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Welcome Message

On behalf of the Executive Committee, we are delighted to welcome you to the IUPAB2024 congress in Kyoto, Japan. This prestigious event, a collaboration between the 21st IUPAB (International Union of Pure and Applied Biophysics) and the 62nd BSJ (Biophysics Society of Japan), will take place from June 24 to 28, 2024, at the Kyoto International Conference Center.

With the theme 'Rocking Out Biophysics', this congress aims to invigorate the field of biophysics by fostering collaboration and innovation. Academic activities play a vital role in updating existing concepts, and we believe that biophysics, with its powerful perspectives and techniques, has the potential to reshape our understanding of life sciences boldly.

Our mission is to create a dynamic environment where researchers from diverse disciplines worldwide can convene, share new perspectives, and push the boundaries of biophysics. Distinguished researchers in biophysics and related fields are invited to deliver plenary and keynote talks, while over 30 sessions will feature presentations by leading scientists. Young researchers will have the opportunity to showcase their cutting-edge work through oral and poster presentations.

To encourage open exchange and collaboration across generations and borders, we have planned a variety of events, including Welcome reception, Kyoto Night, and Conference dinner where you will find excellent cuisine, sake, crafts, and music from Kyoto and other places in Japan.

Join us in 'Rocking Out Biophysics'!

Sincerely yours,

Hiroyuki NOJI

The chair of the organizing committee of IUPAB2024 President of Biophysical Society of Japan (2021-2023) Professor, The University of Tokyo

Outline

Meeting Title: 21st IUPAB Congress 2024 (IUPAB2024)

In Collaboration With: The 62nd Annual Meeting of the Biophysical Society of Japan

Venue: Kyoto International Conference Center

https://www.icckyoto.or.jp/en/visitor-2/access/getting_here/

Date: June 24 (Mon) – 28 (Fri), 2024

Theme: Rocking out Biophysics

Official Language: English

Hosted By: IUPAB: International Union for Pure and Applied Biophysics

BSJ: The Biophysical Society of Japan

SCJ: Science Council of Japan

IUPAB2024 Secretariat Office:

c/o Convention Linkage, Inc.

Sanbancho KS BLDG., 2 Sanbancho, Chiyoda-ku,

Tokyo 102-0075, Japan

TEL: +81-3-3263-8698 FAX: +81-3-3263-8693

E-mail: IUPAB2024-kyoto@c-linkage.co.jp

IUPAB2024 Committee Members

Executive Organizing Committee

ChairHiroyuki NojiVice ChairKei Yura

Secretary General Kazuhito Tabata

Finance Committee

Chair Katsumi ImadaMembers Kazuhito Tabata

Takeharu Nagai

Scientific Program Committee

Chair Takayuki Nishizaka

Members Hiroko Bannai

Kumiko Hayashi Nobuyasu Koga Satoshi Takahashi Shuichi Onami

Tomoko Nishiyama

Yuji Sugita

Sponsorship Committee

Chair Hiromi Imamura
Members Katsumi Imada

Takeharu Nagai

Public Relations Committee

Chair Hideki Nakamura

Member Marie Mita

Poster Committee

Chair Tomoyasu Aizawa

Members Eri Chatani

Daisuke Nakane Kayo Hibino Keiichi Kojima **OMOTENASHI** Committee

Chair Tomomi TaniMembers Chie Hosokawa

Kazuhito Tabata

Shunsuke F. Shimobayashi

Takeharu Nagai

Public Lecture Committee

Chair Shoji Takada

Member Tsuyoshi Terakawa

Eve Fest Committee

Member Kota Katayama

Observer

Members Haruki Nakamura

Kaori Kakiuchi

Meeting Information

Program at a Glance

	Room A	Room B-1	Room B-2	Room C-2
8:00 -				
9:00 -				
10:00 -				
11:00 -				
12:00 -				
13:00 -	12:30-13:10 Opening Ceremony			
14:00 -	13:30-14:20 IUPAB Katchalsky Lecture Prof. Feng Zhang			
15:00 -	14:30-16:50 Symposium 1	14:30-16:50	14:30-16:50	14:30-16:50
16:00 -	Super-resolution and	Symposium 2 Morphogenesis during Development and Repair	Symposium 3 Cryo Electron Microscopy and Tomography	Hands-on Training Session D DNA Nanomachine Tutorial
17:00 -	17:00-17:40 Avanti-IUPAB Prize Lecture Prof. Massimo Olivucci			
18:00 -	TO: Maconilo divaco.	10:30	.12:15	
19:00 -		IUPAB Coun (Venue: R *Invite	oom 555)	
20:00 -		19:00-21:00 Presidential Dinner		
21:00 -		(Venue: Hei *Invite		

Monday, June 24

Room D	Room E	Anne	x Hall	
				- 8:00
				- 9:00
				- 10:00
				- 11:00
				- - 12:00
				- - 13:00
		12:00-17:00 Poster display and Exhibition		- 14:00
				- - 15:00
14:30-16:50 Symposium 4 Correlative Cell Imaging	14:30-16:50 Symposium 5 Theoretical Biology of Complex Systems	15:00-17:00 Coffee break		- 16:00
				- 1 <i>7</i> :00
			17:50-19:15	- 18:00
			Welcome Reception	- 19:00
				- 20:00
				- 21:00

Program at a Glance

	Room A	Room B-1	Room B-2	Room C-2
8:00 -	8:00-8:50 Morning Seminar 1			
9:00 -	(Avanti Polar Lipids)	9:00-9:50 Keynote 1		
10:00 -		Prof. Kunihiko Kaneko		
11:00 -	10:00-12:20 The 20th Early Career Award in Biophysics Candidate Presentations	10:00-12:20 Symposium 6 Mechanosensing and Mechanobiology, Biological Temperature	10:00-12:20 Symposium 7 Protein Structure to Function 1	10:00-12:20 Symposium 8 Unstructured/Disordered Proteins, RNA
12:00 -				
13:00 -	12:35-13:35 BP Seminar 1 (JEOL Ltd.)	12:35-13:35 BP Seminar 2 (Carl Zeiss Co., Ltd.)	12:35-13:35 BP Seminar 3 (Leica Microsystems K.K.)	12:35-13:35 BP Seminar 4
14:00 -				(Nakatani Foundation for Advancement of Measuring Technologies in Biomedical Engineering)
15:00 -				3 4 3/
16:00 -				16:00-18:20 Hands-on Training
17:00 -	16:00-18:20 Symposium 11 Single Molecule Biophysics in Chromosome Science	16:00-18:20 Symposium 12 Cell Motility, Cytoskeletons and Motor Proteins	16:00-18:20 Symposium 13 Protein Structure to Function 2	Session A Millions of Single Live Cell Analysis with the Automated
18:00 -				Trans-scale-scope, AMATERAS
19:00 -				
20:00 -				
21:00 -				

Tuesday, June 25

Room D	Room E	Anr	ex Hall	Sakura	
					- - 8:0
					- - 9:(
					-
					- 10 -
10:00-12:20 Symposium 9 Lipid and Membrane	10:00-12:20 Symposium 10 Data Science for Integrated		00-18:30 display and		- 11
Biophysics	Dynamic Structural Biology		hibition		- - 12
12:20-13:35 12:35-13:35 BP Seminar 5 (SIGMAKOKI CO., LTD.)	12:35-13:35 BP Seminar 6 (On-chip Biotechnologies Co., Ltd)				- - 13 -
		13.50	13:50-14:50 Poster presentations:		- 14
		13:50- 15:50 Coffee break	odd 14:50-15:50 Poster presentations: even		- - 15 -
16:00-18:20 Sponsored Symposium 1	16:00-18:20 Symposium 14				- 16 -
MEXT KAKENHI Grant-in-Aid for Transformative Research Area (A) "Material properties letermine body shapes and their	Data Science, Machine Learning, and Analytical Frameworks for Understanding the				- - 1 <i>7</i> -
constructions" and "Integration of Extracellular Information by Multimodal ECM Activity")	Heterogeneity of Cellular and Multicellular Systems				- 18
			30-19:30 removal time	18:30-20:00 Kyoto Night	- - 19 -
					- 20
					- - 21

Program at a Glance

	Room A	Room B-1	Room B-2		Room C-2
8:00 —	8:00-8:50 Morning Seminar 2				
9:00 —	9:00-9:50 IUPAB Engstrom Lecture				
10:00 -	Prof. Toshio Ando				
11:00 -	10:00-12:20 Symposium 15 Single Molecule Biophysics with Advanced Techniques	10:00-12:20 Symposium 16 Rotary ATPases	10:00-12:20 Symposium 17 Protein Design 8 Engineering		10:00-12:20 Symposium 18 Neural Systems and Excitable Cells
12:00 —					
13:00 —	12:35-13:35 BP Seminar 7 (Refeyn)	12:20-13:5 12:35-13:35 BP Seminar 8 (HAMAMATSU PHOTONICS K.K.)	O Break		
14:00 —					
15:00 —					
16:00 -	16:00-16:40 IUPAB Young Investigator				
17:00 —	Award Lecture Prof. Hideaki Kato	16:40-17:30 BPS Award Lecture Prof. Jerelle A. Joseph			
18:00 —	17:30-18:20 Keynote 2 Prof. Gerhard Hummer	17:30-18:20 Keynote 3 Prof. Rong Li			
19:00 —	18:30-20:30 General Assembly				
20:00 —	(Voting delegates to attend (observers welcome))	12:35-1 Mixer with Presiden (Venue: Ro *Invited	ts and Secretaries oom B-2)		
21:00 —			•)	

Wednesday, June 26

Room D	Room E	Annex Hall	
			- - 8:00 -
			- 9:00 -
10:00-12:20			- 10:00 -
Symposium 19 Understanding Structure and Function of Emerging Viruses	10:00-12:20 Symposium 20 Synthetic Biology	9:00-18:30 Poster display and Exhibition	- 11:00 -
12:20-13:5 12:35-13:35	50 Break		- 12:00 -
BP Seminar 9 (Yokogawa Electric Corporation)	12:35-13:35 BP Seminar 10		- 13:00 -
	(Digital Bioassay Laboratory, The University of Tokyo and TOPPAN Holdings Inc.)	13:50-14:50 Poster presentations: odd 14:50.15:50	- 14:00 -
		break 14:50-15:50 Poster presentations: even	- 15:00 -
			- 16:00 -
			- 17:00 -
		18:30-19:30	- 18:00 - - 19:00
		Poster removal time	- 19:00 - - 20:00
			- 20:00 - - 21:00
			Z 1:00 -

Program at a Glance

	Room A	Room B-1	Room B-2	Room C-2
8:00 -	8:00-8:50 Morning Seminar 3			
9:00 -	(Avanti Polar Lipids)	9:00-9:50 IUPAB Ramachandran Lecture Prof. David Baker		
10:00 -		FIOI. David Dakei		
11:00 -	10:00-12:20 Symposium 21 Computational Molecular Biophysics	10:00-12:20 Symposium 22 Bacterial/Archaeal Supermolecular Assembly	10:00-12:20 Symposium 23 Optogenetics and Photobiology	10:00-12:20 Symposium 24 Chromatin Dynamics and Imaging
12:00 -				
13:00 -	12:35-13:35 BP Seminar 11 (NIKON SOLUTIONS CO.,LTD.)	12:20-13:5 12:35-13:35 BP Seminar 12 (Refeyn)	O Break	
14:00 -				
15:00 -				
16:00 -				
17:00 - -	16:00-18:20 Sponsored Symposium 2 JST PRESTO, Dynamic supra-assembly of biomolecular systems	16:00-18:20 Symposium 26 Applications of Non-equilibrium Physics	16:00-18:20 Symposium 27 DNA/Chromatin Physics	16:00-18:20 Symposium 28 Membraneless Organella, Autophage, Liquid-liquid
18:00 -	biomoleculai systems	, , , , , , , , , , , , , , , , , , , ,		Phase Separation
19:00 -	18:30-19:10 The Bei Lecture Prof. Xiyun Yan			
20:00 -				
21:00 -				

Thursday, June 27

Room D	Room E	Anr	nex Hall	Swan / Japanese Garden	_
					- 8:00
					- - 9:00
					- - 10:00
10:00-12:20 Symposium 25 Biophysics of Disease	10:00-12:20 Hands-on Training Session B Visualizing the Nanometer World in Liquid by Bio-SPMs	Poster	00-18:30 display and hibition		- - 11:00 -
12.00.10					- 12:00
12:35-13:35 BP Seminar 13 (Evident Corporation)	12:35-13:35 BP Seminar 14 (Twist Bioscience)				- - 13:00 -
		13:50- 15:50	13:50-14:50 Poster presentations:		- 14:00 -
		Coffee break	14:50-15:50 Poster presentations:		- 15:00 -
			even		- 16:00
16:00-18:20 Symposium 29 Soft Matter Biophysics (by IUPAP)	16:00-18:20 Asian Biophysics Association (ABA) Symposium				- - 17:00 -
(by lot Al)	Зушрозиш				- 18:00
			30-19:30 removal time		- - 19:00
				19:20-21:20 Conference Dinner	- 20:00
				(Venue in case of rainy weather: Swan/Sakura)	- - 21:00

Program at a Glance

	Room A	Room B-1	Room B-2		Room C-2
8:00 —					
9:00 —		9:00-9:50 Keynote 4 Prof. Hannele Ruohola-Baker			
10:00 —		Proi. Haimele Ruonola-Baker			
11:00 -	10:00-12:20 Hands-on Training Session E Exploring Multi-cellular Mechanics	10:00-12:20 Symposium 30 Structure, Function and Biophysics of the Bacterial Motility and Flagellar Motor	10:00-12:20 Symposium 31 Stem cells and Organ	oids	10:00-12:20 Hands-on Training Session C CHARMM-GUI/GENESIS MD Tutorial
12:00 -					
13:00 -	12:35-13:35 BP Seminar 15 (The Biophysical Society of Japan & Acaric.co.ltd.)	12:20-13:	12:35-13:35 BP Seminar 16 (Nagoya Institute of Techr & SHIMADZU CORPORAT	nology TON)	
14:00 -					
15:00 —					
16:00 -	16:00-17:00				
17:00 —	Closing Ceremony				
18:00 —		10.00	11.00		
19:00 -		Corporate Opinion (Venue: R *Invite	Exchange Meeting oom 555)		
20:00 —		13:50-15:50 IUPAB New Council Meeting			
21:00 -		(Venue: *Invite	коот E) id only		

Friday, June 28

Room D	Room E	Anı	nex Hall	Kyoto University	
					- 8:00
					- - 9:00
					- - 10:00
10:00-12:20 Symposium 32 Origin of Life	10:00-12:20 Symposium 33 Data Sharing and Open Science	Poster	00-16:00 display and hibition		- - 11:00 -
12:20-13:5		EX	nibition		- 12:00 -
. 2.20 . 00					- 13:00 -
		13:50-	13:50-14:50 Poster presentations:		- 14:00 -
		13:50- 15:50 Coffee break	odd 14:50-15:50 Poster presentations:		- 15:00 -
		16:	even 00-17:00	16:15-16:45	- 16:00
		Poster	removal time	Registration 16:45-18:45 Public Lecture	- - 17:00 -
				(at Science Seminar House, Graduate School of Faculty of Science)	- 18:00 -
					- - 19:00
					- - 20:00
					- - 21:00

Hands-on Training Program

Hands-on Training Program

*Pre-registered participants only.

Program A: Millions of single live cell analysis with the automated trans-scale-scope, AMATERAS

Event dates: June 18-21

Venue: Osaka University (June 18-19), RIKEN Kobe Campus (June 20-21)

Learning image processing based on information engineering using AMATERAS (a cutting-edge biological microscope, A Multiple/Multiscale Analytical Tool for Every Rare Activity in Singularity) by Osaka University and RIKEN.

Program B: Visualizing the nanometer world in liquid by Bio-SPMs

Event dates: July 1

Venue: Kanazawa University

One day tour to Kanazawa University to learn about Bio-SPM technologies (super-resolution AFM (FM-AFM & 3D-AFM), high-speed AFM, SICM, AFM for Cell measurement). Participants are given priority to participate in the Bio-SPM summer school conducted annually.

Note: An additional application is required in advance to participate in the Bio-SPM summer school.

Program C: CHARMM-GUI/GENESIS MD tutorial

Event dates: June 30-July 2 Venue: RIKEN Kobe Campus

CHARMM-GUI/GENESIS Workshop held in Kobe to learn MD simulations.

Program D: DNA nanomachine tutorial

Event dates: June 22 Venue: Kansai University

Molecular robotics is a new academic field that aims to create systems that can be called robots using molecules designed from scratch as components. We are pleased to offer a hands-on

program for those interested in molecular robotics to learn the basics of design and evaluation of DNA nanomachines in a short period of time. The program is open to anyone, regardless of specialty or background.

(Sponsored by Grant-in-Aid for Transformative Research Areas (A) "Molecular cybernetics")

Program E: Exploring multi-cellular mechanics

Event dates: June 29 Venue: Kyoto University

This hands-on session will provide an introduction to imaging and image analysis of multi-cellular systems such as tissue and embryo. Participants will learn how to handle these specimens, take images (2D, 3D), and extract biophysical parameters by image analysis.

Program F: Real-time single-molecule experiments with optical tweezers and correlated fluorescence microscopy

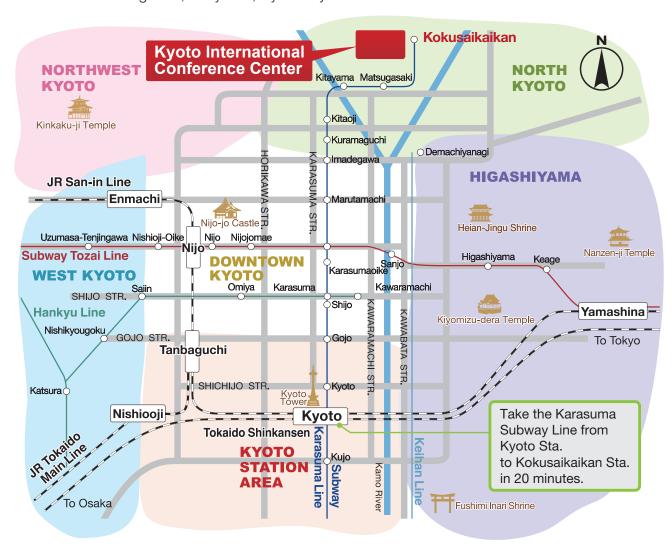
Event dates: June 22-23

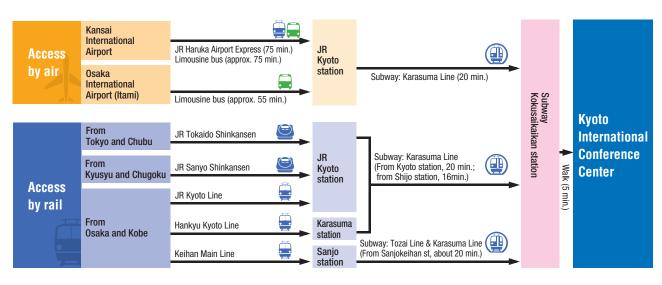
Venue: Institute for Quantitative Bioscience, The University of Tokyo

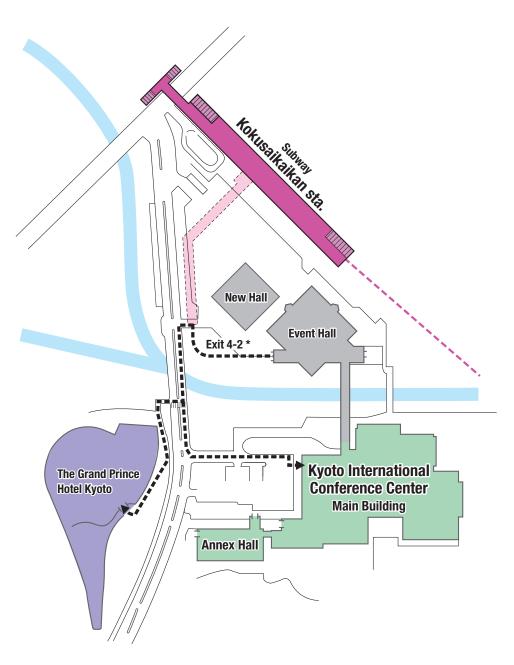
Venue Access

Kyoto International Conference Center

422 Iwakura Oosagi-cho, Sakyo-ku, Kyoto city



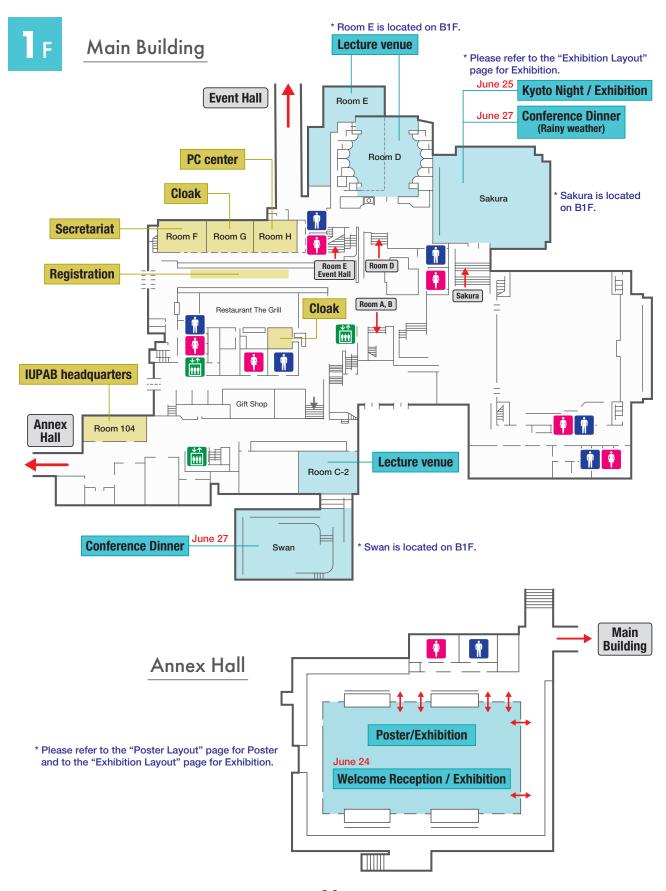




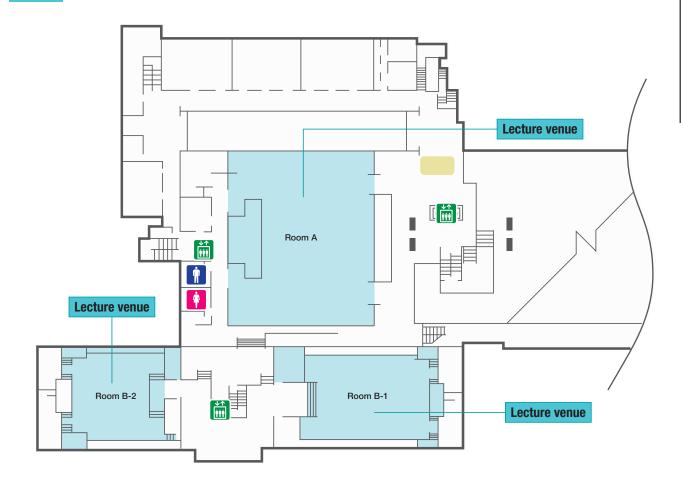
* Exit the ticket gate and walk through the underground passage to Exit 4-2.

