ.*)

2SEP-2 **光合成アンテナ蛋白質フィコシアニンにおける光エネルギー移動の構造研究**
Structural Study of Antenna Protein Phycocyanin in Photosynthetic Light Energy Transfer
○梅名 泰史 [1], 片山 哲郎 [2,3,4], 高山 友理子 [5], 中根 崇智 [6]（[1] 名古屋大・シンクロ, [2] 徳島大・ポスト LED フォトニクス研, [3] 徳島大・院創成科学理工, [4]JST 創発, [5] 自治医科大・生物物理, [6] 大阪大・蛋白研）
Yasufumi Umena[1], Tetsuro Katayama[2,3,4], Yuriko Takayama[5], Takanori Nakane[6] ([1]*NUSR, Nagoya Univ.*, [2]*Inst. of post-LED Photonics, Univ. Tokushima*, [3]*Grad. Sch. Tech. Innov., Univ. Tokushima*, [4]*FOREST/JST*, [5]*Div. of Biophysics., Aichi Medical Univ.*, [6]*Inst. for Protein Research, Osaka Univ.*)

2SEP-3 **フェムト秒顕微過渡吸収分光法を用いた単一結晶中フィコシアニン三量体間のエネルギー移動反応の観測**
Observation of energy transfer dynamics between phycocyanin trimmers in a single crystal by femtosecond transient absorption microscopy
○片山 哲郎 [1,2,4], 上田 柊斗 [2], 古部 昭広 [1,2], 梅名 泰史 [3]（[1] 徳島大・ポスト LED フォトニクス研究所, [2] 徳島大・大学院創成科学研究科理工学専攻, [3] 名古屋大・シンクロトロン光研究センター, [4]JST 創発）
Tetsuro Katayama[1,2,4], Shuto Ueda[2], Akihiro Furube[1,2], Yasufumi Umena[3] ([1]*Institute of post-LED Photonics, Univ. Tokushima*, [2]*Grad. Sch. Sci. Tech. Innov., Univ. Tokushima*, [3]*Synchrotron Radiation Research Center, Univ. Nagoya*, [4]*FOREST/JST*)

2SEP-4 **非断熱 QM/MM 分子動力学計算法の開発と光駆動タンパク質への応用**
Development of non-adiabatic QM/MM molecular dynamics method and applications to light-driven proteins
○八木 清（理化学研究所開拓研究本部）
Kiyoshi Yagi (*RIKEN CPR*)

2SEP-5 **レチナール発色団のねじれとプロトン化が制御するチャネルロドプシン C1C2 のゲーティング機構**
Twisting and Protonation of Retinal Chromophore Regulate Channel Gating of Channelrhodopsin C1C2
○柴田 桂成 [1], 小田 和正 [2], 西澤 知宏 [2], 挾間 優治 [1], 小野 稜平 [1,3], 寶本 俊輝 [1], Reza Bagherzadeh[1], 八尾 寛 [1], 濡木 理 [2], 井上 圭一 [1], 秋山 英文 [1]（[1] 東大物性研, [2] 東大・院理, [3] 群大・院理工）
Keisei Shibata[1], Kazumasa Oda[2], Tomohiro Nishizawa[2], Yuji Hazama[1], Ryohei Ono[1,3], Shunki Takaramoto[1], Bagherzadeh Reza[1], Hiromu Yawo[1], Osamu Nureki[2], Keiichi Inoue[1], Hidefumi Akiyama[1] ([1]*ISSP., Univ. Tokyo*, [2]*Grad. Sch. Sci., Univ. Tokyo*, [3]*Grad. Sch. Sci. & Tech., Gunma Univ.*)

2SEP-6 The *ic*OS Lab at the ESRF: preparing and complementing time-resolved crystallography experiments with *in crystallo* optical spectroscopy
Antoine Royant[1,2] ([1]*Institut de Biologie Structurale, Grenoble, France*, [2]*European Synchrotron Radiation Facility, Grenoble, France*)

2SEP-7 Time-resolved serial femtosecond crystallography on animal-like cryptochrome from *Chlamydomonas reinhardtii*
Yuhei Hosokawa[1,2,3], Mai Nakamura[2], Junpei Yamamoto[2], Manuel Maestre-Reyna[1,3] ([1]*IBC, Academia Sinica*, [2]*Grad. Sch. Eng. Sci., Osaka Univ.*, [3]*Dept. Chem., National Taiwan Univ.*)

2SFP　多様なリズム現象から探る概日時計研究の行方
Future Direction of Circadian Clock Research from the Viewpoint of Diverse Rhythmic Phenomena

オーガナイザー：秋山 修志（分子科学研究所），寺内 一姫（立命館大学）
Organizers: Shuji Akiyama (IMS), Kazuki Terauchi (Ritsumeikan Univ.)

14:00〜16:30
F 会場（会議室 231（2 号館 3F））／Room F（Conference Room 231 (Bldg. 2, 3F)）

Circadian clocks have three common characteristics: free-running oscillations, temperature compensation, and entrainment. While molecular bases for these three properties are being elucidated, the nature of the core oscillator and its diversity remain largely unexplored, and are being actively studied from approaches such as physiology, biophysics, and structural biology. In addition, in response to the growing interest in a style of "create to understand", some research is also being conducted from the perspective of how well sophisticated properties such as circadian clocks can be granted to soft matter. In this symposium, considering complex diversity and commonality found in cyanobacteria, duckweed, and artificial gels, we would like to discuss future approaches to elucidate the circadian clock systems.

はじめに
Opening Remarks

2SFP-1　KaiCI の ATPase 活性が概日振動の最も基礎的な原動力である
ATPase activity of KaiC-CI is the most fundamental process of circadian oscillator of cyanobacteria
○近藤 孝男 [1], 伊藤 – 三輪 久美子 [1], 寺内 一姫 [2]（[1] 名古屋大学, [2] 立命館大学）
Takao Kondo[1], Kumiko Ito-Miwa[1], Kazuki Terauchi[2] ([1]*Nagoya University*, [2]*Ristumeikan University*)

2SFP-2　Activation mechanism of a clock protein KaiC by KaiA
Yasuhiro Onoue, Tomoki Noguchi, Genta Mizuno, Kazuki Terauchi (*Coll. Life Sci., Ritsumeikan Univ.*)

2SFP-3　ウキクサ植物でみられる細胞非自律的な概日リズム
A non-cell-autonomous circadian rhythm in duckweed plant
○渡邊 絵美理 [1], 村中 智明 [2], 中村 駿志 [3], 磯田 珠奈子 [4], 堀川 湧 [5], 相磯 豪志 [5], 伊藤 照悟 [5], 小山 時隆 [5]（[1] 東京大・院新領域, [2] 名古屋大・院生命農学, [3] 東京大・院理, [4] 県立広島大・生物資源科学, [5] 京都大・院理）
Emiri Watanabe[1], Tomoaki Muranaka[2], Shunji Nakamura[3], Minako Isoda[4], Yu Horikawa[5], Tsuyoshi Aiso[5], Shogo Ito[5], Tokitaka Oyama[5] ([1]*Grad. Sch. of Front. Sci., Univ. of Tokyo*, [2]*Grad. Sch. Bioagric. Sci., Nagoya Univ.*, [3]*Grad. Sch. Sci., Univ. of Tokyo*, [4]*Dept. of Bio. Res. Sci., Pref. Univ. of Hiroshima*, [5]*Grad. Sch. Sci., Kyoto Univ.*)

2SFP-4　化学振動ゲルの温度補償機構
Temperature-compensation mechanism of chemical oscillation in gels
○山田 雄平 [1], 伊藤 浩史 [2], 前田 真吾 [1]（[1] 東京工業大学, [2] 九州大学）
Yuhei Yamada[1], Hiroshi Ito[2], Shingo Maeda[1] ([1]*Tokyo Institute of Technology*, [2]*Kyushu University*)

2SFP-5　KaiC の ATPase 制御がシアノバクテリア時計タンパク質の会合と解離を引き起こす
ATPase Regulation in KaiC Triggers Assembly and Disassembly of Clock Proteins in Cyanobacteria
○古池 美彦 [1,2], 秋山 修志 [1,2]（[1] 分子科学研究所, [2] 総合研究大学院大学）
Yoshihiko Furuike[1,2], Shuji Akiyama[1,2] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*)

おわりに
Closing Remarks

2SGP GPCR ダイナミクスの全体像
Holistic concepts in GPCR dynamics

オーガナイザー：片山 耕大（名古屋工業大学），寿野 良二（関西医科大学）
Organizers: Kota Katayama (Nagoya Inst. of Tech.), Ryoji Suno (Kansai Medical Univ.)

14:00〜16:30
G 会場（会議室 232+233（2 号館 3F））／Room G（Conference Room 232+233 (Bldg. 2, 3F)）

Tremendous advances in the structural biology and pharmacology of GPCRs, coupled with rapid advances in computational approaches, have expanded our understanding of both structural and functional aspects of GPCR dynamics and GPCR-ligand or partner protein interactions, providing guidance for new structure-based drug design. The goal of this symposium is to expose scientists to recent discoveries and cross-disciplinary approaches utilized to study GPCRs and provide opportunities for establishing communications that bridge complementary interests in the field of GPCRs. This session will feature speakers who have made exciting discoveries about the molecular mechanisms of GPCRs and partner proteins involved in signal transduction by utilizing spectroscopic, structural biology, single molecule observations, and computational chemistry approaches.

2SGP-1 Structural insights into human kappa opioid receptor signaling by biased ligand
Chiyo Suno-Ikeda[1], **Ryoji Suno[1]**, Ryo Nishikawa[2], Riko Suzuki[3], Seiya Iwata[2], Tomoyo Takai[1], Takaya Ogura[3], Mika Hirose[4], Akitoshi Inoue[1], Eri Asai[1], Ryoji Kise[3], Yukihiko Sugita[5], Tsuyoshi Saito[6], Kota Katayama[2], Asuka Inoue[3], Takayuki Kato[4], Hiroshi Nagase[6], Hideki Kandori[2], Takuya Kobayashi[1] ([1]*Dept. Med., Kansai Med. Univ.*, [2]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [3]*Grad. Sch. Pharm. Sci., Tohoku Univ.*, [4]*IPR, Osaka Univ.*, [5]*LiMe, Kyoto Univ.*, [6]*IIIS, Tsukuba Univ.*)

2SGP-2 NOAH: NOvel AI-assisted High-throughput construct screening for structural analysis
Hideaki Kato (*Univ. Tokyo*)

2SGP-3 G タンパク質と β アレスチンが協奏する GPCR 下流の ERK シグナル伝達
Co-regulation of GPCR-mediated ERK signaling by G protein and β-arrestin
○柳川 正隆 [1,2]（[1] 東北大・院薬, [2] 理研・開拓）
Masataka Yanagawa[1,2] ([1]*Grad. Sch. Pharm., Tohoku Univ.*, [2]*Riken, CPR*)

2SGP-4 分子動力学シミュレーションを用いた GPCRs の安定性とダイナミクスの解析
Investigating Stability and Dynamics of Class A GPCRs using Molecular Dynamics Simulations
○光武 亜代理（明大・物理）
Ayori Mitsutake (*Dept. Physics, Meiji Univ.*)

2SGP-5 Vibrational spectroscopy analyses of ligand recognition and activation mechanisms in G protein-coupled receptors
Kota Katayama[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*OptoBioTechnology Research Center., Nagoya Inst. Tech.*)

2SHP　クライオ電顕を用いたユニークな生体分子構造決定の試み
Challenging structural determination of unique biomolecules using cryo-electron microscopy

オーガナイザー：山本 直樹（自治医科大学），バートンースミス レイモンド（生理学研究所）
Organizers: Naoki Yamamoto (Jichi Medical Univ.), Raymond N. Burton-Smith (NIPS)

14:00〜16:30
H 会場（会議室 234（2 号館 3F））／Room H（Conference Room 234 (Bldg. 2, 3F)）

Cryo-electron microscopy is a powerful tool to determine structures of biomolecules. Especially, it is suitable for those which are difficult to be crystallized such as flexible virus capsids, fibrils, or membrane proteins. In this symposium, young scientists challenging to solve structures of such complicated biomolecules will present their recent results. We will discuss how to solve problems that we encounter in the sample preparation and single-particle analysis.

はじめに
Opening Remarks

2SHP-1　電子顕微鏡を用いたアミロイド線維構造の研究
Electron microscopy of amyloid fibril structures
○山本 直樹（自治医大・医）
Naoki Yamamoto (*Sch. Med., Jichi Med. Univ.*)

2SHP-2　Structural analysis of artificially designed peptide nanofibers by cryo-electron microscopy
Minami Kurokawa[1], Akihiro Kawamoto[2], Mika Hirose[2], Atsuo Tamura[1] ([1]*Grad. Sch. Sci., Univ. Kobe*, [2]*IPR, Univ. Osaka*)

2SHP-3　Cryo-EM structures of human zinc transporter ZnT7 reveal the mechanism of Zn^{2+} uptake into the Golgi apparatus
Ba Han Bui[1,2], Satoshi Watanabe[1,2,3], Kenji Inaba[1,2,3,4,5] ([1]*IMRAM, Tohoku Univ.*, [2]*Dept. Mol. Chem. Life Sci., Grad. Sch. Life Sci., Tohoku Univ.*, [3]*Dept. Chem., Grad. Sch. Life Sci., Tohoku Univ.*, [4]*Med. Inst. Bioregulation, Kyushu Univ.*, [5]*CREST, AMED*)

2SHP-4　シチジン修飾を持つイソロイシン tRNA による遺伝暗号解読の構造基盤
Structural insights into the decoding capability of isoleucine tRNAs with cytidine modification
○秋山 奈穂 [1], 石黒 健介 [1,2], 横山 武司 [2,3], 宮内 健常 [1], 長尾 翌手可 [1], 白水 美香子 [2], 鈴木 勉 [1] ([1] 東大・院工, [2] 理研 BDR・横浜, [3] 東北大・院生命科学）
Naho Akiyama[1], Kensuke Ishiguro[1,2], Takeshi Yokoyama[2,3], Kenjyo Miyauchi[1], Asuteka Nagao[1], Mikako Shirouzu[2], Tsutomu Suzuki[1] ([1]*Grad. Sch. Eng., UTokyo*, [2]*Yokohama Inst., RIKEN BDR*, [3]*Grad. Sch. Life Sci., Tohoku Univ.*)

2SHP-5　ヘム含有型酸素センサータンパク質 HemAT における構造解析の試み
Challenges in the structural analysis of the heme-based oxygen sensor protein HemAT
○東田 怜 [1], 村木 則文 [2], 横山 武司 [3], 奥村 英夫 [4], 馬場 清喜 [4], 河野 能顕 [5], 青野 重利 [1] ([1] 自然科学生命創成, [2] 慶應大 理工, [3] 東北大 生命, [4]JASRI, [5] 理研 RSC）
Rei Tohda[1], Norifumi Muraki[2], Takeshi Yokoyama[3], Hideo Okumura[4], Seiki Baba[4], Yoshiaki Kawano[5], Shigetoshi Aono[1] ([1]*ExCELLS, NINS*, [2]*Dep. of Chem., Keio Univ.*, [3]*Grad. Sch. of Life Sciences., Tohoku Univ.*, [4]*JASRI*, [5]*RIKEN SPring-8 Center*)

2SHP-6　The challenge of studying giant viruses by cryo-electron microscopy
Raymond Burton-Smith[1,2] ([1]*Exploratory Center for Life and Living Systems (ExCELLS), National Institute of Natural Sciences, Okazaki*, [2]*National Institute of Physiological Sciences, National Institute of Natural Sciences, Okazaki*)

おわりに
Closing Remarks

2SIP　液液相分離の生物物理学的研究の最前線
The forefront of biophysical research of liquid-liquid phase separation

オーガナイザー：亀田 倫史（産業技術総合研究所），鎌形 清人（東北大学）
Organizers: Tomoshi Kameda (AIST), Kiyoto Kamagata (Tohoku Univ.)

14:00〜16:30
I 会場（国際会議室（3 号館 3F））／Room I（International Conference Room (Bldg. 3, 3F)）

In this symposium, we focus on five presentations for introducing the current progress of liquid-liquid phase separation of biomolecules or biomolecular systems. The presenters cover various approaches such as single-molecule microscopy, rheology, and molecular dynamics simulations. In addition, wide topics are discussed including enzymatic reactions in condensates, phase separating peptide design, and dynamics of molecules in condensates.

はじめに
Opening Remarks

2SIP-1　DNA 液滴での DNA 結合タンパク質の単分子解析および相分離ペプチドの合理的設計
Single-molecule characterization of DNA-binding proteins in DNA droplets and rational design of artificial phase separating peptides
○鎌形 清人（東北大・多元研）
Kiyoto Kamagata (*IMRAM, Tohoku Univ.*)

2SIP-2　Regulation of Biomolecular Condensation Studied with Large-Scale Coarse-Grained Molecular Dynamics Simulations in GENESIS
Cheng Tan[1], Ai Niitsu[2], Jaewoon Jung[1,2], Yuji Sugita[1,2,3] ([1]*Computational Biophysics Research Team, RIKEN Center for Computational Science*, [2]*Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research*, [3]*Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research*)

2SIP-3　Membraneless active droplets mimic features of living systems
Bevilacqua Alessandro[1], Dindo Mirco[2], Soligo Giovanni[1], Rosti Marco Edoardo[1], Laurino Paola[1] ([1]*Okinawa Institute of Science and Technology*, [2]*University of Perugia*)

2SIP-4　解糖系酵素の液-液相分離
Liquid-liquid phase separation of glycolytic enzymes
○三浦 夏子（大阪公立大・院農）
Natsuko Miura (*Grad. Sch. Agric., Osaka Metropolitan Univ.*)

2SIP-5　液ー液相分離で形成されたオートファジー関連凝集体のマイクロレオロジー
Microrheology of aging autophagy-related aggregates formed by liquid-liquid phase separation
Daisuke Mizuno[1], Kairi Tomita[1], Makoto Fujiwara[1], Haruka Chino[2], Norr Roland[2], Noboru Mizushima[2] ([1]*Kyushu University*, [2]*Tokyo University*)

おわりに
Closing Remarks

2SJP　高解像度な細胞・微粒子解析テクノロジーの最前線
The forefront of high-resolution cell and bioparticle analysis technology
共催 JST/CREST「細胞外微粒子」

オーガナイザー：太田 禎生（東京大学），渡邊 力也（理化学研究所）
Organizers: Sadao Ota (The Univ. of Tokyo), Rikiya Watanabe (RIKEN)

14:00〜16:30
J 会場（会議室 141+142（1 号館 4F））／Room J（Conference Room 141+142 (Bldg. 1, 4F)）

Science and technology feed each other, mutually driving progress in both fields. This symposium assembles leading developers and adopters of cutting-edge technology focused on cell-based, extracellular vesicle (EV)-based, and molecular-based phenotyping. By fostering insightful conversations and engaging presentations, we anticipate the emergence of synergistic and inventive connections among the various strata of biological systems. These include molecules (nucleic acids, peptides, proteins), biological particles (organelles, viruses, EVs), and cells (single cells, organoids).

はじめに
Opening Remarks

2SJP-1　細胞外微粒子解析に向けた CRISPR-Cas によるデジタル核酸検出
Digital nucleic-acid detection with CRISPR-Cas for analysis of extracellular vesicles
○篠田 肇, 渡邉 力也（理研・開拓研究本部）
Hajime Shinoda, Rikiya Watanabe (*CPR, RIKEN*)

2SJP-2　Single-granule RNA-Seq: a comprehensive method for RNA heterogeneity in cellular granules
Yuichi Shichino[1], Mari Mito[1], Shintaro Iwasaki[1,2] ([1]*RIKEN CPR*, [2]*Grad. Sch. Front. Sci., Univ. Tokyo*)

2SJP-3　ヒトの発生過程を in vitro で再現するための幹細胞の分化操作
Manipulation of stem cell differentiation to recapitulate human developmental processes in vitro
○永樂 元次（京都大学・医生物学研究所）
Mototsugu Eiraku (*Institute for Life and Medical Sciences, Kyoto University*)

2SJP-4　人知を超える学習サイトメトリー技術群
Learning Cytometry Technologies
○太田 禎生 [1,2]（[1] 東大・先端研, [2] シンクサイト株式会社）
Sadao Ota[1,2] ([1]*RCAST, Univ Tokyo*, [2]*ThinkCyte Inc*)

2SJP-5　疾患関連エクソソームによる臓器特異的分布と病態寄与機構
Organotropic localization of disease-associated exosomes and its role in etiology
○星野 歩子（東大　先端研）
Ayuko Hoshino (*RCAST, Univ. Tokyo*)

おわりに
Closing Remarks

2SKP　超越分子シンポジウム：分子のシステムを社会に実装する
The symposium of bottom-up creation of cell-free molecular systems: basic research toward social implementation

共催 学術変革領域研究（A）「超越分子システム」

オーガナイザー：川野 竜司（東京農工大学），川村 出（横浜国立大学）
Organizers: Ryuji Kawano (Tokyo Univ. of Agric. and Tech.), Izuru Kawamura (Yokohama Natl. Univ.)

14:00〜16:30
K 会場（会議室 131+132（1 号館 3F））／Room K（Conference Room 131+132 (Bldg. 1, 3F)）

Research on the bottom-up creation of cells has progressed substantially, resulting in reconstituted molecular systems that mimic various cellular functions and properties. However, the bottom-up construction of molecular systems aimed at goals of social implementation has been rarely developed. In this symposium, current research topics including applied and social development based on the basic research of unique molecular systems will be presented. We especially focus on advanced technologies such as cell-free protein synthesis, adhesive nanofiber proteins, and high-throughput single cell-screening.

はじめに
Opening Remarks

2SKP-1　Optimizing the protein synthesis activity of a reconstituted in vitro transcription-translation system
Tomoaki Matsuura (*ELSI, Tokyo Tech*)

2SKP-2　無細胞タンパク質合成系の社会実装
Social implementation of a cell-free protein synthesis system
○清水 義宏（理化学研究所生命機能科学研究センター）
Yoshihiro Shimizu (*RIKEN Center for Biosystems Dynamics Research*)

2SKP-3　希少細胞を対象とした単一細胞遺伝子解析のプラットフォーム開発と応用展開
Development of a platform for single-cell genetic analysis of “rare cells” and their applications
○吉野 知子（東京農工大学）
Tomoko Yoshino (*Tokyo University of Agriculture and Technology*)

2SKP-4　次世代バイオものづくりのための未培養微生物ゲノムデータベース
Uncultured microbial genome database for next-generation biomanufacturing
○細川 正人 [1,2]（[1] 早大院・先進理工, [2]bitBiome（株））
Masahito Hosokawa[1,2] ([1]*Grad. Sch. Adv. Sci. Eng., Waseda Univ.*, [2]*bitBiome*)

2SKP-5　社会実装のための生物物理学分野の研究戦略：一起業家的科学者からの洞察
Research strategies in biophysics for social implementation: Insights from an entrepreneurial scientist
○堀 克敏（名大・院工学）
Katsutoshi Hori (*Grad. Sch. Eng. Nagoya Univ.*)

おわりに
Closing Remarks

2SLP　細胞システムの複雑なメカニクス
Complex mechanics of the cellular system

オーガナイザー：出口 真次（大阪大学），平田 宏聡（金沢工業大学）
Organizers: Shinji Deguchi (Osaka Univ.), Hiroaki Hirata (Kanazawa Inst. of Tech.)

14:00〜16:30
L 会場（会議室 133+134（1 号館 3F））／Room L（Conference Room 133+134 (Bldg. 1, 3F)）

Cells are the unit of living systems, regulating diverse biological processes. It has now become clear that mechanical factors such as the stiffness of intracellular and extracellular components allow cellular systems to function properly, while the whole picture of the mechanisms is yet poorly understood. In this symposium, we focus on the roles of mechanical factors in mediating cellular and subcellular processes and discuss how “mechanics” in such highly complex systems could be probed with techniques/technologies in physics and engineering. Specifically, recent studies from both experimental and theoretical approaches will be presented regarding the embryonic and fetal development and cellular biophysical homeostasis.

2SLP-1　原子間力顕微鏡による発生組織メカニクス
Tissue and embryo mechanics probed by atomic force microscopy
○岡嶋 孝治（北海道大学大学院情報科学研究院）
Takaharu Okajima (*Fac. Inform. Sci. Tech., Hokkaido University*)

2SLP-2　脳の弾性率変動によって駆動される神経分化メカニズムの解明
A systematic strategy to understand the role of microenvironmental stiffness in neurogenesis
○岩下 美里, 小曽戸 陽一（韓国脳研究院）
Misato Iwashita, Yoichi Kosodo (*Korea Brain Research Institute*)

2SLP-3　Nuclear mechanics coordinating biological and mechanical functions in mesenchymal stem cell differentiation
Hiromi Miyoshi (*Mech. Sys. Eng., Tokyo Metro. Univ.*)

2SLP-4　気管軟骨の“パターン”と“形”を生み出す謎を解く
Solving the Mystery of Tracheal Cartilage "Patterns" and "Shapes"
○古川 可奈（阪大・INSD）
Kana Furukawa (*INSD, Osaka Univ.*)

2SLP-5　α-アクチニンによって調節されるストレスファイバーの物性はミオシン由来の力の伝達効率を調節する
Alpha-actinin-mediated physical properties of stress fibers regulate transmission of myosin-generated force
○勝田 紘基 [1,2], 奥田 覚 [3], 長山 和亮 [4], 町山 裕亮 [5], 加藤 昌志 [2], 曽我部 正博 [2,7], 宮田 卓樹 [2], 木戸秋 悟 [6], 平田 宏聡 [2,8]（[1] 岡山大・院・医歯薬, [2] 名大・院医, [3] 金沢大・ナノライフ生命, [4] 茨城大・理工, [5] 東京医大・免疫, [6] 九大・先導物質化学研究所, [7] 金沢工大・産学連携室, [8] 金沢工大・バイオ・化学）
Hiroki Katsuta[1,2], Satoru Okuda[3], Kazuaki Nagayama[4], Hiroaki Machiyama[5], Masashi Kato[2], Masahiro Sokabe[2,7], Takaki Miyata[2], Satoru Kidoaki[6], Hiroaki Hirata[2,8] ([1]*Grad. Sch. Med., Okayama Univ.*, [2]*Grad. Sch. Med., Nagoya Univ.*, [3]*Nano LSL, Kanazawa Univ.*, [4]*Dept. of Biomech. and Eng., Ibaraki Univ.*, [5]*Dept. of Immunol., Tokyo Medical Univ.*, [6]*IMCE, Kyushu Univ.*, [7]*KIT*, [8]*College of Biosci. and Chem., KIT*)

2SLP-6　The Q factor of single cells as a biophysical parameter to decipher cell state
Ilaria Incaviglia, Giulia Ammirati, Sophie Herzog, Daniel J. Müller (*ETH Zürich*)

2SLP-7　細胞の力学的なホメオスタシスと適応のメカニズム
Analyzing cellular mechanical homeostasis and adaptation
○出口 真次（阪大・基礎工）
Shinji Deguchi (*Div. Bioeng., Osaka Univ.*)

2SMP　微小環境で行動する単細胞生物の生存戦略
The survival strategies of unicellular organisms on a microscale
共催 学術変革領域研究（A）「ジオラマ行動力学」

オーガナイザー：鹿毛 あずさ（学習院大学），野村 真未（山形大学），柴 小菊（筑波大学）
Organizers: Azusa Kage (Gakushuin Univ.), Mami Nomura (Yamagata Univ.), Kogiku Shiba (Univ. of Tsukuba)

14:00〜16:30
M 会場（会議室 431+432（4 号館 3F））／Room M（Conference Room 431+432 (Bldg. 4, 3F)）

Movement is one of the fundamental characteristics of life. Although biophysical studies on molecular- and organelle-level motility have elucidated the mechanisms of biological movement, much remains unknown about behavior and its significance at the cellular level. In this symposium, we invite researchers to challenge the behavioral analysis of unicellular organisms and the techniques for capturing cell movement on a microscale. Through the presentations on various subjects including ciliates, amoebae, microalgae, and marine particles, we would like to discuss the behavior and survival strategies of unicellular organisms which are unique to microenvironments, aiming to establish the field of biophysics of behavior.

はじめに
Opening Remarks

2SMP-1　Cooperative hydrodynamics accompany multicellular-like colonial organization in the unicellular ciliate *Stentor*
Shashank Shekhar[1], Hanliang Guo[2], Sean Colin[3], Wallace Marshall[4], Eva Kanso[5], Jack Costello[6] ([1]*Emory University, Atlanta, USA*, [2]*Ohio Wesleyan University, Delaware, USA*, [3]*Roger Williams University, Bristol, USA*, [4]*University of California San Francisco, San Francisco, USA*, [5]*University of Southern California, Los Angeles, USA*, [6]*Providence College, Providence, USA*)

2SMP-2　繊毛虫ソライロラッパムシの細胞外幾何形状に応じた固着場所の選択
Selecting of anchoring location by geometrical cues, in the ciliate, *Stentor coeruleus*
○越後谷 駿 [1], 佐藤 勝彦 [1,2], 中垣 俊之 [1,2], 西上 幸範 [1,2]（[1] 北海道大学大学院生命科学院, [2] 北海道大学電子科学研究所）
Syun Echigoya[1], Katsuhiko Sato[1,2], Toshiyuki Nakagaki[1,2], Yukinori Nishigami[1,2] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Research Institute for Electronic Science, Hokkaido University*)

2SMP-3　Integrative modeling of *Paramecium*, a “swimming neuron”
Romain Brette (*ISIR, Sorbonne Universite, Paris, France*)

2SMP-4　有殻アメーバの被殻構築における巧みな細胞行動
Skillful cell behavior in the construction of testate amoebae shells
○野村 真未（山形大学理学部）
Mami Nomura (*Fac. Sci., Yamagata Univ.*)

2SMP-5　イベントベースビジョンセンサー（EVS）を用いたプランクトンの室内及び自然環境でのミリ秒スケール観測
Millisecond-scale behaviours of plankton quantified in situ and in vitro using the Event-based Vision Sensor (EVS)
○高塚 進[1,2], 宮本 教生[2]（[1] ソニーグループ株式会社, [2] 国立研究開発法人海洋研究開発機構）
Susumu Takatsuka[1,2], Norio Miyamoto[2] ([1]*Sony Group Corporation*, [2]*Japan Agency for Marine-Earth Science Technology*)

2SMP-6　シアノバクテリア鉛直移動における予測不能性
Fundamental unpredictability in the vertical migration of cyanobacteria
○吉山 浩平（滋賀県立大学環境科学部）
Kohei Yoshiyama (*Grad. Sch. Environ. Sci., Univ. Shiga Pref.*)

3 日目（11 月 16 日（木））／Day 3（Nov. 16 Thu.）

3SAA　構造生物学的アプローチに基づく液液相分離（LLPS）の機能解明
Functional elucidation of liquid-liquid phase separation (LLPS) based on structural biology approach

オーガナイザー：西田 紀貴（千葉大学），池谷 鉄兵（東京都立大学）
Organizers: Noritaka Nishida (Chiba Univ.), Teppei Ikeya (Tokyo Metro. Univ.)

09:00〜11:30
A 会場（展示室 211（2 号館 1F））／Room A（Exhibition Room 211 (Bldg. 2, 1F)）

Liquid-liquid phase separation (LLPS) is driven by the dynamic assembly of diverse protein and RNA molecules in the cells. In order to understand how such droplets, which are seemingly disordered structures, regulate various physiological functions, it is necessary to quantitatively measure the behavior of LLPS at the atomic and molecular levels. In this symposium, we would like to introduce recent studies of researchers who are aiming to elucidate the principles of LLPS formation and the regulation of intracellular functions by structural biology approaches such as NMR and computational science, as well as chemical biology.

3SAA-1　溶液 NMR による GRB2 と SOS1 の多価相互作用と液液相分離形成機構の解析
Analysis of the mechanism underlying multivalent interactions between GRB2 and SOS1 and their LLPS using solution NMR
○池谷 鉄兵[1], 大出 真央[2], Ren Weitong[2], 館野 圭太[1], 安藤 孝[1], 菅澤 はるか[1], 杉田 有治[2], 伊藤 隆[1]（[1] 東京都立大・院理, [2] 理研・開拓研究本部）
Teppei Ikeya[1], Mao Oide[2], Weitong Ren[2], Keita Tateno[1], Takashi Ando[1], Haruka Sugasawa[1], Yuji Sugita[2], Yutaka Ito[1] ([1]*Grad. Sch. Sci., Tokyo Metropolitan Univ.*, [2]*RIKEN CBR*)

3SAA-2　Mapping the per-residue surface electrostatic potential of CAPRIN1 along its phase-separation trajectory
Yuki Toyama[1,2,3], Atul Rangadurai[1,2,3,4], Julie Forman-Kay[2,4], Lewis Kay[1,2,3,4] ([1]*Department of Molecular Genetics, University of Toronto*, [2]*Department of Biochemistry, University of Toronto*, [3]*Department of Chemistry, University of Toronto*, [4]*Hospital for Sick Children, Program in Molecular Medicine*)

3SAA-3　がん抑制タンパク質 p53 が形成する凝集体の調製と分析
Preparation and analysis of aggregates formed by the tumor suppressor protein p53
○日比野 絵美[1], 土方 礼嗣[1], 天野 剛志[1,2], 廣明 秀一[1,2]（[1] 名大・院創薬, [2]BeCellBar）
Emi Hibino[1], Reiji Hijikata[1], Takeshi Tenno[1,2], Hidekazu Hiroaki[1,2] ([1]*Grad. Sch. Pharm. Sci, Nagoya Univ.*, [2]*BeCellBar*)

3SAA-4　分子シミュレーションによるタンパク質集合体の液液相分離研究
Liquid-liquid phase separation of protein assemblies studied by molecular simulations
○高田 彰二, 水谷 淳生, 山田 莉彩, 村田 隆（京都大学理学研究科）
Shoji Takada, Azuki Mizutani, Risa Yamada, Yutaka Murata (*Grad. Sch. Sci. Kyoto Univ*)

3SAA-5　細胞シグナル操作のためのデザイナータンパク質コンデンセート
Designer protein condensates for cell signal manipulation
○築地 真也（名工大・院工）
Shinya Tsukiji (*Grad. Sch. Eng., Nagoya Inst. Technol.*)

3SAA-6　細胞内環境下における LLPS 形成タンパク質 FUS の In-cell NMR 観測
In-cell NMR Observation of Liquid-Liquid Phase Separation of FUS
○西田 紀貴（千葉大・院薬）
Noritaka Nishida (*Grad. Sch. Pharm. Sci., Chiba Univ.*)

3SBA　天然変性タンパク質を含む創薬標的に対する生物物理学的アプローチ
Biophysical approaches against the drug target proteins involving intrinsically disordered regions

オーガナイザー：廣明 秀一（名古屋大学），白井 剛（長浜バイオ大学）
Organizers: Hidekazu Hiroaki (Nagoya Univ.),
Tsuyoshi Shirai (Nagahama Inst. of Bio-Science and Tech.)

09:00〜11:30
B 会場（展示室 212（2 号館 1F））／Room B（Exhibition Room 212 (Bldg. 2, 1F)）

Recent progress in proteomics of human diseases and host-pathogen interactions has revealed that potential therapeutic targets contain intrinsically disordered regions (IDRs). Proteins with large amounts of IDRs often lack a fixed or ordered three-dimensional structure, rendering them unsuitable for the modern structure-guided drug discovery methodology. This symposium aims to explore different biophysical approaches to drug discovery and development against IDRs. We will focus on methods that go beyond the classical lock-and-key model, including innovative approaches to understand the structural and dynamic properties of IDRs.

はじめに
Opening Remarks

3SBA-1　典型的でない創薬標的を対象とした溶液 NMR 技術の挑戦〜鍵と鍵穴モデルを超えて
NMR challenges against characterization of non-classical drug targets - beyond the lock-and-key model
○廣明 秀一 [1,2,3]（[1] 東海国立大学機構名古屋大学創薬科学研究科, [2] 合同会社 BeCellBar, [3] 東海国立大学機構　One Medicine 創薬シーズ開発・育成研究教育拠点）
Hidekazu Hiroaki[1,2,3] ([1]*Graduate School of Pharmaceutical Sciences, Nagoya University*, [2]*BeCellBar, LLC*, [3]*Center for One Medicine Innovative Translational Research (COMIT), Tokai National Higher Education and Research System*)

3SBA-2　NMR を用いた天然変性蛋白質の構造解析：アルファーシヌクレイン
NMR Analyses of an intrinsic disordered protein: Alpha-synuclein
○西村 千秋（帝京平成大学薬学部）
Chiaki Nishimura (*Faculty of Pharmaceutical Sciences, Teikyo Heisei University*)

3SBA-3　抗酸菌の天然変性ヒストン様タンパク質　ーその機能と休眠菌形成における役割ー
Mycobacterial intrinsically disordered histone-like protein, its function and role in mycobacterial dormancy
○西山 晃史 [1], 清水 将裕 [2,3], 古寺 哲幸 [2], 尾関 百合子 [1], 真柳 浩太 [4], 山口 雄大 [5], 松本 壮吉 [1]（[1] 新潟大院・医歯学総合・細菌学, [2] 金沢大・ナノ生命科学研, [3] 京都大・複合原子力科学研, [4] 九州大・生体防御医学研, [5] 大阪公大院・医・分子病態薬理学）
Akihito Nishiyama[1], Masahiro Shimizu[2,3], Noriyuki Kodera[2], Yuriko Ozeki[1], Kouta Mayanagi[4], Takehiro Yamaguchi[5], Sohkichi Matsumoto[1] ([1]*Dept. Bacteriol., Niigata Univ. Sch. Med.*, [2]*NanoLSI, Kanazawa Univ.*, [3]*Div. Quantum Beam Mater. Sci., Inst. Integr. Radiat. Nuc. Sci., Kyoto Univ*, [4]*Med. Inst. Bioregulation, Kyushu Univ.*, [5]*Dept. Pharmacol, Osaka Metro Univ. Med. Sch.*)

3SBA-4　天然変性タンパク質における“変性状態”の理解を目指した溶液散乱研究
Solution scattering towards details in flexibility of intrinsically disordered proteins
○清水 将裕 [1], 守島 健 [1], 奥田 綾 [1], 井上 倫太郎 [1], 西山 晃史 [2], 松本 壮吉 [2], 杉山 正明 [1]（[1] 京大・複合研, [2] 新潟大院・医歯学総合・細菌学）
Masahiro Shimizu[1], Ken Morishima[1], Aya Okuda[1], Rintaro Inoue[1], Akihito Nishiyama[2], Sohkichi Matsumoto[2], Masaaki Sugiyama[1] ([1]*KURNS., Kyoto Univ.*, [2]*Dept. Bacteriol., Niigata Univ. Sch. Med.*)

3SBA-5　相分離における分子の動態を捉える
Visualizing molecular dynamics of phase separation
○森 英一朗（奈良医大・未来基礎医学）
Eiichiro Mori (*Dept. Future Basic Med., Nara Med. Univ.*)

おわりに
Closing Remarks

3SCA　自発と応答の情報物理学
Information physics of spontaneity and response

共催 新学術領域研究「生命の情報物理学」

オーガナイザー：青木 一洋（生命創成探究センター），松岡 里実（大阪大学）
Organizers: Kazuhiro Aoki (ExCELLS), Satomi Matsuoka (Osaka Univ.)

09:00〜11:30
C 会場（会議室 221（2 号館 2F））／Room C（Conference Room 221 (Bldg. 2, 2F)）

Physical understanding of information in living systems lies at the leading edge of biophysical studies. The advances in super resolution microscopy and accurate manipulation and measurement techniques have highlighted various unexpected behaviors of molecules and cells under collective motion, which reveals that the essence of the information underlies in the precisely quantified data acquired under the “living” state. In this symposium, we introduce the attempts to investigate the dynamics of living systems in the intrinsic state and in response to the extrinsic stimulus to explore the principles of spontaneous generation, transmission, and processing of biological information.

3SCA-1　バクテリア乱流の空間構造への応答：渦秩序の制御とキラリティー
How bacterial turbulence responds to spatial structures: controlling vortical order and chirality
○西口 大貴（東京大学・理・物理）
Daiki Nishiguchi (*Dept. Phys., Grad. Sch. Sci., Univ. Tokyo*)

3SCA-2 Force transmission via dynamic stretching of Talin as revealed by quantitative live-cell single-molecule imaging
Sawako Yamashiro[1,2], David M. Rutkowski[3], Ying Liu[1], Kelli Ann Lynch[4], Dimitrios Vavylonis[3], Naoki Watanabe[1,2] ([1]*Kyoto Univ. Grad. Sch. Biostudies, Kyoto*, [2]*Dept. Pharmacology, Kyoto Univ.Grad. Sch. Med., Kyoto*, [3]*Dept. Physics, Lehigh Univ., PA/USA*, [4]*Univ. of South Florida, FL/USA*)

3SCA-3 分子レベルでの情報伝達能力の評価から骨格筋ミオシン分子間の協同性を理解する
Understanding cooperativity between skeletal myosin molecules by evaluating information transmission capacity of myosin molecules
○茅 元司（東京大学・院物理）
Motoshi Kaya (*Grad. Sch. Sci., Univ. Tokyo*)

3SCA-4 Characterization of activity-dependent mechanics of the cell cytoplasm
Hiroyuki Ebata, Daisuke Mizuno (*Fac. Sci., Kyushu Univ.*)

3SCA-5 分裂酵母胞子の発芽過程における細胞質流動化の定量解析
Quantitative analysis of cytoplasmic fluidization during germination in fission yeast
○青木 一洋（ExCELLS/基生研）
Kazuhiro Aoki (*ExCELLS/NIBB, NINS*)

3SCA-6 バクテリア遊泳集団の揺らぎと応答
Fluctuation and response of bacterial collective swimming
○鳥谷部 祥一（東北大学・院応用物理）
Shoichi Toyabe (*Applid Physics, Tohoku Univ*)

3SEA 細胞のメゾ構造体の形成と機能の機構：先端イメジング法による解明
Mechanisms for the formation and functions of cellular meso-scale structures: unravelling by advanced imaging methods

オーガナイザー：下林 俊典（京都大学），楠見 明弘（沖縄科学技術大学院大学）
Organizers: Shunsuke Shimobayashi (Kyoto Univ.), Akihiro Kusumi (OIST)

09:00〜11:30
E 会場（会議室 224（2 号館 2F））／Room E（Conference Room 224 (Bldg. 2, 2F)）

To understand how cells work, biophysicists are now discovering the mechanisms by which mesoscale subcellular molecular complexes are formed and function. This approach, particularly that using advanced microscopic imaging methods, is turning out to be very fruitful. Meso-scale, often between 3 and 300 nm, is an interesting spatial scale where non-living nano-scale molecules are assembled to start exhibiting the clear features of micron-scale living cells. Furthermore, recent research advances on the liquid condensates are further activating meso-scale investigations. Therefore, this symposium will focus on this very hot topic of meso-scale structures/events, including liquid signaling platforms, myosin-motor-driven cargo-membrane sculpting, subsynaptic meso-domains, DNA breaks, and fundamental material properties of biomolecular condensates. We hope to make this symposium a place where, together with the audience, new fundamentally important ideas emerge toward the understanding of how subcellular meso-scale structures form and function.

はじめに
Opening Remarks

3SEA-1 細胞膜上のナノ液体複合体が複数の受容体信号を統合する基盤となり、癌細胞の増殖を促進させる
Nano-liquid platform on the plasma membrane that integrates receptor signals for cancer promotion
Taka-aki Tsunoyama[1], Christian Hoffmann[2], Daiki Sasaki[1], Bo Tang[1], Koichiro M Hirosawa[3], Yuri L Nemoto[4], Rinshi R Kasai[3], Takahiro K Fujiwara[5], Kenichi GN Suzuki[3,5], Hiroki Ishikawa[1], Dragomir Milovanovic[2], Akihiro Kusumi[1,5] ([1]*Okinawa Inst. Sci. Tech. Grad. Univ. (OIST)*, [2]*German Cent. Neurodegenerative Diseases (DZNE)*, [3]*Inst. Glyco-Core Res. (iGCORE), Gifu Univ.*, [4]*Biosignal Res. Cent., Kobe Univ.*, [5]*Inst.Integ.Cell-Mat. Sci. (WPI-iCeMS), Kyoto Univ.*)

3SEA-2 Membrane reshaping by myosin-lipid interactions
Claudia Veigel (*Department of Cellular Physiology, Ludwig-Maximilians-University Munich*)

3SEA-3 Emergence of highly ordered meso-structures of multivalent synaptic proteins in living cells
Hirokazu Sakamoto (*Grad. Sch. Med., The Univ. Tokyo*)

3SEA-4 Magnet tweezers studies of PARP binding at single and double strand DNA breaks
Justin Edward Molloy[1], Nicholas A.W. Bell[2] ([1]*Francis Crick Institute, London, UK*, [2]*University College London, Gower Street, London, UK*)

3SEA-5 細胞内相分離メソ液滴の形成、物性、そして機能
Elucidating the formation, material properties, and functions of biomolecular meso-scale condensates
○下林 俊典（京都大学 iPS 細胞研究所）
Shunsuke Shimobayashi (*CiRA, Kyoto University*)

おわりに
Closing Remarks

3SFA 水和による水運動の不均一性から考える生物分子機能
Biomolecular functions based on heterogeneous hydration dynamics

オーガナイザー：今清水 正彦（産業技術総合研究所），菱田 真史（筑波大学）
Organizers: Masahiko Imashimizu (AIST), Masafumi Hishida (Univ. of Tsukuba)

09:00〜11:30
F 会場（会議室 231（2 号館 3F））／Room F（Conference Room 231 (Bldg. 2, 3F)）

How does a biomacromolecular complex like an enzyme work accurately and regulatory in water solvent system dominated by thermal fluctuations? The key to understand this question lies in the fact that, due to hydration, the thermal motions involved in biomolecular functions are temporally and spatially heterogeneous. For example, the collective intermolecular dynamics of protein and water molecules, which are overlapped in the sub-THz frequency region, may be relevant for expressing protein functions. In this symposium, we will attempt to discuss new directions regarding the unexplained phenomena in biomolecular functions based on the measurements of intermolecular dynamics, such as THz-TDS, fs-RIKES, microwave dielectric relaxation and NMR, and the physicochemical theoretical approach.

3SFA-1 サブテラヘルツ波照射によるタンパク質水和への非熱的作用：誘電緩和測定に基づいた研究
Nonthermal Effect of Sub-THz Irradiation on Protein Hydration: Study Based on Dielectric Relaxation Measurements
○今清水 正彦, 杉山 順一, 田中 真人（産総研）
Masahiko Imashimizu, Jun-ichi Sugiyama, Masahito Tanaka (*AIST*)

3SFA-2 **サブテラヘルツ波照射された水溶液中のタンパク質の NMR 法を用いた動的構造解析**
Analyses of structural dynamics of proteins in aqueous solution irradiated with sub-THz electromagnetic waves by using NMR spectroscopy
○徳永 裕二 [1], 竹内 恒 [1], 今清水 正彦 [2]（[1] 東京大学大学院薬学系研究科, [2] 産業技術総合研究所生命分子工学研究部門）
Yuji Tokunaga[1], Koh Takeuchi[1], Masahiko Imashimizu[2] ([1]*Grad. Sch. Pharm. Sci., UTokyo*, [2]*CMB, AIST*)

3SFA-3 **水和イオン液体の含水率による生体分子の溶解性と構造変化**
Solubility and structural changes of biomolecules as a function of water content in hydrated ionic liquids
○藤田 恭子（東京薬科大学　薬学部）
Kyoko Fujita (*Tokyo University of Pharmacy and Life Sciences*)

3SFA-4 **フェムト秒ラマン誘起カー効果分光による凝縮相の低振動数ダイナミクスの観測：生体分子に向けて**
Probing the low-frequency dynamics in condensed phases by femtosecond Raman-induced Kerr effect spectroscopy: Toward biomolecules
○城田 秀明（千葉大・院理）
Hideaki Shirota (*Grad. Sch. Sci., Chiba University*)

3SFA-5 WATER: THE FORGOTTEN BIOLOGICAL MOLECULE THAT CONTROLS LIFE
Biman Bagchi (*Indian Institute of Science, Bengaluru*)

3SFA-6 **タンパク質の構造安定化に対する水和水の役割**
Role of Hydration Water in Protein Conformational Stabilization
○菱田 真史（東京理科大学理学部化学科）
Mafumi Hishida (*Dept. Chem., Tokyo Univ. Sci.*)

3SHA 生体膜の生物物理呼応～生命活動における形と動き～
Biophysical membrane responses: structure and motion in biological activity

オーガナイザー：中瀬 生彦（大阪公立大学），川口 祥正（京都大学）
Organizers: Ikuhiko Nakase (Osaka Metro. Univ.), Yoshimasa Kawaguchi (Kyoto Univ.)

09:00～11:30
H 会場（会議室 234（2 号館 3F））／Room H（Conference Room 234 (Bldg. 2, 3F)）

In biological activity, biomembranes participate in responses for acceptance/rejection of stimulation and structural formations including e.g., cellular uptake, migration, proliferation, and cell death. Understanding and controlling biophysical responses/mechanisms-based membrane systems are highly anticipated to be next-generation therapeutic methodologies for further achievements of disease regulation such as cancers. In this proposal symposium, advanced research technologies and achievements of visualizing and controlling membrane traffic, release of extracellular vesicles, self-organization of tissue formation, exploiting physics and physical chemistry for imaging and analysis of membrane characterization with antimicrobial peptides, biophysical assessment and biological applications (especially drug delivery) of membrane disruptive peptides from the fusion viewpoints of biophysics, molecular cell biology, chemistry, and chemical biology will be presented, and membrane-based therapeutic methodology will be discussed.

はじめに
Opening Remarks

3SHA-1　抗菌ペプチド LL-37 vs HNP1 間ダブルコオペラティブ効果の原理解明
The mechanistic studies of double cooperative effect between antimicrobial peptides LL-37 and HNP1
○杉原 加織（東大生研）
Kaori Sugihara (*IIS, The Univ. of Tokyo*)

3SHA-2　培養場の制御による細胞集団行動の制御
Control of collective cell migration by cell-ECM interactions
○萩原 将也（理化学研究所）
Masaya Hagiwara (*RIKEN*)

3SHA-3　膜傷害性ペプチドを鋳型とした細胞質送達ペプチドの開発
Development of cytosolic delivery peptides by attenuated membrane lytic activity
○川口 祥正, 二木 史朗（京大・化研）
Yoshimasa Kawaguchi, Shiroh Futaki (*Inst. Chem. Res., Kyoto Univ.*)

3SHA-4　抗菌ペプチドによる脂質膜への選択的作用：粗視化分子動力学シミュレーション
Selective action of antimicrobial peptides on lipid membranes: Coarse-grained molecular dynamics study
○篠田 渉（岡山大・基礎研）
Wataru Shinoda (*RIIS, Okayama Univ.*)

3SHA-5　上皮細胞からのエクソソームの非対称分泌の分子機構
Molecular mechanisms of asymmetrical exosome release from polarized epithelial cells
○福田 光則（東北大院・生命科学）
Mitsunori Fukuda (*Grad. Sch. Life Sci., Tohoku Univ.*)

おわりに
Closing Remarks

3SJA　光合成の多様な環境への適応原理
Understanding the Principles of the Adaptation of Photosynthesis to Diverse Environments

共催 学術変革領域研究（A）「光合成ユビキティ」

オーガナイザー：広瀬 侑（豊橋技術科学大学），栗栖 源嗣（大阪大学）
Organizers: Yuu Hirose (Toyohashi Univ. of Tech.), Genji Kurisu (Osaka Univ.)

09:00〜11:30
J 会場（会議室 141+142（1 号館 4F））／Room J（Conference Room 141+142 (Bldg. 1, 4F)）

Photosynthetic organisms synthesize organic compounds from water and carbon dioxides using solar energy. They adapted and expanded over a wide range of environments and sustain all living organisms on Earth. The structure and function of photosynthetic apparatus change dynamically in response to environmental conditions. In 2023, researchers from structural biology, plant physiology, biochemistry, and bioinformatics have teamed up to launch a new research project, "Photosynthetic Ubiquity", which is supported by Grant-in-Aid for Transformative Research Areas (A) from JSPS. In this symposium, the members of this project will discuss approaches to elucidate the molecular principles of adaptation of photosynthetic supramolecular complexes to diverse environments.

3SJA-1 Structure of cyanobacterial photosystem I complexed with ferredoxin and cytochrome c6 at 1.97 Å resolution

Jiannan Li[1,2], Noriyuki Hamaoka[1,2], Fumiaki Makino[3,4], Akihiro Kawamoto[1,2], Keiichi Namba[3,4,5], Christoph Gerle[1], **Genji Kurisu[1,2,5]** ([1]*Inst. Prot. Res., Osaka Univ.*, [2]*Grad. Sch. Sci., Osaka Univ.*, [3]*Grad. Sch. Front. Bio., Osaka Univ.*, [4]*JEOL Co., Ltd.*, [5]*JEOL YOKOGUSHI Res. Lab., Osaka Univ.*)

3SJA-2 チラコイド膜における動的高次分子構造の高速 AFM による可視化

Visualization of dynamic higher-order molecular structure of thylakoid membranes by HS-AFM

○山本 大輔, 西谷 雄大（福岡大・理）

Daisuke Yamamoto, Yudai Nishitani (*Fac. Sci., Fukuoka Univ.*)

3SJA-3 光合成光捕集蛋白質における環境適応機構の解明

Understanding environmental adaptation mechanisms in photosynthetic light-harvesting proteins

○斉藤 圭亮 [1,2], 辻村 真樹 [1], 鍵本 拓海 [1], 石北 央 [1,2]（[1] 東大・先端研, [2] 東大・院工）

Keisuke Saito[1,2], Masaki Tsujimura[1], Takumi Kagimoto[1], Hiroshi Ishikita[1,2] ([1]*RCAST, Univ. Tokyo*, [2]*Grad. Sch. Sci., Univ. Tokyo*)

3SJA-4 祖先型タンパク質による生命マシナリーの環境適応戦略の解読

Decoding the environmental adaptation strategies of biological machineries via ancestral proteins

土屋 裕子 [1], 嶺井 隆平 [2], 土方 敦司 [3], ○白井 剛 [2]（[1] 産総研・人工知能研究センター, [2] 長浜バイオ大・バイオサイエンス, [3] 東薬大・生命科学）

Yuko Tsuchiya[1], Ryuhei Minei[2], Atsushi Hijikata[3], **Tsuyoshi Shirai[2]** ([1]*Artificial Intelligence Research Center (AIRC), National Institute of Advanced Industrial Science and Technology (AIST)*, [2]*Department of Bio-science, Nagahama Institute of Bio-Science and Technology*, [3]*School of Life Sciences, Tokyo University of Pharmacy and Life Sciences*)

3SJA-5 構造から紐解くシアノバクテリアの光色順化

Structural basis of chromatic acclimation in Cyanobacteria

○広瀬 侑（豊橋技科大・院工）

Yuu Hirose (*Toyohashi Univ. of Tech. Dept. of Eng.*)

3SKA 我ら地球生物の可能性～極限微生物から人工細胞まで～

Our Potential as Earthly Organisms: From Extremophile Microbes to Artificial Cells

共催 CREST/さきがけ「ゲノム合成」

オーガナイザー：市橋 伯一（東京大学），鈴木 志野（宇宙航空研究開発機構）

Organizers: Norikazu Ichihashi (The Univ. of Tokyo), Shino Suzuki (JAXA)

09:00～11:30

K 会場（会議室 131+132（1 号館 3F））／Room K（Conference Room 131+132 (Bldg. 1, 3F)）

The recent discovery of new microorganisms with extraordinary characteristics has extended the possibility of living organisms on Earth. Similarly, the recent synthesis of artificial cellular and non-cellular systems has revealed what life could potentially be. As a result of these studies, we have come to realize that the potential of living systems on Earth, including human beings, is much greater than previously thought. In this symposium, we have invited researchers who are actively studying microorganisms in extraordinary habitats or synthesizing artificial systems with extraordinary properties. We hope that this symposium will provide an opportunity for researchers from different fields to broaden their perspectives on living things.

はじめに
Opening Remarks

3SKA-1 **試験管内でセントラルドグマを作ってみて分かったこと**
Lessons from the In vitro construction of the “Central dogma”
○市橋 伯一 [1,2,3]（[1] 東大・総合文化, [2] 東大・先進科学, [3] 東大・生物普遍）
Norikazu Ichihashi[1,2,3] ([1]*Grad. Sch. Arts and Sci, Univ Tokyo*, [2]*KIS, Univ Tokyo*, [3]*UBI, Univ Tokyo*)

3SKA-2 **南極藻類の赤外線利用型光合成メカニズム**
Uphill energy transfer mechanism for photosynthesis performed by far-red light in an Antarctic alga
○小杉 真貴子 [1], 川崎 政人 [2], 柴田 穣 [3], 原 光二郎 [4], 高市 真一 [5], 安達 成彦 [2], 守屋 俊夫 [2], 亀井 保博 [6], 工藤 栄 [7], 菓子野 康浩 [8], 小池 裕幸 [9], 千田 俊哉 [2], 大谷 修司 [10], 豊田 敦 [11], 西出 浩世 [12], 皆川 純 [1]（[1] 基生研・環境光, [2] 高エネ機構・構造生物, [3] 東北大・理, [4] 秋田県立大・生物資源, [5] 東京農大・生命, [6] 基生研・超階層生物, [7] 極地研・生物圏, [8] 兵庫県立大・理, [9] 中央大・理工, [10] 島根大・教育, [11] 遺伝研・ゲノム・進化, [12] 基生研・データ統合）
Makiko Kosugi[1], Masato Kawasaki[2], Yutaka Shibata[3], Kojiro Hara[4], Shinichi Takaichi[5], Naruhiko Adachi[2], Toshio Moriya[2], Yasuhiro Kamei[6], Sakae Kudoh[7], Yasuhiro Kashino[8], Hiroyuki Koike[9], Toshiya Senda[2], Syuji Ohtani[10], Atsushi Toyota[11], Hiroyo Nishide[12], Jun Minagawa[1]
([1]*Div. Env. Photosyn., NIBB*, [2]*SBRC, IMSS, KEK*, [3]*Fac. Sci., Tohoku Univ.*, [4]*Fac. Biores. Sci., Akita Pref. Univ.*, [5]*Fac. Life Sic., Tokyo Univ. Agri.*, [6]*Trans-Scale Biol., NIBB*, [7]*Biosci., NIPR*, [8]*Grad. Sch. Sci., Univ. Hyogo*, [9]*Fac. Sci. Engineering, Chuo Univ.*, [10]*Fac. Education, Shimane Univ.*, [11]*Dep. Genomics Evolution. Biol., NIG*, [12]*Data Integ. Analys. Fac., NIBB*)

3SKA-3 i[3]-screening for an emergent protein function designed by an ML-based generative model
Shunshi Kohyama, Béla Frohn, Leon Babl, Petra Schwille (*Max Planck Institute of Biochemistry*)

3SKA-4 **試験管内合成とタンパク質光操作による人工細胞膜の機能拡張**
Functionalizing artificial cell membrane with cell-free synthesis and light-inducible proteins
○松林 英明（東北大学・学際研）
Hideaki Matsubayashi (*FRIS, Tohoku Univ.*)

3SKA-5 **ウイルス集団内におけるゲノム配列の分布**
Distribution of genomic sequences within a viral population
○田端 和仁（東京大学大学院工学系研究科応用化学専攻）
Kazuhito Tabata (*Department of Applied Chemistry, The University of Tokyo*)

3SKA-6 **酵母を用いた難培養性細菌の全ゲノムクローニング**
Whole genome cloning of unculturable bacteria in yeast
○水谷 雅希 [1], 宮腰 かおり [1], 古賀 隆一 [1], 深津 武馬 [1,2,3], 柿澤 茂行 [1]（[1] 産業技術総合研究所・生物プロセス研究部門, [2] 東京大学大学院理学系研究科・生物科学専攻, [3] 筑波大学大学院・生命環境科学系）
Masaki Mizutani[1], Kaori Miyakoshi[1], Ryuichi Koga[1], Takema Fukatsu[1,2,3], Shigeyuki Kakizawa[1]
([1]*Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology (AIST)*, [2]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, [3]*Graduate School of Life and Environmental Sciences, University of Tsukuba*)

3SKA-7 **鉱物を利用した炭素固定：超還元環境に生きる微生物のもつ効率的な細胞外電子授受蛋白質**
Carbon Fixation Using Minerals: efficient extracellular electron transfer protein in archaea associated with ultra-reducing environments
○鈴木 志野 [1,2]（[1] 宇宙航空研究開発機構・宇宙研, [2] 理研・開拓研究本部,）
Shino Suzuki[1,2] ([1]*ISAS, JAXA*, [2]*CPR, Riken*)

おわりに
Closing Remarks

1 日目（11 月 14 日（火））／Day 1（Nov. 14 Tue.）

1GA　タンパク質：構造、物性、機能
Protein: Structure, Physical Property, Function

座長：古池 美彦（分子科学研究所），谷中 冴子（九州大学），島田 敦広（岐阜大学），
野口 巧（名古屋大学）

Session Chairs: Yoshihiko Furuike (IMS), Saeko Yanaka (Kyushu Univ.), Atsuhiro Shimada (Gifu Univ.), Takumi Noguchi (Nagoya Univ.)