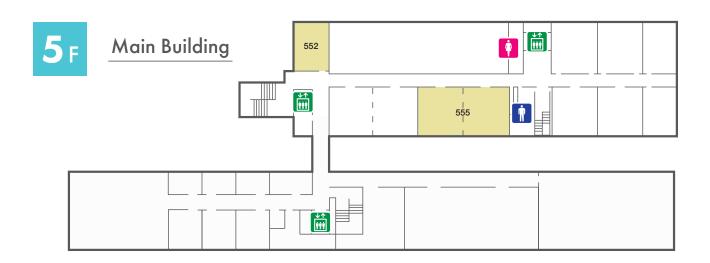
The covered walkway from Exit 4-2 will guide you to our front entrance, keeping you dry on rainy days.

Floor Plan



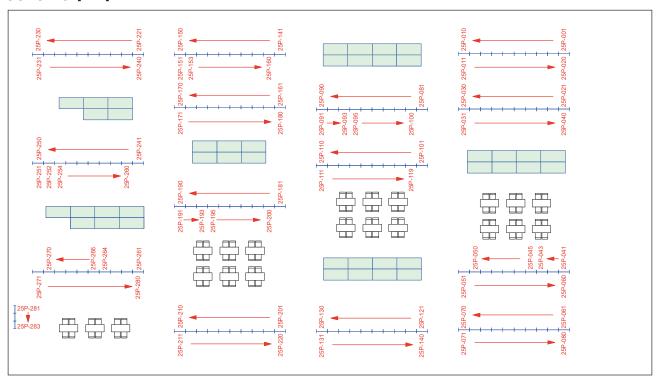
2 F Main Building



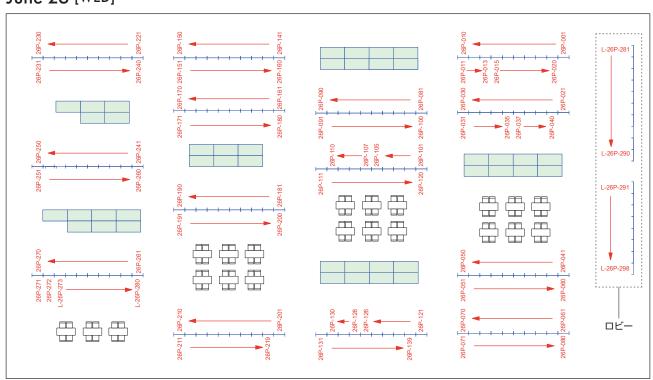


Poster Layout

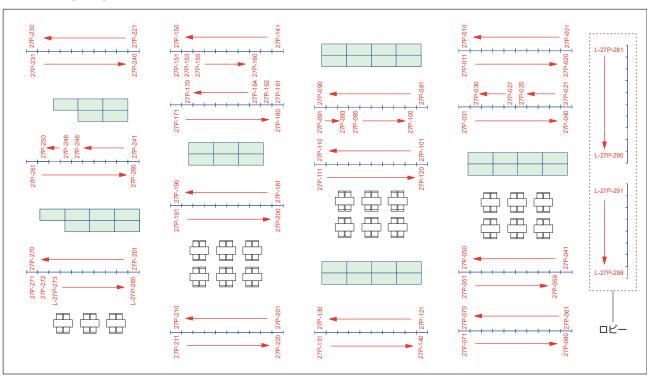
June 25 [TUE]



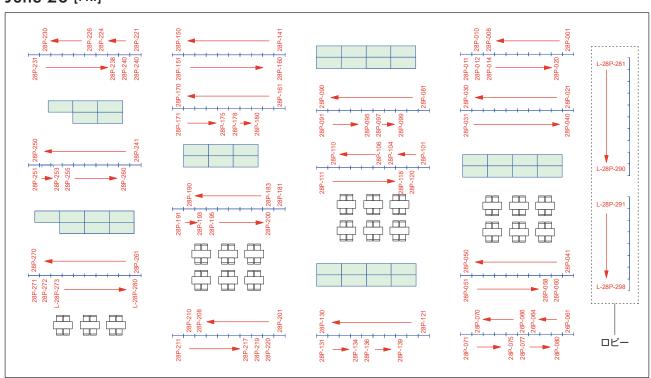
June 26 [WED]



June 27 [THU]

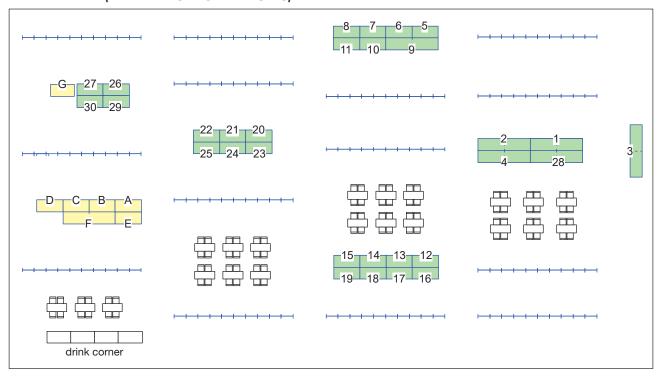


June 28 [FRI]



Exhibition Layout

Annex Hall (June 25 [TUE] - 28 [FRI])



No.	Exhibitor	No.	Exhibitor
1	BLAST Inc.	21	Research Institute of Biomolecule Metrology Co., Ltd.
2	Oxford Instruments K.K.	22	Bruker Japan K.K.
3	Nikon Solutions	23	Yokogawa Electric Corporation
4	Evident Corporation	24	SIGMAKOKI CO., LTD.
5	On-chip Biotechnologies Co., Ltd	25	Japan Laser Corporation
6	TOKYO OHKA KOGYO CO., LTD.	26	FUJIFILM Wako Pure Chemical Corporation
7	NanoAndMore Japan K.K.	27	Yamato Scientific Co., Ltd.
8	HORIBA, Ltd.	28	Quantum Design Japan
9	ORIENTAL GIKEN INC.	29	Pinpoint Photonics, Inc.
10	Chroma Technology Japan	30	CellFree Sciences Co., Ltd
11	Nanion Technologies Japan K.K.	Α	Nakatani Foundation for Advancement of Measuring
12	JEOL Ltd.		Technologies in Biomedical Engineering
13	Refeyn	В	Japan Synchrotron Radiation Research Institute (JASRI)
14	Carl Zeiss Co. Ltd.	С	Worldwide Protein Data Bank
15	Avanti Polar Lipids	D	The DNA Bank, RIKEN BioResource Research Center
16	TAITEC CORPORATION		(RIKEN BRC DNABank)
17	Thorlabs Japan Inc.	Е	Japan Agency for Medical Research and Development
18	Kiko Tech Co., Ltd.	F	The Biophysical Society of Japan
19	Tokai Hit Co., Ltd.	G	Clinica Publishers, LLC
20	HAMAMATSU PHOTONICS K.K.		

For Participants

Registration Desk

Location: Main Entrance Lobby, 1F, Kyoto International Conference Center (ICC Kyoto)

Opening hours: Monday, June 24 11:30-16:30

Tuesday, June 25 07:30-16:30 Wednesday, June 26 07:30-16:30 Thursday, June 27 07:30-16:30 Friday, June 28 08:00-11:00

- <Participants who have completed pre-registration>
- Your name card, certificate of participation and receipt can be downloaded from the "My Page" portal.
- Please download and print out your name card beforehand, and bring it with you.
- If you have forgotten to bring your name card, please present the QR code sent to your email at the Registration Desk, and your name card will be issued onsite.
- <Participants registering on the day of the meeting>
- Please register on the day of the meeting using your own smartphone or PC onsite. Payment is by credit card only.
- <Please wear your name card>

All participants are requested to wear their name card at all times in the congress venue.

Registration fees:

Registration Category		Early Bird	Standard	On-Demand Only
		November 1, 2023-	May 1, 2024-	June 29, 2024-
		April 30, 2024	June 28, 2024	July 31, 2024
		JST (UTC+9)	JST (UTC+9)	JST (UTC+9)
Delegate	Member ¹⁾	JPY 50,000	JPY 70,000	JPY 30,000
	Non-Member	JPY 70,000	JPY 90,000	JPY 40,000
Student ²⁾	Member ¹⁾	JPY 30,000	JPY 40,000	JPY 20,000
	Non-Member	JPY 50,000	JPY 60,000	JPY 30,000
Accompanying Person ³⁾		JPY 10,000		
Conference Dinner		JPY 10,000		

For Participants

- 1) Membership prices apply if you are a member of a national biophysical society.
- 2) Students are asked to submit a valid student ID.
- 3) Up to 5 accompanying persons can be registered.

Registration fees include:

	Onsite participants	On-demand participants	Accompanying persons
Onsite participation in all sessions	✓		
On-demand viewing of sessions	✓	✓	
Exhibition	✓		
Abstract book (online)	✓	✓	
Congress materials	✓		
Handy Program Book	✓		
Welcome Reception	✓		✓
Kyoto Night	✓		✓
Conference Dinner	Please register for Conference Dinner (JPY 10,000 per person)		Please register for Conference Dinner (JPY 10,000 per person)

• Registrants and accompanying persons who have paid their registration fees are invited to the Welcome Reception and Kyoto Night.

On-demand streaming

<Dates>

Streaming period	Monday, July 1 – Wednesday, July 31
Registration period	Saturday, June 29 – Wednesday, July 31
Streamed sessions	Plenary Lectures and Keynote Lectures (other sessions are onsite only)

<How to view the on-demand sessions>

On-demand streaming is only available for registered participants. Those who have completed their registration and payment will receive their unique ID for access to the on-demand streaming

page. Please note that the ID is unique to the individual registrant and cannot be shared with anyone else.

Taking pictures, copying, or downloading of the video or content of the broadcast is strictly prohibited. If any of these actions are discovered or suspected, necessary measures, such as contacting the offending participant's affiliated institution, will be taken accordingly.

Official Language

All sessions will be held in English.

Abstract

<From the congress website>

Abstracts are posted on the congress website in PDF format. Please use the following password to view the abstracts.

Password: iupab2024kyoto

<From the online system>

Abstracts are also posted on the online system. Please login to your "My Page" and click "Time Table" button to view abstracts for each session.

Food and Beverage

Morning Seminars: Danish pastries

BP Seminars (Luncheon Seminars)¹⁾: Boxed sandwiches and Japanese bento (advance

application required)

Coffee Breaks²⁾: Coffee and refreshments

- ¹⁾ Pre-registered users only. There will be no lunch boxes sold onsite.
- * Once a registration for a BP Seminar is made, no cancellations will be accepted.
- * Lunch tickets are printed on your name card and will be checked onsite.
- ²⁾ Coffee breaks will be served after lunch at the Refreshments Corner, located in Annex Hall.

Monday, June 24 15:00-17:00 Tuesday, June 25 13:50-15:50 Wednesday, June 26 13:50-15:50 Thursday, June 27 13:50-15:50 Friday, June 28 13:50-15:50

For Participants

Congress Bags

Congress bags will be distributed at the Registration Desk.

Poster Display and Exhibition

Location: Annex Hall, Kyoto International Conference Center

Exhibition hours: Monday, June 24 12:00-17:00

Tuesday, June 25 09:00-18:30 Wednesday, June 26 09:00-18:30 Thursday, June 27 09:00-18:30 Friday, June 28 09:00-16:00

Digital Point Rally

During the event you can visit the designated exhibition booths and collect points by scanning the QR codes located in each booth using your smartphone. You will need to sign in to your "My Page", choose "Point Rally" menu and allow your camera use to scan the QR codes. The participants who have gathered 10 or more points will enter the draw, and the winners will receive their prizes at the Closing Ceremony.

Location: Annex Hall, 1F, Kyoto International Conference Center

Date & time: Monday, June 24 12:00 - Friday, 28 June 12:00

Cloakroom

The cloakroom service is available during the following hours.

Location 1: Room G, 1F, Kyoto International Conference Center

Location 2: Permanent Cloakroom, 1F, Kyoto International Conference Center

Opening hours: Monday, June 24 11:30-19:30

Tuesday, June 25 07:30-20:30 Wednesday, June 26 07:30-21:00 Thursday, June 27 07:30-21:30 Friday, June 28 08:00-17:30

^{*} Valuables, non-folding umbrellas, or congress bags cannot be accepted.

Social Events

IUPAB 2024 Opening Ceremony

Location: Room A, Kyoto International Conference Center

Date & time: Monday, June 24 12:30-13:10

Performance: Musical performance of traditional Japanese instruments by AUN & HIDE

Welcome Reception

Location: Annex Hall

Date & time: Monday, June 24 17:50-19:15
Performance: Piano performance by Fuyuco

Food & beverage: Drinks and snacks
Fee: Free of charge

Kyoto Night

Location: Sakura

Date & time: Tuesday, June 25 18:30-20:00

Performance: Jazz band

Food & beverage: Sake and snacks
Fee: Free of charge

Conference Dinner

Location: Swan Garden / Sakura (depending on the weather)

Date & time: Thursday, June 27 19:20-21:20

Style: Buffet

Performance: Gagaku (Japanese imperial court music) and a Kyoto rock band

Fee: JPY 10,000

Award ceremony: Nakatani Foundation Award

BPS Student Award

IUPAB 2024 Closing Ceremony

Location: Room A, Kyoto International Conference Center

Date & time: Friday, June 28 16:00-17:00

Award ceremony: IUPAB2024 Student and Early Career Researcher Poster Award

For Participants

Additional Events

IUPAB2024 Eve Fest

Location: Tenchikan, Kyoto Sangyo University
Date & time: Sunday, June 23 13:00-20:00

Fee: Free of charge

*A separate fee (JPY 2,000) is required to attend the social gathering.

*Pre-registered participants only.

Public Lecture

Location: Science Seminar House, Graduate School of Faculty of Science, Kyoto University

Date & time: Friday, June 28 16:45-18:45 (Doors open at 16:15)

Fee: Free of charge

*Please register in advance on the website below (Japanese only):

https://theory.biophys.kyoto-u.ac.jp/iupab-public-seminar

Wi-Fi Access

A Wi-Fi service is available free of charge in public spaces and Event Hall of the Kyoto International Conference Center.

Select the following network: ICCK_Public_WiFi (No password required)

Recordings and Photography

Audio recording, photography, and video recording are strictly prohibited in all venues.

Smoking

All indoor areas are non-smoking.

Lost and Found

Lost property will be kept at the Registration Desk (Main Entrance Lobby, 1F) until Friday, June 28 11:00.

Inquiries

[During the event]

Inquiry Desk: Room F, 1F, ICC Kyoto

[Before/after the event]
IUPAB2024 Secretariat Office
c/o Convention Linkage, Inc.

2 Sanbancho, Chiyoda-ku, Tokyo 102-0075, Japan

E-mail: iupab2024-kyoto@c-linkage.co.jp

For Presenters

Session	Presentation Format	Presentation Time	Data Check on the day of your presentation
All Oral Sessions	Onsite only	As per the information provided to you by your chairperson	Submit your presentation slides to the PC center no later than 45 min. prior to your session's start (if your session is the very first session of the day, no later than 30 min. before the session starts).
Poster Presentation	Onsite only	Please check your Poster number. Presentation time is organized by whether the last part (suffix after hyphen) of the Poster number is odd or even. Odd number: 13:50-14:50 Even number: 14:50-15:50	Posting schedule is listed below.

1. Oral Presentations

If you will be making an oral presentation, please check the following information.

Preparing for your onsite presentation:

- Screen aspect ratio is 16:9. Slides created in 4:3 format will be shown on the screen with black bands on both sides of the slides.
- We recommend that you use OS-standard fonts in your presentation, such as Century Gothic, Courier, Times New Roman.
- Supported software: Windows PowerPoint 2019 and PowerPoint for Microsoft 365.
- If your presentation slides include any video or audio files, please save them in one folder with your slide data.

On your presentation day:

No later than 30 min. before the session starts

• Please visit the PC Center to submit your presentation file. You will be given a short technical instruction.

PC Center

Location: Room H, 1F, Kyoto International Conference Center

Opening hours: Monday, June 24 11:30-16:00

Tuesday, June 25 07:30-16:00 Wednesday, June 26 07:30-16:00 Thursday, June 27 07:30-16:00 Friday, June 28 08:00-12:00

- If you wish to use your own PC:
 - ➤ The Secretariat will prepare an HDMI PC cable connector. If your PC is not compatible with this cable connector, please bring a suitable adaptor.
 - ➤ Please notify the operator in advance if you will be using video or audio in your presentation.
 - ➤ Your presentation file should be named <Session Number>_<Your Full Name>.ppt, and be saved on your desktop.
 - > Please disable your screensaver and any power-saving features on your PC.
 - > Please bring your AC adapter and converter with you.
 - ➤ Please bring your presentation's backup data on a USB flash drive.
 - ➤ After your presentation, do not forget to retrieve your computer from the operator at the venue.
 - > During your presentation, please use the AC adapter included with your computer, not a mini-AC adapter.

No later than 10 min. before the session starts

➤ Please make sure to come to the session room and take the speaker's seat at the left front side of the room.

After the Congress:

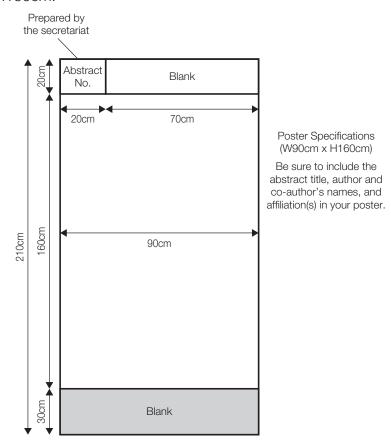
• Your submitted data will be discarded after the congress.

For Presenters

2. Poster Presentations

To present your poster onsite, please follow the steps below:

- Be sure to include the abstract title, author and coauthor names, and the affiliation(s).
- Prepare your poster to fit on the poster board (W90cm x H210cm). Recommended poster size is W90cm×H160cm.



• Bring your poster with you to the Annex Hall of Kyoto International Conference Center on the day of your poster presentation.

Poster set-up/removal times

Presentation date	Set-up	Removal
June 25	June 24 12:00-17:00 or June 25 08:00-09:00	18:30-19:30
June 26	08:00-09:00	18:30-19:30
June 27	08:00-09:00	18:30-19:30
June 28	08:00-09:00	16:00-17:00

^{*} Posters that are left on the poster boards after the removal time has ended will be removed and discarded by the Secretariat after the Congress.

Oral Sessions

Oral Sessions

Monday, June 24

Plenary IUPA	B Katchalsky Lecture Room A
13:30-14:20	Exploration of Biological Diversity
Chair	Takeharu Nagai (Osaka University)
PL-1	Exploration of Biological Diversity
	Feng Zhang ^{1,2,3} ¹ Howard Hughes Medical Institute, ² Broad Institute of MIT and Harvard, ³ McGovern
	Institute for Brain Research, Department of Brain and Cognitive Sciences, Department of Biological Engineering, Massachusetts Institute of Technology

Symposium ²	1 Room A
14:30-16:50	Super-resolution and Advanced Microscopy Imaging
Chairs	Takanobu Katoh (The University of Tokyo)
	Elizabeth Hinde (School of Physics, Faculty of Science, The University of Melbourne)
\$1-1	Cryo-optical microscopy for super-resolution imaging of the moment Katsumasa Fujita ^{1,2} ¹Osaka University, ²AIST
\$1-2	3D architectural dynamics of super-molecular assembly in live cells by using single molecule orientation imaging with advanced fluorescence polarization probes
	Tomomi Tani ¹ , Nori Nakai ² , Keisuke Sato ² , Kenta Saito ² , Sumio Terada ² ¹ Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology, ² Graduate School of Medicine, Tokyo Medical and Dental University
\$1-3	Ångström-resolution fluorescence microscopy <u>Luciano A. Masullo</u> ¹ , Susanne Reinhardt ^{1,2} , Isabelle Baudrexel ^{1,3} ,

Luciano A. Masullo¹, Susanne Reinhardt^{1,2}, Isabelle Baudrexel^{1,3}, Philipp Steen^{1,2}, Rafal Kowalewski^{1,2}, Alexandra Eklund^{1,3}, Sebastian Strauss^{1,2}, Eduard Unterauer^{1,2}, Thomas Schlichthaerle^{1,2}, Maximilian Strauss^{1,2}, Christian Klein^{3,4}, Ralf Jungmann^{1,2}

¹Max Planck Institute of Biochemistry, Planegg, Germany, ²Faculty of Physics and Center for NanoScience, Ludwig Maximilian University, Munich, Germany, ³Department of Chemistry and Biochemistry, Ludwig Maximilian University, Munich, Germany, ⁴Roche Innovation Center Zurich, Roche Pharma Research and Early Development, Schlieren, Switzerland

Development, Schliefen, Switzenand

Monday, June 24

\$1-4 Fluorescence fluctuation spectroscopy of protein transport as a function of oligomeric state

Elizabeth Hinde, Ashleigh Solano, Xiaomeng Zhang

University of Melbourne

\$1-5 Biophysical Characterization of Cancer Metabolism: Multiparametric Imaging and Phenotypic Tracking in Mitochondrial Dynamics

Michelle Digman, Giulia Tedeschi, Lorenzo Scipioni, Austin Lefebvre,

Francesco Palomba

Department of Biomedical Engineering and the Laboratory for Fluorescence

Dynamics, University of California Irvine, Irvine, CA, USA

\$1-6 Immotile cilia mechanically sense the direction of fluid flow for left-right determination

Takanobu A. Katoh^{1,2}

¹Grad. Sch. Med., The Univ. of Tokyo, Tokyo, Japan, ²BDR., Riken, Kobe, Japan

Symposium 2	
14:30-16:50	Morphogenesis during Development and Repair
Chairs	Satoru Okuda (Nano Life Science Institute, Kanazawa University)
	Yanlan Mao (Laboratory for Molecular Cell Biology, University College London)
00.4	
S2-1	Mechano-hydraulic control of mammalian ovarian follicle development
S2-1	Mechano-hydraulic control of mammalian ovarian follicle development Chii Jou Chan ^{1,2} , Arikta Biswas ¹ , Boon Heng Ng ¹ , Yuting Lou ¹ ,
S2-1	•

\$2-2 A 3D Vertex Model to analyse the Drosophila wing disc during wound healing

Pablo Vicente Munuera¹, Jose J Muñoz², Yanlan Mao¹

¹Laboratory for Molecular Cell Biology, University College London, London, UK, ²Laboratori de Càlcul Numèric (LaCàN), Centre Internacional de Mètodes Numèrics en Enginyeria (CIMNE), Universitat Politècnica de Catalunya (UPC), Barcelona, Spain

\$2-3 Comparative study of interspecies diversity in cortical stiffness using atomic force microscopy

Misato Iwashita, Yoichi Kosodo

Korea Brain Research Institute

\$2-4 Robust cytoplasmic partitioning by resolving an intrinsic cytoskeletal instability

Melissa Rinaldin^{1,2,3}, Alison Kickuth^{1,2,3}, Benjamin Dalton⁴, Yitong Xou⁵, Stefano Di Talia⁵, Jan Bruqués^{1,2,3}

¹Cluster of Excellence Physics of Life, TU Dresden, Dresden, 01307 Germany, ²Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, 01307 Germany, ³Center of Systems Biology Dresden, 01307 Germany, ⁴Department of Physics, Freie Universität Berlin, Berlin, 14195 Germany, ⁵Department of Cell Biology, Duke University Medical Center, Durham, NC 27710 USA

\$2-5 "Telescope model" for coordinated organ morphogenesis and stem cell formation

Ritsuko Morita

Graduate School of Frontier Biosciences, Osaka University

\$2-6 The role of nuclear properties and packing for movements in pseudostratified epithelia

Mariana Gil, Lucrezia Ferme, <u>Caren Norden</u> Instituto Gulbenkian de Cienca, Oeiras, Portugal