14:00〜16:00

A 会場（展示室 211（2 号館 1F））／Room A（Exhibition Room 211 (Bldg. 2, 1F)）

1GA1400 Structural analysis of disease-associated proteins in the brain for PET ligand development

Kaede Goto[1], Junta Tomono[1], Ryuichi Harada[2], Takeshi Yokoyama[1], Yoshikazu Tanaka[1] ([1]*Grad. Sch. Life Sci., Tohoku Univ.*, [2]*Grad. Sch. Med., Tohoku Univ.*)

1GA1415 自然免疫シグナル伝達を制御する MyD88 多量化機序の分子論的な解明

The molecular analysis of MyD88 oligomerization that regulates innate immune signaling

○笠井 一希 [1], 今村 香代 [1], 宮田 知子 [2], 牧野 文信 [2], 加藤 貴之 [3], 成田 哲博 [4], 紺野 宏記 [5], 難波 啓一 [2], 大西 秀典 [6], 杤尾 豪人 [1]（[1] 京大・院理・生物科学, [2] 阪大・生命機能, [3] 阪大・蛋白研, [4] 名大・院理・生命理学, [5] 金大・ナノ生命科学研, [6] 岐大・院医・小児科学）

Kazuki Kasai[1], Kayo Imamura[1], Tomoko Miyata[2], Fumiaki Makino[2], Takayuki Kato[3], Akihiro Narita[4], Hiroki Konno[5], Keiichi Namba[2], Hidenori Onishi[6], Hidehito Tochio[1] ([1]*Dept. of Biol. Sci., Grad. Sch. of Sci., Kyoto Univ*, [2]*Grad. Sch. of FBS., Osaka Univ.*, [3]*IPR., Osaka Univ.*, [4]*Dept. of Biol. Sci., Grad. Sch. of Sci., Nagoya Univ.*, [5]*WPI-NanoLSI., Kanazawa Univ.*, [6]*Dept. of Peds., Grad. Sch. of Med., Gifu Univ.*)

1GA1430 ハイスループット蛋白質熱安定性データ収集系の開発

Development of a high-throughput data collecting system for thermal stability of proteins

○伊藤 沙衣 [1], 松長 遼 [1], 中木戸 誠 [1], 河村 大輔 [2], 加藤 洋人 [2], 石川 俊平 [2], 津本 浩平 [1,3]（[1] 東京大学大学院工学系研究科バイオエンジニアリング専攻., [2] 東京大学大学院医学系研究科衛生学分野., [3] 東京大学大学院工学系研究科化学生命工学専攻.）

Sae Ito[1], Ryo Matsunaga[1], Makoto Nakakido[1], Daisuke Komura[2], Hiroto Kato[2], Shumpei Ishikawa[2], Kouhei Tsumoto[1,3] ([1]*Department of Bioengineering, Graduate School of Engineering, University of Tokyo.*, [2]*Department of Preventive Medicine, Graduate School of Medicine, The University of Tokyo.*, [3]*Department of Chemistry and Biotechnology, Graduate School of Engineering, University of Tokyo.*)

1GA1445 ウシ由来インスリンのアミロイドオリゴマーおよびプロトフィブリル形成のモデリング

Mechanistic modeling of amyloid oligomer and protofibril formation of bovine insulin

○柚 佳祐 [1], 今村 比呂志 [2], 野崎 拓郎 [1], 藤井 悠生 [1], 守島 健 [3], 奥田 綾 [3], 井上 倫太郎 [3], 杉山 正明 [3], 茶谷 絵理 [1]（[1] 神戸大・院理, [2] 長浜バイオ大・バイオサイエンス, [3] 京大・複合研）

Keisuke Yuzu[1], Hiroshi Imamura[2], Takuro Nozaki[1], Yuki Fujii[1], Ken Morishima[3], Aya Okuda[3], Rintaro Inoue[3], Masaaki Sugiyama[3], Eri Chatani[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Dept. Bio-Sci., Nagahama Inst. Bio-Sci. Tech.*, [3]*KURNS, Kyoto Univ.*)

1GA1500 相分離液滴によるホタルの生物発光の発光量子収率向上

Quantum yield enhancement of firefly bioluminescence with phase-separated condensates

○木原 良樹 [1,2], 西原 諒 [2,3], 丹羽 一樹 [2], 冨田 峻介 [2], 栗田 僚二 [1,2]（[1] 筑波大学 大学院数理物質研究群., [2] 産業技術総合研究所., [3] 科学技術振興機構.）

Yoshiki Kihara[1,2], Ryo Nishihara[2,3], Kazuki Niwa[2], Syunsuke Tomita[2], Ryoji Kurita[1,2] ([1]*Faculty of Pure and Applied Sciences, University of Tsukuba.*, [2]*National Institute of Advanced Industrial Science and Technology (AIST).*, [3]*Japan Science and Technology Agency (JST), PRESTO.*)

1GA1515 **可変領域スーパーチャージ抗体–抗原相互作用の熱力学的解析と相互作用パラメータの制御**
Thermodynamic analysis of Fv-supercharged antibody–antigen interactions and control of interaction parameters
○笠原 慶亮 [1], 黒田 大祐 [2], カアベイロ ホセ [3], 長門石 曉 [4], 津本 浩平 [1,4]（[1] 東大・院工学・バイオエンジ, [2] 感染研・治ワク, [3] 九大・院薬, [4] 東大・院工学・医工 RS）
Keisuke Kasahara[1], Daisuke Kuroda[2], Jose Caaveiro[3], Satoru Nagatoishi[4], Kouhei Tsumoto[1,4] ([1]*Dept. Bioeng., Grad. Sch. Eng., Univ. Tokyo*, [2]*Res. Ctr. Drug Vaccine Dev., NIID*, [3]*Grad. Sch. Pharm. Sci., Kyusyu Univ.*, [4]*Med. Dev. Dev. Reg. Res. Ctr., Grad. Sch. Eng., Univ. Tokyo*)

1GA1530 **統計力学モデルの拡張による酵素反応の自由エネルギー地形の予測**
Predicting free energy landscapes of enzyme reactions by an extended statistical mechanical model
○劉 潤晶 [1], 大岡 紘治 [2], 新井 宗仁 [1,2,3]（[1] 東大・総合文化・生命環境, [2] 東大・教養, [3] 東大・理・物理）
Runjing Liu[1], Koji Ooka[2], Munehito Arai[1,2,3] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Col. Arts & Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

1GA1545 **ウイルスヘリオロドプシン V2HeR3 のプロトン輸送メカニズム解明に向けた FTIR 研究**
FTIR spectroscopic study for clarifying proton transporting mechanisms of viral heliorhodopsin (V2HeR3)
○水鳥 律 [1], 片山 耕大 [1,2], Béjà Oded[3], 神取 秀樹 [1,2]（[1] 名工大・院工, [2] オプトバイオテクノロジー研究センター, [3]Technion-Israel Inst. Tech.）
Ritsu Mizutori[1], Kota Katayama[1,2], Oded Béjà[3], Hideki Kandori[1,2] ([1]*Nagoya Inst. Tech.*, [2]*OptoBioTechnology Research Center*, [3]*Technion-Israel Inst. Tech.*)

1GB タンパク質：構造機能相関
Protein: Structure & Function

座長：加藤 晃一（生命創成探究センター），加藤 祐樹（名古屋大学），大貫 隼（分子科学研究所），鎌足 雄司（岐阜大学）
Session Chairs: Koichi Kato (ExCELLS), Yuki Kato (Nagoya Univ.), Jun Ohnuki (IMS), Yuji Kamatari (Gifu Univ.)

14:00〜16:30
B 会場（展示室 212（2 号館 1F））／Room B（Exhibition Room 212 (Bldg. 2, 1F)）

1GB1400 **pH 応答性伸縮タンパク質集合体の変形メカニズム**
Shape morphing mechanism of pH-responsive piston protein
○伊達 弘貴 [1], 菊池 幸祐 [1], 鱒村 颯太 [1], Li Xin[1], Thuc Toan Pham[1], 内橋 貴之 [2], 上久保 裕生 [3], 村田 和義 [4], 上野 隆史 [1]（[1] 東工大生命理工, [2] 名大院理, [3] 奈良先端大物質, [4]ExCELLS・生理学研究所）
Koki Date[1], Kosuke Kikuchi[1], Souta Masumura[1], Xin Li[1], Toan Pham Thuc[1], Takayuki Uchihashi[2], Hironari Kamikubo[3], Kazuyoshi Murata[4], Takafumi Ueno[1] ([1]*School of Life Science and Technology, Tokyo Institute of Technology*, [2]*Graduate School of Science, Nagoya University*, [3]*School of Science and Technology, NAIST, MS*, [4]*ExCELLS/NIPS*)

1GB1415 **緑色感受性色覚タンパク質のクライオ電子顕微鏡を用いた構造決定への挑戦**

The challenge to determine the structure of a green-sensitive cone pigment by cryo-EM

○大橋 沙也佳 [1], 片山 耕大 [1,2], 福田 昌弘 [3], 小島 朝翔 [3], 寿野 良二 [4], 杉田 征彦 [5], Nipawan Nuemket[6,7], 岩田 想 [6,8], 南後 恵理子 [8,9], 小林 拓也 [4], 野田 岳志 [3], 加藤 英明 [3], 神取 秀樹 [1,2]（[1] 名工大・院工, [2] オプトバイオロテクノロジー研究センター, [3] 東大院・総文, [4] 関西医科大学, [5] 京大・医生研, [6] 京大・医, [7] 高輝度光科学研究センター, [8] 理研, [9] 東北大・多元）

Sayaka Ohashi[1], Kota Katayama[1,2], Masahiro Fukuda[3], Asato Kojima[3], Ryoji Suno[4], Yukihiko Sugita[5], Nipawan Nuemket[6,7], So Iwata[6,8], Eriko Nango[8,9], Takuya Kobayashi[4], Takeshi Noda[3], Hideaki Kato[3], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst.Tech.*, [2]*OptoBioTechnology Research Center*, [3]*Arts and Science, The Univ. of Tokyo*, [4]*Kansai Medical University*, [5]*Institute for Life and Medical Sciences, Kyoto University*, [6]*Graduate School of Medicine, Kyoto University*, [7]*Japan Synchrotron Radiation Research Institute*, [8]*RIKEN Spring-8 Center*, [9]*Institute of Multidisciplinary Research for Advanced Materials*)

1GB1430 **グルタミン酸脱水素酵素におけるリガンド結合解離動態のクライオ電子顕微鏡構造解析**

Conformational and ligand-association dynamics of glutamate dehydrogenase in the mixture with ligands visualized by cryo-EM

○若林 大貴 [1,2,3], 大出 真央 [3,4], 中迫 雅由 [1,2]（[1] 慶應大・理工, [2] 理研・RSC, [3] 理研・CPR, [4]JST・さきがけ）

Taiki Wakabayashi[1,2,3], Mao Oide[3,4], Masayoshi Nakasako[1,2] ([1]*Dept. Phys., Keio Univ.*, [2]*RSC, RIKEN*, [3]*CPR, RIKEN*, [4]*PRESTO, JST*)

1GB1445 **M2 ムスカリン受容体（M_2R）活性化のための機能的ホットスポット残基を特定**

Identifying functional hotspot residues for activation in M2 muscarinic receptor (M_2R)

○杉浦 勇也 [1], 片山 耕大 [1,2], 住井 裕司 [1], 寿野 良二 [3], Putri Nur Arina Binti Mohd Ariff[1], 柴田 哲男 [1], 神取 秀樹 [1,2]（[1] 名工大・院工, [2] 名工大・オプトバイオテクノロジー研究センター, [3] 関西医大・医）

Yuya Sugiura[1], Kota Katayama[1,2], Yuji Sumii[1], Ryoji Suno[3], Putri Nur Arina Binti Mohd Ariff[1], Norio Shibata[1], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*OptoBioTechnology Research Center., Nagoya Inst. Tech.*, [3]*Kansai Medical University. Medical*)

1GB1500 **人工設計したペプチドナノポアの *β*-ターン周辺配列の再設計**

Redesign around *β*-turn of *de novo* peptide nanopore

○小川 莉奈 [1], 藤田 祥子 [1], 栢森 史浩 [2], 臼井 健二 [2], 川野 竜司 [1]([1] 東京農工大学工学府生命工学専攻, [2] 甲南大学　フロンティアサイエンス学部　生命化学科）

Rina Ogawa[1], Shoko Fujita[1], Fumihiro Kayamori[2], Kenji Usui[2], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, [2]*Faculty of Frontiers of Innovative Research in Science and Technology, Konan University*)

1GB1515 Structural Dynamics Study of a Bacterial Diterpene Cyclase CotB2 during Enzymatic Reaction

Atika Nur Rochmah[1], Masahiko Taguchi[1,2], Takaaki Fujiwara[1,2], Tomohisa Kuzuyama[3], Eriko Nango[1,2] ([1]*Grad. Sch. Sci., Univ. Tohoku*, [2]*IMRAM, Univ. Tohoku*, [3]*Grad. Sch. Agr. and Life Sci., Univ. Tokyo*)

1GB1530 **バーチャルスクリーニングに適した AlphaFold2 タンパク質立体構造モデルの選択**

Identifying suitable AlphaFold2 protein structure models for improved structure-based virtual screening

○内河 慶輔, 古井 海里, 大上 雅史（東京工業大学 情報理工学院 情報工学系）

Keisuke Uchikawa, Kairi Furui, Masahito Ohue (*Department of Computer Science, School of Computing, Tokyo Institute of Technology*)

1GB1545 SARS-CoV-2 スパイクタンパク質の二重蛍光ラベル化とラベル化試料の一分子蛍光分光法による構造ダイナミクスの解明

Double fluorophore labeling of SARS-CoV-2 spike protein and its structural dynamics revealed by single molecule fluorescence spectroscopy

○森 大晟 [1,2], 伊藤 優志 [1,2], 鈴木 干城 [3], 橋口 隆生 [3], 高橋 聡 [1,2]（[1] 東北大・多元研, [2] 東北大・院生命科学, [3] 京都大・医生研）

Taisei Mori[1,2], Yuji Itoh[1,2], Tateki Suzuki[3], Takao Hashiguchi[3], Satoshi Takahashi[1,2] ([1]*IMRAM, Univ. Tohoku*, [2]*Grad. Sch. Life Sci., Univ. Tohoku*, [3]*Inst. Life Med. Sci., Univ. Kyoto*)

1GB1600 ヒト抗菌ペプチド LL-37 とそのオルソログのヘリックス性に依存した DNA およびミセルとの相互作用様式の多様性

Helicity-dependent diversification of interaction modes of human antimicrobial peptide LL-37 and its orthologs with DNA and micelles

○柴垣 光希 [1], クリスナント ジェレミア オクタビアン [1], テフェラ デサレニ アベジェ [1], 月岡 耕太郎 [1], 上田 和佳 [1], 加納 康平 [1], 谷 昊 [1], 平井 芙実 [1], 相沢 智康 [1,2]（[1] 北大・院生命, [2] 北大・院先端生命）

Mitsuki Shibagaki[1], Oktavian Chrisnanto Jeremia[1], Abeje Tefera Dessalegn[1], Kotaro Tsukioka[1], Waka Ueda[1], Kohei Kano[1], Hao Gu[1], Fumi Hirai[1], Tomoyasu Aizawa[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

1GB1615 全原子分子動力学計算で明らかになった F_O モーターのトルク発生機構

Torque generation mechanism of F_O motor elucidated by the all-atom molecular dynamics simulation

○神山 幸成 [1], パーキン 暖 [2], 高野 光則 [1,2]（[1] 早大・先進理工・物理応物, [2] 早大・理工総研）

Yukinari Kamiyama[1], Dan Parkin[2], Mitsunori Takano[1,2] ([1]*Dept. of Pure & Appl. Phys., Grad. Scl. Adv. Sci. & Eng., Waseda Univ.*, [2]*Waseda Res. Inst. for Sci. & Eng.*)

1GC タンパク質：計測・解析、タンパク質工学／進化工学
Protein: Measurement & Analysis, Engineering

座長：田中 康太郎（名古屋大学），小杉 貴洋（分子科学研究所），三野 広幸（名古屋大学），鈴木 雄太（京都大学）

Session Chairs: Kotaro Tanaka (Nagoya Univ.), Takahiro Kosugi (IMS), Hiroyuki Mino (Nagoya Univ.), Yuta Suzuki (Kyoto Univ.)

14:00〜16:30

C 会場（会議室 221（2 号館 2F））／Room C（Conference Room 221 (Bldg. 2, 2F)）

1GC1400 真空紫外円二色性分光法による β-lactoglobulin の生体膜相互作用過程の時間分解観測

Time-resolved observation of the membrane interaction process of β-lactoglobulin by vacuum-ultraviolet circular-dichroism spectroscopy

○橋本 聡 [1], 松尾 光一 [2]（[1] 広島大・先進理工, [2] 広島大・放射光）

Satoshi Hashimoto[1], Koichi Matsuo[2] ([1]*Grad. Sch. Adv. Sci. Eng., Univ. Hiroshima*, [2]*HiSOR., Univ. Hiroshima*)

1GC1415 密着結合タンパク質 ZO-1 による液-液相分離の生細胞内 Raman-Brillouin 観測

Raman-Brillouin observation of LLPS of a tight junction protein ZO-1 in a living cell

○永井 海地 [1], 澁谷 蓮 [1], 梶本 真司 [1,2], 田原 進也 [1], 平野 咲雪 [4], 木下 典之 [3], 上野 直人 [3], 中林 孝和 [1]（[1] 東北大学大学院 薬学部, [2]JST さきがけ, [3] 自然科学研究機構 基礎生物研究所, [4] 自然科学研究機構 生命創生探究センター）

Kaichi Nagai[1], Ren Shibuya[1], Shinji Kajimoto[1,2], Shinya Tahara[1], Sayuki Hirano[4], Noriyuki Kinoshita[3], Naoto Ueno[3], Takakazu Nakabayashi[1] ([1]*Graduate school of pharmaceutical sciences Tohoku univ.*, [2]*JST PRESTO*, [3]*National institute for Basic Biology National Institutes of National Science*, [4]*Exploratory Research Center on Life and Living Systems National Institutes of Natural Sciences*)

1GC1430 **タンパク質間相互作用を利用したナノポアによるペプチド検出の検討**
Investigation of Peptide Detection with Nanopore Using Protein-Protein Interaction
○山地 未紗, 川野 竜司（東京農工大学・生命工学）
Misa Yamaji, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

1GC1445 **液-液相分離法：水溶液中でのタンパク質の濃縮と高感度ラマン測定への応用**
Liquid-liquid phase separation method: protein condensation and its application to highly sensitive Raman measurements in aqueous solution
○齋藤 彩夏 [1], 飛田 怜央奈 [1], 田原 進也 [1], 梶本 真司 [1,2], 中林 孝和 [1]（[1] 東北大院・薬, [2]JST さきがけ）
Ayaka Saito[1], Reona Tobita[1], Shinya Tahara[1], Shinji Kajimoto[1,2], Takakazu Nakabayashi[1] ([1]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [2]*JST PRESTO*)

1GC1500 **進化を遡る 2step アプローチを用いた単量体 IFNγ の設計とがん免疫療法への適用に向けた検討**
Design of monomeric IFNγ via a two-step evolutionary tracing back approach and biological investigation for cancer immunotherapy
○後藤 陽太 [1,2], 宮房 孝光 [3], 本田 真也 [1,2]（[1] 東京大学大学院 新領域創成科学研究科, [2] 産業技術総合研究所 バイ オメディカル研究部門, [3] 産業技術総合研究所 生物プロセス研究部門）
Yota Goto[1,2], Takamitsu Miyafusa[3], Shinya Honda[1,2] ([1]*Graduate School of Frontier Sciences, The University of Tokyo*, [2]*Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology*, [3]*Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology*)

1GC1515 **mRNA 提示法において mRNA 配列がライブラリ多様性に及ぼす影響の大規模解析**
Large-scale analysis of the effect of mRNA sequences on the library diversity in mRNA display technology
○梅本 駿 [1], 近藤 太志 [1], 藤野 公茂 [1], 林 剛介 [1], 村上 裕 [1,2]（[1] 名大・院工学, [2] 名大・ナノライフ）
Shun Umemoto[1], Taishi Kondo[1], Tomoshige Fujino[1], Gosuke Hayashi[1], Hiroshi Murakami[1,2] ([1]*Grad. Sch. Eng., Nagoya Univ.*, [2]*Inst. Nano-Life-Systems, Inst. of Innov. for Future Society, Nagoya Univ.*)

1GC1530 **疎水性 β バレルナノポア形成 *de novo* ペプチドの無細胞合成手法探索**
Exploration of cell-free synthesis methods for hydrophobic β-barrel nanopore-forming *de novo* peptides
○藤田 祥子 [1], 川村 出 [2], 川野 竜司 [1]（[1] 東京農工大学 工学府 生命工学専攻, [2] 横浜国立大学 大学院理工学府 化学・生命系理工学専攻）
Shoko Fujita[1], Izuru Kawamura[2], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, [2]*Graduate School of Engineering Science, Yokohama National University*)

1GC1545 **リポソームディスプレイを用いた *de novo* ナノポア形成ペプチドの指向性進化**
A direct evolution of *de novo* nanopore-forming peptide with liposome display
○佐藤 茉奈 [1], 藤田 祥子 [1], 松浦 友亮 [2], 川野 竜司 [1]（[1] 東京農工大学　工学部　生命工学科, [2] 東京工業大学　地球生命研究所）
Mana Sato[1], Shoko Fujita[1], Tomoaki Matsuura[2], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology.*, [2]*Earth-Life Science Institute, Tokyo Institute of Technology*)

1GC1600 **酵母によるシステインリッチタンパク質の遺伝子組換え発現におけるジスルフィド架橋ミスペアリング分子種の異常分泌**
Abnormal secretion of disulfide bridge mispairing molecular species in the recombinant expression of cysteine-rich protein by yeast
○花岡 杏美 [1], 吉川 一歩 [1], 飯塚 友菜 [1], 鄭 靖康 [1], 蔡 文清 [1], 中嶋 友里枝 [1], 石原 颯馬 [2], 相沢 智康 [1,2]（[1] 北大・院生命, [2] 北大・理）
Ami Hanaoka[1], Ichiho Yoshikawa[1], Tomona Iizuka[1], Jingkang Zheng[1], Wenqing Cai[1], Yurie Nakajima[1], Soma Ishihara[2], Tomoyasu Aizawa[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Sch. Sci., Hokkaido Univ.*)

1GC1615　**進化分子工学による cis 型アゾベンゼン特異的人工抗体の創製と光細胞操作ツールへの応用**
In vitro evolution of cis-azobenzene-specific artificial antibodies for chemo-optogenetic control of cell function
○宮崎 友輝 [1], 藤野 公茂 [2], 吉井 達之 [1], 舟根 守 [2], 村田 直哉 [2], Kim Chung Nguyen[2], 田原 海 [1], 吉川 優 [1], 深谷 菜摘 [1], 長門石 曉 [4], 津本 浩平 [4], 林 剛介 [2], 村上 裕 [2,3], 築地 真也 [1]（[1] 名工大院工, [2] 名大院工, [3] 名大未来ナノ, [4] 東大院工）
Tomoki Miyazaki[1], Tomoshige Fujino[2], Tatsuyuki Yoshii[1], Mamoru Funane[2], Naoya Murata[2], Chung Nguyen Kim[2], Kai Tahara[1], Masaru Yoshikawa[1], Natsumi Fukaya[1], Satoru Nagatoishi[4], Kouhei Tsumoto[4], Gosuke Hayashi[2], Hiroshi Murakami[2,3], Shinya Tsukiji[1] ([1]*Graduate School of Engineering, Nagoya Institute of Technology*, [2]*Graduate School of Engineering, Nagoya University*, [3]*Institute of Nano-Life-Systems, Institute of Innovation for Future Society, Nagoya University*, [4]*Graduate School of Engineering, The University of Tokyo*)

1GD　天然変性、ヘム、膜タンパク質、神経・感覚
Intrinsic disorder, Heme, Membrane protein, Neuroscience & Sensory systems

座長：伊藤 暁（分子科学研究所），阿部 一啓（名古屋大学），岩本 真幸（福井大学）
Session Chairs: Satoru Itoh (IMS), Kazuhiro Abe (Nagoya Univ.), Masayuki Iwamoto (Fukui Univ.)

14:00〜16:30
D 会場（会議室 222+223（2 号館 2F））／Room D（Conference Room 222+223 (Bldg. 2, 2F)）

1GD1400　**タンパク質の液-液相分離からの凝集に対する分子ピンセット CLR01 の適用**
Application of molecular tweezer CLR01 to protein aggregation from liquid-liquid phase separation
○髙宮 諒翔 [1], 田原 進也 [2], Schrader Thomas[3], Klärner Frank-Gerrit[3], Bitan Gal[4], 中林 孝和 [2]（[1] 東北大学薬学部, [2] 東北大学大学院薬学研究科, [3]Department of Chemistry, University of Duisburg-Essen, [4]Department of Neurology, University of California at Los Angeles）
Masato Takamiya[1], Shinya Tahara[2], Thomas Schrader[3], Frank-Gerrit Klärner[3], Gal Bitan[4], Takakazu Nakabayashi[2] ([1]*Faculty of Pharmaceutical Sciences, Tohoku University*, [2]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [3]*Department of Chemistry, University of Duisburg-Essen*, [4]*Department of Neurology, University of California at Los Angeles*)

1GD1415　**蛍光顕微鏡と光ピンセットを用いた FUS タンパク質液滴の融合ダイナミクスの研究**
Elucidating fusion dynamics of FUS protein droplets using fluorescence microscopy and optical tweezers
Syamil Muharror Ahsanul Husna[1,2], Atsumi Hando[1,3], Saori Kanbayashi[1], Kiyoto Kamagata[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Dept. Chem., Fac. Sci., Tohoku Univ.*, [3]*Dept. Life Sci., Grad. Sch. Sci., Tohoku Univ.*)

1GD1430　**天然変性タンパク質による相分離濃縮を利用した少量短鎖オリゴの連結技術**
Assembly of short and small amounts of DNAs using the DNA concentration ability of IDP droplets
○上野 大慈, 皆川 慶嘉, 野地 博行（東京大・工学系研究科応用化学）
Taiji Ueno, Yoshihiro Minagawa, Hiroyuki Noji (*Grad. Engeneering, Applied Chemistry., Univ. Tokyo*)

1GD1445　**転写関連蛋白質による多層的液液相分離に関する粗視化分子動力学シミュレーション研究**
Coarse-grained MD simulations for the formation of multi-layered phase separation of transcription-related proteins
○水谷 淳生 [1], タン チェン [2], 杉田 有治 [2,3,4], 高田 彰二 [1]（[1] 京大・院理学, [2] 理研・RCCS, [3] 理研・CPR, [4] 理研・BDR）
Azuki Mizutani[1], Cheng Tan[2], Yuji Sugita[2,3,4], Shoji Takada[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*RIKEN, RCCS*, [3]*RIKEN, CPR*, [4]*RIKEN, BDR*)

1GD1500 **祖先型ヘモグロビン α 鎖および β 鎖の構造ダイナミクス**
Structural dynamics of ancestral hemoglobin α and β chains
○入谷 悠, 石川 春人, 水谷 泰久（阪大・院理学）
Yu Iritani, Haruto Ishikawa, Yasuhisa Mizutani (*Grad. Sch. Sci., Univ. Osaka*)

1GD1515 **キメラシン：β バレル構造をもつポア形成ペプチドとポア形成タンパク質 α ヘモリシンの統合**
Chimerasin: Pore-forming peptide with β-barrel structure integrated into pore-forming protein, α-hemolysin
○中田 彩夏 [1], 山地 未紗 [1], 小川 莉奈 [1], 田中 良和 [2], 川野 竜司 [1]（[1] 東京農工大・生命工学, [2] 東北大学　大学院　生命科学研究科）
Ayaka Nakada[1], Misa Yamaji[1], Rina Ogawa[1], Yoshikazu Tanaka[2], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, [2]*Graduate School of Life Sciences, Tohoku University.*)

1GD1530 Harnessing the power of machine learning and high-throughput molecular dynamics simulations to predict protein-lipid interactions
Kyle Ian Peter Le Huray[1,2], Frank Sobott[1], He Wang[3], Antreas Kalli[2] ([1]*School of Molecular and Cellular Biology, Faculty of Biological Sciences, University of Leeds, Leeds, UK*, [2]*Leeds Institute of Cardiovascular and Metabolic Medicine, School of Medicine, University of Leeds, Leeds, UK*, [3]*School of Computing, University of Leeds, Leeds, UK*)

1GD1545 **化学受容ニューロンで発現する GPCR SRX は温度受容体候補である**
GPCR SRX expressed in a pair of chemosensory neurons is a thermoreceptor candidate gene
○森本 千夏 [1,2], 宮崎 智瑛 [2], 三浦 徹 [1,2], 大西 康平 [1,2], 太田 茜 [1,2], 久原 篤 [1,2,3]（[1] 甲南大学 大学院自然科学研究科, [2] 甲南大学 統合ニューロバイオロジー研究所, [3]PRIME, AMED）
Chinatsu Morimoto[1,2], Chie Miyazaki[2], Tohru Miura[1,2], Kohei Ohnishi[1,2], Akane Ohta[1,2], Atsushi Kuhara[1,2,3] ([1]*Graduate School of Natural Science, Konan University*, [2]*Institute for integrative Neurobiology, Konan University*, [3]*PRIME, AMED*)

1GD1600 **ヒト神経細胞の活動依存的転写は転写調節因子 CREB がヒストンアセチル化酵素 CBP で決定された標的遺伝子に繰り返し結合することで促進される**
Repetitive CREB binding to gene loci predetermined by CBP induces activity-dependent gene expression in human cortical neurons
○渥美 友梨 [1], 菅生 紀之 [1], 岩田 亮平 [2], Vanderhaeghen Pierre[2], 山本 亘彦 [1,3]（[1] 大阪大学大学院生命機能研究科, [2]VIB-KU Leuven, Center for Brain & Disease Research, [3]Institute of Neurological and Psychiatric disorders, Shenzhen Bay Laboratory）
Yuri Atsumi[1], Noriyuki Sugo[1], Ryohei Iwata[2], Pierre Vanderhaeghen[2], Nobuhiko Yamamoto[1,3] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*VIB-KU Leuven, Center for Brain & Disease Research*, [3]*Institute of Neurological and Psychiatric disorders, Shenzhen Bay Laboratory*)

1GD1615 **新規蛍光寿命プローブを用いたシナプス可塑性の長期的維持に関わるメモリー分子の網羅的探索**
Identification of memory molecules involved in synaptic plasticity using novel fluorescence lifetime probes
○長澤 裕太郎 [1,2], 村越 秀治 [1,2]（[1] 自然科学研究機構 生理学研究所 脳機能計測・支援センター 多光子顕微鏡室, [2] 総合研究大学院大学 生命科学研究科 生理科学専攻）
Yutaro Nagasawa[1,2], Hideji Murakoshi[1,2] ([1]*Supportive Center for Brain Research, National Institute for Physiological Sciences*, [2]*Department of Physiological Sciences, SOKENDAI (The Graduate University for Advanced Studies)*)

1GE　DNA・DNA 結合タンパク質、RNA・RNA 結合タンパク質、DNA/RNA ナノテクノロジー、クロマチン・染色体
DNA & DNA binding proteins, RNA & RNA binding proteins, DNA/RNA nanotechnology, Chromatin & Chromosomes

座長：前島 一博（国立遺伝学研究所），島本 勇太（国立遺伝学研究所），木村 暁（国立遺伝学研究所）
Session Chairs: Kazuhiro Maeshima (NIG), Yuta Shimamoto (NIG), Akatsuki Kimura (NIG)

14:00〜16:45
E 会場（会議室 224（2 号館 2F））／Room E（Conference Room 224 (Bldg. 2, 2F)）

1GE1400　Single molecule microscopy reveals that importin α slides along DNA while transporting cargo molecules
Trishit Banerjee[1,2], Kazuya Jibiki[3], Hinata Sugasawa[4], Noriko Yasuhara[3,4], Kiyoto Kamagata[1,2] ([1]*IMRAM, Tohoku Univ.*, [2]*Dep. of Chem., Grad. Sch. of Sci., Tohoku Univ.*, [3]*Dep. of Biosci., College of Humanities and Sci., Nihon Univ.*, [4]*Grad. Sch. of Integrated Basic Sci., Nihon Univ.*)

1GE1415　Single-molecule fluorescence studies of the reaction mechanism of replication fork remodeling enzyme
Liu Chieh-Kai[1], Chiu Yu-Hui[2], Chen Yen-Ju[2], Chi Peter[2], Li Hung-Wen[1] ([1]*Department of Chemistry, National Taiwan University, Taipei, Taiwan*, [2]*Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan*)

1GE1430　細胞核内における DNA underwinding の力学的理解
Mechanical understanding of DNA underwinding in a cell nucleus
○福手 淳平 [1,2], 牧 功一郎 [1,2,3], 安達 泰治 [1,2,3]（[1] 京大・院生命科学, [2] 京大・医生研, [3] 京大・院工学）
Jumpei Fukute[1,2], Koichiro Maki[1,2,3], Taiji Adachi[1,2,3] ([1]*Grad. Sch. Biostudies, Kyoto Univ.*, [2]*Inst. Life & Med. Sci., Kyoto Univ.*, [3]*Grad. Sch. Eng., Kyoto Univ.*)

1GE1445　DNA カーテン上の転写因子 YY1 の 1 分子蛍光イメージング
Single-molecule fluorescence imaging of transcription factor YY1 on DNA curtain
○晏 晞, 高田 彰二, 寺川 剛（京都大学大学院理学研究科）
Xi Yan, Shoji Takada, Tsuyoshi Terakawa (*Graduate School of science, Kyoto University.*)

1GE1500　液-液相分離により生じる FUS 液滴と RNA の相互作用のラマン顕微分光での検出
Interaction between FUS proteins and RNA in droplets formed via liquid-liquid phase separation detected by Raman microscopy
○松浦 宇宙 [1], 田原 進也 [1], 梶本 真司 [1,2], 中林 孝和 [1]（[1] 東北大学院・薬学部, [2]JST・さきがけ）
Uchu Matsuura[1], Shinya Tahara[1], Shinji Kajimoto[1,2], Takakazu Nakabayashi[1] ([1]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [2]*JST PRESTO*)

1GE1515　一分子蛍光測定を用いた SARS-CoV-2 N タンパク質と RNA の結合様式の解明
Structural characterization of RNA upon the binding with SARS-CoV-2 N protein by single molecule fluorescence measurements
○金田 直也 [1,2], 遠藤 隼 [1,3], 鈴木 怜和 [1,3], 伊藤 優志 [1,2,3], 小井川 浩之 [1,2,3], 高橋 聡 [1,2,3]（[1] 東北大・多元研, [2] 東北大院・理学, [3] 東北大院・生命）
Naoya Kaneda[1,2], Shun Endo[1,3], Leo Suzuki[1,3], Yuji Itoh[1,2,3], Hiroyuki Oikawa[1,2,3], Satoshi Takahashi[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Dep. Chem., Grad. Sch. Sci., Tohoku Univ.*, [3]*Grad. Sch. Life Sci., Tohoku Univ.*)

1GE1530　リング状 DNA を用いた計算とナノポアデコーディングによる microRNA パターン認識
Recognizing Over/Under-expression Patterns of microRNA using ring-shaped DNA-based computing and its Nanopore Decoding
○江村 聡馬, 神原 史佳, 滝口 創太郎, 川野 竜司（東京農工大学　工学部　生命工学科）
Soma Emura, Fumika Kambara, Sotaro Takiguchi, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology.*)

1GE1545 **複製フォークにおけるヒストン H3/H4 リサイクリングの分子動力学シミュレーション**
Molecular dynamics simulations of parental histone H3/H4 recycling at a replication fork
○長江 文立津, 高田 彰二, 寺川 剛（京都大・院理学・生物物理）
Fritz Nagae, Shoji Takada, Tsuyoshi Terakawa (*Dept. of Biophys., Grad. Sch. of Sci., Kyoto Univ.*)

1GE1600 Replication-dependent histone (Repli-Histo) labeling revealed that chromatin motion can determine DNA replication timing
Katsuhiko Minami[1,2], Satoru Ide[1,2], Sachiko Tamura[1], Masato T. Kanemaki[1,2], Kazuhiro Maeshima[1,2] ([1]*National Institute of Genetics*, [2]*Graduate Institute for Advanced Studies, SOKENDAI*)

1GE1615 **リンカーヒストンはクロマチンドメインの液体状の「のり」として働く**
Linker histone H1 serves as liquid-like “glue” of chromatin domain
○島添 將誠 [1,2], 井手 聖 [1,2], 田村 佐知子 [1], 前島 一博 [1,2]（[1] 遺伝研 ゲノムダイナミクス研究室, [2] 総研大 遺伝学専攻）
Masa A. Shimazoe[1,2], Satoru Ide[1,2], Sachiko Tamura[1], Kazuhiro Maeshima[1,2] ([1]*Genome Dynamics Lab, National Institute of Genetics*, [2]*Dep. of Genetics, SOKENDAI*)

1GE1630 **微小空間への閉じ込めが 12-mer ヌクレオソームアレイの高次構造形成を促進する**
Microspace confinement promotes the formation of higher-order structures of 12-mer nucleosome arrays
○岡部 誠大 [1], 飯塚 怜 [1], 赤津 綜隆 [1], 越後谷 健太 [1], 鯨井 智也 [2], 胡桃坂 仁志 [1,2], 上村 想太郎 [1]（[1] 東大・院理・生科, [2] 東大・定量研）
Masahiro Okabe[1], Ryo Iizuka[1], Munetaka Akatsu[1], Kenta Echigoya[1], Tomoya Kujirai[2], Hitoshi Kurumizaka[1,2], Sotaro Uemura[1] ([1]*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. of Tokyo*, [2]*Inst. For Quant, Biosci., The Univ. of Tokyo*)

1GF 分子モーター
Molecular motor

座長：寺田 智樹（名古屋大学），大友 章裕（分子科学研究所），原島 崇徳（分子科学研究所）
Session Chairs: Tomoki P. Terada (Nagoya Univ.), Akihiro Otomo (IMS), Takanori Harashima (IMS)

14:00〜16:15
F 会場（会議室 231（2 号館 3F））／Room F（Conference Room 231 (Bldg. 2, 3F)）

1GF1400 **構成的手法により 2 つの異なるメカニズムが分子モーターの一方向性運動を生む仕組みを明らかにする**
Constructive approach revealed the existence of two distinct mechanisms that generate unidirectionality of biomolecular motors
○中山 慎太郎 [1,2], 古田 茜 [2], 吉雄 麻喜 [2], 網野 美紗子 [2], 大岩 和弘 [1,2], 古田 健也 [2]（[1] 兵県大・院理学, [2] 情報通信研究機構・未来 ICT 研究所）
Shintaro Nakayama[1,2], Akane Furuta[2], Maki Yoshio[2], Misako Amino[2], Kazuhiro Oiwa[1,2], Ken'ya Furuta[2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICT Res. Inst., NICT*)

1GF1415 **ミトコンドリア型特異的阻害因子 IF_1 に感受的な、好熱菌 PS3 由来 F_1-ATPase の再設計**
Redesigning of F_1-ATPase from thermophilic *Bacillus* PS3 with mitochondrial-specific IF_1-inhibition sensitivity
○畑崎 優一郎 [1], 小林 稜平 [2], 渡邉 亮 [1], 上野 博史 [1], 野地 博行 [1]([1] 東京大学工学系研究科応用化学専攻, [2] 自然科学研究機構 分子科学研究所 計算科学研究センター）
Yuichiro Hatasaki[1], Ryohei Kobayashi[2], Ryo Watanabe[1], Hiroshi Ueno[1], Hiroyuki Noji[1] ([1]*Department of Applied Chemistry, Graduate School of Engineering, University of Tokyo.*, [2]*Research Center for Computational Science, Institute for Molecular Science.*)

1GF1430 微小管の集団運動における細胞質ダイニンの機械的特性の効果
Effects of mechanical properties of cytoplasmic dynein on collective motion of microtubules
○原田 洋祐 [1,2], 大岩 和弘 [1,2]（[1] 兵県大・院理学, [2]NICT 未来 ICT 研究所）
Yosuke Harada[1,2], Kazuhiro Oiwa[1,2] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICT Res. Inst., NICT*)

1GF1445 複数のプロトン駆動トルク発生ユニットを有する ATP 合成酵素の *pmf* 依存性
The *pmf* dependence of ATP synthesis/hydrolysis of ATP synthase with multiple torque generating units
○安田 秩都, 丸井 里駆, 上野 博史, 野地 博行（東大院・工・応用化学）
Kiyoto Yasuda, Riku Marui, Hiroshi Ueno, Hiroyuki Noji (*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

1GF1500 Directionality on kinesin-1 motility can be determined depending on the anchor points
Rieko Sumiyoshi, Masahiko Yamagishi, Junichiro Yajima (*Grad. Arts & Sci., Univ. Tokyo*)

1GF1515 アクチン結合ヌクレオチドの交換はミオシン II+ATP によって促進される
Exchange of actin-bound nucleotides is enhanced by myosin II in the presence of ATP
○歳納 健太, 上田 太郎（早稲田大学 理工学術院 先進理工学研究科 物理学及応用物理学専攻）
Kenta Toshino, Taro QP Uyeda (*Dept.Pure &Appl. Physics, Grad. Sch. Adv. Sci & Eng., Waseda Univ.*)

1GF1530 流動的な脂質膜表面に結合したミオシン-1c が生み出すアクチンフィラメントのキラルな 3 次元運動
Myosin-1c bound to fluid lipid membranes drives the 3D chiral motion of F-actin
○佐藤 優成 [1], 吉村 孝平 [2], 松田 恭平 [1], 丸茂 哲聖 [1], 原口 武士 [3], 山岸 雅彦 [1], 須河 光弘 [1], 伊藤 光二 [2,3], 矢島 潤一郎 [1]（[1] 東京大・院・総合文化・ 広域科学, [2] 千葉大・院・融合理工・生物, [3] 千葉大・院・理学・生物）
Yusei Sato[1], Kohei Yoshimura[2], Kyohei Matsuda[1], Akisato Marumo[1], Takeshi Haraguchi[3], Masahiko Yamagishi[1], Mitsuhiro Sugawa[1], Kohji Ito[2,3], Junichiro Yajima[1] ([1]*Dep. of Life Sci., Grad. School of Arts and Sci., The Uni. of Tokyo*, [2]*Dep. of Biology, Chiba Uni.*, [3]*Dep. of Biology, Chiba Uni.*)

1GF1545 巨大繊毛虫 *Spirostomum ambiguum* における繊毛基底小体から伸びる表層微小管束間の滑り運動
Elongation mechanism of the giant unicellular ciliate *Spirostomum ambiguum*:Active sliding between cortical microtubule ribbons
○中村 公祐 [1,2], 端山 拓希 [1], 小嶋 寛明 [2], 大岩 和弘 [1,2], 園部 誠司 [1]（[1] 兵県大・院理学, [2] 情報通信研究機構・未来 ICT 研究所）
Kosuke Nakamura[1,2], Hiroki Hayama[1], Hiroaki Kojima[2], Kazuhiro Oiwa[1,2], Seiji Sonobe[1] ([1]*Grad. Sch. Sci., Univ. Hyogo*, [2]*Adv. ICT Res. Inst., NICT*)

1GF1600 クライオ電子顕微鏡による 14 本から 16 本プロトフィラメント GMPCPP 微小管の構造解析
14 to 16 protofilament GMPCPP-microtubules structures revealed by cryo-EM
○前嶋 捷久 [1], 岡本 玲菜 [1], 今井 洋 [1], 梶村 直子 [2], 光岡 薫 [2], 廣瀬 未果 [3], 加藤 貴之 [3], 成田 哲博 [4], 昆 隆英 [1]（[1] 阪大・院理, [2] 阪大・超高圧電子顕微鏡センター, [3] 阪大・蛋白質研究所, [4] 名古屋大学大学院理学研究科）
Toshihisa Maeshima[1], Reina Okamoto[1], Hiroshi Imai[1], Naoko Kajimura[2], Kaoru Mitsuoka[2], Mika Hirose[3], Takayuki Kato[3], Akihiro Narita[4], Takahide Kon[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Res. Ctr. for UHVEM, Osaka Univ.*, [3]*IPR, Osaka Univ.*, [4]*Grad. Sch. Sci., Nagoya Univ.*)

1GG 細胞生物学的課題
Cell biology

座長：大嶋 篤典（名古屋大学），廣澤 幸一朗（岐阜大学），村越 秀治（生理学研究所）
Session Chairs: Atsunori Oshima (Nagoya Univ.), Koichiro M. Hirosawa (Gifu Univ.), Hideji Murakoshi (NIPS)

14:00〜16:45
G 会場（会議室 232+233（2 号館 3F））／Room G（Conference Room 232+233 (Bldg. 2, 3F)）

1GG1400 **1 粒子・超解像顕微鏡観察による細胞外小胞の標的細胞への選択的結合機構の解明**
Mechanisms of selective binding of extracellular vesicles to cells as revealed by single-particle tracking and super-resolution microscopy
○磯貝 樹 [1], 廣澤 幸一朗 [2], 菅野 未希 [3], 木塚 康彦 [2,4], 横田 康成 [5], 鈴木 健一 [2,4,6]（[1] 岐阜大・院・連農, [2] 岐阜大・iGCORE, [3] 岐阜大・院・自然研, [4] 科技振・CREST, [5] 岐阜大・工, [6] 国立がん研）
Tatsuki Isogai[1], Koichiro M. Hirosawa[2], Miki Kanno[3], Yasuhiko Kizuka[2,4], Yasunari Yokota[5], Kenichi G. N. Suzuki[2,4,6] ([1]*UGSAS, Univ. Gifu*, [2]*iGCORE, Univ. Gifu*, [3]*Grad. Sch. Nat. Sci. Tech., Univ. Gifu*, [4]*CREST, JST*, [5]*Dept. Eng., Univ. Gifu*, [6]*Natl. Cancer Ctr. Res. Inst.*)

1GG1415 **共生細菌はドリル運動で狭小通路を突破する**
Symbiotic bacteria break through narrow passage by flagellar wrapping
○吉岡 青葉 [1], 菅 哲朗 [2], 菊池 義智 [3], 中根 大介 [1]（[1] 電通大・基盤理工, [2] 電通大・機械知能, [3] 産総研・生物プロセス）
Aoba Yoshioka[1], Tetsuo Kan[2], Yoshitomo Kikuchi[3], Daisuke Nakane[1] ([1]*Dept. Eng. Sci., UEC*, [2]*Dept. Mech. and Int. Sys. Eng., UEC*, [3]*Dept. BPRI, AIST*)

1GG1430 **ATP 枯渇時の細胞内小胞運動の劇的な低下と細胞骨格との関係**
Drastic decrease in intracellular vesicle motility during ATP depletion and its relationship to the cytoskeleton
○太田 英暁, 樋口 秀男（東大院・理）
Hideaki Ota, Hideo Higuchi (*Grad. Sch. Sci., Univ. Tokyo*)

1GG1445 **温泉の水流がナビゲートする表面付着細菌の長旅**
Water flow navigates the long journey of surface-associated bacteria living in hot springs
○上村 直輝 [1], 玉腰 雅忠 [2], 中根 大介 [1]（[1] 電通大・基盤理工, [2] 東京薬大・生命科学部）
Naoki Uemura[1], Masatada Tamakoshi[2], Daisuke Nakane[1] ([1]*Dept. Eng. Sci., UEC*, [2]*Dept. Mol. Biol., TUPLS*)

1GG1500 Boundary-driven separation and reassembly of migrating cell sheets induce fluctuating dynamics and morphology by tuning local interactions
Mitsuru Sentoku[1], Masaharu Endo[1], Miki Takei[1], Yusuke Koshita[2], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

1GG1515 **サイトカラシン D のアクチンダイナミクス阻害におけるアロステリック効果**
Cytochalasin D inhibits actin polymerization dynamics allosterically
○三谷 隆大 [1], 武田 修一 [2], 藤原 郁子 [1], 本多 元 [1]（[1] 長岡技大・物質生物, [2] 岡山大・異分野基礎研）
Takahiro Mitani[1], Shuichi Takeda[2], Ikuko Fujiwara[1], Hajime Honda[1] ([1]*Dept. of Matl. Sci. and Bioeng., Nagaoka Univ. of Tech.*, [2]*Okayama Univ., RIIS*)

1GG1530 **微小管の機械的性質におけるチューブリン C 末端尾部の役割**
Role of tubulin C terminal tail on the mechanical properties of microtubules
Senjuti Nowroz[1], Syeda Rubaiya Nasrin[2], Takefumi Yamashita[3], Kazuki Sada[1,4], Akira Kakugo[2] ([1]*Grad. Sch. Chem.Sci. and Eng., Hokkaido univ*, [2]*Grad. Sch. Sci., Kyoto Univ*, [3]*Res.Cent. Adv. Sci. Tech., Tokyo univ.,*, [4]*Fac. Sci. , Hokkaido University,*)

1GG1545 **RasGEFX は Ras の自発的な興奮を制御し、RasGEFB/M/U とともランダムな細胞運動に寄与する**
RasGEFX regulates spontaneous Ras excitability with RasGEFB/M/U for random cell migration
○岩本 浩司 [1], 松岡 里実 [1,2,3], 上田 昌宏 [1,2,3]（[1] 大阪大学 大学院理学研究科, [2] 大阪大学 大学院生命機能研究科, [3] 理化学研究所 生命機能科学研究センター）
Koji Iwamoto[1], Satomi Matsuoka[1,2,3], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. of Front. Biosci., Osaka Univ.*, [3]*BDR, RIKEN*)

1GG1600 Membrane backtracking in phagocytosis against opsonized glass microneedle revealed maximum engulfment capacity regulation in macrophages
Dan Horonushi[1], Amane Yoshida[1], Yoshiki Nakata[1], Mitsuru Sentoku[1], Yuya Furumoto[1], Toshiki Azuma[1], Sota Suzuki[1], Maiha Ando[1], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

1GG1615 巨大化細胞を用いた一細胞内シグナル伝達機構の研究
Use of giant cells to study intracellular signaling mechanisms
○林田 幸久, 森本 雄祐（九州工業大学大学院情報工学府）
Yukihisa Hayashida, Yusuke V Morimoto (*Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*)

1GG1630 Roles of Potassium in Mitochondrial Functions
Jannatul Naima[1,2], Yoshihiro Ohta[1] ([1]*Department of Biotechnology and Life Science, Graduate School of Engineering, Tokyo University of Agriculture and Technology*, [2]*Department of Pharmacy, University of Chittagong, Bangladesh*)

1GH 生体膜・人工膜、化学受容
Biological & Artificial membrane, Chemoreception

座長：岡 俊彦（静岡大学），山崎 昌一（静岡大学），湊元 幹太（三重大学）
Session Chairs: Toshihiko Oka (Shizuoka Univ.), Masahito Yamazaki (Shizuoka Univ.), Kanta Tsumoto (Mie Univ.)

14:00〜16:15
H 会場（会議室 234（2 号館 3F））／Room H（Conference Room 234 (Bldg. 2, 3F)）

1GH1400 膜タンパク質の一分子解析のためのナノフルイディクス基板支持モデル細胞膜
Nanofluidic supported model cell membrane for single molecular analysis of membrane-bound proteins
○吉村 優[1], 小松 亮太[1], 遊佐 真一[2], 森垣 憲一[3]（[1] 神戸大・院農学, [2] 兵庫県立大・院工学, [3] 神戸大・バイオシグナル総合研究センター）
Yu Yoshimura[1], Ryota Komatsu[1], Shin-ichi Yusa[2], Kenichi Morigaki[3] ([1]*Grad. Sch. Agri., Kobe Univ*, [2]*Department of Materials Science and Chemistry, University of Hyogo*, [3]*Biosignal Research Center, Kobe Univ.*)

1GH1415 人工膜とナノ空間を用いた膜結合分子の動的挙動の計測
Membrane-based nanofluidic channel for studying lateral diffusion of membrane-bound molecules in nanometric confinement
○長塚 ななみ[1], 宮田 優里[2], 吉村 優[2], 肥塚 雅人[2], 森垣 憲一[2,3]（[1] 神戸大・農学, [2] 神戸大・院農学, [3] 神戸大バイオシグナル総合研究センター）
Nanami Nagatsuka[1], Yuri Miyata[2], Yu Yoshimura[2], Masato Koezuka[2], Kenichi Morigaki[2,3] ([1]*Fac. Agri., Kobe Univ.*, [2]*Grad. Sch. Agri., Kobe Univ.*, [3]*Biosignal Resarch Center, Kobe Univ.*)

1GH1430 β-hairpin 構造を有する抗菌ペプチドの電気生理学的分析
Electrophysiological analysis of antimicrobial peptides with β-hairpin structure
○羽切 夕貴, 橋本 若奈, 川野 竜司（東京農工大・生命工学）
Yuki Hagiri, Wakana Hashimoto, Ryuji Kawano (*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

1GH1445 細菌膜オンアチップ：異なる活性を示す抗菌ペプチドのグラム陰性細菌外膜への作用評価
Reconstitution of the outer membrane of Gram-negative bacteria on a chip
○橋本 若奈, 川野 竜司（東京農工大・院生命工学）
Wakana Hashimoto, Ryuji Kawano (*Dep. of Biotech. and Life Sci., Tokyo Univ. of Agri. and Tech.*)

1GH1500　マイクロ流体デバイス内での細胞サイズの 2 個組リポソームの一斉配置
Simultaneous rearrangement of cell-sized liposome dyads trapped in a microfluidic device
○小淵 晴仁 [1], 章 逸汀 [2], 浜田 省吾 [3], 杉山 博紀 [4], 安部 桂太 [5], 稲田 晃大 [6], 礒川 悌二郎 [6], 村田 智 [5], 豊田 太郎 [1,7]（[1] 東大・院総合文化, [2] 立教大・理, [3] 東工大・情報理工学院, [4] 自然科学研究機構・生命創成探究セ, [5] 東北大・院工, [6] 兵庫県立大・院工, [7] 東大・生物普遍性連携研究機構）
Haruto Obuchi[1], Yiting Zhang[2], Shogo Hamada[3], Hironori Sugiyama[4], Keita Abe[5], Akihiro Inada[6], Teijiro Isokawa[6], Satoshi Murata[5], Taro Toyota[1,7] ([1]*Grad. Sch. Arts Sci., Univ.*, [2]*Coll. Sci, Rikkyo Univ.*, [3]*Int. Grad. Sch. Sci. Eng., Tokyo Inst. Tech.*, [4]*ExCELLS, NINS.*, [5]*Grad. Sch. Eng., Tohoku Univ.*, [6]*Grad. Sch. Eng., Univ. Hyogo.*, [7]*Univ. Biol. Inst., Univ. Tokyo.*)

1GH1515　Mechanism study of antimicrobial peptide synergistic effects of LL37 and HNP1
Yuge Hou, Kaori Sugihara (*Institute of Industrial Science, The University of Tokyo,*)

1GH1530　支持脂質二層膜に GPCR を方向性を制御して組込む [II] GPCR の C 末特異性 Fab´を使って
Reconstituting GPCR into supported lipid bilayer with controlled orientation. [2] Prebinding of the Fab´ fragment to C-terminus of GPCR
○肥塚 雅人 [1], 森垣 憲一 [1,3], 林 文夫 [2]（[1] 神戸大・院農学, [2] 神戸大・院理学, [3] 神戸大・バイオシグナル総合研究センター）
Masato Koezuka[1], Kenichi Morigaki[1,3], Fumio Hayashi[2] ([1]*Grad. Sch. Agri., Kobe Univ.*, [2]*Grad. Sch. Agri., Univ. Kobe*, [3]*Biosignal Research Center, Univ. Kobe*)

1GH1545　RND 型異物排出系内膜トランスポーター MdtB, MdtC のヘテロ三量体形成
Heterotrimer formation of MdtB and MdtC, inner membrane transporters of the RND-type xenobiotic efflux complex
○中村 勇斗（法政大・院理工）
Yuto Nakamura (*Grad. Sch. Sci. and Engin., Hosei Univ*)

1GH1600　コレラ菌ピルビン酸/オキサロ酢酸走性受容体 Mlp2 のリガンド認識機構
Ligand recognition of the pyruvate/oxaloacetate chemoreceptor of *Vibrio cholerae*
○大森 楓河 [1], 八尾 和輝 [1], 山元 季実子 [1,4], 田島 寛隆 [2,3], 川岸 郁朗 [1,2,3]（[1] 法政大学・院理工, [2] 法政大学・生命・生命機能, [3] 法政大学・ナノテクセンター, [4] 農研機構・農環研）
Fuga Omori[1], Kazuki Yao[1], Kimiko Yamamoto[1,4], Hirotaka Tajima[2,3], Ikuro Kawagishi[1,2,3] ([1]*Grad. Sch. Sci. and Engin., Hosei Univ*, [2]*Fac. of Biosci. and Appl. Chem., Hosei Univ*, [3]*Res. Cent. for Micro-Nano Tech., Hosei Univ*, [4]*Inst. Agro-Environ. Sci., NARO*)

1GI　生命の起源・進化、合成生物学・人工細胞、ゲノム生物学、非平衡・生体リズム
Origin of life & Evolution, Synthetic biology & Artificial cells, Genome biology, Nonequilibrium state & Biological rhythm

座長：今井 啓雄（京都大学），向山 厚（福井県立大学），広瀬 侑（豊橋技術科学大学），瀧口 金吾（名古屋大学）
Session Chairs: Hiroo Imai (Kyoto Univ.), Atsushi Mukaiyama (Fukui Pref. Univ.), Yuu Hirose (Toyohashi Univ. Tech.), Kingo Takiguchi (Nagoya Univ.)

14:00〜16:45
I 会場（国際会議室（3 号館 3F））／Room I（International Conference Room (Bldg. 3, 3F)）

1GI1400　L-トレオニン由来の人工核酸 L-*a*TNA を用いた化学的な自己複製
Chemical replication of L-*a*TNA derived from L-threonine
○沖田 ひかり, 村山 恵司, 浅沼 浩之（名古屋大・院工学）
Hikari Okita, Keiji Murayama, Hiroyuki Asanuma (*Grad. Sch. Eng., Nagoya Univ.*)

1GI1415 **配列情報とベシクル再生産の連携による生命の起源**
Origin of Life by Linking Sequence Information and Vesicle Reproduction
○馬場 晶子 [1], 佐藤 啓大 [1], ヘンキース イヴォ [1], ウルフ オルソン [2], ワング アナ [3], 今井 正幸 [1]
([1] 東北大・院理学, [2] ルンド大・院理学, [3] ニュー・サウス・ウェールズ大・院理学)
Akiko Baba[1], Keidai Sato[1], Ivo Henkys[1], Olsson Ulf[2], Anna Wang[3], Masayuki Imai[1] ([1]*Grad. Sch. Sci., Univ. Tohoku*, [2]*Grad. Sch. Sci., Univ. Lund*, [3]*Grad. Sch. Sci., Univ. New South Wales*)

1GI1430 **バイオハイブリッドロボットの作製に向けたクラミドモナス除膜細胞および単離軸糸の巨大リポソームへの封入**
Encapsulation of Chlamydomonas demembranated models or isolated axonemes in giant liposomes for the preparation of bio-hybrid robots
○秋山 浩一朗, 林 真人, 金子 智行（法政大・院理工・生命機能）
Koichiro Akiyama, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad.Sch.Sci.&Eng., Hosei Univ.*)

1GI1445 **RNA ファミリー配列の深層生成設計**
Deep generative design of RNA family sequences
○角 俊輔 [1,2], 浜田 道昭 [2,3,4], 齊藤 博英 [1]（[1] 京都大学 iPS 細胞研究所, [2] 早稲田大学先進理工学部, [3] 産業技術総合研究所 生体システムビッグデータ解析オープンイノベーションラボラトリ, [4] 日本医科大学）
Shunsuke Sumi[1,2], Michiaki Hamada[2,3,4], Hirohide Saito[1] ([1]*Center for iPS Cell Research and Application (CiRA), Kyoto University*, [2]*Graduate School of Advanced Science and Engineering, Waseda University*, [3]*Computational Bio Big-Data Open Innovation Laboratory (CBBD-OIL), National Institute of Advanced Industrial Science and Technology (AIST)*, [4]*Graduate School of Medicine, Nippon Medical School*)

1GI1500 **リン脂質-タンパク質非対称膜小胞内膜上でのタンパク質集積**
Protein accumulation on the inner leaflet of asymmetric phospholipid-protein vesicles
○鈴木 允人, 神谷 厚輝（群馬大学 大学院 理工学府）
Masato Suzuki, Koki Kamiya (*Graduate School of Science and Technology, Gunma University.*)

1GI1515 **インフルエンザウイルスゲノムの in vitro 構築**
In vitro reconstruction of the influenza virus genome
○田中 良汰 [1], 末次 正幸 [2], 野地 博行 [1], 田端 和仁 [1]（[1] 東京大学 大学院工学系研究科 応用化学専攻, [2] 立教大学 理学部 生命理学科）
Ryota Tanaka[1], Masayuki Su'etsugu[2], Hiroyuki Noji[1], Kazuhito Tabata[1] ([1]*Department of Applied Chemistry, Graduate School of Engineering, The University of Tokyo*, [2]*Department of Life Science, College of Science, Rikkyo University*)

1GI1530 **試験管内での DNA 複製・転写・翻訳反応における最適条件の非互換性について**
Incompatibility of optimum conditions for *in vitro* DNA replication, transcription, and translation
○瀬尾 海渡 [1], 市橋 伯一 [1,2,3]（[1] 東大・院総合文化, [2] 東大・先進研, [3] 東大・生物普遍性研）
Kaito Seo[1], Norikazu Ichihashi[1,2,3] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*Komaba Inst. Sci., Univ. Tokyo*, [3]*Universal Biol Inst., Univ. Tokyo*)

1GI1545 **DNA 自己複製に伴って成長する Dextran 型人工細胞系の構築**
Development of Dextran-based artificial cell that grows in coupled with internal DNA self-replication
○藪田 萌, 皆川 慶嘉, 野地 博行（東大・院応用化学）
Moe Yabuta, Yoshihiro Minagawa, Hiroyuki Noji (*Department of applied chemistry, School of engineering, The University of Tokyo*)

1GI1600 **炎症性老化における NFκB ダイナミクスと遺伝子発現制御**
NFκB dynamics and gene regulation in inflammatory aging
○松田 啓汰 [1], 田畑 祥 [1], 茂呂 和世 [2], 岡田 眞里子 [1]（[1] 大阪大学蛋白質研究所, [2] 大阪大学医学系研究科生体防御学教室）
Keita Matsuda[1], Sho Tabata[1], Kazuyo Moro[2], Mariko Okada[1] ([1]*Institute for Protein Research, Osaka University*, [2]*Laboratory for Innate Immune Systems, Graduate School of Medicine, Osaka University*)

1GI1615 Geometry of spontaneous beating cardiomyocyte networks dominates emerged adaptive slower beating synchronization and ion channel responses

Kazufumi Sakamoto[1], Suguru Matsumoto[1], Nanami Abe[1], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

1GI1630 アクティブ細胞骨格系における状態転移と非平衡収縮ダイナミクス

State transitions and non-equilibrium contractile dynamics in active cytoskeletons

○柏原 智香, 前多 裕介（九州大学　理・物理）

Tomoka Kashiwabara, Yusuke T. Maeda (*Department of Physics, Kyushu University*)

1GJ 光生物：視覚・光受容、光遺伝学・光制御

Photobiology: Vision & Photoreception, Optogenetics & Optical control

座長：木村 明洋（名古屋大学），角田 聡（名古屋工業大学），山下 高廣（京都大学）

Session Chairs: Akihiro Kimura (Nagoya Univ.), Satoshi Tsunoda (Nagoya Inst. Tech.), Takahiro Yamashita (Kyoto Univ.)