Symposium 3 Room B-	
14:30-16:50	Cryo Electron Microscopy and Tomography
Chairs	Fei Sun (CAS)
	Masahide Kikkawa (Graduate School of Medicine, The University of Tokyo)
S3-1	In-cell structure of microtubule doublet in mouse sperm flagella reveals the structural stability essential for motility Fei Sun National Key Laboratory of Biomacromolecules, CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences, Beijing 100101, China.
S3-2	Combination of genetics and cryo-electron tomography to study the calcium-dependent regulation of outer arm dynein in zebrafish sperm Hiroshi Yamaguchi, Motohiro Morikawa, Masahide Kikkawa Department of Cell Biology and Anatomy, Graduate School of Medicine, The Univ. of Tokyo

Monday, June 24

S3-3 Deciphering the Mechanism of Ribosomal Methylase Mediated Antibiotic Resistance

Ruchi Anand

Department of Chemistry, Indian Institute of Technology Bombay, Mumbai India 400076

Structural physiology of gastric proton pump and related cation pumps

Kazuhiro Abe^{1,2}

¹Graduate School of Science, Hokkaido University, Sapporo, Japan, ²Cellular and Structural Physiology Institute, Nagoya University, Nagoya, Japan

S3-5 CryoEM brings new mechanistic insights into double-stranded DNA break repair

Gabriel Lander, Chris Zerio

Scripps Research, La Jolla CA 92037, USA

S3-6 Structural Studies of SLC Transporters Relevant to Health and Diseases

Yongchan Lee

Graduate School of Medical Life Science, Yokohama City University, Kanagawa, Japan

Symposium 4	₽ R	oom D
14:30-16:50	Correlative Cell Imaging	
Chairs	Tokuko Haraguchi (Frontier of Biosciences, Osaka University)	
	Ioanna Mela (Department of Pharmacology, University of Cambridge)	
	Tomonobu Watanabe (Center for Biosystems Dynamics Research/Resear Institute for Radiation Biology and Medicine, RIKEN/Hiroshima University)	rch

S4-1 Correlative Atomic Force Microscopy with Super-resolution Microscopy for the characterisation of biological specimens

Ioanna Mela

University of Cambridge, Department of Pharmacology

S4-2 The endoplasmic reticulum connects to the nucleus by constricted junctions that mature after open mitosis in mammalian cells

Helena Bragulat-Teixidor^{1,2,3}, Keisuke Ishihara⁴, Gréta Martina Szücs^{1,2}, Shotaro Otsuka^{1,2}

¹Max Perutz Labs, Vienna Biocenter Campus (VBC), Vienna, Austria, ²Medical University of Vienna, Center for Medical Biochemistry, Vienna, Austria, ³Vienna BioCenter PhD Program, Doctoral School of the University of Vienna and Medical University of Vienna, Vienna, Austria, ⁴Department of Computational and Systems Biology, School of Medicine, University of Pittsburgh, Pittsburgh, PA, USA

\$4-3 From Transcription to Translation: Single Molecule Imaging of Endogenous Gene Activity

<u>Timothy Stasevich</u>, Matthew Saxton, Tatsuya Morisaki, O'Neil Wiggan Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO, USA

S4-4 Label-free correlative imaging reveals the heterogeneity of tumor microenvironments

<u>Guan-Yu Zhuo</u>, Wei-Hsun Wang, Ming-Chi Chen Institute of Translational Medicine and New Drug Development, China Medical University, Taiwan

S4-5 Live CLEM imaging for studies of nuclear envelope dynamics

Tokuko Haraguchi

Graduate School of Frontier Biosciences, Osaka University

Symposium 5	Room E
14:30-16:50	Theoretical Biology of Complex Systems
Chairs	Mikhail Tikhonov (Physics, Washington University)
	Masayo Inoue (Graduate School of Engineering, Kyushu Institute of Technology)
	Chikara Furusawa (Center for Biosystems Dynamics Research, RIKEN)
S5-1	Emergent simplicity in microbial ecosystems Mikhail Tikhonov Washington University in St Louis, St Louis, MO, USA
\$5-2	The origin of non-equilibrium order Arvind Murugan University of Chicago

Monday, June 24

S5-3 Impact of population spatial structure on mutant fixation, from models on graphs to the gut

Anne-Florence Bitbol

EPFL

S5-4 Revealing global stoichiometry conservation architecture in cells by Raman and gene expression correspondences

Ken-ichiro F. Kamei¹, Koseki Kobayashi-Kirschvink^{2,3}, Takashi Nozoe¹,

Hidenori Nakaoka⁴, Miki Umetani¹, Yuichi Wakamoto¹

¹The University of Tokyo, ²Broad Institute of MIT and Harvard, ³Massachusetts Institute of Technology, ⁴Kyoto University

S5-5 Stability and death of in silico Escherichia coli metabolism

Yusuke Himeoka¹, Chikara Furusawa^{1,2}

¹Universal biology institute, The University of Tokyo, ²Center for Biosystems Dynamics Research, RIKEN

Hands-on Training Session D Room C-2 14:30-16:50 **DNA Nanomachine Tutorial** Chair Shin-ichiro Nomura (Tohoku University) HT-D-1 DNA origami-based integrated molecular systems and functional nanomachines Masavuki Endo^{1,2} ¹Research Development Division, Kansai University, ²WPI-iCeMS, Kyoto University HT-D-2 Nanomechanical DNA Origami Devices Akinori Kuzuya Department of Chemistry and Materials Engineering, Kansai University

Multi-reconfigurable and multi-responsive DNA origami nanodevices

Yuki Suzuki Mie University

HT-D-3

HT-D-4 Online user interface of computational tools for accelerating DNA nanotechnology research

Ibuki Kawamata **Kyoto University**

HT-D-5 Long DNA strands' insertion into DNA droplets as a potential model for chromatin condensates studies

Nathan Nunes Evangelista¹, Chimura Takahiko², Koki Kamiya³,

Masahiro Takinoue^{1,2}

¹Department of Life Science and Technology, Tokyo Institute of Technology, ²Department of Computer Science, Tokyo Institute of Technology, ³Division of Molecular Science, Graduate School of Science and Technology, Gunma University

HT-D-6 DNA nanopore sensor for cell secretion measurement

Hiromu Akai, Kan Shoji

Nagaoka University of Technology

The Avanti Prize Lecture		Room A
17:00-17:40	From color-tuning to optogenetics: modeling the relationsh between red-light absorption and fluorescence intensity in archaerhodopsins	ip
Chairs	Manuel Prieto (iBB/IST-Institute for Bioengineering and Bioscience, UniLisbon, Portugal) Anthony Watts (University of Oxford, UK)	versity of

AP From color-tuning to optogenetics: modeling the relationship between red-light absorption and fluorescence intensity in archaerhodopsins

Massimo Olivucci^{1,2}

¹Department of Biotechnology, Chemistry and Pharmacy, University of Siena, Siena, Italy, ²Department of Chemistry, Bowling Green State University, Bowling Green, OH, USA

Tuesday, June 25

Keynote 1	Room B-1
9:00-9:50	Searching for Universal Laws in Evolved and Evolvable Complex Biological Systems
Chair	Chun-Biu Li (Stockholm University)
KL-1	Searching for Universal Laws in Evolved and Evolvable Complex Biological Systems Kunihiko Kaneko Niels Bohr Institue

The 20th Early Career Award in Biophysics Candidate Presentations Room A 10:00-12:20 Chairs Takayuki Nishizaka (Gakushuin Univesity) Shuji Akiyama (Institute for Molecular Science)

YF-1 Microtubule/kinesin complexes spontaneously emerge vortices in cell-sized droplet generated by water/water phase separation

<u>Hiroki Sakuta</u>^{1,2}, Naoki Nakatani³, Takayuki Torisawa⁴, Yutaka Sumino⁵, Kanta Tsumoto⁶, Kazuhiro Oiwa^{7,8}, Kenichi Yoshikawa³

¹Universal Biology Institute, University of Tokyo, ²Graduate School of Arts and Sciences, University of Tokyo, ³Faculty of Life and Medical Sciences, Doshisha University, ⁴Cell Architecture Laboratory, National Institute of Genetics, ⁵Department of Applied Physics, Faculty of Advanced Engineering Tokyo University of Science, ⁶Graduate School of Engineering, Mie University, ⁷Advanced ICT Research Institute, National Institute of Information and Communications Technology, ⁸Graduate School of Science, University of Hyogo

YF-2 Oxygen-evolving photosystem II structures during S1–S2–S3 transitions

Hongjie Li, Yoshiki Nakajima, Michihiro Suga, Jian-Ren Shen Research Institute for Interdisciplinary Science and Graduate School of Natural Science and Technology, Okayama University, Okayama, Japan

YF-3 A high-throughput analysis of cancer-cell dormancy under mechanical confinement with micro-hydrogel beads

Misa Minegishi^{1,2}, Keiji Nozaki^{2,3}, Kaori Nishikawa¹, Hirofumi Shintaku^{1,2,3}
¹RIKEN Cluster for Pioneering Research, RIKEN., ²Institute for Life and Medical Science, Kyoto University., ³Department of Micro Engineering, Graduate School of Engineering, Kyoto University.

YF-4 Crosstalk of two bacterial actins composed of the force generation unit of Spiroplasma swimming

Daichi Takahashi^{1,2}, Makoto Miyata^{2,3}, Ikuko Fujiwara⁴

¹Research Institute for Interdisciplinary Science, Okayama University, Japan, ²Graduate School of Science, Osaka Metropolitan University, Japan, ³The OMU Advanced Research Institute for Natural Science and Technology, Osaka Metropolitan University, Japan, ⁴Department of Materials Sciences and Bioengineering, Nagaoka University of Technology, Japan

YF-5 Spatiotemporal formation of a single liquid-like condensate of α-synuclein and subsequent aging by optical trapping

<u>Keisuke Yuzu^{1,2}</u>, Ching-Yang Lin², Po-Wei Yi², Chih-Hao Huang², Hiroshi Masuhara², Eri Chatani¹

¹Graduate School of Science, Kobe University, Kobe, Japan, ²Department of Applied Chemistry, National Yang Ming Chiao Tung University, Hsinchu, Taiwan

YF-6 Encapsulation of cell nucleolus by single-stranded DNA

Koichiro Maki^{1,2,3,4}, Jumpei Fukute^{1,3}, Taiji Adachi^{1,2,3,4}

¹Laboratory of Biomechanics, Institute for Life and Medical Sciences, Kyoto University, Japan, ²Department of Micro Engineering, Graduate School of Engineering, Kyoto University, Japan, ³Department of Mammalian Regulatory Network, Graduate School of Biostudies, Kyoto University, Japan, ⁴Department of Medicine and Medical Science, Graduate School of Medicine, Kyoto University, Japan

YF-7 From cellular chirality to large-scale chirality: Emergence of chiral spiral in migrating cellular system

Masayuki Hayakawa¹, Biplab Bhattacherjee¹, Lihao Guo¹, Hidekazu Kuwayama², Tatsuo Shibata¹

¹Laboratory for Physical Biology, RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, ²Faculty of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Japan

YF-8 Myosin and tropomyosin-troponin complementarily regulate thermal activation of striated muscles

<u>Shuya Ishii</u>^{1,2}, Kotaro Oyama^{1,2}, Fuyu Kobirumaki-Shimozawa², Tomohiro Nakanishi^{2,3}, Naoya Nakahara⁴, Madoka Suzuki⁵, Shin'ichi Ishiwata⁶, Norio Fukuda²

¹QST, Gunma, Japan, ²Dept Cell Physiol, Sch Med, Jikei Univ, Tokyo, Japan, ³Dept Anesthesiology, Sch Med, Jikei Univ, Tokyo, Japan, ⁴Dept Mol Physiol, Sch Med, Jikei Univ, Tokyo, Japan, ⁵IPR, Osaka Univ, Osaka, Japan, ⁶Fac Sci Engn, Waseda Univ, Tokyo, Japan

Tuesday, June 25

YF-9 Prediction of detailed structures over the entire free energy landscape of protein folding using extended statistical mechanical models and restrained simulations

Koji Ooka¹, Munehito Arai^{1,2,3}

¹College of Arts and Sciences, The University of Tokyo, Tokyo, Japan., ²Department of Life Sciences, The University of Tokyo, Tokyo, Japan., ³Department of Physics, The University of Tokyo, Tokyo, Japan.

YF-10 Pseudo-luciferase activity of the SARS-CoV-2 spike protein

Ryo Nishihara^{1,2}, Hisham M Dokainish^{3,4}, Yoshiki Kihara^{1,5}, Yuji Sugita^{4,6,7}, Ryoji Kurita^{1,5}

¹Health and Medical Research Institute, National Institute of Advanced Industrial Science and Technology, ²Japan Science and Technology Agency, PRESTO, ³Faculty of Pharmaceutical Sciences, Hokkaido University, ⁴Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research, ⁵Faculty of Pure and Applied Sciences, University of Tsukuba, ⁶Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, ⁷Computational Biophysics Research Team, RIKEN Center for Computational Science

Symposium 6	Room B-1
10:00-12:20	Mechanosensing and Mechanobiology, Biological Temperature
Chairs	Mitsuhiro Iwaki (Protein Biophysics Group, Bio-ICT Lab, National Institute of Information and Communications Technology)
	Kate Poole (Faculty of Medicine & Health, School of Biomedical Sciences, University of New South Wales)

S6-1 Mammalian mechanosensing via ion channels

Kate Poole, Abie Cargando, Phoebe Dunbabin, Lioba Schroeter,

Amrutha Patkunarajah

School of Biomedical Sciences, Faculty of Medicine and Health, University of New South Wales, Sydney, Australia

Visualization and Control of Biological Temperature Using Subcellular-Targeted Chemical Dyes

Satoshi Arai

WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa University

S6-3 Mechanotransduction at cell-cell junctions: beyond the usual suspects

Alexander Dunn Stanford University

S6-4 DNA nanodevices for single-molecule biology in mechanosystems

Mitsuhiro Iwaki^{1,2,3}

¹Advanced ICT Research Institute, National Institute of Information and

Communications Technology, ²RIKEN Center for Biosystems Dynamics Research,

³Immunology Frontier Research Center, Osaka University

S6-5 A high-throughput analysis of cancer-cell dormancy under mechanical

confinement with micro-hydrogel beads

Misa Minegishi^{1,2}, Keiji Nozaki^{2,3}, Kaori Nishikawa¹, Hirofumi Shintaku^{1,2,3}
¹RIKEN Cluster for Pioneering Research, RIKEN., ²Institute for Life and Medical Science, Kyoto University., ³Department of Micro Engineering, Graduate School of Engineering, Kyoto University.

\$6-6 Platelet migration behavior is dependent on substrate stiffness

Hendrik von Eysmondt, Jan Seifert, Johannes Rheinlaender,

Tilman E. Schäffer

Institute of Applied Physics, University of Tübingen, Germany

Symposium 7	Room B-2
10:00-12:20	Protein Structure to Function 1
Chairs	Ho Min Kim (Korea Advanced Institute of Science and Technology)
	Mikako Shirouzu (Center for Biosystems Dynamics Research, RIKEN)
\$7-1	Structural dynamics of parathyroid hormone receptor and development of biased agonist Osamu Nureki, Kazuhiro Kobayashi The University of Tokyo, Tokyo, Japan
\$7-2	Structure and Function of TMEM87A, a unique Voltage-dependent Cation Channel in Golgi apparatus Ho Min Kim KAIST
\$7-3	Structural basis for antiepileptic drugs and botulinum neurotoxin recognition of SV2A Atsushi Yamagata RIKEN Center for Biosystems Dynamics Research

Tuesday, June 25

\$7-4 Multi-dimensional crystallography: how do enzymes work?

Pedram Mehrabi¹, Eike Schulz⁴, Sihyun Sung³, David von Stetten³, Caitlin Hatton¹, Stephan Kleine-Doepke¹, Jan-Philipp Leimkohl², Hendrik Schikora², Martin Kollewe², Friedjof Tellkamp²

¹Institute for Nanostructure and Solid State Physics, University of Hamburg, Hamburg, Germany., ²Max-Planck-Institute for the Structure and Dynamics of Matter, Hamburg, Germany., ³EMBL-Hamburg, ⁴University Medical Center Hamburg-Eppendorf (UKE), Hamburg, Germany

S7-5 SAM lyases – small, divergent and multifunctional proteins in bacteriophage counter defense

Maria Selmer

Department of Cell and Molecular Biology, Uppsala University, Sweden

S7-6 Unraveling the Energy Transition Network That Dictates Allosteric Activation of Proapoptotic High-Temperature Requirement Protease A2

<u>Kakoli Bose</u>¹, Aasna Parui¹, Vandana Mishra², Shubhankar Dutta¹, Prasenjit Bhaumik²

¹Bose Lab, ACTREC Tata Memorial Centre, NAVI MUMBAI, India; Homi Bhabha National Institute, Mumbai, India, ²Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, India

Symposium 8	Room C-2
10:00-12:20 Chair	Unstructured/Disordered Proteins, RNA Shintaro Iwasaki (Cluster for Pioneering Research, RIKEN)
S8-1	DEAD-box ATPases are global regulators of phase-separated organelles and RNA flux Maria Hondele Biozentrum, University of Basel, Spitalstrasse 41, 4056 Basel, Switzerland
\$8-2	Engineering phase separations in cells to manipulate RNA condensates Zoher Gueroui Ecole Normale Supérieure

S8-3 Transcriptomics in P-bodies reveals the selective mRNA release to modulate translation

Yuichi Shichino¹, Mari Mito¹, Shintaro Iwasaki^{1,2}

¹RIKEN CPR, ²Dept. Comp. Biol. Med. Sci., Grad. Sch, Front. Sci., Univ. Tokyo

S8-4 Stress Granule Fusion Mediated by Mitochondrial Dynamics Is **Essential for Cell Survival**

Tae Lim Park, Won-Ki Cho

Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST), Daejeon 34141, Republic of Korea

S8-5 Amyloid conformation-dependent disaggregation revealed by singlemolecule fluorescence imaging

Yoshiko Nakagawa^{1,2}, Howard C.H. Chen¹, Yusuke Komi¹,

Shinju Sugiyama¹, Takaaki Kurinomaru³, Yuri Tomabechi⁴,

Elena Krayukhina³, Kenji Okamoto⁵, Takeshi Yokoyama⁴, Mikako Shirouzu⁴,

Susumu Uchiyama^{3,6}, Megumi Inaba², Tatsuya Niwa⁷, Yasushi Sako⁵,

Takahiro Nakayama⁸, Hiroki Konno⁸, Noriyuki Kodera⁸, Hideki Taguchi⁷,

Motomasa Tanaka¹

¹RIKEN Center for Brain Science, Saitama, Japan, ²School of Life Science and Technology, Tokyo Institute of Technology, Kanagawa, Japan, ³Research Department, U-Medico Inc., Osaka, Japan, ⁴RIKEN Center for Biosystems Dynamics Research, Kanagawa, Japan, ⁵Cellular Informatics Laboratory, RIKEN, Saitama, Japan, ⁶Graduate School of Engineering, Osaka University, Osaka, Japan, ⁷Cell Biology Center, Institute of Innovative Research, Tokyo Institute of Technology, Kanagawa, Japan, ⁸WPI Nano Life Science Institute, Kanazawa University

Symposium 9	Room D
10:00-12:20	Lipid and Membrane Biophysics
Chairs	Chiho Watanabe (Graduate school of integrated sciences for life, Hiroshima University)
	Roberto Covino (Frankfurt Institute for Advanced Studies)
S9-1	Exploring Lipid and Membrane Biophysics Chiho Watanabe

Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan

Tuesday, June 25

\$9-2 High-throughput analysis of membrane fluidity unveils a hidden dimension in immune cell states

<u>Luca Andronico</u>¹, Yidan Jiang^{1,2}, Valentina Carannante³, Sofia Iskrak¹, Patrick A. Sandoz³, Jaromir Mikes¹, Andrey Klymchenko⁴, Marcus Buggert⁵, Anders Österborg^{6,7}, Björn Önfelt^{3,5}, Petter Brodin¹, Erdinc Sezgin¹

¹Science for Life Laboratory, Department of Women's and Children's Health, Karolinska Institutet, 17165 Solna, Sweden, ²European Molecular Biology Laboratory (EMBL), 69117, Heidelberg, Germany, ³Science for Life Laboratory, Department of Applied Physics, KTH Royal Institute of Technology, 114 28 Stockholm, Sweden, ⁴Laboratoire de Bioimagerie et Pathologies, UMR 7021 CNRS, Université de Strasbourg 74 Route du Rhin 67401 Illkirch France, ⁵Department of Medicine Huddinge, Centre for Infectious Medicine, Karolinska Institutet, 171 77, Stockholm, Sweden, ⁶Department of Hematology, Karolinska University Hospital, Stockholm, Sweden, ⁷Department of Oncology-Pathology, Karolinska Institutet, 171 77, Stockholm, Sweden

S9-3 Biological tuning of the membrane phase transition facilitates plasma membrane organization and function.

Sarah Veatch

University of Michigan

S9-4 Lipid heterogeneity within giant vesicles confer robust protein pattern formation

Nishu Kanwa

Max Planck Institute for Biochemistry, Germany

\$9-5 Electron diffraction reveals substructures in lipid raft-like ordered membrane domains

Masanao Kinoshita, Mayu Maeda, Shimpei Yamaguchi, Nobuaki Matsumori Kyushu University

\$9-6 Elastic and viscous properties of model lipid bilayers measured using dynamic neutron scattering

Michihiro Nagao^{1,2,3}

¹National Institute of Standards and Technology Center for Neutron Research,

²Department of Materials Science and Engineering, University of Maryland,

³Department of Physics and Astronomy, University of Delaware

S9-7 Investigating how membranes control the thermodynamics and kinetics of membrane protein complexes with molecular simulations.

Roberto Covino

Frankfurt Institute for Advanced Studies, Ruth-Moufang-Straße 1, 60438 Frankfurt am Main, Germany.

Symposium [*]	10 Room E	
10:00-12:20	Data Science for Integrated Dynamic Structural Biology	
Chairs	Florence Tama (Nagoya University & RIKEN Center for Computational Science)	
	Jianhan Chen (Chemistry, University of Massachusetts Amherst)	
\$10-1	Solving 3D puzzles of biomolecular interactions by integrative modelling	
	Alexandre Bonvin	
	Utrecht University, Faculty of Science, Bijvoet Centre	
\$10-2	Searching the Molecular Space using Neural Network Energy Models Chaok Seok Seoul National University	
\$10-3	Dynamic structure of monomeric Grb2 revealed via integrative	

modeling

Mao Oide¹, Teppei Ikeya², Weitong Ren³, Hisham Dokainish⁴, Takaharu Mori⁵, Yutaka Ito², Yuji Sugita^{1,6,7}

¹Theoretical Molecular Science Laboratory, RIKEN Clusters for Pioneering Research, Saitama, Japan, ²Department of Chemistry, Graduate School of Science, Tokyo Metropolitan University, Tokyo, Japan, ³Wenzhou Institute, University of Chinese Academy of Sciences, Zhejiang, China, ⁴Laboratory of Biomolecular Science, Faculty of Pharmaceutical Sciences, Hokkaido University, Hokkaido, Japan, ⁵Department of Chemistry, Faculty of Science Division I, Tokyo University of Science, Tokyo, Japan, ⁶Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, Hyogo, Japan, ⁷Computational Biophysics Research Team, RIKEN Center for Computational Science, Hyogo, Japan

S10-4 Dynamics of Intrinsically Disordered Proteins via Simulations and Machine Learning

Michael Feig

Michigan State University, East Lansing, MI, USA

Tuesday, June 25

\$10-5 Protein structural ensembles from 3D and 2D cryo-EM data

Massimiliano Bonomi

Institut Pasteur, Université Paris Cité, CNRS UMR 3528, Computational Structural Biology Unit, Paris, France

Symposium 11 Ro		1 Room A
	16:00-18:20	Single Molecule Biophysics in Chromosome Science
	Chairs	Kayo Hibino (Department of Chromosome Science, National Institute of Genetics)
		Je-Kyung Ryu (Seoul National University)

\$11-1 Single-nucleosome imaging unveils dynamic organization of mitotic chromosomes.