14:00〜16:45

J 会場（会議室 141+142（1 号館 4F））／Room J（Conference Room 141+142 (Bldg. 1, 4F)）

1GJ1400 オプシンのレチナール結合特性の制御メカニズム解析

The regulatory mechanism underlying the binding preference of retinal isomers in opsins

○藤藪 千尋 [1], 佐藤 恵太 [2], 今元 泰 [1], 大内 淑代 [2], 七田 芳則 [3], 山下 高廣 [1] ([1] 京大・院理, [2] 岡山大・院医歯薬, [3] 立命館大・総研機構）

Chihiro Fujiyabu[1], Keita Sato[2], Yasushi Imamoto[1], Hideyo Ohuchi[2], Yoshinori Shichida[3], Takahiro Yamashita[1] ([1]*Grad. Sch. of Sci., Kyoto Univ.*, [2]*Grad. Sch. of Med., Dent. and Pharm. Sci., Okayama Univ.*, [3]*Research Organization for Science and Technology., Ritsumeikan Univ.*)

1GJ1415 プロトン移動反応によって制御される青感受性視物質の早期光反応過程

Early photoreaction process of primate blue-sensitive pigment controlled by proton transfer reaction

○水野 陽介 [1], 片山 耕大 [1,2], 今井 啓雄 [3], 神取 秀樹 [1,2] ([1] 名工大・院工, [2] 名工大・オプトバイオテクノロジー研究センター, [3] 京大・ヒト行動進化研究センター）

Yosuke Mizuno[1], Kota Katayama[1,2], Hiroo Imai[3], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng, Nagoya Inst. Tech.*, [2]*OptoBio Technology Research Center, Nagoya Inst. Tech.*, [3]*Center for the Evolutionary Origins of Human Behavior, Kyoto Univ.*)

1GJ1430 低温ラマン分光法による Photoactive Yellow Protein の初期構造変化過程の解析

Cryogenic Raman study of early photointermediates of photoactive yellow protein

Shota Kawasaki[1], Tomotsumi Fujisawa[2], Wouter D Hoff[3], Masasi Unno[2] ([1]*Grad. Sch. Adv. Health Sci., Saga Univ.*, [2]*Fac. Sci. Eng., Saga Univ.*, [3]*Oklahoma state Univ.*)

1GJ1445 光高感度なチャネルロドプシンの分光学的解析

Spectroscopic study of a channelrhodopsin with high reactivity to weak light

○山下 陽 [1], 杉本 哲平 [1], 片山 耕大 [1,2], 角田 聡 [1,2], 田中 達基 [3], 志甫谷 渉 [3], 濡木 理 [3], 神取 秀樹 [1,2] ([1] 名工大・院工, [2] オプトバイオテクノロジー研究センター, [3] 東大・院理）

Yo Yamashita[1], Teppei Sugimoto[1], Kota Katayama[1,2], Satoshi Tsunoda[1,2], Tatsuki Tanaka[3], Wataru Shihoya[3], Osamu Nureki[3], Hideki Kandori[1,2] ([1]*Grad. Sch. of Eng., Nagoya Inst. of Tech.*, [2]*OptoBio Tech. Res. Cent.*, [3]*Grad. Sch. of Sci., The Univ. Tokyo.*)

1GJ1500 **非視覚オプシン OPN3 によるメラノコルチン 1 型受容体（MC1R）活性阻害効果の解析**
Analysis of the inhibitory effect of nonvisual opsin, OPN3, on melanocortin 1 receptor (MC1R) function
○石村 有沙 [1], Yan Xiaochan[2], 今井 啓雄 [1,2]（[1] 京都大・院理学, [2] 京都大・ヒト行動進化研究センター）
Arisa Ishimura[1], Xiaochan Yan[2], Hiroo Imai[1,2] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*EHUB, Kyoto Univ.*)

1GJ1515 **Gs タンパク質共役型受容体クラゲロドプシンの光反応早期過程の分光解析**
Spectroscopic studies of the early photoreaction process of the light-sensitive Gs protein-coupled receptor, jellyfish rhodopsin
○犬飼 紫乃 [1], 片山 耕大 [1,2], 小柳 光正 [3], 寺北 明久 [3], 神取 秀樹 [1,2]（[1] 名工大・院工, [2] 名工大・オプトバイオテクノロジー研究センター, [3] 大阪公大・院理）
Shino Inukai[1], Kota Katayama[1,2], Mitsumasa Koyanagi[3], Akihisa Terakita[3], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*OptoBioTechnology Research Center, Nagoya Inst. Tech.*, [3]*Grad. Sch. Sci., Osaka Metro. Univ.*)

1GJ1530 **カリウム選択的チャネルロドプシン KCR のカリウム選択性の構造基盤**
Structure basis of potassium selectivity in potassium-selective channelrhodopsin KCR
Seiya Tajima[1], Yoon Seok Kim[2], Masahiro Fukuda[1], YoungJu Jo[2], Peter Y. Wang[2], Joseph M. Paggi[3], Eamon F.X. Byrne[2], Koichiro Kishi[1], Seiwa Nakamura[1], Charu Ramakrishnan[4], Shunki Takaramoto[5], Takashi Nagata[5], Masae Konno[5], Masahiro Sugiura[6], Kota Katayama[6], Toshiki Matsui[1], Keitaro Yamashita[7], Suhyang Kim[1], Hisako Ikeda[1], Masatoshi Inoue[2], Jaeah Kim[2], Hideki Kandori[6], Ron O. Dror[3], Keiichi Inoue[5], Karl Deisseroth[2,4], Hideaki. E. Kato[1] ([1]*Komaba Inst. Sci., Univ. Tokyo*, [2]*Dept. Bioeng., Stanford Univ.*, [3]*Dept. Comp. Sci., Stanford Univ.*, [4]*CNC Program, Stanford Univ.*, [5]*ISSP, The Univ. Tokyo.*, [6]*Life Sci. Appl. Chem., Grad. Sch. Eng. Nagoya Inst. Tech.*, [7]*MRC LMB, Cambridge Biomedical Campus*)

1GJ1545 **光駆動性プロトンポンプロドプシンを用いた細菌べん毛運動の光操作法の開発**
Development of an optical method to control bacterial motility using light-driven proton pumping rhodopsins
○中西 浩太郎 [1], 小島 慧一 [2], 曽和 義幸 [3], 須藤 雄気 [2]（[1] 岡山大院・医歯薬, [2] 岡山大・学術研究院・医歯薬学域, [3] 法政大・生命科学・生命機能）
Kotaro Nakanishi[1], Keiichi Kojima[2], Yoshiyuki Sowa[3], Yuki Sudo[2] ([1]*Grad. Sch., Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*Fac., Med. Dent. & Pharm., Okayama Univ.*, [3]*Dep. Front. Biosci. Res. Cen. Micro Nano Tech, Hosei Univ.*)

1GJ1600 **ウイルスロドプシンにチャネル機能をもたらす特異な水素結合系**
Atypical hydrogen bonding network bringing channel function to viral rhodopsin
○青山 真子 [1], 片山 耕大 [1,2], 神取 秀樹 [1,2]（[1] 名工大・院工, [2] 名工大 オプトバイオテクノロジー研究センター）
Mako Aoyama[1], Kota Katayama[1,2], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Nagoya Inst. Tech., OptoBio Technology Research Center*)

1GJ1615 **深海エビ *Rimicaris hybisae* は可視光感受性オプシンのレパートリーを持つ**
Repertoire of visible light-sensitive opsins in the deep-sea hydrothermal vent shrimp *Rimicaris hybisae*
○長田 祐也 [1], 宮本 教生 [2], 佐藤 恵太 [3], 山中 悠嗣 [4], 西村 陽介 [5], 吉澤 晋 [6], 高井 研 [2], 大内 淑代 [3], 山下 高廣 [7], 須藤 雄気 [3], 小島 慧一 [3]（[1] 岡山大・院医歯薬（薬学系）, [2] 海洋研究開発機構 超先鋭研究開発部門, [3] 岡山大・学術研究院医歯薬, [4] 岡山大・薬, [5] 海洋研究開発機構 生命理工学センター, [6] 東京大・大気海洋研, [7] 京都大・院理）
Yuya Nagata[1], Norio Miyamoto[2], Keita Sato[3], Yuji Yamanaka[4], Yosuke Nishimura[5], Susumu Yoshizawa[6], Ken Takai[2], Hideyo Ohuchi[3], Takahiro Yamashita[7], Yuki Sudo[3], Keiichi Kojima[3] ([1]*Grad. Sch. Med. Dent. & Pharm. Sci., Okayama Univ.*, [2]*X-STAR, JAMSTEC*, [3]*Fac. Med, Dent & Pharm Sci., Okayama Univ.*, [4]*Sch. Pharm. Sci., Okayama Univ.*, [5]*CeBN, JAMSTEC*, [6]*AORI, Univ. Tokyo*, [7]*Grad. Sch. Sci., Kyoto Univ.*)

1GJ1630 **短波長吸収カチオンチャネルロドプシン KnChR のイオン輸送メカニズムの解明**
Ion transport mechanism of short wavelength absorbing cation channelrhodopsin KnChR
○夏目 航希 [1], 細島 頌子 [1], 角田 聡 [1,2], 神取 秀樹 [1,2] ([1] 名古屋工業大学　工学研究科, [2] オプトバイオテクノロジー研究センター）
Koki Natsume[1], Shoko Hososhima[1], Satoshi Tsunoda[1,2], Hideki Kandori[1,2] ([1]*Nagoya Institute of Technology*, [2]*Opto-Biotechnology Research Center*)

1GK　水・水和／電解質、計算生物学、数理生物学・理論生物学
Water & Hydration & Electrolyte, Computational biology, Mathematical & Theoretical biology

座長：吉田 紀生（名古屋大学），奥村 久士（生命創成探究センター），白井 伸宙（三重大学）
Session Chairs: Norio Yoshida (Nagoya Univ.), Hisashi Okumura (ExCELLS), Nobu C. Shirai (Mie Univ.)

14:00〜16:45
K 会場（会議室 131+132（1 号館 3F））／Room K（Conference Room 131+132 (Bldg. 1, 3F)）

1GK1400 **深層学習と経験分布の融合的手法による膜蛋白質の水和構造予測**
Prediction of hydration structures over membrane proteins using deep learning in combination with the empirical hydration distribution
○佐藤 航地 [1,2,3], 大出 真央 [4,5], 中迫 雅由 [1,2] ([1] 慶應大・理工, [2] 理研・RSC, [3]JST・SPRING, [4] 理研・CPR, [5]JST・さきがけ）
Kochi Sato[1,2,3], Mao Oide[4,5], Masayoshi Nakasako[1,2] ([1]*Dept. of Phys., Keio Univ.*, [2]*RSC, RIKEN*, [3]*SPRING, JST*, [4]*CPR, RIKEN*, [5]*PRESTO, JST*)

1GK1415 **AlphaFold2 を用いた親水的なアミノ酸配列空間の探索によるフォールド可能なタンパク質の特定**
Exploring hydrophilic sequence space to search for uncharted foldable proteins by AlphaFold2
○冨田 尚希 [1], シャバス レオナルド [1,2], 千見寺 浄慈 [1] ([1] 名大・工・応物, [2] 名大・シンクロトロン光センター）
Naoki Tomita[1], Chavas Leonard[1,2], Chikenji George[1] ([1]*Dept. of Appl. Phys., Grad. Sch. of Eng., Nagoya Univ.*, [2]*Synchrotron Radiation Center, Nagoya Univ.*)

1GK1430 The Effect of Tricaprylin Surface on The Lid Region Dynamics of *Candida antarctic*a Lipase B
Tegar Nurwahyu Wijaya[1,2], Akio Kitao[1] ([1]*School of Life Science and Technology, Tokyo Institute of Technology.*, [2]*Department of Chemistry, Universitas Pertamina*)

1GK1445 **粗視化力場 SPICA における二次構造依存のタンパク質主鎖モデルの開発**
Development of a secondary structure-dependent protein backbone model for SPICA coarse-grained force field
○山田 哲平 [1], 宮崎 裕介 [2], Kumar Ashutosh[3], Vanni Stefano[3], 篠田 渉 [2] ([1] 岡山大・院自然科学, [2] 岡山大・異分野基礎科学研究所, [3] フリブール大・生物学科）
Teppei Yamada[1], Yusuke Miyazaki[2], Ashutosh Kumar[3], Stefano Vanni[3], Wataru Shinoda[2] ([1]*Grad. Sch. Sci. & Tech., Okayama Univ.*, [2]*RIIS, Okayama Univ.*, [3]*Dept. of Biol., University of Fribourg, Switzerland.*)

1GK1500 **オレキシン 2 受容体の活性化における動的性質と中間状態の計算論的洞察**
Structural and Computational Insight into Dynamics and Intermediate State in OX2R Activation
○横井 駿 [1,2], 光武 亜代理 [1] ([1] 明治大学 大学院 理工学研究科 物理学専攻, [2] スタンフォード大学 医学部 構造生物学科）
Shun Yokoi[1,2], Ayori Mitsutake[1] ([1]*Department of Physics, Graduate School of Science and Technology, Meiji University*, [2]*Structural Biology Department, School of Medicine, Stanford University*)

1GK1515 **ハイブリッド型 *in silico* 創薬による SARS-CoV-2 メインプロテアーゼの新規共有結合阻害剤の探索**

Discovery of potent covalent inhibitors against SARS-CoV-2 main protease by hybrid *in silico* drug study

○小清水 初花 [1], 小野 純一 [2], 福西 快文 [3], 中井 浩巳 [1,2]（[1] 早大先進理工, [2] 早大理工総研, [3] 産総研生命工学）

Uika Koshimizu[1], Junichi Ono[2], Yoshifumi Fukunishi[3], Hiromi Nakai[1,2] ([1]*Department of Chemistry and Biochemistry, School of Advanced Science and Engineering, Waseda University*, [2]*Waseda Research Institute for Science and Engineering (WISE), Waseda University*, [3]*Cellular and Molecular Biotechnology Research Institute, National Institute of Advanced Industrial Science and Technology*)

1GK1530 **大規模な自由エネルギー摂動法計算のための効率的な摂動マップ構築の検討**

Study of efficient perturbation map construction for large-scale free energy perturbation calculations

○古井 海里, 大上 雅史（東工大・情報理工学院）

Kairi Furui, Masahito Ohue (*School of Computing, Tokyo Institute of Technology*)

1GK1545 **3D 細胞画像の構造抽出と特徴付けに基づく細胞分裂機構の定量的解析**

Quantitative Analysis of Cell Division Mechanisms through the Structure Extraction and Characterization of 3D Cell Images

○高坂 仁 [1], 岩根 敦子 [2], 冨樫 祐一 [1,2]（[1] 立命館大学 生命科学部生物計算研究室, [2] 理化学研究所 生命機能科学研 究センター）

Jin Kousaka[1], Atsuko H. Iwane[2], Yuichi Togashi[1,2] ([1]*Ritsumeikan University*, [2]*RIKEN Center for Biosystems Dynamics Research*)

1GK1600 **自然言語処理による細胞内ネットワーク構造の抽出と数理モデル構築の自動化**

Extracting Intracellular Networks and Constructing Mathematical Models with Natural Language Processing

○荒金 究, 岡田 眞里子（大阪大・蛋白研）

Kiwamu Arakane, Mariko Okada (*Inst. for Protein Res., Osaka Univ.*)

1GK1615 **細胞内ネットワークにおける Bow-tie 構造の進化原理**

Evolutionary mechanism of bow-tie architecture in intracellular network

○伊藤 冬馬 [1,2,3], 近藤 洋平 [1,2,3], 青木 一洋 [1,2,3], 斉藤 稔 [3,4]（[1] 基生研・ 定量生物, [2] 総研大, [3] 生命創成探究センター, [4] 広大・統合生命）

Thoma Itoh[1,2,3], Yohei Kondo[1,2,3], Kazuhiro Aoki[1,2,3], Nen Saito[3,4] ([1]*Div. Quant. Biol., NIBB*, [2]*SOKENDAI*, [3]*ExCELLS*, [4]*Grad. Sch. Integrated Sci. for Life, Hiroshima Univ.*)

1GK1630 **一遺伝子欠損は遺伝子発現状態にグローバルな影響を与える**

Single-gene deletions impact global gene expression states

○千葉 元太 [1], 亀井 健一郎 [1], 小田 有沙 [1,2], 太田 邦史 [1,2,3], 若本 祐一 [1,2,3]（[1] 東大・院総合文化, [2] 東大・複雑系生命システム研究センター, [3] 東大・生物普遍性研究機構）

Genta Chiba[1], Ken-ichiro F. Kamei[1], Arisa Oda[1,2], Kunihiro Ohta[1,2,3], Yuichi Wakamoto[1,2,3] ([1]*Grad. Sch. Arts and Sci., Univ. Tokyo*, [2]*Res. Cent. Complex Syst. Biol., Univ. Tokyo*, [3]*UBI, Univ. Tokyo*)

1GL 光合成、計測、バイオエンジニアリング
Photosynthesis, Measurements, Bioengineering

座長：村田 和義（生命創成探究センター），廣明 秀一（名古屋大学），米田 勇祐（分子科学研究所），出羽 毅久（名古屋工業大学）

Session Chairs: Kazuyoshi Murata (ExCELLS), Hidekazu Hiroaki (Nagoya Univ.), Yusuke Yoneda (IMS), Takehisa Dewa (Nagoya Inst. Tech.)

14:00〜16:15

L 会場（会議室 133+134（1 号館 3F））／Room L（Conference Room 133+134 (Bldg. 1, 3F)）

1GL1400 **集光アンテナを持つキサントロドプシンの光活性化研究**

Photoactivation study of Xanthorhodopsin with a Light-Harvesting Antenna

○板倉 彰汰 [1], 水野 陽介 [1], 片山 耕大 [1,2], 吉住 玲 [1], Ariel Chazan[3], Oded Béjà[3], 神取 秀樹 [1,2]（[1] 名古屋工業大学 大学院工学研究科, [2] オプトバイオテクノロジー研究センター, [3]Technion –Israel Institute of Technology）

Shota Itakura[1], Yosuke Mizuno[1], Kota Katayama[1,2], Rei Yoshizumi[1], Chazan Ariel[3], Béjà Oded[3], Hideki Kandori[1,2] ([1]*Graduate School of Engineering, Nagoya Institute of Technology*, [2]*OptoBioTechnology Research Center*, [3]*Technion –Israel Institute of Technology*)

1GL1415 **Mn を Fe に置換した水分解酸素発生反応触媒における反応性の解明**

Structural and energetic insights into Mn-to-Fe substitution in the oxygen-evolving complex

○齊藤 昌弘 [1], 斉藤 圭亮 [1,2], 石北 央 [1,2]（[1] 東京大学大学院工学系研究科応用化学専攻, [2] 東京大学先端科学技術研究センター）

Masahiro Saito[1], Keisuke Saito[1,2], Hiroshi Ishikita[1,2] ([1]*Department of Applied Chemistry, The University of Tokyo*, [2]*Research Center for Advanced Science and Technology, The University of Tokyo*)

1GL1430 **光合成アンテナクロロソームの微視的な構造不均一性と光捕集機能の相関解析**

Relationship between light-harvesting function and microscopic structural heterogeneity in the photosynthetic antenna chlorosome

○新井 峻 [1], 稲垣 知実 [2], 原田 二郎 [3], 浅井 智広 [4], 近藤 徹 [1]（[1] 東工大・生命理工, [2] 立命館大院・生命科学, [3] 久留米大・医, [4] 中央大・理工）

Shun Arai[1], Tomomi Inagaki[2], Jiro Harada[3], Chihiro Azai[4], Toru Kondo[1] ([1]*Dept. of Life & Sci., Tokyo Tech.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [3]*Sch. of Med., Kurume Univ.*, [4]*Fac. of Sci. & Eng., Chuo Univ.*)

1GL1445 **光化学系 II における Mn_4CaO_5 クラスターの中間 S_2 状態形成を制御する重要な因子**

Important Factors Influencing the Intermediate-S_2-State Formation of the Mn_4CaO_5 Cluster in Photosystem II

○陳 楊 [1], 斉藤 圭亮 [1,2], 石北 央 [1,2]（[1] 東大・院工, [2] 東京大学先端科学技術研究センター）

Yang Chen[1], Keisuke Saito[1,2], Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*RCAST, Univ. Tokyo*)

1GL1500 **顕微ラマン分光法による神経分化に伴う熱産生のラベルフリー計測**

Label-free measurement of heat production during neuronal differentiation by Raman microscopy

○入倉 桜介 [1], 幡本 拓哉 [2], 高橋 大智 [2], 梶本 真司 [1,2,3], 中林 孝和 [1,2]（[1] 東北大学薬学部, [2] 東北大学大学院薬学研究科, [3]JST さきがけ）

Ohsuke Irikura[1], Takuya Hatamoto[2], Hiroaki Takahashi[2], Shinji Kajimoto[1,2,3], Takakazu Nakabayashi[1,2] ([1]*Faculty of Pharmaceutical Sciences, Tohoku University*, [2]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [3]*JST PRESTO*)

1GL1515 **細胞死の不可逆性の理解に向けた、一細胞遺伝子発現解析と機械学習による細胞の運命予測の統合**

Integrating single-cell transcriptomics and cell fate prediction by deep learning for understanding the point of no return to cell death

○岡庭 有明 [1,2], 城口 克之 [1]（[1] 理研・BDR, [2] 阪大・院生命機能）

Tomoaki Okaniwa[1,2], Katsuyuki Shiroguchi[1] ([1]*RIKEN BDR*, [2]*Grad. Sch. Frontier Biosciences, Osaka Univ.*)

1GL1530 **銅イオンの定量計測を可能にする二つのルシフェラーゼの経時的発光減衰の違いを基盤としたレシオメトリ**

Ratiometry based on differences of luminescence decay kinetics of two luciferases enabling quantitative Cu^{2+} concentration measurement

○呉 題（大阪大学　産業科学研究所）

Ti Wu (*Osaka University SANKEN*)

1GL1545　ナノポア計測を用いた CALHM2 チャネル 1 分子の電気的特性解析
Electrical characterization of a single CALHM2 channel molecule using nanopore measurement
○中村 宗太郎 [1], 山崎 洋人 [2], 志甫谷 渉 [1], 濡木 理 [1], 上村 想太郎 [1]（[1] 東京大学・大学院理学系研究科生物科学専攻, [2] 長岡技術科学大学 産学融合トップランナー養成センター）
Sotaro Nakamura[1], Hirohito Yamazaki[2], Wataru Shihoya[1], Osamu Nureki[1], Sotaro Uemura[1]
([1]*Department of Biological Sciences, The University of Tokyo*, [2]*Nagaoka University of Technology, Top Runner Incubation Center for Academia-Industry Fusion*)

1GL1600　フラグメントリンキング法に基づく PROTAC 分子リンカー設計
PROTAC molecular linker design using fragment linking method
○石沢 涼太, 大上 雅史（東京工業大学 情報理工学院 情報工学系）
Ryota Ishizawa, Masahito Ohue (*Department of Computer Science, School of Computing, Tokyo Institute of Technology*)

1GM　バイオイメージング
Bioimaging

座長：笠井 倫志（国立がん研究センター研究所），中村 彰彦（静岡大学），菊島 健児（名古屋市立大学）
Session Chairs: Rinshi S. Kasai (NCCRI), Akihiko Nakamura (Shizuoka Univ.), Kenji Kikushima (Nagoya City Univ.)

14:00〜16:45
M 会場（会議室 431+432（4 号館 3F））／Room M（Conference Room 431+432 (Bldg. 4, 3F)）

1GM1400　クライオ三次元ナノスコピーの開発：DNA オリガミによる評価
Development of cryogenic 3D nanoscopy: Evaluation with DNA origami
○成瀬 寛太 [1], 松田 剛 [1], 溝内 雄太 [1], 中田 栄司 [2], 森井 孝 [2], 松下 道雄 [1], 藤芳 暁 [1]（[1] 東京工業大学理学院物理学系物理学コース, [2] 京都大学エネルギー理工学研究所）
Kanta Naruse[1], Tsuyoshi Matsuda[1], Yuta Mizouchi[1], Eiji Nakata[2], Takashi Morii[2], Michio Matsushita[1], Satoru Fujiyoshi[1] ([1]*Department of physics,Tokyo institute of technology*, [2]*Institute of Advanced Energy, Kyoto University*)

1GM1415　緑色蛍光タンパク質を基盤とするバイオセンサーを用いた細胞内乳酸振動の観察
Direct observation of intracellular L -lactate oscillations with green fluorescent protein-based biosensors
○針尾 紗彩 [1], リー ジャン N. T.[2], 杉本 光 [3], 高橋-山城 恵生 [4], 那須 雄介 [1], 黒田 真也 [5], キャンベル E. ロバート [1]（[1] 東京大学・院理学・化学, [2] トロント大学・院化学, [3] 東京大学・院医学・生化学分子生物学, [4] アルバータ大学・院化学, [5] 東京大学・院理学・生物科学）
Saaya Hario[1], Gaing. N. T. Le[2], Hikaru Sugimoto[3], Kei Takahashi-Yamashiro[4], Yusuke Nasu[1], Shinya Kuroda[5], E. Robert Campbell[1] ([1]*Dept. Chem., Grad. Sch. Sci., Univ. Tokyo*, [2]*Dept. Chem., Grad. Sch., Univ. Toronto*, [3]*Dept. Biochem and Molbio., Grad. Sch. Med., Univ. Tokyo*, [4]*Dept. Chem., Grad. Sch., Univ. Alberta.*, [5]*Dept. Bio. Sci., Grad. Sch., Sci., Univ. Tokyo.*)

1GM1430　ラマン／ブリルアンイメージングを用いた生細胞内におけるストレス顆粒の異常相転移の観察
Observation of aberrant phase transition of stress granules in living cells using Raman/Brillouin microscopy
○澁谷 蓮 [1], 梶本 真司 [1,2], 柳沼 秀幸 [3,4], 有吉 哲郎 [3,4], 岡田 康志 [3,4], 中林 孝和 [1]（[1] 東北大院・薬, [2]JST さきがけ, [3] 東京大・国際高等研究所 IRCN, [4] 理研 BDR）
Ren Shibuya[1], Shinji Kajimoto[1,2], Hideyuki Yaginuma[3,4], Tetsuro Ariyoshi[3,4], Yasushi Okada[3,4], Takakazu Nakabayashi[1] ([1]*Grad. Sch. Pharm. Sci., Tohoku Univ.*, [2]*JST PRESTO*, [3]*WPI-IRCN, Univ. Tokyo*, [4]*RIKEN BDR*)

1GM1445 **超解像イメージングのための光スイッチング赤色蛍光タンパク質の開発**
Development of a photoswitchable red fluorescent protein for super-resolution imaging
○野間 涼平 [1,2], 和沢 鉄一 [1], 杉浦 一徳 [1], 設樂 久志 [3], 竹本 研 [3], 永井 健治 [1,2] ([1] 阪大・産研, [2] 阪大・院・生命機能, [3] 三重大・院・医)
Ryohei Noma[1,2], Tetsuichi Wazawa[1], Kazunori Sugiura[1], Hisashi Shidara[3], Kiwamu Takemoto[3], Takeharu Nagai[1,2] ([1]*SANKEN, Osaka Univ.*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*Grad. Sch. Med., Mie Univ.*)

1GM1500 **高速 AFM 観察とシミュレーションを用いた、E6AP/E6/p53 三者複合体の構造ダイナミクスの解明**
Revealing structural dynamics of E6AP/E6/p53 complex by using HS-AFM and computational simulation
Kazusa Takeda[1], Ikumi Muro[1], Flechsig Holger[2], Hiroki Konno[2] ([1]*Graduate School Nat. Sci. & Technol., Kanazawa Univ.*, [2]*WPI Nano Life Sci. Inst. (WPI-NanoLSI), Kanazawa Univ.*)

1GM1515 Multicolor Autoluminescent Reporters based on Bacterial Bioluminescence System
Kusuma Subhan Hadi[1,2], Mitsuru Hattori[2], Takeharu Nagai[1,2] ([1]*Graduate School of Frontier Bioscience, Osaka University*, [2]*Department of Biomolecular Science and Engineering, SANKEN (The Institute of Scientific and Industrial Research), Osaka University.*)

1GM1530 **バクテリアべん毛Ⅲ型輸送装置を利用した新規膜電位センサーの開発**
Development of a novel membrane voltage sensor based on the bacterial flagellar type III secretion system
○坂田 桧 [1], 南野 徹 [2], 森本 雄祐 [3] ([1] 九州工業大学 大学院情報工学府, [2] 大阪大学 大学院生命機能研究科, [3] 九州工業大学 大学院情報工学研究院 物理情報工学研究系)
Kai Sakata[1], Tohru Minamino[2], V. Yusuke Morimoto[3] ([1]*Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech*, [2]*Grad. Sch. Front. Biosci., Osaka Univ.*, [3]*Dept. Phys. and Info. Eng., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*)

1GM1545 **高速高分解能生細胞観察のための新規定量位相顕微鏡法**
Computational phase microscopy for live cell imaging with high spatiotemporal resolution
○犬塚 悠剛 [1,2], 岡田 康志 [1,2,3,4,5] ([1] 東京大学・院理学, [2] 理研・生命機能, [3] 東京大学・院医学, [4] 東京大学・生物普遍性研究機構, [5] 東京大学・ニューロインテリジェンス国際研究機構)
Yugo Inutsuka[1,2], Yasushi Okada[1,2,3,4,5] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*BDR., Riken*, [3]*Grad. Sch. Med., Univ. Tokyo*, [4]*UBI., Univ. Tokyo.*, [5]*IRCN., Univ. Tokyo.*)

1GM1600 **情報理論に基づくラマン画像と他計測法による画像に含まれる情報の関係性の定量**
Quantification of the relationship between information contained in Raman images and other types of images based on information theory
○近藤 僚哉 [1], 水野 雄太 [1,2,3], Clement Jean-Emmanuel[2,3], 藤田 克昌 [4], 原田 義規 [5], 小松崎 民樹 [1,2,3] ([1] 北大・院総化, [2] 北大・電子研, [3] 北大・ICReDD, [4] 阪大・院工, [5] 京都府立医大)
Ryoya Kondo[1], Yuta Mizuno[1,2,3], Jean-Emmanuel Clement[2,3], Katsumasa Fujita[4], Yoshinori Harada[5], Tamiki Komatsuzaki[1,2,3] ([1]*Grad. Sch. Chem. Sci. & Eng., Univ. Hokkaido*, [2]*Res. Inst. Electronic Sci.*, [3]*WPI-ICReDD, Univ. Hokkaido*, [4]*Grad. Eng., Univ. Osaka*, [5]*Kyoto Pref. Univ. Med.*)

1GM1615 **生体内 3D 温度計測技術の開発と応用**
In vivo 3D thermometry
○中根 有梨奈 [1], 前岡 遥花 [2], 五十嵐 龍治 [3], 臼杵 深 [4], 杉 拓磨 [1,2] ([1] 広島大学理学部生物科学科, [2] 広島大学大学院統合生命科学研究科生命医科学プログラム, [3] 量子科学技術研究開発機構, [4] 静岡大学電子工学研究所)
Yurina Nakane[1], Haruka Maeoka[2], Ryuji Igarashi[3], Shin Usuki[4], Takuma Sugi[1,2] ([1]*Department of Biological Science, School of Science, Hiroshima University*, [2]*Program of Biomedical Science, Graduate School of Integrated Sciences for Life, Hiroshima University*, [3]*Quantum Science and Technology Organization*, [4]*Research Institute of Electronics, Shizuoka University*)

1GM1630　**凍結固定細胞のラマン/超解像蛍光マルチモーダルイメージング**

Raman and super-resolution fluorescence imaging of cryo-fixed cells

○辻 康介[1], 山中 真仁[1], 熊本 康昭[2], 田村 昌子[3], 水島 健太[1], 河野 駆[1], 久保 俊貴[4], 平野 花咲[1], 杉浦 一徳[5], 福島 俊一[5], 國本 拓実[1], 西田 健太郎[1], 原田 義規[3], スミス ニコラス[6], ハインツマン ライナー[7,8], 永井 健治[5], 田中 秀央[3], 藤田 克昌[1,2,9]（[1]大阪大学 大学院工学研究科, [2]大阪大学 先導的学際研究機構, [3]京都府立医科大学 細胞分子機能病理学, [4]大阪大学 大学院医学研究科, [5]大阪大学 産業科学研究所, [6]大阪大学 免疫学フロンティア研究センター, [7]ライプニッツ光科学研究所, [8]フリードリヒシラー大学イエナ, [9]産総研・阪大 先端フォトバイオ OIL）

Kosuke Tsuji[1], Masahito Yamanaka[1], Yasuaki Kumamoto[2], Shoko Tamura[3], Kenta Mizushima[1], Kakeru Kono[1], Toshiki Kubo[4], Hanae Hirano[1], Kazunori Sugiura[5], Shun-ichi Fukushima[5], Takumi Kunimoto[1], Kentaro Nishida[1], Yoshinori Harada[3], Nicholas Smith[6], Rainer Heintzmann[7,8], Takeharu Nagai[5], Hideo Tanaka[3], Katsumasa Fujita[1,2,9] ([1]*Dept. of Appl. Phys., Osaka Univ.*, [2]*OTRI, Osaka Univ.*, [3]*Dept. of Pathology and Cell Regulation, Kyoto Prefectural Univ. of Medicine*, [4]*Dept. of Dermatol., Osaka Univ.*, [5]*SANKEN, Osaka Univ.*, [6]*IFReC, Osaka Univ.*, [7]*Leibniz Inst.*, [8]*Jena Univ.*, [9]*AIST Advanced Photo-BIO OIL*)

座長：倭 剛久（名古屋大学），加藤 祐樹（名古屋大学）
Session Chairs: Takahisa Yamato (Nagoya Univ.), Yuki Kato (Nagoya Univ.)

09:00〜11:45
L 会場（会議室 133+134（1 号館 3F））／Room L（Conference Room 133+134 (Bldg. 1, 3F)）

3HL0900 重力屈性と光屈性の関係性～光屈性は重力屈性を阻害する？！～
Relationship between gravitropism and phototropism ~ Does phototropism inhibit gravitropism?
Haruka Inoue, Itsuki Shibamiya, Chihiro Nishikawa, Akari Mochihara, Kouki Ishikawa (*Koyo H.S.*)

3HL0915 水耕栽培した植物はなぜ色水を吸い上げるのか
Why do hydroponic plants pump up colored water
Kota Abe, Ayaka Kamijo, Mana Kamiya, Naoki Niyomura (*Nagoya city Koyo High School*)

3HL0930 関西におけるアカハライモリの警告色の模様の分布
Distribution of warning coloration pattern in Kansai red bellied newts
Sora Kazumi[1,2], Rikiya Ogawa[2] ([1]*Osaka Prefecture Tondabayashi High School*, [2]*Rikijuku Science School*)

3HL0945 大和川水系石川のオオシマドジョウの採餌生態
Foraging ecology of *Cobitis* sp. BIWAE type A in Yamato River system Ishi river
Takemasa Otsuka[1,2], Ryoto Nakajima[1,2], Rikiya Ogawa[2] ([1]*Osaka Prefecture Tondabayashi High School*, [2]*Rikijuku Science School*)

3HL1000 近縁種アブラハヤとの共存によるタカハヤの形質置換
Substitution of *Rhynchocypris oxycephalus jouyi* trait by coexistence with closely related species *Rhynchocypris lagowskii steindachneri*
Kazuma Hirai[1,2], Takemasa Otsuka[1,2], Ryoto Nakajima[1,2], Sora Kazumi[1,2], Syuto Machii[1], Tomoyuki Maeda[1], Rikiya Ogawa[2] ([1]*Osaka Prefecture Tondabayashi High School*, [2]*Rikijuku Science School*)

3HL1015 ヒマワリのフィボナッチ螺旋構造
Fibonacci Spiral Structure of Sunflower
Fuga Suzuki (*Aichi Prefectural Okazaki High School*)

3HL1030 イエユウレイグモの初期胚における細胞の集団運動
Collective Cell Dynamics during the Early Embryonic Stage of Pholcus phalangioides
Hiroto Shoji, Toshiya Usui (*Aichi Institute of Technology Meiden High School*)

3HL1045 深層学習を用いたタンパク質の立体構造と機能予測
Prediction of protein structure and function by deep learning
Yui Nishikawa[1], Haruto Yajima[2], Tsuyoshi Shirai[3], Shigure Saito[4], Tingting Wang[4], Takahisa Yamato[4] ([1]*Chikusa H.S.*, [2]*Shizuoka H.S.*, [3]*Nagahama Inst. Bio-Sci. Tech.*, [4]*Grad. Sch. Sci.,Nagoya Univ.*)

3HL1100 髪の修復可能範囲
The Fixable Range of Hair
Norihito Hashi, Nachi Okamoto, Yukine Takamatsu, Hayato Morishita, Shuji Fujita (*Komatsu High School*)

3HL1115 豆苗の密度効果に与える条件の研究
Study on Conditions Affecting the Density Effect of Bean Seedlings
Haruka Kometani, Hibiki Tokuda, Momo Yoshita, Ryosuke Kasamaki, Shunsuke Takahashi (*Komatsu High School*)

3HL1130　Aβ の線維成長におけるポリフェノールの影響に関する研究

The research on the influence of polyphenols in the fibril growth of Amyloid Beta

Sara Takahashi[1], Saho Izawa[2], Yui Kanaoka[3], Yuto Nonaka[3], Yuki Tajimi[3], Maho Yagi[4], Takayuki Uchihashi[3] ([1]*Ichinomiya High School*, [2]*Tajimi Kita High School*, [3]*Nagoya University Graduate School*, [4]*Nagoya City University*)

ポスター発表　Poster Presentations

1 日目（11 月 14 日（火））／Day 1（Nov. 14 Tue.） 17:00 〜 19:00

01A. タンパク質：構造／01A. Protein: Structure

1Pos001 金属イオン結合により構造変化する α ヘリカルペプチドにおける疎水性コア形成残基の影響
Effects of hydrophobic core residues on conformational changes of α-helical peptides induced upon metal-ion binding
Shinya Nishatani[1], Yumi Kitagawa[2], Satoshi Nagao[3], Hiroshi Sekiguchi[3], Masayuki Oda[1,2] ([1]*Faculty Life. Environ. Sci., Kyoto Pref. Univ*, [2]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ*, [3]*Japan Synchrotron Radiation Research Institute (JASRI)*)

1Pos002 AlphaFold 構造データベースからの「二刀流 NTPase」の発見
Dual-wield NTPases: a novel protein family mined from AlphaFold protein structure database
Koya Sakuma[1], Ryotaro Koike[1], Motonori Ota[1,2] ([1]*Grad. Sch. Informatics, Nagoya University*, [2]*Inst. for Glyco-core Research, Nagoya University*)

1Pos003 乾眠クマムシのリボソーム in-situ 構造解析
In-situ Structural Analysis of Tardigrades Ribosomes in Anhydrobiotic State
Hiroko Takazaki[1], Taiga Horii[2], Takayuki Kato[1] ([1]*IPR, Univ. Osaka*, [2]*Grad. Sch. Sci., Univ. Osaka*)

1Pos004 Real-time imaging and analysis of human SAA aggregation using quantum dots
Liangquan Shi, Tuya Gegen, Masahiro Kuragano, Kiyotaka Tokuraku (*Muroran Institute of Technology University*)

1Pos005 量子ドットを用いたアミリン凝集体のリアルタイム 3D イメージングと阻害解析
Real-time 3D Imaging and Inhibition Analysis of Amylin Aggregations Using Quantum Dots
Xiaoyu Yin, Ziwei Liu, Tuya Gegen, Hayate Sawatari, Keiya Shimamori, Masahiro Kuragano, Kiyotaka Tokuraku (*Muroran Institute of Technology*)

1Pos006 マイクロフルイディックチップを使った室温条件下でのフェリチンの構造決定
Structure determination of Ferritin at room temperature in microfluidic chips
Yusuke Kono[1], Leonard Chavas[1,2] ([1]*Dept. of Appl. Phys., Nagoya Univ.*, [2]*Synchrotron Radiation Center, Nagoya Univ.*)

1Pos007 Map p ing an enzyme active site with time-resolved serial femtosecond crystallography by mixing injectors
Fangjia Luo[1], Michihiro Sugahara[2], Tetsunari Kimura[3], Takanori Nakane[4], Keitaro Yamashita[5], Kazuya Hasegawa[1], Ayumi Yamashita[2,6], Tomoyuki Tanaka[2,6], Toshi Arima[2,6], Rie Tanaka[2,6], Eiichi Mizohata[4], Mamoru Suzuki[4], Tetsuya Masuda[7], Kensuke Tono[1], So Iwata[2,6], Eriko Nango[2,8] ([1]*JASRI*, [2]*RIKEN Harima*, [3]*Kobe University*, [4]*Osaka University*, [5]*MRC Laboratory of Molecular Biology*, [6]*Kyoto University*, [7]*Ryukoku University*, [8]*Tohoku University*)

1Pos008 Damage-free Crystal Structure of Fluorescent Protein, mBanana Reveals the Actual Chromophore Conformation
Nipawan Nuemket[1,2], Fangjia Luo[1], Takaaki Fujiwara[3], Norimichi Nomura[4], So Iwata[2,4], Eriko Nango[2,3] ([1]*Japan Synchrotron Radiation Research Institute*, [2]*RIKEN*, [3]*Tohoku University*, [4]*Kyoto University*)

1Pos009 時計タンパク質 KaiA-KaiC 複合体の溶液構造解析
Structural analysis of clock protein KaiA-KaiC complex in solution
Ken Morishima[1], Masahiro Shimizu[1], Yasuhiro Yunoki[1], Lionel Porcar[2], Anne Martel[2], Rintaro Inoue[1], Masaaki Sugiyama[1] ([1]*Institute for Integrated Radiation and Nuclear Science, Kyoto University*, [2]*Institut Laue-Langevin*)

1Pos010 左巻き *βαβ* モチーフを含む新規フォールドタンパク質のデノボデザイン
De novo design of left-handed βαβ-motifs-containing proteins
Hiroto Murata[1], Riu Hirano[1], Swagatha Ghosh[1], Leonard Chavas[1,2], George Chikenji[1] ([1]*Dept of Appl. Phys., Grad. Sch of Eng., Nagoya. Univ*, [2]*Synchrotron Radiation Research Center, Nagoya Univ.*)

1Pos011 Cryo-EM structure of the Mfa1 minor type V pilus from the periodontal pathogen *Porphyromonas gingivalis*
Satoshi Shibata[1,2], Mikio Shoji[3], Hideyuki Matsunami[2], Matthias Wolf[2] ([1]*Div. Bacteriology, Fac. Med., Tottori Univ.*, [2]*Mol. cryo-EM unit, OIST*, [3]*Grad. Sch. Biomed. Sci., NagaNagasaki Univ.*)

1Pos012 Crystal Structures of AMPA Receptor Complexed with a Ligand by X-ray Free Electron Laser
Hansel Adriel[1], Takaaki Fujiwara[1], Kyohei Soga[2], Fangjia Luo[3], Shigeki Kiyonaka[2], Eriko Nango[1,3] ([1]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, Katahira 2-1-1, Aoba-ku, Sendai, Japan, 980-8577*, [2]*Graduate School of Engineering, Nagoya University, Furo-cho, Chigusa-ku, Nagoya, Japan, 464-8603*, [3]*RIKEN SPring-8 Center, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan*)

01B. タンパク質：構造機能相関／01B. Protein: Structure & Function

1Pos013 ヒスタミン H_1 受容体に対する E/Z-Doxepin 立体異性体の結合評価
Binding properties of E/Z-Doxepin isomers to histamine H_1 receptor
Hiroto Kaneko[1], Ryunosuke Korenaga[1], Ryota Nakamura[2], Shinnosuke Kawai[2], Tadashi Ando[2], **Mitsunori Shiroishi**[1] ([1]*Dept.of Biol. Sci. and Technol., Tokyo Univ. of Sci.*, [2]*Dept. of Appl. Electronics, Tokyo Univ. of Sci.*)

1Pos014 ヒスタミン H1 受容体に対する E/Z-Doxepin 立体異性体の結合自由エネルギー計算
Free energy calculations of E- and Z-doxepin isomers binding to histamine H1 receptor
Ryota Nakamura[1], Shinnosuke Kawai[1], Hiroto Kaneko[2], Ryunosuke Korenaga[2], Tadashi Ando[1], Mitsunori Shiroishi[2] ([1]*Dept. of Appl. Electronics., Tokyo Univ. of Sci.*, [2]*Dept. of Biol. Sci. and Technol., Tokyo Univ. of Sci.*)

1Pos015 Glu48 と His124 の変異による大腸菌リボヌクレアーゼ HI の金属イオン配位解析
Metal-ion coordination in *Escherichia coli* ribonuclease HI, as revealed by mutation analyses of Glu48 and His124
Yumi Kitagawa[1], Zengwei Liao[1], Takuji Oyama[2], Kosuke Morikawa[1], Masayuki Oda[1] ([1]*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*, [2]*Faculty Life Environ. Sci., Yamanashi Univ.*)

1Pos016 重鎖 CDR3 ループ内ジスルフィド結合が抗原結合や安定性に与える影響
Role of a disulfide bond in H-CDR3 loop of antibody for antigen binding and stability
Mutsumi Yoshida[1], Yumi Kitagawa[1], Masayuki Oda[1], Nobutaka Numoto[2], Nobutoshi Ito[2] ([1]*Grad. Sch. Life. Environ. Sci., Kyoto Pref. Univ.*, [2]*Med. Res. Inst., Tokyo Med. Dent. Univ.*)

1Pos017 ショウジョウバエの左右非対称性を制御する MyoIC と MyoID の解析
Analysis of MyoIC and MyoID controlling left-right asymmetry in Drosophila
Suguru Sato[1], Kohe Yoshimura[1], Takeshi Haraguchi[2], Asuka Yamaguchi[3], Kenji Matsuno[3], Kohji Ito[2] ([1]*Grad. Sch. Sci., Univ. Chiba*, [2]*Sch. Sci., Univ.Chiba*, [3]*Grad. Sch. Sci., Univ. Osaka*)

1Pos018 電荷ペプチドタグ付き抗 EGFR-VHH 抗体の生物物理学的解析と EGFR への結合評価
Biophysical characterization of charged peptide-tagged anti-EGFR-VHHs and evaluation of their binding to EGFR
Yukako Shimatake[1], Md. Golam Kibria[1], Sawaros Onchaiya[1], Yoko Akazawa[2], Yoshihisa Hagihara[2], Yutaka Kuroda[1] ([1]*Grad. Sch. Eng., TUAT*, [2]*Kansai Inst., AIST*)

1Pos019 時間分解蛍光異方性測定による緑色蛍光タンパク質 eGFP の蛍光共鳴エネルギー移動の観測
FRET processes of enhanced green fluorescent protein (eGFP) observed by picosecond time-resolved fluorescence anisotropy measurements
Yuna Kinoshita[1], Mamoru Shigeno[1], Haruko Hosoi[1,2] ([1]*Grad. Sch. Sci., Toho Univ.*, [2]*Fac. Sci., Toho Univ.*)

1Pos020 Crystallographic, SAXS and simulation studies on LTA4 hydrolases reveal conformational differences related to catalytic mechanism
Mahmudul Hasan[1,2], **Sandhya P. Tiwari**[2], Jesper Z. Haeggström[3], Gert-Jan Bekker[2], Kenji Mizuguchi[2], Marjolein Thunnissen[4] ([1]*Biochemistry and Structural Biology, Lund University, Sweden*, [2]*Institute for Protein Research, Osaka University*, [3]*Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm, Sweden*, [4]*MAX IV Laboratory, Lund University, Sweden*)

01C. タンパク質：物性／01C. Protein: Physical Property

1Pos021 分子動力学計算による変性剤中におけるタンパク質の熱力学的研究
Molecular dynamics study of thermodynamics of proteins in denaturants
Hitomi Baba[1], Mafumi Hishida[2], Go Watanabe[1,3,4] ([1]*Grad. Sch. Sci., Kitasato Univ.*, [2]*Sch. Sci., Tokyo Univ. Sci.*, [3]*Sch. Front. Eng., Kitasato Univ.*, [4]*KISTEC*)

1Pos022 X 線小角散乱解析による磁場応答蛋白質の構造学的研究
Structural studies of magnetic field-responsive proteins by small-angle X-ray scattering analysis
Shigeki Arai[1], Rumi Shimizu[1], Motoyasu Adachi[1], Mitsuhiro Hirai[2] ([1]*Institute for Quantum Life Science, QST*, [2]*Gunma University*)

1Pos023 ニワトリ卵白由来リゾチームの熱凝集の前駆体とされる不可逆的なオリゴマーの物性解析
Physicochemical characterization of irreversible oligomers considered precursors of thermal aggregation of hen egg white lysozyme
Tomonori Saotome, Shun-ichi Kidokoro (*Nagaoka Univ. of Tech.*)

1Pos024 日本脳炎ウイルス由来 ED3 タンパク質と金属イオンの相互作用による会合体形成の物理化学的解析
Physicochemical analysis of aggregation of Japanese encephalitis virus-derived ED3 protein with metal ions
Nanaka Morikoshi, MD. Din Islam, Subbaian Brindha, Takahiro Yosizue, Yutaka Kuroda (*Grad. Sch. Eng., TUAT*)

1Pos025 Bacterial expression of the influenza A H1N1 receptor-binding domain protein
Le Ngoc Thao Tu, Tharangani Rathnayaka, Yutaka Kuroda (*Grad. Sch. Eng, TUAT*)

1Pos026 ペプチド結合平面性の部位特異的緩和が β タンパク質の熱安定性に及ぼす影響
Effect of site-specific relaxation of peptide bond planarity on thermal stability of beta-proteins
Kaori Chiba[1], Tomonori Saotome[2] ([1]*Indust. Eng. Natl. Inst. Tech, Ibaraki Coll.*, [2]*Dept. of Mate. Sci. and Bio., Nagaoka Univ. of Tech.*)

1Pos027 高圧 native 電気泳動速度法を用いたオリゴマータンパク質の安定性に関する研究
The thermodynamical and kinetic studies on the stability of oligomeric protein by using high-pressure native PAGE velocity method
Ryo Ishiguro, **Tetsuro Fujisawa** (*Fac. Eng., Gifu Univ.*)

1Pos028 クモ糸フィブロインから再構成されたナノファイバーを用いたフィルムの調製
Preparation of films with nanofibers reconstructed from spider silk fibroin
Haruya Kajimoto[1], Kento Yonezawa[2], Takehiro Sato[3], Yoichi Yamazaki[1], Sachiko Toma-Fukai[1], Hironari Kamikubo[1,2] ([1]*NAIST, MS*, [2]*NAIST, CDG*, [3]*Spiber Inc.*)

1Pos029 アミロイド β タンパク質の分子構造動態と凝集に D-アスパラギン酸が与える影響
Effect of D-Aspartic Acid on the Conformational Dynamics and Aggregation of Amyloid-$\beta_{1\text{-}42}$ Protein
Yu Fukuda[1], Takeru Kameda[1], Shin-ichi Tate[3], Yuichi Togashi[1,2] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Riken BDR*, [3]*Grad. Sch. Integ. Sci. Life, Hiroshima Univ.*)

1Pos030 ミトコンドリアにおけるタンパク質膜挿入の構造基盤
Structural basis of the protein membrane insertion by the mitochondrial protein assembly gate
Hironori Takeda (*Grad. Sch. Sci. Tech. Inno., Kobe Univ.*)

01D. タンパク質：機能／01D. Protein: Function

1Pos031 Investigation of the effect of ATP/ADP for formation of 2-Cys peroxiredoxin (Prx2) high molecular weight complex
NgocTrang Tran[1], Hiroki Konno[2] ([1]*Grad. Sch. Frontier Science Initiative, Kanazawa Univ.*, [2]*WPI Nano Life Science Institute, Kanazawa Univ.*)

1Pos032 Orchestration of proteins in a Kai clock system 2
Masaaki Sugiyama[1], Ken Morishima[1], Yasuhiro Yunoki[1], Rintaro Inoue[1], Hirokazu Yagi[2], Koichi Kato[3] ([1]*KURNS*, [2]*Grad. Sch. Phar., Nagoya City Univ.*, [3]*ExCELLS*)

1Pos033 エネルギー再生系酵素であるポリリン酸キナーゼ 2 クラス III の広い基質特異性のメカニズムの解明
Characterization of promiscuity of energy regeneration enzyme polyphosphate kinase 2 class III
Ako Kagawa[1], Ryusei Matsumoto[2], Takayoshi Watanabe[1], Liam Longo[1], Tomoaki Matsuura[1] ([1]*ELSI, Tokyo Tech*, [2]*Dept. Life Sci. Tech., Tokyo Tech*)

1Pos034 ファージディスプレイ法によるポリエチレンテレフタレート吸着タンパク質の開発
Development of polyethylene terephthalate binding protein by phage display method
Yoshihito Hashino[1], Akihiko Nakamura[1,2] ([1]*Faculty of Agriculture, Shizuoka University*, [2]*Institute for Molecular Science*)

1Pos035 高活性 PET 分解酵素の高速スクリーニング法の確立と実証
Development and demonstration of high-throughput screening method for highly active PET hydrolase
Yui Ogura[1], Akihiko Nakamura[1,2] ([1]*Faculty of Agriculture, Shizuoka University*, [2]*Institute for Molecular Science*)

1Pos036 一過的な静水圧印加後における GEF ドメイン存在時の Ras の遅発的活性化
Delayed activation of Ras in the presence of GEF after application of transient hydrostatic pressure
Teruhiko Matsuda[1], Minki Chang[2], Yuki Taninaka[2], Katsuko Furukawa[2], Takashi Ushida[3], Taro QP Uyeda[1] ([1]*Dept. Pure & Appl. Physics, Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Bio Eng., Fac. Eng., Univ. Tokyo*, [3]*Dept. Mech. Eng., Fac. Eng., Univ. Tokyo*)

1Pos037 Clarification of the color tuning mechanism between GPR and BPR by FTIR spectroscopy
Tatsuro Nishikino[1], Teppei Sugimoto[1], Hideki Kandori[1,2] ([1]*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology*, [2]*OptoBioTechnology Research Center, Nagoya Institute of Technology*)

1Pos038 QM/MM metadynamnics を使った *Eco*RV の DNA 加水分解における複数の反応経路
Reaction Pathways in DNA Hydrolysis of *Eco*RV Calculated by QM/MM Metadynamics
Itaru Onishi[1], Mika Mitsumatsu[1], Ryoutarou Matsuda[1], Norio Yoshida[2], Fumio Hirata[3], **Masayuki Irisa**[1] ([1]*Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*Grad. Sch. Inform.. Nagoya Univ.*, [3]*Inst. Mol. Sci.*)

1Pos039 深層学習を用いた GIST マップの高速計算：リガンド結合に伴う水の自由エネルギー変化の計算への応用
A Fast Computation of GIST Maps Using a Deep Learning: Application to the Computation of Free-Energy Change of Water upon Ligand Binding
Yusaku Fukushima, Yuki Ito, **Takashi Yoshidome** (*Dep. of Appl. Phys., Tohoku Univ.*)

1Pos040 二次元蛍光寿命相関分光法による酵素反応観測の試み： CRISPR-Cas13a の RNA 分解反応
An attempt to detect enzymatic reaction by two-dimensional fluorescence lifetime correlation spectroscopy: RNA cleavage by CRISPR-Cas13a
Tsukasa Tokita[1], Bidyut Sarkar[1], Hajime Shinoda[2], Kunihiko Ishii[1,3], Rikiya Watanabe[2], Tahei Tahara[1,3] ([1]*Molecular Spectroscopy Laboratory, RIKEN, Japan*, [2]*Molecular Physiology Laboratory, RIKEN, Japan*, [3]*RIKEN Center for Advanced Photonics, Japan*)

1Pos041 全光子記録方式による二色蛍光相関分光法：ナノ秒からミリ秒領域におけるタンパク質ダイナミクスの観測
Lossless photon recording of two-color fluorescence correlation spectroscopy for protein dynamics investigations from nano to milliseconds
Yutaka Sano[1,2], Yuji Itoh[1,2], Atsuhito Fukasawa[3], Hiroyuki Oikawa[1,2], Satoshi Takahashi[1,2] ([1]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*, [2]*Department of Chemistry, Graduate School of Science, Tohoku University*, [3]*Hamamatsu Photonics K. K.*)

1Pos042 リコンビナント LOX-1,CD36 および LDL 受容体に結合する LDL の硬さ特性
Physical properties of low-density lipoproteins recognized by recombinant LOX-1,CD36 and LDL receptor
Seiji Takeda[1], Kanako Ushirogata[2], Takehiro Kikuchi[1], Yunoshin Sasaki[1], Subagyo Agus[3], Taichi Takasuka[2] ([1]*Dept. Pharm., Hokkaido Univ. of Sci.*, [2]*Grad. Sch. GFR., Hokkaido University*, [3]*Grad. Sch. Info. Sci.Tech., Hokkaido University*)

1Pos043 非生物発光タンパク質における擬似ルシフェラーゼ活性の発見と利用
Discovery and utilization of pseudo-luciferase activities in non-bioluminescent proteins
Ryo Nishihara[1,2], Ryoji Kurita[1] ([1]*National Institute of Advanced Industrial Science and Technology (AIST)*, [2]*Japan Science and Technology Agency (JST), PRESTO*)

1Pos044 Advancing X-ray Diffraction: Versatile Capabilities and Future Prospects of BL2S1 at the Aichi Synchrotron
Leonard MGH Chavas, Yasufumi Umena, Hiroki Onoda (*Nagoya University Synchrotron-radiation Research center*)

1Pos045 グラファイト上におけるペプチドの自己組織化を利用した EggPC 脂質膜の展開
Utilizing Peptide Self-Assembly on Graphite for the formation of EggPC Lipid Membranes
Soichiro Kato[1], Kantaro Kikuchi[1], Takayuki Watanabe[2], Tomoaki Matsuura[2], Yuhei Hayamizu[1] ([1]*Dept. of Mat. Sci. and Eng., Tokyo Tech.*, [2]*ELSI, Tokyo Tech.*)

1Pos046 Automated Density Extraction of Isomorphous Difference map and Occupancy-estimation for Conformer Fitting
Sriram Srinivasa Raghavan[1], Osamu Miyashita[1], Tama Florence[1,2,3] ([1]*RIKEN Center for Computational Science, Kobe, Japan*, [2]*Institute of Transformative Biomolecules (WPI-ITbM), Nagoya University, Aichi, Japan*, [3]*Department of Physics, Graduate School of Science, Nagoya University, Aichi, Japan.*)

01F. タンパク質：タンパク質工学／進化工学／01F. Protein: Engineering

1Pos047 タンパク質ディスプレイとマイクロウェルアレイチップを組み合わせた、個別生化学的評価型タンパク質スクリーニングシステムの開発
Protein screening system based on individual biochemical evaluation by the combination of protein display and microwell array chip
Shingo Ueno[1], Fumi Toshioka[1], Shoichi Tsuchiya[1], Takanori Ichiki[1,2] ([1]*iCONM, Kawasaki Inst. Industry. Promo.*, [2]*Grad. Sch. Eng., Univ. Tokyo*)

1Pos048 ファインチューニング済み言語モデルを用いた VHH 抗体配列のベイズ最適化
Bayesian optimization of nanobody sequences with a fine-tuned language model
Hironori Matsubara, Yasuhiro Matsunaga (*Grad. Sch. Sci. Eng., Saitama Univ.*)

1Pos049 L グルタミン酸酸化酵素の基質認識の構造基盤
Structural basis of substrate recognition of L-glutamate oxidase
Yuka Ueda[1], Natsume Nakayama[2], Yoshika Yano[2], Kenji Inagaki[2], Takekawa Norihiro[1], Katsumi Imada[1] ([1]*Dept. Macromol. Sci., Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Env. & Life Sci.*)

1Pos050 非天然アミノ酸を用いたペプチド生合成を目指した AzpC の改変体の計算デザイン
Computational design of modified AzpC for peptide biosynthesis using nonnatural amino acids
Koki Miyake, Takashi Maruyama, Yoshitaka Moriwaki, Yohei Katsuyama, Yasuo Ohnishi, Tohru Terada (*The Graduate School of Agricultural and Life Sciences, The University of Tokyo*)

1Pos051 Development of fluorescent peptide aptamer targeting the SARS-CoV-2 spike protein using ribosome display
Shin Woong Kim[1,2], Yoshito Ito[3], Noriko Minagawa[3], Akiko Yumoto[3], Yoshihiro Ito[1,2,3], Takanori Uzawa[2,3] ([1]*Department of Biological Sciences, Tokyo Metropolitan University*, [2]*Nano Medical Engineering Laboratory, RIKEN Cluster for Pioneering Research*, [3]*Emergent Bioengineering Materials Research Team, RIKEN Center for Emergent Matter Science*)

1Pos052 3D ドメインスワッピングに基づいた計算機設計による安定な *c* 型シトクロム 2 量体の創製
Construction of stable *c*-type cytochrome dimers utilizing computational design inspired by 3D domain swapping
Naoya Kobayashi[1], Yuma Yoshida[1], Hideaki Ogata[2], Tsuyoshi Mashima[1], Shun Hirota[1] ([1]*NAIST, Mat. Sci.*, [2]*Univ. Hyogo, Grad. Sch. Sci.*)

1Pos053 立体的に類似した構造モチーフを介した構造ドメイン組換えによるヘテロオリゴマータンパク質のコンビナトリアル設計法
Combinatorial design of heterooligomeric proteins by recombination of structural domains through sterically analogous structure motifs
Marino Yamamoto, Naoya Kobayashi, Shun Hirota (*Mat. Sci., NAIST*)

1Pos054 ペプチドアプタマー選出に向けたサイバー・フィジカルシステムの構築
Development of a cyber-physical system for peptide aptamer selection
Yoshito Ito, Noriko Minagawa, Akiko Yumoto, Yoshihiro Ito, **Takanori Uzawa** (*RIKEN*)

03. 膜タンパク質／03. Membrane proteins

1Pos055 膜内切断プロテアーゼ RseP のネイティブ質量分析による特性解析
Characterization of the intramembrane-cleaving protease RseP by native mass spectrometry
Michiko Tajiri, Tomoya Shida, Terukazu Nogi, Satoko Akashi (*Yokohama City Univ.*)

1Pos056 高速 AFM による多剤排出トランスポーター P-gp の機能ダイナミクス解析
HS-AFM Observation of Conformational Dynamics of ABC transporter P-gp
Yuto Nonaka[1], Norie Hamaguchi[2], Fumi Nakagawa[2], Takeshi Murata[2], Takayuki Uchihashi[1] ([1]*Grad. Sch. Phys., Univ. Nagoya*, [2]*Grad. Sch. sci., Univ. Chiba*)

1Pos057 異なる膜様環境下でのプロトンポンプ型ロドプシン RxR の物性、構造および機能の解析
Analysis of the physical properties, structure and function of proton-pumped rhodopsin RxR under different membrane-mimetic environments
Chihiro Kikuma[1], Rika Suzuki[1], Keiichi Kojima[2], Yuji Tokunaga[3], Koh Takeuchi[3], Yuki Sudo[2], Hideo Takahashi[1] ([1]*Grad. Sch. Med. Life Sci., YCU*, [2]*Grad. Sch. Msd., Dent. and Pharma Sci., Univ. Okayama*, [3]*Grad. Sch. Pharma Sci., Univ. Tokyo*)

1Pos058 液胞膜内 delta-rhodopsin 発現酵母による光を用いた H^+輸送と物質生産能の向上
Enhancement of H^+ transport and bioproduction capacity by light for yeast expressing delta-rhodopsin in vacuolar membrane
Kaoru Daicho, Yoko Hirono, Hiroshi Kikukawa, Kentaro Tamura, Kiyotaka Hara (*Grad.Sch.Integr.Pharm. Nutr. Sci.,Univ.Shizuoka*)

1Pos059 アデノシン A2a 受容体と G タンパク質との結合のダイナミクスの解明： 分子動力学シミュレーション研究による
Unveiling the dynamics of Adenosine A2a receptor coupling to the G proteins: a molecular dynamics simulation study
PhuocDuy Tran, Sari Hagimoto, Akio Kitao (*Sch. Life Sci. Tech., TokyoTech*)

1Pos060 高フッ素化ジパルミトイルホスファチジルコリン膜に再構成したバクテリオロドプシンの構造・機能の特徴
Structural and functional properties of bacteriorhodopsin reconstituted in highly fluorinated dipalmitoylphosphatidylcholine membranes
Daiki Kojima[1], Ai Nakagawara[1], Takafumi Shimoaka[1], Takashi Kikukawa[2], Toshiyuki Takagi[3], Hiroshi Takahashi[1], Hideki Amii[1,4], Masashi Sonoyama[1,4,5] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*, [3]*AIST*, [4]*GIAR, Gunma Univ.*, [5]*GUCFW, Gunma Univ.*)

1Pos061 リガンド結合の有無による MAO-B 二量体のダイナミクスの違い
The differences between the dynamics in MAO-B dimer with/without a ligand binding
Yoshitaka Tadokoro[1], Naoyuki Miyashita[1,2] ([1]*Grad. Sch. BOST, KINDAI Univ.*, [2]*BOST., KINDAI Univ.*)

04. DNA・DNA 結合タンパク質／04. DNA & DNA binding proteins

1Pos062 Hop2-Mnd1 and Swi5-Sfr1 Stimulate Dmc1 Filament Assembly Using Distinct Mechanisms
Hung-Wen Li[1], Wei Lee[1], Hiroshi Iwasaki[2], Hideo Tsubouchi[2] ([1]*Chemistry, Nat'l Taiwan Univ.*, [2]*Institute of Innovative Research, Tokyo Institute of Technology*)

1Pos063 分子動力学シミュレーションによるインターカレーションした DNA の構造解析
Analysis of conformation of intercalated DNA using molecular dynamics simulations
Hisashi Ishida[1], Hidetoshi Kono[1,2] ([1]*National Institutes for Quantum Science and Technology*, [2]*Chiba University*)