<u>Kayo Hibino</u>^{1,2}, Yuji Sakai³, Sachiko Tamura¹, Masatoshi Takagi⁴, Katsuhiko Minami^{1,2}, Toyoaki Natsume^{1,2,6}, Masa A. Shimazoe^{1,2}, Masato T. Kanemaki^{1,2,5}, Naoko Imamoto⁴, Kazuhiro Maeshima^{1,2}

¹National Institute of Genetics, Mishima, Japan, ²SOKENDAI, Mishima, Japan, ³Kyoto University, Kyoto, Japan, ⁴RIKEN Cluster for Pioneering Research, Wako, Japan, ⁵The University of Tokyo, Tokyo, Japan, ⁶Present address: Research Center for Genome & Medical Sciences, Tokyo

\$11-2 Mechanics and microrheology of native human mitotic chromosomes

Gijs JL Wuite

Vrije Universiteit, De Boelelaan 1081, 1081 HV, Amsterdam, The Netherlands

\$11-3 Unpaused and Loosened Unwinding of Nucleosomal DNA on H2A.B Variants

Hikaru Nozawa¹, Fritz Nagae², Satoshi Ogihara¹, Rina Hirano³, Hirohito Yamazaki⁴, Ryo Iizuka¹, Munetaka Akatsu³, Tomoya Kujirai³, Shoji Takada², Hitoshi Kurumizaka³, <u>Sotaro Uemura</u>¹

¹Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Tokyo, Japan, ²Department of Biophysics, Graduate School of Science, Kyoto University, Kyoto, Japan, ³Institute for Quantitative Biosciences, The University of Tokyo, Tokyo, Japan, ⁴Department of Mechanical Engineering, Nagaoka University of Technology, Niigata, Japan

\$11-4 Super-resolution imaging of transcription in living cells

Ibrahim Cissé

Department of Biological Physics Max Planck Institute of Immunobiology and Epigenetics

\$11-5 Bridging-induced phase separation by cohesin complexes

Je-Kyung Ryu

Department of physics and astronomy, Seoul National University, South Korea

Symposium 1	Room B-1
16:00-18:20	Cell Motility, Cytoskeleton and Motor Proteins
Chairs	Sarah Köster (Faculty of Physics / Institute for X-Ray Physics, University of Goettingen)
	Ikuko Fujiwara (Dep. of Materials Science and Bioengineering, Nagaoka University of Technology)

\$12-1 Inhibitory mechanisms of actin polymerization dynamics at the molecular level by Cytochalasin D and Archea gelsolin

Ikuko Fujiwara¹, Takahiro Mitani¹, Horyo Mizuki¹, Toshiro Oda²,

Shuichi Takeda³

¹Material Sciences and Bioengineering, Nagaoka University of Technology, Japan, ²Faculty of Health and Welfare, Tokai Gakuin University, Kakamigahara, Japan, ³Okayama University, Okayama, Japan

\$12-2 COLLECTIVE MOTOR AND MICROTUBULE MECHANICS UNDERLYING SPINDLE SELF-ORGANIZATION

Yuta Shimamoto^{1,2}

¹National Institute of Genetics, ²SOKENDAI University

\$12-3 Intermediate filaments in the cytoskeleton: safety belt and shock absorber for the cell?

Sarah Köster

University of Göttingen, Germany

\$12-4 Intra- and extra-cellular functions of vimentin: mechanics, signaling, and adhesion

Paul Janmey¹, Robert Bucki¹, Alison Patteson²

¹Department of Physiology, University of Pennsylvania, Philadelphia PA, USA,

²Physics Department, Syracuse University, Syracuse NY, USA

\$12-5 Cell biophysics: phase diagrams, phase portraits and trajectories

Cécile Sykes

Laboratoire de Physique de l'École normale supérieure, ENS, Université PSL, CNRS, Sorbonne Université, Université Paris Cité, F-75005 Paris, France

Tuesday, June 25

Symposium '	
16:00-18:20	Protein Structure to Function 2
Chairs	Shun-ichi Sekine (RIKEN)
	Heeyoun Bunch (Applied Biosciences, Kyungpook National University)
S13-1	Structural basis of promoter-proximal pausing of RNA polymerase II at +1 nucleosome Shun-ichi Sekine
	RIKEN Center for Biosystems Dynamics Research, Yokohama, Japan
\$13-2	Coarse-grained molecular dynamics simulations of parental histone H3/H4 recycling by a replisome
	Fritz Nagae ¹ , Yasuto Murayama ² , Tsuyoshi Terakawa ¹
	¹ Department of Biophysics, Graduate School of Science, Kyoto University Kyoto, Japan, ² Department of Chromosome Science, National Institute of Genetics, Shizuoka, Japan
\$13-3	Structural and biochemical analysis of a unique structural unit of chromatin
	Kayo Nozawa ¹ , Hitoshi Kurumizaka ²
	¹ School of Life Science and Technology, Tokyo Institute of Technology, ² Institute for Quantitative Biosciences, The University of Tokyo

\$13-4 A dual interaction between RSV NS1 protein and MED25 underlies RSV virulence and interferon antagonism

Celia Ait-Mouhoub², Jiawei Dong¹, Alexis Verger³, Marie Galloux², Delphyne Descamps², Jean-Francois Eleouet², Monika Bajorek², Christina Sizun¹

¹Institut de Chimie des Substances Naturelles, CNRS, Université Paris-Saclay, Gif-sur-Yvette, France, ²Virologie et Immunologie Moléculaires, INRAE, Université Paris-Saclay, UVSQ, Jouy-en-Josas, France, ³Integrative Structural Biology, CNRS, INSERM, Université de Lille, Institut Pasteur de Lille, Lille, France

\$13-5 ERK2-topoisomerase II regulatory axis is important for gene activation in immediate early genes

Heeyoun Bunch^{1,2}, Deukyeong Kim², Masahiro Naganuma³, Reiko Nakagawa⁴, Anh Cong⁵, Jaehyeon Jeong¹, Haruhiko Ehara³, Hongha Vu⁶, Jeong Ho Chang⁶, Matthew Schellenberg⁵, Shun-ichi Sekine³

¹Department of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea, ²School of Applied Biosciences, College of Agriculture & Life Sciences, Kyungpook National University, Daegu, Republic of Korea, ³Laboratory for Transcription Structural Biology, RIKEN Center for Biosystems Dynamics Research, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Japan, ⁴RIKEN BDR Laboratory for Phyloinformatics, Hyogo, Japan, ⁵Department of Biochemistry and Molecular Biology, Mayo Clinic, Rochester, Minnesota, USA, ⁶Department of Biology Education, Kyungpook National University, Daegu, Republic of Korea

\$13-6 Topological formation of transcriptional condensates relative to subnuclear compartments

Won-Ki Cho

Korea Advanced Institute of Science and Technology (KAIST)

\$13-7 Spatial regulation of ribosomal RNA transcription by phase separation and transition

Satoru Ide^{1,2}, Yasuto Murayama^{1,2}, Kazuhiro Maeshima^{1,2}

¹National Institute of Genetics, Shizuoka, Japan, ²SOKENDAI (the Graduate University for Advanced Studies), Japan

Symposium 14 16:00-18:20 Data Science, Machine Learning, and Analytical Frameworks for Understanding the Heterogeneity of Cellular and Multicellular Systems Chairs Susanne Rafelski (Allen Institute for Cell Science) Katsuyuki Shiroguchi (Center for Biosystems Dynamics Research (BDR), RIKEN)

\$14-1 Integrated intracellular organization dynamics and its variations in human iPS cells

Allen Institute for Cell Science¹, Julie A Theriot², <u>Susanne Rafelski</u>¹
Allen Institute for Cell Science Seattle, WA, USA, ²Department of Biology and Howard Hughes Medical Institute, University of Washington Seattle, WA USA

Tuesday, June 25

\$14-2 Machine learning interpretable models of cell mechanics and mophogenesis

Vincenzo Vitelli

University of Chicago, Chicago, USA

\$14-3 Enhancing Identification of Cancer Stem Cells through Line

Illumination Raman Microscopy and Hydrogel-Based Platforms

Jean-Emmanuel Clement Hokkaido University WPI-ICReDD

\$14-4 Cellular gradient flow structure connects single-cell-level rules and

population-level dynamics

<u>Shuhei Horiguchi</u>^{1,2}, Tetsuya Kobayashi²
¹Kanazawa University, ²The University of Tokyo

\$14-5 Imaged-based prediction of single-cell transcriptomic phenotypes

using robotic data acquisition

Katsuyuki Shiroguchi

RIKEN Center for Biosystems Dynamics Research (BDR), Japan

\$14-6 Machine learning for Overcoming Heterogeneity of Single-cell

Datasets

Maria Brbic

EPFL

Hands-on Training Session A 16:00-18:20 Millions of Single Live Cell Analysis with the Automated Trans-scale-scope, AMATERAS Chairs Shuichi Onami (RIKEN Center for Biosystems Dynamics Research) Takeharu Nagai (Osaka University)

HT-A-1 Automated trans-scale scope opens up a new horizon in life science research

Takeharu Nagai^{1,2,3}

¹SANKEN, Osaka University, ²OTRI, Osaka University, ³RIES, Osaka University

HT-A-2 Activatable Raman probes for multiplexed vibrational imaging in live cells and tissues

Mako Kamiya

Department of Life Science and Technology, Tokyo Institute of Technology

HT-A-3 Engineering high performance biosensors to analyze signaling and metabolism in live cells

Robert E. Campbell

Department of Chemistry, School of Science, The University of Tokyo

HT-A-4 Analyzing the Invisible: Advanced Techniques in Microscopy and Spectroscopy for Internal State Characterization

Imari Sato

National Institute of Informatics

HT-A-5 Cell Tracking and Data Management for AMATERAS

Shuichi Onami^{1,2,3}

¹RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, ²RIKEN Information R&D and Strategy Headquarters, Kobe, Japan, ³RIKEN, TRIP Headquarters, Kobe, Japan

Wednesday, June 26

Plenary IUP	AB Engstrom Lecture	Room A
9:00-9:50	Filming Biomolecules in Dynamic Action by High-speed AF	M
Chair	Christina Sizun (CNRS/ICSN, Université Paris Saclay)	
PL-2	Filming biomolecules in dynamic action by high-speed AFI Toshio Ando	М

Symposium '	Symposium 15 Room A		
10:00-12:20	Single Molecule Biophysics with Advanced Techniques		
Chairs	Doory Kim (Department of Chemistry, Hanyang University)		
	Masataka Yanagawa (Tohoku University)		
S15-1	Unveiling receptor dynamics with single-molecule high-content analysis		
	Masataka Yanagawa ^{1,2}		
	¹ Molecular and Cellular Biochemistry, Graduate School of Pharmaceutical Sciences, Tohoku University, Miyagi, Japan, ² Cellular Informatics Laboratory, RIKEN Cluster for Pioneering Research, Saitama, Japan		
\$15-2	Multidimensional Super-Resolution Microscopy of the Living Cell Ke Xu University of California, Berkeley		
\$15-3	Subcellular localization and diffusion dynamics of RNA degradosome proteins in live bacteria cells Sangjin Kim University of Illinois at Urbana-Champaign		
S15-4	mRNA decoding in human is kinetically and structurally distinct from bacteria. Scott C Blanchard ^{1,2} ¹Department of Structural Biology, St Jude Children's Research Hospital, Memphis,		
S15-5	TN, USA, ² Chemical Biology & Therapeutics, St Jude Children's Research Hospital, Memphis, TN, USA. Ultrastructural Studies of Gram-positive Bacteria and Their		

\$15-5 Ultrastructural Studies of Gram-positive Bacteria and Their Extracellular Vesicles

Doory Kim

Hanyang University

Symposium ⁻	16 Room B-1
10:00-12:20	Rotary ATPases
Chairs	Tomoko Masaike (Faculty of Science and Technology / Department of Applied Biological Science, Tokyo University of Science)
	Alastair Stewart (Structural Biology, The Victor Chang Cardiac Research Institute)
S16-1	Mechanisms of rotary ATPases Tomoko Masaike
	Department of Applied Biological Science, Faculty of Science and Technology, Tokyo University of Science
\$16-2	E. coli ATP synthase after the addition of ATP or ADP Alastair Stewart
	The Victor Chang Cardiac Research Institute, Darlinghurst, Australia
S16-3	Inferring subsystem efficiencies in bipartite molecular machines Matthew Leighton, <u>David Sivak</u> Department of Physics, Simon Fraser University
S16-4	Biophysical characterization of the archaellar motor rotation Yoshiaki Kinosita, Rikiya Watanabe RIKEN, Saitama, Japan
S16-5	Molecular Mechanism of V-ATPase Reversible Disassembly Stephan Wilkens SUNY Upstate Medical University, Department of Biochemistry and Molecular Biology, 750 East Adams Street, Syracuse, NY 13210, USA
S16-6	Sodium motive force-driven ATP synthesis by EhV-ATPase Akihiro Otomo ^{1,2} , Lucy Zhu ³ , Mayuko Yamamoto ¹ , Yasuko Okuni ¹ , Takanori Harashima ^{1,2} , Ryota lino ^{1,2} ¹ Institute for Molecular Science, ² SOKENDAI, ³ ParisTech

Wednesday, June 26

\$16-7 Engineering of ATP synthase to enhance proton-to-ATP ratio

<u>Hiroshi Ueno</u>¹, Kiyoto Yasuda¹, Norie Hamaguchi², Riku Marui¹, Naruhiko Adachi³, Toshio Moriya³, Satomi Inaba³, Toshiya Senda³, Takeshi Murata², Hiroyuki Noji¹

¹Department of Applied Chemistry, Graduate School of Engineering, The University of Tokyo, Tokyo, Japan, ²Department of Chemistry, Graduate School of Science, Chiba University, Chiba, Japan, ³Structural Biology Research Center, Institute of Materials Structure Science, High Energy Accelerator Research Organization (KEK), Ibaraki, Japan

Symposium [*]	Room B-2
10:00-12:20	Protein Design & Engineering
Chairs	Guto Rhys (Chemistry, Cardiff University)
	Ai Niitsu (CPR, RIKEN)
\$17-1	EMBO Keynote Lecture Modular protein design for new protein folds and regulation of protein and biological processes

Roman Jerala

National Institute of Chemistry, Ljubljana, Slovenia

\$17-2 Indels: The Evolutionary Switches Bridging Protein Functions and Topologies

Paola Laurino

Protein Engineering and Evolution Unit, Okinawa Inst. of Sci. & Tech. Graduate Univ.

\$17-3 How will we catalyse unnatural reactions using proteins?

Guto Rhys

Cardiff University, UK

\$17-4 Computational design of highly active SNARE-like membrane fusion proteins

Masaharu Somiya^{1,2}, Sydney Funk¹, Neil King¹

¹Institute for Protein Design, University of Washington, ²SANKEN, Osaka University

\$17-5 Protein Structure Prediction and Design using RoseTTAFold

Minkyung Baek

Department of Biological Sciences, Seoul National University, Seoul, Republic of Korea

\$17-6 Data Efficient Protein Function Improvement by Machine Learning with Molecular Simulation

<u>Teppei Deguchi</u>^{1,2}, Yoichi Kurumida³, Shinji Iida³, Yutaka Saito^{1,2,3}

¹Graduate School of Frontier Sciences, The University of Tokyo, Chiba, Japan.,

²Artificial Intelligence Research Center, AIST, Tokyo, Japan.,

³Department of Data Science, School of Frontier Engineering, Kitasato University, Kanagawa, Japan.

Compression 40			
Symposium 1			
10:00-12:20	Neural Systems and Excitable Cells Chief Llocal (Overly to Calculate Calcul		
Chairs	Chie Hosokawa (Graduate School of Science / Department of Chemistry, Osaka Metropolitan University)		
	Sung Hyun Kim (Department of Physiology, School of Medicine,, Kyung Hee University)		
\$18-1	$A\beta$ -MISFOLDING AS PRECISE RISK PLASMA BIOMARKER FOR ALZHEIMER DEMENTIA IN A SYMPTOM-FREE STAGE		
	Klaus Gerwert ^{1,2}		
	¹ Ruhr University Bochum, Bochum, Germany, ² Center for Protein Diagnostics, Bochum, Germany		
\$18-2	Harnessing thermoplasmonics to modulate neuronal excitability and network activity Yoonkey Nam		
	Department of Bio and Brain Engineering, KAIST (Korea Advanced Institute of Science and Technology)		
\$18-3	Distinct synaptic vesicle recycling in inhibitory nerve terminals is coordinated by SV2A Sung Hyun Kim		
	Department of Physiology, School of Medicine, Kyung Hee University		
S18-4	Optical Manipulation of Molecular Dynamics in Neurons Chie Hosokawa Osaka Metroplitan University		
\$18-5	Measuring the stiffness of neuronal growth cones with scanning ion conductance microscopy		

Institute of Biochemistry (IFIB), University of Tübingen, Tübingen, Germany

¹Institute of Applied Physics, University of Tübingen, Tübingen, Germany, ²Interfaculty

Aylin Balmes¹, Hannes Schmidt², Tilman E. Schäffer¹

Wednesday, June 26

\$18-6 Optimal power-law encoding is self-organized in cultured neuronal networks

Asahi Nakamuta, Jun-nosuke Teramae

Grad Sch Informatics, Kyoto University, Kyoto, Japan

Symposium 19 Room D 10:00-12:20 Understanding Structure and Function of Emerging Viruses Chairs Juha Huiskonen (Institute of Biotechnology, Helsinki Institute of Life Science HiLIFE, University of Helsinki) Katsumi Maenaka (Faculty of Pharmaceutical Sciences, Hokkaido University)

\$19-1 Functional annotation of viral protein sugarcoats

Shang-Te Danny Hsu^{1,2,3}

¹Institute of Biological Chemistry, Academia Sinica, Taipei 11529, Taiwan, ²Institute of Biochemical Sciences, National Taiwan University, Taipei 106319, Taiwan, ³International Institute for Sustainability with Knotted Chiral Meta Matter (SKCM2), Hiroshima University, Higashihiroshima, Hiroshima 739-8527, Japan

\$19-2 Host Recognition of SARS-CoV-2 Spike: A Double-Edged Sword

Firdaus Samsudin¹, Palur Raghuvamsi^{1,2}, Lorena Zuzic¹, Ganna Petruk³, Manoj Puthia³, Jitka Petrlova³, Paul MacAry⁴, Ganesh Anand⁵, Artur Schmidtchen⁶, Peter J. Bond^{1,2}

¹Bioinformatics Institute, A*STAR, Singapore, ²Dept. of Biological Sciences, NUS, Singapore, ³Dept. of Clinical Sciences, Lund University, Sweden, ⁴Life Sciences Institute, NUS, Singapore, ⁵Dept. of Chemistry, The Pennsylvania State University, PA, USA, ⁶Dept. of Biomedical Sciences, University of Copenhagen, Denmark

\$19-3 Cryo-ET of SARS-CoV-2 provided insights into its architecture and neutralization

Sai Li

School of Life Sciences, Tsinghua University, Beijing 100084, China

S19-4 Elucidating Spike Protein Conformations from Simulation and **Experiment**

Hisham M. Dokainish^{1,2}, Yuji Sugita^{2,3,4}, Katsumi Maenaka^{1,5,6}

¹Center for Research and Education on Drug Discovery, Faculty of Pharmaceutical Sciences, Hokkaido University, Sapporo, Japan, ²Theoretical Molecular Science Laboratory, RIKEN Cluster for Pioneering Research, Wako, Japan, ³Laboratory for Biomolecular Function Simulation, RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, ⁴Computational Biophysics Research Team, RIKEN Center for Computational Science, Kobe, Japan, ⁵Hokkaido University Institute for Vaccine Research & Development, Sapporo, Japan, ⁶International Institute for Zoonosis Control, Hokkaido University, Sapporo, Japan

Direct inhibition of human APOBEC3 deaminases by HIV-1 Vif S19-5 independent of the ubiquitination/degradation pathway

Keisuke Kamba¹, Li Wan^{1,2}, Kentaro Tozawa^{1,2}, Satoru Unzai³, Ryo Morishita⁴, Akifumi Takaori-Kondo⁵, Takashi Nagata^{1,2}, Masato Katahira^{1,2}

¹Institute of Advanced Energy, Kyoto University, Kyoto, Japan, ²Graduate School of Energy Science, Kyoto University, Kyoto, Japan, ³Department of Frontier Bioscience, Hosei University, Tokyo, Japan, ⁴CellFree Sciences Co., Ltd., Ehime, Japan, ⁵Graduate School of Medicine, Kyoto University, Japan

S19-6 Restructuring of bacteriophage Φ6 viral particle activates semiconservative transcription

Serban L. Ilca^{1,2}, Xiaoyu Sun³, Esa-Pekka Kumpula⁴, Katri Eskelin³, David I. Stuart², Minna M. Poranen³, Juha Huiskonen^{2,4}

¹New York Structural Biology Center, Simons Electron Microscopy Center, New York, NY, USA, ²Division of Structural Biology, Centre for Human Genetics, University of Oxford, Oxford, UK, ³Molecular and Integrative Biosciences Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland, ⁴Institute of Biotechnology, Helsinki Institute of Life Science HiLIFE, University of Helsinki, Helsinki, Finland

Symposium 20 Room E 10:00-12:20 Synthetic and Constructive Biology Chairs

Tomoaki Matsuura (Tokyo Institute of Technology)

Sheref S. Mansy (Chemistry, University of Alberta)

S20-1 A potential path to the Darwinian evolution of protocells

Sheref Mansy

University of Alberta, Department of Chemistry, Edmonton, Alberta T6G 2G2, Canada

Wednesday, June 26

\$20-2 Design and construction of artificial cells reproducing cellular functions

<u>Yutetsu Kuruma</u>^{1,2}, Yasuhiro Shimane¹, Rumie Matsumura¹, Sumie Eto³, Samuel Berhanu³

¹Japan Agency for Marine-Earth Science and Technology (JAMSTEC), ²Yokohama City University, ³Earth-Life Science Institute (ELSI)

\$20-3 SUGARS FOR FUNCTION: Enabling protein post-translational modifications in cell-free systems

<u>Karen Polizzi</u>¹, Elli Makrydaki¹, Oscar Marshall¹, Rochelle Aw², Farzana Alam¹, Tejasvi Shivakumar¹, Akashaditya Das¹, Cleo Kontoravdi¹ Department of Chemical Engineering and Imperial College Centre for Synthetic Biology, London, UK, ²Department of Bioengineering, Stanford University, Stanford, CA, USA

\$20-4 Pigment Reporters for Further Development of Cell Free Systems for Synthetic Biology with Secondary Metabolism

Constance B. Bailey¹, Tien T. Sword², Jaime Lorenzo N. Dinglasan^{2,3}, J. William J. William Barker², Ghaeath S.K. Abbas¹, Madeline E. Spradley², Scott J. Emrich¹, Michael A. Gilchrist², Mitchell J. Doktycz²

¹University of Sydney, School of Chemistry, Sydney NSW, Australia, ²University of Tennessee-Knoxville, Knoxville, TN, USA, ³Oak Ridge National Laboratory, Oak Ridge, TN, USA

\$20-5 Synthetic approaches to biomolecular motors

Ken'ya Furuta^{1,2}

¹Advanced ICT Research Institute, National Institute of Information and Communications Technology, Hyogo, Japan, ²Department of Biological Sciences, Graduate School of Science, Osaka University, Osaka, Japan