1Pos064 高速原子間力顕微鏡による FnCas9 の機能動態解明
High-speed atomic force microscopy reveals functional dynamics of Francisella novicida Cas9
Hideaki Tsukada[1], Mikihiro Shibata[2,3] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ*, [2]*WPI-NanoLSI, Kanazawa Univ*, [3]*InFiniti, Kanazawa Univ*)

1Pos065 大腸菌 UvrD C 末端非構造化領域全欠損変異体の DNA 結合・巻き戻しダイナミクス
Dynamics of DNA binding and unwinding by *Escherichia coli* UvrD lacking the entire unstructured C-terminal region
Hiroaki Yokota (*Grad. Sch. Creation New Photon. Indust.*)

1Pos066 高速原子間力顕微鏡による転写因子 Photozipper の DNA 上での動態過程の観察
Dynamic process of a transcription factor, Photozipper, on DNA observed by high-speed atomic force microscopy
Akihiro Tsuji[1], Hayato Yamashita[1], Osamu Hisatomi[2], Masayuki Abe[1] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*Grad. Sch. Sci., Osaka Univ.*)

1Pos067 スピンラベル ESR によるヘテロクロマチンタンパク質 HP1 の動的構造研究：リン酸化・DNA・H3K9me3・相分離の効果
Structural dynamics of heterochromatin protein HP1 by spin labeling ESR: Effects of phosphorylation, DNA, H3K9me3, and phase separation
Isao Suetake[2,3], Kazunobu Sato[4], Tomoaki Sugishita[3], Yuichi Mishima[3], Takeji Takui[4], Hironobu Hojo[3], Yoh Matsuki[3], Toshimichi Fujiwara[3], Makoto Miyata[1], **Toshiaki Arata[1,3]** ([1]*Dept. Biol., Grad. Sch. Sci., Osaka Met. Univ.*, [2]*Nakamura Gakuen Univ.*, [3]*IPR, Osaka Univ.*, [4]*Dept. Chem., Grad. Sch. Sci., Osaka Met. Univ.*)

1Pos068 RNA ポリメラーゼⅡがクロマチン構造を壊さずにヌクレオソームを通過する粗視化分子シミュレーション
Coarse-grained molecular simulations of RNA polymerase II passing through nucleosomes without disruption of chromatin
Takafumi Yamauchi, Fritz Nagae, Genki Shino, Tsuyoshi Terakawa, Giovanni Brandani, Shoji Takada (*Kyoto University*)

08. クロマチン・染色体／08. Chromatin & Chromosomes

1Pos069 Effect of the molecular crowding environment on the structure of polynucleosome
Tomoko Sunami[1], Amarjeet Kumar[1], Hidetoshi Kono[1,2] ([1]*National Institutes for Quantum Science and Technology*, [2]*Chiba University*)

1Pos070 生きた細胞核内での粘弾性測定
Measurement of Viscoelasticity in Nucleus of Living Cell
Akinori Miyamoto[1,2], Ryota Orii[3], Tetsuya Hiraiwa[2,4], Hirokazu Tanimoto[3], Yoshihiro Murayama[1] ([1]*Department of Applied Physics, Tokyo University of Agriculture and Technology, Japan*, [2]*Mechanobiology Institute, National University of Singapore, Singapore*, [3]*Department of Science, Yokohama City University, Japan*, [4]*Department of Physics, Academia Sinica, Taiwan*)

1Pos071 Building a Coarse-Grained Model to Investigate the Effects of Post-Translational Modifications on Nucleosome Packing and Gene Expression
Wai Soon Chan[1], Giovanni B. Brandani[2], Shoji Takada[2], Hidetoshi Kono[1] ([1]*Molecular Modeling and Simulation Team, iQLS, QST, Japan*, [2]*Department of Biophysics, Graduate School of Science, Kyoto University, Japan*)

1Pos072 Decoding the Mg^{2+} Ion Effects on Polynucleosomal Array Dynamics: Insights from Single-Molecule Optical Tweezers
Amarjeet Kumar[1], Tomoko Sunami[1], Shoko Sato[2], Hitoshi Kurumizaka[2], Hidetoshi Kono[1,3] ([1]*Institutes for Quantum Life Science, National institutes for Quantum Science and Technology, Chiba, Japan*, [2]*Institute for Quantitative Biosciences, The University of Tokyo, Tokyo, Japan*, [3]*Graduate School of Science, Chiba University, Chiba, Japan*)

1Pos073 クロマチンの高次構造はクロマチンの局所的な動きとクロマチンのかたさを制御する
Higher order structure of chromatin regulates local chromatin motion and chromatin stiffness
Shiori Iida[1,2], Masahito Tanaka[3], Sachiko Tamura[1], Masato Kanemaki[2,4], Yuta Shimamoto[2,3], Kazuhiro Maeshima[1,2] ([1]*Genome Dynamics Lab., Natl. Inst. of Genetics*, [2]*Graduate Institute for Advanced Studies, SOKENDAI*, [3]*Physics and Cell Biology Lab., Natl. Inst. of Genetics*, [4]*Molecular Cell Engineering Lab., Natl. Inst. of Genetics*)

09. 電子状態／09. Electronic

1Pos074 The electrical spike of *Escherichia coli*

Chiao-Chen Chuang[1], Fan Bai[2,3], Chien-Jung Lo[1] ([1]*Department of Physics and Center for Complex Systems, National Central University, JhongLi, Taoyuan 32001, Republic of China.*, [2]*Biomedical Pioneering Innovation Center (BIOPIC), School of Life Sciences, Peking University, Beijing, China.*, [3]*Beijing Advanced Innovation Center for Genomics (ICG), Peking University, Beijing, China.*)

1Pos075 酸素耐性を持つ[NiFe]ヒドロゲナーゼの電子・幾何構造に基づく理論的考察

Theoretical investigation into the electronic and geometrical structures for the oxidation tolerance of [NiFe]-hydrogenases

Yuta Hori[1], Ayaka Sato[2], Yasuteru Shigeta[1] ([1]*Center for Computational Sciences, Univ. Tsukuba*, [2]*Grad. Sch. Sci. Tech., Univ. Tsukuba*)

10. 水・水和／電解質／10. Water & Hydration & Electrolyte

1Pos076 高い透水性をもつ細胞を用いた凍結保存過程における脱水の効果に関する研究

Study on the effects of dehydration in the cryopreservation process by using high water permeability cells

Sumire Matsuo[1], Kenji Yamazaki[2], Masato Yasui[3], Youichiro Abe[3], Tsutomu Uchida[2] ([1]*Graduate school of engineering, Hokkaido University*, [2]*Faculty of Engineering, Hokkaido University*, [3]*School of Medicine, Keio University*)

1Pos077 構造予測法と統計熱力学を組み合わせた「ペプチド薬デザイン法」の開発

A methodology for designing peptide drugs by combining structure prediction methods and statistical thermodynamics

Shunsuke Miyamoto, Tomohiko Hayashi (*Grad. Sch. Sci. and Tech., Niigata Univ.*)

1Pos078 機械学習をもちいた水の構造記述子による溶液の低密度-高密度構造の検出

A structural descriptor for liquid water constructed by machine-learning method that detects low-density and high-density structure

Taku Mizukami[1], Nguyen Viet Cuong[2], Dam Hieu Chi[3] ([1]*JAIST, Materials Science*, [2]*HPC systems*, [3]*JAIST Knowledge Science*)

1Pos079 ペプチドおよびタンパク質周囲の水和ダイナミクスの分子動力学シミュレーションによる解明

Elucidation of hydration dynamics around peptides and proteins by molecular dynamics simulation

Takuya Takahashi[1], Ryutaro Inou[2], Yui Nakamura[2], Shingo Nobunaga[2], Simon Hikiri[1] ([1]*Coll. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ.*)

1Pos080 テラヘルツ分光で解き明かす細胞内の水の世界

Exploring the world of intracellular water with terahertz spectroscopy

Keiichiro Shiraga[1,2], Suzune Nagao[3] ([1]*Grad. Sch. Agri., Kyoto Univ.*, [2]*JST PRESTO*, [3]*Dep. Agri., Kyoto Univ.*)

1Pos081 酵素反応における水の役割の解明に向けたタンパク質周りの水和状態の検証

Investigation of hydration state around proteins to elucidate the role of water in enzyme reactions

Mizuki Yamamoto[1], Naoshi Kondo[2], Yuichi Ogawa[2], Keiichiro Shiraga[2,3] ([1]*Dep. Agri., Kyoto Univ.*, [2]*Grad. Sch. Agri., Kyoto Univ.*, [3]*JST PRESTO*)

1Pos082 トレハローストランスポーター TRET1 発現細胞を用いた接着状態での凍結保存技術の開発
Study on the development of cryopreservation technology in an adherent state using cells expressing trehalose transporter TRET1
Koki Watanabe[1], Takahiro Kikawada[2,3], Kenji Yamazaki[4], Tsutomu Uchida[4] ([1]*Graduate School of Engineering, Hokkaido University*, [2]*National Agriculture and Food Research Organization (NARO)*, [3]*Graduate School of Frontier Sciences, The University or Tokyo*, [4]*Faculty of Engineering, Hokkaido University*)

14. 分子モーター／14. Molecular motor

1Pos083 粗視化 MD 計算を用いた F_OF_1 ATPase の F_O モーターと F_1 モーターの回転対称性のミスマッチに関する理論研究
Theoretical study on rotational symmetry mismatch between F_O and F_1 motor of F_OF_1 ATPase using coarse-grained MD simulation
Shintaroh Kubo, Yasushi Okada (*Grad. Sch. Med., Univ. Tokyo*)

1Pos084 高速 AFM によるべん毛 III 型分泌装置の ATPase FliI の動態観察
Observation of flagellar type III secretion system ATPase FliI by HS-AFM
Yuki Tajimi[1], Asako Usui[2], Tatsunari Yano[2], Norihiro Takekawa[2], Katsumi Imada[2], Takayuki Uchihashi[1,3] ([1]*Department of Physics, Nagoya University*, [2]*Department of Macromol, Osaka University*, [3]*ExCELLS*)

1Pos085 繊毛打中のクシクラゲ櫛板の軸糸からのミリ秒時間分解 X 線回折像記録
Millisecond time-resolved recordings of X-ray diffraction patterns from axonemes in beating comb plates of ctenophore
Hiroyuki Iwamoto[1], Mio Kosaka[2], Ryo Yokoya[2], Kei Jokura[2], Kazuhiro Oiwa[3], Kazuo Inaba[2] ([1]*SPring-8, JASRI*, [2]*Univ. Tsukuba, Shimoda Marine Research Ctr.*, [3]*NICT・Bio-ICT*)

1Pos086 細菌鞭毛馬達的分布
Bacterial Flagellar Motor Distribution
Chien-Jung Lo (*National Central University*)

1Pos087 キネシン 1 のネックリンカーが頭部のメカノケミカルサイクルを制御する仕組み
How the neck linker controls mechanochemical cycle of kinesin-1's catalytic domain
Yamato Niitani[2], Kohei Matsuzaki[1,2], Erik Jonsson[3], Ron Vale[3], **Michio Tomishige**[1] ([1]*Dept. Phys. Sci., Aoyama Gakuin Univ.*, [2]*Dept. Appl. Phys., Univ. Tokyo*, [3]*Dept. Cell. Mol. Pharmacol., UCSF*)

1Pos088 モータータンパク質の運動の理解を目指した第一通過時間による負荷を伴う化学反応速度の計算
Chemical reaction rates with loads calculated from first-passage time towards understanding motions of motor proteins
Takakuni Fukumoto[1], Hideo Higuchi[1], Kazuo Sasaki[2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Grad. Sch. Eng. Univ. Tohoku*)

1Pos089 QCM によるモータータンパク質の ATPase と結合解離の計測
Measurement of motor protein ATPase and binding dissociation by QCM
Taiki Nishimura[1], Honoka Kobayashi[1], Hideki Ashizawa[2], O. Yuhei Tahara[3,4], Makoto Miyata[3,4], Hajime Honda[1], Ikuko Fujiwara[1] ([1]*Dept. Matl. Sci. Bioeng., Nagaoka Univ. Tech*, [2]*RIVER ELETEC CORPORATION*, [3]*Grad. Sch. Sci., Osaka Metropolitan Univ*, [4]*OCARINA, Osaka Metropolitan Univ*)

1Pos090 水頭症マウスの免疫染色法による内腕ダイニンのタンパク質発現量の解析
Analysis of protein expression levels of inner arm dynein in hydrocephalus mice by immunostaining
Riko Ota, Madoka Kondo, Hironori Ueno (*Edu.,Aichi Univ. Edu.*)

1Pos091 マウスにおける内腕ダイニンの組織依存的発現解析とストーク部位発現
Tissue-dependent expression analysis of inner arm dynein and stalk expression in mice
Yuka Iwasa, Mio Kosaka, Nozomu Ida (*Edu., Aichi Univ. Edu.*)

1Pos092 Active Buckling of Microtubule Driven by Kinesin Motor
Douglas K. Ng'ang'a, Takahiro Nitta (*Applied physics, Gifu Univ.*)

1Pos093 Cooperativity in force generation by kinesin propelled microtubule ' s swarm using an electromagnetic tweezer
Mst Rubaya Rashid[1], Mousumi Akter[2], Arif Md. Rashedul Kabir[2], Kazuki Sada[2], Akira Kakugo[1] ([1]*Division of Physics and Astronomy, Kyoto University*, [2]*Graduate School of Science, Hokkaido University*)

1Pos094 QCM はミオシンの結合と解離によって起こるアクチンフィラメントの変化を検出する可能性がある
QCM may detect changes in actin filaments brought by the association and dissociation of myosin
Honoka Kobayashi[1], Taiki Nishimura[1], Naoki Matsumoto[2], Hideki Ashizawa[3], Ikuko Fujiwara[1,2], Hajime Honda[1,2] ([1]*Dept. of Matl. Sci. and Bioeng., Nagaoka Univ. of Tech*, [2]*Dept. of Bioeng. , Nagaoka Univ. of Tech*, [3]*RIVER ELETEC CORPORATION*)

1Pos095 圧力変化によるべん毛モーターの回転コントロール
Control of flagellar rotation with pressure change
Seiichiro Kinoshita, Masayoshi Nishiyama (*Grad.Sch.Sci. and Eng., Kindai Univ.*)

1Pos096 Whole structural modeling of budding yeast condensin complex by high-speed atomic force microscopy and semi-automatic analysis
Hiroki Koide[1], Noriyuki Kodera[2], Mayu Terakawa[1], Shoji Takada[1], Tsuyoshi Terakawa[1] ([1]*Faculty of Science, Kyoto University*, [2]*Biophysics Group, Kanazawa University*)

15A. 細胞生物学的課題：接着／15A. Cell biology: Adhesion

1Pos097 生細胞内における応力伝播
Stress propagation in a living cell
Ayama Tokuyasu, Hirokazu Tanimoto (*Grad. Sch.Nanobioscience., Yokuhama City Univ.*)

1Pos098 接着性 GPCR、CELSR が細胞間に形成する分子複合体の解析
Stably formed trans protein complex of adhesion GPCR at the cell-cell interface
Rinshi Kasai[1], Shigetaka Nishiguchi[2], Takayuki Uchihashi[3] ([1]*Natl. Cancer Ctr. Res. Inst.*, [2]*Osaka U.*, [3]*Nagoya U.*)

15B. 細胞生物学的課題：運動／15B. Cell biology: Motility

1Pos099 大腸菌単一細胞における走化性応答時の走化性タンパク質の細胞内動態の観察
Observation of intracellular dynamics of chemotaxis proteins during chemotactic response in a single *E. coli* cell
Hajime Fukuoka, Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima (*Grad. Sch. Front Biosci., Osaka Univ.*)

1Pos100 アーキアべん毛モーターは周期光刺激に応答して回転方向を変える
Archeallar motor changes the direction of rotation in response to periodic light stimuli
Azusa Kage[1], Ayaka Ihara[1], Daisuke Nakane[2], Takayuki Nishizaka[1] ([1]*Dept. Physics, Gakushuin Univ.*, [2]*Dept. Engineering Science, The Univ. of Electro-Communications*)

1Pos101 キイロショウジョウバエ精子鞭毛の 2 重らせん波形成と伝播
The extremely long flagellum of *Drosophila melanogaster* spermatozoon beats with small helical waves superimposed on large helical waves
Sho Tamai[1], Kosei Sato[1,2], **Kazuhiro Oiwa**[1,2] ([1]*Grad. Sch. Sci., Univ.Hyogo*, [2]*Natl. Inst. Info.Commun.Technol.*)

1Pos102 真核生物の走化性における β-arrestin を介した濃度レンジの拡張
β-arrestin mediates the extension of the concentration ranges in eukaryotic chemotaxis
Masaki Muromoto[1], Satomi Matsuoka[1,2,3], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. of Front. Biosci., Osaka University.*, [2]*Grad. Sch. Sci., Osaka University.*, [3]*BDR, RIKEN*)

1Pos103 Amyloid β aggregation inhibits cell motility of human brain microvascular endothelial cells through the disruption of actin cytoskeleton
Masahiro Kuragano[1], Takuma Maeda[1,2,3], Keiya Shimamori[1], Hiroki Kurita[3], Kiyotaka Tokuraku[1] ([1]*Graduate School of Engineering, Muroran Institute of Technology*, [2]*Ohkawara Neurosurgical Hospital*, [3]*Department of Cerebrovascular Surgery, International Medical Center, Saitama Medical University*)

1Pos104 腸炎ビブリオの乳酸・ピルビン酸・短鎖脂肪酸への走化性応答
Chemotaxis to lactate, pyruvate, and short-chain fatty acid (SCFA) in *Vibrio parahaemolyticus*
Hiroyuki Terashima, Toshio Kodama (*Dept. Bacteriol., Inst. Trop. Med.(NEKKEN), Nagasaki Univ.*)

1Pos105 セミインタクト化マウス気管上皮細胞の 3 次元繊毛運動解析
3D tracking of ciliary beating in semi-intact murine tracheal epithelial cells
Tatsuya Ichikawa[1], Kentaro Seri[1], Nobukiyo Tanaka[1], Koji Ikegami[2], Tomoko Masaike[1] ([1]*Dept. Appl. Biol. Sci., Tokyo Univ. of Sci.*, [2]*Dept. Anatomy and Dev. Biol., Sch. Med., Hiroshima U.*)

1Pos106 ケラトサイト細胞はムチンの高濃度域へ移動する
Cultured keratocytes showed a migratory response to the area of high mucin concentration
Seira Tachibana, Hitoshi Tatsumi (*Department of Applied Bioscience, Kanazawa Inst. of Technol., Ishikawa, Japan*)

1Pos107 海洋性ビブリオ菌べん毛モーター固定子 PomB のプラグ領域への化学修飾による固定子活性化の検討
Flagellar stator activation by a site-specific chemical modification in the plug region of PomB
Hiroaki Koiwa, Michio Homma, Seiji Kojima (*Grad. Sch. Sci., Univ. Nagoya*)

1Pos108 ゼブラフィッシュ原腸形成過程において観察された特徴的な細胞ブレブ挙動
Characteristic cell membrane blebs observed in zebrafish gastrulation
Ayaka Miyahara, Toshiyuki Mitsui, Yuuta Moriyama (*Aogaku Univ. Dept,of Phys.*)

1Pos109 ヒト原腸形成の自己組織化を模倣する：ヒト iPS 細胞のマイクロパターン培養
Mimicking the self-organization movement of human gastrulation: micro pattern culture of human iPS cells
Hazuki Tsuboi[1], Miyu Mori[1], Chihiro Takeuchi[1], Kiyoshi Ohnuma[2] ([1]*Grad. Sch. Eng., Univ. Nagaoka Tech*, [2]*Inn., Univ. Nagaoka Tech*)

1Pos110 細胞性粘菌の運動に関するグラフ理論を用いた解析
Analysis on the movement of crawling amoeba cells based on graph theory
Kazuko Hamaoka[1], Shinya Fujita[2], Hirokazu Tanimoto[1] ([1]*Grad. Sch. Nanobioscience, Yokohama City Univ.*, [2]*Grad. Sch. Data Science, Yokohama City Univ.*)

1Pos111 適応を担う 2 種類の酵素である CheR と CheB の細胞内動態の比較
Comparison of the intracellular dynamics of CheR and CheB, the two enzymes responsible for adaptation in chemotaxis system
Taketo Oshima, Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci. Osaka Univ.*)

1Pos112 魚類表皮ケラトサイト集団のリーダー細胞のフォロワーへの脱落
Demotion of leader cells to followers during the late stages of re-epithelialization in wound repair
Chika Okimura, Yoshiaki Iwadate (*Department of Biology, Yamaguchi University.*)

15C. 細胞生物学的課題：細胞骨格・膜骨格／15C. Cell biology: Cytoskeleton & Membrane Skeleton

1Pos113 デスミン中間径線維と相互作用するアクチン線維の指向的挙動
Oriented behavior of single actin filaments interacting with single desmin intermediate filaments
Kuniyuki Hatori, Takumi Ishizaka (*Yamagata Univ. Grad. Sci., Eng.*)

1Pos114 Jasplakinolide または Phalloidin を結合させたアクチンフィラメントの内部状態を FRET 観察によって理解する
Understanding the orientation of actin subunits conjugating with jasplakinolide or phalloidin by FRET measurements
Ai Takahashi[1], Miku Nezasa[1], Ichiro Nishikata[2], Kenji Kamimura[3], Ikuko Fujiwara[1], Hajime Honda[1] ([1]*Dept. of Matl. Sci. and Bioeng., Nagaoka Univ. of Tech.*, [2]*ACEM., NIT. Nagaoka college*, [3]*Dept. of Elect.Ctrl.Eng ., NIT. Nagaoka College*)

1Pos115 原子間力顕微鏡による粘膜下層由来線維芽細胞（SMFs）および漿膜下層由来線維芽細胞（SPFs）のレオロジー特性
Rheological properties of Submucosal and subperitoneal fibroblasts measured by atomic force microscopy
Haruka Yamasaki[1], Kaori Kuribaysdhi-shigetomi[1], Motohiro Kojima[2], Takaharu Okajima[1] ([1]*Hokkaido University*, [2]*National Cacner Center Exploratory Oncology Research & Clinical Trial Center*)

1Pos116 Physical integration of microtubule and actin cytoskeletons
Ryota Orii, Hirokazu Tanimoto (*Grad. Sch. Nanobioscience., Yokohama City University*)

1Pos117 微小管星状体の細胞内移動に伴う細胞質流れ場の測定
Measurement of the cytoplasmic flow field associated with microtubule aster centration
Mao Ikeda, Hirokazu Tanimoto (*Grad. Sch. Nanobioscience, Yokohama City Univ*)

1Pos118 Regulation of muscle membrane robustness against mechanical stress by membrane remodelling proteins
Kenshiro Fujise, Kohji Takei, **Tetsuya Takeda** (*Grad. Sch. Med. Dent. Pharma. Sci., Okayama Univ.*)

1Pos119 ラメリポディアアクチン流動の自己組織化機構
Self organization of reaward actin flow in lamellipodia
Tomomi Tani[1], Nori Nakai[2], Keisuke Sato[2], Sumio Terada[2] ([1]*National Institute of Advanced Industrial Science and Technology*, [2]*Tokyo Medical and Dental University*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

1Pos120 培地中 K^+濃度上昇による心筋細胞シートの伝導速度遅延
Slowing of conduction velocity in cardiomyocytes by increasing concentration of K^+ in cultured medium
Kentaro Kito, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

1Pos121 近赤外レーザーを用いた環状心筋ネットワークの伝導制御
Control of initiation site of excitation in Circular Cardiomyocyte Network Using Near-Infrared Laser
Momo Akada, Kentaro Kito, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, Dept. Frontier Biosci., Hosei Univ.*)

1Pos122 PI3K-PAK1 シグナル伝達は S-G2 期における ERK の活性化ダイナミクスを制御する
PI3K-PAK1 signaling regulates the activation dynamics of ERK in S-G2 phase
Ryo Yoshizawa, Nobuhisa Umeki, Yasushi Sako (*Wako Inst., Riken*)

1Pos123 同種の受容体からなる受容体アレイがもたらす短い適応時間
Short adaptation time brought about by receptor arrays composed of homogeneous species of receptors
Saki Ueda, Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front Sci., Osaka Univ.*)

1Pos124 シグナル伝達を惹起する細胞膜 EGFR 動態の 1 分子解析
Single-molecule analysis of EGFR behavior inducing signal transduction in the plasma membran
Michio Hiroshima[1,2,3], Masahiro Ueda[1,2] ([1]*Grad. Sch. FBS., Osaka Univ.*, [2]*RIKEN BDR*, [3]*RIKEN CPR*)

1Pos125 Promotion of cancer stem cell-like formation by administration of anticancer drugs
Akane Sato[1,2], Etsuro Ito[1,2] ([1]*Department of Biology, Waseda University*, [2]*BioPhenoMA Inc.*)

1Pos126 Geometric correlation of simultaneous plural phagocytoses on single macrophage
Maiha Ando (*ASE., Univ.Waseda*)

16A. 生体膜・人工膜：構造・物性／16A. Biological & Artificial membrane: Structure & Property

1Pos127 長鎖セラミドは一価不飽和リン脂質の相転移温度を生理的温度まで上昇させる
Long chain ceramides raise the chain-melting transition of monounsaturated phospholipids to physiological temperature
Hiroshi Takahashi[1,2], Tomohiro Hayakawa[2], Asami Makino[2], Kunihiko Iwamoto[2], Kazuki Ito[3], Satoshi B. Sato[2,4], Toshihide Kobayashi[2,5] ([1]*Grad.Sch.Sch. &Tech. Gunma Univ.*, [2]*Wako Inst., Riken*, [3]*SPring-8, Riken*, [4]*Grad. Sch. Sci., Kyoto Univ.*, [5]*UMR, CNRS, Univ. Strasbourg*)

1Pos128 長さの異なるアシル鎖をもつスフィンゴミエリンが脂質ラフト様相分離膜に及ぼす影響
Impact of sphingomyelin acyl chain heterogeneity upon properties of raft-like membranes
Masanao Kinoshita, Kana Hirano, Nobuaki Matsumori (*Grad. Sch. Sci., Kyushu Univ.*)

1Pos129 １本の疎水鎖末端にパーフルオロアルキル基を導入した新規二本鎖部分フッ素化 Hybrid 脂質の二分子膜の熱物性
Thermophysical properties of bilayers of double-chain-hybrid phospholipids with perfluoroalkyl groups at the end of one hydrophobic chain
Ai Nakagawara[1], Takafumi Shimoaka[1], Toshiyuki Takagi[2], Hiroshi Takahashi[1], Hideki Amii[1,3], Masashi Sonoyama[1,3,4] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*AIST*, [3]*GIAR, Gunma Univ.*, [4]*GUCFW, Gunma Univ.*)

1Pos130 光誘起マイクロバブルによる超長尺チューブ状リポソーム形成
Formation of ultralong liposome tubes by laser-induced microbubble
Akemi Noguchi, Ken-ichi Yuyama, Chie Hosokawa, Yasushi Tanimoto, Yasuyuki Tsuboi (*Grad. Sch. Sci., Univ. Osaka Metropolitan*)

1Pos131 神経芽腫細胞を用いた局所麻酔薬による脂質ラフトの形成抑制
Local anesthetics suppress the formation of lipid rafts in mouse neuroblastoma (Neuro2a) cell membranes
Aoi Nishimura, Yasuhiro Tanaka, Masanao Kinoshita, Kohei Torikai, Takayuki Kawai, Nobuaki Matsumori (*Grad. Sch. Sci. Kyushu Univ.*)

1Pos132 Vesosome-Based Drug Carrier for Conrolled and Sustained Release of Multiple Components
Tae-Joon Jeon[1], Deborah Lee[1], Seoyoon Song[1], Suheon Kim[1], Mina Lee[1], Eunsoo Kim[1], Sunhee Yoon[1], Han-ul Kim[2], Sejin Son[1], Hyun Suk Jung[2], Yun Suk Huh[1], Sun Min Kim[1] ([1]*Department of Bioengineering and Biological Sciences, Inha University, Korea*, [2]*Department of Biochemistry, Kangwon National University, Korea*)

16D. 生体膜・人工膜：輸送・情報伝達／16D. Biological & Artificial membrane: Transport & Signal transduction

1Pos133 改変型 β バレルナノポアタンパク質のリポソーム上での機能検討
Investigating the function of modified β-barrel nanopore protein on liposome
Toshiyuki Tosaka, Koki Kamiya (*Grad. Sch. Sci. & Tech., Gunma Univ.*)

1Pos134 膜タンパク質膜挿入に関わる糖脂質 MPIase と基質タンパク質の相互作用解析
Intermolecular Interactions between Membrane Proteins and Glycolipids Essential for Membrane Protein Integration
Shoko Mori[1], Kaoru Nomura[1], Kohki Fujikawa[1], Tsukiho Osawa[1], Ken-ichi Nishiyama[2], Keiko Shimamoto[1,3] ([1]*Bioorg. Res. Inst., Suntory Fdn. Life Sci.*, [2]*Fac. Agric., Iwate Univ.*, [3]*Grad. Sch. Sci., Osaka Univ.*)

1Pos135 支持脂質二層膜に GPCR を方向性を制御して組み込む [I] 共役する G タンパク質を使って
Reconstituting GPCR into supported lipid bilayer with controlled orientation. [I] Prebinding of the G protein transducin
Fumio Hayashi[1], Masato Koezuka[2], Kenichi Morigaki[2,3] ([1]*Grad. Sch. Sci., Univ. Kobe*, [2]*Grad. Sch. Agri., Univ. Kobe*, [3]*Biosignal Research Center, Univ. Kobe*)

1Pos136 リポソーム膜を介した DNA 配列情報伝達に向けた分子トランスデューサの研究
DNA Sequence Information Transfer Across Liposome Membrane Using Designed Molecular Transducers
Kai Yoshida[1], Shinichiro Nomura[1], Satoshi Murata[1], Ibuki Kawamata[1], Hideaki Matubayashi[1], Shogo Hamada[2] ([1]*Graduate School of Engineering, Tohoku University*, [2]*School of Computing, Tokyo Institute of Technology*)

18 神経・感覚／18 Neuroscience & Sensory systems

1Pos137 高速 AFM による CaMKII オリゴマー間に生じる分子間相互作用の解析
Interaction between inter CaMKII holoenzymes revealed by high-speed AFM
Taisei Suzuki[1], Hideji Murakoshi[2], Mikihiro Shibata[3] ([1]*Grad. Sch. NanoLS., Kanazawa Univ.*, [2]*Supportive Center for Brain Research, NIPS.*, [3]*WPI-NanoLSI, Kanazawa Univ.*)

1Pos138 High-speed atomic force microscopy reveled structural dynamics of CaMKIIβ at single-molecule level
Keisuke Matsushima[1], Hideji Murakoshi[2], Mikihiro Shibata[3,4] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Supportive Center for Brain Research, NIPS.*, [3]*WPI-NanoLSI, Kanazawa Univ.*, [4]*InFiniti, Kanazawa Univ.*)

1Pos139 カエル神経筋接合部シナプスにおける短期可塑性各成分間の数学的関係性：増進・増強・促通成分の関係性は積なのか和なのか
Relationship of components of short-term synaptic plasticity: Are augmentation, potentiation, and facilitation multiplicative or additive?
Naoya Suzuki (*Dept. physics, Sch. Sci., Nagoya Univ.*)

1Pos140 ゲノム編集によるタウ標識とタウ凝集過程の生細胞観察
Labeling of Tau by genome editing and live cell imaging analysis of tau aggregation process
Iona Katayama[1], Shigeo Sakuragi[2], Yoshiyuki Soeda[3], Akihiko Takashima[3], Hiroko Bannai[2] ([1]*Dept. of Elec. Eng. Biosci., Grad. Sch. of Adv.Sci.Eng.,Waseda univ.*, [2]*Fac. of Sci. Eng., Waseda univ.*, [3]*Fac. of Sci., Gakusyuin univ.*)

1Pos141 Effects of CPTX on Dendritic Spines in Primary Cultures of Rat Hippocampal Neurons
Boxiao Zhao[1], Hiroko Bannai[1], Michisuke Yuzaki[2] ([1]*Grad. Sch. of Adv. Sci. Eng., Waseda univ.*, [2]*Sch. of Med., Keio Univ.*)

1Pos142 イソフルランによる AMPA・$GABA_A$ 受容体クラスターの分布変化
Isoflurane-induced changes in AMPA and $GABA_A$ receptor cluster distribution
Shigeo Sakuragi[1], Taro Katagiri[2], Junichiro Ono[3,4], Hiroko Bannai[1] ([1]*Fac. Sci. Eng., Waseda Univ.*, [2]*Dept. Elec. Eng. Biosci., Grad. Sch. Adv. Sci. Eng., Waseda Univ.*, [3]*KKR Takamatsu Hosp.*, [4]*Dep. Anesthesiol., Fac. Med., Kagawa Univ.*)

20. 行動／20. Behavior

1Pos143 有効打と回復打からなるボルボックスの繊毛運動の粘弾性依存性
Viscoelasticity dependence of ciliary motion consisting of effective and recovery strokes in Volvox
Saki Tamura, Yoshihiro Murayama (*Tokyo Univ. of Agri. and Tech.*)

1Pos144 体細胞の状態変化がボルボックスの走光性に及ぼす影響
Effect of change of somatic cell state on phototaxis of *Volvox*
Mitsuki Sato, Yoshihiro Murayama (*Tokyo Univ. of Agri. and Tech.*)

1Pos145 リスク下にある真性粘菌の脱出行動における質量,経路幅,リスク強度の依存性
Dependence of mass, escape path width, and risk intensity on escape behavior of true slime mold under risk
Tomoki Fukuhara (*Grad. Sch, Sys. info. Sci., Future University Hakodate*)

21A. 光生物：視覚・光受容／21A. Photobiology: Vision & Photoreception

1Pos146 アニオンチャネルロドプシンのゲート閉鎖過程と過渡的なプロトン放出反応の同時性
Synchronicity of gate closing and transient proton release from Asp234 in *Guillardia theta* anion channelrhodopsin 1
Miu Sudo[1], Sayo Inoko[1], Takuma Watanabe[1], Makoto Demura[1,2], Takashi Kikukawa[1,2], Takashi Tsukamoto[1,2] ([1]*Division of Macromolecular Functions, Department of Biological Science, School of Science, Hokkaido University*, [2]*Faculty of Advanced Life Science, Hokkaido University*)

1Pos147 Electrophysiological characterization of the ion transport mechanism of proton pump rhodopsin in rhizobacteria
Zikun Lyu, Shunki Takaramoto, María del Carmen Marín, Hiromu Yawo, Keiichi Inoue (*ISSP, Univ. Tokyo*)

1Pos148 ウニオプシンの分子特性の比較解析
Comparative analysis of the molecular properties of sea urchin opsins
Atsushi Horiuchi[1], Kazumi Sakai[1], Shion Aoki[1], Junko Yaguchi[2], Shunsuke Yaguchi[2], Takahiro Yamashita[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Shimoda Marine Res. Cent., Univ. of Tsukuba*)

1Pos149 ラマン光学活性分光を用いたクロライドポンプ微生物型ロドプシンの活性部位構造に関する研究
Structure and Heterogeneity of Retinal Chromophore in Chloride Pump Rhodopsins Revealed by Raman Optical Activity
Masashi Unno[1], Masaiku Ohya[1], Takashi Kikukawa[2], Junpei Matsuo[1], Takashi Tsukamoto[2], Ryota Nagaura[1], Tomotsumi Fujisawa[1] ([1]*Department of Chemistry and Applied Chemistry, Saga University*, [2]*Faculty of Advanced Life Science, Hokkaido University*)

1Pos150 ナトリウムポンプロドプシンにおけるレチナールシッフ塩基の配座変化
Configurational change of retinal Schiff base chromophore in a sodium pump rhodopsin
Tomotsumi Fujisawa[1], Kouta Kinoue[1], Ryouhei Seike[1], Takashi Kikukawa[2], Masashi Unno[1] ([1]*Fac. Sci. Eng., Saga Univ.*, [2]*Fac. Adv. Life Sci., Hokkaido Univ.*)

1Pos151 双安定性かつ G タンパク質双共役性を示すオプシン
Characterization of an opsin having bi-stable and bi-coupling properties
Tomoki Kawaguchi, Hisao Tsukamoto (*Department of Biology, Graduate School of Science, Kobe University*)

1Pos152 哺乳類メラノプシンと特異的アンタゴニストとの相互作用の生化学的・理論的解析
Biochemical and computational analyses of interactions between mammalian melanopsins and a specific antagonist
Kohei Obayashi[1], Ruisi Zou[2,3], Toshifumi Mori[3], Hisao Tsukamoto[1] ([1]*Department of Biology, Graduate School of Science, Kobe University*, [2]*Interdisciplinary Graduate School of Engineering Sciences, Kyushu University*, [3]*Institute for Materials Chemistry and Engineering, Kyushu University*)

1Pos153 リン酸化ロドプシンとの相互作用における桿体アレスチン 4 量体の役割
Role of Tetramer of Rod Visual Arrestin in the Interaction with Phosphorylated Rhodopsin
Yasushi Imamoto[1], Keiichi Kojima[1,2], Toshihiko Oka[3], Ryo Maeda[1], Yoshinori Shichida[4] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Fac. Med. Dent. Pharm. Sci., Okayama Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*, [4]*Ritsumeikan Univ.*)

1Pos154 分子センサーを用いた、無脊椎動物型オプシンによる G タンパク質の活性化・下流のシグナル伝達キネティクスの解析
Analysis of invertebrate-type opsin-mediated G protein activation and downstream signaling kinetics using luminescent biosensors
Marina Narimiya, Michihiro Ohta, Hisao Tsukamoto (*Grad. Sch. Sci., Kobe Univ.*)

1Pos155 溶液 NMR 法によるプロトンポンプ型ロドプシン RxR のアルギニン残基の機能における役割の解析
Roles of the conserved arginine residue in a proton pumping rhodopsin RxR revealed by solution NMR spectroscopy
Reika Hironishi[1], Rika Suzuki[1], Masahumi Hirohata[1], Keiichi Kojima[2], Toshio Nagashima[3], Toshio Yamazaki[3], Yuki Sudo[2], Hideo Takahashi[1] ([1]*Grad. Sch. of Med. Life Sci., YCU*, [2]*Grad. Sch. of Med., Dent. and Pharma. Sci., Univ. of Okayama*, [3]*BDR, RIKEN*)

1Pos156 ラマン分光法による青／橙色シアノバクテリオクロムの青色吸収型の構造解析
Structural analysis of the blue-absorbing form of blue/orange cyanobacteriochrome by Raman spectroscopy
Ryoka Seto[1], Masako Hamada[2], Yuu Hirose[2], Tomotsumi Fujisawa[1], Masashi Unno[1] ([1]*Department of Chemistry and Applied Chemistry, Faculty of Science and Engineering, Saga University*, [2]*Department of Applied Chemistry and Life Science, Toyohashi University of Technology*)

1Pos157 ラマン分光法およびアミノ酸置換体を用いたシアノバクテリオクロム RcaE における Lys261 の役割の解明
Role of Lys261 in Cyanobacteriochrome RcaE Studied by Mutagenesis and Raman Spectroscopy
Taisei Koga[1], Masako Hamada[2], Yuu Hirose[2], Tomotsumi Fujisawa[1], Masashi Unno[1] ([1]*Department of Chemistry and Applied Chemistry, Faculty of Science and Engineering, Saga University*, [2]*Department of Applied Chemistry and Life Science, Toyohashi University of Tecnology*)

21B. 光生物：光合成／21B. Photobiology: Photosynthesis

1Pos158 光合成カルボニルカロテノイド、シフォナキサンチンの発光準位の同定：蛍光スペクトルの溶媒効果
Characterization of the emissive state of a photosynthetic carbonyl carotenoid, siphonaxanthin: Solvent effect of fluorescence spectra
Ritsuko Fujii[1,2,5], **Kazuhiro Yoshida**[1], Soichiro Seki[2], Yumiko Yamano[3], Naohiro Oka[4] ([1]*Grad. Sch. Sci., Osaka Metropolitan Univ.*, [2]*Grad. Sch. Sci., Osaka City Univ.*, [3]*Edu. Res. Ctr., Kobe Pharmac. Univ.*, [4]*Bio-Innovation Res. Ctr., Tokushima Univ.*, [5]*Research Ctr. for Artificial Photosynth., Osaka Metropolitan Univ.*)

1Pos159 高速原子間力顕微鏡を用いた植物光合成膜におけるタンパク質複合体の動態観察
Dynamics of protein complexes in plant photosynthetic membrane observed by high-speed atomic force microscopy
Yudai Nishitani, Daisuke Yamamoto (*Fac. Sci., Fukuoka Univ.*)

1Pos160 1 分子励起-蛍光スペクトル分光法による光化学系 I のアンテナ分子への観察
Access to the Antenna System of Photosystem I via Single-Molecule Excitation -Emission Spectroscopy
XianJun Zhang[1], Joachim Martin Seibt[2], Rin Taniguchi[1], Ryo Nagao[3], Tatsuya Tomo[4], Takumi Noguchi[5], Shen Ye[1], Thomas Renger[2], Yutaka Shibata[1] ([1]*Tohoku University*, [2]*Johannes Kepler University Linz*, [3]*Shizuoka University*, [4]*Tokyo University of Science*, [5]*Nagoya University*)

1Pos161 AutoDock vina を用いた *T. elongatus* 光化学系 I のキノン結合サイトにおける分子結合シミュレーション
Molecular Docking Simulations at Quinone Binding Site of Photosystem I from *T. elongatus* Using AutoDock vina
Ayumu Takagi[1], Shigeru Itoh[2], Akihiro Kimura[2], Hirotaka Kitoh[1] ([1]*Grad. Sch. Sci. Eng., Kindai Univ.*, [2]*Dept. Phys., Grad. Sch. Sci., Univ. Nagoya*)

1Pos162 Purification and characterization of a new thermophilic purple sulfur bacterium *Caldichromatium japonicum*
Akane Minamino[1], K. Saini Mohit[3], Shinji Takenaka[1], Zheng-Yu Wang-Otomo[2], Yukihiro Kimura[1] ([1]*Department of Agrobioscience, Graduate School of Agriculture, Kobe University*, [2]*Faculty of Science, Ibaraki University*, [3]*Centre Algatech*)

1Pos163 紅色光合成細菌の辺縁光捕集タンパク質のバクテリオクロロフィル *a* のスペクトル特性に対する色素脱離と界面活性剤の影響
Spectral changes of bacteriochlorophyll *a* in peripheral antenna proteins of purple photosynthetic bacteria by B800 removal and detergents
Yoshitaka Saga, Syota Kawato, Kohei Hamanishi, Yuhi Sasamoto (*Fac. Sci. Eng., Kindai Univ.*)

1Pos164 ベイズ最適化による光合成 I 型反応中心 3 種の励起子モデルの修正
Modification of the exciton models of three photosynthetic type-I reaction centers with Bayesian optimization
Wataru Shimooka[1], Hirotaka Kitoh[2], Shigeru Itoh[1], Akihiro Kimura[1] ([1]*Grad. Sch., Nagoya Univ.*, [2]*Fac. Sci. and Engi., Kindai Univ.*)

1Pos165 光化学系 II の酸素発生系における翻訳後アミノ酸変換：脂肪族アミノ酸の変換
Post-translational amino acid conversion in the O_2-evolving complex of photosystem II: Conversion of aliphatic amino acids
Hatsune Mizue[1], Takehiro Suzuki[2], Takumi Matsubara[1], Tomomi Kitajima-Ihara[1], Minako Hirano[1], Yuichiro Shimada[1], Yuki Kato[1], Naoshi Dohmae[2], Takumi Noguchi[1] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*RIKEN CSRS*)

1Pos166 光化学系Ⅱにおけるクロロフィル励起三重項状態の消光機構
Quenching mechanism of the excited triplet state of chlorophyll in photosystem II
Mizuki Yokokawa, Yuki Kato, Takumi Noguchi (*Grad. Sch. Sci, Univ. Nagoya*)

1Pos167 Q-band パルス電子常磁性共鳴（EPR）法による光化学系Ⅱ マンガンクラスターの S_2 High Spin 状態の構造
Structure of S_2 High-Spin State Manganese Cluster of Photosystem II by Q-band Pulsed Electron Paramagnetic Resonance (EPR) Spectroscopy
Shinya Kosaki, Hiroyuki Mino (*Grad. Sch. Sci., Nagoya Univ.*)

1Pos168 *Synechocystis* PCC 6803 フィコビリソームロッドにおける周辺環境を含む発色団の光吸収スペクトルの理論的研究
Theoretical study of energy states of chromophores including the surrounding environment in *Synechocystis* PCC 6803 Phycobilisome rod
Hiroto Kikuchi (*Dept. of Phys. Nippon Med. Sch.*)

22. 放射線生物／活性酸素／22. Radiobiology & Active oxygen

1Pos169 **電子線照射による細胞伸長は ROS が原因か**
Is ROS the main factor for cell elongation caused by electron beam irradiation?
Junya Katai[1], Yuta Nagano[1], Kenshi Suzuki[2], Tetsuo Narumi[1], Masaki Shintani[1], Yosuke Tashiro[1], Yoshimasa Kawata[3], Wataru Inami[3], Hiroyuki Futamata[4] ([1]*Dept. Appl. Chem. Biological Eng., Univ. Shizuoka*, [2]*Grad. Sch. Scie. Tech., Univ. Shizuoka*, [3]*Res. Inst. Elect., Univ. Shizuoka*, [4]*Res. Inst. Green. Sci. Tech., Univ. Shizuoka*)

1Pos170 **人工多能性幹細胞とラマン顕微鏡を用いた放射線感受性の個人差推定法**
Estimation of human individual radiosensitivity using Raman spectroscopy and iPSC
Hideaki Fujita[1], Kensuke Sasaki[2], Tomonobu Watanabe[1,2] ([1]*Department of Stem Cell Biology, Research Institute for Radiation Biology and Medicine, Hiroshima University*, [2]*Laboratory for Comprehensive Bioimaging, RIKEN Center for Biosys-tems Dynamics Research*)

1Pos171 **一分子観察による DNA 二本鎖切断の定量的解析：抗酸化物質の保護効果**
Quantitative Evaluation on the Kinetics of Double-Strand Breaks of DNA from Single Molecule Observation: Protective Effect of Antioxidants
Haruto Ogawa[1], Takashi Nishio[1,2], Yuko Yoshikawa[1], Koichiro Sadakane[1], Kenichi Yoshikawa[1] ([1]*Facul. Life. Med. Sci., Doshisha Univ.*, [2]*PoL, TU Dresden*)

24. 合成生物学・人工細胞／24. Synthetic biology & Artificial cells

1Pos172 **細胞を創る研究から見えてきた生命の仕組み**
Characteristics of living cells revealed by cell reconstitution studies
Kei Fujiwara (*Dept. Biosci. Info., Keio Univ.*)

1Pos173 Design and construction of artificial DNA condensates with nanoscale biomolecules
Nathan Nunes Evangelista, Masahiro Takinoue (*Sch. Life Sci., Tokyo Tech*)

1Pos174 **リボソーム生合成の細胞外における再構成**
Reconstitution of ribosome biogenesis outside of cells
Yuishin Kosaka[1,2], Yumi Miyawaki[1], Megumi Mori[1], Shunsuke Aburaya[3], Mao Fukuyama[4,5], Mitsuyoshi Ueda[1,6], Wataru Aoki[5,6,7] ([1]*Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Kyoto, Japan*, [2]*Research Fellow of JSPS, Tokyo, Japan*, [3]*Division of Metabolomics, Medical Institute of Bioregulation, Kyushu University, Fukuoka, Japan*, [4]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, Sendai, Japan*, [5]*JST FOREST, Tokyo, Japan*, [6]*Kyoto Integrated Science & Technology Bio-Analysis Center, Kyoto, Japan*, [7]*Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan*)

1Pos175 **機械刺激依存性チャネルを用いた脂質-タンパク質非対称膜小胞内への分子輸送**
Molecular transportations via mechanosensitive channels into the asymmetric lipid-protein vesicles
Kotaro Baba, Koki Kamiya (*Graduate School of Science and Technology, Gunma University*)

1Pos176 **大腸菌細胞集団における走化性誘導の自己組織的パターン形成**
Self-organized pattern formation induced by chemotaxis in *E. coli* cell populations
Hironori Fujita[1,2] ([1]*Astrobiology Center*, [2]*National Institute for Basic Biology*)

1Pos177 **外部刺激に応答したリポソームの非対称膜形成制御システムの開発**
Development of Controllable System of Lipid Asymmetry in Liposome by External Stimulations
Sumin Lee, Koki Kamiya (*Grad. Sch. Sci. Tec., Gunma Univ.*)

1Pos178 人工細胞の粘性変化がもらたす新たな機能
Viscous changes in synthetic cells drive novel functionalities
Aileen Cooney[1,2,4], Tomoaki Matsuura[1], Yuval Elani[3], Lorenzo Di Michele[4] ([1]*Earth-Life Science Institute: ELSI, Tokyo Institute of Technology*, [2]*Department of Chemistry, Imperial College London*, [3]*Department of Chemical Engineering, Imperial College London*, [4]*Department of Chemical Engineering and Biotechnology, University of Cambridge*)

1Pos179 界面通過法によるリポソームへのチラコイド封入
Encapsulation of thylakoids into liposomes by emulsion transfer method
Shintaro Nishizaki, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ.*)

1Pos180 アフリカツメガエル卵抽出液を用いた人工細胞内核形成への挑戦
A challenge for nuclear assembly in synthetic cells using *Xenopus* egg extract
Sho Takamori[1], Hisatoshi Mimura[1], Toshihisa Osaki[1], Tomo Kondo[2], Miyuki Shintomi[3], Keishi Shintomi[4], Miho Ohsugi[2], Shoji Takeuchi[1,5,6] ([1]*Artificial Cell Membrane Systems Group, Kanagawa Institute of Industrial Science and Technology*, [2]*Graduate School of Arts and Sciences, The University of Tokyo*, [3]*Life Science Network, The University of Tokyo*, [4]*Chromosome Dynamics Laboratory, RIKEN*, [5]*Institute of Industrial Science, The University of Tokyo*, [6]*Graduate School of Information Science and Technology, The University of Tokyo*)

1Pos181 リポソームの機能化を目的とした DNA ハイドロゲル裏打ち構造の構築に向けて
Toward construction of DNA hydrogel-based cortex-like structures for liposome functionalization
Takuro Yoshinaga[1], Yusuke Sato[2] ([1]*Sch. Comp. Sci. Syst. Eng., Kyutech*, [2]*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech*)

1Pos182 動的な静止構造：人工細胞内に創られたチューリングパターン
Creation of Turing pattern in artificial cells by PAR system-like mutual inhibition network
Sakura Takada[1], Natsuhiko Yoshinaga[2,3], Nobuhide Doi[1], Kei Fujiwara[1] ([1]*Dept. Biosci. and Info., Keio Univ.*, [2]*AIMR, Tohoku Univ.*, [3]*MathAM-OIL, AIST*)

25. ゲノム生物学／25. Genome biology

1Pos183 染色体動態と関連している因子は何か？
What factors are associated with chromosome dynamics?
Takuya Nara[1], Haruko Takahashi[1], Akinori Awazu[2], Y Kikuchi[1] ([1]*Program of Basic Biology, Graduate School of Integrated Sciences for Life, Hiroshima University*, [2]*Program of Mathematical and Life Sciences, Graduate School of Integrated Sciences for Life, Hiroshima University*)

1Pos184 インフルエンザウイルスゲノムの変異分布計測
Mutational distribution of influenza virus genomes
Kazuki Ikeda (*the university of tokyo*)

26A. 計算生物学: 生命情報学／26A. Computational biology: Bioinformatics

1Pos185 Analysis of structure–function correlation in the active sites of heme proteins
Hiroko X. Kondo[1], Hiroyuki Iizuka[2], Gen Masumoto[3], Yusuke Kanematsu[4], Yu Takano[5] ([1]*Fac. Eng., Kitami Inst. Tech.*, [2]*CHAIN, Hokkaido Univ.*, [3]*RIKEN R-IH*, [4]*Grad. Sch. Adv. Sci. Eng., Hiroshima Univ.*, [5]*Grad. Sch. Info. Sci., Hiroshima City Univ.*)

1Pos186 CARMIL と twinfilin-tail の結合がキャッピング蛋白質の揺らぎに与える影響；弾性ネットワークモデルによる網羅的解析
Elastic network model reveals distinct flexibilities of capping proteins bound to CARMIL and twinfilin-tail
Ryotaro Koike, Motonori Ota (*Grad. Sch. Info., Nagoya Univ.*)

1Pos187 電子顕微鏡を用いた肺がん検出に向けたディープラーニングのための各種データ量増強と YOLO バージョン評価
Various Data Volume Augmentation and YOLO Versions Evaluation for Deep Learning to Detect Lung Cancers Using Electron Microscopy
Tatsumi Mizoe[1], Kenji Etchuya[2], Makiko Suwa[1,2], Chikara Sato[1,3] ([1]*Grad. Biol. Sci., Aoyama Gakuin Univ.*, [2]*Chem. Biol. Sci.,Aoyama Gakuin Univ*, [3]*National Institute of Advanced Industrial Science and Technology*)

1Pos188 生成モデルのよるタンパク質距離行列及び立体構造の生成
Generation of distance matrices and tertiary structures of proteins using a generative model
Ryo Okada[1], Yoshitaka Moriwaki[1], Kentaro Shimizu[2], Tohru Terada[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri and Life Science., The Univ. of Tokyo*, [2]*Agricultural Bioinformatics Research Unit, Grad. Sch. of Agri and Life Science., The Univ. of Tokyo*)

1Pos189 乳がんバイオマーカー候補の選定に有用な中心性指標の特定
Identification of useful centrality indicators for selection of breast cancer biomarker candidates
Saito Torii, Takanori Sasaki (*Grad. Sch. Adv. Math. Sci., Meiji Univ.*)

1Pos190 匂い地図シミュレータの構築と匂い分類のへの応用
Construction of odor map simulator and its application to odor classification
Kuria Takahashi[1], Kenji Etchuya[2], Makiko Suwa[1,2] ([1]*Biol. Sci., Grad. Sci. Eng., Aoyama Gakuin Univ.*, [2]*Chem. Biol. Sci., Sci. Eng., Aoyama Gakuin Univ.*)

1Pos191 免疫炎症関連のがんホールマーク遺伝子群に基づいた乳がんの遺伝子相関ネットワーク解析および生存分析
Gene correlation network analysis and survival analysis of breast cancer with cancer hallmark genes related to inflammation and immunity
Ayaka Yakushi[1], Masahiro Sugimoto[2], Takanori Sasaki[1] ([1]*Grad. Sch. Adv. Math. Sci., Meiji Univ.*, [2]*Ins. Adv. Bio., Keio Univ.*)

1Pos192 マルチオミクス解析による海馬神経系細胞の刺激応答の不均一性を生み出すメカニズムの解
Multi-omics analysis of stimulus-response heterogeneity in hippocampal neural cells
Katsunari Saito[1], Ken Murakami[1], Kaho Ito[1], Yutaka Suzuki[2], Yukiko Goda[3], Mariko Okada[1] ([1]*Institute for Protein Research, Osaka University*, [2]*Graduate School of Frontier Sciences, The University of Tokyo*, [3]*Synapse Biology Unit, Okinawa Institute of Science and Technology Graduate University*)

1Pos193 遺伝子発現の量比保存構造の尺度として細胞ラマンスペクトルを最大限に活用する
Maximizing the potential of cellular Raman spectra as a proxy of the stoichiometry conservation structure of gene expression
Takashi Nozoe[1,2], Ken-ichiro F. Kamei[1] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*UBI, Univ. Tokyo*)

26B. 計算生物学: 分子シミュレーション／26B. Computational biology: Molecular simulation

1Pos194 構造ゆらぎと薬剤結合モードに基づいたインシリコスクリーニングの高度化
Advancement of in silico screening based on protein structural fluctuation and drug binding mode
Hiroto Terada, Kei Moritsugu (*Grad. Sch. Sci., Osaka Pref. Univ*)

1Pos195 ABC 多剤排出トランスポーター構造変化の最小自由エネルギーパス計算
Minimum free energy path calculation for the structural change of ABC multi-drug efflux transporter
Kei Moritsugu[1,2], Takumi Someya[2], Ryuji Ishida[2], Akinori Kidera[2] ([1]*Grad. Sch. Sci., OMU*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

1Pos196 HIV-1 プロテアーゼの薬剤耐性機構に関する理論的研究： 残基相互作用ネットワーク解析
Computational Study of HIV-1 Protease for Drug Resistance Mutations: Residue Interaction Network Analysis
Yuto Miyamoto, Norifumi Yamamoto (*Chiba Tech*)

1Pos197 ヌクレオチドに依存したアクチンの構造サンプリング
Structural samplings of actin that are dependent on the bound nucleotides
Kenta Omoto, Kei Moritsugu (*Grad.Sch.Sci.,Osaka Pref.Univ*)

1Pos198 格子ポリマー鎖の負のエネルギー弾性に対する曲げエネルギーの効果
Effect of bending energy on negative energetic elasticity in a lattice polymer chain
Nobu C. Shirai[1], Naoyuki Sakumichi[2] ([1]*Mie Univ.*, [2]*Grad. Sch. Eng., Univ. Tokyo*)

1Pos199 グルタミンペプチドの自己集合構造に関する分子動力学的研究
A Molecular Dynamics Study on the Self-Assembled Structure of Glutamine Peptides
Daiki Miura[1], Itsuki Ajioka[2,5], Takahiro Muraoka[3,5], Go Watanabe[1,4,5] ([1]*Grad. Sch. Sci., Kitasato Univ.*, [2]*CBIR., Tokyo Medical and Dental Univ.*, [3]*Grad. Sch. Eng., Tokyo Univ. Agric. and Tech.*, [4]*Sch. Front. Eng., Kitasato Univ.*, [5]*KISTEC*)

1Pos200 オートファゴソーム脂質輸送の分子動力学シミュレーション
Molecular dynamics of autophagosomal lipid transfer
Yuji Sakai[1], Kazuaki Matoba[2], N. Nobuo Noda[3], Yuji Sugita[4] ([1]*Inst. Life Med. Sci, Kyoto Univ.*, [2]*Inst. Microbial Chem.*, [3]*Inst. Genetic Med, Hokkaido Univ.*, [4]*RIKEN*)

1Pos201 Dynamin-1 assembly and membrane tubule constriction mechanism revealed by coarse-grained simulations
Md. Iqbal Mahmood[1], Shintaroh Kubo[2], Kei-ichi Okazaki[1] ([1]*Research Center for Computational Science, Institute for Molecular Science, National Institutes of Natural Sciences, Okazaki*, [2]*Graduate School of Medicine, The University of Tokyo, Japan.*)

1Pos202 レプリカ置換法によるポリグルタミンタンパク質の凝集に対するアルギニンの阻害機構の理論的解析
Theoretical analysis of the inhibition mechanism of arginine on polyglutamine protein aggregation by the replica permutation method
Shoichi Tanimoto[1], Hisashi Okumura[1,2,3] ([1]*ExCELLS*, [2]*IMS*, [3]*SOKENDAI*)

1Pos203 QM/MM 法によるプレニル基転移酵素 Fur7 の反応機構解析
QM/MM study on the catalytic mechanism of the aromatic prenyltransferase Fur7
Fan Zhao[1], Yoshitaka Moriwaki[1], Tomohisa Kuzuyama[1,2], Tohru Terada[1] ([1]*Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo*, [2]*CRIIM, Univ. of Tokyo*)

1Pos204 天然アニオンチャネルロドプシン GtACR1 の塩化物イオンの自由エネルギープロファイルとイオン輸送経路に関する理論的研究
Theoretical study on free energy profile of chloride ion and ion conducting pathway of natural anion channelrhodopsin GtACR1
Takafumi Shikakura, Shigehiko Hayashi (*Grad. Sch. Sci., Kyoto Univ.*)

1Pos205 生物発光タンパク質イクオリンの発光反応過程についての理論的研究
Theoretical study on the luminescent reaction process of bioluminescent protein Aequorin
Tomohiro Ando, Shigehiko Hayashi (*Grad. Sch. Sci., Kyoto Univ.*)

1Pos206 実験構造に基づく $Ca_V1.2$ イオンチャネルと薬剤間の結合自由エネルギー計算
Calculation of the binding free energies of drugs to the $Ca_V1.2$ ion channel based on the experimental structure
Tatsuki Negami, Tohru Terada (*Grad. Sch. Agri. and Life Sci., Univ. Tokyo*)

1Pos207 ラン藻由来アルカン合成酵素の基質結合と生成物解離ダイナミクスの分子動力学シミュレーション
Molecular dynamics simulations of substrate binding and product dissociation dynamics of a cyanobacterial alkane synthase
Masataka Yoshimura[1], Shino Oda[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

1Pos208 How fast is fast enough: computer modeling of host-guest binding in a 3D cell-adaptable hydrogel network
Yi Wang (*Department of Physics, the Chinese University of Hong Kong*)

1Pos209 自由エネルギー解析によるトリプトファン合成酵素の β-reaction stage I と α-Ligand 結合との関係性の解明
Allosteric regulation of β-reaction stage I in tryptophan synthase by free energy analysis
Shingo Ito, Kiyoshi Yagi, Yuji Sugita (*Theor. Mol. Sci. Lab., CPR, RIKEN*)

1Pos210 経路探索手法によるヒトアミノ酸トランスポーター LAT1-CD98hc の構造変化の解析
Pathway sampling simulations to understand dynamically conformational changes in human amino acid transporter LAT1
Natsumi Yoshida[1], Masao Inoue[1], Toru Ekimoto[1], Tsutomu Yamane[2], Mitsunori Ikeguchi[1,2] ([1]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [2]*RIKEN R-CCS*)

1Pos211 Accelerated molecular dynamics and AlphaFold discover a conformational state of transporter protein OxlT
Jun Ohnuki, Kei-ichi Okazaki (*Institute for Molecular Science*)

1Pos212 Theoretical Study of Solvent Effect and Stability of Complex Structure of Aspirin and Hydroxyprophyl-ß-Cyclodextrin by MD Simulation
Helmia Jayyinunnisya, Dedy Rendrawan, Lince Meriko, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Nat. Sci. Tech, Kanazawa Univ.*)

1Pos213 Evaluation of MD-based high-throughput screening methods using supercomputer Fugaku
Tomoya Nabetani[1], Toru Ekimoto[1,2], Tsutomu Yamane[3], Mitsunori Ikeguchi[1,2,3] ([1]*Dept. Sci, Yokohama City Univ.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [3]*RIKEN R-CCS*)

1Pos214 Characterization of dynamic conformation of high mannose-type oligosaccharides based on molecular simulation and data clustering
Yue Zhang[1], Takumi Yamaguchi[1,2,3] ([1]*Sch. Materials Sci., JAIST*, [2]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [3]*ExCELLS, NINS*)

1Pos215 銅含有アミン酸化酵素における反応自由エネルギーの QM/MM 解析
QM/MM Free energy simulation for the catalytic reaction of bacterial copper amine oxidase
Mitsuo Shoji[1], Takeshi Murakawa[2], Yuta Hori[1], Yasuteru Shigeta[1], Hideyuki Hayashi[2], Toshihide Okajima[3] ([1]*CCS U.Tsukuba*, [2]*OMPU*, [3]*Sanken Osaka U.*)

26C. 計算生物学：生体モデリングとシミュレーション／26C. Computational biology: Biological modeling and simulation

1Pos216 NRK による CK2 活性制御の構造モデリングと解析
Structural modeling and analysis of NRK-mediated regulation of CK2 activity
Rena Yoshimura[1], Beni Lestari[2], Toshiaki Fukushima[2], Kei Moritsugu[1] ([1]*Grad. Sch. Sci., Osaka Pref. Univ.*, [2]*IIR, Tokyo Inst. Tech.*)