The Young In	vestigator Award Lecture	Room A
16:00-16:40	Structural and functional diversity in light-gated ion channel channel rhodopsins	els:
Chairs	Manuel Prieto (iBB/IST-Institute for Bioengineering and Bioscience, UniLisbon, Portugal) Anthony Watts (University of Oxford, UK)	iversity of
YIA	Structural and functional diversity in pump-like cation	

channelrhodopsins Hideaki Kato

The University of Tokyo

BPS Award Lecture Room B-1		
16:40-17:30	Accurate Models for Interrogating and Engineering Biomo	lecular
Chair	Kumiko Hayashi (The University of Tokyo)	
Presenter	Jennifer Pesanelli (Biophysical Society)	
BPS	Accurate models for interrogating and engineering biomole condensates Jerelle A Joseph ^{1,2} ¹ Department of Chemical and Biological Engineering, Princeton University, USA	

Keynote 2	Room A
17:00-17:50	Molecular Simultations Open a Window into Cellular Dynamics
Chair	Yuji Sugita (RIKEN)
KL-2	Molecular simulations open a window into cellular dynamics Gerhard Hummer ^{1,2} ¹ Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Frankfurt am Main, Germany, ² Institute for Biophysics, Goethe University Frankfurt, Frankfurt am Main, Germany

Wednesday, June 26

Keynote 3	Room B-1
17:00-17:50	Cytoplasmic Dynamics and Mechanics in the Maturation and Aging of Mammalian Oocytes
Chair	Jie Yan (National University of Sinagpore)
KL-3	Cytoplasmic Dynamics and Mechanics in the Maturation and Aging of Mammalian Oocytes Rong Li Mechanobiology Institute, National University of Singapore

Thursday, June 27

Plenary IUPAB Ramachandran Lecture		Room B-1
9:00-9:50	Design of New Protein Functions using Deep Learning	
Chair	Nobuyasu Koga (Osaka University)	
PL-3	Design of New Protein Functions using Deep Learning David Baker	
	Biochemistry, Genome Sciences, Bioengineering, Chemical Engineering, Science and Physics, University of Washington, USA	ng, Computer

Symposium 2	Room A
10:00-12:20	Computational Molecular Biophysics
Chairs	Shoji Takada (Graduate School of Science, Kyoto University)
	Cecilia Clementi (Physics, Freie Universität Berlin)
S21-1	Modeling the Genome: A View by a Physicist José Onuchic Center for Theoretical Biological Physics, Rice University, Houston TX 77005, USA
\$21-2	Physicochemical regulation of the liquid-like organisation of chromatin
	Rosana Collepardo-Guevara ^{1,2,3} , Stephen Farr ² , Maria Julia Maristany ² , Jan Huertas ¹
	¹ Yusuf Hamied Department of Chemistry, University of Cambridge, Cambridge, ² Cavendish Laboratory, Department of Physics, University of Cambridge, Cambridge, UK, ³ Department of Genetics, University of Cambridge, Cambridge, UK
\$21-3	Solvent constraints for biopolymer folding and evolution in
	extraterrestrial environments
	Ignacio Sánchez ^{1,2} , Ezequiel Galpern ^{1,2} , <u>Diego U. Ferreiro</u> ^{1,2}
	¹ Universidad de Buenos Aires, Facultad de Ciencias Exactas y Naturales, Departamento de Química Biológica, Laboratorio de Fisiología de Proteínas, Buenos Aires, Argentina, ² CONICET-Universidad de Buenos Aires, Instituto de Química Biológica de la Facultad de Ciencias Exactas y Naturales (IQUIBICEN), Buenos Aires, Argentina.
S21-4	Changes in VEGFR by VEGF: Pursuing activation mechanism and drug targeting via computer simulations

Young Min Rhee, Yeon Ju Go, Mahroof Kalathingal Korea Advanced Institute of Science and Technology

Thursday, June 27

\$21-5 Multiscale biomolecular simulations for chromatin and transcription regulation

Shoji Takada

Shufneg Zhao

Graduate School of Science, Kyoto University

Symposium 2	22 Room B-1
10:00-12:20	Bacterial/Archaeal Supermolecular Assembly
Chairs	Isil Tulum (Faculty of Science/ Department of Biology, Istanbul University)
	Daisuke Nakane (Department of Engineering Science, The University of Electro-Communications)
S22-1	Phototaxis and control of type IV pilus functions Annegret Wilde ¹ , Nils Schuergers ¹ , Jonas Hammerl ¹ , Yu Han ¹ , Shylaja Mohandass ² , Conrad Mullineaux ² ¹ University of Freiburg, Germany, ² Queen Mary University of London, United Kingdom
\$22-2	Cell surface architecture of a nano-sized archaeon Nanobdella aerobiophila Shingo Kato Japan Collection of Microorganisms (JCM), RIKEN BioResource Research Center
\$22-3	Development of Protein-Based Strategies for Detection, Identification and Controlling Plant Pathogenic Phytoplasmas <u>Isil Tulum</u> , Kayhan Derecik Istanbul University, Faculty of Science, Department of Biology
S22-4	Coevolution of glycosylation, flagellar motor and cell shape in Campylobacter jejuni for efficient host Eli Cohen Imperial College London
\$22-5	Dissecting the structure and function of the bacterial flagellar motor. Anna Roujeinikova Department of Microbiology, Infection and Immunity Program, Monash Biomedicine Discovery Institute, Monash University, Melbourne, Victoria, Australia
\$22-6	From Inactivity to Motion: Uncovering Motility Dynamics of Alcanivorax Borkumensis

Grad. Sch. of Sci. and tech., Univ. of Tsukuba

Symposium 2	23 Room B-2
10:00-12:20 Chairs	Optogenetics and Photobiology Keiichi Inoue (The Institute for Solid State Physics, The University of Tokyo) Kota Katayama (Life Science and Applied Chemistry, Nagoya Institute of Technology)
\$23-1	The search for new carotenoid light-harvesting systems in microbial rhodopsins Oded Béjà Faculty of Biology, Technion – Israel Institute of Technology, Haifa, Israel
\$23-2	MULTIPLE RETINAL ISOMERIZATIONS DURING THE EARLY PHASE OF THE BESTRHODOPSIN PHOTOREACTIONS Spyridon Kaziannis ^{1,4} , Matthias Broser ³ , Ivo H.M. van Stokkum ² , Jakub Dostal ⁴ , Wayne Busse ³ , Arno Munhoven ³ , Cesar Bernardo ⁴ , Miroslav Kloz ⁴ , Peter Hegemann ³ , John T.M. Kennis ² ¹ University of Ioannina, Ioannina, ² Vrije Universiteit, Amsterdam, ³ Humboldt University, Berlin, ⁴ ELI Beamlines, Prague
\$23-3	Structural Dynamics of Microbial Rhodopsins Captured by X-ray Free Electron Lasers Eriko Nango Institute of Multidisciplinary Research for Advanced Materials, Tohoku University
\$23-4	Photoisomerization Mechanism of Retinal in Different Microbial Rhodopsins - Insight from Multiscale Simulation Igor Schapiro Institute of Chemistry, The Hebrew University of Jerusalem, Israel
\$23-5	Coral opsins: unique spectral tuning and G protein selectivity Akihisa Terakita Department of Biology, Graduate School of Science, Osaka Metropolitan University, Osaka, Japan

Thursday, June 27

Symposium 2	24 Room C-2
10:00-12:20	Chromatin Dynamics and Imaging
Chairs	Kazuhiro Maeshima (Department of Chromosome Science, National Insitute of Genetics)
	Vadim Backman (Biomedical Engineering, Northwestern University)
S24-1	Chromatin domains as an emergent property: how cells learn to regulate epigenetic memory and transcriptional reprogramming Vadim Backman ^{1,2} ¹Department of Biomedical Engineering, Northwestern University, ²Center for Physical Genomics & Engineering, Northwestern University
S24-2	Replication-dependent histone (Repli-Histo) labeling specifically visualizes physical properties of euchromatin/heterochromatin in living human cells. Katsuhiko Minami ^{1,2} , Satoru Ide ^{1,2} , Sachiko Tamura ^{1,2} , Kazuhiro Maeshima ^{1,2} ¹ National Institute of Genetics, Japan, ² Graduate Institute for Advanced Studies, SOKENDAI
\$24-3	Understanding the Regulatory Grammar of Enhancers and Silencers: Biophysical Insights from Machine Learning Ryan Friedman, Avinash Ramu, Sara Lichtarge, Yawei Wu, Lloyd Tripp, Daniel Lyon, Connie Myers, David Granas, Maria Gause, Joeseph Corbo, Barak Alon Cohen, Michael White Washington University School of Medicine, Saint Louis, MO 63110
\$24-4	What phase of matter is the chromosome and why should the living cell care? Olga K. Dudko University of California at San Diego
\$24-5	THE PIONEER TRANSCRIPTION FACTOR OCT4 ALTERS CHROMATIN PACKING

PACKING

Jan Huertas^{1,2}, M. Julia Maristany³, Rosana Collepardo-Guevara^{1,2} ¹Yusuf Hamied Department of Chemistry - University of Cambridge, ²Department of Genetics - University of Cambridge, ³Department of Physics - University of Cambridge

Symposium 2	25 Room D
10:00-12:20	Biophysics of Disease
Chairs	Eri Chatani (Graduate School of Science / Department of Chemistry, Kobe University)
	Motomasa Tanaka (RIKEN Center for Brain Science)
	Lukasz Joachimiak (Center for Alzheimer's and Neurodegenerative Diseases, University of Texas Southwestern Medical Center)
S25-1	Engineered chaperone-mediated disaggregation and degradation of yeast prions Motomasa Tanaka RIKEN Center for Brain Science, Japan
\$25-2	How heterotypic amyloid interactions determine amyloid pathology Nikolaos Louros ^{1,2} , Katerina Konstantoulea ^{1,2} , Frederic Rousseau ^{1,2} , <u>Joost Schymkowitz</u> ^{1,2} Switch Laboratory, VIB Center for Brain and Disease Research, Herestraat 49, 3000 Leuven, Belgium, Switch Laboratory, Department of Cellular and Molecular Medicine, KU Leuven, Herestraat 49, 3000 Leuven, Belgium

\$25-3 Visualizing Amyloid Oligomers, the Dark Matter of Alzheimer's Disease

<u>David Robert Boyer</u>¹, Peng Ge¹, Romany Abshkaron¹, Roni Haj Hussein¹, Yi Xiao Jiang¹, Alejandro Foley², Ka Chan², Jevgenji Raskatov², David Eisenberg¹

¹Department of Biological Chemistry, University of California, Los Angeles, USA, ²Department of Chemistry and Biochemistry, University of California, Santa Cruz, USA

S25-4 Unveiling the Mechanism of Protein Aggregation to Form Oligomers and Protofibrils: A Study Using Insulin as a Model

Eri Chatani, Keisuke Yuzu

Graduate School of Science, Kobe University

\$25-5 Chemical and structural bases for fibril aggregate formation of RNA-binding proteins with low-complexity domains by neurodegenerative disease mutations.

Masato Kato^{1,2}, Nobuo Maita², Kim Sunyong², Yuko Kajino²

¹Department of Biochemistry, University of Texas Southwestern Medical Center, Dallas, TX USA,, ²Institute for Quantum Life Science, National Institutes for Quantum Science and Technology (QST), Chiba, JAPAN

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S25-6 Investigation of Toxicity and Structural Mechanism of Dipeptide Repeats in ALS and the Therapeutic Strategy

Yun-Ru (Ruby) Chen

Genomics Research Center, Academia Sinica

\$25-7 Engineering proteins to control amyloid assembly

Lukasz Joachimiak

University of Texas Southwestern Medical Center

\$25-8 Unlocking Ribosome Heterogeneity: High-Resolution Genome-Wide Positional Sequencing and Its Implications in Disease Research

<u>Gabriella Viero</u>¹, Fabio Lauria¹, Toma Tebaldi², Lorenzo Lunelli³,

Gregor Anderluh⁴, Thomas Gillingwater⁵

¹Institute of Biophysics CNR Italy, ²University of Trento, Trento, Italy, ³Bruno Kessler Foundation (FBK), Trento, Italy, ⁴National Institute of Chemistry, Ljubljana, Slovenia,

⁵University of Edinburgh, Edinburgh, United Kingdom

Symposium 26 Room B-	
16:00-18:2	20 Applications of Non-equilibrium Physics
Chairs	Kumiko Hayashi (The University of Tokyo)
	Chun-Biu Li (Faculty of Science/Mathematics Department, Stockholm University)
\$26-1	Kinetic basis of G-quadruplex selective stabilizing ligands revealed by
S26-1	

\$26-2 Nonequilibrium energetics and noise-induced acceleration of molecular motor, kinesin-1

Takayuki Ariga

Technology

Graduate School of Frontier Biosciences, Osaka University, Osaka, Japan

\$26-3 Active fluctuations of cytoplasmic actomyosin networks facilitate dynein-driven intracellular transports along microtubules

Takayuki Torisawa^{1,2}, Kei Saito^{2,3}, Ken'ya Furuta⁴, Akatsuki Kimura^{1,2}

¹Cell Architecture Laboratory, National Institute of Genetics, ²Department of Genetics, Graduate University for Advanced Studies (SOUKENDAI), ³Physics and Cell Biology Laboratory, National Institute of Genetics, ⁴Advanced ICT Research Institute, National Institute of Information and Communications Technology

S26-4 Drug the Allosteric Site of a Cancer Target Revealed by Time-Dependent Linear Response Theory

<u>Lee-Wei Yang</u>^{1,2,3,5}, Bang-Chieh Huang¹, Pramod Shah¹, Yi-Yun Cheng⁴, Chi-Hong Chang-Chein¹, Kuan-Chou Chen⁶, Chao-Ling Yao⁶

¹Institute of Bioinformatics and Structural Biology, National Tsing Hua University, Hsinchu 300044, Taiwan, ²PhD program in Biomedical Artificial Intelligence, National Tsing Hua University, Hsinchu 300044, Taiwan, ³Physics Division, National Center for Theoretical Sciences, Taipei 106319, Taiwan, ⁴Praexisio Inc., San Diego, CA92121, USA, ⁵Bioinformatics & CBMB Programs, Academia Sinica, Taipei 115201, Taiwan, ⁶Department of Chemical Engineering. National Cheng Kung University, Tainan 70101, Taiwan

\$26-5 Microbial competition in expanding colony: Emergent collective alignment gives an advantage to longer cells

Nathan van den Berg, Kristian Thijssen, Thu Trang Nguyen, Adrien Sarlet, Mireia Cordero, Alba Garcia Vazquez, Namiko Mitarai,

Amin Doostmohammadi, Liselotte Jauffred The Niels Bohr Institute, University of Copenhagen

Single-molecule dynamics across phase boundaries in active biomolecular condensates

<u>Stefano Bo</u>¹, Lars Hubatsch², Jonathan Bauermann³, Christoph Weber⁴, Frank Jülicher⁵

¹King's College London, London, United Kingdom, ²Max Planck Institute for Cell Biology and Genetics, Dresden, Germany, ³Harvard University, Cambridge, United States of America, ⁴Augsburg University, Augsburg, Germany, ⁵Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Symposium 27 Room B-2 16:00-18:20 DNA/Chromatin Physics Chairs Tsuyoshi Terakawa (Faculty of Science / Department of Biophysics, Kyoto University) Eric C. Greene (Biochemistry & Molecular Biophysics, Columbia University)

\$27-1 Unveiling the Molecular Mechanism of Histone Recycling through Biophysical Approaches

Tsuyoshi Terakawa

Department of Biophysics, Graduate School of Science, Kyoto University

Thursday, June 27

S27-2 New Paradigms for Rad51 paralog function

Eric Greene

Columbia University, Department of Biochemistry and Molecular Biophysics

\$27-3 Machines on Genes: A Single-Molecule Perspective

Shixin Liu

The Rockefeller University, New York, USA

\$27-4 Mismatch Elimination in human DNA mismatch repair

Jong-Bong Lee

Department of Physics, School of Interdisciplinary Bioscience & Bioengineering, Medical Science & Engineering POSTECH, Pohang, Korea

\$27-5 G-quadruplex Structures Formed by Human Telomeric and C9orf72 DNA and RNA

<u>Guang Zhu</u>, Changdong Liu, Naining Xu, Monica Suen, Bin Yan, Qing Yi The Hong Kong University of Science and Technology

Symposium 2	Room C-2	
16:00-18:20	Membraneless Organella, Autophage, Liquid-liquid Phase Separation	
Chairs	Miho Yanagisawa (Graduate School of Arts and Sciences, University of Tokyo) Arslan Siddique (Chemistry, University of New South Wales)	
S28-1	How does membrane confinement at the cell size change the phase separation of macromolecules? Miho Yanagisawa Graduate School of Arts and Sciences, The University of Tokyo	

\$28-2 Cell-inspired biomimetic droplets

Anderson Ho Cheung Shum^{1,2}

¹The University of Hong Kong, ²Advanced Biomedical Instrumentation Centre

\$28-3 Capillary force in cells: functional bio-condensate wetting

Roland L. Knorr^{1,2,3}

¹Interfacial Cell Biology Lab, Humboldt-Universität zu Berlin, Germany, ²University of Cologne, Faculty of Medicine and University Hospital Cologne, Germany, ³Graduate School and Faculty of Medicine, The University of Tokyo, Japan

Oral Sessions

\$28-4 Deciphering the molecular mechanism of DNA-protein interactive co-condensates

Zhi Qi¹, Cheng Li¹, Yunqiang Bian², Wenfei Li^{2,3}

¹Center for Quantitative Biology, Peking-Tsinghua Center for Life Sciences, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing 100871, China, ²Wenzhou Key Laboratory of Biophysics, Wenzhou Institute, University of Chinese Academy of Sciences, Wenzhou, Zhejiang 325000, China, ³Department of Physics, National Laboratory of Solid-State Microstructure, and Collaborative Innovation Center of Advanced Microstructures, Nanjing University, Nanjing 210093, China

\$28-5 Condensates' interface triggers the liquid-to-solid transition

Yi Shen¹, David Weitz², Daniele Vigolo³, Tuomas Knowles⁴

¹School of Chemical and Biomolecular Engineering, The University of Sydney, ²School of Engineering and Applied Sciences, Harvard University, ³School of Biomedical Engineering, The University of Sydney, ⁴Yusuf Hamied Department of Chemistry, University of Cambridge

Symposium 2	Room D	
16:00-18:20	Soft Matter Biophysics	
Chairs	Patricia Bassereau (Physical Chemistry Curie, Institut Curie)	
	Masaki Sasai (Fukui Institute for Fundamental Chemistry, Kyoto University)	
S29-1	Active Topological Defects and Universal Symmetries in Living Biological Matter	
	Amin Doostmohammadi	

S29-2 On the role of polymerases in shaping the 4D Genome

Niels Bohr Institute, University of Copenhagen

<u>Daniel Jost</u>¹, Dario D'Asaro^{1,2}, Hossein Salari^{1,2}, Cedric Vaillant², Jean-Michel Arbona¹

¹Laboratoire de Biologie et Modélisation de la Cellule, École Normale Supérieure de Lyon, CNRS, UMR5239, Inserm U1293, Université Claude Bernard Lyon 1, 46 Allée d'Italie, 69007 Lyon, France, ²École Normale Supérieure de Lyon, CNRS, Laboratoire de Physique, 46 Allée d'Italie, 69007 Lyon, France

\$29-3 Formation of chromatin domains without loop extrusion: the chromatin capture model of interphase cohesin

Shin Fujishiro¹, Masaki Sasai^{1,2}

¹Fukui Institute for Fundamental Chemistry, Kyoto University, Kyoto, Japan,

²Department of Complex Systems Science, Nagoya University, Nagoya, Japan

Thursday, June 27

\$29-4 Lipid membranes and membrane proteins: Not a coexistence but an intimate relationship.

Alicia Damm¹, Raju Regmi¹, Su-Jin Paik¹, Raj-Kumar Sadhu¹,

Jacob Kaestel-Hansen², Maxime Dahan¹, Nikos Hatzakis², Pierre Sens¹,

Daniel Lévy¹, Patricia Bassereau¹

¹Institut Curie, Paris, France, ²Nano-Science Center, Copenhagen, Denmark

S29-5 Nonlinear Dynamics of the Auditory System

Dolores Bozovic, Justin Faber

Dept. of Physics and Astronomy, University of California Los Angeles, USA

Hands-on Tra	aining Session B Room E
10:00-12:20	Visualizing the Nanometer World in Liquid by Bio-SPMs
Chair	Noriyuki Kodera (Kanazawa University)
HT-B-1	Visualizing Nanoscale Dynamics and Mechanics in Living Cells by Nanoendoscopy AFM Takeshi Fukuma Kanazawa University
HT-B-2	Nanoscale analysis of microbial cell walls using AFM Keisuke Miyazawa ^{1,2} , Takeshi Fukuma ^{1,2} ¹Kanazawa University, ²WPI-NanoLSI
HT-B-3	Visualizing surface dynamics of living cells at nanometer scale resolution with scanning ion conductance microscopy Shinji Watanabe Nano Life Science Institute (WPI-NanoLSI), Kanazawa University, Ishikawa, Japan
HT-B-4	Biological Nanopore Probes for Scanning Ion Conductance Microscopy Kan Shoji Nagaoka University of Technology
HT-B-5	Single-molecule imaging of AMPA-type glutamate receptors by high-speed atomic force microscopy Mikihiro Shibata Kanazawa University

ABA-8

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HT-B-6 HS-AFM analysis of microtubule-binding proteins in solution

Marina Ohno¹, Hayato Shibuya¹, Noriyuki Kodera², <u>Ikuko Hayashi</u>¹Biomed. Sci., Yokohama City Univ., ²NanoLSI, Kanazawa Univ.

Asian Biophys	sics Association (ABA) Symposium Room E
16:00-18:20 Chairs	Asian Biophysics Association (ABA) Symposium Shang-Te Danny Hsu (Institute of Biological Chemistry, President of ABA, member of Biophysical Society of R.O.C, Academia Sinica) Haibin Su (Chemistry, Member of The Biophysical Society of Hong Kong, Hong Kong University of Science and Technology)
ABA-1	Elizabeth Hinde School of Physics, Faculty of Science, President of The Australian Society for Biophysics (ASB), The University of Melbourne
ABA-2	Tao Xu President of Biophysica Society of China (BSC), Guangzhou Laboratory
ABA-3	Haibin Su Chemistry, Member of The Biophysical Society of Hong Kong, Hong Kong University of Science and Technology
ABA-4	Ruchi Anand Vice-President of The Indian Biophysical Society (IBS), Indian Institute of Technology Bombay
ABA-5	Satoshi Takahashi Institute of Multidisciplinary Research for Advanced Materials, President of the Biophysical Society of Japan (BSJ), Tohoku University
ABA-6	Hyun-Ho Lim Lab Head, Molecular Physiology and Biophysics Laboratory, President of The Korean Biophysical Society (KBPS), Korea Brain Research Institute
ABA-7	Shang-Te Danny Hsu Institute of Biological Chemistry, President of ABA, member of Biophysical Society of R.O.C, Academia Sinica

Earth Life Science Institute (ELSI), Tokyo Institute of Technology, Tokyo, Japan

Deciphering the Complexity in Biological Interaction

ABA Young Investigator Award Lecture

Tetsuhiro S. Hatakeyama

Thursday, June 27

The Bei Lecture		Room A
18:30-19:10	Nanozyme, a new biological catalyst and its applications	
Chair	Tao Xu (National Laboratory of Biomacromolecules, Guangzhou)	
BL Nanozyme, a new biological catalyst and its applications		
	Xiyun Yan	
	Institute of Biophysics, Chinese Academy of Sciences	

Oral Sessions

Keynote 4	Room B-1	
9:00-9:50	Decoding regeneration using computer designed proteins	
Chair	Ikuko Fujiwara (Nagaoka University of Technology)	
KL-4	Decoding regeneration using computer designed proteins Hannele Ruohola-Baker ^{1,2}	
	¹ Department of Biochemistry, University of Washington, Seattle, WA, USA, ² Institute for Stem Cell & Regenerative Medicine, University of Washington, Seattle, WA, USA)

Symposium 30	Room B-1
10:00-12:20	Structure, Function and Biophysics of the Bacterial Motility and Flagellar Motor
Chairs	Matthew Baker (School of Biotechnology and Biomolecular Science, University of New South Wales)
	Seiji Kojima (Department of Biological Science, Graduate School of Science, Nagoya University)
\$30-1	Spatio-temporal dynamics of the proton motive force on single bacterial cells Anaïs Biquet-Bisquert¹, Baptiste Carrio¹, Nathan Meyer¹, Thales Fernandes¹, Manouk Abkarian¹, Farida Seduk², Axel Magalon², Ashley Nord¹, Francesco Pedaci¹ ¹Centre de Biologie Structurale, Université de Montpellier, CNRS, INSERM, Montpellier, France, ²Aix Marseille Université, CNRS, Laboratoire de Chimie Bactérienne (UMR7283), IMM, IM2B, 13402, Marseille, France
\$30-2	Diversity of flagellar system – What do we learn from H. pylori? Wing Ngor Shannon Au, Kailei Sun, Liyang Sun, Wendy Wai Ling Lam Chinese University of Hong Kong
\$30-3	EMBO Young Investigator Lecture 5:2 molecular motors – from bacterial motility to anti-phage defense Nicholas M. I. Taylor NNF Center for Protein Research, University of Copenhagen
\$30-4	Adhesins and flagella-dependent bacterial surface motility Shuichi Nakamura Grad. Sch. Eng., Tohoku Univ.

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\$30-5 A cell-surface conveyor belt controls the rotational direction of its driver

Abhishek Shrivastava

Biodesign Institute, Arizona State University

\$30-6 Protein engineering via directed evolution of the stator subunit of the bacterial flagellar motor

Pietro Ridone¹, Tsubasa Ishida³, Angela Lin¹, David Humphreys⁴,

Eleni Giannoulatou⁴, Yoshiyuki Sowa³, Matthew Baker^{1,2}

¹School of Biotechnology and Biomolecular Science, UNSW Sydney, Sydney, Australia, ²Institute of Molecular Biology and Biotechnology, FoRTH, Heraklion, Crete, Greece, ³Hosei University, Kanagawa, Japan, ⁴Victor Chang Cardiac Research Institute, Darlinghurst, Australia

Symposium 3	Room B-2	
10:00-12:20	Stem Cells and Organoids	
Chairs	Minoru Takasato (Center for Biosystems Dynamics Research, RIKEN)	
	Andras Lakatos (Department of Clinical Neurosciences, University of Cambridge)	

S31-1 Generation of Urinary Tract Organoids from Human Pluripotent Stem Cells

Minoru Takasato^{1,2,3}

¹RIKEN Center for Biosystems Dynamics Research, ²Graduate School of Biostudies, Kyoto University, ³Graduate School of Medicine, Osaka University

S31-2 Tailoring autonomous trial-and-error by robots and AI (robotic search system) for Biophysics

Genki Kanda¹, Taku Tsuzuki², Auto Culture Project Team^{1,2,3,4,5}, Yosuke Ozawa², Masayo Takahashi^{3,4}, Koichi Takahashi¹, Tohru Natsume⁵ ¹RIKEN, ²Epistra Inc., ³Vision Care Inc., ⁴VCCT Inc., ⁵Robotic Biology Institute Inc.

\$31-3 3D human neural organoid models for interrogating mechanisms and therapeutics in neurodegeneration

Andras Lakatos

Department of Clinical Neurosciences, University of Cambridge, Cambridge, UK

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\$31-4 Hepato-Biliary-Pancreatic Organogenesis in a Dis

Takanori Takebe^{1,2,3,4,5}

¹Division of Stem Cell & Organoid Medicine, Osaka University, ²Institute of Research, Tokyo Medical and Dental University, ³Center for Stem Cell & Organoid Medicine (CuSTOM), Cincinnati Children's Hospital Medical Center, ⁴Divisions of Gastroenterology, Hepatology and Nutrition and Developmental Biology, Cincinnati Children's Hospital Medical Center, ⁵Communication Design Center, Yokohama City University

S31-5 Large-scale generation of uniform-sized miniature adipocyte spheroids in hydrogel capsules

Ruri Maekawa, Kazuki Hattori, Sadao Ota

Research Center for Advanced Science and Technology, The University of Tokyo

S31-6 A state of partial Rb inactivation and intermediate E2F activation safeguards proliferation commitment

Yumi Konagaya

RIKEN Center for Biosystems Dynamics Research

Symposium 3	Room D
10:00-12:20	Origin of Life
Chairs	Ryo Mizuuchi (Department of Electrical Engineering and Bioscience, Faculty of Science and Engineering, Waseda University)
	Tony Z. Jia (Earth-Life Science Institute, Tokyo Institute of Technology)

S32-1 Evolution of Complex Chemical Mixtures Reveals Combinatorial Compression and Population Synchronicity

Moran Frenkel-Pinter¹, Kavita Matange², Vahab Rajaei²,

Pau Capera-Aragonès¹, John T Costner², Adelaide Robertson², Jennifer Seoyoung Kim², Anton S Petrov², Jessica C Bowman²,

Loren Dean Williams²

¹Institute of Chemistry, The Hebrew University of Jerusalem, Israel 91904, ²School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA 30332-0400 USA

Friday, June 28

\$32-2 The peptides increase the compartmentalization and stability of the protoribosome

Tomoko Yamaguchi^{1,2,3}

¹Earth-Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan, ²Department of Cell Biology, Faculty of Science, Charles University, Prague, Czech Republic, ³Graduate School of Pharmaceutical Sciences, Kyoto University, Kyoto, Japan

S32-3 Investigating Biophysical Impacts of Prebiotic Milieu on the Membrane Stability using Model Systems

Arslan Siddique^{1,2}, Lauren A. Lowe^{1,2}, Soumya Kanti De^{1,2}, Daniel Loo^{1,2}, Andrew Nelson³, Anna Wang^{1,2}

¹Australian Centre for Astrobiology, University of New South Wales, NSW 2052, Australia, ²School of Chemistry, University of New South Wales, NSW 2052, Australia, ³Australian Centre for Neutron Scattering, ANSTO Sydney, NSW 2232, Australia

In vitro selection of primitive catalysts to fill the gap between chemical and enzymatic RNA self-replication systems

Seung Soo Oh1, Lijun Zhu2, Jack Szostak3

¹Department of Materials Science and Engineering, Pohang University of Science and Technology (POSTECH), 77 Cheongam-Ro, Nam-Gu, Pohang, Gyeongbuk 37673, South Korea, ²Department of Biochemistry and Biophysics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA, ³Howard Hughes Medical Institute, Department of Chemistry, The University of Chicago, Chicago, Illinois 60637, USA

S32-5 Reconstruction of Ancient Protein Folds in the Central Dogma Machinery

Shunsuke Tagami RIKEN BDR

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Symposium 3	Room E
10:00-12:20 Chairs	Data Sharing and Open Science Shuichi Onami (RIKEN Center for Biosystems Dynamics Research) Caterina Strambio-De-Castillia (Molecular Medicine, University of Massachusetts Chan Medical School)
\$33-1	SSBD and Global Sharing of Bioimaging Data Shuichi Onami ^{1,2,3} ¹RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, ²RIKEN Information R&D and Strategy Headquarters, Kobe, Japan, ³RIKEN, TRIP Headquarters, Kobe, Japan
\$33-2	Managing the image-data life cycle for the real world: connecting the dots from sample preparation to image acquisition, analysis, publication, and data reuse Caterina Strambio-De-Castillia Program in Molecular Medicine, UMass Chan Medical School, Worcester, MA, USA
\$33-3	Chinese Cohort Studies and Data Sharing Tao Xu ^{1,2} ¹Guangzhou Laboratory, ²Institute of Biophysics, Chinese Academy of Sciences
\$33-4	GEMS Informatics: advancing data-driven innovation in agri-food and natural resources management. Oluwaseun F. Gakenou ¹ , David M. Drew ¹ , Jan Greyling ² Department of Forestry and Wood Science, Stellenbosch University, South Africa, Stellenbosch Agroinformatics Initiative, Stellenbosch University, South Africa
\$33- 5	Scalable strategies for a next-generation of FAIR bioimaging Josh Moore ^{1,2} ¹German Biolmaging-Gesellschaft für Mikroskopie und Bildanalyse e.V., Constance, Germany, ²Open Microscopy Environment (OME) Consortium

Friday, June 28

Hands-on Training Session E

Room A

10:00-12:20 Exploring Multi-cellular Mechanics

Chairs Makoto Sato (Kanazawa University)

Tatsuo Shibata (RIKEN)

Shige H. Yoshimura (Kyoto University)

HT-E-1 Active cytoskeleton controlled through force and shape

Yusuke T Maeda¹, Ryota Sakamoto^{1,2}

¹Department of Physics, Kyushu University, ²Department of Biomedical Engineering, Yale University

HT-E-2 Cellular-level left-right asymmetry, cell chirality, induces the chiral collective rotation of multicellular colony

Tomoki Ishibashi¹, Ryohei Nishizawa^{1,2}, Goshi Ogita¹, Tatsuo Shibata¹ ¹RIKEN Center for Biosystems Dynamics Research, Japan, ²Graduate School of Frontier Biosciences, Osaka University

HT-E-3 Analysis of Differential Growth in Curved Surface Morphogenesis through Constructing a Conformal Map

<u>Kentaro Morikawa</u>¹, Shinichi Morita^{2,3}, Kazuki Sakura^{2,4}, Akiteru Maeno⁵, Hiroki Gotoh⁶, Teruyuki Niimi^{2,3}, Yasuhiro Inoue¹

¹Department of Micro Engineering, Graduate School of Engineering, Kyoto University, Kyoto, Japan, ²Division of Evolutionary Developmental Biology, National Institute for Basic Biology, Okazaki, Japan, ³Basic Biology Program, Graduate Institute for Advanced Studies, The Graduate University for Advanced Studies, SOKENDAI, Okazaki, Japan, ⁴Japan Society for The Promotion of Science Research Fellowship, ⁵National Institute of Genetics, Shizuoka, Japan, ⁶Department of Biological Science, Faculty of Science, Shizuoka University, Shizuoka, Japan

HT-E-4 Tiling mechanisms of the compound eye through geometrical tessellation

Steven Davis¹, Takashi Hayashi¹, Takamichi Sushida², Masakazu Akiyama³, Shin-Ichiro Ei⁴, <u>Makoto Sato</u>¹

¹Kanazawa University, ²Salesian Polytechnic, ³Toyama University, ⁴Hokkaido University

Oral Sessions

HT-E-5 Mechanical waves decode positional information to calibrate wound healing response in zebrafish

<u>Fu-Lai Wen</u>¹, Marco P. De Leon², Keng-Hui Lin³, Chen-Hui Chen²

¹Department of Science Education, National Taipei University of Education, Taipei, Taiwan, ²Institute of Cellular and Organismic Biology, Academia Sinica, Taipei, Taiwan, ³Institute of Physics, Academia Sinica, Taipei, Taiwan

HT-E-6 PIEZO1-mediated mechanosensing regulates the fate of neural progenitor cells during cerebral development

Mayumi Okamoto^{1,2}, Tsukasa Shimamura², Takaki Miyata², Keiko Nonomura^{3,4}

¹Graduate School of Science, Nara Women's University, ²Graduate School of Medicine, Nagoya University, ³School of Life Science and Technology, Tokyo Institute of Technology, ⁴Division of Embryology, National Institute of Basic Biology

Hands-on Training Session C 10:00-12:20 CHARMM-GUI/GENESIS MD Tutorial Chairs Wonpil Im (Lehigh University) Yuji Sugita (RIKEN) HT-C-1 Three routes to molecular movies Holmut Grubmullor Maxim Igaay Lare Book, Stoffen Schultze

Helmut Grubmuller, Maxim Igaev, Lars Bock, Steffen Schultze Max Planck Institute for Multidisciplinary Sciences, Goettingen, Germany

HT-C-2 Modeling multi-state structures of proteins and simulating their conformational transitions

Jiaxuan Li, Song Yang, Chen Song

Peking University, Beijing, China

HT-C-3 Multiscale Simulations of Enzyme Mechanisms: Bridging Catalysis, Conformational Changes and Ligand Release

Kwangho Nam

Department of Chemistry and Biochemistry, University of Texas at Arlington, Arlington, TX 76019, USA

Friday, June 28

HT-C-4 Exploring Allosteric Changes in the Conformational Landscape of Src Kinase upon Substrate Binding by GENESIS

Song-Ho Chong^{1,2}, Hiraku Oshima^{1,3}, Yuji Sugita^{1,4,5}

¹RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, ²Faculty of Life Sciences, Kumamoto University, Kumamoto, Japan, ³Graduate School of Science, University of Hyogo, Hyogo, Japan, ⁴RIKEN Center for Computational Science, Kobe, Japan, ⁵RIKEN Center for Pioneering Research, Saitama, Japan

HT-C-5 Computational Explorations of Chromatin Structure and Dynamics: from Single Nucleosomes to Entire Genes

Giovanni Brandani

Department of Biophysics, Graduate School of Science, University of Kyoto

HT-C-6 WHAT CAN CHARMM-GUI DO FOR YOU?

Wonpil Im

Biological Sciences, Lehigh University, Bethlehem, PA USA

Notes

Tuesday, June 25

Presentation time is organized by whether the last part (suffix) of Poster Session number is odd/even.

Abstracts marked with * in the abstract number eligible for IUPAB2024 Student and Early Career Researcher Poster Award voting

Ex) *25P-999

Protein: Structure

*25P-001 The molecular strucutre of an axle-less F1-ATPase

Emily Furlong^{1,2}, Ian Reiniger-Chatzigian¹, Yi Zeng^{1,3}, Simon Brown⁴, Meghna Sobti^{1,3}, Alastair Stewart^{1,3}

¹Molecular, Structural and Computational Biology Division, The Victor Chang Cardiac Research Institute, Darlinghurst, Australia, ²Division of Biomedical Science and Biochemistry, Research School of Biology, Australian National University, Acton, ACT, Australia, ³St Vincent's Clinical School, Faculty of Medicine, UNSW Sydney, Kensington, Australia, ⁴School of Chemistry and Molecular Bioscience, Molecular Horizons, and Australian Research Council Centre for Cryo-electron Microscopy of Membrane Proteins, University of Wollongong, Wollongong, NSW, Australia

*25P-002 The role of charges in the enzymatic mechanism of acetoacetate decarboxylase

Masato Ishizaka^{1,2}, Sören Rindfleisch^{1,2}, Florian Auer^{1,2}, Lukas Gingeleit^{1,2}, Tat Cheng³, Michael Bielecki⁴, Fabian Rabe von Pappenheim^{1,2}, Elke Penka^{1,2}, Ronald Kluger⁴, Eri Sakata³, Kai Tittmann^{1,2}

¹Department of Molecular Enzymology, Georg-August University Göttingen, Göttingen, Germany., ²Max-Planck-Institute for Multidisciplinary Sciences, Göttingen, Germany., ³Institute for Neuropathology, University Medical Center Göttingen, Göttingen, Germany., ⁴Davenport Chemistry Laboratories, Department of Chemistry, University of Toronto, Toronto, Canada.

*25P-003 Structural insights into the allosteric inhibition of P2X4 receptors

<u>Cheng Shen</u>¹, Yuqing Zhang², Wenwen Cui², Yimeng Zhao¹, Danqi Sheng¹, Xinyu Teng¹, Miaoqing Shao², Muneyoshi Ichikawa¹, Jin Wang², Motoyuki Hattori¹

¹Fudan University, Shanghai, China, ²China Pharmaceutical University, Nanjing, China

*25P-004 Cryo-EM Structure of P-glycoprotein Bound by Three Elacridar P-gp-Inhibitor Molecules

Norie Hamaguchi^{1,2,3}, Naruhiko Adachi⁴, Toshio Moriya⁴, Masato Kawasaki⁴, Satoshi Yasuda³, Naohiko Anzai², Toshiya Senda⁴, Satoshi Ogasawara³, Takeshi Murata³

¹Graduate School of Medical and Pharmaceutical Sciences, Chiba University, ²Graduate School of Medicine, Chiba University, ³Graduate School of Science, Chiba University, ⁴Structural Biology Research Center, Institute of Materials Structure Science, High Energy Accelerator Research Organization

*25P-005 Structural insights into the orthosteric inhibition of P2X receptors by classical non-ATP-analog antagonists

Danqi Sheng¹, Chenxi Yue²

¹Fudan University, Shanghai China, ²China Pharmaceutical University, Nanjing, China

*25P-006 Ion selectivity mechanism of the MgtE channel for Mg2+ over Ca2+ Xinyu Tenq¹, Danqi Shenq¹, Ye Yu², Jin Wanq², Motoyuki Hattori¹

¹Fudan University, Shanghai, China, ²China Pharmaceutical University, Nanjing, China

*25P-007 Tracking the glucose/ xylose isomerase mechanism using freezing under high pressure

Agnieszka Klonecka^{1,2,3}, Joanna Slawek¹, Philippe Carpentier^{4,5}, Christoph Mueller-Dieckmann⁴, Katarzyna Kurpiewska⁶, Maciej Kozak^{1,7}

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*25P-008 Structure-activity relationship (SAR) study of hydrophobic moiety of nonsecosteroidal VDR ligands using diphenylsilane scaffold

Narasinghe Mudiyanselage Hansaka Nirupama Thilakarathne^{1,2}, Takashi Misawa³, Yosuke Demizu³, Yuya Hanazono², Nobutoshi Ito², Hiroyuki Kagechika¹, Shinya Fujii¹

¹Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University, ²Medical Research Institute, Tokyo Medical and Dental University, ³National Institute of Health Sciences

*25P-009 Structural transformation of a dipeptide Gly-Phe by coffee-ring effect

<u>Ayaka Sako</u>, Masaki Saito, Kazuo Eda, Atsuo Tamura Kobe University, Graduate School of Science

25P-010 Exploring the Continuous Conformational Variability of Glutamate Dehydrogenase Using Cryo-EM Single-particle Images and MD Simulations

<u>Tingting Wang</u>¹, Osamu Miyashita¹, Hideki Shigematsu², Masaki Yamamoto³, Florence Tama^{1,4}

¹Computational Structural Biology Research Team, R-CCS, RIKEN, Japan, ²Japan Synchrotron Radiation Research Institute (JASRI), SPring-8, Hyogo, Japan, ³RIKEN SPring-8 Center, Hyogo, Japan, ⁴Department of Physics and ITbM, Nagoya University, Japan

25P-011 Preliminary Cryo-EM study of Arabidopsis Magnesium Transporter MRS2-1

Hexin Xu¹, Xinyu Teng¹, Cheng Shen¹, Yimeng Zhao¹, Xiaoyu Yang², Natsuko I. Kobayashi², Keitaro Tanoi², Motoyuki Hattori²

¹Fudan University, Shanghai, China, ²The University of Tokyo, Tokyo, Japan

25P-012 Application of de novo protein design to structural analysis of noncanonical MgtE Mg2+ channel

Zhixuan Zhao¹, Kimiho Omae², Ziyi Zhang¹, Xinyu Teng¹, Cheng Shen¹, Danqi Sheng¹, Wataru Iwasaki², Motoyuki Hattori¹

¹Fudan University, Shanghai, China, ²The University of Tokyo, Tokyo, Japan

25P-013 Native lipid NanoDisc application for structural determination of RND transporter

Kenta Tsutsumi, Atsushi Nakagawa, Eiki Yamashita Institute for Protein Research, Osaka, Japan

25P-014 Preliminary cryo-EM study of the MgtE Mg2+ channel with the PRC-barrel domain

Ziyi Zhang¹, Kimiho Omae², Cheng Shen¹, Wataru Iwasaki², Motoyuki Hattori¹

¹Fudan University, Shanghai, China, ²The University of Tokyo, Tokyo, Japan

Protein: Structure & Function

*25P-015 Interpretation of Protein-Corona Formation and Inhibition of Fibrillation by Polyphenol Capped Gold Nanoparticles

Atanu Singha Roy¹, Kakali Baruah¹, Ajit Kumar Singh², Anupam Nath Jha² ¹Department of Chemistry, National Institute of Technology Meghalaya, Shillong 793003, India, ²Department of Molecular Biology and Biotechnology, Tezpur University, Assam 784028, India

*25P-016 CryoEM-sampling of metastable conformations appearing in cofactorligand association and catalysis of glutamate dehydrogenase

<u>Taiki Wakabayashi</u>^{1,2}, Mao Oide^{3,4}, Masayoshi Nakasako^{1,2}
¹Dept. Phys., Keio Univ., Kanagawa, Japan, ²RIKEN RSC, Hyogo, Japan, ³Inst. Prot. Res., Osaka Univ., Osaka, Japan, ⁴PRESTO, JST, Tokyo, Japan

*25P-017 Coarse-Grained Molecular Dynamics Simulations of Rotational Asymmetry in FOF1 ATPase

Shintaroh Kubo¹, Yasushi Okada^{1,2}

¹the University of Tokyo, ²RIKEN

*25P-018 Predicting enzyme function using an empirical approach with machine learning

Suguru Fujita, Tohru Terada

Graduate School of Agricultural and Life Science, Faculty of Agriculture, The university of Tokyo.

*25P-019 Ca2+-induced formation of ice-like water network on the surface of type II antifreeze protein from Japanese smelt

<u>Tatsuya Arai</u>^{1,2}, Yue Yang¹, Sakae Tsuda¹, Kazuhiro Mio², Yuji Sasaki^{1,2} ¹Graduate School of Frontier Sciences, The University of Tokyo, ²AIST-UTokyo Advanced Operando-Measurement Technology Open Innovation Laboratory (OPERANDO-OIL)

*25P-020 Predicting protein conformational motions with AlphaFold2 dictated by physical energy landscape

Xingyue Guan^{1,2}, Qianyuan Tang³, Weitong Ren², Wenfei Li^{1,2}, Wei Wang¹
¹Department of Physics, National Laboratory of Solid State Microstructure, Nanjing University, Nanjing 210093, China, ²Wenzhou Key Laboratory of Biophysics, Wenzhou Institute, University of Chinese Academy of Sciences, Wenzhou, Zhejiang 325000, China, ³Department of Physics, Hong Kong Baptist University, 224 Waterloo Road, Kowloon Tong, Hong Kong SAR, China

*25P-021 Thermodynamic insights into the antiamyloid activity of lobeline on lysozyme fibrillation

<u>Vibeizonuo Rupreo</u>¹, Jhimli Bhattacharyya¹, Ria Saha², Rajib Kumar Mitra² ¹Department of Chemistry, National Institute of Technology Nagaland, Dimapur, Nagaland - 797103, India, ²Department of Chemical and Biological Sciences, S.N. Bose National Centre for Basic Sciences, Kolkata - 700106, West Bengal, India

*25P-022 Functional mechanism of a short wavelength absorbing cation channelrhodopsin, KnChR

Koki Natsume¹, Shoko Hososhima^{1,2}, Yuzhu Wang³, Tatsuki Tanaka³, Wataru Shihoya³, Osamu Nureki³, Hideki Kandori^{1,2}, Satoshi Tsunoda^{1,2}
¹Nagoya Institute of Technology, ²Opto-Biotechnology Research Center, ³The University of Tokyo

*25P-023 Structural basis of inhibition and transport in Organic Cation Transporter 1

<u>Yi Cheng Zeng</u>^{1,2}, Meghna Sobti^{1,2}, Ada Quinn³, Esther Kristianto⁴, Simon Brown⁵, Nicola Smith⁶, Jamie Vandenberg^{2,7}, Renae Ryan⁸, Alastair Stewart^{1,2}

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*25P-024 Rational Design of High-Affinity Protein Binders by Side Chain Dihedral Correlation Network

<u>Yun-Jung Hsieh</u>^{1,2}, Ta I Hung^{3,4}, Wei-Lin Lu¹, Chia-en Chang^{3,4}, Kuen-Phon Wu^{1,2}

¹Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan, ²Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan, ³Department of Chemistry, University of California, Riverside, United States, ⁴Department of Bioengineering, University of California, Riverside, United States

*25P-025 Cytoplasmic domain of GtACR1 regulations the channel gating.