1Pos217 Unraveling the mechanisms of drug resistance in the MAPK pathway using structure-based modeling
Hiroaki Imoto[1], Nora Rauch[1], Ayaka Ichikawa[2], Mariko Okada[2,3], Oleksii Rukhlenko[1], Boris Kholodenko[1,4,5] ([1]*Systems Biology Ireland, University College Dublin*, [2]*Institute for Protein Research, Osaka University*, [3]*WPI Premium Research Institute for Human Metaverse Medicine (WPI-PRIMe), Osaka University*, [4]*Conway Institute of Biomolecular & Biomedical Research, University College Dublin*, [5]*Department of Pharmacology, Yale University School of Medicine*)

1Pos218 細胞がクラスターとなって移動する仕組みを解き明かす膜モデル
A cell membrane model that reproduces single and cluster cell migration
Katsuhiko Sato (*RIES, Hokkaido Univ.*)

1Pos219 Predicting the placement of biomolecular structures on AFM substrates based on electrostatic interactions
Romain Amyot, Noriyuki Kodera, Holger Flechsig (*NanoLSI, Kanazawa University*)

1Pos220 カルマンフィルタによる上皮組織の力推定
Kalman force inference for epithelial deformation: a force inference method for time-lapse movies
Goshi Ogita[1], Shuji Ishihara[2], Kaoru Sugimura[3], Tatsuo Shibata[1] ([1]*Riken BDR*, [2]*Grad. Sch. Arts and Sci., U Tokyo*, [3]*Grad. Sch. Sci., U Tokyo*)

1Pos221 A Gradient-Based Approach for Optimizing Molecular Structures using Atomic Force Microscopy Images and Normal Mode Analysis
Xuan Wu[1], Osamu Miyashita[2], Florence Tama[1,2,3] ([1]*Department of Physics, Nagoya University*, [2]*RIKEN Center for Computational Science*, [3]*Institute of Transformative Bio-Molecules, Nagoya University*)

1Pos222 Theoretical analysis of fruiting body development by *Dictyostelium discoideum*
Seiya Nishikawa[1], Shuji Ishihara[1,2] ([1]*Dept. of Integrated Sci., Grad. Sch. of Arts and Sci., The Univ. of Tokyo*, [2]*Universal Biol. Inst., The Univ. of Tokyo.*)

1Pos223 タンパク質-RNA 複合体のリファインメントのための AI に基づくモデリングとフレキシブルドッキング
Integrated AI-based Modeling and Flexible Docking for Protein-RNA Complexes Refinement
Kowit Hengphasatporn, Yasuteru Shigeta, Ryuhei Harada (*Center for Computational Sciences, University of Tsukuba, 1-1-1 Tennodai, Tsukuba, Ibaraki 305-8577, Japan*)

1Pos224 ハイブリッド QM/MM 自由エネルギー法によるタンパク質機能発現の理解
Understanding of protein functional expression using hybrid QM/MM free energy method
Masahiko Taguchi[1,2,3], Ryo Oyama[2], Masahiro Kaneso[2], Cheng Cheng[2], Chika Higashimura[2], Yoshihiro Uchida[2], Shun Sakuraba[3], Justin Chan[3], Shigehiko Hayashi[2], Hidetoshi Kono[3] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Sci., Kyoto Univ.*, [3]*iQLS, QST*)

28. 生態／環境／28. Ecology & Environment

1Pos225 微生物群集の機能的役割分担が複合微生物系の機能的恒常性を可能にする
Functional sharing of microbial community enables homeostasis in complex microbial systems
Rei Ikeda[1], Masahiro Honjo[2], Nobuhiro Takahashi[1], Reika Mimoto[3], Yasuhisa Saito[4], Takashi Okada[5], Motohiko Kimura[1], Yosuke Tashiro[1], Hiroyuki Futamata[6] ([1]*Grad. Sch. Integr. Sci. Technol., Shizuoka Univ.*, [2]*Grad. Sch. Sci. Technol. Shizuoka Univ.*, [3]*Fac. Eng. Shizuoka Univ.*, [4]*Grad. Sch. Sci. Eng. Shimane Univ.*, [5]*Inst. Med. Biol. Kyoto Univ.*, [6]*Res. Inst. Green Sci. Technol., Shizuoka Univ.*)

1Pos226 *Rhodococcus qingshengi* A3-8 株による独立栄養条件下での有機酸生産機構の解析
Analysis of mechanism for organic acid production by *Rhodococcus qingshengii* strain A3-8 under autotrophic conditions
Nobuhiro Takahashi[1], Yosuke Tashiro[1], Hiroyuki Futamata[2] ([1]*Department of Applied Chemistry and Biochemical Engineering, Graduate School of Engineering, Shizuoka University*, [2]*Research Institution of Green Science and Technology, Shizuoka University*)

1Pos227 Selective IR measurement of fluorescent protein chromophores in aqueous solution by resonance IR spectroscopy
Hirona Takahashi, Makoto Sakai (*Faculty of Science, Okayama University of Science*)

1Pos228 Effects of heat and chemical treatments on human hair detected by IR super-resolution imaging based on non-linear optical processes
Hirona Takahashi, Natsuki Okano, Hiroka Ishikawa, **Makoto Sakai** (*Faculty of Science, Okayama University of Science*)

1Pos229 tRNA post-transcriptional modifications enhance tRNA structural stability
Kazuki Nagashima[1], Ren Nakazaki[2], Asuteka Nagao[2], Ryo Iizuka[1], Hirohito Yamazaki[3], Tsutomu Suzuki[2], Sotaro Uemura[1] ([1]*Grad. Sch. Sci., The Univ. of Tokyo*, [2]*Grad. Sch. Eng., The Univ. of Tokyo*, [3]*TRI, Nagaoka Univ. of Tech*)

1Pos230 3D structural determination of biomolecules using spatial correlations in X-ray free-electron laser data
Wenyang Zhao[1], Osamu Miyashita[1], Miki Nakano[1], Florence Tama[1,2,3] ([1]*RIKEN Center for Computational Science*, [2]*Institute of Transformative Bio-Molecules, Nagoya University*, [3]*Department of Physics, Nagoya University*)

1Pos231 交流音を受容した内耳感覚上皮帯に生じる直流動作の検出とその起源
Induction of the offset motion by sinusoidal acoustic stimuli in cochlear sensory epithelium
Takeru Ota, Hiroshi Hibino (*Grad. Sch. Med., Osaka Univ.*)

1Pos232 原子間力顕微鏡を用いた転移能の異なる生きたがん細胞内核膜硬さ測定
Measurement of nuclear membrane properties in living cancer cells with different metastatic abilities using atomic force microscopy
Takehiko Ichikawa[1], Kundan Sivashanmugan[2], Takeshi Shimi[1,3], Kojiro Ishibashi[3], Takeshi Yoshida[1,4], Rikinari Hanayama[1,4], Eishu Hirata[1,3], Hiroshi Kimura[5,6], Takeshi Fukuma[1,7] ([1]*Kanazawa Univ., NanoLSI*, [2]*Univ. Maryland Sch. Med.*, [3]*Kanazawa Univ., Canc. Res. Inst.*, [4]*Kanazawa Univ., Grad. Sch. Med. Sci.*, [5]*Tokyo Inst. Tech., Inst, Inno, Res.*, [6]*Tokyo Inst. Tech., Grad. Sch. Biosci. Biotech.*, [7]*Kanazawa Univ., Dev. Nano Life Sci.*)

1Pos233 高速 AFM/ラマンマルチモーダル計測装置の開発
Development of high-speed AFM/Raman multimodal system
Keishi Yang[1], Feng-Yueh Chan[2], Hiroki Watanabe[2], Shingo Yoshioka[1], Prabhat Verma[1], Takayuki Uchihashi[2], Takayuki Umakoshi[1] ([1]*Grad. Sch. Eng., Univ. Osaka*, [2]*Grad. Sch. Sci., Univ. Nagoya*)

1Pos234 深層学習を用いた XFEL 単粒子解析実験の回折パターンの選別
Deep learning strategy for identifying hit diffraction patterns in experimental single particle XFEL data
Miki Nakano[1], Bhaskar Dasgputa[2], Sandhya P. Tiwari[3], Osamu Miyashita[1], Florence Tama[1,4,5] ([1]*RIKEN, R-CCS*, [2]*UTokyo, RCAST*, [3]*Osaka Univ., IPR*, [4]*Grad. Sch. Sci., Nagoya Univ.*, [5]*Nagoya Univ., ITbM*)

1Pos235 生細胞表面構造の動態計測に向けた走査型イオン伝導顕微鏡の電流ノイズの低減の検討
Current noise reduction of scanning ion conductance microscopy for visualizing structural dynamics of living cell membranes
Shoma Kamei[1], Shinji Watanabe[2] ([1]*Grad. Sch. NanoLS., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

1Pos236 ダイナミックレンジを増大させた FRET 型 ATP バイオセンサーによる単一細胞 ATP 計測
FRET-based ATP biosensors with expanded dynamic range for single-cell ATP measurement with fluorescence microscopy and flow cytometry
Akane Yonemitsu, Mizuho Nishida, **Hiromi Imamura** (*Grad. Sch. Biost., Kyoto Univ.*)

1Pos237 標的タンパク質を高効率で光不活化する光増感蛍光タンパク質
A photosensitizing fluorescent protein for high efficiency light inactivation of target proteins
Hisashi Shidara, Taku Shirai, Susumu Jitsuki, Kiwamu Takemoto (*Grad. Sch. Med., Mie Univ.*)

1Pos238 雲母格子上に整列した単一ポリペプチド鎖の光熱オフレゾナンスモード AFM による観察
Observation of single polypeptide chains aligned on a mica lattice by using photothermal off-resonance tapping AFM
Ikuo Obataya (*Quantum Design Japan*)

1Pos239 3 次元構造化照明顕微鏡の光軸方向分解能向上における画像取得枚数の減少
Reduction of image acquisition for the 3D-structured illumination microscopy with an axial resolution improvement
Wataru Minoshima, Yamato Matsuo, Atsushi Matsuda (*Adv. Res. Inst., NICT*)

1Pos240 荷電ペプチドを付加して最小ルシフェラーゼの活性を高める: picALuc2.0
Adding a charged peptide to enhance the activity of a minimal luciferase: picALuc2.0
Yuki Ohmuro-Matsuyama[1], Hayato Matsui[1], Masaki Kanai[1], **Tadaomi Furuta[2]** ([1]*Shimadzu Corporation*, [2]*Sch. Life Sci Tech., Tokyo Tech*)

1Pos241 リソソーム周辺の局所的な細胞質 ATP 濃度イメージング
Imaging local ATP concentrations at the cytoplasmic surface of lysosomes
Momoko Aoyama[1], Taiichi Tsuyama[2], Hiromi Imamura[3], Ken Yokoyama[1,2] ([1]*Graduate School of Life Science, Kyoto Sangyo University*, [2]*Faculty of Life Science, Kyoto Sangyo University*, [3]*Graduate School of Biostudies, Kyoto University*)

1Pos242 超高速 AFM の実現に向けたカンチレバーの変位検出レーザースポットの最小化
Miniaturization of the laser spot for cantilever deflection detection to realize ultra-high-speed AFM
Karen Kamoshita[1], Kenichi Umeda[2], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

1Pos243 生細胞における転写中の RNA ポリメラーゼ II 分子の力学的特性
Mechanical properties of single RNA Polymerase II molecules during transcription in living cells
Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech*)

1Pos244 Glow 発光する最小サイズ発光酵素 picALuc 変異体の作製
Glow-type conversion of a minimal luciferase, picALuc
Yuki Ohmuro-Matsuyama[1], Hayato Matsui[1], Masaki Kanai[1], Tadaomi Furuta[2] ([1]*Technol. Res. Lab., Shimadzu Co., Ltd.*, [2]*Sch. Life Sci Tech., Tokyo Tech*)

1Pos245 Effects of the astaxanthin against amyloid β aggregation on SH-SY5Y cells
Sahithya Hulimane Ananda, Gegen Tuya, Masahiro Kuragano, Kiyotaka Tokuraku (*Graduate School of Engineering, Muroran Institute of Technology*)

1Pos246 高速拡散 1 分子の位置推定精度向上にむけた軌跡追跡シミュレーション解析
Simulation analysis of improved trajectory tracking of single molecules undergoing fast diffusion
Hodaka Abiko, Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech*)

1Pos247 C2C12 筋芽細胞の分化過程における核内 1 分子動態の変化
Changes in single-molecule dynamics in the nucleus during differentiation of C2C12 myoblasts
Masanori Hirose, Yuma Ito, Makio Tokunaga (*Sch. Life Sci. Tech., Tokyo Tech*)

1Pos248 神経分化における細胞内発熱の寄与
Implication of Intracellular Thermogenesis in Neuronal Differentiation
Shunsuke Chuma[1,2], Kohki Okabe[3,4], Yoshie Harada[2,5,6] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*IPR, Osaka Univ.*, [3]*Grad. Sch. Pharm. Sci., The Univ. Tokyo*, [4]*JST PRESTO*, [5]*QIQB Osaka Univ.*, [6]*WPI-PRIMe Osaka Univ.*)

1Pos249 カフェインがニワトリ胚心臓の発生に及ぼす影響の SS-OCT による観察
Cardiac development in chick embryos exposed to caffeine imaged with swept source OCT
Ryuichiro Yamazaki, Takashi Yamaoka, Tomoya Tanaka, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ. Dept,of Phys.*)

2 日目（11 月 15 日（水））／Day 2（Nov. 15 Wed.） 16:50 〜 18:50

01A. タンパク質：構造／01A. Protein: Structure

2Pos001 海洋放線菌由来新規酵素の構造解析
Structual analysis of a novel enzyme from marine *Streptomyces*
Takumi Oshiro[1], Shuta Uehara[1], Yoshikazu Tanaka[2], Takuya Ito[3], Yoshio Kodera[1,4], Takashi Matsui[1,4] ([1]*Grad. Sch. Sci., Kitasato Univ.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*, [3]*Fac. Farm., Osaka Ohtani Univ.*, [4]*Center for Desease Proteomics, Sch. Sci., Kitasato Univ.*)

2Pos002 ディープラーニングによる電子顕微鏡画像中の生体分子の同定手法の開発
Identification of biomolecules in electron microscopy images with deep learning
Atsushi Matsumoto (*Institute for Quantum Life Science, National Institutes for Quantum Science and Technology*)

2Pos003 ヒト・ノイラミニダーゼ 1（hNeu1）の構造特定に向けたモデル作成
Model creation for structure determination of human neuraminidase1(hNeu1)
Takeru Nakajima[1], Leonard Chavas[1,2], Swagatha Ghosh[1], Hiroki Onoda[2] ([1]*Grad. Sch. Appl. Phys., Nagoya Univ*, [2]*NUSR, Nagoya Univ*)

2Pos004 硫酸還元細菌 *Desulfovibrio vulgaris* Miyazaki F 株由来 APS 還元酵素の結晶構造
Crystal structure of APS reductase from *Desulfovibrio vulgaris Miyazaki F.*
Rio Hamada, Koji Nishikawa, Hideaki Ogata (*Grad. Sch.Sci.,Univ.Hyogo*)

2Pos005 海洋性ビブリオ菌べん毛モーター固定子タンパク質 PomB のリンカー領域の役割
Roles of linker region of PomB, flageller stator protein in Vibrio alginolyticus
Yusuke Miyamura[1], Tatsuro Nishikino[2], Hiroaki Koiwa[1], Kanji Takahashi[3], Yuki Tajimi[3], Michio Homma[3], Takayuki Uchihashi[3], Seiji Kojima[1] ([1]*Dept. Biol. Sci., Grad.*, [2]*Det. Life Sci., Appl. Chem., Nagoya Inst. Tech.;*, [3]*Dept. Phys.,, Grad. Sch. Sci., Nagoya Univ*)

2Pos006 F_oF_1-ATPase の非触媒部位の機能
Function of the non-catalytic site of F_oF_1-ATPase
Ren Kobayashi, Atsuki Nakano, Ken Yokoyama (*Faculty of Life Science, Kyoto Sangyo University*)

2Pos007 Studying structural and dynamic properties of urinary human serum albumin fragments: simulation studies
Chanya Archapraditkul[1], Kanokwan Janon[1], Deanpen Japrung[2], Prapasiri Pongprayoon[1,3] ([1]*Department of Chemistry, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand*, [2]*National Nanotechnology Center, National Science and Technology Development Agency, Thailand Science Park, Khlong Luang, Pathum Thani, Thailand*, [3]*Center for Advanced Studies in Nanotechnology for Chemical, Food and Agricultural Industries, KU Institute for Advanced Studies, Kasetsart University, Bangkok, Thailand*)

2Pos008 Computational studies of inhibitory effect of brazilin and hematein from *Caesalpinia sappan* Linn. against *Cutibacterium acnes*

Maneenuch Pengsawang[1], Apaporn Boonmee[2], Phoom Chairatana[3], Prapasiri Pongprayoon[1] ([1]*Department of Chemistry, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand*, [2]*Department of Chemistry, Faculty of Science and Technology, Rambhai Barni Rajabhat University, Chanthaburi 22000, Thailand*, [3]*Department of Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand*)

2Pos009 持続可能なフードシステムに向けたエネルギー豊富なタンパク質の構造決定
Structural characterization of energy-rich proteins for sustainable food systems

Yuuma Tanaka[1], Swagatha Ghosh[1], Leonard Chavas[1,2] ([1]*Dept. of Appl. Phys., Grad. Such. of Eng., Nagoya Univ.*, [2]*Synchrotron Radiation Research Center, Nagoya Univ.*)

2Pos010 Analysis of the electronic state of the metal sites of cytochrome *c* oxidase using simultaneous XES and XRD measurements

Keigo Tsuiki[1], Takahumi Kamei[1], Takanori Nakane[2], Tetsuo Katayama[3], Atsuhiro Shimada[1] ([1]*Dept. Appl. Life Sci., Fac. Appl. Biol. Sci., Univ. Gifu*, [2]*Inst. Protein Res., Univ. Osaka*, [3]*JASRI*)

2Pos011 Electron transfer mechanism proposed by the cryo-EM structure of cytochrome *c* and cytochrome *c* oxidase complex

Yuto Taguchi[1], Daisuke Kouzai[2], Haruna Naitou[1], Kouki Nishikawa[3,4], Yoshinori Huziyoshi[3,4], Kazutoshi Tani[5], Kouichirou Ishimori[6], Atsuhiro Shimada[1] ([1]*Dept. Appl. Life Sci., Fac. Appl. Biol. Sci., Univ. Gifu*, [2]*Inst. Cellular and Structural Physiology , Univ. Nagoya*, [3]*Inst. Adv. Res., Univ. Tokyo Medical and Dental*, [4]*CeSPIA Inc.*, [5]*Grad. Sch. Med., Univ.Mie*, [6]*Faculty of science, Univ. Hokkaidou*)

01B. タンパク質：構造機能相関／01B. Protein: Structure & Function

2Pos012 膜内切断プロテアーゼ RseP の結晶構造及び基質の進入と切断を制御する新規ゲーティング機構モデル
Crystal structure and novel gating mechanistic model to regulate substrate entry and its cleavage of the intramembrane protease RseP

Yohei Hizukuri[1], Yuki Imaizumi[2], Kazunori Takanuki[2], Takuya Miyake[1], Tatsuya Kobayashi[1], Tatsuhiko Yokoyama[1], Rika Oi[2], Terukazu Nogi[2], Yoshinori Akiyama[1] ([1]*Inst. Life Med. Sci., Kyoto Univ.*, [2]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*)

2Pos013 インバース共溶媒分子動力学法によるタンパク質-化合物部分構造相互作用の定量的評価手法の開発
Quantitative Evaluation of Protein-Chemical Substructure Interaction with Inverse Mixed-Solvent Molecular Dynamics Simulation

Keisuke Yanagisawa[1], Ryunosuke Yoshino[2,3], Genki Kudo[4], Takatsugu Hirokawa[2,3] ([1]*Comput. Sci., Sch. Comput., Tokyo Tech*, [2]*Faculty Med., Univ. Tsukuba*, [3]*TMRC, Univ. Tsukuba*, [4]*Appl. Sci., Grad. Sch. Sci. Tech., Univ. Tsukuba*)

2Pos014 フラボ酸化還元酵素の光化学的性質を利用したタンパク質構造ダイナミクス解析
Investigation of protein dynamics using photochemistry of a flavin prosthetic group in oxidoreductase

Daisuke Seo[1], Bo Zhuang[2], Alexey Aleksandrov[2], Marten Vos[2] ([1]*Division of Material Science, Graduate School of Natural Science and Technology, Kanazawa University*, [2]*LOB, CNRS, INSERM, École Polytechnique, Institut Polytechnique de Paris*)

2Pos015 A synthetic biology approach to reconstituting defined amyloid fibrils for FAD-related Aβ that reproduce features of cotton-wool plaque

Mohammad Jafar Tehrani[1], Isamu Matsuda[1], Atsushi Yamagata[2], Tatsuya Matsunaga[1,2], Mikako Shirouzu[2], **Yoshitaka Ishii**[1,2] ([1]*School of Life Science and Technology, Tokyo Institute of Technology*, [2]*RIKEN Center for Biosystems Dynamics Research*)

2Pos016 海洋生物由来の抗 SARS-CoV-2 活性を有するタンパク質の血球凝集活性を抑制するタンパク質工学的手法
Protein engineering for suppressing hemagglutination activity of anti-SARS-CoV-2 protein from marine organism
Mami Okabe[1], Hiromi Watari[2], Yokoyama Takeshi[1], Ayato Takada[3], Ryuichi Sakai[2], Yoshikazu Tanaka[1] ([1]*Graduate School of Life Science, Tohoku University*, [2]*Faculty of Fisheries Sciences, Hokkaido University*, [3]*International Institute for Zoonosis Control, Hokkaido University*)

2Pos017 CD28 結合における Gads SH2 の構造機能特性
Structural and functional properties of Gads SH2 dimer in CD28 binding
Yusuke Sakakibara, Saki Ochi, Masayuki Oda (*Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ.*)

2Pos018 細菌の運動と形態を規定する細胞内べん毛の in situ 構造解析
In situ structural analysis of the periplasmic flagella that regulates bacterial motility and morphology
Akihiro Kawamoto[1], Toshiki Kuribayashi[2], Masatomo Morita[3], Shuichi Nakamura[2], Nobuo Koizumi[3] ([1]*IPR., Univ. Osaka*, [2]*Grad. Sch. Engineer., Univ. Tohoku*, [3]*NIID*)

01C. タンパク質：物性／01C. Protein: Physical Property

2Pos019 タンパク質の液液相分離に対する尿素とトリメチルアミン N-オキシドの効果
Effects of small molecular compounds on protein liquid-liquid phase separation: Urea and trimethylamine N-oxide (TMAO)
Keiji Kitamura[1], Ryo Kitahara[1,2] ([1]*Graduate School of Pharmacy, Ritsumeikan University*, [2]*College of Pharmaceutical Sciences, Ritsumeikan University*)

2Pos020 タンパク質の高分解能熱流解析：2 次構造の役割
High resolution heat current analysis of proteins: Role of secondary structure
Yoichi Arita, Tingting Wang, Wataru Sugiura, Shigure Saito, Takahisa Yamato (*Grad. Sci., Nagoya Uni.*)

2Pos021 中性子準弾性散乱により明らかとなった α-シヌクレインの内部ダイナミクス
Internal dynamics of α-synuclein revealed by quasielastic neutron scattering
Satoru Fujiwara[1], Kai Nishikubo[2], Taiki Tominaga[3] ([1]*Inst. Quantum Life Science, QST*, [2]*Ibaraki Univ.*, [3]*Neutron R&D Div., CROSS*)

2Pos022 タンパク質の熱流計算：アミノ酸残基間コミュニケーションの原子レベル観測
Computational study of heat flow in proteins: Observation of residue-residue communication at the atomic level
Shigure Saito, Tingting Wang, Wataru Sugiura, Yoichi Arita, Takahisa Yamato (*Grad. Sch. Sci., Univ. Nagoya*)

2Pos023 ケージ状蛋白質に閉じ込めた蛋白質の安定性
Stability of the proteins inside the caged protein
Shuji Kanamaru (*Dep. of Life Sci. and Tech., Tokyo Inst. of Tech.*)

2Pos024 2 つの変性タンパク質が互いに結合してフォールディングする反応機構の統計力学モデルによる予測
Predicting mechanisms of mutual synergistic folding by a statistical mechanical model
Shun Nagai[1], Koji Ooka[2], Runjing Liu[3], Munehito Arai[1,2,3] ([1]*Dept. Phys., Univ. Tokyo*, [2]*Col. Arts & Sci., Univ. Tokyo*, [3]*Dept. Life Sci., Univ. Tokyo*)

2Pos025 αB クリスタリンによる早期アミロイド形成阻害の分子機構
Molecular mechanism of early inhibition of amyloid formation by αB-crystallin
Yuki Kokuo[1], Keisuke Yuzu[1], Naoki Yamamoto[2], Ken Morishima[3], Aya Okuda[3], Rintaro Inoue[3], Masaaki Sugiyama[3], Junna Hayashi[4], John A. Carver[4], **Eri Chatani**[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Grad. Sch. Med., Jichi Med. Univ.*, [3]*KURNS., Kyoto Univ.*, [4]*Res. Sch. Chem., Austral. Natl. Univ.*)

2Pos026 統計力学モデルによるタンパク質のフォールディング経路の理論的デザイン
Theoretical design of protein folding pathways by a statistical mechanical model
Sae Kato[1], Koji Ooka[2], Runjing Liu[1], Munehito Arai[1,2,3] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Col. Arts & Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

2Pos027 RNA 結合タンパク質 FUS による液-液相分離と不可逆凝集：高圧吸光光度法と蛍光顕微鏡によるアプローチ
Liquid-liquid phase separation and irreversible aggregation of FUS: High-pressure UV-visible spectrophotometry and fluorescence microscopy
Ryu Yamamoto (*Graduate School of Pharmacy, Ritsumeikan Univeristy*)

01D. タンパク質：機能／01D. Protein: Function

2Pos028 Photoregulation of Ras GTPase Activity using regulatory Factor GAP modified with azobenzene derivatives
Rajib Ahmed, Nobuyuki Nishibe, Alrazi Islam MD, Kazunori Kondo, Shinsaku Maruta (*Department of Biosciences, Graduate School of Science and Engineering Soka University, Hachioji, Tokyo.*)

2Pos029 脂肪酸結合タンパク質 FABP4 と脂肪酸における網羅的な結合特性に関する研究
A comprehensive study of binding properties between fatty acid binding protein FABP4 and fatty acids
Haruka Terawaki[1], Hazuki Namiki[1], Shun Tokudome[1], Fumio Hayashi[2], Yusuke Inoue[1,3], Shigeru Sugiyama[4], Shigeru Matsuoka[5], Michio Murata[6], Masashi Sonoyama[1,3,7] ([1]*Grad. Sch. Sci. Tech., Gunma Univ*, [2]*Ctr. Inst. Analysis, Gunma Univ.*, [3]*GUCFW, Gunma Univ.*, [4]*Fac. Sci. Tech., Kochi Univ.*, [5]*Fac. Med., Oita Univ.*, [6]*Grad. Sch. Sci., Osaka Univ.*, [7]*GIAR, Gunma Univ.*)

2Pos030 プロピオン酸菌由来乳清発酵物質によるダイオキシン受容体 AhR 活性化を介した免疫賦活化機構の解析
Analysis of immunostimulatory mechanism through activation of dioxin receptor AhRby fermented whey derived from propionic acid bacteria
Yukihiko Narita[1], Atsuko Miura[1,2], Taku Sugawara[2], Hiroaki Shimizu[1], Hideaki Itoh[3] ([1]*Akita University Graduate School of Medicine/Department of Neurosurgery*, [2]*Akita Cerebrospinal and Cardiovascular Center*, [3]*Graduate School of Agricultural and Life Sciences, The University of Tokyo*)

2Pos031 Antifreeze proteins possibly control cellular water transport to protect cells from hypothermic damage
Yue Yang[1], Tatsuya Arai[1,2], Yuji C. Sasaki[1,2] ([1]*Grad Sch. of Fron. Sci., Univ. Tokyo*, [2]*AIST-UTokyo*)

2Pos032 Guanidine/Biguanide 系薬剤とミトコンドリア呼吸鎖末端酵素の相互作用解析
Interaction analysis between Guanidine/Biguanides and a terminal enzyme of mitochondrial respiratory chain
Seungwan Woo[1], Gerald I Shulman[2], Atsuhiro Shimada[3] ([1]*Grad. Sch. Nat. Sci. Tech., Univ. Gifu*, [2]*Sch. Med., Univ. Yale*, [3]*Fac. Appl. Biol. Sci., Univ. Gifu*)

2Pos033 大腸菌フェリチンの鉄酸化活性に及ぼす無機リン酸の影響
Effect of inorganic phosphate on the iron oxidation activity of *Escherichia coli* ferritin A
Takumi Kuwata, Kazuo Fujiwara, Masamichi Ikeguchi (*Dept. of Biosci., Grad. Sch. of Sci and Eng., Soka Univ.*)

2Pos034 TAT ロドプシンが 77K で示すプロトン移動反応に対する分光解析
Spectroscopic analysis of proton transfer reaction of TAT rhodopsin at 77 K
Teppei Sugimoto[1], Kota Katayama[1,2], Hideki Kandori[1,2] ([1]*Graduation school of Engineering, Nagoya institute of technology*, [2]*OptoBio Technology Research Center, Nagoya institute of technology*)

01E. タンパク質：計測・解析／01E. Protein: Measurement & Analysis

2Pos035 A platform for testing the properties of peptide-based siderophore mimics using computational and biophysical methods
Piotr Sebastian Maj, Uladzislava Tsylents, Monika Wojciechowska, Joanna Trylska (*Centre of New Technologies, University of Warsaw, Poland*)

2Pos036 生細胞中の CRAF は 14-3-3 との相互作用を介して 2 種類の閉構造をとる
CRAFs in living cells adopt two types of closed conformations through interaction with 14-3-3
Kenji Okamoto, Yasushi Sako (*RIKEN CPR*)

2Pos037 ラマン分光法を用いた心臓アミロイドーシスの鑑別診断
Differential diagnosis of cardiac amyloidosis using Raman spectroscopy
Mizuki Yoshimoto[1], Takeshi Honda[2], Hiroki Takanari[3], Shin-ichiro Yanagiya[3], Hirokazu Miki[4] ([1]*Graduate school of medicine, Tokushima university*, [2]*Graduate school of sciences and technology for innovation, Tokushima university*, [3]*Institute of Post-LED Photonics, Tokushima university*, [4]*Tokushima university Hospital*)

2Pos038 高効率で特異的なシステインの修飾法の開発
Development of Highly efficient and specific modification technique for Cys residue
Arisa Suto[1], Yoshio Kodera[1,2], Takashi Matsui[1,2] ([1]*Grad. Sch. Sci., Kitasato Univ*, [2]*Center for Disease Proteomics, Sch. Sci., Kitasato Univ*)

2Pos039 MDCC 標識リン酸結合タンパクを含む droplet chamber array による高感度無機リン酸検出
Highly sensitive detection of inorganic phosphate using droplet chamber arrays containing MDCC-labeled phosphate-binding protein
Tomohiro Aoyama[1], Yoshihiro Minagawa[2], Hiroshi Ueno[2], Nobukiyo Tanaka[1], Hiroyuki Noji[2], Tomoko Masaike[1] ([1]*Dept. Appl. Biol. Sci., Tokyo Univ. of Sci.*, [2]*Dept. Appl. Chem., Sch. Eng., Univ. of Tokyo*)

2Pos040 原子間力顕微鏡像の探針形状推定法計算の高速化
Accelerating end-to-end differentiable blind tip reconstruction algorithm for fast reconstruction of molecular surfaces
Ryuhei Oshima, Yasuhiro Matsunaga (*Grad. Sch. Sci. Eng., Saitama Univ.*)

2Pos041 アミロイド β42 と 40 検出のためのチオ NAD サイクリング ELISA 法の開発
Development of thio-NAD cycling ELISA for detection of amyloid beta 42 and 40
Yuta Kyosei[1], Etsuro Ito[1,2] ([1]*Department of Biology, Waseda University*, [2]*BioPhenoMA Inc.*)

01F. タンパク質：タンパク質工学／進化工学／01F. Protein: Engineering

2Pos042 単量体化した人工赤色蛍光蛋白質 AzamiRed の構造
Structure of monomerized AzamiRed, an artificial red fluorescent protein engineered from AzamiGreen
Shiho Otubo[1], Hiromi Imamura[2], Isamu Nagatomi[1], Norihiro Takekawa[1], **Katsumi Imada[1]** ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Biost., Kyoto Univ.*)

2Pos043 MD シミュレーション・レプリカ交換モンテカルロ法と機械学習によるデータ効率的なタンパク質機能改良
Data Efficient Protein Function Improvement by Machine Learning with MD Simulation and Replica Exchange Monte Carlo Method
Teppei Deguchi[1,2], Shinji Iida[3], Yutaka Saito[1,2,3] ([1]*Grad. Sch. FS., Univ. Tokyo*, [2]*AIRC, AIST*, [3]*Sch. FR., Univ. Kitasato*)

2Pos044 深層学習による小型 PD-1 アンタゴニストの理論的設計
Theoretical design of a small PD-1 antagonist with deep learning
Shinya Inoue[1], Shunji Suetaka[1], Munehito Arai[1,2] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Dept. Phys., Univ. Tokyo*)

2Pos045 内包分子を鋳型としたウイルス模倣粒子の構築
Assembly of virus-like architectures directed by cargo molecules
Kenya Tajima, **Naohiro Terasaka** (*Earth-Life Science Institute, Tokyo-Tech*)

2Pos046 ダーウィン進化を用いたスクリーニング不要の in vitro 指向性進化系の実現に向けて
Toward screening-free in vitro directed evolution with natural selection
Taro Furubayashi[1], Thibault Di Meo[1], Yoshihiro Minagawa[1], Hiroyuki Noji[1], Yannick Rondelez[2] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*ESPCI, Paris*)

2Pos047 カルモジュリンを利用した G タンパク質 Ras のイオノクロミック制御
Iono-chromic control of G-protein Ras using calmodulin
Ziyun Zhang[1], Yassine Sabek[1], Nobuyuki Nishibe[1], Kazunori Kondo[2], Sinsaku Maruta[1,2] ([1]*Grad. Sch. Sci., Univ.Soka*, [2]*Sci., Univ. Soka*)

2Pos048 相互作用データのハイスループットな収集による抗体特異性制御残基の特定
Identification of residues which regulate antibody specificity by high-throughput collection of interaction data
Mayuko Inagaki[1], Ryo Matsunaga[1], Shigeru Okumura[2], Toshiaki Maruyama[2], Kevin Entzminger[2], Kouhei Tsumoto[1,3,4] ([1]*Department of Bioengineering, Graduate School of Engineering, The University of Tokyo*, [2]*Abwiz Bio Inc.*, [3]*Department of Chemistry and Biotechnology, Graduate School of Engineering, The University of Tokyo*, [4]*The Institute of Medical Science, The University of Tokyo*)

2Pos049 ウシ由来抗菌ペプチドの高収率組換え発現系の構築及び機能の検討
Construction of a high-yield recombinant expression system of bovine antimicrobial peptides and elucidation of function and mode of action
Fumi Hirai[1], Mitsuki Shibagaki[1], Hao Gu[1], Yuya Hizume[2], Tomoyasu Aizawa[1,2] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Sch. Sci., Hokkaido Univ.*)

01G. タンパク質：天然変性／01G. Protein: Intrinsic disorder

2Pos050 天然変性タンパク質の液液相分離に関する MD シミュレーション
MD simulation of liquid-liquid phase separation of intrinsically disordered proteins
Tetsu Koyama, Naoki Iso, Yuki Norizoe, Takuya Saito, Takahiro Sakaue (*Univ. Aoyama Gakuin*)

2Pos051 ストレスセンサーの会合を制御する多様な相互作用の分子機構
Molecular mechanisms of multiple interactions regulating stress sensor assembly
Soichiro Kawagoe[1], Takuya Mabuchi[2,3], Hiroyuki Kumeta[4], Motonori Matsusaki[1], Munehiro Kumashiro[1], Koichiro Ishimori[5], Tomohide Saio[1] ([1]*Inst. of Adv. Med.Sci., Tokushima Univ.*, [2]*Front. Res. Inst. for Interdiscip. Sci., Tohoku Univ.*, [3]*Inst. of Fluid Sci., Tohoku Univ.*, [4]*Fac. of Adv. Life Sci., Hokkaido Univ.*, [5]*Dept. of Chem., Fac. of Sci., Hokkaido Univ.*)

2Pos052 Hyperphosphorylation of nucleolar protein Nopp140 drives mitotic nucleolar disassembly
Hisashi Shimamura[1], Yuki Norizoe[2], Takahiro Sakaue[2], Shige H. Yoshimura[3] ([1]*Fac. Int. Human Studies, Kyoto University*, [2]*Col. Science and Engineering, Aoyama Gakuin University*, [3]*Grad. Sch. Biostudies, Kyoto University*)

2Pos053 タンパク質液液相分離過程の細胞内と試験管での違いとその機構の解明
Exploring the mechanism to explain the difference in protein liquid-liquid phase separation (LLPS) processes between in vitro and in cells
Hitomi Kimura[1,2], Natsumi Tane[1], Kyota Yasuda[1,2], **Shin-ichi Tate**[1,2] ([1]*Grad. Sch. Int. Sci. Life, Hiroshima Univ.*, [2]*WPI-SKCM2, Hiroshima Univ.*)

2Pos054 二機能性クリプトクロム C 末端領域における構造ダイナミクスの NMR 解析
NMR analysis of dynamics of the C terminal extension in bi-functional cryptochrome
Yuki Kaide, Satoshi Nagao, Wataru Sato, Minoru Kubo (*Grad. Sch. Sci., Univ. Hyogo*)

2Pos055 光誘起 TDP-43 IDR 凝縮体の細胞質における特徴的脱会合過程
Distinct disassemble process of light-induced condensates of TDP-43 intrinsically disordered region in the cytoplasm
Yuta Hamada[1], Akira Kitamura[2] ([1]*Grad. Sch. of Life Sci., Hokkaido Univ.*, [2]*Fac. of Adv. Life Sci., Hokkaido Univ*)

2Pos056 ストレス顆粒の形成・機能に必要な構成因子の近傍分子ラベルを用いた同定・解析
Proximity labaleling identified a protein essential for the proper formation and function of stress granule
Kyota Yasuda (*Grad. Sch. Int. Life Sci. Hiroshima*)

2Pos057 α-シヌクレインの液-液相分離を誘導・制御する *de novo* ペプチドの開発
De novo peptides that induce and modulate the liquid-liquid phase separation of α-synuclein
Tatsuya Ikenoue[1], Masatomo So[2], Naohiro Terasaka[1], Wei-En Huang[1], Yasushi Kawata[3], Yohei Miyanoiri[4], Hiroaki Suga[1] ([1]*Department of Chemistry, The University of Tokyo*, [2]*Department of Future Basic Medicine, Nara Medical University*, [3]*Department of Chemistry and Biotechnology, Tottori University*, [4]*Institute for Protein Research, Osaka University.*)

05. RNA・RNA 結合タンパク質／05. RNA & RNA binding proteins

2Pos058 ハンマーヘッドリボザイムの酵素反応に関する理論的研究
Theoretical study on an enzymatic reaction of the hammerhead ribozyme
Ayaka Matsuyama[1], Masahiko Taguchi[2], Shigehiko Hayashi[1] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*IMRAM, Tohoku Univ.*)

2Pos059 ウイルス RNA 構造の理解のための RNA 構造の測定と推定
Investigation and prediction of RNA structure towards the understanding of viral RNA structure
Yuji Itoh[1,2,3], Takuya Katayama[1,2], Naoya Kaneda[1,3], Shrutarshi Mitra[1], Satoshi Takahashi[1,2,3] ([1]*IMRAM, Tohoku Univ.*, [2]*Grad. Sch. Life Sci., Tohoku Univ.*, [3]*Grad. Sch. Sci., Tohoku Univ.*)

2Pos060 Conformational elucidation of SARS-CoV-2 genomic RNA elements by single-molecule FRET measurements
Shrutarshi Mitra[1], Yuji Itoh[1,2], Takuya Katayama[1,2], Satoshi Takahashi[1,2] ([1]*Institute of Multidisciplinary Research for Advanced Materials (IMRAM), Tohoku University*, [2]*Graduate School of Life Science, Tohoku University*)

2Pos061 NMR 法による DNA-RNA ハイブリッドグアニン四重鎖構造とペプチドの相互作用解析
Detection of the interaction between DNA-RNA hybrid G-quadruplex structure and G-quadruplex-binding peptide using NMR
Taisei Masunaga[1,2], Yudai Yamaoki[1,2], Chihiro Nakayama[2], Keiko Kondo[1], Takashi Nagata[1,2], Masato Katahira[1,2] ([1]*Institute of Advanced Energy, Kyoto University*, [2]*Graduate School of Energy Science, Kyoto University*)

06. DNA/RNA ナノテクノロジー／06. DNA/RNA nanotechnology

2Pos062 **酵素を用いた時間遅れ反応による DNA 液滴ベース人工細胞の分裂制御**
Controlled division of DNA droplet-based artificial cells coupled with enzymatic time delay circuit
Tomoya Maruyama[1], Ryohei Furuichi[2], Akihiro Yamamoto[2], Gong Jing[1], Masahiro Takinoue[1,2,3] ([1]*School of Life science and Technology, Tokyo Institute of Technology*, [2]*School of Computer Science, Tokyo Institute of Technology*, [3]*Living Systems Materialogy (LiSM) Research Group, International Research Frontiers Initiative (IRFI), Tokyo Institute of Technology*)

2Pos063 Kissing-loop **相互作用により構築された RNA 液滴による AND 論理演算**
'AND' logic operation of RNA droplets assembled via kissing-loop interaction
Hirotake Udono[1], Minzhi Fan[1], Yoko Saito[1], Hirohisa Ohno[2], M. Shin-ichiro Nomura[3], Yoshihiro Shimizu[4], Hirohide Saito[2], Masahiro Takinoue[1] ([1]*Sch. Comp., Tokyo Tech.*, [2]*CiRA, Kyoto Univ.*, [3]*Sch. Eng., Tohoku Univ.*, [4]*Riken*)

2Pos064 **DNA 液滴のための相分離スイッチ素子の設計**
Design of phase-separation switch element for DNA droplet
Yuta Aizaki[1], Masahiro Takinoue[1,2] ([1]*Department of Computer Science, Tokyo Institute of Technology*, [2]*Living Systems Materialogy (LiSM) Research Group, International Research Frontiers Initiative (IRFI), Tokyo Institute of Technology*)

2Pos065 **人工 DNA ナノ粒子モーターの高速化戦略**
Strategy for acceleration of artificial DNA-nanoparticle motor
Takanori Harashima[1,2], Akihiro Otomo[1,2], Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*)

2Pos066 **DNA 液滴の時空間的形成の制御**
Regulation of spatiotemporal formation of DNA droplets
Shogo Kai[1], Yusuke Sato[2] ([1]*Sch. Comp. Sci. Syst. Eng., Kyutech*, [2]*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech*)

2Pos067 Toward a DNA origami-based motor with power stroke mechanism and tunable parameters
Akihiro Fukuda[1], Yusuke Sato[2], Takeshi Yokoyama[3,4], Yoshikazu Tanaka[3], Shoichi Toyabe[1] ([1]*Grad. Sch. Eng., Univ. Tohoku*, [2]*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech*, [3]*Grad. Sch. Life Sci., Univ. Tohoku*, [4]*JST PRESTO*)

2Pos068 3D DNA nanostructure-based assembled structures for the construction of chromatin-like heterogeneous system
Hong Xuan Chai[1], Masahiro Takinoue[1,2] ([1]*Tokyo Institute of Technology, School of Life Science and Technology*, [2]*Tokyo Institute of Technology, School of Computing*)

2Pos069 **DNA 液滴コンピュータによる核酸酵素反応の制御**
Control of deoxyribozyme activity by computational DNA droplets
Naoki Yoshida[1], Masahiro Takinoue[1,2] ([1]*Grad. Sch. Life. Sci. & Tech., Tokyo Tech.*, [2]*Grad. Sch. Comput., Tokyo Tech.*)

2Pos070 Functionalization of vertices on wireframe DNA origami polyhedron
Takuma Nishimura, Kanta Tsumoto, Yuki Suzuki (*Grad. Sch. Eng., Mie. Univ.*)

14. 分子モーター／14. Molecular motor

2Pos071 **細菌べん毛モーター固定子 MotB の L118P 変異がモーター負荷応答に与える影響**
The L118P mutation in the stator protein MotB affects motor adaptation to load in the bacterial flagellar motor
Shuo Peng Wang[1], Tsubasa Ishida[2], Naoki Hidaka[1], Shoichi Toyabe[3], Seiji Kojima[4], Yoshiyuki Sowa[1,2] ([1]*Dep. Front. Biosci., Hosei Univ.*, [2]*Micro-Nano Tech., Hosei Univ.*, [3]*Grad. Sch. Eng., Tohoku Univ.*, [4]*Grad. Sch. Sci., Nagoya Univ.*)

2Pos072 哺乳類 V-ATPase の構造機能解明
Structure-function elucidation of mammalian V-ATPase
Yui Nishida[1], Atsuko Nakanishi[2], Atsuki Nakano[1], Shiori Saeki[1], Kaoru Mitsuoka[2], Ken Yokoyama[1] ([1]*Grad. Sch. Bioscience., Kyoto Sangyo Univ.*, [2]*Research Center for UHVEM., Osaka Univ.*)

2Pos073 細菌べん毛モーターにおけるステップ回転の固定子数依存性
Stator-number dependence of stepwise rotation in the bacterial flagellar motor
Shusuke Kuboi, Shuichi Nakamura (*Dept. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*)

2Pos074 光渦を用いた光ピンセットと DNA オリガミによる生体分子モーター F_1-ATPase の静止トルク測定
Quantitative force manipulation and measurement of F_1-ATPase via DNA Origami probe optically trapped with an optical vortex
Yu Hashimoto, Tomoko Otsu-Hyodo, Yoshiyuki Ohtake, Sayaka Kazami, Yuji Kimura, Hiroyasu Itoh (*Hamamatsu Photonics K.K. Central research laboratory*)

2Pos075 F_oF_1-ATP 合成酵素 *c*-サブユニットローター回転の熱力学的メカニズム
Thermodynamic mechanism underlying the rotation of the *c*-subunit rotor of F_oF_1-ATP synthase
Hideo Akutsu[1,7], Yasuto Todokoro[2], Su-Jin Kang[3], Toshiharu Suzuki[4], Takahisa Ikegami[1], Masatune Kainosho[5], Masasuke Yoshida[6], Toshimichi Fujiwara[7] ([1]*Grad. Sch. Med Life Sci., Yokohama City Univ.*, [2]*Sch. Sci., Osaka Univ.*, [3]*Seoul Natl. Univ.*, [4]*Lab. Chem. Life Sci., Tokyo Inst. Tech.*, [5]*Grad. Sch. Sci., Tokyo Metro. Univ.*, [6]*Grad. Sch. Life Sci., Kyoto Sangyo Univ.*, [7]*IPR, Osaka Univ.*)

2Pos076 Na^+-駆動型べん毛モーターキメラ固定子の動態観察
Stator dynamics of chimeric Na^+-driven *E. coli* flagellar motor observed with fluorescent microscopy
Tomoya Shoji[1], Naoki Hidaka[1], Yong-Suk Che[3], Yoshiyuki Sowa[1,2] ([1]*Department of Frontier Bioscience, Hosei University*, [2]*Micro-Nano Technology, Hosei University*, [3]*Graduate School of Frontier Bioscience, Osaka University*)

2Pos077 Deciphering the actin structure-dependent preferential cooperative binding of cofilin
Kien Xuan Ngo[1], Huong T Vu[2], Kenichi Umeda[1], Noriyuki Kodera[1], Taro Q.P. Uyeda[3], Toshio Ando[1] ([1]*WPI NanoLSI, Kanazawa Univ., Jpn.*, [2]*Cent. Mechanochem. Cell Biol., Warwick Med. Sch., UK.*, [3]*Fact. Sci. Eng., Waseda Uni., Jpn.*)

2Pos078 べん毛 III 型輸送 ATPase 複合体の CryoEM 構造
CryoEM structure of the ATPase ring complex of the flagellar Type III export apparatus
Asako Usui[1], Miki Kinoshita[3], Yuki Tajimi[2], Takayuki Uchihashi[2], Tohru Minamino[3], Norihiro Takekawa[1], Katsumi Imada[1] ([1]*Dept. of Macromol. Sci., Grad. Sch. of Sci., Osaka Univ.*, [2]*Dept. of phys. Sci., Grad. Sch. of Sci., Nagoya Univ.*, [3]*Grad. Sch. of Frontier Biosci., Osaka Univ.*)

2Pos079 Physical pictures of rotation mechanisms of F_1- and V_1-ATPases: Leading roles of translational, configurational entropy of water
Satoshi Yasuda[1,2], Tomohiko Hayashi[3,4], Takeshi Murata[1,2], Masahiro Kinoshita[4,5] ([1]*Grad. Sc. Sci., Chiba Univ.*, [2]*Membrane Protein Research and Molecular Chirality Research Centers, Chiba Univ.*, [3]*Facul. Eng., Niigata Univ.*, [4]*Institute of Advanced Energy, Kyoto Univ.*, [5]*Center for the Promotion of Interdisciplinary Education and Research, Kyoto Univ.*)

2Pos080 ミトコンドリアまたは α プロテオバクテリアの共通祖先型 F_1-ATPase の 1 分子回転解析
Single-molecule analysis of the rotation of the common ancestral F_1-ATPase of mitochondria or α-proteobacteria
Hiroki Homma[1], Hiroshi Ueno[1], Ryutaro Furukawa[2], Satoshi Akanuma[2], Hiroyuki Noji[1] ([1]*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*, [2]*Facul. Human Sci., Waseda Univ.*)

2Pos081 深海環境における海洋微生物の運動能
Compounding deep sea physical impacts on marine microbial motility
Kelli K. Mullane[1], **Masayoshi Nishiyama**[2], Tatsuo Kurihara[3], Douglas H. Bartlett[1] ([1]*Scripps Inst. Oceanography, UCSD, USA*, [2]*KINDAI Univ.*, [3]*Kyoto Univ.*)

2Pos082 ADP 結合型細胞質ダイニンの 2 つのリンカー構造
Not one but two different cytoplasmic dynein ADP linker structures
Hiroshi Imai[1], Riko Kanazawa[1], Rieko Shimo-Kon[1], Shinji Kamimura[2], Naoko Kajimura[3], Kaoru Mitsuoka[3], Mika Hirose[4], Takayuki Kato[4], Takahide Kon[1] ([1]*Dept. Biol. Sci., Grad.Sch.Sci.,Osaka Univ.*, [2]*Dept. Biol. Sci., Fac. Sci. & Eng., Chuo Univ*, [3]*Res. Ctr. for UHVEM, Osaka Univ*, [4]*Inst. for Protein Res., Osaka Univ.*)

2Pos083 10 nm ナノ粒子の散乱光イメージングによる F_1-ATPase の回転可視化
Visualization of rotation of F_1-ATPase based on scattering imaging of 10 nm nanoparticle
Keigo Shinoda (*Department of Applied Chemistry, Graduate School of Engineering, University of Tokyo.*)

2Pos084 腸球菌由来 V-ATPase はナトリウムイオン駆動力で ATP を合成する
Enterococcus hirae V-ATPase synthesizes ATP driven by the sodium ion motive force
Akihiro Otomo[1,2], Lucy Zhu[3], Takanori Harashima[1,2], Ryota Iino[1,2] ([1]*Institute for Molecular Science*, [2]*SOKENDAI*, [3]*Chime ParisTech*)

15B. 細胞生物学的課題：運動／15B. Cell biology: Motility

2Pos085 Exploration of isoleucine recognition sites in chemoreceptor using chimeric receptors
Shinnosuke Kawahara, Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Front Biosci, Osaka Univ.*)

2Pos086 遊泳性緑藻ボルボックス目におけるレイノルズ数と繊毛運動調節様式の連関
Reynolds-number-dependent ciliary regulation in the swimming green algae Volvocales
Noriko Ueki[1,2], Ken-ichi Wakabayashi[2,3] ([1]*Science Research Center, Hosei Univ, Tokyo, Japan*, [2]*CLS, Tokyo Tech, Kanagawa, Japan*, [3]*Faculty of Life Sciences, Kyoto Sangyo Univ, Kyoto, Japan*)

2Pos087 Emerging cell size transition modes of collective endothelial cell migration induced by geometrical wide-narrow-wide pathway constraints
Masaharu Endo (*Grad. Sch. Sci., Univ. Waseda*)

2Pos088 べん毛 III 型分泌装置のポリペプチドチャネル複合体のクライオ電子顕微鏡構造
CryoEM structure of the polypeptide channel complex of the bacterial flagellar type III secretion system
Miki Kinoshita[1], Tomoko Miyata[1], Fumiaki Makino[1,2], Takayuki Kato[3], Katsumi Imada[4], Keiichi Namba[1,5,6], Tohru Minamino[1] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*JEOL Ltd.*, [3]*IPR, Osaka Univ.*, [4]*Grad. Sch. Sci., Osaka Univ.*, [5]*JEOL YOKOGUSHI, Osaka Univ.*, [6]*RIKEN SPring-8*)

2Pos089 クシクラゲ 平衡器官形成における繊毛表面の細胞運動
Cell movement on ciliary surface during the statolith formation of Ctenophores
Naoki Noda (*Nihon Univ. School of Medicine*)

2Pos090 Evaluation of the dominant distance of the leader cells over the follower cells in collective migration using Y-shape micro-pathway assay
Miki Takei, Mitsuru Sentoku, Masaharu Endo, Yusuke Koshita, Kenji Yasuda (*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

2Pos091 スピロヘータ細菌の遊泳と形態変化の関係
Association of swimming and morphological variation in a spirochete bacterium
Souichi Ugawa[1], Kyosuke Takabe[2], Nobuo Koizumi[2], Shuichi Nakamura[1] ([1]*Dept. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*, [2]*Department of Bacteriology I, NIID, Japan*)

2Pos092 海洋性ビブリオ菌べん毛モーター固定子 PomB とストマチン様タンパク質 FliL との相互作用解析
Investigation of interaction between flagellar motor stator PomB and stomatin-like protein FliL in marine *Vibrio*
Michio Homma[1], Tatsuro Nishikino[2], Norihiro Takekawa[3], Mitsuru Ikeda[4], Yuki Tajimi[1], Kazuyoshi Murata[4], Katsumi Imada[3], Seiji Kojima[5], Takayuki Uchihashi[1] ([1]*Physics, Grad. Sch. Sci., Nagoya Univ.*, [2]*Dep. Life Sci. Appl. Chem., Nagoya Inst.Tech.*, [3]*Dept. of Macromol. Sci. Grad. Sch. Sci., Osaka Univ.*, [4]*ExCELLS, Nat. Inst. Nat. Sci.*, [5]*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*)

2Pos093 細菌べん毛フック成長端の構造
Structure of the growing end of the bacterial flagellar hook
Sae Hashimoto[1], Tomoko Miyata[2], Fumiaki Makino[2,3], Keiichi Namba[2,4], Norihiro Takekawa[1], Katsumi Imada[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*JEOL Ltd.*, [4]*JEOL YOKOGUSHI Res. Alliance. Lab., Osaka Univ.*)

2Pos094 海洋性ビブリオ菌におけるべん毛本数制御因子 FlhF と MS リング構成因子 FliF の相互作用の生化学的解析
Biochemical analysis for interactions between the flagellar number regulator FlhF and the MS ring protein FliF in marine *Vibrio*
Yuria Fukushima[1], Seiji Kojima[1], Michio Homma[2] ([1]*Dept. Biol. Sci., Grad. Sch. Sci., Nagoya Univ*, [2]*Dept. Phys., Grad. Sch. Sci., Nagoya Univ*)

2Pos095 ゼブラフィッシュ自己組織化細胞塊における細胞ダイナミクスの解析
Analysis of cell dynamics during the self-organizing process in zebrafish explant
Kosuke Hashimoto, Ryuta Watanabe, Toshiyuki Mitsui, Yuuta Moriyama (*Aogaku Univ. Dept,of Phys.*)

2Pos096 A novel swimming strategy of *Alivibrio fischeri* revealed by single-cell tracking microscopy
Xiang Yu Zhuang, Chien-Jung Lo (*Department of Physics, National Central University, Jhongli, Taoyuan, Taiwan 32001*)

2Pos097 共培養系における線維芽細胞の牽引力解析
Analysis of fibroblast's traction force in co-culture system
Arata Nagai, Kaito Kojima, Hiromu Kuwabara, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ.*)

2Pos098 細菌べん毛フック-ジャンクション-フィラメントキャップ複合体の構造
Structure of the complex composed of the hook, junction, and filament-cap in the bacterial flagellum
Norihiro Takekawa[1], Kurumi Mori[1], Tomoko Miyata[2,3], Fumiaki Makino[4], Keiichi Namba[2,3], Katsumi Imada[1] ([1]*Grad. Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [3]*JEOL YOKOGUSHI Res. Alliance Lab., Osaka Univ.*, [4]*JEOL Ltd.*)

2Pos099 回転方向に依存した大腸菌べん毛モーターの回転ゆらぎ
Rotational fluctuations of the *E. coli* depending on the rotational direction of their flagellar motor
Taisei Miyamoto, Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci. Osaka Univ.*)

15C. 細胞生物学的課題：細胞骨格・膜骨格／15C. Cell biology: Cytoskeleton & Membrane Skeleton

2Pos100 コフィリン–アクチン動態の熱力学的解析
Thermodynamic analysis of cofilin-induced actin dynamics
Nayu Itou, Yukino Yamada, Hideyuki Komatsu (*Department of Bioscience and Bioinformatics, Faculty of Systems Engineering and Computer Science, Kyushu Institute of Technology*)

2Pos101 細胞性粘菌のアクチンフィラメントの可視化に向けた取り組み
Challenges visualization of actin filaments in *Dictyostelium discoideum* cells
Yuki Gomibuchi, Yukihisa Hayashida, Yusuke V. Morimoto, Takuo Yasunaga (*Grad. Sch Comp. Sci and Sys. Eng., Kyushu Inst. Tech.*)

2Pos102 Myosin or its fragments influences F-actin dynamics and deformation of droplets under the liquid-liquid phase separation
Tatsuyuki Waizumi[1], Hiroki Sakuta[2], Mahito Kikumoto[1], Masahito Hayashi[3], Kanta Tsumoto[4], Kingo Takiguchi[1], Kenichi Yoshikawa[5] ([1]*Grad. Sch. Sci., Univ. Nagoya*, [2]*Grad. Sch. Arts and Sci., Univ. Tokyo*, [3]*Dept. Frontier BioSci., Univ. Hosei*, [4]*Grad. Sch. Eng., Univ. Mie*, [5]*Sci Ctr. Self-Organization., Univ. Doshisha*)

2Pos103 Formation of lamellipodia-like and filopodia-like structures by self-organization of actin filaments
Masaya Fukui[1], Nen Saito[1,2], Naoki Honda[1,2,3] ([1]*Grad. Sch. Sci of life., Univ. Hiroshima*, [2]*National Institutes of Natural Sciences, Exploratory Research Center on Life and Living Systems*, [3]*Grad. Sch. Bio., Univ. Hiroshima*)

2Pos104 マイクロ流路を用いた多数の微小対象物への機械刺激
Mechanical stimulation of a large number of micro objects using microfluidic channels
Masaru Kojima[1], Masahiro Totani[1], Mitsuhiro Horade[2], Toshihiko Ogura[3], Tatsuo Arai[4] ([1]*Grad. Sch. Eng.Sci., Osaka Univ.*, [2]*Grad. Sch. Sci. and Eng., NDA*, [3]*IDAC, Tohoku Univ.*, [4]*CNBE, UEC*)

2Pos105 マウス初期胚発生時の核膜 lamin B1 による核の構造、力学と遺伝子発現の動的変化
Dynamic changes in the nuclear structure, mechanics, and gene expression by lamin B1 during early mouse embryogenesis
Masahito Tanaka[1], Rin Sakanoue[2], Atsushi Takasu[2], Yasuki Miyagawa[2], Naoko Watanabe[1], Kei Miyamoto[2], Yuta Shimamoto[1,3] ([1]*National Institute of Genetics.*, [2]*Graduate School of Biology-Oriented Science and Technology, Kindai University*, [3]*Department of Genetics, Sokendai University*)

2Pos106 Fatigue Failure of Microtubules Under Repetitive Mechanical Stress
Syeda Rubaiya Nasrin[1], Neda M. Bassir Kazeruni[2], Henry Hess[2], Akira Kakugo[1] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Dept. of Biomed. Engg. Columbia Univ.*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

2Pos107 *Dictyostelium* の走化性受容体 cAR1 は細胞前側でより緊密に集まる
The *Dictyostelium* chemotaxis receptor cAR1 more tightly gathers on the front side of the cell
Atsuhiro Mii[1,2], Satomi Matsuoka[1,2,3], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. Front. Biosci., Osaka Univ.*, [2]*BDR, Riken*, [3]*Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.*)

2Pos108 ホスホリパーゼによる膜流動性の調節と信号増幅
Slow diffusion and signal amplification on the membrane regulated by a phospholipase
Gen Honda[1], Satoshi Sawai[2,3], Miho Yanagisawa[1,2,3] ([1]*Komaba Institute for Science, Graduate School of Arts and Sciences, University of Tokyo*, [2]*Department of Basic Science, Graduate School of Arts and Sciences, University of Tokyo*, [3]*Research Center for Complex Systems Biology, Graduate School of Arts and Sciences, University of Tokyo*)

2Pos109 Unveiling the regulation mechanisms of AMPA receptors' synaptic dwell lifetimes by single-molecule imaging
Yuri L. Nemoto[1,2,4], Rinshi S. Kasai[3], Hiroko Hijikata[4], Taka A. Tsunoyama[1], Kazuma Naito[4], Nao Hiramoto-Yamaki[4], Takahiro K. Fujiwara[4], Akihiro Kusumi[1,4] ([1]*Membrane Cooperativity Unit, OIST*, [2]*Biosignal Research Center, Kobe University*, [3]*National Cancer Center*, [4]*WPI-iCeMS, Kyoto University*)

2Pos110 細胞が遊走後に形成するミグラソームが示す炎症誘導能の評価
Evaluation of inflammation inducing ability of migrasomes formed by cells after migration
Koki Yoshikawa, Shogo Saito, Masayoshi Tanaka, Mina Okochi (*Sch. Mat. and Chem. Tech., Tokyo Tech*)

2Pos111 自発運動する細胞の興奮系 Ras を抑制する GAP の同定
Identification of GAP that suppresses the excitatory Ras in spontaneous cell motility
Guangyu Cheng[1], Satomi Matsuoka[1,2,3], Masahiro Ueda[1,2,3] ([1]*Grad. Sch. Sci., Osaka University*, [2]*Grad. Sch. of Front. Biosci., Osaka University*, [3]*BDR, RIKEN*)

2Pos112 細胞外環境に暴露したミトコンドリアの機能変化
Functional changes in mitochondria during exposure to the extracellular environment
Chisato Negoro (*Grad.Sch.Eng.,Tokyo. Univ. Agr.& Tech.*)

2Pos113 ミトコンドリア投与が細胞増殖に及ぼす影響
Effects of mitochondrial administration on cell growth
Akiho Nishimura, Yoshihiro Ohta (*Grad.Sch.Eng.,Tokyo. Univ.Agr.& Tech*)