Hana Maruyama¹, Shoko Hososhima¹, Satoshi Tsunoda^{1,2}, Yuya Ohki³, Takashi Kikukawa^{3,4}, Takashi Tsukamoto^{3,4}, Hideki Kandori^{1,2}

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*25P-026 Beyond the Active site: The addition of a remote loop reveals a new complex biological function for chitinase enzymes

Dan Kozome¹, Adnan Sljoka^{2,3}, Paola Laurino¹

¹Protein Engineering and Evolution Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan, ²Center for Advanced Intelligence Project, RIKEN, ³York University, Canada

*25P-027 Towards the Cryo-EM Structures of Viral Annealase Proteins

<u>Lucy Johanna Fitschen</u>^{1,2}, Jodi Brewster^{1,2}, Jordan Nicholls^{1,2}, Stefan Mueller¹, Gökhan Tolun^{1,2}

¹School of Chemistry and Molecular Bioscience, and Molecular Horizons, University of Wollongong, Wollongong, Australia, ²ARC Industrial Transformation Training Centre for Cryo-electron Microscopy of Membrane Proteins (CCeMMP)

***25P-028** Targeting the oncoprotein GOLPH3

Anastasia Theodoropoulou¹, Luciano Abriata¹, Anita Nasrallah², Francesco Talotta², Sarah Vacle¹, Fernando Meireles¹, Maria J. Marcaida¹, Giovanni D'Angelo², Matteo Dal Peraro¹

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25P-029 IgG subclass oligomerization upon antigen binding - Full biophysical

characterization of the missing link between antibody binding and complement activation

<u>Jürgen Strasser</u>¹, Nikolaus Frischauf¹, Aran F. Labrijn², Frank J. Beurskens², Johannes Preiner¹

¹University of Applied Sciences Upper Austria, Linz, Austria, ²Genmab, Utrecht, Netherlands

25P-030 Regulation of enzyme structure and function by weak metal-ion binding

Masayuki Oda¹, Yumi Kitagawa¹, Takuji Oyama², Kosuke Morikawa¹ ¹Kyoto Prefectural University, ²University of Yamanashi

25P-031 Structure and function of stomatin-like protein FliL to assist flagellar motor stator PomAB in marine Vibrio

Norihiro Takekawa¹, Tatsuro Nishikino², Ray Burton-Smith³, Yuki Tajimi⁴, Mitsuru Ikeda³, Kazuyoshi Murata³, Seiji Kojima⁵, Takayuki Uchihashi⁴, Katsumi Imada¹, Michio Homma⁴

¹Dep Macromol Sci, Grad Sch Sci, Osaka Univ, ²Dep Life Sci Appli Chem, Nagoya Inst Tech, ³ExCELLS, Nat Inst Nat Sci, ⁴Div Material Sci, Grad Sch Sci, Nagoya Univ, ⁵Div Biol Sci, Grad Sch Sci, Nagoya Univ

25P-032 Factors influencing pH-sensitive color changes in firefly

bioluminescence were studied through computational analysis of hydrogen bond networks in close proximity to catalytic centers of luciferase and its mutants using QM/MM

Kota Nosaka¹, Naohisa Wada²

¹Graduate School of Life Sciences, Toyo University, Gunma, Japan, ²kyoto Luminous Science Laboratory, Kyoto, Japan

25P-033 A double-edged sword: Bacteriophage PlyGRCS endolysin targeting MRSA Staphylococcus aureus isolates and serendipitous discovery of its interaction with a cold shock protein C (CspC)

Padmanabhan Balasundaram

Department of Biophysics, National Institute of Mental Health and Neuro Sciences (NIMHANS)

25P-034 Deciphering Protein Dynamics and Evolution: Insights from AlphaFold 2's Predicted Aligned Error

Qian-Yuan Tang¹, Liangxu Xie², Xiangze Zeng¹

¹Hong Kong Baptist University, Hong Kong, China, ²Jiangsu University of Technology, China

25P-035 Conformational Heterogeneity and Fluorescence Resonance Energy Transfer in the Calcium Indicator Yellow Cameleon YC3.60

Hiroki Tsubota, Yuna Kinoshita, Mamoru Shigeno, <u>Haruko Hosoi</u> Toho University

25P-036 Protein Dynamics and Mechanisms from Multiple Structures

Robert L Jernigan, Mesih Kilinc, Kejue Jia, Weixia Deng, Pradeep Bk, Rthan Bush

Department of Biochemistry, Biophysics and Molecular Biology, Iowa State University, Ames, IA, USA

Protein: Physical property

*25P-037 Role of aggregation-prone segments in fibril formation of the amyloidogenic apolipoprotein A-I variant

Norihiro Namba¹, Takashi Ohgita¹, Hiroko Tamagaki-Asahina², Toshinori Shimanouchi³, Takeshi Sato², Hiroyuki Saito¹

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*25P-038 Feasibility of immunoglobulin A purification using phosphate-modified zirconia particles

Shogo Kanoh^{1,2}, Kentaro Shiraki¹, Katsuya Kato³, Atsushi Hirano²
¹Faculty of Pure and Applied Sciences, University of Tsukuba, 1-1-1 Tennodai,
Tsukuba, Ibaraki 305-8573, Japan, ²Nanomaterials Research Institute, National
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305-8565, Japan, ³Chubu Center, National Institute of Advanced Industrial Science
and Technology (AIST), Nagoya, Aichi 463-8560, Japan

*25P-039 Development of a high-throughput data collecting system for antibody optimization: thermal stability and interaction kinetics

<u>Sae Ito</u>¹, Ryo Matsunaga¹, Makoto Nakakido¹, Daisuke Komura², Hiroto Katoh², Shumpei Ishikawa², Kouhei Tsumoto^{1,3}

¹Department of Bioengineering, School of Engineering, The University of Tokyo., ²Department of Preventive Medicine, Graduate School of Medicine, The University of Tokyo., ³Department of Chemistry and Biotechnology, School of Engineering, The University of Tokyo.

*25P-040 Air/water-interface-induced self-assembly of biosurfactant protein RolA from filamentous fungus Aspergillus oryzae

Nao Takahashi¹, Yuki Terauchi², Takumi Tanaka³, Akira Yoshimi⁴, Hiroshi Yabu⁵, Keietsu Abe¹

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*25P-041 pKa, stretching vibrational frequencies, and nuclear magnetic resonance chemical shifts in H-bond networks of protein environments

Masaki Tsujimura¹, Keisuke Saito^{1,2}, Hiroshi Ishikita^{1,2}

¹Graduate School of Engineering, The University of Tokyo, Tokyo, Japan, ²Research Center for Advanced Science and Technology, The University of Tokyo, Tokyo, Japan

25P-042 The common feature of fibril formation mechanism of α -synuclein and apolipoprotein A-I

<u>Takashi Ohgita</u>, Norihiro Namba, Hiroki Kono, Hiroyuki Saito Kyoto Pharmaceutical University

Protein: Function

*25P-043 Regulatory mechanism of HADH and its localization in cell organelles during temperature acclimation in Caenorhabditis elegans

<u>Yukina Mori</u>¹, Misaki Okahata¹, Akihisa Fukumoto¹, Yohei Minakuchi², Atsushi Toyoda², Akane Ohta¹, Atushi Kuhara^{1,3}

¹Faculty of Science and Engineering Konan University & Institute for Integrative Neurobiology, Kobe, Japan, ²National Institute of Genetics, ³PRIME, AMED

*25P-045 Proposed design of kinetic parameters for agonist antibodies that induce OX40 clustering.

<u>Kan Ujiie</u>¹, Aki Tanabe², Satoru Nagatoishi³, Ryo Matsunaga^{1,4}, Kouhei Tsumoto^{1,4,5}

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*25P-046 In vitro assembly of a protein capsule and cargo molecules into virus-like particles.

<u>Kenya Tajima</u>¹, Yusuke Sakai², Naohiro Terasaka¹
¹Earth-Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan, ²Center for Biosystems Dynamics Research, RIKEN, Osaka, Japan

25P-047 FHL complex as a cell strategy to regulate proton motive force and survive under energy limited fermentative conditions

Heghine Gevorgyan, Anna Poladyan, Anait Vassilian, <u>Karen Trchounian</u> Laboratory of Microbiology, Bioenergetics and Biotechnology, Research Institute of Biology, Yerevan State University

25P-048 Regulation Mechanism of Liquid-Liquid Phase Separation and Following Aggregation of Fused in Sarcoma by RNA Revealed by Raman Microscopy

Shinya Tahara, Uchu Matsuura, Shinji Kajimoto, Takakazu Nakabayashi Graduate School of Pharmaceutical Sciences, Tohoku University

Protein: Measurement & Analysis

*25P-049 Platinum (II) stabilizes a molten-globule conformation of a small globular cytosolic protein

Suman Tiwari, A.S.R. Koti

Department of Chemical Sciences, TIFR, Mumbai, India.

*25P-050 Visualization and quantitative analysis of protein-protein interaction and cell fusion events using split Akaluc complementation in deep tissues

<u>Yiling Li</u>, Genki Kawamura, Qiaojing Li, Takeaki Ozawa Department of Chemistry, School of Science, The University of Tokyo, Japan

*25P-051 Time-resolved study of the interaction mechanism between α1-acid glycoprotein and membrane by vacuum-ultraviolet circular-dichroism spectroscopy

Satoshi Hashimoto¹, Koichi Matsuo^{1,2}

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25P-052 Real-time Visualization of Structural Maintenance of Chromosomes Complexes by High-Speed Atomic Force Microscopy

<u>Kenichi Umeda</u>^{1,2}, Yumiko Kurokawa³, Yasuto Murayama³, Noriyuki Kodera¹ Nano Life Science Institute, Kanazawa University, Japan, ²PRESTO/JST, Japan, ³Department of Chromosome Science, National Institute of Genetics, Japan

25P-053 Sensitivity of various occupancy estimation for synthetic data related to time-resolved serial femtosecond crystallography.

<u>Sriram Srinivasa Raghavan</u>¹, Florence Tama^{1,2,3}, Osamu Miyashita¹

¹RIKEN Center for Computational Science, Kobe, Japan., ²Institute of Transformative Biomolecules (WpI-ITbM), Nagoya University, Aichi, Japan., ³Department of Physics, Graduate School of Science, Nagoya University, Aichi, Japan.

25P-054 A state of partial Rb inactivation and intermediate E2F activation safeguards proliferation commitment

Yumi Konagaya

RIKEN Center for Biosystems Dynamics Research

25P-055 Real-time HS-AFM observation of EEA1-mediated vesicle fusion in the absence of canonical regulators

<u>Tareg Omer Mohammed</u>, Prem Babu, Shingo Fukuda, Toshio Ando Nano Life Science Institute, Kanazawa University, Kakuma-machi, Kanazawa 920-1192, Japan

Protein: Design & Engineering

*25P-056 PMBiT: A Bioluminescent Probe for Large Antigen Detection

<u>Cheng Qian</u>¹, Ayumu Ninomiya¹, Natsuki Shibukawa¹, Hiroshi Ueda², Takanobu Yasuda², Bo Zhu², Tetsuya Kitaguchi²

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*25P-057 Stabilizing Talin R3 in its Folded State: De Novo Design of a Peptide Binder as a Molecular Lock

Yuze Sun, Jie Yan

National university of singapore mechanobiology institute

*25P-058 Hibody: A Bioluminescent Immunosensor Based on "Trap & Release" of Luciferase-derived Peptide Fused to Antibody

Takanobu Yasuda, Bo Zhu, Hiroshi Ueda, Tetsuya Kitaguchi

Laboratory for Chemistry and Life Science, Institute of Innovative Research, Tokyo Institute of Technology, Kanagawa, Japan

*25P-059 Increased reaction efficiency by external stimuli-sensitive linker

Momoka Takazawa, Koki Kamiya

Graduate School of Science and Technology, Gunma University, Kiryu, Gunma, Japan

*25P-060 Design of Proteins that adopt interconvertible two distinct functional conformations

Toma Ikeda¹, Tatsuya Nojima², Hideki Taguchi^{1,2}

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²Institute of Innovative Research, Tokyo Institute of Technology, Japan

*25P-061 The symmetric SAKe protein scaffold

<u>Staf Wouters</u>¹, Andreu Mor Maldonado², Hiroki Noguchi¹, Kenichi Kamata¹, Wim Maes³, Karen Vanhoorelbeke³, Jeremy Tame⁴, Steven De Feyter², Arnout Voet¹

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*25P-062 Characterization of novel scFv×VHH format of biparatopic antibody against MtsA from Streptococcus pyogenes

Risa Asano¹, Miyu Takeuchi¹, Makoto Nakakido¹, Chihiro Aikawa², Takeshi Yokoyama³, Yoshikazu Tanaka³, Ichiro Nakagawa², Kouhei Tsumoto^{1,4,5}

¹Dept of Bioeng.Eng., Sch. of Eng., The Univ of Tokyo, ²Dept. of Microbiol., Sch. of Med., Kyoto Univ, ³Grad.Sch.of Life Sci., Tohoku Univ, ⁴Dept. of Chem. Biotech., Sch. of Eng., The Univ of Tokyo, ⁵Inst. of Med. Sci., The Univ of Tokyo

25P-063 Functional protein complexes from symmetric designer proteins

<u>Arnout RD Voet</u>, Staf Wouters, Bram Mylemans, Hiroki Noguchi KU Leuven, Belgium

25P-064 Development of a general methodology to design sensor proteins

Rie Tatsumi, Nobuyasu Koga

Institute for Protein Research (IPR), Osaka University, Osaka, Japan

25P-065 A one-pot detection system using β -glucuronidase-based enzyme switch and label-free antibody

<u>Bo Zhu</u>¹, Yukihiko Yamasaki², Takanobu Yasuda¹, Cheng Qian³, Zhirou Qiu³, Hiroshi Ueda¹, Tetsuya Kitaguchi¹

¹Laboratory for Chemistry and Life Science, Institute of Innovative Research, Tokyo Institute of Technology, Yokohama, Japan, ²BioDynamics Laboratory Inc., Tokyo, Japan, ³Graduate School of Life Science and Technology, Tokyo Institute of Technology, Yokohama, Japan

Protein: Intrinsic disorder

*25P-066 The Relationship between Self-assembly and Local Dynamics of Intrinsically Disordered Proteins

Ryoga Kobayashi¹, Takashi S. Kodama², Norio Yoshida³, Hideki Nakamura^{4,5}, Yohei Miyanoiri², Hidehito Tochio¹, Naotaka Sekiyama¹ Department of Biophysics, Graduate School of Science, Kyoto University, Kyoto, Japan, ²Institute for Protein Research, Osaka University, Osaka, Japan, ³Department of Complex systems science, Graduate School of Informatics, Nagoya University, Nagoya, Japan, ⁴Department of Synthetic Chemistry and Biological Chemistry, Graduate School of Engineering, Kyoto University, Kyoto, Japan, ⁵Hakubi Center for Advanced Research, Kyoto University, Kyoto, Japan

*25P-067 Interaction Mechanism of α -Synuclein with Synapsin in the Liquid Condensates

Shunki Takaramoto, Keiichi Inoue

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25P-068 Global Analysis of Disordered Proteome in Cells

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Heme proteins

*25P-069 Crystal structures of bovine heart cytochrome c oxidase with inhibitor complex

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25P-070 Gold Nanoparticle Thin Film Electrode Enables Direct Electrochemical Control of Cytochrome P450 Reaction

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Membrane proteins

*25P-071 Engineering cardiolipin binding to an artificial membrane protein reveals determinants for lipid-mediated stabilization

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*25P-072 Identification of Novel Receptor for Polyphenolic Metabolites

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*25P-073 Mechanism of caffeine-induced functional recovery in RyR2 loss-offunction mutant

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*25P-074 A proton-transfer mechanism in the malaria parasite lactate/H+ symporter suggests a transporter without conformational changes

<u>Ciara J F Wallis</u>, Kasimir Gregory, Stephen Fairweather, Ruitao Jin, Sitong He, Giel van Dooren, Adele Lehane, Ben Corry Research School of Biology, The Australian National University, Canberra, Australia

*25P-075 Ligand binding mechanism analysis of muscarinic acetylcholine receptors utilizing vibrational spectroscopy

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25P-076 Structural dynamics of potassium ion selective and cyclic nucleotide binding in a CNG channel SthK using ATR-FTIR

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25P-077 Where is the N-tail? A Computational Study of Intrinsically Disordered Regions of Human ATP-sensitive Potassium Channel

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25P-078 A Novel Gate Operation Pathway of Lipopolysaccharide Transport by Bacterial ABC Transporter MsbA and LptC

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25P-079 Pulmonary Surfactant Protein C (SP-C): The role of palmitoyl chains on protein-protein interaction and oligomerization, from time-resolved fluorescence methodologies

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DNA & DNA binding proteins

*25P-080 Single molecule imaging of DNA higher-order structural formation by human transcription factor Yin Yang 1.

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*25P-081 Differential dynamics specify MeCP2 function at nucleosomes and methylated DNA

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25P-082 Mediator Mei5-Sae3 Stabilizes Dmc1 Recombinase Clusters for Efficient Assembly on RPA-Coated Single-Stranded DNA

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RNA & RNA binding proteins

*25P-083 Molecular mechanisms of interaction between RNase I and ribosomes

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25P-084 Nascent pre-ribosomal RNA acts as surfactants that suppress fusion of fibrillar centers in nucleolus

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DNA/RNA nanotechnology

*25P-085 Agent model for numerical simulation of the DNA active droplet

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*25P-086 Construction of DNA droplets capable of autonomously moving by sensing nucleic acids

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*25P-087 Specific cell binding of functionalized DNA droplets

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*25P-088 DNA droplets based on self-assembled DNA nanostructure polymers with programmable multivalency

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*25P-089 DNA Nanostructure-based Chromatin-inspired Heterogeneous Fluid Gel Structures

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Nucleic acid: Others

*25P-090 Mechanical diversity and folding intermediates of parallel-stranded G-quadruplexes with a bulge

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*25P-091 Force propagation in dense DNA solution

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Chromatin & Chromosomes

*25P-092 Molecular motor in a box: a model for chromatin remodelers

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*25P-093 Coarse-grained Simulations for Unidirectional Translocation of Bacterial SMC Complex via DNA-segment Capture

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25P-095 Theory of viscoelasticity of chromatin and its surrounding environment

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Water & Hydration & Electrolyte

*25P-096 Effect of osmolytes on the activity of α -amylase

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25P-097 Investigations of hydration structures and dynamics around proteins and peptides with MD simulations

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Molecular genetics & Gene expression

*25P-098 Effects of transcription termination elements on in vitro genome transcription

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Morphogenesis and Development

*25P-099 Three-dimensional Mechanical Cooperativity Optimises Epithelial Wound Healing

Shu En Lim, Rob Tetley, Yanlan Mao

University College London

Muscle

*25P-100 Myosin and tropomyosin-troponin complementarily regulate thermal activation of striated muscles

Shuya Ishii^{1,2}, Kotaro Oyama^{1,2}, Fuyu Kobirumaki-Shimozawa², Tomohiro Nakanishi^{2,3}, Naoya Nakahara⁴, Madoka Suzuki⁵, Shin'ichi Ishiwata⁶, Norio Fukuda²

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25P-101 Observation of power stroke coordination in DNA Origami based artificial myosin filaments

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Molecular motor

*25P-102 Spontaneous γ subunit rotation upon conformational changes of the α , β subunits in F1-ATPase

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*25P-103 Characterization of the motility of tetrahymena kinesin 9A and 9B

<u>Hiroto Ishii</u>, Masahiko Yamagishi, Junichiro Yajima Graduate School of Arts and Science, The University of Tokyo, Tokyo, Japan

*25P-104 Modeling the motion of heterodimeric kinesins reveals head-head coordination in a KIF1A dimer

Tomoki Kita, Kazuo Sasaki, Shinsuke Niwa Tohoku University

*25P-105 Structural analysis of ATP synthases embedded in a lipid bilayer under proton motive force by cryoEM

Atsuki Nakano¹, Jun-ichi Kishikawa², Kaoru Mitsuoka³, Ken Yokoyama¹ ¹Fac. of Life Sci., Kyoto Sangyo Univ, ²Applied Biology, Kyoto Institute of Technology, ³Research Center for Ultra-High Voltage Electron Microscopy, Osaka University

25P-106 Application of information theory to understand cooperative force generation between skeletal myosin molecules

Motoshi Kaya, Arun Kasimchetty, Hideo Higuchi Department of Physics, University of Tokyo

25P-107 Extreme-Value Analysis of Intracellular Cargo Transport by Motor Proteins

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25P-108 Comparative analysis of cilia force production in effective and recovery strokes of isolated Volvox carteri cells

Ryuta Yamaguchi, Katsuya Shimabukuro National Institute of Technology, Ube College

25P-109 Cryo-EM structure of mammalian V-ATPase.

<u>Yui Nishida</u>¹, Atsuko Nakanishi², Atsuki Nakano¹, Fuka Ueda¹, Kaoru Mitsuoka², Ken Yokoyama¹

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Single Molecule Biophysics

*25P-110 Regulation of anticalin-CTLA4 binding mechano-stability by altering protein pulling geometry

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*25P-111 Versatile peptide probes for labeling cell-surface GPCR

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*25P-112 The role of von Willebrand factor-like Domains in Mucin Adhesion

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*25P-113 Self-fueled Peptide Assembly Investigated via AFM-based Imaging

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*25P-114 Force-Dependent Structural Changes of Filamin C Rod Domains Regulated by Filamin C Dimer

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25P-115 State-of-the-art high-speed atomic force microscopy for filming faster biomolecular dynamics

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25P-116 In-cell single-molecule FRET measurement of cytosolic RAF proteins

Kenji Okamoto, Yasushi Sako RIKEN CPR

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*25P-117 Extent of stochasticity in folding dynamics determines the forcetolerance and longevity of mechanosensing proteins

<u>Pritam Saha</u>, Vishavdeep Vashisht, Ojas Singh, Gaurav Kumar Bhati, Surbhi Garg, Dr. Sabyasachi Rakshit

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Cell biology: Adhesion

25P-118 A Novel Semi-Automatic Software Tool for Focal Adhesion Analysis

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Cell biology: Motility

*25P-119 Effect of Substrate Elasticity on Adhesion and Motility of Cancer Cells

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*25P-120 Decoding Antidote Access: Binding/Unbinding Pathways toward Organophosphate-Inhibited HuAChE

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*25P-121 β -arrestin acts as an inhibitor of trimeric G protein signaling in eukaryotic chemotaxis

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*25P-122 Conversion from Linear Contraction to Rotation of Stress Fibers in Migrating Keratocytes

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*25P-123 Rebirth of Fish Epidermal Keratocyte Sheets

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*25P-124 Integration between Epidermal Keratocyte Sheets Accompanied by Rapid Disassembly of Actomyosin Cables

<u>Kazuma Shimizu</u>, Chika Okimura, Yoshiaki Iwadate Department of Biology, Yamaguchi University

*25P-125 Side-by-side interaction of adjacent cells dominates the collaborative dynamics and ordering of collective cells

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*25P-126 Mimicking dynamics of human gastrulation: microprint culture of two types of cells derived from human iPS cells

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25P-127 Structural and Functional Insights into Drosophila melanogaster Sperm Flagella: A Focus on Axonemal Architecture and Beating Patterns

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25P-128 Structural Changes of Beating Comb Plates of Ctenophores during Effective and Recovery Strokes as Probed by Time-resolved X-ray Diffraction Recording

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25P-129 Identifying direct and indirect interactions among collectively moving individuals using pairwise information flow metric

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25P-130 Structural and functional analyses of the C-terminal cytoplasmic domain of a flagellar export gate protein, FlhB

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Cell biology: Cytoskeleton & Membrane skeleton

*25P-131 Crosstalk of two bacterial actins composed of the force generation unit of Spiroplasma swimming

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*25P-132 Microtubule Fatigue Under Repetitive Mechanical Stress

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25P-133 Dominant negative mutations in γ -tubulin cause partial loss of protofilaments in centriole triplet microtubules

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25P-134 Actin fluctuations regulate cofilin binding

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25P-135 Signaling Mechanisms to Regulate Activation of Actin Depolymerization Factor Cofilin in Mast Cells

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Cell biology: Signal transduction & Cell membrane

*25P-136 The maximum phagocytic limit of macrophages is determined by the maximum expansion ability of the local cell membrane surrounding antigens.