2Pos114 種々の培養条件におけるミトコンドリア電子伝達複合体活性の比較
Comparison of mitochondrial electron transfer complex activity under various culture conditions
Momoka Kutami, Yoshihiro Ohta (*Grad.Sch.Eng.,Tokyo. Univ. Agr.&Tech.*)

16A. 生体膜・人工膜：構造・物性／16A. Biological & Artificial membrane: Structure & Property

2Pos115 モデル生体膜における分子充填と膜間相互作用に対するコレステロールとラノステロールの影響比較
Comparison of the effects of cholesterol and lanosterol on the molecular packing of model membranes and their bilayer-bilayer interactions
Ayumi Okayama, Kohei Wada, Hiroshi Takahashi (*Graduate School of Science and Technology, Gunma University*)

2Pos116 ウイルス様粒子開発にむけた分子動力学シミュレーションによる SARS-CoV-2 膜タンパク質を含む膜の構造・性質変化の探索
Investigation of membrane properties including SARS-CoV-2 membrane proteins by molecular dynamics simulation for VLP development
Ryo Urano, Wataru Shinoda (*Okayama Univ. Res. Inst. Interdiscip. Sci.*)

2Pos117 蛍光プローブ Prodan を用いた蛍光測定によるラノステロールとコレステロールの生体膜への影響評価
Impact of lanosterol and cholesterol on model biomembranes evaluated by Prodan fluorescence measurement
Michael Postrado, Hiroshi Takahashi (*Biophysics Lab., Division of Pure and Applied Science,Graduate School of Science and Technology, Gunma University*)

2Pos118 Creation of liposomes intended to be phagocytosed by macrophages
Akari Saito, Masahito Hayashi, Tomoyuki Kaneko (*LaRC,FB,Grad.Sch.Sci.&Eng.,Hosei Univ.*)

2Pos119 三成分リポソームの相挙動に対するアセトニトリルの効果
Effect of acetonitrile on phase behaviors of ternary liposomes
Shota Matsuzawa[1], **Kazunari Yoshida**[1,2] ([1]*Fac. Eng., Yamagata Univ.*, [2]*Grad. Sch. Sci. Eng., Yamagata Univ.*)

2Pos120 蛍光寿命相関解析に基づく脂質三成分相図における単層膜特異的脂質拡散
Leaflet-specific lipid diffusion on ternary phase diagram of lipids studied by fluorescence lifetime correlation analyses
Takuhiro Otosu, Miyuki Sakaguchi, Shoichi Yamaguchi (*Grad. Sch. Sci. Eng., Saitama Univ.*)

16B. 生体膜・人工膜：ダイナミクス／16B. Biological & Artificial membrane: Dynamics

2Pos121 ポリリジン吸着が巨大リポソームの単層膜特異的脂質拡散に与える影響
The Effect of Polylysine Adsorption on the Leaflet-specific Lipid Diffusion in a Giant Unilamellar Vesicle
Kosei Shimizu, Miyuki Sakaguchi, Shoichi Yamaguchi, Takuhiro Otosu (*Grad. Sch. Sci. Eng., Saitama Univ.*)

2Pos122
Mechanism of membrane activity of NEMURI protein
Moynul Hasan[1], Yuta Ogasawara[1], Yuko Fujioka[1], Suguru Nishinami[2], Hirofumi Toda[2], Nobuo N. Noda[1] ([1]*Hokkaido University*, [2]*University of Tsukuba*)

2Pos123 抗菌ペプチドが誘起するナノポアに由来する巨大リポソームの破裂
Evolution of a nanopore induced by antimicrobial peptides to the rupture of giant unilamellar vesicles
Md. Masum Billah[1,2], Ahmed Marzuk[1], Masahito Yamazaki[1,3,4] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Dept. Phys., Jashore Univ. Sci. Tech.*, [3]*Res. Inst. Ele., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ*)

2Pos124 抗菌ペプチドによる単一細菌の細胞膜損傷と単一細胞レベルでの細胞死の相関
Correlation between antimicrobial peptides (AMPs)-induced membrane damage of single bacterial cells and cell death at single-cell level
Md. Zahidul Islam[1,2], Farzana Hossain[1], Md. Hazrat Ali[3], Masahito Yamazaki[1,3,4] ([1]*Res. Inst. Ele., Shizuoka Univ.*, [2]*Dept. Biotech. Genetic Eng., Jahangirnagar Univ.*, [3]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [4]*Grad. Sch. Sci., Shizuoka Univ.*)

2Pos125 相分離した三成分ベシクルにグラフトされた高分子の膜流動性への影響
Effect of polymer chains grafted onto the phase-separated ternary GUVs on the membrane fluidity
Yuka Sakuma (*Grad. Sch. Sci., Tohoku Univ.*)

2Pos126 浸透圧ストレス下における脂質二重膜の挙動に対するアクチン封入の影響
Effect of actin encapsulation on the behavior of lipid bilayers under osmotic stress
Ken Bessho[1], Mahito Kikumoto[1], Yuki Mizutani[2], Moka Ito[1], Kingo Takiguchi[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Sch. Sci., Nagoya Univ.*)

17. 化学受容／17. Chemoreception

2Pos127 コレラ菌の走化性を媒介するペリプラズム結合蛋白質 SatA の構造
Crystal structure of SatA, a periplasmic binding protein that mediates chemotaxis to serine in *Vibrio cholerae*
Miyuki Aoyama[1], Norihiro Takekawa[1], So-ichiro Nishiyama[2], Hirotaka Tajima[3], Ikuro Kawagishi[3], Katsumi Imada[1] ([1]*Dept. Macromol. Sci., Grad. Sch. Sci., Osaka Univ.*, [2]*Dept. Appl Life Sci, Niigata Univ of Pharm and Appl Life Sci.*, [3]*Dept. Front Biosci., Hosei Univ.*)

2Pos128 大腸菌再構成系を用いたクロストリジウム属細菌走化性受容体の入力刺激の解明
Elucidation of input signals of *Clostridium* chemoreceptors by *E. coli* reconstitution system
So-ichiro Nishiyama, Nao Iwahashi, Shohei Koike (*Fac. App. Life Sci., Niigata Univ. Pharm. App. Life Sci.*)

2Pos129 腸炎ビブリオ由来走化性受容体 VP183 のリガンド結合メカニズム
Ligand binding mechanism of VP183, a chemotaxis receptor of Vibrio parahaemolyticus
Ririka Iida[1], Yuka Ueda[2], Norihiro Takekawa[2], Hiroyuki Terashima[3], Mayuko Sakuma[4], Katsumi Imada[2] ([1]*Sch. Sci., Osaka Univ.*, [2]*Grad. Sch. Sci., Osaka Univ.*, [3]*Inst. of Tropical Medicine, Nagasaki Univ.*, [4]*Dept. Pharm., Kinjo Gakuin Univ.*)

2Pos130 低温ラマン分光法によるシアノバクテリオクロム RcaE の緑色吸収型から赤色吸収型への光変換過程の研究
Cryogrnic Raman study of photoconversion process from green to red absorbing state of the cyanobacteriochrome RcaE
Yasuhiro Jyojima[1], Masako Hamada[2], Yuu Hirose[2], Masashi Unnno[1], Tomotsumi Fujisawa[1] ([1]*Grad.Sch.Adv.Health Sci.,Saga Univ.*, [2]*Dep. App. Chem. Life Sci., Toyohashi Univ. Tech.*)

2Pos131 *Rhodospirillum centenum* 由来の photoactive yellow protein の低温分光分析
Low-temperature spectroscopy of photoactive yellow protein from *Rhodospirillum centenum*
Kirari Ogata[1], Tomotsumi Fujisawa[2], Wouter D Hoff[3], Masashi Unno[2] ([1]*Grad.Sch.Adv.Health Sci.,Saga Univ.*, [2]*Fac.Sci.Eng.,Saga Univ.*, [3]*Oklahoma state Univ.*)

2Pos132 新奇カチオンチャネルロドプシン HulaCCR の機能解析
Electrophysiological characterization of a novel cation channelrhodopsin HulaCCR with an ET(C)D motif
Shunki Takaramoto[1], Shai Fainsod[2], Takashi Nagata[1], Andrey Rozenberg[2], Oded Béjà[2], Keiichi Inoue[1] ([1]*ISSP, Univ. Tokyo*, [2]*Technion-Israel Inst. Tech.*)

2Pos133 脊椎動物が広くもつ紫外光感受性 Opn5 の吸収波長制御に関わるアミノ酸残基
Amino acid residue responsible for the spectral tuning of UV-sensitive vertebrate Opn5
Kazuyuki Asamoto, Kengo Fujii, Chihiro Fujiyabu, Takahiro Yamashita (*Grad. Sch. of Sci., Kyoto Univ*)

2Pos134 ロドプシンダイマー列上における G 蛋白質トランスデューシンの 1 分子拡散過程
Single molecular diffusion process of G protein transducin on rhodopsin dimer rows
Hayato Yamashita[1], Akihiro Tsuji[1], Fumio Hayashi[2], Kenichi Morigaki[3,4], Masashi Fujii[5,6], Akinori Awazu[5,6], Masayuki Abe[1] ([1]*Grad. Sch. Eng. Sci., Osaka Univ.*, [2]*Grad. Sch. Sci., Kobe Univ.*, [3]*Grad. Sch. Agr. Sci., Kobe Univ.*, [4]*Biosignal Research Center, Kobe Univ.*, [5]*Grad. Sch. Sci., Hiroshima Univ.*, [6]*Grad. Sch. Int., Hiroshima Univ.*)

2Pos135 固体 NMR を用いた TaHeR のレチナール近傍の His23 と His82 の構造解析
Characterization of His23 and His82 near the retinal chromophore of *Thermoplasmatales* archaeon heliorhodopsin by solid-state NMR
Sari Kumagai[1], Toshio Nagashima[2], Toshio Yamazaki[2], Hideki Kandori[3], Izuru Kawamura[1] ([1]*Graduate School of Engineering Science, Yokohama National University*, [2]*RIKEN RSC*, [3]*Nagoya Institute of Technology*)

2Pos136 脊椎動物が持つレチナール光異性化酵素ロドプシン・RGR の吸収波長の多様性
Diversified absorption spectra in vertebrate retinal photo-isomerase rhodopsins
Takashi Nagata, Naoya Morimoto, Chunyangguang Li, Keiichi Inoue (*ISSP, Univ. Tokyo*)

2Pos137 RcPYP と PBP の多量体形成機構の解明
Elucidation of oligomer formation mechanism of RcPYP and PBP
Yoichi Yamazaki[1], Daiki Takenaka[1], Kento Yonezawa[1,2], Sachiko Toma-Fukai[1], Hironari Kamikubo[1,2] ([1]*NAIST, MS*, [2]*NAIST, CDG*)

2Pos138 光サイクル型脊椎動物ロドプシンを用いた細胞内セカンドメッセンジャーレベルの光依存的変化
Light-dependent changes in the intracellular second messenger levels using photocyclic vertebrate rhodopsin
Kazumi Sakai, Shion Aoki, Takahiro Yamashita (*Graduate school of Science, Kyoto University*)

2Pos139 イオンポンプ型ロドプシンの効率的機能改変の試み
Attempts to strategic functional modifications of ion pump rhodopsins
Kaito Hasegawa[1], Tomoya Maeda[2], Satoru Fukiya[2], Takashi Tsukamoto[1,3], Makoto Demura[1,3], Takashi Kikukawa[1,3] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Res. Fac. Argic., Hokkaido Univ.*, [3]*Fac. Adv. Life Sci., Hokkaido Univ.*)

2Pos140 ニワトリクリプトクロム 4 の C 末端伸長領域は暗酸化反応と、その温度依存性を調節する
Carboxyl-terminal extension of chicken cryptochrome 4 modulates dark oxidation reaction and its temperature dependency
Tensho Yanagi, Takayuki Miyazaki, Hiroaki Otsuka, Keiko Okano, Toshiyuki Okano (*Dept. Elec. Eng., Grad. Sch. ASE., Waseda Univ.*)

21B. 光生物：光合成／21B. Photobiology: Photosynthesis

2Pos141 緑色硫黄細菌の光合成反応中心複合体におけるカロテノイドの三重項励起状態
Triplet-excited state of carotenoid in the photosynthetic reaction center complex of green sulfur bacteria
Tomomi Inagaki[1], Masatoshi Kida[2], Daisuke Kosumi[3], Chihiro Azai[4] ([1]*Graduate School of Life Sciences, Ritsumeikan University*, [2]*Graduate School of Science and Technology, Kumamoto University*, [3]*Institute of Industrial Nanomaterials, Kumamoto University*, [4]*Faculty of Science and Engineering, Chuo University*)

2Pos142 2 次元パターン化ポリマー膜を支持体とした人工チラコイド膜の極低温顕微分光性能観察
Characterization of artificial thylakoid membrane supported by 2-D lattice of polymerized lipid bilayer by Cryogenic spectral microscopy
Hayata Sakai[1], Koki Takagi[2], Shen Ye[1], Kenichi Morigaki[3], Yutaka Shibata[1] ([1]*Graduate School of Science Tohoku Univ.*, [2]*Faculty of Agriculture Kobe Univ.*, [3]*Graduate School of Biosignal Reserch Center Kobe Univ.*)

2Pos143 I 型光合成反応中心の多様性と光捕集機構
Photosynthetic Type-I Reaction Centers: Diversities and Light Harvesting Mechanisms
Akihiro Kimura[1], Hirotaka Kitoh[2], Shigeru Itoh[1] ([1]*Grad. Sch. Sci., Nagoya Univ.*, [2]*Fac. Eng. Sci., Kindai Univ.*)

2Pos144 Studies on energy transfer and charge separation mechanisms in heliobacterial reaction center with ultrafast time-resolved spectroscopy
Risa Kojima[1], Masatoshi Kida[2], Daisuke Kosumi[3], Hirozo Oh-oka[4] ([1]*Col. Life Sci., Ritsumeikan Univ.*, [2]*Grad. Sch. Sci. & Tech., Kumamoto Univ.*, [3]*IINa, Kumamoto Univ.*, [4]*CELAS, Osaka Univ.*)

2Pos145 クロロフィル *f* を含む光化学系 I の近赤外光吸収のレッドシフトメカニズム解明を目指した蛍光バンドの帰属
Assignment of fluorescence bands of chlorophyll-*f* in photosystem I to elucidate its mechanism of red-shift into near-infrared region
Rin Taniguchi[1], Toshiyuki Shinoda[2], Tatsuya Tomo[2], Shen Ye[1], Yutaka Shibata[1] ([1]*Department of Chemistry, Graduate School of Science, Tohoku University*, [2]*Department of Biology, Faculty of Science, Tokyo University of Science*)

2Pos146 光化学系 II の酸素発生中心における $CaMn_4O_6$ クラスターの S_3 状態から初期 S_4 状態の DFT と DLPNO-CC 法による解析
DFT and DLPNO-CC investigation of the S_3 to early S_4 state of the $CaMn_4O_6$ clusters in the Kok cycle in the OEC of PSII
Koichi Miyagawa[1], Takashi Kawakami[2,3], Mitsuo Shoji[1], Kizashi Yamaguchi[3,4,5], Yasuteru Shigeta[1] ([1]*Center for Computational Sciences, University of Tsukuba*, [2]*Graduate School of Science, Osaka University*, [3]*RIKEN Center for Computational Science*, [4]*Center for Quantum Information and Quantum Biology, Osaka University*, [5]*SANKEN, Osaka University*)

2Pos147 2.5 億年前地層試料中の光合成色素の顕微分光分析
Microspectroscopic analysis of photosynthetic pigments in 250-million-years-old geological samples
Tomohiro Ishikawa[1], Ryosuke Saito[2], Toru Kondo[1] ([1]*Dept. of Life Sci. and Tech. Tokyo Tech.*, [2]*Dept. of Earth Sci., Yamaguchi Univ.*)

2Pos148 1粒子レベルで見たリング型クロロフィル色素自己会合体の光物理学特性
Photophysical properties of ring-shaped self-aggregates of chlorophyll molecules at the single-particle level
Shinnosuke Masuda[1], Shun Arai[1], Tatsuma Ishii[2], Shogo Matsubara[3], Toru Kondo[1] ([1]*Dept. of Life Sci. and Tech., Tokyo Tech.*, [2]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [3]*Grad. Sch. Eng., Nagoya Tech.*)

2Pos149 暗発酵と光発酵の二段階発酵を用いたウイスキー廃液からのバイオ水素生産
Biohydrogen production from whiskey waste liquid by two stage of dark and photo fermentation
Masahiro Hibino[1], Moeka Fukushima[2] ([1]*Div. Sust. Enviro. Eng., Muroran Inst. Tech.*, [2]*Dept. Sci. Inf., Muroran Inst. Tech.*)

2Pos150 一次元状クロロフィル自己会合体における一粒子レベルでの光学特性
Optical properties of one-dimensional chlorophyll self-aggregates at the single-particle level
Yuki Kamiie[1], Shogo Matsubara[2], Toru Kondo[1] ([1]*Dept. of Life Sci. and Tech., Tokyo Tech.*, [2]*Grad. Sch. Eng, Nagoya Tech.*)

23. 生命の起源・進化／23. Origin of life & Evolution

2Pos151 天然および人工ランダムペプチドの量子分子進化指標
Quantum molecular evolution index for natural and artificial random peptides
Masanori Yamanaka (*CST, Nihon Univ.*)

2Pos152 遺伝子発現ノイズによる原始的適応の実験的検証
Experimental verification of primitive adaptation via gene expression noise
Miki Umetani[1,2,3], Asako Kitai[4], Yuichi Wakamoto[1,2,3] ([1]*Graduate School of Arts and Sciences, The University of Tokyo*, [2]*Research Center for Complex Systems Biology, The University of Tokyo*, [3]*Universal Biology Institute, The University of Tokyo*, [4]*School of Medicine, The University of Tokyo*)

2Pos153 機械学習を用いた RNA 分子のホストパラサイトネットワークの複雑性予測
Predicting Complexity of Host-Parasite Networks of RNA Molecules Using Machine Learning
Kei Nishida[1], Yusuke Himeoka[2], Chikara Furusawa[1,2,3] ([1]*Department of Physics, Graduate School of Science, The University of Tokyo*, [2]*Universal Biology Institute, Graduate School of Science, The University of Tokyo*, [3]*Center for Biosystems Dynamics Research, RIKEN*)

2Pos154 古生代ミオグロビンの分子進化
Myoglobin evolution in Paleozoic era
Yasuhiro Isogai[1], Antonio Tsuneshige[2], Mitsuki Mori[1], Miwa Yoshida[1], Hiroshi Imamura[3], Tsuyoshi Shirai[3] ([1]*Dept. Pharmaceutical Engineering, Toyama Prefectural Univ.*, [2]*Dept. Frontier Bioscience and Research Center for Micro-Nano Technology, Hosei University*, [3]*Dept. Bio-science, Nagahama Inst. Bio-Science and Technology*)

2Pos155 表現型システム生物学：多要素構造システムのマクロ進化ダイナミクス
Phenotypic systems biology: Macro-evolutionary dynamics of multi-component systems
Takao K. Suzuki, Wataru Iwasaki (*Grad. Sch. Front. Sci., UTokyo*)

2Pos156 Proliferation of phospholipid vesicles induced by freeze and thaw cycles and its effect on the lipid composition
Tatsuya Shinoda[1], Kazumu Kaneko[2], Yoshikazu Tanaka[3], Yasuhito Sekine[4], Tomoaki Matsuura[4] ([1]*Dept. Life Sci. Tech., Tokyo Tech*, [2]*Dept. Earth Planet. Sci., Tokyo Tech*, [3]*Grad. Sch. Life Sci., Tohoku Univ*, [4]*ELSI, Tokyo Tech*)

2Pos157 遺伝子発現制御ネットワークの進化における汎化能の解析
Computational analysis of generalization capacity in evolution of gene expression network
Chikara Furusawa (*BDR, RIKEN*)

2Pos158 Environment-driven structural phase transitions of primitive LLPS protocells

Tony Z Jia[1,2], Tommaso Fraccia[3], Chen Chen[1], Ruiqin Yi[1], Motoko Igisu[4], Chie Sakaguchi[5], Rehana Afrin[1], Christian Potiszil[5], Tak Kunihiro[5], Katsura Kobayashi[5], Eizo Nakamura[5], Yuichiro Ueno[6], Andre Antunes[2,7], Anna Wang[8,9,10], Kuhan Chandru[11], Jihua Hao[2,12] ([1]*Earth-Life Science Institute, Tokyo Institute of Technology*, [2]*Blue Marble Space Institute of Science*, [3]*Institut Pierre-Gilles de Gennes, CBI, ESPCI Paris, Université PSL*, [4]*Institute for Extra-cutting-edge Science and Technology Avant-garde Research (X-star), Japan Agency for Marine-Earth Science and Technology (JAMSTEC)*, [5]*The Pheasant Memorial Laboratory for Geochemistry and Cosmochemistry, Institute for Planetary Materials, Okayama University*, [6]*Department of Earth and Planetary Sciences, Tokyo Institute of Technology*, [7]*State Key Laboratory of Lunar and Planetary Sciences, Macau University of Science and Technology (MUST)*, [8]*School of Chemistry, UNSW Sydney.*, [9]*Australian Centre for Astrobiology, UNSW Sydney*, [10]*RNA Institute, UNSW Sydney*, [11]*Space Science Center (ANGKASA), Institute of Climate Change, National University of Malaysia*, [12]*Deep Space Exploration Laboratory/CAS Laboratory of Crust-Mantle Materials and Environments, University of Science and Technology of China*)

2Pos159 原始的な RNA 集団の調査から見つかった自己複製する最小の RNA

Minimal RNA self-reproduction discovered from a random pool of oligomers

Ryo Mizuuchi[1,2], Norikazu Ichihashi[3,4,5] ([1]*Fac. Sci. Eng., Waseda Univ.*, [2]*JST, FOREST*, [3]*Grad. Sch. Arts and Sci., Univ. Tokyo*, [4]*Komaba Inst. Sci., Univ. Tokyo*, [5]*UBI, Univ. Tokyo*)

24. 合成生物学・人工細胞／24. Synthetic biology & Artificial cells

2Pos160 DNA 液滴における選択的なリポソーム捕捉

Selective liposome capture in DNA droplets

Ryoya Hasegawa[1], Jing Gong[1], M. Shin-ichiro Nomura[2], Masahiro Takinoue[1,3,4] ([1]*Department of Life Science and Technology, Tokyo Institute of Technology*, [2]*Department of Robotics, Graduate School of Engineering, Tohoku University*, [3]*Department of Computer Science, Tokyo Institute of Technology*, [4]*Living Systems Materialogy (LiSM) Research Group, International Research Frontiers Initiative*)

2Pos161 リポソーム内無細胞タンパク質発現の転写と翻訳における脂質電荷の影響

Lipid charge affects the protein transcription and translation inside Giant unilamellar vesicle

Akari Miwa[1], Masatoshi Wakamori[2], Takashi Umehara[2], Koki Kamiya[1] ([1]*Grad. Sch. Sci. Tech., Gunma. univ.*, [2]*BDR ., Riken*)

2Pos162 LLPS-mediated artificial cell holding the artificial organelle with its interface stabilized

Kanji Tomohara, Yoshihiro Minagawa, Hiroyuki Noji (*Dept. Appl. Chem., Grad. Sch. Eng., Univ. Tokyo*)

2Pos163 コンパートメント化された刺激応答性ドラッグデリバリーのための脂質ベースの人工多細胞システム

Lipid Based Artificial Multicellular Systems for Compartmentalized and Stimuli-Responsive Drug Delivery

Tsuyoshi Inaba[1], James Richard Archer[1], Shogo Hamada[2], Hideaki Matsubayashi[1], Keita Abe[1], Ibuki Kawamata[1,3], Satoshi Murata[1], Shin-ichiro Nomura[1] ([1]*Grad.Sci.Eng., Tohoku Univ.*, [2]*Int. Grad. Sch. Sci. Eng., Tokyo Inst. Tech.*, [3]*Grad. Sch. Nat. Sci. Ochanomizu Univ.*)

2Pos164 人工細胞光操作系を用いた基板の接着力と細胞運動の構成的理解

Light-inducible artificial cell motility on diverse adhesion surfaces: a bottom-up approach to understanding cell migration

Daichi Nakajima[1], Shiva Razavi[2,3], Takanari Inoue[2], Shin-ichiro M. Nomura[1], Hideaki Matsubayashi[2,4] ([1]*Grad. Sch. Robotics., Univ. Tohoku*, [2]*Department of Cell Biology, Johns Hopkins University School of Medicine*, [3]*Department of Biological Engineering, Massachusetts Institute of Technology*, [4]*Frontier Research Institute for Interdisciplinary Sciences, Univ. Tohoku*)

2Pos165 トランスファー RNA の自律合成系の試験管内構築に向けた合理的 tRNA 発現系の設計および実証
Rationally designed *in vitro* transfer RNA expression system for the construction of a tRNA self-reproductive system
Ryota Miyachi[1], Yoshihiro Shimizu[2], Norikazu Ichihashi[1,3,4] ([1]*Grad. Sch. Arts Sci., Univ. Tokyo*, [2]*Riken BDR*, [3]*Komaba Institute for Sci., Univ. Tokyo*, [4]*Research Center for Complex System Biology, Universal Biology Institute Univ. Tokyo*)

2Pos166 合成ポリペプチド鎖とオリゴ核酸の設計に基づく固-液多相分離階層構造の開発
Development of the solid-liquid multiphase hierarchical structures based on chemically-designed polypeptides and oligonucleotides
Hiroshi Kamizawa[1], Yiwei Liu[2], Takumi Yamada[1], Kanjiro Miyata[3], Teruki Nii[2], Takeshi Mori[2,4], Yoshiki Katayama[2,4,5,6], Akihiro Kishimura[2,4,5] ([1]*Grad. Sch. Sys. Life Sci., Kyushu Univ*, [2]*Dept. of Applied Chem., Fac. of Eng., Kyushu Univ*, [3]*Dept. of Materials Eng., The Univ of Tokyo*, [4]*Ctr. for, Future Chem., Kyushu Univ*, [5]*Ctr. for Molecular Systems, Kyushu Univ*, [6]*The Ctr. For Adv. Med. Innov., Kyushu Univ*)

2Pos167 コンプレックスコアセルベートの電荷密度調節によるタンパク質内包機能をもつ人工生体分子凝縮体の設計
Charge density modulation in complex coacervate for protein sequestration to mimic biomolecular condensates
Ryoma Omae[1], Biplab K C[1], Teruki Nii[1], Takeshi Mori[1,2], Yoshiki Katayama[1,2,3,4], Akihiro Kishimura[1,2,3] ([1]*Dep. of Applied Chem., Faculty of Eng., Kyushu Univ.*, [2]*Ctr. for Future Chem., Kyushu Univ.*, [3]*Ctr. for Mol. Sys., Kyushu Univ.*, [4]*Ctr. for Adv. Med. Innov., Kyushu Univ.*)

2Pos168 DNA オリガミマイクロカプセルと DNA ハイドロゲルでできた異種人工細胞間の通信
Communication between different types of artificial cells based on DNA origami microcapsules and DNA hydrogels
Nagi Yamashita[1], Marcos Masukawa[2], Mayumi Chano[2], Yusuke Sato[3], Kanta Tsumoto[4], Kenichi Yoshikawa[5], Masahiro Takinoue[1,2] ([1]*School of Life Science and Technology, Tokyo Institute of Technology*, [2]*School of Computing, Tokyo Institute of Technology*, [3]*Graduate School of Computer Science and Systems Engineering, Kyushu Institute of Technology*, [4]*Graduate School of Engineering, Mie University*, [5]*Institute for Advanced Study, Kyoto University*)

2Pos169 多様な膜・高分子組成でのベシクル成長実験: 進化する人工ミニマルセルを目指して
Growth rates of synthetic cells with the various vesicle-polymer compositions: Toward implementing the evolution
Taro Suzuki (*Grad.Sch.Sci. , Univ. Tohoku*)

2Pos170 自己生産する細胞のコンセプトを人工系で単純に再設計する：モデル実験系で繋ぐ物質と生命
Reproduction of a synthetic minimal cell: An experimental approach connecting matter and cell
Minoru Kurisu[1], Peter Walde[2], Masayuki Imai[1] ([1]*Dept. Phys., Grad. Sch. Sci., Tohoku Univ.*, [2]*Dept. Materials, ETH Zürich*)

26A. 計算生物学: 生命情報学／26A. Computational biology: Bioinformatics

2Pos171 グラフ NN による化学分子表現学習とその匂い認知予測への応用
Molecular Representation Learning by Graph Neural Networks and its Application to Odor Perception Prediction
Tetsuya Kobayashi[1], Mengji Zhang[2], Akira Funahashi[3] ([1]*IIS, UTokyo*, [2]*Shanghai Jiao Tong University*, [3]*Keio Univ*)

2Pos172 敵対的生成ネットワークに基づくクライオ電子顕微鏡画像解像度改善法の開発
Development of the method to improve the resolution of cryo-EM map based on the Generative Adversarial Networks
Xinyuan Li (*FBS. Osaka Univ.*)

2Pos173 経験的アプローチによる酵素の機能予測
Predicting enzyme function using an empirical approach
Suguru Fujita, Tohru Terada (*Dept. of Biotechnol., Grad. Sch. of Agri. and Life Aci., Univ. of Tokyo*)

2Pos174 脳神経回路の配線規則を読み解くデータ駆動型解析
Data-driven analysis to decipher the wiring rules of brain neural circuits
Jigen Koike[1], Naoki Honda[1,2,3] ([1]*Grad. Sch. Int. Sci. Life, Hiroshima Univ.*, [2]*Grad. Sch. Biostudies, Kyoto Univ.*, [3]*ExCELLS*)

2Pos175 アンサンブルドッキングにおけるタンパク質相互作用表面の解析
Analysis of protein interaction surfaces in ensemble docking
Nobuyuki Uchikoga[1], Yuri Matsuzaki[2] ([1]*Sch. Interdiscip. Math. Sci., Meiji Univ.*, [2]*Acad. Leadership, Tokyo Inst. Tech.*)

2Pos176 構造比較を利用した不凍タンパク質の特徴付け
Characterization of Antifreeze proteins by using structural comparison
Yuki Konaka, Motonori Ota, Ryotaro Koike, Koya Sakuma (*Grad.Sch.Info., Univ. Nagoya*)

2Pos177 Basal-like 乳がんにおいて染色体間相互作用が消失した遺伝子ペア群のオントロジー解析
Ontology analysis for gene pairs with disrupted inter-chromosomal interactions in basal-like breast cancer
Yuta Shintani, Takanori Sasaki (*Fac. Adv. Math. Sci., Meiji Univ.*)

2Pos178 A multimer structure prediction method: generating multiple decoy structures via docking software and ranking confidence with AlphaFold2
Masaki Koyama[1], Hiroki Onoda[2], George Chikenji[1] ([1]*Dept. of Appl. Phys., Grad. Sch. of Eng., Nagoya Univ.*, [2]*Synchrotron Radiation Research Center, Nagoya Univ.*)

2Pos179 かゆみ伝達に関与するタンパク質の研究
Proteins involved in itch transmission
Kota Tsurumi, Motonori Ota, Ryotaro Koike (*Grad Sch. Inf., Univ. Nagoya*)

26B. 計算生物学: 分子シミュレーション／26B. Computational biology: Molecular simulation

2Pos180 1 分子 FRET 計測と分子動力学シミュレーションを統合した Protein G のフォールディング経路解析
Integrative modeling of protein G folding dynamics from single-molecule FRET and molecular dynamics simulations
Soichiro Oda, Yasuhiro Matsunaga (*Grad. Sch. Sci. Eng., Saitama Univ.*)

2Pos181 FRET-assisted structural modeling of dynamic protein ensembles
Bianca Reschke, Christian A. Hanke, Alexander Larbig, Claus A. M. Seidel (*Institute for Molecular Physical Chemistry, Heinrich Heine University, Duesseldorf, Germany*)

2Pos182 Gromacs ソフトウェアと Martini 粗視化力場を用いたタンパク質表面電荷分布とその溶解性の関係性の探索
Exploring the relationship between the surface charge of a protein and its solubility using the MARTINI model and GROMACS software
Ryusei Nomura[1], Hiromichi Turui[2], Yutaka Kuroda[1] ([1]*Grad. Sch. Eng., TUAT*, [2]*Grad. Sch. Med., Juntendo*)

2Pos183 拡張アンサンブル分子動力学シミュレーションに基づいた環状ペプチドの膜透過性予測技術の開発
Development of a Protocol for Predicting Membrane Permeability of Cyclic Peptides Based on Molecular Dynamics Simulations
Masatake Sugita, Takuya Fujie, Keisuke Yanagisawa, Masahito Ohue, Yutaka Akiyama (*Sch. Computing, Tokyo Tech*)

2Pos184 グリッドを用いた主成分分析による分子集団の運動モードの解析
Cooperative modes for collective molecules using grid-based principal-component analysis
Koji Ogata, Kentaro Oishi (*Fac. Pharm. Sci., Sanyo-Onoda City Univ.*)

2Pos185 脂質二重膜における大腸菌 site-2 protease RseP の分子動力学シミュレーション
Molecular dynamics simulations of E. coli site-2 protease RseP in the lipid bilayer
Kenta Tanaka[1], Toru Ekimoto[1], Tsutomu Yamane[2], Terukazu Nogi[1], Mitsunori Ikeguchi[1] ([1]*Grad. Sch. Med. Life Sci., Yokohama City Univ.*, [2]*RIKEN R-CCS*)

2Pos186
Targeting G-Quadruplex Structures in SARS-CoV-2 Nsp3; SARS Unique Domain (SUD) as a Novel Target of Pyridostatine Against Covid-19
Rendrawan Dedy, Jayyinunnisya Helmia, Meriko Lince, Kazutomo Kawaguchi, Hidemi Nagao (*Grad.Sch.Nat.Sci.Tech.,Kanazawa Univ.*)

2Pos187 Learning QM/MM Potential by Equivariant Multiscale Model
YaoKun Lei[1,2], Kiyoshi Yagi[1,2], Yuji Sugita[1,2,3] ([1]*Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research, RIKEN*, [2]*Computational Biophysics Research Team, RIKEN Center for Computational Science, RIKEN*, [3]*Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, RIKEN*)

2Pos188 Atomic-Level Characterization of Protein Kinase - Inhibitors binding through massive Molecular Dynamics Simulations
Ai Shinobu[1,2], Re Suyong[1,3], Hiraku Oshima[1,4], Yuji Sugita[1] ([1]*RIKEN*, [2]*Osaka University*, [3]*National Institutes of Biomedical Innovation, Health, and Nutrition*, [4]*University of Hyogo*)

2Pos189 SARS-CoV-2 スパイクタンパク質とユニバーサル中和抗体との相互作用： 残基間相互作用ネットワークに基づく理論的解析
Interaction of the SARS-CoV-2 spike protein with a universal neutralizing antibody: Insights from Residue Interaction Network Analysis
Hirokazu Murata, Norifumi Yamamoto (*Chiba Tech*)

2Pos190 HIV-1 逆転写酵素の薬剤耐性機構に関する理論的研究： 残基相互作用ネットワーク解析
Computational Study of HIV-1 Reverse Transcriptase for Drug Resistance Mechanism: Residue Interaction Network Analysis
Ryuki Hashimoto, Norifumi Yamamoto (*Chiba Tech*)

2Pos191 SOD1 変性過程に関する理論的研究： 銅イオンと亜鉛イオンの解離に伴う残基間相互作用の変化
Insights into the denaturation process of SOD1: Changes in residue interactions associated with dissociation of Cu and Zn ions
Kento Takeuchi[1], Shinya Tahara[2], Takakazu Nakabayashi[2], Norifumi Yamamoto[1] ([1]*Chiba Tech*, [2]*Univ.Tohoku*)

2Pos192 SOD1 変性過程に関する理論的研究：分子内 S-S 結合の解離に伴う残基間相互作用の変化
Insights into the denaturation process of SOD1: Changes in residue interactions associated with dissociation of intramolecular SS bonds
Tomu Fukasawa[1], Shinya Tahara[2], Takakazu Nakabayashi[2], Norifumi Yamamoto[1] ([1]*Chiba Tech*, [2]*Univ.Tohoku*)

2Pos193 QM/MM 分子シミュレーションによるミオシンの ATP 加水分解反応機構に関する理論的研究
Insights into the Reaction Mechanism of ATP Hydrolysis in Myosin through QM/MM Molecular Simulations
Tatsuki Tominaga, Norifumi Yamamoto (*Chiba Tech*)

2Pos194 Theoretical study of the influence of solvent conditions on the structure and interaction of core region in LC domain of FUS
Suzuka Tokunaga, Isseki Yu (*Maebashi Institute of Technology Information Systems Program*)

2Pos195 インフルエンザウイルス・ノイラミニダーゼの薬剤耐性機構に関する理論的研究： 残基相互作用ネットワーク解析
Computational study of the drug resistance of influenza virus neuraminidase: Residue interaction network analysis
Yuki Kagusa, Norihumi Yamamoto, Manabu Igarashi (*Chiba tech*)

2Pos196 メソスケールシミュレーションによるシナプス後肥厚タンパク質が形成する多相凝集体の次元比較
Mesoscale simulation demonstrates the dimensional comparison of multi-phased condensates formed by postsynaptic density proteins
Risa Yamada, Shoji Takada (*Grad. Sch. Sci., Kyoto Univ.*)

2Pos197 Molecular dynamics simulation of the substrate channeling in tryptophan synthetase
Isseki Yu[1], Shingo Ito[2], Kiyoshi Yagi[2], Yui Sugita[2] ([1]*Maebashi Institute of Technology Information Systems Program*, [2]*Riken Theoretical Molecular Science Laboratory*)

2Pos198 Exploring the Structural Characteristics of Erythropoietin Based on Glycosylation Patterns Using Molecular Dynamics Simulations
Haeri Im[1], Song-Ho Chong[2], Yuji Sugita[1,3,4] ([1]*Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research, Wako, Japan*, [2]*Global Center for Natural Resources Sciences, Faculty of Life Sciences, Kumamoto University, Kumamoto, Japan*, [3]*Computational Biophysics Research Team, RIKEN Center for Computational Science, Kobe, Japan*, [4]*Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, Kobe, Japan*)

2Pos199 光駆動塩化物イオンポンプロドプシンの分子動力学シミュレーション
Molecular dynamics simulation of light-driven chloride ion pump rhodopsin
Akiya Moriuchi[1,2], Masahiko Taguchi[1,2], Hinano Ogawa[1,2], Takaaki Fujiwara[1,2], Osamu Miyashita[3], Eriko Nango[1,2] ([1]*Graduate School of Science, Tohoku University.*, [2]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University.*, [3]*RIKEN Center for Computational Science*)

2Pos200 アデニル酸キナーゼの構造転移とアンフォールディングのカメレオンモデルによる研究
Conformational transition and unfolding of adenylate kinase studied by chameleon model
Tomoki P. Terada (*Grad. Sch. Eng., Nagoya Univ.*)

2Pos201 味覚受容体 1 型の全原子分子動力学シミュレーション
All-atom molecular dynamics simulations of Taste receptor type 1
Kazuma Okada, Yasuhiro Matsunaga (*Grad. Sch. Sci. Eng., Saitama Univ.*)

27. 数理生物学・理論生物学／27. Mathematical & Theoretical biology

2Pos202 構造感度解析を用いたドーパミン化学反応ネットワークの理論解析
Theoretical analysis of dopamine chemical reaction network using structural sensitive analysis
Shun Sawada, Kei Tokita (*Grad. Sch. Info., Nagoya Univ.*)

2Pos203 大脳皮質における組織特異的な血管パターン形成の数理モデル
Computational Model Exploring Characteristic Pattern Regulation in Periventricular Vessels
Hisako Takigawa-Imamura[1], Saito Hirano[2] ([1]*Grad. Sch. Med. Sci., Kyushu Univ.*, [2]*Yahata Kousei Hosp.*)

2Pos204 Chemical thermodynamics for growing compartments with stoichiometric constraints
Atsushi Kamimura, Yuki Sughiyama, Tetsuya J. Kobayashi (*IIS, The University of Tokyo*)

2Pos205 イオン輸送タンパク質による細胞中のジュール熱発生の理論的研究
Joule heating in cells involving ion transport proteins: A theoretical study
Tetsuichi Wazawa, Takeharu Nagai (*SANKEN, Osaka Univ.*)

2Pos206 ライブイメージング画像を用いた多細胞組織内の細胞間相互作用の力の推定
Live imaging-based inference of mechanical potential of cell-cell interaction in multicellular systems
Hiroshi Koyama[1,2], Toshihiko Fujimori[1,2] ([1]*Div. Embryology, NIBB*, [2]*SOKENDAI (Grad. Univ. Advanced Studies)*)

2Pos207 Disruption of metabolic homeostasis: Responsiveness due to the cofactor dynamics and network sparsity
Yusuke Himeoka[1], Chikara Furusawa[1,2] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*BDR, Riken*)

2Pos208 線虫の確率的行動選択に関する非線形神経回路モデル
Nonlinear neural circuit model of stochastic behavioral choice in C. elegans
Makoto Fukui, Yuishi Iwasaki (*Grad. Sch. Sci. Eng., Ibaraki Univ*)

2Pos209 遺伝子発現時系列データのモード分解解析
Data-driven study of gene expression time-series patterns
Masayo Inoue (*Grad. Sch. Eng., Kyushu Inst. Tech.*)

2Pos210 相互作用する動的可塑的結合力学系を用いた生物個体間コミュニケーションのモデル
A model of communication between individual organisms using dynamic-plastic coupled dynamical systems
Haruto Nakata, Akinori Awazu (*Graduate School of Integrated Sciences for Life, Univ. Hiroshima*)

30. 計測／30. Measurements

2Pos211 高速 AFM による Sec トランスロコンの 1 分子計測
Single molecule observation of Sec translocon by High Speed AFM
Yui Kanaoka[1], Takaharu Mori[2], Tomoya Tsukazaki[3], Takayuki Uchihashi[1,4] ([1]*Graduate School of Science, Nagoya University*, [2]*School of Science, Tokyo University of Science*, [3]*Division of Biological Science, NAIST*, [4]*ExCELLS*)

2Pos212 液液相分離を形成するペプチドと RNA の分子間相互作用を検知するグラフェンバイオセンサー
Molecular Interactions of Peptides and RNA Forming Liquid-Liquid Phase Separation Evaluated by Graphene Electrochemical Transistors
Kantaro Kikuchi, Yui Yamazaki, Yuhei Hayamizu (*Dept. of Mat. Sci. and Eng. , Tokyo Tech.*)

2Pos213 Universality of single-cell rheology during cell division in developing embryo observed by atomic force microscopy
Takahiro Kotani, Yuki Miyata, Yosuke Tsuboyama, Megumi Yokobori, Tomohiro Matsuo, Yuki Fujii, Takaharu Okajima (*Grad. Sch. Inform. Technol., Hokkaido. Univ.*)

2Pos214 超高感度タンパク質 ELISA 測定法を用いた不活化ウイルスの測定
Ultrasensitive ELISA detection of inactivated viruses
Yuki Kobayashi[1,2], Etsuro Ito[1,2] ([1]*Department of Biology, Waseda University*, [2]*BioPhenoMA Inc.*)

2Pos215 蛍光ビーズを用いた CLEM の研究
Research on CLEM method using fluorescent beads
Miho Nakafukasako[1], Tomoya Higo[1], Yuki Gomibuchi[2], Hiroko Takazaki[3], Yusuke V. Morimoto[2], Takayuki Kato[3], Takuo Yasunaga[2] ([1]*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech.*, [2]*Dept. of Phys. Info. Tech., Kyutech.*, [3]*IPR, Univ. Osaka*)

2Pos216 Development of a method for conformational analysis of oligosaccharides using ion mobility spectrometry
Hao Feng[1], Takumi Yamaguchi[1,2,3] ([1]*Sch. Materials Sci., JAIST*, [2]*Grad. Sch. Pharm. Sci., Nagoya City Univ.*, [3]*ExCELLS, NINS*)

2Pos217 原子間力顕微鏡を用いた大腸粘液層の力学的評価
Mechanical Evaluation of Colonic Mucus Layer by Atomic Force Microscopy
Momoka Horikiri[1], Mugen Taniguchi[2], Naritaka Kobayashi[3], Hiroshi Y. Yoshikawa[1], Kiyoshi Takeda[2], Ryu Okumura[2], Takahisa Matsuzaki[1] ([1]*Grad. Sch. Eng., Univ. Osaka*, [2]*Grad. Sch. Med., Univ. Osaka*, [3]*Sch. Eng., Univ. Shiga*)

2Pos218 DNA Origami Nanospring: Probing the Dynamics of Single Integrin motion, Force Magnitude and Orientation in Living Cells
Hitomi Matsubara[1], Hiroki Fukunaga[2], Takahiro Saito[3], Keigo Ikezaki[4], Mitsuhiro Iwaki[2] ([1]*BDR, RIKEN*, [2]*Adv ICT Res Inst, NICT*, [3]*Grad. Sch. FBS., Univ. Osaka*, [4]*Grad. Sch. Sci., Univ. Tokyo*)

2Pos219 ポリジメチルシロキサン膜で被覆したグラフェンセンサーを用いた電気的バイオセンシング
Electrical biosensing using graphene sensors covered with poly(dimethylsiloxane) membrane
Takao Ono[1], Miho Kannaka[1], Yasushi Kanai[1,2], Naruto Miyakawa[3], Ayumi Shinagawa[3], Shin-ichi Nakakita[4], Yohei Watanabe[5], Shota Ushiba[3], Shinsuke Tani[3], Yasuo Suzuki[6], Masahiko Kimura[3], Daichi Chiba[1,2,7,8], Kazuhiko Matsumoto[1] ([1]*SANKEN, Osaka Univ.*, [2]*OTRI, Osaka Univ.*, [3]*Murata Manufacturing Co., Ltd.*, [4]*Fac. Med., Kagawa Univ.*, [5]*Grad. Sch. Med. Sci., Kyoto Pref. Univ. Med.*, [6]*Sch. Pharm. Sci., Univ. Shizuoka*, [7]*CSRN, Osaka Univ.*, [8]*SRIS, Tohoku Univ.*)

31. バイオイメージング／31. Bioimaging

2Pos220 pyroptosis における IL-1β 放出動態の一細胞イメージング
Single-cell imaging of IL-1β release dynamics in pyroptosis
Mika Kato[1], Zhuohao Yang[2], Nobutake Suzuki[3], Mai Yamagishi[3], Takashi Funatsu[2], Yoshitaka Shirasaki[2] ([1]*Dep. Pharm., The Univ. of Tokyo*, [2]*Grad. Pharm. Sci., The Univ. of Tokyo*, [3]*Live Cell Diagnosis, Ltd.*)

2Pos221 Development of a fluorescence lifetime biosensor for quantitative imaging of intracellular GTP levels in living cells
Thi Ngoc Loan Nguyen, Quang Cong Vu, Satoshi Arai (*WPI Nano Life Science Institute, Kanazawa Univ.*)

2Pos222 Quantification of intracellular Ca^{2+} levels by Red/Green/Blue fluorescence lifetime biosensors
Cong Quang Vu[1], Yasushi Okada[2,3], Satoshi Arai[1] ([1]*NanoLSI, Kanazawa Univ.*, [2]*Laboratory for Cell Polarity Regulation, Center for Biosystems Dynamics Research, RIKEN*, [3]*Department of Cell Biology, Department of Physics, The Univ. of Tokyo*)

2Pos223 Investigation of cell membrane exposed to nanopipette-based non-thermal atmospheric pressure plasma using scanning probe microscope
Han Gia Nguyen[1], Linhao Sun[2], Shinya Kumagai[3], Shinji Watanabe[2] ([1]*Grad. Sch. Nano Life Sci, Univ. Kanazawa*, [2]*WPI NanoLSI, Univ. Kanazawa*, [3]*Univ. Meijo*)

2Pos224 マウスノード不動繊毛は変形の向きを感知して左右軸を決定する
Immotile cilia mechanically sense the direction of fluid flow for left-right determination
Takanobu A. Katoh[1,2], Toshihiro Omori[3], Katsutoshi Mizuno[4], Takeshi Itabashi[2], Atsuko H. Iwane[2], Takuji Ishikawa[3], Takayuki Nishizaka[5], Hiroshi Hamada[2], Yasushi Okada[1,2,6] ([1]*Grad. Sch. Med., The Univ. of Tokyo*, [2]*BDR, Riken*, [3]*Grad. Sch. Eng., Tohoku Univ.*, [4]*Fac. Med. Sci., Univ. of Fukui*, [5]*Fac. Sci., Gakushuin Univ.*, [6]*Grad. Sch. Sci., UBI, WPI-IRCN, The Univ. of Tokyo*)

2Pos225 Attempt of intracellular imaging by high-speed atomic force microscopy
Hikaru Ichida[1], Kenichi Umeda[2], Alam Mohammad Shahidul[1], Risa Omura[2], Makiko Kudo[2], Takehiko Ichikawa[2], Takeshi Fukuma[2], Takahiro Nakayama[2], Mikihiro Shibata[2,3], Noriyuki Kodera[2] ([1]*Grad. Sch. NanoLS., Kanazawa Univ*, [2]*WPI-NanoLSI, Kanazawa Univ.*, [3]*InFiniti, Kanazawa Univ*)

2Pos226 Post-acquisition super resolution for cryo-EM
Raymond Burton-Smith[1,2], Kazuyoshi Murata[1,2] ([1]*Exploratory Center for Life and Living Systems (ExCELLS), National Institute of Natural Sciences, Okazaki*, [2]*National Institute of Physiological Sciences, National Institute of Natural Sciences, Okazaki*)

2Pos227 透過型電子顕微鏡の最大感度をもたらす新規位相板（II）
Novel Hilbert Phase Plates for Maximum Sensitivity in Transmission Electron Microscopy (II)
Kuniaki Nagayama (*N-EM Laboratories Inc.*)

2Pos228 蛍光グルコース誘導体を用いたグルコースの細胞内における局在解析
Analysis of intracellular glucose localization by fluorescent glucose analogs
Mio Yanagida, Hirofumi Nakano, **Hironori Ueno** (*Grad. Sch. Edu., Aichi univ. Edu.*)

2Pos229 Investigation of the photophysical property of a fluorescent calcium-ion indicator, Yellow Cameleon 3.60, under cryogenic condition

Wakana Miyamura[1], Takumi Kunimoto[1], Masahito Yamanaka[1], Toshiki Kubo[2], Kosuke Tsuji[1], Kazunori Sugiura[3], Shun-ichi Fukushima[3], Nicholas Smith[4], Takeharu Nagai[3,5], Katsumasa Fujita[1,5,6] ([1]*Dept. Appl. Phys., Osaka Univ.*, [2]*Dept. Dermatol., Osaka Univ.*, [3]*SANKEN, Osaka Univ.*, [4]*IFReC., Osaka Univ.*, [5]*OTRI., Osaka Univ.*, [6]*PhotoBIO-OIL., AIST*)

2Pos230 シングルセル 3D オプトジェネティクス技術の開発と応用

Development and application of single-cell 3D optogenetics technology

Tomoyoshi Inoue[1], Ryuki Imamura[1], Naoya Kataoka[2], Shin Usuki[3], Takuma Sugi[1] ([1]*Program of Biomedical Science, Graduate School of Integrated Sciences for Life, Hiroshima University*, [2]*Department of Integrative Physiology, Graduate school of Medicine, Nagoya University*, [3]*Research Institute of Electronics, Shizuoka University*)

2Pos231 ナノメートル精度を有する極低温光電子相関顕微鏡システムの開発

Development of cryogenic correlative light and electron microscope system with nanometer-scale

Takuma Yorita[1], Yoshimasa Takizawa[2], Hitoshi Kurumizaka[2], Satoru Fujiyoshi[2] ([1]*Grad. sch. Sci., Tokyo Tech*, [2]*IQB., Univ. Tokyo*)

2Pos232 高分解能ライトフィールド顕微鏡によるリアルタイム三次元多粒子トラッキングの開発

Development of real-time 3D multi-particle tracking by high-resolution light-field microscopy

Ryuki Imamura[1], Shin Usuki[2], Takuma Sugi[1] ([1]*Program of Biomedical Science, Graduate School of Integrated Sciences for Life, Hiroshima University*, [2]*Research Institute of Electronics, Shizuoka University*)

2Pos233 超低侵襲高速原子間力顕微鏡の開発

Ultra-low-invasive high-speed atomic force microscopy for visualization of fragile molecular complexes

Shingo Fukuda, Toshio Ando (*WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University*)

32. バイオエンジニアリング／32. Bioengineering

2Pos234 Lectin-conjugated nanoparticles selectively binding to cancer cell surface glycans for the capture of pacreatic cancer cell exosomes

Jonghoon Choi (*School of Integrative Engineering, Chung-Ang University*)

2Pos235 集光レーザービームの物理作用による生体分子濃縮の時空間制御

Spatiotemporal control of condensation of biomolecules via photophysical effects of a focused laser beam

Shuma Matsumoto[1], Ren Shirata[1,2], Genki Fukasawa[3], Takahisa Matsuzaki[1], Teruki Sugiyama[4,5], Ryuzo Kawamura[6], Tomoaki Matsuura[7], Hiroshi Yoshikawa[1] ([1]*Grad. Sch. Eng., Osaka Univ.*, [2]*Grad. Sch. Chem., Saitama Univ.*, [3]*Grad. Sch. Life Sci. Tech., Tokyo Tech.*, [4]*Dep. Appl. Chem., NYCU*, [5]*Div. Mater. Sci., NAIST*, [6]*Grad. Sch. Sci and Eng., Saitama Univ.*, [7]*ELSI, Tokyo Tech.*)

2Pos236 微小曲面電極を用いた電気化学発光の細胞表面分子検出への応用

Application of electrochemiruminescence with cup-shaped microelectrodes for detection of cell surface molecules

Taro Sasaki[1,2], Koki Uchiyama[1,2], Tomoyuki Kamata[3], Dai Kato[3], Naoshi Kojima[3], Shohei Yamamura[3], Hyonchol Kim[1,2] ([1]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [2]*Cell. Mol. Biotechnol. Res. Inst., AIST*, [3]*Health Med. Res. Inst., AIST*)

2Pos237 非熱平衡大気圧プラズマを用いた細胞成長促進用マイクロ潅流デバイスシステム

A micro perfusion system for promoted cell growth using non-thermal atmospheric pressure plasma

Hayata Okino, Shinya Kumagai (*Meijo University*)

2Pos238 パルスレーザーが骨の溶解性に与える影響の評価 ～骨構造の時空間制御に向けて～
Influence of pulsed laser irradiation on dissolution behavior of bone to understand the structural and chemical origins of old bone region
Anna Konishi[1], Erika Yamashita[2,3], Mihoko Maruyama[1], Takahisa Matsuzaki[1], Heqi Xi[1], Menglu Li[1], Katsumasa Fujita[1], Junichi Kikuta[2,4], Yusuke Mori[1], Masaru Ishii[2,3,4,5], Hiroshi Yoshikawa[1] ([1]*Grad. Sch. Eng., Univ. Osaka*, [2]*Grad. Sch. Med., Univ. Osaka*, [3]*StemRIM Institute of Regeneration-Inducing Medicine., Univ. Osaka*, [4]*Grad. Sch. FBS., Univ. Osaka*, [5]*iFReC., Univ. Osaka*)

2Pos239 スリットナノポア近傍の DNA のダイナミクスに対するイオン種の影響
Effect of ionic species on Dynamics of DNA near slit nanopore
Takuma Yoshinaga, Seiwa Yamagishi, Yunosuke Fuji, Shin Takano, Yuuta Moriyama, Toshiyuki Mitsui (*Aoaku. Univ, Dept, of Phys.*)

2Pos240 相分離マイクロリアクタを用いたオンチップ濃縮系の開発
Development of on-chip enrichment system using microreactor for phase separation
Yoshihiro Minagawa, Shoki Nakata, Hiroyuki Noji (*Dep. App. Chem, Univ. Tokyo.*)

2Pos241 マグネタイトナノ粒子を内包したフェリチン結晶の FIB 加工とその結晶を利用したスピン波デバイスの開発
FIB machining of crystals of magnetite nanoparticles encapsulated in ferritin and development of spin-wave device using the arrays
Mitsuhiro Okuda[1,2], Gabriela Pretre[2] ([1]*Meiji Univ.*, [2]*Komie corp.*)

2Pos242 マイクロビーズに提示したライブラリーによる蛍光アプタマーの in vitro セレクション
Selection of fluorogenic RNA aptamers by *in vitro* compartmentalization using microbead-display libraries
Tomotaka Tayama[1], Keisuke Ito[2], Sotaro Uemura[2], Ryo Iizuka[2] ([1]*Dept. Biol. Sci., Fac. Sci., The Univ. Tokyo*, [2]*Dept. Biol. Sci., Grad. Sch. Sci., The Univ. Tokyo*)

2Pos243 硬さの空間パターンによる細胞の集団運動の制御
Control of self-organization of cells by mechanically patterned hydrogel
Takahisa Matsuzaki (*Grad. Sch. Eng. Osaka Univ.*)

34. その他／34. Miscellaneous topics

2Pos244 高分子鎖における First Passage 問題の理論的解析
Theorical analytics of First Passage Problems for polymer model
Yuta Sakamoto, Takahiro Sakaue (*Grad. Sci and Eng., Univ. Aoyama Gakuin*)

2Pos245 Phase separation of soft polymer mixtures
Naoki Iso, Yuki Norizoe, Takahiro Sakaue (*Aoyama Gakuin University*)

2Pos246 Antifungal effect of nanostructured copper oxide: Synthesis and Application
Yuki Nishida (*Faculty of Agriculture, Kagoshima University*)

2Pos247 インクジェット技術を用いたバクテリアのパターン化植菌方法
Development of patterned inoculation of microbial cell using inkjet technology
Mikiko Tsudome, Shigeru Deguchi (*JAMSTEC*)

2Pos248 種依存的な細胞レベルの温度適応機構の探索
Identifying species-dependent mechanisms of temperature adaptation at the cellular level
Haruya Suzuki[1], Akira Murakami[1,2], Takashi Funatsu[1], Koki Okabe[1,3] ([1]*Grad. Sch. Pharm. Sci., The Univ. of Tokyo*, [2]*Sch. Pharm. Sci., Univ. Shizuoka*, [3]*PRESTO, JST*)

2Pos249 213nm 深紫外線パルスレーザ を用いる微生物殺菌効果の定量性に関する検討
Quantitative Study of Microbial Sterilization by using Deep UV Pulse Laser at 213nm
Koichi Murayama[1], Riri Miura[1], Kazuhiro Dainaka[2], Nobuhiro Umemura[2] ([1]*Hokkaido Univ. of Education*, [2]*Chitose Insti. Sci. Tech.*)

2Pos250 Medusavirus の新規カプシド構造と粒子形成過程に伴う構造変化
Novel capsid structure and structural changes during particle formation of Medusavirus
Ryoto Watanabe[1,2,3], Chihong Song[1,2,3], Masaharu Takemura[4], Kazuyoshi Murata[1,2,3] ([1]*The Graduate University for Advanced Studies (SOKENDAI)*, [2]*NIPS*, [3]*ExCELLS*, [4]*Tokyo University of Science*)

3 日目（11 月 16 日（木））／Day 3（Nov. 16 Thu.） 13:10 〜 15:10

01A. タンパク質：構造／01A. Protein: Structure

3Pos001 Structure and dynamics of β-hairpin peptide SVG28 by solid-state nuclear magnetic resonance spectroscopy
Izuru Kawamura[1], Shuhei Yoshida[2], Fumihiro Kayamori[2], Yuto Suzuki[1], Daisuke Sato[1], Shoko Fujita[3], Kenji Usui[2], Ryuji Kawano[3] ([1]*Grad. Sch. Eng. Sci., Yokohama Natl. Univ.*, [2]*Konan Univ.*, [3]*Tokyo Univ. Agric. Technol. (TUAT)*)

3Pos002 クライオ電子顕微鏡によるナトリウム共役型中性アミノ酸トランスポーター SNAT2 の立体構造解析
Cryo-EM Structure Analysis of SNAT2, the Sodium-Coupled Neutral Amino Acid Transporter
Haruna Inuzuka, Yongchan Lee, Tomohiro Nishizawa (*Grad. Sch. of Med. Life Sci., Yokohama City Univ.*)

3Pos003 ゼアキサンチン結合型のキサントロドプシン kin4B8 のクライオ電子顕微鏡構造解析
Cryo-EM structure of the zeaxanthin-bound xanthorhodopsin kin4B8
Wataru Shihoya[1], Syunya Murakoshi[1], Ariel Chazan[2], Hideki Kandori[3], Keiichi Inoue[4], Susumu Yoshizawa[5], Oded Beja[2], Osamu Nureki[1] ([1]*Grad. Sch. Sci., The Univ of TOkyo*, [2]*Faculty of Biology, Technion-Israel Institute of Technology*, [3]*OptoBioTechnology Research Center, Nagoya Institute of Technology*, [4]*The Institute for Solid State Physics, The University of Tokyo*, [5]*Atmosphere and Ocean Research Institute, The University of Tokyo*)

3Pos004 Molecular basis of host recognition and antigenic drift of human coronavirus 229E
Yu-Xi Tsai (*IBC, Academia Sinica*)

3Pos005 cyclic offset を導入した AlphaFold Multimer による環状ペプチド複合体構造予測
Structure prediction of cyclic peptide complexes by AlphaFold Multimer with cyclic offset
Keinoshin Togashi, Takatsugu Kosugi, Masahito Ohue (*Department of Computer Science, School of Computing, Tokyo Institute of Technology*)

3Pos006 Molecular basis of the hyper-activity of anti-cancer bispecific antibody due to domain rearrangement revealed by cryo-EM
Kyohei Sato[1], Ryutaro Asano[2], Koki Makabe[3], Izumi Kumagai[2], Takashi Matsui[4], Shiro Uehara[1], Atsushi Tsugita[1], Takeshi Yokoyama[1], Yoshikazu Tanaka[1] ([1]*Grad. Sch. Life Sci., Univ. Tohoku*, [2]*Grad. Sch. Eng., Univ. Tokyo of Agriculture and Technology*, [3]*Grad. Sch. Sci and Eng., Univ. Yamagata*, [4]*Grad. Sch. Sci., Univ. Kitasato*)

3Pos007 Structural study on the bacteriocin pectocin M1 from *Pectobacterium catorovorum*
Nawee Jantarit[1,2], Hideaki Tanaka[2], Genji Kurisu[1,2] ([1]*Grad.Sch.Sci., Osaka Univ.*, [2]*IPR, Osaka Univ.*)

3Pos008 新規細胞内ポケットを介した class B1 GPCR の活性化機構の解明
A novel activation mechanism of class B1 GPCRs via a conserved intracellular pocket
Kazuhiro Kobayashi[1], Kouki Kawakami[1], Tsukasa Kusakizako[2], Atsuhiro Tomita[2], Michihiro Nishimura[2], Kazuhiro Sawada[2], Hiroyuki Okamoto[2], Suzune Hiratsuka[3], Gaku Nakamura[3], Riku Kuwabara[3], Hiroshi Noda[4], Hiroyasu Muramatsu[4], Masaru Shimizu[4], Tomohiko Taguchi[5], Asuka Inoue[3], Takeshi Murata[6], Osamu Nureki[2] ([1]*Komaba Institute for Science, the University of Tokyo*, [2]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*, [3]*Graduate School of Pharmaceutical Sciences, Tohoku University*, [4]*Research Division, Chugai Pharmaceutical*, [5]*Laboratory of Organelle Pathophysiology, Department of Integrative Life Sciences, Graduate School of Life Sciences, Tohoku University*, [6]*Department of Chemistry, Graduate School of Science, Chiba University*)

3Pos009 CENP-E モータードメインの加水分解前後の結晶構造の比較
Comparison of crystal structures of the CENP-E motor domain before and after hydrolysis
Asuka Shibuya[1,2], Akira Suzuki[2], Naohisa Ogo[3], Jun-ichi Sawada[3], Akira Asai[3], Hideshi Yokoyama[2] ([1]*Fac. Pharm. Sci., Josai Itn. Univ.*, [2]*Fac. Pharm. Sci., Tokyo Univ. Sci.*, [3]*Ctr. Drug Discov., Grad. Sch. Pharm. Sci., Univ. Shizuoka*)

3Pos010 新規化学修飾グラフェングリッドを利用した細胞分裂タンパク質 FtsZ フィラメントのクライオ電顕構造解析
Cryo-EM structure analysis of cell division protein FtsZ filaments using a novel chemically modified graphene grid
Junso Fujita[1,2,3], Hiroshi Amesaka[4], Takuya Yoshizawa[5], Kota Hibino[5], Fumiaki Makino[1,2,6], Haruyasu Asahara[3], Maiko Moriguchi[3], Tsuyoshi Inoue[3], Keiichi Namba[1,2,7], Shun-ichi Tanaka[4], Hiroyoshi Matsumura[5] ([1]*Grad. Sch. Frontier Biosci., Osaka Univ.*, [2]*JEOL YOKOGUSHI Res. Alliance Lab., Osaka Univ.*, [3]*Grad. Sch. Pharm. Sci., Osaka Univ.*, [4]*Grad. Sch. Life & Env. Sci., Kyoto Pref. Univ.*, [5]*Coll. of Life Sci., Ritsumeikan Univ.*, [6]*JEOL Ltd.*, [7]*RIKEN BDR/SPring-8 Center*)

3Pos011 高感度チャネルロドプシン GtCCR4 の構造基盤
Structural basis for the highly sensitive channelrhodopsin GtCCR4
Tatsuki Tanaka[1], Shoko Hososhima[2], Yo Yamashita[2], Teppei Sugimoto[2], Wataru Iida[1], Fumiya K. Sano[1], Kota Katayama[2,3], Satoshi P. Tsunoda[2,3], Wataru Shihoya[1], Hideki Kandori[2,3], Osamu Nureki[1] ([1]*Grad. Sch. of Sci., Univ. of Tokyo*, [2]*Grad. Sch. of Eng., Nagoya Inst. of Tech.*, [3]*OptoBio Tech. Res. Cent.*)

01B. タンパク質：構造機能相関／01B. Protein: Structure & Function

3Pos012 Prediction of the quantitative function of artificially-designed protein from structural information
Ryosaku Ota[1], Naoki Honda[1,2,3,4] ([1]*Graduate School of Integrated Sciences for Life, Hiroshima University*, [2]*Exploratory Research Center on Life and Living Systems*, [3]*Graduate School of Biostudies, Kyoto University*, [4]*Center for Brain, Mind and Kansei sciences research, Hiroshima University*)

3Pos013 Effects of cancer-associated mutations on the allosteric network within the carboxyl-terminal hydrolase domain of BAP1
Chih-Hsuan Lai[1], Hao-Ting Chang[2], Shang-Te Danny Hsu[1,2,3] ([1]*Institute of Biological Chemistry, Academia Sinica, Taipei 11529, Taiwan*, [2]*Institute of Biochemical Sciences, National Taiwan University, Taipei 10617, Taiwan*, [3]*International Institute for Sustainability with Knotted Chiral Meta Matter, Hiroshima University, Higashihiroshima 739-8527, Japan*)

3Pos014 クライオ電子顕微鏡によるチャネルロドプシンの構造解析
Cryo-EM structure of a channelrhodopsin
Yuzhu Wang[1], Tatsuki Tanaka[1], Fumiya K. Sano[1], Hiroaki Akasaka[1], Satoshi P. Tsunoda[2], Wataru Shihoya[1], Hideki Kandori[2], Osamu Nureki[1] ([1]*Graduate School of Science, The University of Tokyo*, [2]*Graduate School of Engineering, Nagoya Institute of Technology*)

3Pos015 Efficient recombinant production, structural and functional study of mouse-derived α-defensin family, cryptdins
Shaonan Yan, Yuchi Song, Yi Wang, Shinya Yoshino, Tomoyasu Aizawa (*Graduate School of Life Science, Hokkaido University*)

3Pos016 X 線 1 分子追跡法を用いた TRP チャネルの分子内動態計測
Measurement of intramolecular dynamics of TRP channels using Diffracted X-ray Tracking
Kazuhiro Mio[1,2], Tatsunari Ohkubo[2], Tatsuya Arai[1,3], Yuji C. Sasaki[1,3] ([1]*AIST Operando-OIL*, [2]*Med. Life Sci., Yokohama City Univ.*, [3]*Grad. Sch. Front. Sci., Univ. Tokyo*)

3Pos017 海洋性珪藻 *Phaeodactylum tricornutum* の細胞質局在性 θ 型炭酸脱水酵素の構造と機能解析
Structural and functional analysis of the cytosolic θ carbonic anhydrase from marine diatom *Phaeodactylum tricornutum*
Hiroto Negoro[1,2], Hideaki Tanaka[1,2], Ginga Shimakawa[3], Hiroyasu Koteishi[1,2], Akihiro Kawamoto[1,2], Yusuke Matsuda[3], Genji Kurisu[1,2] ([1]*Institute for Protein Research, Osaka University*, [2]*Department of Biotechnology, Graduate School of Engineering, Osaka University*, [3]*Department of Bioscience, School of Biological & Environmental Sciences, Kwansei Gakuin University*)

3Pos018 小型 AsCas12f 酵素のクライオ電子顕微鏡を用いた構造解析およびその改変
An AsCas12f-based compact genome editing tool derived by deep mutational scanning and structural analysis
Satoshi Omura[1], Tomohiro Hino[2], Ryoya Nakagawa[1], Tomoki Togashi[3], Tsukasa Ohmori[3], Atsushi Hoshino[2], Osamu Nureki[1] ([1]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo.*, [2]*Department of Cardiovascular Medicine, Graduate School of Medical Science, Kyoto Prefectural University of Medicine.*, [3]*Department of Biochemistry, Jichi Medical University School of Medicine.*)

3Pos019 Ultrahigh-affinity transport proteins from ubiquitous marine bacteria: structure, function, and environmental significance
Benjamin Clifton[1], Uria Alcolombri[2], Colin Jackson[3], Paola Laurino[1] ([1]*Protein Eng. Evol. Unit, Okinawa Inst. Sci. Tech. (OIST)*, [2]*Inst. Environ. Eng., ETH Zurich*, [3]*Research School of Chem., Aust. Nat. Univ. (ANU)*)

01C. タンパク質：物性／01C. Protein: Physical Property

3Pos020 抗体の変性によるコンパクト化と理想的球状化
Antibodies get smaller and ideally globular by denaturation
Hiroshi Imamura[1], Ayako Ooishi[2], Shinya Honda[2] ([1]*Dept. Bio-sci., Nagahama Inst. Bio-Sci. Tech.*, [2]*Biomed. Res. Inst., AIST*)

3Pos021 あらゆるタンパク質のフォールディング機構を予測できる統計力学モデルの開発
Development of statistical mechanical models that can predict folding mechanisms of any protein
Koji Ooka[1], Munehito Arai[1,2,3] ([1]*Col. Arts & Sci., Univ. Tokyo*, [2]*Dept. Life Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

3Pos022 AlphaFold2 を用いた大型タンパク質の新生鎖フォールディング予測
Prediction of nascent chain folding of large multidomain proteins by AlphaFold2
Shunji Suetaka[1], Masataka Yoshimura[1], Koji Ooka[2], Munehito Arai[1,2,3] ([1]*Dept. Life Sci., Univ. Tokyo*, [2]*Col. Arts & Sci., Univ. Tokyo*, [3]*Dept. Phys., Univ. Tokyo*)

3Pos023 小麦由来グリアジンペプチドの凝集形成に関する研究
Characterization of Aggregation Process of Wheat Gliadin 33-mer Peptides
Yuri Emoto[1], Mio Nakashima[1], Natsuko Goda[1], Emi Hibino[1], Takeshi Tenno[1,2], Hidekazu Hiroaki[1,2,3] ([1]*Grad. Sch. Pharm. Sci., Nagoya Univ.*, [2]*BeCellBar, LLC*, [3]*COMIT*)

3Pos024 一倍体状態に起因する中心体足場タンパク質の不足はヒト体細胞のゲノム不安定性を引き起こす
Haploidy-linked insufficiency of pericentriolar material (PCM) protein causes a genome instability in human somatic cells
Koya Yoshizawa[1], Ryota Uehara[2] ([1]*Graduate School of Life Science, Hokkaido University*, [2]*Faculty of Advanced Life Science, Hokkaido University*)

3Pos025 血清アミロイド A の線維形成における主要な構造変化
A key conformational change for the fibril formation by serum amyloid A
Taishi Okunishi, Katsumi Matsuzaki, Masaru Hoshino (*Grad. Sch. of Pharm. Sci., Univ. Kyoto*)

3Pos026 蛋白質凝集の免疫原性は凝集体の生物物理学的特徴によって決まる
The biophysical properties of protein aggregates determine i*n vivo* immunogenicity
Yutaka Kuroda (*Tokyo University of Agriculture and Technology (TUAT)*)

3Pos027 VHH 抗体 FR2 残基による特徴的な親和性-安定性トレードオフ機構の解明
Elucidation of unique affinity-stability trade-off mechanisms by FR2 residues in VHH antibodies
Koichi Yamamoto[1], Makoto Nakakido[1], Daisuke Kuroda[1,2], Satoru Nagatoishi[1], Kouhei Tsumoto[1,3] ([1]*Grad. Sch. of Eng., Univ. of Tokyo*, [2]*Nat. Inst. of Infect. Dis.*, [3]*Inst. of Med. Sci., Univ. of Tokyo*)

3Pos028 フロリゲン活性化複合体による LLPS 形成と花成制御機構
The LLPS formation by flowering activation complex and flowering regulating mechanism
Mayu Enomoto[1], Suai Anzawa[1], Yuka Koizumi[1], Kyoko Furuita[2], Kenichiro Taoka[3,4], Keiji Nishida[4], Akihiko Kondo[4], Takashi Kodama[2], Toshimichi Fujiwara[2], Hiroyuki Tsuji[3,5], Chojiro Kojima[1,2] ([1]*Grad. Sci., YNU*, [2]*IPR, Univ. Osaka*, [3]*KIBR, YCU*, [4]*EGBRC, Univ. Kobe*, [5]*BBC, Univ. Nagoya*)

01E. タンパク質：計測・解析／01E. Protein: Measurement & Analysis

3Pos029 構造コンプライアンス特性のロボット機構学的解析に基づくタンパク質の運動生成
Generation of Protein Motions based on Robot Kinematic Analysis of Structural Compliance Properties
Keisuke Arikawa (*Fcl. Eng., Kanagawa Inst. of Tech.*)

3Pos030 細胞内環境に酷似した細胞残骸密集環境下でのヒトアミロイドベータタンパク質の凝集体形成
Aggregate formation of Human Amyloid-beta Protein in cell debris crowding environment closely resembling the intracellular environment
Mitsuhiro Hirai[1], Hiroki Iwase[2], Shigeki Arai[3] ([1]*Gunma University*, [2]*Comprehensive Research Organization for Science and Society*, [3]*National Institute for Quantum and Radiological Science and Technology*)

3Pos031 Optimization of MD-derived conformational ensemble in information content space and its application to experimental SAXS data
Tomotaka Oroguchi (*Faclt. Sci. Tech., Keio Univ.*)

3Pos032 あいち SR の名古屋大学 X 線回折ビームライン BL2S1 の即応性と多様性の利用支援
Rapid Access and Multi-Use Diffraction Beamline BL2S1 from Nagoya University in Aichi-SR
Yasufumi Umena[1], Hiroki Onoda[1], Leonard Chavas[1,2] ([1]*NUSR, Nagoya Univ.*, [2]*Grad. Sch. Eng., Nagoya Univ.*)

3Pos033 量子カスケードレーザーを用いた時間分解赤外分光法による古細菌と細菌由来の 2 つのヘリオロドプシンの構造変化計測
Time-resolved infrared dual-comb spectroscopy using quantum cascade laser reveals differences in structual changes of two heliorhodopsins
Toshiki Nakamura[1], Soichiro Kato[1], Ryo Yamamoto[2], Manish Singh[1,3], Hideki Kandori[1,3], Yuji Furutani[1,3] ([1]*Nagoya Institute of Technology*, [2]*Nagoya Institute of Technology*, [3]*OptoBio Technology Research Center*)

3Pos034 電気生理学的手法によるディフィシル菌二成分毒素の膜透過アッセイ系構築
Construction of a membrane translocation assay system for *C. difficile* binary toxin by electrophysiological technique
Yuki Mitani[1], Sotaro Takiguchi[2], Ryuji Kawano[2], Hideaki Tsuge[1] ([1]*Graduate School of Life Science, Kyoto Sangyo University*, [2]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*)

3Pos035 パルス電子顕微鏡のための液中試料観察法の開発
Development of the Liquid Sample Observation Method for Pulse Electron Microscopy
Ryoya Katayama, Takeru Yamasaki, Tomoharu Matsumoto, Akihiro Narita (*Grad. Sch. Sch., Nagoya Univ.*)

02. ヘムタンパク質／02. Heme proteins

3Pos036 Electrochemically boosted P450 reactions to produce pharmaceutical hydroxyvitamin D_3
Yasuhiro Mie[1], Chitose Mikami[1], Yoshiaki Yasutake[1,2] ([1]*Bioproduction Res. Inst., AIST*, [2]*CBBD-OIL, AIST-Waseda Univ.*)

3Pos037 ウシ心筋シトクロム酸化酵素のカルシウム結合構造
Calcium-bound structure of bovine heart cytochrome *c* oxidase
Kazumasa Muramoto, Kyoko Shinzawa-Itoh (*Grad. Sch. Sci., Univ. Hyogo*)

3Pos038 Fe-Tyr 配位結合をもつ 4 種類の天然変異ヘモグロビン M の結晶構造
Crystallographic structures of four kinds of Hemoglobin M which has Fe-Tyr coordination bond
Shigenori Nagatomo[1], Ayana Sato-Tomita[2], Yumi Semba[1], Akihisa Miyagawa[1], Kiyoharu Nakatani[1], Mio Ohki[3], Kenji Mizutani[3], Sam-Yong Park[3], Naoya Shibayama[2] ([1]*Dept. Chem., Univ. Tsukuba*, [2]*Div. of Biophysics, Jichi Medical Univ.*, [3]*Protein Design Lab., Yokohama City Univ.*)

3Pos039 CHCHD2 によるチトクロム酸化酵素活性化作用機序解明を目指した可視共鳴ラマン分光学的研究
Visible resonance Raman Study to elucidate the action mechanism of CHCHD2 for activating cytochrome oxidase
Takuto Kamei[1], Sachiko Yanagisawa[1], Atsuhiro Simada[2], Gladyck Stephanie[3], Aras Siddhesh[2], Huettemann Maik[3], Glossman Lawrence[3], Minoru Kubo[1] ([1]*Grad. Sch. Sci., Univ. Hyogo, Japan.*, [2]*Fac. Appl. Biol. Sci., Gifu Univ.*, [3]*Wayne State Univ. Sch. Med.*)

3Pos040 アロステリック蛋白質の構造会合と特性に対する両親媒性溶質の影響
Effects of an amphipathic solute on the structural assembly and properties of an allosteric protein
Antonio Tsuneshige (*Frontier Bioscience HOSEI UNIVERSITY*)

03. 膜タンパク質／03. Membrane proteins

3Pos041 両親媒性ポリマーで再構成された BhuUV-T の分光学的解析
Spectroscopic analysis of BhuUV-T reconstituted with amphiphilic polymers
Yuki Sumida[1], Ayaka Naka[1], Yasuhiro Kobori[1,2], Yoshitsugu Shiro[3], Hiroshi Sugimoto[4], Tetsunari Kimura[1,2] ([1]*Dept. of Chem., Grad. Sch. Sci., Univ. Kobe*, [2]*Mol. Photo. Res. Cent., Univ. Kobe*, [3]*Dept. of Life Sci., Grad. Sch. of Sci., Univ. Hyogo*, [4]*SPring-8, RIKEN*)

3Pos042 クライオ電子顕微鏡と分子動力学計算によって明らかとなった植物 YS1 トランスポーターによる鉄・フィトシデロホア複合体の輸送機構
Iron-phytosiderophore uptake mechanism of plant YS1 transporter revealed by cryo-EM structure and MD simulations
Atsushi Yamagata (*RIKEN Center for Biosystems Dynamics Research*)

3Pos043 K オピオイド受容体とモルフィナン骨格を保有するリガンドとの相互作用解析
Vibrational spectroscopy study of chemical interaction between k-opioid receptor (KOR) and ligands having morphinan structure
Ryo Nishikawa[1], Kota Katayama[1,2], Seiya Iwata[1], Ryoji Suno[3], Chiyo Suno[3], Takuya Kobayashi[3], Hideki Kandori[1,2] ([1]*Graduate School of Engineering, Nagoya Institute of Technology*, [2]*OptoBio Technology Research Center, Nagoya Institute of Technology*, [3]*Graduate School of Medicine, Kansai Medical University*)

3Pos044 フィタニル基および膜貫通架橋をもつエーテル型リン脂質膜が再構成したバクテリオロドプシンの四次構造と光機能中間体に与える影響
Effect of the phytanyl groups and membrane-spanning cross-linkage on structure and photocycle of bR in ether-linked phospholipid membrane
Ami Harasawa[1], Ai Nakagawara[1], Takafumi Shimoaka[1], Toshiyuki Takagi[2], Takashi Kikukawa[3], Hiroshi Takahashi[1], Masashi Sonoyama[1,4,5] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*AIST*, [3]*Fac. Adv. life Sci., Hokaido Univ.*, [4]*GIAR, Gunma Univ.*, [5]*GUCFW, Gunma Univ.*)

3Pos045 脂質膜パッチに再構成されたコレステロールトランスポーター ABCA1 の高速 AFM 観察
High-speed AFM imaging of the cholesterol transporter ABCA1 reconstituted in lipid membrane patch
Kaho Nakamoto[1], Atsushi Kodan[2], Romain Amyot[1,4], Kazuki Sakata[3], Yasuhisa Kimura[3], Kenichi Umeda[4], Kazumitsu Ueda[2], Noriyuki Kodera[4] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-iCeMS, Kyoto Univ.*, [3]*Div. Appl. Life Sci., Grad Sch. Agric., Kyoto Univ.*, [4]*WPI-NanoLSI, Kanazawa Univ.*)

3Pos046 光捕集タンパク質 LH1-RC の光受容における分子動態解析
Intramolecular dynamics analysis of light-harvesting protein LH1-RC in photoreception using the DXT technique
Tatsunari Ohkubo[1,2], Tatsuya Arai[2,3], Kazuhiro Mio[1,2], Yuji C. Sasaki[2,3] ([1]*Grad. Sch. Med. Sci., Yokohama CU*, [2]*Operand OIL, AIST*, [3]*Grad. Sch. of Front. Sci., The Univ of Tokyo*)

3Pos047 CGMD シミュレーションを用いた ErbB2, FGFR, EGFR の膜貫通部位のそれぞれの二量体化とそれらの構造の比較
Dimerizations of TM domains in ErbB2, FGFR, and EGFR Using CGMD Simulations and the Comparisons of These Structures
Naoto Tonogaito[1], Chika Minami[1], Naoyuki Miyasita[1,2] ([1]*Grad. Sch. BOST, KINDAI Univ.*, [2]*BOST, KINDAI Univ.*)

06. DNA/RNA ナノテクノロジー／06. DNA/RNA nanotechnology

3Pos048 プライマー伸長にともなう鎖置換反応で駆動される DNA 状態機械の生物学応用に向けた検証
Characterization of a DNA state machine driven by primer extension accompanying strand displacement reaction toward biological application
Ken Komiya, Koji Sakamoto (*X-star, JAMSTEC*)

3Pos049 サブマイクロスケールのトラス DNA 構造体の設計手法
Design method of sub-micrometer scale truss DNA structures
Ibuki Kawamata[1,2], Yudai Yamashita[1], Satoshi Murata[1] ([1]*Graduate School of Engineering, Tohoku University*, [2]*Faculty of Core Research, Ochanomizu University*)

3Pos050 Multi-stimuli-responsive DNA origami nanolattice
Yuri Kobayashi, Kanta Tsumoto, Yuki Suzuki (*Grad. Sch. Eng., Mie. Univ.*)

3Pos051 DNA 反応拡散系における波型ハイドロゲルパターン
Waving hydrogel pattern in DNA-based reaction–diffusion system
Jaehyeok Eom[1], Keita Abe[1], Ibuki Kawamata[1,2], Shin-ichiro Nomura[1], Satoshi Murata[1] ([1]*Grad. Sch. Eng. Tohoku Univ.*, [2]*Grad. Sch. Faculty of Core Research Ochanomizu Univ.*)

3Pos052 利用光鉗技術探討 RNA 偽結結構對核醣體框架位移之影響
Exploring how RNA pseudoknots affect ribosomal frameshifting using optical tweezers
YuTong Huang (*National Taiwan University / Taiwan (R.O.C)*)

3Pos053 外界とのコミュニケーションが可能なリポソーム型分子ロボットの構築に向けて
Toward the construction of giant unilamellar vesicle type molecular robots that can communicate with outside environment
Shoji Iwabuchi, Ryuji Kawano (*Tokyo University of Agriculture and Technology*)

3Pos054 統合情報理論に基づく意識をもった DNA システムのボトムアップ構築
Bottom-up Construction of DNA System with Consciousness based on Integrated Information Theory
Fumika Kambara[1], Sotaro Takiguchi[1], Hiroki Watanabe[2], Masahiro Takinoue[2], Ryuji Kawano[1] ([1]*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology.*, [2]*Department of Computer Science, Tokyo Institute of Technology.*)

3Pos055 DNA コンピューティングを用いたカスケード酵素の可逆的空間制御系を応用した miRNA 検出
Reversible spatial control of cascade enzymes for miRNA detection system based on DNA computing
Aoi Mameuda[1], Masahiro Takinoue[2], Koki Kamiya[1] ([1]*Grad. Sch. Sci. Tech. , Gunma Univ.*, [2]*Dept. Comp. Sci. , Tokyo Tech.*)

3Pos056 単分散 GUV を用いた複数の相分離コンパートメントを持つ人工細胞モデルの生成
Generation of an Artificial Cell Model with Multiple Phase-separated Compartments within Monodisperse GUVs
Ryotaro Yoneyama[1], Ryota Ushiyama[1], Tomoya Maruyama[2], Masahiro Takinoue[2,3], Hiroaki Suzuki[1] ([1]*Graduate School of Science and Engineering, Chuo University*, [2]*Life Science and Technology, Tokyo Institute of Technology*, [3]*Department of Computer Science, Tokyo Institute of Technology*)

3Pos057 疎水環境のナノスケール配置制御技術の開発
Development of nanoscale positional control technique for hydrophobic environment
Issei Kusunoki, Lwin Aye Seaim, Yusuke Sato (*Grad. Sch. Comp. Sci. Syst. Eng., Kyutech*)

07. 核酸：その他／07. Nucleic acid: Others

3Pos058 Direct visualization of nucleosome sliding in nucleosomes containing a histone variant and tailless histones by HS-AFM
Shin Morioka[1], Shoko Sato[2], Takumi Oishi[2], Suguru Hatazawa[2], Naoki Horikoshi[2], Tomoya Kujirai[2], Yoshimasa Takizawa[2], Hitoshi Kurumizaka[2], Mikihiro Shibata[3,4] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*Institute for Quantitative Biosciences, The Univ. of Tokyo*, [3]*WPI-NanoLSI, Kanazawa Univ.*, [4]*InFiniti, Kanazawa Univ.*)

3Pos059 Synthetic siderophores as the Trojan horse carriers for peptide nucleic acids through the *E. coli* membrane
Uladzislava Tsylents[1], Michał Burmistrz[1], Piotr Maj[1], Adam Mieczkowski[2], Monika Wojciechowska[1], Joanna Trylska[1] ([1]*Centre of New Technologies, University of Warsaw, Banacha 2c, 02-097 Warsaw, Poland*, [2]*Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Pawinskiego 5a, 02-106 Warsaw, Poland*)

3Pos060 光ピンセットを用いたソレ効果による相分離ドロップレットの生成と DNA 濃縮 III
Generation of Phase-Separated Droplets Induced by the Soret Effect and DNA Enrichment by Optical Tweezers III
Mika Kobayashi[1,2], Hiroyuki Noji[2] ([1]*Tokyo Univ. of Agriculture and Tech.*, [2]*Univ. Tokyo*)

3Pos061 局所的配列の力学的特性が DNA の変形に及ぼす影響
Effects of mechanical properties of local sequence on DNA conformational changes
Anzu Kawamura[1], Shiho Ishii[1], Naoaki Sakamoto[2], Akinori Awazu[2], Yoshihiro Murayama[1] ([1]*Tokyo Univ. of Agri. and Tech.*, [2]*Hiroshima Univ.*)

3Pos062 線形および環状 DNA の交流電場応答の直接観測
Dynamics of circular and linear DNA under AC fields in viscous solutions
Yunosuke Fuji, Seiwa Yamagishi, Shin Takano, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ. Dept. of Phys.*)

3Pos063 鎖状及び環状 DNA の絡み合い構造における変形の伝播距離の測定
Measurements of propagation distance of deformation in entangled structure of linear and circular DNA
Saki Matsuyama, Akinori Miyamoto, Yoshihiro Murayama (*Tokyo Univ. of Agri. and Tech.*)

3Pos064 シミュレーテッド分岐マシンを使用した RNA 二次構造の予測の改善
Improved Prediction of RNA Secondary Structure Using Simulated Bifurcation Machine
Yuki Matsubara[1], Kengo Tsuda[1], Masaru Suzuki[2], Hiroaki Hata[1] ([1]*Mitsui Knowledge Industry*, [2]*TOSHIBA DIGITAL SOLUTIONS*)

3Pos065 Structural Dynamics Role of AGG Interruptions in Preventing CGG Repeat Expansion Associated with Fragile X Syndrome
I-Ren Lee, Yang-I Shen, Kai-Chun Cheng (*National Taiwan Normal University*)

12. 発生・分化／12. Development & Differentiation

3Pos066 子宮平滑筋の収縮による子宮内圧力が器官形成期の胚の発生に与える影響
The effects of intrauterine pressure by uterine smooth muscle contractions for embryos in early organogenesis stage
Misuzu Okuno[1,2], Yoko Ueda[1], Kyoko Mochida[1], Yasumasa Bessho[2], Chiharu Kimura-Yoshida[1], Isao Matsuo[1] ([1]*Department of Molecular Embryology, Research Institute, Osaka Women's and Children's Hospital, Osaka Prefectural Hospital Organization*, [2]*Laboratory of Gene Regulation Research, Division of Biological Science, Graduate School of Science and Technology, Nara Institute of Science and Technology*)

3Pos067 Atomic force microscopy reveals that rheological properties of developing embryos in the gastrula stage depend on the cell fates
Yuki Miyata, Takahiro Kotani, Yosuke Tsuboyama, Tomohiro Matsuo, Yuki Fujii, Takaharu Okajima (*Grad. Sch. Inform. Technol., Hokkaido. Univ.*)

3Pos068 細胞外環境の硬さから読み解く脊椎動物心臓の発生と進化
The role of stiffness for evolution and development of vertebrates heart
Sho Matsuki, Ryuta Watanabe, Toshiyuki Mitsui, Yuuta Moriyama (*Grad. Sch. Sci., Univ.Aogaku*)

3Pos069 次世代 SPIM によるマウス E5.5 胚発生のトランススケール解析
Trans-scale analysis of a whole E5.5 mouse embryo during development with Next-generation SPIM
Go Shioi[1], Tomonobu M Watanabe[1], Junichi Kaneshiro[1], Yusuke Azuma[2], Shuichi Onami[2] ([1]*Laboratory for Comprehensive Bioimaging, RIKEN Center for Biosystems Dynamics Research*, [2]*Laboratory for Developmental Dynamics, RIKEN Center for Biosystems Dynamics Research*)

3Pos070 線虫の背側／腹側軸確立における極性確立反応ネットワークの同定
Identifying the reaction network for polarity establishment in C. elegans dorsal/ventral axis establishment
Ryunosuke Saito[1], Masatoshi Nishikawa[1,2], Sungrim Seirin Lee[3] ([1]*Grad. Sch. Sci &Eng., HoseiUniv*, [2]*Dep. Frontier Biosci., Hosei Univ*, [3]*ASHBi., Kyoto Univ*)

3Pos071 Combination of force measurement and inference decipher non-linear involvement of E-cad shaping early *C. elegans* embryos

Kazunori Yamamoto[1,2,3], Charras Guillaume[1] ([1]*LCN, UCL*, [2]*Applied Bioscience, Kanagawa Institute of Technology*, [3]*Institute for Genetic Medicine, Hokkaido University*)

13. 筋肉／13. Muscle

3Pos072 骨格筋の粘弾性における微小管の役割

The role of microtubules on viscoelastic properties in skeletal muscle

Takuya Kobayashi[1], Motoshi Kaya[2], Nagomi Kurebayashi[1], Takashi Murayama[1], Takashi Sakurai[1] ([1]*Dept. of Cellular and Molecular Pharmacology, Juntendo University*, [2]*Faculty of Physics, The University of Tokyo*)

3Pos073 スピロプラズマの遊泳装置を構成する細菌アクチン MreB1 の精製と機能解析

Purification and characterization of bacterial actin MreB1: a component of swimming machinery in *Spiroplasma*

Daichi Takahashi[1], Makoto Miyata[1,2], Ikuko Fujiwara[3] ([1]*Grad. Sch. Sci., Osaka Metropolitan Univ.*, [2]*OCARINA, Osaka Metropolitan Univ.*, [3]*Dept. Mater. Sci. Bioeng., Nagaoka Univ. Tech.*)

3Pos074 アクチンフィラメントの末端を数ナノメートルの精度で観察

Observation of an end of actin filament with several nanometer accuracies

Hikaru Empuku[1], Takahiro Mitani[1], Itsuki Kunita[2], Hajime Honda[1] ([1]*Dept. Matl. Sci. Bioeng., Nagaoka Univ.*, [2]*Faculty of Engineering, University of the Ryukyus.*)

3Pos075 X 線回折法と張力測定法によるウサギ外眼筋の構造・機能特性

Structural and functional property of the rabbit extraocular muscle studied by X-ray diffraction experiment and tension measurement

Maki Yamaguchi[1], Toru Kurihara[2], Naoya Nakahara[1], Hideki Yamauchi[1], Kazuhiro Hirano[1], Mai Yamaguchi[1], Toshiko Yamazawa[1], Tetsuo Ohno[3], Shigeru Takemori[1], Naoto Yagi[4] ([1]*The Jikei Univ. Sch.Med.*, [2]*Sougou Tokyo Hosp.*, [3]*Teikyo Heisei Univ.*, [4]*SPring8/JASRI*)

3Pos076 心筋細胞における生理的レベルの圧負荷のカルシウムハンドリングへの影響

Effect of physiological hydrostatic pressure on Ca^{2+} handling in mouse cardiomyocytes

Yohei Yamaguchi[1], Toshiyuki Kaneko[2], Susumu Ohya[1], Masayoshi Nishiyama[3] ([1]*Dept. Pharm., Grad. Sch. Med., Nagoya City Univ.*, [2]*Dept. Physio., Asahikawa Med. Univ.*, [3]*Dept. Physics, Kindai Univ.*)

3Pos077 アクトミオシン相互作用の計算モデルにおける筋収縮の巨視的性質に対するバイアスブラウン運動の効果

The effect of biased Brownian motion on the macroscopic properties of muscle contraction in the simulation model of actomyosin interaction

Shunta Oda, Tomoki P. Terada (*Dept. Appl. Phys., Grad. Sch. Eng., Nagoya Univ.*)

3Pos078 DNA オリガミ-ミオシンⅡ融合ナノシステムの単分子解像度計測によるパワーストローク協調の可視化

Visualization of the cooperative power stroke revealed by single molecule measurement of DNA origami-based myosin II nano system

Hiroki Fukunaga[1,10], Masashi Ohmachi[9], Takumi Washio[2,7], Hiroaki Takagi[3], Keisuke Fujita[4,10], Keigo Ikezaki[8], Toshio Yanagida[6], Mitsuhiro Iwaki[1,5,10] ([1]*Adv ICT Res Inst, NICT*, [2]*UT-Heart Inc*, [3]*Dept. phys., Nara Med. Univ*, [4]*FBS, Univ. Osaka*, [5]*IFReC, Univ. Osaka*, [6]*IST, Univ. Osaka*, [7]*FS, Univ. Tokyo*, [8]*Grad. Sch. sci., Univ. Tokyo*, [9]*SIGMA KOKI*, [10]*BDR, Riken*)

3Pos079 アクチン分子の局所構造について

Semi-local conformations of actin molecules

Toshiro Oda (*Faculty of Health and Welfare, Tokai-gakuin Univ.*)

3Pos080 プロトン駆動力下でのクライオ電子顕微鏡単粒子解析によって明らかにする ATP 合成酵素の回転機構
Single particle Cryo-EM under proton motive force reveals the rotational mechanism of ATP synthase
Atsuki Nakano[1], Jun-ichi Kishikawa[2], Kaoru Mitsuoka[3], Ken Yokoyama[1] ([1]*Fac. of Life Sci., Kyoto Sangyo Univ*, [2]*Applied Biology, Kyoto Institute of Technology*, [3]*Research Center for Ultra-High Voltage Electron Microscopy, Osaka University*)

3Pos081 CHD ファミリーの α アクチニン ABD とフィラミン ABD はアクトミオシンⅡ運動を阻害しない
Unlike CHD of Rng2,two members of the CHD family, α-actinin ABD and filamin ABD, do not inhibit actomyosin II motility in vitro
Kameyama Shuhei (*Dept. Pure & Appl. Physics, Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos082 Creation of ATP synthase with multiple torque generating units
Hiroshi Ueno[1], Riku Marui[1], Naruhiko Adachi[2], Norie Hamaguchi[3], Toshio Moriya[2], Masato Kawasaki[2], Akihito Ikeda[2], Satomi Inaba[2], Satoshi Yasuda[3], Toshiya Senda[2], Takeshi Murata[3], Hiroyuki Noji[1] ([1]*Grad. Sch. Eng., Univ. Tokyo*, [2]*Tsukuba, KEK*, [3]*Grad. Sch. Sci., Univ. Chiba*)

3Pos083 全原子計算によるアクトミオシンの結合モードの探索と biased binding の再現
Investigation of binding modes and reproduction of biased binding of actomyosin by all-atom calculations
Kyoko Shimanuki, Daichi Kubo, Kyohei Shoji, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Grad. Scl. Adv. Sci. & Eng., Waseda Univ.*)

3Pos084 マイナスキネシン kinesin-14 の微小管上マイナス端方向運動には N 末側で固定されることが重要
Anchoring geometry is a significant factor in determining the direction of kinesin-14 motility on microtubules
Masahiko Yamagishi, Rieko Sumiyoshi, Junichiro Yajima (*Grad. Arts & Sci., Univ. Tokyo*)

3Pos085 KIF1A-微小管結合における K-loop の結合安定性および結合速度への寄与
Contribution of K-loop to the KIF1A-microtubule binding stability and the binding rate
Koki Adachi, Mitsunori Takano (*Dept. of Pure & Appl. Phys., Grad. Scl. Adv. Sci. & Eng., Waseda Univ.*)

3Pos086 情報理論を用いた骨格筋ミオシンの協同性の評価
Evaluation of skeletal myosin cooperativity based on information theory
Arun Kasimchetty (*Department of Physics, School of Science, The University of Tokyo.*)

3Pos087 周毛性細菌におけるべん毛間の回転速度差
Rotation-speed difference between flagella in peritrichous bacteria
Tsubasa Ishihara, Shuichi Nakamura (*Dept. Appl. Phys., Grad. Sch. Eng., Tohoku Univ.*)

3Pos088 F_1-ATPase の回転を駆動する構造変化メカニズム
Conformational change mechanisms driving the rotation of F_1-ATPase
Masahiro Motohashi[1,2], Mao Oide[2,3], Chigusa Kobayashi[4], Jung Jaewoon[2,4], Eiro Muneyuki[1], Yuji Sugita[2,4] ([1]*Grad. Sch. Sci. Eng., Univ. Chuo*, [2]*Wako Inst., Riken*, [3]*PRESTO, JST*, [4]*Kobe Inst., Riken*)

3Pos089 繊毛の屈曲波運動を実現する繊毛キネシンの力学特性
The mechanical properties of ciliary kinesin: an essential motor for the bending wave motion of cilia
Hiroto Ishii, Masahiko Yamagishi, Junichiro Yajima (*Grad. Sch. of Arts and Sci., Univ. Tokyo*)

3Pos090 新規評価方法を用いたバクテリアべん毛モーターの回転揺らぎの周期性の解析
Investigation of periodicity of rotational fluctuations in the bacterial flagellar motor using a novel evaluation method
Kenta Takemori, V. Yusuke Morimoto (*Fac, Comp. Sci. and Sys. Eng., Kyushu Inst. Tech*)

3Pos091 ヘテロダイマーモーターの運動を数学的にモデル化することで明らかにする KIF1A ダイマーのヘッド間の協調性
Modeling the motion of heterodimeric motors uncovers head-head coordination in a KIF1A dimer
Tomoki Kita[1], Kazuo Sasaki[2], Shinsuke Niwa[1,3] ([1]*Grad. Life. Sci., Tohoku Univ.*, [2]*Grad. Eng., Tohoku Univ.*, [3]*FRIS., Tohoku Univ.*)

3Pos092 *A Novel Photochromic inhibitor SP-AB-SP exhibits multiple stages of inhibitory activity on mitotic kinesin Eg5*
MD Alrazi Islam[1], Shinsaku Maruta[2], Tostani Fofou Yonta[2] ([1]*Dept. Sci & Eng. for Sustainable Innovation, Soka University*, [2]*Grad. Sch. of Bio Science , Soka University*)

3Pos093 ミトコンドリア型 ATP 合成酵素の阻害因子 IF_1 が示す回転方向依存的な制御機構: 1 分子操作実験と分子動力学シミュレーション
Direction-dependent regulation of IF_1 in the mitochondrial ATP synthase by single-molecule manipulation and molecular dynamics simulation
Ryohei Kobayashi, Kei-ichi Okazaki (*Inst. for Mol. Sci.*)

15B. 細胞生物学的課題：運動／15B. Cell biology: Motility

3Pos094 リアルタイムフィードバックを用いた機械的刺激による心筋細胞集合体の拍動リズムの制御
Control of cardiac aggregate beat rhythm by mechanical stretch with real-time feedback
Kyotaro Kanazashi, Ayu Sasaki, Yuuta Moriyama, Toshiyuki Mitsui (*Aogoku Univ.Dept,of Phys*)

3Pos095 機械学習を用いた共培養下における線維芽細胞の動態予測
Prediction of fibroblast dynamics in co-culture using machine learning
Hiromu Kuwabara, Arata Nagai, Kaito Kojima, Ayu Sasaki, Kyotaro Kanazashi, Yuuta Moriyama, Toshiyuki Mitsui (*Aogaku Univ. Dept,of Phys.*)

3Pos096 細胞個体レベルでの大腸菌走化性応答の定量解析
Quantitative analysis of E. coli chemotactic response at individual cell level
Hiroto Tanaka, Yasuaki Kazuta, Erica Kobayashi, Hiroaki Kojima (*Frontier Research Lab, Adv ICT Res Inst, NICT*)

3Pos097 繊毛運動の温度による制御
Control of ciliary motility by temperature
Shunta Fueki, Megumi Yoshida, **Kenjiro Yoshimura** (*Col. Sys. Engineer. Sci., Shibaura Inst. Technol.*)

3Pos098 深層学習を用いて血管新生に関わる動的な自由度を抜き出す
Extracting dynamic degrees of freedom involved in angiogenesis using deep learning
Hiroshi Fujisaki[1], Kenta Odagiri[2], Hiromichi Suetani[3], Hiroya Takada[1], Rei Ogawa[1] ([1]*Nippon Medical School*, [2]*Senshu Univ.*, [3]*Oita Univ.*)

3Pos099 細菌の遊泳に対する菌体サイズの影響
Effect of the cell size on bacterial swimming
Riu Osanai (*Grad.Eng.,Univ.Tohoku*)

3Pos100 海洋細菌 Vibrio alginolyticus の集団運動における 1 細胞運動解析
Single cell dynamics in collective migration of Vibrio alginolyticus
Hiyori Tokumori, Ikuro Kawagishi, Masatoshi Nishikawa (*Dep. Frontier Bioscience, Hosei Univ.*)

3Pos101 Phosphatidylserine is an essential regulator of Ras excitability and cell motility
Satomi Matsuoka[1,2,3], Da Young Shin[2,3], Hyeyun Jung[2], Hiroaki Takagi[3,4], Michio Hiroshima[1,3], Masahiro Ueda[1,2,3] ([1]*Graduate School of Frontier Biosciences, Osaka University*, [2]*Graduate School of Science, Osaka University*, [3]*Center for Biosystems Dynamics Research, RIKEN*, [4]*School of Medicine, Nara Medical University*)

3Pos102 クラミドモナス後退遊泳固定株に前進遊泳を復帰させる変異
Chlamydomonas Move-Backwards-Only mutants restored forward swimming by a point mutation in the outer-arm dynein β heavy chain
Toshiki Yagi, Ai Sumiyoshi, Shogo Sawada (*Dept. of Life Sci., Prefectural Univ. Hiroshima*)

3Pos103 カルシウム感受性があるクラミドモナス鞭毛内部構造のラセン配置
The Calcium Sensitive Helical Arrangement of Axonemal Structures in Chlamydomonas Flagella
Hitoshi Sakakibara[1], Kenta Ishibashi[1], Hiroyuki Iwamoto[2], Hiroaki Kojima[1], Kazuhiro Oiwa[1,3] ([1]*BioICT., NICT*, [2]*SPring8, JASRI*, [3]*Life Sci., Univ. Hyogo*)

3Pos104 電子顕微鏡法によるスピロプラズマ遊泳運動をもたらす MreB4 と MreB5 の可視化
Visualization of MreB4 and MreB5 Filaments Driving *Spiroplasma* Swimming by Electron Microscopy
Haruka Yuasa[1], Yuya Sasajima[1], Hana Kiyama[1], Daichi Takahashi[1], Takuma Toyonaga[1,3], Tomoko Miyata[2], Fumiaki Makino[2], Keiichi Namba[2], Makoto Miyata[1,3] ([1]*Grad. Sch. Sci., Osaka Metropolitan Univ.*, [2]*Osaka Univ.*, [3]*OCARINA, Osaka Metropolitan Univ.*)

3Pos105 *Spiroplasma* swimming mechanism suggested by fluorescently labeled MreBs expressed in JCVI-syn3B
Yoshiki Tanaka[1], Hana Kiyama[1], Makoto Miyata[1,2] ([1]*Grad. Sch. Sci., Osaka Metro Univ*, [2]*OCARINA, Osaka Metro Univ*)

3Pos106 JCVI-syn3B における 2 つの MreB タンパク質による *Haloplasma* 運動能の再構築
Haloplasma Motility Reconstituted in JCVI-syn3B by Combination of Two MreB Proteins
Mone Mimura[1], Hana Kiyama[1], Shingo Kato[2], Yuya Sasajima[1], Atsuko Uenoyama[1], Shigeyuki Kakizawa[3], André Antunes[4], Tomoko Miyata[5], Fumiaki Makino[5], Keiichi Namba[5], Makoto Miyata[1,6] ([1]*Grad. Sch. Sci., Osaka Metropolitan Univ., Japan*, [2]*RIKEN BRC., JCM., Japan*, [3]*Bioproduction Res. Inst., AIST., Japan*, [4]*Macau Univ. of Sci. and Tech., China*, [5]*Osaka Univ., Japan*, [6]*OCARINA, Osaka Metropolitan Univ., Japan*)

3Pos107 光ピンセットによる外力印加に対する細胞境界の変形応答
Force-induced remodeling of cell contacts by two-point optical manipulation
Kenji Nishizawa[1], Shao-Zhen Lin[2], Claire Chardès[3], Jean-François Rupprecht[2], Pierre-François Lenne[3] ([1]*Graduate School of Science, The University of Tokyo.*, [2]*CNRS, Centre de Physique Théorique.*, [3]*CNRS, The Institute of Developmental Biology of Marseille.*)

3Pos108 水／水の相分離により生じる細胞サイズ液滴内での微小管ーキネシン複合体の自発的な対流生成
Microtubule-kinesin complexes spontaneously generate vortex flow in the cell-sized droplets created by water/water phase separation
Hiroki Sakuta[1,2], Naoki Nakatani[3], Takayuki Torisawa[4], Yutaka Sumino[5], Kanta Tsumoto[6], Kazuhiro Oiwa[7,8], Kenichi Yoshikawa[3,9] ([1]*UBI, Univ. Tokyo*, [2]*Grad. Sch. Arts Sci., Univ. Tokyo*, [3]*Facul. Life Med. Sci., Doshisha Univ.*, [4]*Cell Arch. Lab., Natl. Inst. Genet.*, [5]*Facul. Adv. Eng., Tokyo Univ. Sci.*, [6]*Grad. Sch. Eng., Mie Univ.*, [7]*Adv. ICT Res. Inst., NICT*, [8]*Grad. Sch. Sci., Univ. Hyogo*, [9]*Inst. Adv. Study, Kyoto Univ.*)

15D. 細胞生物学的課題：情報伝達・細胞膜／15D. Cell biology: Signal transduction & Cell membrane

3Pos109 環状心筋細胞ネットワークにおける 64 電極同時細胞外電位計測
Simultaneous 64-electrode extracellular potential measurement of circular cardiomyocyte networks
Akito Yoshikawa, Momo Akada, Masahito Hayashi, **Tomoyuki Kaneko** (*LaRC, Dept. Frontier Biosci., Hosei Univ.*)

3Pos110 デコンボリューション法を用いた大腸菌走化性受容体の三次元観察
Three-dimensional observation of *Escherichia coli* chemotaxis receptors using the deconvolution method
Yumiko Uchida, Yong-Suk Che, Akihiko Ishijima, Hajime Fukuoka (*Grad. Sch. Frontier Biosci. Osaka Univ.*)

3Pos111 Effects of mitochondrial administration on reduction of oxidative damage of cells
Sadab Sipar Ibban[1,2], Sayaka Doi[1], Yoshihiro Ohta[1] ([1]*Department of Biotechnology and Life Science, Graduate School of Engineering, Tokyo University of Agriculture and Technology*, [2]*Department of Pharmacy, International Islamic University Chittagong, Bangladesh*)

3Pos112 A method for measuring the maximal membrane extension of macrophages using the cylindrical inner surface of opsonized capillary tubes
Sota Suzuki[1], Dan Horonushi[1], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos113 Hydrostatic pressure stimuli increase intracellular calcium concentration
Masatoshi Morimatsu[1], Zidan Gao[2], Keiji Naruse[1] ([1]*Graduate School of Medicine,Dentistry and Pharmaceutical Sciences*, [2]*Graduate School of Medicine,Dentistry and Pharmaceutical Sciences*)

3Pos114 大腸菌センサーキナーゼ BaeS によるインドール感知機構
Indole-sensing mechanism of the sensor kinase BaeS of *Escherichia coli*
Hirotaka Tajima[1,2], Tomoka Iseri[2], Kennichiro Kashihara[3], Ikuro Kawagishi[1,2,3] ([1]*Res. Cen. for Micro-Nano Tech., Hosei Univ.*, [2]*Dept. Biosci., Hosei Univ.*, [3]*Grad. Sch. Sci. Eng., Hosei Univ.*)

3Pos115 高カルシウム濃度環境において増殖可能な細胞株の解析
Analysis of cell strains capable of proliferating in high Ca^{2+} concentration environment
Fumiya Shimizu[1], Yusuke V. Morimoto[2] ([1]*Grad. Sch. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*, [2]*Dept. Phys. and Info. Eng., Fac. Comp. Sci. and Sys. Eng., Kyushu Inst. Tech.*)

3Pos116 大腸菌走化性受容体による誘引応答シグナリングの光架橋解析
Photo-crosslinking analyses of attractant signaling via the chemoreceptor of *Escherichia coli*
Momoka Nakano[1], Hirotaka Tajima[2,3], Ikuro Kawagishi[1,2,3] ([1]*Grad. Sch. Sci., Univ. Hosei*, [2]*Dept. Biosci., Univ. Hosei*, [3]*Res. Cen. Micro-Nano Tech., Univ. Hosei*)

3Pos117 導電性を利用した微生物のエネルギー戦略
Electron conduction conserves energy in bacterial assemblages
Yoshihide Tokunou[1,2], Hiromasa Tongu[3], Masanori Toyofuku[1,4], Nobuhiko Nomura[1,4] ([1]*Faculty of Life and Environmental Sciences, University of Tsukuba.*, [2]*International Center for Materials Nanoarchitectonics, National Institute for Materials Science.*, [3]*Degree Programs in Life and Earth Sciences, University of Tsukuba.*, [4]*Microbiology Research Center for Sustainability, University of Tsukuba.*)

16A. 生体膜・人工膜：構造・物性／16A. Biological & Artificial membrane: Structure & Property

3Pos118 両親媒性ランダムコポリマーによる曲がった膜の認識
Recognition of curved membrane by amphiphilic random copolymers
Kazuma Yasuhara, Ryo Yamanaka, Jun-ichi Kikuchi (*Div. Mat. Sci., Nara Inst. Sci. Tech.*)

3Pos119 人工膜を用いた脂質膜表面における分子認識の研究
A biomimetic molecular recognition platform based on functionalized lipid bilayer membrane
Yuuri Miyata[1], Nanami Nagatsuka[2], Masato Koezuka[1], Fumio Hayashi[3], Kenichi Morigaki[1,4] ([1]*Grad. Sch. Agri., Kobe Univ*, [2]*Fac. Agri., Kobe Univ*, [3]*Grad. Sch. Sci., Kobe Univ*, [4]*Biosignal Research Center, Kobe Univ*)

3Pos120 脂質膜組成と高分子相分離の相関
Correlation between lipid membrane composition and macromolecular phase separation
Chiho Watanabe (*Grad. Sch. Int. Sci. Life, Hiroshima Univ.*)

3Pos121 The mammalian cell protective synergy of antimicrobial peptides LL-37 and HNP1
Ariane Melissa Schwitter[1,2], Kaori Sugihara[2] ([1]*Grad. Scho. Eng., The University of Tokyo, Tokyo*, [2]*Institute of Industrial Science, The University of Tokyo, Tokyo*)

3Pos122 脂質膜の長期的な水透過に対する膜特性の影響
Effect of membrane properties on long-term water permeation through lipid membranes
Natsuki Fukuda, Nozomi Watanabe, Yukihiro Okamoto, Hiroshi Umakoshi (*Graduate School of Engineering Science, Osaka University.*)

3Pos123 Global-TRES 法を用いたリポソーム膜特性の新規評価手法の開発
Multiplicity of Solvent Environments in Lipid Bilayer Systems Revealed by Comparative Global-TRES of Twin Probes: Laurdan and Prodan
Natsuumi Ito, Nozomi Watanabe, Yukihiro Okamoto, Hiroshi Umakoshi (*Bio-Inspired Chemical Engineering Laboratory / Division of Chemical Engineering / Graduate School of Engineering Science / Osaka University*)

16B. 生体膜・人工膜：ダイナミクス／16B. Biological & Artificial membrane: Dynamics

3Pos124 クロモグリク酸ナトリウム封入リポソームにおける形状変化と膜の相分離
Shape change and membrane phase separation on disodium cromoglycate-encapsulated liposomes
Kaori Udagawa, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. Sci.&Eng., Hosei Univ.*)

3Pos125 体外式膜型人工肺の新規中空糸膜細孔構造モデルにおける水分子と酸素分子の透過シミュレーションの検討
Simulation study of Water and Oxygen Molecule's Permeations in the partial model of a Novel Hollow Fiber Membrane Pore Structure in ECMO
Takahiro Chujo[1], Yoshitaka Tadokoro[1], Makoto Fukuda[1,2], Naoyuki Miyashita[1,2] ([1]*Grad. Sch. BOST, KINDAI Univ.*, [2]*BOST., KINDAI Univ.*)

3Pos126 相分離した三成分系ベシクルにおける膜粘度の温度依存性
Viscosity Landscape of Phase-Separated Ternary Vesicles in Composition-Temperature Space
Julia Tanaka, Kenya Haga, Masayuki Imai, Yuka Sakuma (*Grad. Sch. Sci., Tohoku Univ.*)

3Pos127 一定張力による脂質膜中のポア形成やプリポアの縁の線張力に対する単分子膜自発曲率の効果
Effect of monolayer spontaneous curvature on constant tension-induced pore formation and the line tension of a pre-pore in lipid bilayers
Kanta Tazawa[1], **Masahito Yamazaki**[1,2,3] ([1]*Grad. Sch. Sci., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ*, [3]*Grad. Sch. Sci. Tech., Shizuoka Univ*)

3Pos128 抗菌ペプチド・PGLa のポア形成に対する膜張力と単分子膜自発曲率の効果
Effect of membrane tension and monolayer spontaneous curvature on antimicrobial peptide PGLa-induced pore formation
Marzuk Ahmed[1], Md. Zahidul Islam[2], Masahito Yamazaki[1,2,3] ([1]*Grad. Sch. Sci. Tech., Shizuoka Univ.*, [2]*Res. Inst. Ele., Shizuoka Univ.*, [3]*Grad. Sch. Sci., Shizuoka Univ.*)

3Pos129 光ピンセットを用いた人工脂質膜ドメイン操作
Manipulation of lipid membrane domains in artificial membrane by optical tweezers
Yasushi Tanimoto, Shunya Moriyama, Kyoko Masui, Chie Hosokawa (*Grad. Sch. Sci., OMU*)

3Pos130 ポリマー脂質膜のチャネルにおける脂質膜の自発展開
Self-spreading lipid bilayers in preformed polymeric lipid bilayer channels
Masako Fujii[1], Kenichi Morigaki[1,2] ([1]*Grad. Sch. Agri., Univ. Kobe*, [2]*Biosignal Research Center, Univ. Kobe*)

16C. 生体膜・人工膜：興奮・チャネル／16C. Biological & Artificial membrane: Excitation & Channels

3Pos131 **細菌機械受容チャネル MscL のメカノゲーティング調節における細胞外ループの役割に関する解析**
Analysis on the role of the periplasmic loop in the regulation of Mechano-Gating in the Bacterial Mechanosensitive Channel MscL
Yasuyuki Sawada[1], Masahiro Sokabe[2], Hisashi Kawasaki[3] ([1]*Institute of Materials Innovation, Institutes of Innovation for Future Society, Nagoya University*, [2]*Human Information Systems Labs, Kanazawa Institute of Technology*, [3]*Agro-Biotechnology Research Center, University of Tokyo*)

3Pos132 Importance of Spatial Arrangement Shape of Cardiomyocyte Network for Precise and Stable On-Chip Predictive Cardiotoxicity Measurement
Nanami Abe, Kazufumi Sakamoto, Hideki Matsumoto, Mitsuru Sentoku, Kenji Yasuda (*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng, Waseda Univ., Japan*)

3Pos133 **原核生物由来ナトリウムチャネルを用いた分子動力学計算**
Molecular dynamics simulation with prokaryotic sodium channels
Katsumasa Irie (*Pharm. Sci., Wakayama Med. Univ.*)

3Pos134 **簡便な単一チャネル電流計測システムの開発**
Development of a simple single-channel current measurement system
Tomomi Murata[1], **Toru Ide**[1,2], Minako Hirano[1], Mami Asakura[2] ([1]*Grad. Sch. Health Sys., Okayama Univ.*, [2]*Dept. Engn., Okayama Univ.*)

3Pos135 **アガロースゲルビーズを用いたチャネル電流測定装置の開発**
Development of channel current measurement device using agarose gel beads
Mami Asakura[1], Shuyan Wang[2], Minako Hirano[2], Toru Ide[2] ([1]*Dept. of Comp. Tech. Soln., Okayama Univ.*, [2]*Grad. Sch. Health Sys., Okayama Univ.*)

3Pos136 **細胞排出イオンの測定によるがん浸潤関連塩化物イオンチャネル Clic1 の機能解析**
Functional analysis of the cancer invasion-associated chloride ion channel Clic1 by measuring cell efflux ions
Ayana Yamagishi[1,2], Akane Nagata[2], Koki Uchiyama[2], Tsukuru Minamiki[3], Toshihiro Takeshita[4], Chikashi Nakamura[1,2] ([1]*Cell. Mol. Biotech. Res. Inst., AIST*, [2]*Grad. Sch. Eng., Tokyo Univ. Agric. Technol.*, [3]*Health Med. Res. Inst., AIST*, [4]*Sens. Sys. Res. Cent., AIST*)

3Pos137 **TRAAK チャネルの特徴的なフリッカーゲーティングは内葉張力によって制御されている**
The inner leaflet tension regulates the characteristic flicker gating of the single TRAAK channel
Takahisa Maki[1], Yuka Matsuki[2], Toshiyuki Yoshida[3], Shigetoshi Oiki[4], **Masayuki Iwamoto**[1] ([1]*Dept. Mol. Neurosci., Univ. Fukui. Facul. Med. Sci.*, [2]*Dept. Anesth. Reanimatol., Univ. Fukui. Facul. Med. Sci.*, [3]*Dept. Info. Sci., Univ. Fukui. Facul. Eng.*, [4]*Biomed. Imaging Res. Cent., Univ. Fukui*)

19. 神経回路・脳の情報処理／19. Neuronal circuit & Information processing

3Pos138 **集光フェムト秒レーザーの高頻度照射により誘発された神経活動の時空間パターン**
Spatio-temporal patterns of neuronal activity induced by high-frequency irradiation with a focused femtosecond laser
Kan Otani[1], Yumi Segawa[1], Wataru Minoshima[1,2], Kyoko Masui[1], Chie Hosokawa[1] ([1]*Grad.Sch.Sci.,osaka Metro.Univ./Osaka City Univ*, [2]*NICT*)

3Pos139 **赤外線レーザーによる神経回路の刺激**
Stimulation of neural network by infrared laser
Rika Fuchikami, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, FB, Grad. Sch. SCi. & Eng., Hosei Univ.*)

3Pos140 **線虫の全脳活動データに対する機能的神経クラスタ推定**
Estimation of functional neuron ensembles for whole-brain activity data in *C. elegans*
Harutaka Takeshita, Shun Kimura, Koujin Takeda, Yuishi Iwasaki (*Grad. Sch. Sci. Eng., Ibaraki Univ.*)

3Pos141 低酸素密閉空間における 1 細胞レベルでの神経細胞培養に最適な細胞濃度の検証
Optimal Cell Concentration for Culturing Neuronal Cells at Single Cell Level in Hypoxic Sealed Space
Ayuri Sakaguchi, Masahito Hayashi, Tomoyuki Kaneko (*LaRC, Dept. Frontier Biosci., Hosei Univ.*)

3Pos142 スパース制約を課した新たな ICA とタスク付き fMRI データ解析への応用
A novel ICA with sparse constraint and application to task-related fMRI data analysis
Yusuke Endo, Koujin Takeda (*Grad. Sch. Eng., Univ. Ibaraki*)

3Pos143 神経細胞-微小電極接合部の分子特異的形成に向けた小型人工シナプスオーガナイザーの分子設計
Molecular design of compact engineered synapse organizer toward molecule-specific formation of neuron-microelectrode junctions
Kosuke Sekine[1], Sam Young Kim[1], Sm Ahasanul Hamid[1], Mieko Imayasu[1], Tomoyuki Yoshida[2], Hidekazu Tsutsui[1] ([1]*School of Material Science,Japan Advanced Institute of Science and Technology.Ishikawa*, [2]*Department of Molecular Nuroscience, faculty of mecdicine,University of Toyama*)

3Pos144 哺乳類および鳥類の一次ニューロンにおけるペプチドタグを介した人工シナプスオーガナイザーのシナプス形成活性
Peptide-tag mediated synaptogenic activity of engineered synapse organizer in mammalian and avian primary neurons
Wataru Haga[1], Sm. Ahasanul Hamid[1], Sam Young Kim[1], Mieko Imayasu[1], Tomoyuki Yoshida[2] ([1]*School of Materials Science, Japan Advanced Institute of Science and Technology. Ishikawa*, [2]*Department of Molecular Neuroscience, Faculty of Medicine, University of Toyama*)

3Pos145 海馬が合成する男性・女性ホルモンやストレスホルモンは記憶シナプスを蛋白キナーゼ信号系で制御する
Kinase-dependent modulation of neuronal synapses by hippocampus-synthesized androgen, estrogen and stress hormone
Suguru Kawato[1,2], Mika Soma[1,2], Mari Ogiue-Ikeda[1,2], Saira Mabashi[2], Minoru Saito[2] ([1]*Dep. Urology, Grad. Sch. Medicine, Juntendo Univ.*, [2]*Dep. Bioscience, Nihon Univ.*)

3Pos146 ミミズ古典的条件づけの分子メカニズム
Molecular mechanisms of classical conditioning in earthworm, *Eisenia fetida*
Sukehiro Kabayama[1], Yoshiichiro Kitamura[2] ([1]*Appl Matl Life Sci, Grad Sch Eng, Kanto Gakuin Univ*, [2]*Dept Math Sci Phys, Col Sci Eng, Kanto Gakuin Univ*)

3Pos147 長距離に情報伝達する神経ネットワークは脳表面の最短経路に配線される --- ヒト胎児脳の形の数理解析
Geodesic theory of long association fibers arrangement in the human fetal cortex
Kazuya Horibe[2,3], Gentaro Taga[4], **Koichi Fujimoto**[1,2] ([1]*Math. Life Sci., Horoshima Univ.*, [2]*Biol. Sci., Osaka Univ.*, [3]*Grad. Sci. Eng., Osaka Univ.*, [4]*Grad. Sci. Edu., Univ. Tokyo*)

3Pos148 Axonal differentiation of embryonic hippocampal neurons is governed by the length of neurite outgrowth rather than growth order
Ryohei Yamazaki[1], Nanami Abe[1], Soya Hagiwara[2], Naoya Takada[2], Kenji Yasuda[1,2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos149 味覚嫌悪学習後に見られる GABA 応答変化の濃度依存性
Dose-dependence of GABA response in the nervous system after conditioned taste aversion training
Yoshimasa Komatsuzaki[1], Samui Chiba[2], Ayaka Itoh[3], Minoru Saito[3] ([1]*Dept. Phys., CST, Nihon Univ.*, [2]*Grad. Sch. of Sci. and Tech., Nihon Univ.*, [3]*Grad. Sch. of Integ. Bas. Sci., Nihon Univ.*)

3Pos150 SynGAP LLPS condensates recruit PSD95 and receptor oligomers, serving as a basic platform for generating neuronal excitatory synapses
Saahil Acharya[1], Taka-aki Tsunoyama[1], Christian Hoffmann[2], Gerard Aguilar[2], Irina Meshcheryakova[1], Yuri L. Nemoto[1], Aya Nakamura-Norimoto[1], Takahiro Fujiwara[3], Dragomir Milovanovic[2], Akihiro Kusumi[1] ([1]*Okinawa Institute of Science and Technology Graduate University (OIST), Okinawa, Japan*, [2]*German Centre for Neurodegenerative Diseases (DZNE), Berlin, Germany*, [3]*Institute for Integrated Cell-Material Sciences (WPI-iCeMS), Kyoto University, Kyoto, Japan*)

21A. 光生物：視覚・光受容／21A. Photobiology: Vision & Photoreception

3Pos151 光活性化型アデニル酸シクラーゼの ATP 依存的な液ー液相分離
ATP-dependent liquid-liquid phase separation of photoactivated adenylate cyclase
Yusuke Nakasone[1], Kazuhiro Sakamaki[2], Masahide Terazima[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Grad. Sch. Biostudies., Univ. Kyoto*)

3Pos152 QM/MM RWFE-SCF 法を用いたアニオンポンプロドプシン *Np*HR のイオン輸送過程に関する理論的研究
Theoretical study on ion transport process of anion pump rhodopsin *Np*HR using QM/MM RWFE-SCF method
Tomo Ejiri, Ryo Oyama, Shigehiko Hayashi (*Grad. Sch. Sci., Univ. Kyoto*)

3Pos153 光センサー RsPYP と下流分子 RsPBP の光可逆的な相互作用ダイナミクス
Photo-reversible intermolecular interaction dynamics between light sensor protein RsPYP and its downstream protein RsPBP
Mizuki Hirata[1], Yusuke Nakasone[1], Suhyang Kim[2], Masahide Terazima[1] ([1]*Grad. Sch. Sci., Univ. Kyoto*, [2]*Grad. Sch. Arts and Sci., Univ. Tokyo*)

3Pos154 光合成集光タンパク質の高温高圧抽出におけるフィコビオロビンからフィコシアノビリンへの変換
Conversion of phycoviolobilin to phycocyanobilin during pressurized liquid extraction of cyanobacterial photosynthetic antenna protein
Takaaki Matsushita, Yuya Fujita, Takanari Kamo, Toshihiko Eki, Yuu Hirose (*Toyohashi Univ. of Tech. Dep. of Eng.*)

3Pos155 同位体標識色素を用いたシアノバクテリオクロム型光受容体 RcaE の光感知機構の解析
Analysis of photosensing mechanism of the cyanobacteriochrome RcaE using isotope-labeled bilin chromophore
Yuya Fujita[1], Takanari Kamo[1], Takaaki Matsushita[1], Masako Hamada[1], Tatsuya Tsuchida[2], Takayuki Nagae[3], Toshihiko Eki[1], Masaki Mishima[3], Yutaka Ukaji[2], Yuu Hirose[1] ([1]*Toyohashi Univ. of Tech. Dep. of Eng.*, [2]*Kanazawa Univ. Coll. of Sci. and Eng.*, [3]*Tokyo Univ. of Phar. and Life Sci.*)

3Pos156 光センサータンパク質 OCP とその制御タンパク質 FRP の光依存的な相互作用ダイナミクス
Time-resolved study on intermolecular interaction dynamics between orange carotenoid protein and fluorescence recovery protein
Tadayuki Tokashiki[1], Takatoshi Ohata[1], Syunrou Tokonami[2], Yusuke Nakasone[1], Masahide Terazima[1] ([1]*Grad. Sch. Sci., Kyoto Univ.*, [2]*Grad. Sch. Sci., Gakushuin Univ.*)

3Pos157 ヘリオロドプシンのプロトン移動に伴う水素結合ネットワーク上の構造変化
Proton transfer and conformational changes along the hydrogen bond network in heliorhodopsin
Masaki Tsujimura[1], Yoshihiro Chiba[1], Keisuke Saito[1,2], Hiroshi Ishikita[1,2] ([1]*Grad. Sch. Eng., UTokyo*, [2]*RCAST, UTokyo*)

3Pos158 長い光サイクルをもつアクチノバクテリア由来の新規外向き H^+ポンプロドプシン
Actinobacteria-derived novel outward proton-pumping rhodopsins having long photocycle
Shota Takahashi[1], Mako Ueno[1], Fumio Hayashi[2], Takashi Kikukawa[3], Ichiro Kasano[1], Yusuke Inoue[1], Masashi Sonoyama[1,4,5] ([1]*Grad. Sch. Sci. Tech., Gunma Univ.*, [2]*Ctr. Inst. Analysis, Gunma Univ.*, [3]*Fac. Adv. Life. Sci., Hokkaido Univ.*, [4]*GIAR, Gunma Univ.*, [5]*GUCFW,Gunma Univ.*)

3Pos159 ロドプシン-ベストロフィン巨大イオンチャネル複合体の光誘起構造変化の研究
Light-induced structural changes of a rhodopsin-bestrophin giant ion channel complex studied by infrared spectroscopy
Natsuki Honda[1], Rei Yoshizumi[1], Hideki Kandori[1,2], Yuji Furutani[1,2] ([1]*Grad. Sch. Eng., Tech. Nagoya*, [2]*OptoBiotechnology Research Center., Tech. Nagoya*)

3Pos160 レチナール発色団を結合するリジン 255 の共有結合は KR2 のナトリウムポンプ機能に必須である
Covalent binding at Lys-255 residue connecting the retinal chromophore is essential for a sodium pump function of Krokinobacter Rhodopsin2
Yuki Ichikawa[1], Shoha Ochiai[1], Sahoko Tomida[1], Yuji Furutani[1,2] ([1]*Department of Engineering, Nagoya Institute of Technology, Japan*, [2]*OptoBioTechnology Research Center, Nagoya Institute of Technology, Japan*)

3Pos161 固体 NMR を用いたシゾロドプシンのレチナールと Cys75 の立体相互作用の解析
Steric interaction of Cys75 with retinal in schizorhodopsin using solid-state NMR
Akito Kitaguchi[1], Takashi Okitsu[2], Hideki Kandori[3], Keiichi Inoue[4], Izuru Kawamura[1] ([1]*Graduate School of Engineering Science, Yokohama National University, Japan*, [2]*Faculty of Pharmaceutical Sciences, University of Toyama, Japan*, [3]*Department of Life Science and Applied Chemistry, Nagoya Institute of Technology, Japan*, [4]*The Institute for Solid State Physics, The University of Tokyo, Japan*)

3Pos162 近赤外光吸収ロドプシンの特異な光化学反応
Unique photochemical reactions in near-infrared light absorbing rhodopsins
Masahiro Sugiura[1], Ritsu Mizutori[1], Kazuki Ishikawa[1], Kota Katayama[1,2], Yuji Sumii[1], Rei Abe-Yoshizumi[1], Satoshi Tsunoda[1,2], Yuji Furutani[1,2], Norio Shibata[1], Leonid S. Brown[3], Hideki Kandori[1,2] ([1]*Dept. Life Sci. & App. Chem, Nagoya Inst. Tech.*, [2]*OptoBioTechnology Research Center*, [3]*Dept. of Phys. Univ. of Guelph*)

21C. 光生物：光遺伝学・光制御／21C. Photobiology: Optogenetics & Optical Control

3Pos163 可視光でオン・オフできる Gs 共役型光遺伝学ツールの開発
Development of a Gs-coupled optogenetic tool that can be turned on and off by visible light
Akinari Sakayori[1], Yusuke Sakai[2], Naoyuki Taira[1], Yusei Sakata[1], Mitsumasa Koyanagi[2], Akihisa Terakita[2], Saori Tani-Matsuhana[1], Kunio Inoue[1], Hisao Tsukamoto[1] ([1]*Grad. Sch. Sci., Kobe Univ.*, [2]*Grad. Sch. Sci., Osaka Metropolitan Uni.*)

3Pos164 無脊椎動物由来の Gi/o 共役型可視光受容タンパク質の分子特性
Molecular characteristics of an invertebrate Gi/o-coupled and visible light-sensitive opsin
Sachiko Fukuzawa, Hisao Tsukamoto (*Grad. Sch. Sci., Kobe Univ.*)

3Pos165 光ジッパー融合タンパク質の光依存的な Lac オペレーター配列への結合
A light-dependent binding of the lacI-Photozipper fusion protein to the lac operator sequence
Osamu Hisatomi, Nagomi Matsumoto (*Grad. Sch. Sci., Osaka Univ.*)

3Pos166 大腸菌に対する青色光の光毒性
Phototoxicity of blue light to *E. coli* cells
Nagomi Matsumoto, Osamu Hisatomi (*Grad. Sch. Sci., Osaka Univ.*)

3Pos167 ユレモ由来の光活性化アデニル酸シクラーゼの活性に影響を与える重要なアミノ酸の同定
Identification of Key Amino Acids affecting the Activity of Photoactivated Adenylyl Cyclase from *Oscillatoria acuminata*
Minako Hirano[1], Masumi Takebe[2], Syunshi Yano[1], Hinase Kondo[1], Ayu Yuasa[1], Toru Ide[1] ([1]*Grad Schl Interdiscip Sci Engn Health Syst, Okayama Univ.*, [2]*Hamamatsu Photonics K.K.*)

3Pos168 近赤外線レーザーによる分散培養心筋細胞シートに対する光ペーシング
Optical pacing in cardiomyocytes by near-infrared laser
Takaaki Nishikawa[1], Yasumasa Furuie[1], Kentaro Kito[2], Masahito Hayashi[2], Tomoyuki Kaneko[2] ([1]*LaRC, Dept. Frontier Biosci, Hosei Univ.*, [2]*LaRC, FB, Grad. Sch.Sci&Eng, Hosei Univ.*)

3Pos169 光駆動内向きプロトンポンプのツール開発
Tool development for the light-driven inward-proton pumps
Rei Abe-Yoshizumi[1], Shinji Matsuda[2], Wataru Kakegawa[3], Takao Imai[2], Itaru Arai[3], Satoshi Tsunoda[1], Michisuke Yuzaki[3], Hideki Kandori[1,4] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech.*, [2]*Grad. Sch. Inform. and Eng., UEC*, [3]*Dept. Physiol., Keio Univ. Sch. Med.*, [4]*OptoBio., Nagoya Inst. Tech.*)

3Pos170 Photoregulation of Small GTPase Ras using Photoresponsive Protein
Nobuyuki Nishibe[1], Zhang Ziyun[1], Kazunori Kondo[2], Shinsaku Maruta[1,2] ([1]*Department of Bioinformatics, Soka University Graduate School of Engineering*, [2]*Department of Science and Engineering for Sustainable Innovation, Faculty of Science and Engineering, Soka University*)

3Pos171 光センサータンパク質 eBLUF の選択的ダイマー化を利用した光操作ツールの開発
Opto-control of protein activity utilizing selective dimerization of light sensor eBLUF
Takafumi Kuno[1], Yusuke Nakasone[1], Kazuhiro Sakamaki[2], Masahide Terazima[1] ([1]*Grad.Sci.,Univ.Kyoto*, [2]*Grad.Bio.,Univ.Kyoto*)

3Pos172 バクテリオロドプシンの酸性青色状態の分光学的解析
Spectroscopic analysis of the acid blue form of bacteriorhodopsin
Tsutomu Kouyama, Kunio Ihara (*Nagoya Yniversity*)

3Pos173 アニオンチャネルロドプシン GtACR1 における細胞内ドメインによるイオンチャネル機能の制御
The cytoplasmic domain regulates the photocurrent lifetime of anion channelrhodopsin GtACR1
Hana Maruyama[1], Shoko Hososhima[1], Satoshi Tsunoda[1,2], Yuya Ohki[3], Takashi Kikukawa[3,4], Takashi Tsukamoto[3,4], Hideki Kandori[1,2] ([1]*Grad. Sch. Eng., Nagoya Inst. Tech*, [2]*Opto Bio Technology Research Center*, [3]*Grad. Sch. Life Sci., Univ. Hokkaido*, [4]*Grad. Sch. Faculty of Advanced Life Sci., Univ. Hokkaido*)

3Pos174 光遺伝学を用いた p53 シグナル伝達経路の操作法開発
Optogenetic control of p53 signaling pathway
Tatsuki Tsuruoka[1,2,3], Yuhei Goto[1,2,3], Kazuhiro Aoki[1,2,3] ([1]*Quantitative Biology Research Group, Exploratory Research Center on Life and Living Systems (ExCELLS), National Institutes of Natural Sciences*, [2]*Division of Quantitative Biology, National Institute for Basic Biology*, [3]*Department of Basic Biology, School of Life Science, SOKENDAI (The Graduate University for Advanced Studies)*)

26A. 計算生物学: 生命情報学／26A. Computational biology: Bioinformatics

3Pos175 深層学習および SVM を用いた GPCRーG タンパク質結合選択性予測プログラムの開発
Development of Program for Predicting GPCR - G protein Coupling Selectivity, Using Deep Learning and SVM
Kento Fujishima[1], Kenji Etchuya[1], Hiroshi Arai[2], Ikuo Masuho[3,4], Makiko Suwa[1,2] ([1]*Chem. Biol. Sci., Sci. Eng., Aoyama Gakuin Univ.*, [2]*Biol. Sci., Grad. Sci. Eng., Aoyama Gakuin Univ.*, [3]*Pediatrics & Rare Dis. Group, Sanford Res.*, [4]*Dept. of Pediatrics, Sanford Sch. of Med., Univ. of South Dakota*)

3Pos176 乳がん患者ごとの最適な治療法の予測のための乳がん細胞モデルのシミュレーション
Simulation of breast cancer cell models for predicting optimal treatment strategies for individual breast cancer patients
Shogo Sonoyama, Takanori Sasaki (*Grad.Sch.Adv.Math.Sci.,Meiji Univ.*)

3Pos177 Metainference method applied on Hi-C data to study heterogeneous chromatin conformations and their dynamics
Chenyang Gu, Shoji Takada, Giovanni Brandani (*Grad. Sch. Sci., Univ. Kyoto*)

3Pos178 頻出する ψ ループモチーフと稀に確認される ψ ループモチーフを区別する構造ルールの解析
Analysis of structural rules that distinguish frequently and rarely occurring psi-loop motif
Tomoki C. Terada, Takumi Nishina, George Chikenji (*Dept of Appl. Phys., Grad. Sch. of Eng., Nagoya Univ.*)

3Pos179 生体膜上で相互作用する GPCR ペアの特徴
Characteristics of the interacting GPCR pairs on biological membrane
Wataru Nemoto[1,2], Yuki Ishioka[1], Kyokuhou Sya[1], Aoi Fukushima[2] ([1]*Dept. Sci. & Eng., Tokyo Denki Univ.*, [2]*Grad. Sch. Sci. & Eng., Tokyo Denki Univ.*)

3Pos180 GPCR ヘテロダイマー結合リガンドの特徴解析
Computational analysis of ligands to GPCR heterodimer
Ryota Takishima[1], Tatsuki Okamoto[2], Kurumi Tsuda[2], Wataru Nemoto[1,2] ([1]*Grad. Sch. Sci. & Eng, Tokyo Denki Univ.*, [2]*Dept. Sci. & Eng, Tokyo Denki Univ.*)

3Pos181 膜タンパク質間相互作用ペア予測
Membrane protein interaction pair prediction
Takuma Gunji[1], Gota Saito[1], Aoi Fukushima[1,2], Wataru Nemoto[1,2] ([1]*Dept. Sci. & Eng., Tokyo Denki Univ.*, [2]*Grad. Sch. Sci. & Eng., Tokyo Denki Univ.*)

3Pos182 GPCR 間相互作用予測器の開発と応用
Development and application of GPCR-GPCR interaction pairs predictor
Aoi Fukushima[1], Gouta Saito[2], Hiroaki Teruse[3], Sakie Shimamura[1], Hiroyuki Toh[3], Wataru Nemoto[1,2] ([1]*Dept. Sci. & Eng., Tokyo Denki Univ.*, [2]*Grad. Sci. & Eng., Tokyo Denki Univ.*, [3]*Dept. Sci. & Tech., Kwanseigakuin Univ.*)

3Pos183 Machine learning-based quantification of nuclear behavior to understand chiral properties of multicellular epithelial colonies
Ryohei Nishizawa[1,2], Tomoki Ishibashi[1], Goshi Ogita[1], Tatsuo Shibata[1] ([1]*BDR, RIKEN*, [2]*Grad. FBS., Univ. Osaka*)

3Pos184 言語モデルを使った液-液相分離 client タンパク質の予測
Language Model-Based Prediction of LLPS Client Proteins
Kazuki Miyata[1], Wataru Iwasaki[1,2,3,4,5] ([1]*Graduate School of Science, the University of Tokyo*, [2]*Graduate School of Frontier Sciences, the University of Tokyo*, [3]*Atmosphere and Ocean Research Institute, the University of Tokyo*, [4]*Institute for Quantitative Biosciences, the University of Tokyo*, [5]*Collaborative Research Institute for Innovative Microbiology, the University of Tokyo*)

26B. 計算生物学: 分子シミュレーション／26B. Computational biology: Molecular simulation

3Pos185 PI3K SH2 ドメインの基質結合と構造ダイナミクスの gREST シミュレーション
Substrate binding-coupled conformational dynamics of PI3K SH2 domain revealed by gREST simulation
Suyong Re[1], Kenji Mizuguchi[1,2] ([1]*NIBIOHN*, [2]*IPR, Osaka Univ.*)

3Pos186 粗視化分子動力学シミュレーションを用いた多成分脂質二重膜における膜貫通タンパク質パーティショニング
Transmembrane protein partitioning in multicomponent lipid bilayers using coarse-grained molecular dynamics simulations
Diego Ugarte[1], Yuji Sugita[1,2,3] ([1]*Computational Biophysics Research Team, RIKEN Center for Computational Science*, [2]*Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research*, [3]*Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research*)

3Pos187 α チューブリンおよび KRas4B の天然変性領域における遊離状態と結合状態に関する分子動力学シミュレーション解析
Molecular dynamics simulation for the isolated and complex states of the intrinsically disordered regions in α-tubulin and KRas4B
Masato Morikawa[1], Kazuki Kawada[2], Taimu Maeda[2], Koji Umezawa[1,2,3] ([1]*Grad. Sch. Of Sci. & Tech., Shinshu Univ*, [2]*Agri., Shinshu Univ*, [3]*IBS., Shinshu Univ*)

3Pos188 Binding Pathway of Hydroxycarboxylic acid receptor 2 (HCAR2) — Niacin Explored by Tree-Search Molecular Dynamics (TS-MD)
Yukina Nakai[1], Toru Ekimoto[1], Tsutomu Yamane[2], Kei Terayama[1], Sam-Yong Park[1], Mitsunori Ikeguchi[1,2] ([1]*Dept. of Med. Life Sci., Yokohama City Univ.*, [2]*R-CCS, Riken*)

3Pos189 主成分分析の逆変換を用いた構造生成によるタンパク質構造のサンプリング
Enhanced conformational sampling based on structural generation by the inverse transformation using principal component analysis
Rikuri Morita, Yasuteru Shigeta, Ryuhei Harada (*CCS, Univ. Tsukuba*)

3Pos190 単一アミノ酸ポテンシャル力場 SAAP を用いたアミロイド形成ペプチドの分子シミュレーション
Molecular simulation of amyloid-forming peptides using the Single Amino Acid Potential (SAAP)
Sayako Misawa[1,2], Taku Shimosato[3], Michio Iwaoka[1,2,3] ([1]*Graduate School of Science and Technology, Tokai University*, [2]*Institute of Advanced Biosciences, Tokai University*, [3]*Department of Chemistry, School of Science, Tokai University*)

3Pos191 変異型タンパク質複合体の結合自由エネルギー計算
Binding free energy calculation for mutated protein complex system
Kazutomo Kawaguchi, Hidemi Nagao (*Inst. Sci. Eng., Kanazawa Univ.*)

3Pos192 Development of GENESIS CGDYN for large-scale coarse-grained MD simulation of heterogeneous biomolecule systems
Jaewoon Jung[1,2], Cheng Tan[1], Yuji Sugita[1,2,3] ([1]*RIKEN R-CCS*, [2]*RIKEN CPR*, [3]*RIKEN BDR*)

3Pos193 光合成反応中心ー光捕集アンテナ超分子複合体におけるユビキノン／ユビキノール移動経路の解明
Ubiquinone/ubiquinol exchange pathway in the photosynthetic RC–LH1 supercomplex
Yosuke Teshirogi[1], Yoshitaka Moriwaki[1], Kentaro Shimizu[2], Tohru Terada[1] ([1]*Dept. of Biotechnol., Grad. Sch. of Agri and Life Science., The Univ. of Tokyo*, [2]*Agricultural Bioinformatics Research Unit, Grad. Sch. of Agri and Life Science., The Univ. of Tokyo*)

3Pos194 Semi-automated derivation of SPICA force field parameters for glycosaminoglycans (GAGs)
Grzegorz Lazarski[1,3], Yusuke Miyazaki[2], Ryo Urano[2], Mariusz Kępczyński[3], Wataru Shinoda[2] ([1]*Grad. Sch. of Natural Science and Technology, Okayama University*, [2]*Okayama University*, [3]*Doc. Sch. of Exact and Natural Sciences, Jagiellonian University*)

3Pos195 植物のチラコイド膜の曲率に対する脂質の種類と比率の依存性に関する理論的研究
Theoretical study of the dependence of different lipid types and ratios on the curvature of plant thylakoid membranes
Kaichi Kokubo, Ryuta Imayoshi, Tatsuhiro Kawashima, Kazutomo Kawagutchi, Hidemi Nagao (*Grad. Sch. Nat. Sci. Tech., Univ. Kanazawa*)

3Pos196 長時間分子動力学シミュレーションによる植物型フェレドキシンの構造や運動状態に関する計算化学的研究
Computational analysis of the structure and motion of the plant-type ferredoxin using long-time molecular dynamics simulations
Tomoki Nakayoshi[1], Yusuke Ohnishi[2], Hideaki Tanaka[2], Genji Kurisu[2], Yu Takano[1] ([1]*Grad. Sch. Inf. Sci., Hiroshima City Univ.*, [2]*Inst. Protein Res., Osaka Univ.*)

3Pos197 抗肺炎球菌薬開発に向けた FtsXECL1 の D&C-MD シミュレーションと自由エネルギー解析
D&C-MD Simulation and Free Energy Analysis of FtsXECL1 toward an Anti-pneumococcus Drug Development
Hiromitsu Shimoyama (*Noguchi Institute*)

3Pos198 The Spike protein Conformational Shift in the Omicron Variant of SARS-CoV-2
Hisham Dokainish[1,2], Yuji Sugita[3,4,5], Katsumi Maenaka[1,2] ([1]*Faculty of Pharmaceutical Sciences, Hokkaido University*, [2]*Hokkaido University Institute for Vaccine Research & Development*, [3]*Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research, Wako, Japan*, [4]*Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, Kobe, Japan*, [5]*Center for Drug Design Research, National Institutes of Biomedical Innovation*)

3Pos199 GPU を用いた粗視化分子動力学シミュレータの開発と大規模系への適用
Development of GPU-accelerated coarse-grained molecular dynamics simulator and application to large-scale systems
Yutaka Murata, Shoji Takada (*Dept. Biophysics, Div. Biology Grad. Sch. of Science, Kyoto University, Takada Lab*)

3Pos200 SPICA 力場を用いた粗視化分子動力学シミュレーションによる脂質ナノ粒子の研究
Coarse-grained molecular dynamics simulation of lipid nanoparticles using the SPICA force field
Yusuke Miyazaki, Wataru Shinoda (*RIIS, Okayama Univ.*)

3Pos201 弾性エネルギーを用いた混合正規分布分子の基準振動解析
Normal mode analysis of Gaussian mixture molecule using spring and strain energy
Takeshi Kawabata, Kengo Kinoshita (*Grad.Sch.Info.Sci., Tohoku Univ.*)

3Pos202 新生ペプチド鎖のリボソームトンネルにおける 2 次構造形成に関する計算科学的研究
The computational study on the secondary structure formation of nascent peptides inside the ribosome tunnel
Takunori Yasuda[1], Rikuri Morita[2], Yasuteru Shigeta[2], Ryuhei Harada[2] ([1]*Doctoral Program in Biology, University of Tsukuba*, [2]*Center for Computational Sciences, University of Tsukuba*)

3Pos203 光活性化アデニル酸シクラーゼ OaPAC のシグナル伝達機構の分子シミュレーションによる解析
Analysis of signal transmission mechanism of photoactivated adenylate cyclase OaPAC by molecular simulation
Akiya Fukuda[1], Masahiko Taguchi[1,2,3], Shun Sakuraba[3], Justin Chan[3], Eriko Nango[1,2], Hidetoshi Kono[3] ([1]*Graduate School of Science, Tohoku University*, [2]*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University*, [3]*Institute for Quantum Life Science, National Institutes for Quantum Science and Technology*)

3Pos204 TDP-43 のマルチドメイン構造と RNA とともに形成する非膜性構造体の物性の関係
The Relationship between Multiple-domain Structures of TDP-43 and the Physical Properties of Membraneless Organelles Formed with RNA
Yui Matsushita[1], Eiji Yamamoto[2] ([1]*Graduate School of Science and Technology, Keio University*, [2]*Department of System Design Engineering, Keio University*)

3Pos205 インシリコとインビトロ解析による広範なコロナ変異株に結合可能な抗体の開発
Development of antibodies with broadly binding affinity to SARS-CoV-2 variants *in silico* and *in vitro* assays
Xu Pan[1], Takashi Tadokoro[1,3], Yuki Anraku[1], Cong Tian[1], Hideo Fukuhara[1,2], Takao Nomura[1], Shunsuke Kita[1], Taishi Onodera[4], Yu Adachi[4], Saya Moriyama[4], Kohei Yumoto[4], Tateki Suzuki[5], Jiei Sasaki[5], Takao Hashiguchi[5], Yoshimasa Takahashi[4], Hisham M. Dokainish[1], Katsumi Maenaka[1] ([1]*Faculty of Pharmaceutical Sciences, Hokkaido University*, [2]*International Institute for Zoonosis Control, Hokkaido University*, [3]*Sanyo-Onoda City University*, [4]*National Institute of Infectious Diseases*, [5]*Laboratory of Medical Virology, Institute for Frontier Life and Medical Sciences, Kyoto University*)

27. 数理生物学・理論生物学／27. Mathematical & Theoretical biology

3Pos206 Biomolecular Set Theory-分子生物学のための測度論的確率論の展開-
Biomolecular Set Theory -Measure-theoretic probability theory for molecular biology-
Ryoichi Sato, Masami Yokota Hirai (*CSRS., RIKEN*)

3Pos207 魚類の網膜における錐体モザイク形成に関する力学モデルを用いた考察
Study of cone mosaic formation in fish retinas using a mathematical model
Keiichi Yamamoto[1], Yuji Sakai[2], Atsushi Mochizuki[2] ([1]*Graduate school of Science, Kyoto University*, [2]*Institute for life and medical sciences, Kyoto University*)

3Pos208 上皮シートにおける極性細胞と非極性細胞の相分離
Phase separation of polar and nonpolar cells in epithelial sheet
Ryunosuke Karimata[1], Satoru Okuda[2] ([1]*School of Mathematics and Physics, Kanazawa University*, [2]*Nano Life Science Institute, Kanazawa University*)

3Pos209 細胞膜上の分子密度に依存したクラスター形成とシグナル伝達の数理的研究
Mathematical study of molecular density-dependent cluster formation and signal transduction on the plasma membrane
Hiroaki Takagi (*Dep. Phys., Sch. Med., Nara Med. Univ.*)

3Pos210 周期構造上の紡錘形細胞集団におけるトポロジカル欠陥のダイナミクス
Dynamics of topological defects in spindle-shaped cell populations on periodic structures
Hiroki Miyazako[1], Naoki Matsuda[1], Takashi Sakajo[2], Takaaki Nara[1] ([1]*Grad. Sch. IST, Univ. of Tokyo*, [2]*Grad. Sch. Sci., Kyoto Univ.*)

3Pos211 相互作用する複数の要素から成るシステムの挙動に関する理論解析
Modeling the behavior of a system consisting of multiple interacting elements
Naoto Yonekura[1], Shinji Deguchi[2] ([1]*School of Engineering Science, Osaka University*, [2]*Graduate School of Engineering Science, Osaka University*)

3Pos212 Simultaneous Optimization of the Structure and Control of Machines: A Model Study
Yuki Hamada[1], Yuichi Togashi[1,2] ([1]*Grad. Sch. Life Sci., Ritsumeikan Univ.*, [2]*RIKEN BDR*)

3Pos213 液滴誘導型細胞内走化性の理論
Theory of droplet-induced intracellular chemotaxis
Takeshi Sugawara (*CDS, Univ. Kochi*)

29. 非平衡・生体リズム／29. Nonequilibrium state & Biological rhythm

3Pos214 微小管集団によって運搬・蓄積されるコロイド粒子のクラスター形成
Cluster Formation of Colloidal Particles Transported and Accumulated by Microtubule Populations
Yuki Matsuo[1], Yutaka Sumino[1], Mousumi Akter[2], Mst. Rubaya Rashid[3], Akira Kakugo[3] ([1]*Department of Applied Physics, Faculty of Science Division I, Tokyo University of Science*, [2]*Institute of Molecular Biology, University of Oregon*, [3]*Department of Physics, Graduate School of Science, University of Kyoto*)

3Pos215 Emergence of adaptive slower coupled oscillations of spontaneously beating cardiomyocyte networks using on chip cell network assay
Suguru Matsumoto[1], Kazufumi Sakamoto[1], Kenji Yasuda[1,2], Kosuke Fujimoto[2] ([1]*Dept. Pure & Appl. Phys., Grad. Sch. Adv. Sci. & Eng., Waseda Univ.*, [2]*Dept. Pure & Appl. Phys., Sch. Adv. Sci. & Eng., Waseda Univ.*)

3Pos216 運動ニューラルネットワークの局所不可逆性の定量化
Quantifying the local irreversibility of a motor neural network
Yoshiaki Horiike[1,2], Shin Fujishiro[3], Rune W. Berg[2], Karel Josef A. Proesmans[4] ([1]*Dept. Appl. Phys., Nagoya Univ.*, [2]*Dept. Neurosci., Univ. Copenhagen*, [3]*Fukui Inst. Fundam. Chem., Kyoto Univ.*, [4]*Niels Bohr Intl. Acad., Univ. Copenhagen*)

3Pos217 細胞の意思決定における理論的な精度限界
Theoretical limits on the precision of cellular decision making
Nobumasa Ishida, Yoshihiko Hasegawa (*Grad. Sch. Info. Sci. Tech., Univ. Tokyo*)

3Pos218 確率論に基づくシミュレーションを用いた１次元振動パターンにおけるピーク位置の理論的研究
Theoretical Study of Peak Position in One Dimensional Oscillation Patterns by using Stochastic Simulation
Ryuta Imayoshi, Kaichi Kokubo, Tatsuhiro Kawashima, Kazutomo Kawaguchi, Hidemi Nagao (*Grad. Sch. Nat. Sci, Kanazawa Univ.*)

3Pos219 精子形成の周期と波：マウス精巣の細胞集団秩序を支える生物リズム
The spermatogenic cycle and wave: biological rhythms for the collective cellular order in mouse testis
Toshiyuki Sato[1], Shosei Yoshida[1,2] ([1]*NIBB*, [2]*Grad. Inst. for Adv. Stud., SOKENDAI*)

3Pos220 走化性を示さない細胞性粘菌変異株の集団が示すキラルなパターン形成
Large-scale chiral pattern formation in population of non-chemotactic *Dictyostelium* cells
Masayuki Hayakawa[1], Hidekazu Kuwayama[2], Tatsuo Shibata[1] ([1]*Riken, BDR*, [2]*Faculty of Life and Environmental Sciences, University of Tsukuba*)

3Pos221 高周波強制振動によるニューロンのモデル方程式の発火抑制
Suppression of repetitive spiking in neural model equation with high frequency forced oscillation
Keito Yamasaki (*IGSES,Univ.Kyushu*)

3Pos222 心筋細胞に備わった恒常性的安定性を併せ持つカオス特性、S4C の発見
Discovery of S4C, a chaotic property of cardiomyocytes with homeostatic stability
Seine A. Shintani[1,2,3] ([1]*Department of Biomedical Sciences, College of Life and Health Sciences, Chubu University.*, [2]*Center for Mathematical Science and Artificial Intelligence, Chubu University.*, [3]*Institute for Advanced Research, Nagoya University*)

3Pos223 細胞集団における位相欠陥の幾何的制御と流れの発生
Geometric control of topological defects and emergent flow in cell population
Ryo Ienaga[1], Yusuke Maeda[1], Kazusa Beppu[2] ([1]*Grad. Sch. Sci.Phys., Univ. Kyushu*, [2]*Applied Phys., Univ. Aalto*)

3Pos224 Inducing simple and short-termed phosphorylation oscillation by using a phosphorylation site variant of clock protein KaiC
Kosuke Maki, Yuji Nishimura, Rie Kumagai, Yuto Iura (*Grad. Sch. Sci., Nagoya Univ.*)

30. 計測／30. Measurements

3Pos225 NMR analysis of 2'-fucosyllactose in human breast milk
Zhiyan Hu[1], Jiaxi Jiang[1], Li Gan[1], Zihao Song[1], Yuki Ohnishi[1], Seiji Osada[2], Hiroyuki Kumeta[1], Yasuhiro Kumaki[1], Kazuo Yamauchi[3], Tomoyasu Aizawa[1] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Nakayama Co.,Ltd.*, [3]*IAS, OIST*)

3Pos226 卓上型 NMR 装置を用いたヒト母乳中の乳糖濃度の定量
Determination of lactose concentration in human breast milk utilizing a benchtop NMR spectrometer
Jiaxi Jiang[1], Zhiyan Hu[1], Zihao Song[1], Li Gan[1], Yuki Ohnishi[1], Seiji Osada[2], Hiroyuki Kumeta[1], Yasuhiro Kumaki[1], Kazuo Yamauchi[3], Tomoyasu Aizawa[1] ([1]*Grad. Sch. Life Sci., Hokkaido Univ.*, [2]*Nakayama Co.,Ltd.*, [3]*IAS, OIST*)

3Pos227 センサシステム研究のための水素化アモルファスシリコンで増強された脂肪酸とクマリンの複合分子薄膜
Composite molecular thin films of fatty acids and coumarins enhanced with hydrogenated amorphous silicon for sensor system research
Koyu Akiyama[1], Kazunori Takada[1], Kohei Saito[1], Hiroshi Masumoto[2], Yutaka Tsujiuchi[1,2] ([1]*Material Science and Engineering, Akita University*, [2]*Frontier Research Institute for Interdisciplinary, Tohoku University*)

3Pos228 Plunus Lanessiana から抽出した蛍光色素の解析と水素化アモルファスシリコン薄膜上での特性
Analysis of fluorescent pigments extracted from Plunus Lanessiana and their properties on hydrogenated amorphous silicon thin films
Yutaka Tsujiuchi[1,2], Kazunori Takada[1], Koyu Akiyama[1], Akihito Nakajima[1], Hiroshi Masumoto[2] ([1]*Material Science and Engineering, Akita University*, [2]*Frontier Research Institute for Interdisciplinary, Tohoku University*)

3Pos229 タンパク質間相互作用検出のための 4 チャンネル偏光蛍光相関分光装置の構築と検証
Construction and verification of 4ch polarization-dependent fluorescence correlation spectroscopy for detection of protein interaction
Masastaka Kinjo, Riku Ando, Akira Kitamura (*Ad. Lif. Sci.Hokkaido U.*)

3Pos230 補償光学系による位相変調と機械学習を用いて 1 分子輝点 3 次元座標を光軸方向に広範囲に高精度計測する方法のシミュレーション研究
A simulation study of precise 3D single-molecule localization over a large axial range using PSF engineering and deep learning
Yuma Ito, Ryota Sasaki, Kosuke Ohira, Xiang Zhou, **Makio Tokunaga** (*Sch. Life Sci. Tech., Tokyo Tech*)

3Pos231 Development of Electrochemical DNA Sensors for Nondestructive Inspection of Molecular Robots
Haruki Tanabe, Hiromu Akai, Kan Shoji (*Graduate School of Engineering, Nagaoka University of Technology*)

3Pos232 血中 CEA 腫瘍マーカーの 1 分子識別のためのアプタマーを用いたナノポア測定技術開発
Development of aptamer-based nanopore measurement technology for single molecule identification of CEA tumor markers in blood
Ryo Akita, Hikaru Nozawa, Tatsuhiko Tsunoda, Sotaro Uemura (*Grad. Sch. Sci., Univ. Tokyo*)

3Pos233 ウイルスゲノムの分節化による多重感染条件での細胞感染率の違い
Differences in cell infection rates under multiple infection conditions due to viral genome segmentation
Yuu Kawahara, Hiroyuki Noji, Kazuhito Tabata (*Grad. Eng. App., Univ. Tokyo*)

31. バイオイメージング／31. Bioimaging

3Pos234 Establishment of a screening system for bioluminescent indicator development
Rikuto Tanaka[1], Kazunori Sugiura[2], Mitsuru Hattori[2], Takeharu Nagai[1,2] ([1]*Grad. Sch. FBS. Osaka*, [2]*SANKEN. Osaka*)

3Pos235 Versatile design for genetically-encoded fluorescent indicator based on excited state proton transfer
Kazunori Sugiura, Takeharu Nagai (*SANKEN, Osaka university*)

3Pos236 高速 AFM の更なる高速化に向けた Z-スキャナシステムの改良
Improvement of the Z-scanner system for faster high-speed AFM
Kazuma Tatsumi[1], Kenichi Umeda[2], Noriyuki Kodera[2] ([1]*Grad. Sch. Math. & Phys., Kanazawa Univ.*, [2]*WPI-NanoLSI, Kanazawa Univ.*)

3Pos237 High-throughput system for real-time single-cell secretion imaging with optical waveguide chip
Zhuohao Yang[1], Mai Yamagishi[2], Nobutake Suzuki[2], Etsushi Kuroda[3], Shinya Sakuma[4], Takashi Funatsu[1], Yoshitaka Shirasaki[1] ([1]*Grad. Sch. Pharm. Sci., The Univ. of Tokyo*, [2]*Live Cell Diagnosis, Ltd.*, [3]*Dep. Immun., Hyogo Coll. Med.*, [4]*Fac. Eng., Kyushu Univ.*)

3Pos238 Aβ 凝集体が Tau の凝集に与える影響
Effects of preformed amyloid β aggregates on tau aggregation
Soichiro Ogura (*Graduate school of Engineering, Muroran Institute of Technology*)

3Pos239 SSBD:repository/SSBD:database: バイオイメージングデータのグローバルな共有
SSBD:repository/SSBD:database: A global sharing of bioimaging data
Koji Kyoda[1], Hiroya Itoga[1], Fangfang Wang[1,2], Miguel Miranda-Miranda[1], Haruna Yamamoto[1], Yuki Yamagata[2,3], Yukako Tohsato[1,4], Shuichi Onami[1,2] ([1]*RIKEN BDR*, [2]*RIKEN R-IH*, [3]*RIKEN BRC*, [4]*Ritsumeikan University*)

3Pos240 脂質・ヌクレオチド依存的なペルオキシレドキシン高分子量複合体形成メカニズムの解明
Study on the formation mechanism of peroxiredoxin high molecular weight complex with lipid and nucleotide
Ryusei Yamada[1], Hiroki Konno[2] ([1]*Grad. Sch. Sci., Univ. Kanazawa*, [2]*WPI Nano Life Science Inst., Univ. Kanazawa*)

3Pos241 がん免疫において細胞傷害性指標となる液性因子分泌のライブセルイメージング
Live Cell Imaging of Liquid Factor Secretion as an Indicator of Cytotoxicity in Cancer Immunity
Yuto Kurisu[1], Zhuohao Yang[1], Koji Nagaoka[2], Kazuhiro Kakimi[2,3], Takashi Funatsu[1], Yoshitaka Shirasaki[1] ([1]*Grad. Sch. Pharm. , UTokyo.*, [2]*UTokyo Hospital*, [3]*Faculty of Medicine ,Kindai Univ.*)

3Pos242 Single Polypeptide Detection Using a Translocon SecYEG
Wenqing Xu[1], Ryoji Miyazaki[2], Ryo Iizuka[1], Tomoya Tsukazaki[2], Sotaro Uemura[1] ([1]*Grad. Sch. Sci., Univ. Tokyo*, [2]*Nara Inst. of Sci. and Tech.*)

3Pos243 凍結固定された生体試料内分子のラマンイメージング
Raman imaging of intracellular molecules in cryo fixed biological specimens
Mizushima Kenta[1,2], Yasuaki Kumamoto[1,3], Shoko Tamura[4], Masahito Yamanaka[1], Kentaro Mochizuki[4], Menglu Li[1,2], Shunsuke Egoshi[5,6], Kosuke Dodo[5,6], Yoshinori Harada[4], Isac Smith Nicholas[7], Mikiko Sodeoka[5,6], Hideo Tanaka[4], Katsumasa Fujita[1,2,3] ([1]*Department of Applied Physics, Osaka University*, [2]*Advanced Photonics and Bioengineering Open Innovation Laboratory AIST-Osaka University*, [3]*Institute of Open and Transdisciplinary Research Initiatives, Osaka University*, [4]*Department of Pathology and Cell Regulation, Kyoto Prefectural University of Medicine*, [5]*Synthetic Organic Chemistry Laboratory, RIKEN Cluster for Pioneering Research*, [6]*Catalysis and Integrated Research Group, RIKEN Center for Sustainable Resource Science*, [7]*Biophotonics Laboratory, Immunology Frontier Research Center, Osaka University*)

3Pos244 光機能性ラマンプローブの開発とその応用
Development of photoactivatable and photoswitchable Raman probes
Minoru Kawatani[1,2], Ayumi Komazawa[3], Jingwen Shou[4], Hiroyoshi Fujioka[1,2], Yoshio Mita[4,5], Yasuteru Urano[2,3], Yasuyuki Ozeki[4,6], Mako Kamiya[1,2,7] ([1]*Sch. Life Sci. Tech., Tokyo Tech.*, [2]*Grad. Sch. Med., Univ. Tokyo*, [3]*Grad. Sch. Pharm. Sci., Univ. Tokyo*, [4]*Dep. Electr. Eng. Info. Sys., Univ. Tokyo*, [5]*LIMMS, Univ. Tokyo*, [6]*RCAST, Univ. Tokyo*, [7]*IRFI, Tokyo Tech.*)

3Pos245 小胞ライブイメージングが解き明かす新しい細胞間情報伝達様式
New Mode of Intercellular Communication Unveiled by Vesicle Live Imaging
Tomohiro Minakawa[1], Fumiyoshi Ishidate[2], Takahiro Fujiwara[2], Jun K. Yamashita[1] ([1]*Graduate School of Medicine, the University of Tokyo Department of Cellular and Tissue Communication*, [2]*Analysis Center, Institute for Integrated Cell-Material Sciences (WPI-iCeMS), KUIAS, Kyoto University*)

3Pos246 非標識光学顕微鏡を用いた細胞内熱伝導と加熱による温度変化の計測
Intracellular heat conduction and heat-induced temperature change measurements by label-free optical microscopy
Keiichiro Toda[1], Masaharu Takarada[2], Genki Ishigane[1], Hiroyuki Shimada[1], Venkata Ramaiah Badarla[1], Kohki Okabe[2], Takuro Ideguchi[1] ([1]*Department of Science, The University of Tokyo*, [2]*Department of Pharmaceutical Science, The University of Tokyo*)

3Pos247 クラスター型プロトカドヘリンの同種親和性相互作用を可視化する蛍光指示薬の開発
Development of fluorescent indicators for visualizing homophilic interaction of clustered protocadherin
Takashi Kanadome[1,2], Nanami Hoshino[3], Takeharu Nagai[2], Takeshi Yagi[3], Tomoki Matsuda[2] ([1]*PRESTO, JST*, [2]*SANKEN, Osaka Univ.*, [3]*FBS, Osaka Univ.*)

3Pos248 プロリンを含有するテトラペプチドの結晶化
Crystallization of Proline-containing Tetrapeptides
Shogo Hayashi, Kazunori Motai, Yuhei Hayamizu (*Dept. of Mat. Sci. and Eng., Tokyo Tech.*)

3Pos249 ヒスチジンを含むテトラペプチドと銅イオンの結晶化におけるリアルタイムイメージングとラマン分光解析
Real-Time Imaging of Crystallization and Raman Spectral Analysis of Histidine-Containing Tetrapeptides and Metal Ions
Yumie Nishiyama, Kazunori Motai, Shogo Hayashi, Yuhei Hayamizu (*Dept. of Mat. Sci. and Eng., Tokyo Tech*)

3Pos250 Integrating In Vivo Crystallography and De Novo Protein Design at Nagoya University
Etsuko Tokunaga[1], Hiroki Onoda[1], Yasufumi Umena[1], Swagatha Ghosh[2], George Chikenji[2], Tomoki Terada[2], Hidehiko Akiyama[3], Leonard MGH Chavas[1,2] ([1]*NUSR, Nagoya University*, [2]*Dept Applied Physics, Nagoya University*, [3]*Faculty of Medical Sciences, Fujita Health University*)

名字（Family Name）のアルファベット順にソートしています。すべて，オンラインで入力されたデータのまま，表示しています。演題番号の末尾が 00 または 99 は，シンポジウムのオーガナイザーによる開会挨拶等を示しています。

	2Pos242
	3Pos232
	3Pos242
Ueno, Hironori (上野 裕則)	1Pos090
	2Pos228
Ueno, Hiroshi (上野 博史)	1GF1415
	1GF1445
	2Pos039
	2Pos080
	3Pos082
Ueno, Mako (上野 真琴)	3Pos158
Ueno, Naoto (上野 直人)	1SJA-4
	1GC1415
Ueno, Shingo (上野 真吾)	**1Pos047**
Ueno, Taiji (上野 大慈)	**1GD1430**
Ueno, Takafumi (上野 隆史)	1GB1400
Ueno, Yuichiro	2SAP-2
	2Pos158
Uenoyama, Atsuko (上野山 敦子)	3Pos106
Ugarte, Diego (Ugarte Diego)	**3Pos186**
Ugawa, Souichi (宇川 聡一)	**2Pos091**
Ukaji, Yutaka (宇梶 裕)	3Pos155
Ulf, Olsson (ウルフ オルソン)	1GI1415
Umakoshi, Hiroshi (馬越 大)	3Pos122
	3Pos123
Umakoshi, Takayuki (馬越 貴之)	1Pos233
Umeda, Kenichi	2Pos077
Umeda, Kenichi (梅田 健一)	1SBA-2
	1SEA-6
	1Pos242
	2Pos225
	3Pos045
	3Pos236
Umehara, Takashi (梅原 崇史)	2Pos161
Umeki, Nobuhisa (梅木 伸久)	1Pos122
Umemoto, Shun (梅本 駿)	**1GC1515**
Umemura, Nobuhiro (梅村 信弘)	2Pos249
Umena, Yasufumi	1Pos044
Umena, Yasufumi (梅名 泰史)	**2SEP-2**
	2SEP-3
	3Pos032
	3Pos250
Umetani, Miki (梅谷 実樹)	**2Pos152**
Umezawa, Koji (梅澤 公二)	3Pos187
Unabara, Daisuke (海原 大輔)	1SHA-5
Unnno, Masashi (海野 雅司)	2Pos130
Unno, Masashi (海野 雅司)	**1Pos149**
	1Pos150
	1Pos156
	1Pos157
	2Pos131
Unno, Masasi (海野 雅司)	1GJ1430
Urano, Ryo (浦野 諒)	**2Pos116**
	3Pos194
Urano, Yasuteru (浦野 泰照)	3Pos244
Ushiba, Shota (牛場 翔太)	2Pos219
Ushida, Takashi (牛田 多加志)	1Pos036
Ushirogata, Kanako (後潟 夏菜子)	1Pos042
Ushiyama, Ryota (牛山 諒太)	3Pos056
Usui, Asako (碓井 亜瑳子)	1Pos084
	2Pos078
Usui, Kenji (臼井 健二)	1SGA-8
	1GB1500
	3Pos001
Usui, Toshiya (臼井 俊哉)	3HL1030
Usuki, Gikyo (臼杵 義亨)	2SIA-1
Usuki, Shin (臼杵 深)	1GM1615
	2Pos230
	2Pos232
Uyeda, Taro Q.P.	2Pos077
Uyeda, Taro QP (上田 太郎)	1GF1515
	1Pos036
Uzawa, Takanori	1Pos051
Uzawa, Takanori (鵜澤 尊規)	**1Pos054**
Vale, Ron	1Pos087
Vanderhaeghen, Pierre (Vanderhaeghen Pierre)	
	1GD1600
Vanni, Stefano (Vanni Stefano)	1GK1445
Vavylonis, Dimitrios	3SCA-2
Veigel, Claudia	**3SEA-2**
Verma, Prabhat (バルマ プラブハット)	1Pos233
Viet Cuong, Nguyen (グェン ヴィエット クーン)	
	1Pos078
Vos, Marten (Vos Marten)	2Pos014
Vu, Cong Quang	**2Pos222**
Vu, Huong T	2Pos077
Vu, Quang Cong	2Pos221
Wada, Kohei (和田 康平)	2Pos115
Waizumi, Tatsuyuki (和泉 達幸)	**2Pos102**
Wakabayashi, Ken-ichi (若林 憲一)	2Pos086
Wakabayashi, Taiki (若林 大貴)	**1GB1430**
Wakamori, Masatoshi (若森 昌聡)	2Pos161
Wakamoto, Yuichi (若本 祐一)	1GK1630
	2Pos152
Walde, Peter (Walde Peter)	2Pos170
Walinda, Erik (ヴァリンダ エリック)	2SAA-7
Wang, Anna	2SAP-2
	2Pos158
Wang, Anna (ワング アナ)	1GI1415
Wang, Fangfang (王 放放)	3Pos239
Wang, He	1GD1530
Wang, Peter Y.	1GJ1530
Wang, Shuo Peng (王 碩鵬)	**2Pos071**
Wang, Shuyan (王 姝儼)	3Pos135
Wang, Tingting (Tingting Wang)	2Pos020
Wang, Tingting (Wang Tingting)	3HL1045

ランチョンセミナー　BP-1　Presented by ZEISS

超解像領域でのイメージングから一分子レベルの挙動を捉える

New modified confocal based super resolution technique Airyscan 2 and Airyscan based FCS technology Dynamics Profilerのご紹介

ZEISS共焦点レーザ顕微鏡ベース超解像技術 Airyscan はその発表以来、誰もが気軽に使える超解像手法として、広がりと進化を遂げてきました。Airyscan 2となり、新たなプロセス Joint Deconvolutionとのコンビネーションで最大分解能は90nm（XY）と大きく飛躍しました。

Airyscanの技術を次のステップ進めるDynamics Profilerがこの度登場しました。現在、Fluorescence Correlation Spectroscopy （FCS）は一分子の動態解析に広く用いられています。しかし、その概念やデリケートな設定などから嫌厭される方もいらっしゃるのではないでしょうか？そこで、これまでの問題点を解決し、分子レベルの挙動解析を多くのイメージングユーザの方が利用できるように工夫したのがDynamics Profilerです。

さらに、Dynamics Profiler では、32 ch で構成された Airyscan 検出器の特性を活かし、分子の点領域内での動きまで導き出すことができます。これにより、近年話題の液-液層分離、膜構造のない境界面での拡散ダイナミクスの測定や分子のフロー解析など新たなソリューションをご提供します。

本セミナーでは超解像から分子動態解析まで可能になった Airyscan 2 Dynamics Profilerをご紹介します。

日　時：11月14日（火）11:50-12:40

会　場：D会場（部屋番号222&223）

講演者：佐藤康彦 カールツァイス株式会社
リサーチマイクロスコピーソリューション
プロダクト＆アプリケーションセールススペシャリスト

ZEISS
Seeing beyond

皆様のご来場をお待ち申し上げます。

カールツァイス株式会社　microscopy.ja@zeiss.com

第６１回日本生物物理学会年会

浜松ホトニクス株式会社
BP セミナー

日時：2023年11月14日（火）11：50～12：40

会場：名古屋国際会議場　E会場（部屋番号：224）

演題1　qCMOSカメラを用いた蛍光１分子観察で、分子が働く仕組みを探る

演者　**笠井 倫志**　先生

国立研究開発法人国立がん研究センター研究所
先端バイオイメージング研究分野

セミナー内容

Gタンパク質共役型受容体（GPCR）は、ヒトでは約８００種類もあることが知られており、機能も多岐にわたるため、生命現象を理解するうえでカギとなる分子の一つである。近年、GPCRは従来の知見と異なり、寿命約１００ミリ秒の動的なダイマーを最小単位とする会合体を形成することが分かってきた。さらに、ダイマーがシグナル生成に関わる等、会合体形成によるシグナル制御の機構の一端も明らかになりつつある一方で、会合体形成の一般性や、生体内での実際の働きや意義については、未だ不明な点が多い。私たちは、qCMOSカメラをはじめとした様々な高感度カメラを用いた細胞内蛍光１分子観察技術によって、こうした疑問に答えようとするアプローチを続けており、本発表では最近の知見をご紹介したい。

演題2　浜松ホトニクスの最新イメージング技術

演者　**三浦 大輝**

浜松ホトニクス株式会社　システム事業部　システム営業推進部

浜松ホトニクス株式会社
www.hamamatsu.com

□ システム営業推進部　〒431-3196　静岡県浜松市東区常光町812
TEL (053)431-0150　FAX (053)433-8031　E-mail sales@sys.hpk.co.jp

第61回日本生物物理学会年会
HORIBA バイオフィジックスセミナーのご案内

「生命凝縮系の分光学」

国立研究開発法人理化学研究所

脳神経科学研究センター　細胞機能探索技術研究チーム
光量子工学研究センター　生命光学技術研究チーム

宮脇敦史 先生

開催日時　11月15日（水）11:40-12:30

会場　C会場（部屋番号：221）

1センチ角（光路長１センチ）の石英セルを用いる古典的分光装置は現行の生物蛍光スペクトル測定に妙な束縛をかけている。すなわち内部遮断効果の排除を理由に測定対象を希薄溶液に限定している。しかしながら細胞質をはじめ細胞内各コンパートメントの中味は理想溶液からほど遠い。molecular crowdingの名のとおり高濃度の生体高分子を含む濃厚水溶液であり、さらに必ずしも均一系ではなく、液―液相分離にもとづく混合系であり、凝集体（固体）を伴う液体としての凝縮系でもある。こうした生物の複雑万丈をなるべく反映した状況で蛍光標識分子の挙動を解析する方法として堀場製作所の蛍光吸光分光装置Duettaの活用を推奨してみたい。True FRET（無放射性）をTrivial FRET（放射性）から区別する目的でも使える。当該分光装置の吸光分光と蛍光分光は決して1+1=2の関係にはない。

蛍光吸光分光装置
Duetta

日本蛋白質構造データバンク(PDBj)BP セミナー

日時:2023 年 11 月 15 日(2 日目) 11:40-12:30
会場:D 会場 (部屋番号:222+223)

Protein Data Bank: From Two Epidemics to the Global Pandemic to mRNA Vaccines and Paxlovid

Stephen K. Burley, M.D., D.Phil.

RCSB Protein Data Bank, Institute for Quantitative Biomedicine, Department of Chemistry and Chemical Biology, Rutgers, The State University of New Jersey and
RCSB Protein Data Bank, San Diego Super Computer Center, University of California, San Diego

Structural biologists and the Protein Data Bank (PDB) played decisive roles in combatting the COVID-19 pandemic. This talk will explain how global three-dimensional (3D) biostructure data was turned into global knowledge, allowing scientists and engineers around the world to understand the inner workings of coronaviruses and develop effective countermeasures against SARS-CoV-2.

State-of-the-art mRNA vaccines, initially designed with guidance from single-particle cryo-electron microscopy structures of the SARS-CoV and MERS Spike Proteins, benefited more than five billion individuals around the world by preventing viral infections entirely or significantly reducing morbidity and mortality. Structure-guided drug discovery efforts at Pfizer, first initiated in the 2000s in response to the SARS-CoV epidemic and reactivated in 2020 early in the global pandemic, yielded nirmatrelvir -- a potent, orally-bioavailable, covalently-acting, peptidomimetic inhibitor of the SARS-CoV-2 Main Protease. This targeted anti-viral drug received Emergency Use Authorization from the United States Food and Drug Administration in December 2021, less than two years following public release of the viral genome sequence. It is used clinically for the treatment of acute SARS-CoV-2 infections in a fixed dose combination with ritonavir and sold under the brand name Paxlovid.

Biomedicine and biotechnology delivered! Bolstered by open access to research data generated with public and private monies, particularly 3D structures of coronavirus proteins and their complexes with one another, with antibodies, and with small-molecule inhibitors archived in the PDB, basic and applied researchers made a difference that made a difference when the world desperately needed them to succeed. To underscore the importance of these contributions, I quote Dr. Anthony Fauci, former head of the National Institute of Allergy and Infectious Disease, "Show me a person who's vaccinated, got infected, took Paxlovid and died. I can't find anybody."

Chaired by Genji Kurisu, Head, Protein Data bank Japan,
Professor, Institute for Protein Research, Osaka University

The 61st Annual Meeting of Biophysical Society of Japan

第61回日本生物物理学会大会

Refeyn Japan BPセミナー

日時：2023年11月15日　11:40 – 12:30

場所：E会場（部屋番号: 224）

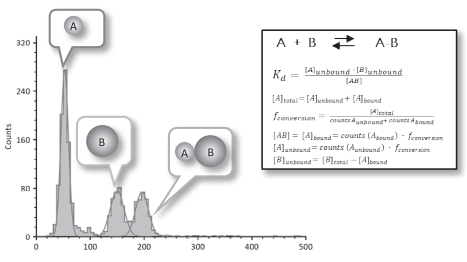
高効率の蛋白質Dynamics解析に向けた Mass photometry

レフェイン・ジャパン株式会社　志波公平

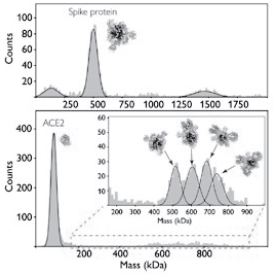
近年より蛋白質の立体構造の重要性が議論され出し、CryoEMなどの解析ツールが実際に蛋白質研究に活用され出して、蛋白質のDynamics解析への注目がさらに高まっている。Dynamics解析を行う上で、解析される対象試料調製などの精度向上が要求される。このことは、例えば実際に複合体解析を行う場合、用いる試料が正しく複合体を形成しているかどうかを知ったうえで測定するのかどうかということとなり、仮にわからない状況で解析を行うことで多くの工数を無駄にしてしまうことにつながる。

Mass photometry法（以下、MP法）は、英国のOxford大学で開発された手法で、極微量の試料量で分子量分布を獲得することができる技術である。当社ではMP法を用いた分析装置の開発・製造・販売・サポートを行っている。今回の発表では、MP法を用いた蛋白質の溶液中Dynamicsに向けたアプリケーション事例を紹介するとともに、実際の研究においてどの程度効率化が図れるのかについても触れる予定である。また、複合体解析に欠かせない分子間相互作用解析についても、その定量評価手法（K_D算出）を交えて紹介したい。

Mass Photometryを用いたアプリケーション事例



MP法を用いた蛋白質Aと蛋白質Bの分子間相互作用解析
20 nM IgG存在下における、BSAのタイトレーション結果



新型コロナウイルス（SARS-CoV2）
スパイク蛋白質の分子量分布（上）と、
ACE2との相互作用による複合体分布（下）

REFEYN®
WEIGHING MOLECULES WITH LIGHT

レフェイン・ジャパン株式会社
657-0036　神戸市灘区桜口町1−1−14
https://www.refeyn.co.jp/

日本カンタム・デザイン株式会社

abberior instruments
STED超解像顕微鏡 ランチョンセミナー

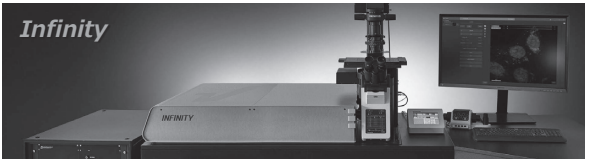
プログラム

◆ 日時：11月15日（水） 11:40-12:30

◆ 会場： J会場

◆ 演題：State-of-the-art super-resolution fluorescence imaging
seminar and online demonstration by Abberior Instruments

◆ 演者：石原 あゆみ （日本カンタム・デザイン）
Dr.Dirk Luchtman （Abberior Instruments GmbH ※オンライン講演）



STEDデモンストレーション

◆ 小間番号： 2
◆ 展示内容： abberior instruments STED超解像顕微鏡STEDYCON
◆ お問合せ： 日本カンタム・デザイン株式会社 第2事業本部
URL： https://www.qd-japan.com/
〒171-0042 東京都豊島区高松1-11-16 西池袋フジタビル2階
TEL： 03-5964-6624 E-mail： info@qd-Japan.com

日本カンタム・デザイン株式会社

Prof.Stefan Hell from Max Planck Institute
スペシャルトーク

プログラム

◆ 日時：11月16日（木）12:00-12:50　　◆ 会場：J会場

◆ 演題：Molecule-scale resolution and dynamics in fluorescence microscopy

◆ 座長：岡田　康志先生

理化学研究所・生命機能科学研究センター チームリーダー
東京大学・大学院医学系研究科・分子細胞生物学専攻 教授
東京大学・大学院理学系研究科・物理学専攻 教授

◆ 演者：Prof. Dr. Stefan W Hell （オンライン講演）

Max Planck Institute for Multidisciplinary Sciences, Göttingen &
Max Planck Institute for Medical Research, Heidelberg

I will show how an in-depth description of the basic principles of diffraction-unlimited fluorescence microscopy has spawned MINFLUX [1-4], a recent super resolution method that has reached the resolution of the size of a fluorophore molecule. Providing 1–3 nanometer resolution in fixed and living cells, as well as localization precisions in the Angström range, MINFLUX and the related MINSTED concept [5,6] are being established for routine applications in the biomedical sciences [4]. Relying on fewer fluorescence photons than other methods, these techniques are also poised to characterize dynamic processes at the single protein level, as already demonstrated by tracking sub(nanometer) details of the unhindered stepping of the motor protein kinesin-1 on microtubules at up to physiological ATP concentrations [7].

[1] Balzarotti, F., Eilers, Y., Gwosch, K. C., Gynnå, A. H., Westphal, V., Stefani, F. D., Elf, J., Hell, S.W. Nanometer resolution imaging and tracking of fluorescent molecules with minimal photon fluxes. **Science** 355, 606-612 (2017).

[2] Eilers, Y., Ta, H., Gwosch, K. C., Balzarotti, F., Hell, S. W. MINFLUX monitors rapid molecular jumps with superior spatiotemporal resolution. **PNAS** 115, 6117-6122 (2018).

[3] Gwosch, K. C., Pape, J. K., Balzarotti, F., Hoess, P., Ellenberg, J., Ries, J., Hell, S. W. MINFLUX nanoscopy delivers 3D multicolor nanometer resolution in cells. **Nat. Methods** 17, 217–224 (2020).

[4] Schmidt, R., Weihs, T., Wurm, C. A., Jansen, I., Rehman, J., Sahl, S. J., Hell, S. W. (2021) MINFLUX nanometer-scale 3D imaging and microsecond-range tracking on a common fluorescence microscope. **Nat. Commun.** 12:1478.

[5] Weber, M., Leutenegger, M., Stoldt, S., Jakobs, S., Mihaila, T. S., Butkevich, A. N., Hell, S. W. MINSTED fluorescence localization and nanoscopy. **Nat. Photon.** 15, 361-366 (2021).

[6] Weber, M., von der Emde, H., Leutenegger, M., Gunkel, P., Sambandan, S., Khan, T. A., Keller-Findeisen, J., Cordes, V. C., Hell, S.W. MINSTED nanoscopy enters the Ångström localization range. **Nat. Biotechnol.**, 41, 569-576 (2023).

[7] Wolff, J.O., Scheiderer, L., Engehard, T., Engelhardt, J., Matthias, J., Hell, S.W. MINFLUX dissects the unimpeded walking of kinesin-1, **Science**, 379, 1004-1010 (2023).