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*25P-137 Lipid domains in the inner leaflet of cell plasma membranes serve as a signaling platform for K-Ras

Toshiki Mori¹, Koichiro M. Hirosawa², Rinshi S. Kasai³, Tomohiko Taguchi⁴, Yasunari Yokota⁵, Kenichi G.N. Suzuki^{1,2,3}

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25P-138 ERK-mediated STAT3 inhibition causes dynamic heterogeneity in IL-6 signaling

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25P-139 Intracelluar information flow in RAS-MAPK signaling

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Biological & Artificial membrane: Structure & Property

*25P-140 Protein accumulation on amphiphilic protein-phospholipid hybrid leaflet

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*25P-141 Creation of Asymmetric Membrane Vesicles with a Protein Inner Membrane Mixed with Phospholipids

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*25P-142 Triglyceride-Tethered Membrane Lipase Sensor

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25P-143 Characterization of Lipid Vesicles Adsorbed on Bovine Serum Albumin: Adhesion and Large Nano-indentation

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25P-144 Decoding functional oligomeric states of membrane-associated protein oligomers forming membrane pores

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25P-145 Solid-Supported-Membrane-Based Electrophysiology: Application to the Analysis of Membrane Binding

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Biological & Artificial membrane: Dynamics

*25P-146 Unraveling of the mechanisms of hierarchical mesoscale domain organization in cell plasma membranes by super-resolution microscopy and single-molecule tracking.

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*25P-147 Impact of peptides on the solubility of Amphotericin B and its sterolspecific membrane activity

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*25P-148 Acceleration of lipid exchange reaction between human cells and supported lipid bilayers

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25P-149 Antibacterial activity of C-terminal fragments of NEMURI

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Biological & Artificial membrane: Excitation & Channels

*25P-150 Photocaged amino acid method elucidates the potency of individual positively-charged residues in PIP2-dependency of the Kir2.1 inwardly rectifying potassium channel

<u>Junxian Zhou</u>, Natsuki Mizutani, Kohei Yamamoto, Yoshifumi Okochi, Yasushi Okamura

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25P-151 ATP directly regulates the voltage-gated proton channel

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Membraneless Organella, autophage, Liquid-liquid phase separation

*25P-153 Coalescence of liquid or gel-like DNA-encapsulating micro-droplets

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*25P-154 Aberrant phase transition of stress granules in living cells observed by Raman/Brillouin microscopy and machine learning

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*25P-155 Molecular weight polydispersity initiates nucleation of polymer blends around the phase separation boundary

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*25P-156 Hyperphosphorylation of nucleolar protein Nopp140 drives mitotic nucleolar disassembly.

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25P-157 Molecular dynamics of autophagosomal lipid transfer

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25P-158 Designer coacervates for protein sequestration

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25P-159 Highly Charged Proteins and Their Repulsive Interactions in Regulation of Biomolecular Condensation

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25P-160 A Key Role of Less Bulky-Hydrophobic Amphipathic α -helix in Autophagy

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Chemoreception

*25P-161 Ligand recognition of the Vibrio cholerae chemoreceptor for two distinct attractants, pyruvate and serine

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Neuroscience & Sensory systems

*25P-162 HS-AFM reveals the structural role of CaMKII in synaptic structural plasticity

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*25P-163 Physics of transport through capillaries and the blood-brain barrier: comparative study of hydrogel phantom and living mouse models

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25P-164 Spontaneous depolarization wave in the embryonic CNS: optical imaging with a voltage-sensitive dye

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25P-165 Oscillations in the embryonic chick olfactory bulb: optical imaging with a voltage-sensitive dye

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Neuronal circuit & Information processing

*25P-166 Environmental oxygen information generates temperature response diversity in C. elegans

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25P-167 Construction of Single-Cell Level Linear Neural Network with Agarose Micro Fabrication Technology

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Behavior

25P-168 Anticipation Behavior of the Physarum Plasmodia to Periodic Light Stimulus

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Photobiology: Vision & Photoreception

*25P-169 The mechanism regulating the binding properties of retinal isomers in opsins

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*25P-170 Light-induced structural changes of a rhodopsin domain in a rhodopsin-bestrophin giant ion channel complex studied by time-resolved infrared spectroscopy

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*25P-171 Exploration of the Diversity of Absorption Spectra in Vertebrate Retinal Photo-isomerase, RGR

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*25P-172 Exploring the spectral tuning mechanism of bestrhodopsin from Phaeocystis antarctica

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25P-173 In Vitro Analysis of the Effect of Narrowband and Broadband Light in Visible Range on Lens Epithelial Cell Migration

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25P-174 Insights into light-driven chloride ion pump mechanism of NM-R3 and NpHR by molecular dynamics simulation

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Photobiology: Photosynthesis

*25P-175 Structure of S2 High-Spin State Manganese Cluster of Photosystem II by Multi-frequency Electron Paramagnetic Resonance (EPR) Spectroscopy

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***25P-176** Oxygen-evolving photosystem II structures during S1–S2–S3 transitions

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25P-177 Theoretical analysis of the light-harvesting process in C. thermophilum type-I reaction center that binds three different species of chlorophyll molecules

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25P-178 Electron Transfer Reactions in the Photosynthetic Reaction Center Complex lacking Iron-Sulfur Cluster Fx of Green Sulfur Bacterium Chlorobaculum tepidum

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Photobiology: Optogenetics & Optical control

*25P-179 Antitumor effects of photo-induced cell death using an outward proton pump rhodopsin

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25P-180 Microbial Rhodopsin Engineering through Machine Learning and Automated Experiments

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Radiobiology & Active oxygen

25P-181 Analysis of Radiation-induced Stem Cell Competition and Bystander Response Using Titanium Characteristic X-ray Microbeam

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Origin of life & Evolution

*25P-182 The role of non-biological membraneless polyester microdroplets as protocells at the origins of life

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*25P-183 Creation of a Membraneless Protocell with Earth-abundant Transition Metal Catalysts

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*25P-184 Primordial Evolution by Linking Sequence Information and Vesicle Reproduction

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25P-185 Genetic properties influencing transcriptional variability

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Synthetic biology & Artificial cells

*25P-186 Optimizing the in vitro expression profile of central dogma-related proteins

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*25P-187 Characterization of ribosome biogenesis in vitro

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*25P-188 Light-Induced Control of Directional Movement in Chlamydomonas-Encapsulated Liposomes

<u>Hiromasa Shiraiwa</u>, Koichiro Akiyama, Shunsuke Shiomi, Masahito Hayashi, Tomoyuki Kaneko

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*25P-189 Construction of asymmetric lipid-protein membrane tension sensing system by using mechanosensitive channels

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25P-190 Designing a reproduction cycle of vesicles coupled with artificial metabolic pathways

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25P-191 Dynamic Instability of Totally-synthetic Supramolecular Dipeptide Fibers upon Hybridization of Surfactant Micelles

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Genome biology

*25P-192 Heterogeneity of Genomic Sequence within Population in Single Plaque of Influenza Virus Revealed by Revio analysis

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Computational biology: Bioinformatics

*25P-193 Improving Protein Complex Prediction through the Generation of Multiple Decoy Structures using Docking Software and Aggressive Refinement by AlphaFold2

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Computational biology: Molecular simulation

*25P-195 Elucidating the Binding Pathway of 'Abltide' to Abl Kinase through Enhanced 2D Replica Exchange Molecular Dynamics Simulations

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*25P-196 Exploring Protein-Lipid Interactions in Membranes: A Coarse-Grained Perspective with Implicit Solvent Modeling

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*25P-197 Investigating TDP43 Condensation and Contributions of Ions: A Multiscale Comparative Analysis of Coarse-Grained Models

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*25P-198 Virtual alanine scan for entire sequence of SARS-CoV-2 main protease complexed with ensitrelyir

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*25P-199 Simulation of Lipid Membranes and Their Interaction with Polystyrene

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*25P-200 Enhancing protein conformation sampling with coevolution

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*25P-201 Charge-Charge Interactions in Molecular Dynamics Simulations of Glycans, Glycosaminoglycans, and Lipopolysaccharides

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*25P-202 Quantifying chromosome structural dynamical pathways during cell fate decision making process

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*25P-203 Physical determinants of multiphase organisation in protein/RNA condensates

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*25P-204 Molecular determinants of lipid selectivity of VPS13 lipid transport protein

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*25P-205 Ligand dependent conformational plasticity that guides substrate transport cycle of ABC transporters

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25P-206 Exploring 3D cell spreading in supramolecular hydrogels and dynamics-induced hydrogel surface reconfiguration through molecular simulations

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25P-207 The role of computational approaches in uncovering mechanisms of ferroptotic cell death signal

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25P-208 Dimerization of APP-C99 using BE-ABMD simulations

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25P-209 Computer aided engineering of nonstandard biotechnological enzyme – nitrile hydratase case

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25P-210 Why bestatin inhibitor prefers human carnosinase II (CN2) to human carnosinase I (CN1): Simulation study.

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25P-211 Computational and Biochemical Studies on the Molecular Interactions Between Melanopsin and its AntagonistsC

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25P-212 Atom Filtering Algorithm and GPU-Accelerated Calculation of Simulation Atomic Force Microscopy Images

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25P-213 Small GTPase Ran: exploring nucleotide-specific conformations

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25P-214 Large-scale coarse-grained MD simulations for heterogeneous biomolecular systems by efficient parallelization

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25P-215 Molecular dynamics simulation of amyloid- β aggregates

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Computational biology: Biological modeling and simulation

*25P-216 Mathematical model of glioma cell migration and deformation dependent on adhesion dynamics to extracellular matrix

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*25P-217 Reassessing the Exon-Foldon correspondence using Frustration Analysis

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*25P-218 Computational study of the agonism/antagonism effect of small molecules to toll-like receptor (TLR) 7

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***25P-219** Torsion Angles to Map Protein Conformational Changes

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*25P-220 Simulating three dimensional epithelial monolayer tissue deformation using cell center model

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*25P-221 Development and validation of novel anticancer drugs against protein kinase D2

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*25P-222 An investigation of the molecular mechanisms underpinning the aggregation of POR-BT isomers within membranes using molecular dynamics simulations

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25P-223 Membrane morphology of Clathrin-Mediated Endocytosis

<u>Suguru Ushioda</u>, Masashi Tachikawa Tachikawa Lab, Faculty of Science, Yokohama City Univ.

25P-224 Novel Dengue Vaccine Development – A Multiscale Simulation Study

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25P-225 Navigating Bio-Systems Through A Deep Learnt Lens-Scape of Multiscale Analytics

Haibin Su

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25P-226 Exploring intermediate states along binding of inhibitors to protein kinases using large-scale molecular dynamics simulations

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Computational biology: machine learning for molecules or cell systems

*25P-227 Prediction of Olfactory Perception From Learned Molecular Representation

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*25P-228 Label-free detection of senescent cells using Raman imaging and machine learning

<u>Hiroko Kodama</u>¹, Ren Shibuya², Hiroaki Takahashi², Shinji Kajimoto^{1,2,3}, Takakazu Nakabayashi^{1,2}

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Mathematical & Theoretical biology

*25P-229 Theory for Optimal Estimation and Control with Resource Limitations in Biological Information Processing

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*25P-230 Framework for efficient drug selection using machine learning

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*25P-231 THEORETICAL STUDY ON PARTIAL AND TOTAL ADAPTATION OF MULTIPLE TISSUES UNDER FORCE INTERACTION

Ryunosuke Suzuki, Taiji Adachi Kyoto University, Kyoto, Japan

25P-232 Stoichiometric constraints alter thermodynamic fates of growing systems

<u>Atsushi Kamimura</u>¹, Yuki Sughiyama², Tetsuya J. Kobayashi¹ ¹The University of Tokyo, ²Tohoku University

25P-233 Information Geometry of Equilibrium and Nonequilibrium Chemical Reaction Networks

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Ecology & Environment

*25P-234 Mutual Reinforcement Between Spatial Structure and Species Coexistence in a Living Soil Model

<u>Riz Fernando Noronha</u>, Kim Sneppen, Kunihiko Kaneko Niels Bohr Institute, Copenhagen, Denmark

Nonequilibrium state & Biological rhythm

*25P-235 Mechanism of scaling behavior of an intracellular reaction-diffusion wave in cell-size space

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25P-236 Chaotic Oscillations of Sarcomeres within Cardiomyocytes Induced by Calcium Fluctuations: Identification and Physiological Significance of 'S4C'

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Measurements

*25P-237 Quantitative correspondence between drug-response curves in the REMA test measured fluoromerically and colourimetrically

<u>Alexander V. Sychev</u>¹, Anastasia Lavrova², Eugene Postnikov¹ ¹Kursk State University, ²Saint-Petersburg State Research Institute of Phthisiopulmonology

*25P-238 Development of a dual-luciferase indicator for 'Mix-and-read' detection of Cu2+

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*25P-239 Combined analysis of static and dynamic cell-mechanics with unbiased transcriptomics for thousands of single cells

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25P-240 Nanoendoscopy-AFM measurement of nuclear stiffness in living different metastatic cancer cells

Takehiko Ichikawa¹, Kundan Sivashanmugan², Takeshi Shimi^{1,3}, Kojiro Ishibashi³, Takeshi Yoshida^{1,4}, Akiko Kudo¹, Eishu Hirata^{1,3}, Rikinari Hanayama^{1,4}, Hiroshi Kimura^{5,6}, Takeshi Fukuma^{1,7}

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25P-241 Enzyme reaction measurement using graphene biosensors and its application to SARS-CoV-2 detection

Takao Ono¹, Yohei Watanabe², Shin-ichi Nakakita³, Yasushi Kanai^{1,4}, Naruto Miyakawa⁵, Ayumi Shinagawa⁵, Shota Ushiba⁵, Shinsuke Tani⁵, Yasuo Suzuki⁶, Masahiko Kimura⁵, Daichi Chiba^{1,4,7,8}, Kazuhiko Matsumoto¹ SANKEN, Osaka Univ., Osaka, Japan, ²Kyoto Pref. Univ. Med., Kyoto, Japan, ³Kagawa Univ., Kagawa, Japan, ⁴SRIS, Tohoku Univ., Sendai, Japan, ⁵Murata Manufacturing Co., Ltd., Kyoto, Japan, ⁶Univ. Shizuoka, Shizuoka, Japan, ⁷OTRI, Osaka Univ., Osaka, Japan, ⁸CSRN, Osaka Univ., Osaka, Japan

25P-242 Construction 4 channels polarization-dependent fluorescence correlation spectroscopy for detection of protein interaction.

Masataka Kinjo, Riku Ando, Akira Kitamura Hokkaido University, Sapporo, Japan.

Bioimaging

*25P-243 Development of luminescent glucose sensor and its application

<u>Tanaka Rikuto</u>¹, Sugiura Kazunori², Hattori Mitsuru², Nagai Takeharu^{1,2} ¹Graduate School of Frontier Biosciences, Osaka University, ²SANKEN, Osaka University

*25P-244 Quantitative chemical and physical imaging of heterochromatin in a living cell using Raman-Brillouin microscopy

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*25P-245 Investigating the Mechanical Properties and Dynamics of Focal Adhesions in Living Cells by Nanoendoscopy-AFM Technique

Alam Mohammad Shahidul, Tetsuya Shirokawa, Takehiko Ichikawa, Clemens M. Franz, Takeshi Fukuma

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*25P-246 Native molecular properties of full-length SARS-CoV-2 Open Reading Frame 6 (ORF6) protein observed using HS-AFM

Goro Nishide¹, Keesiang Lim², Maiki Tamura³, Akiko Kobayashi⁴, Qingci Zhao³, Masaharu Hazawa^{2,4}, Toshio Ando², Noritaka Nishida³, Richard W. Wong^{2,4}

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*25P-247 Shannon entropy and complexity in describing and visualizing the chemical diversity of surrounding cells by mass spectrometry imaging techniques

<u>Lili Xu</u>¹, Manabu Machida², Tomoaki Kahyo¹, Mitsutoshi Setou¹

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*25P-248 Label-free detection of supersulfides in aliving cell using Raman microscopy

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*25P-249 Mechanical properties of human platelets in biochemical confinement

Vincent Gidlund, Jan Seifert, Johanna Rodriguez, Carmela Rianna,

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*25P-250 Oblique Line Scan Illumination Enables Expansive, Accurate and Sensitive Single Protein Measurements in Solution and in Living Cells

Amine Driouchi¹, Mason Bretan¹, Brynmor Davis¹, Alec Heckert¹, Markus Seeger¹, Maité Bradley Silva¹, William Forrest¹, Jessica Hsiung¹, Jiongyi Tan¹, Hongli Yang¹, Eric Betzig², Xavier Darzacq², Russ Berman¹, Daniel Anderson¹

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*25P-251 Characterization of a novel membrane voltage sensor in the bacterial flagellar type III export apparatus

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25P-252 Atomic force microscopy (AFM)-based nanoindentation of the RSJ2 Ralstonia phage

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25P-254 Scanning-free functional Fluorescence Microscopy Imaging Toward Spatial Mapping of Biomolecular Information in Live Cell

Sho Oasa¹, Aleksandar Krmpot^{2,3}, Stanko Nikolic^{2,3}, Andrew Clayton⁴, Igor Tsigelny⁵, Jean-Pierre Changeux⁶, Lars Terenius¹, Milivoj Belic³, Rudolf Rigler⁷, Vladana Vukojevic¹

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25P-255 Characteristics of extracellular collagen in cartilage revealed by polarization-resolved second harmonic generation imaging

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Bioengineering

*25P-256 Exploring Biological Changes in Whole and Serum Blood of Healthy and Diabetic Patients Using Drying Droplets

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*25P-257 Fabrication of a Nanobody-based Ratiometric Bioluminescent Immunosensor for Point-of-care Testing

Yinghui Yang¹, Akihito Inoue¹, Takanobu Yasuda², Hiroshi Ueda², Bo Zhu², Tetsuya Kitaguchi²

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*25P-258 High-throughput nano/micro biological particle analyzer with unsupervised denoising for enhanced sensitivity

<u>Yuichiro Iwamoto</u>¹, Benjamin Salmon², Yusuke Yoshioka³, Bin Xu¹, Ryosuke Kojima¹, Alexander Krull², Sadao Ota¹

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*25P-259 Multicolor autonomous bioluminescence imaging based on bacterial bioluminescence system

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25P-260 Isolation of novel fluorogenic RNA aptamers via affinity- and fluorescence-based in vitro selection

Ryo Iizuka¹, Keisuke Ito¹, Tomotaka Tayama¹, Sotaro Uemura^{1,2}

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Crystal growth & Crystallization technique

*25P-261 Protein – calixarene crystal engineering

<u>Niamh Maria Mockler</u>¹, Kiefer Ramberg¹, Colin Raston², Peter Crowley¹ ¹School of Biological and Chemical Sciences, University of Galway, H91 TK33, Galway, Ireland, ²Flinders University, Adelaide, Australia.

*25P-262 Investigation of crystallization of crystallized protein expressed using E. coil

Yume Kosuge, Koki Kamiya Graduate School of Science and Technology, Gunma University, Kiryu, Gunma, Japan

Virus structure, function, SARS-CoV-2

*25P-263 Study of the binding site dynamics, druggability and cryptic pocket formation in different human coronaviruses' main protease (Mpro)

Ahmed Adel Ezat

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*25P-264 Cryo-EM structure of the Borna disease virus 1 RNA-free nucleoprotein complex

Shinya Goto^{1,2}, Yuya Hirai³, Keizo Tomonaga^{4,5,6}, Takeshi Noda^{1,2}, Masayuki Horie^{7,8}, Yukihiko Sugita^{1,2,9}

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25P-266 Unraveling the Dynamics of SARS-CoV-2 Spike: From Glycosylation States to Cryptic Pockets and Antibody Binding

Mohd Firdaus Samsudin¹, Lorena Zuzic¹, Palur Raghuvamsi^{1,2}, Aishwary Shivgan¹, Nikhil Tulsian², Himanshi Chawla³, Joel Allen³, Max Crispin³, Paul MacAry⁴, Ganesh Anand⁵, Peter Bond^{1,2}
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Mechanosensing and Mechanobiology, Biological Temperature

*25P-267 Development of a high-frequency focused ultrasound system for applying noninvasively localized mechanical stimulation to cells in culture

Natsumi Fujiwara, Shao Ying Tan, Akira Nagakubo, Masahiro Kino-oka, Hirotsugu Ogi

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25P-268 Force transmission by retrograde actin flow-induced dynamic stretching of Talin

<u>Sawako Yamashiro</u>^{1,2}, David Rutkowski³, Kelli Ann Lynch^{3,4}, Ying Liu¹, Dimitrios Vavylonis³, Naoki Watanabe^{1,2}

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25P-269 Modulating E-Cadherin Engagement to Alter Cell Junctional Tension in Spheroids

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Biophysics of disease

*25P-270 Opportunities of Raman spectroscopy in pulmonary arterial hypertension

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*25P-271 Exploring Dapagliflozin Therapy Effects on Nanomechanics and Morphology of Red Blood Cells in Type I Diabetes Mellitus

Patrycja Lidia Twardawa^{1,2}, Bartłomiej Matejko³, Agata Kubisiak^{1,2}, Katarzyna Cyranka^{3,4}, Tomasz Klupa^{3,4}, Marta Targosz-Korecka¹

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25P-272 Opposite effects of extracellular chloride and pH on closely related CIC-6 and CIC-7 transporters suggest non-overlapping function in endo-lysosomes

Maria Antonietta Coppola¹, Paola Gavazzo¹, Ilaria Zanardi¹, Abraham Tettey-Matey¹, Antonella Liantonio², Paola Imbrici², Peying Fong³, Michael Pusch¹

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Miscellaneous topics

*25P-273 Structural and Magneto Absorption Study of Hard and Soft Ferrite

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25P-274 FUNCTIONALIZED CNT AND ACTIVATED CARBON

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Single Molecule Biophysics

25P-275 Quantifying ligand binding kinetics in G-quadruplex DNA with fluorescence lifetime correlation analyses

<u>Chao-Han Cheng</u>, Chih-Chieh Ko, Yong-Zhan Hong, Chung-Chieh Wu Department of Applied Chemistry, National Pingtung University, Pingtung, Taiwan

Cell biology: Motility

25P-276 Inference of cellular traction forces using temporal information

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Computational biology: Molecular simulation

25P-277 Secondary Proton Transfer in the Qo Site of Cytochrome bc1

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Computational biology: Biological modeling and simulation

25P-278 Phase-field model of Dictyostelium fruiting body formation

<u>Seiya Nishikawa</u>¹, Satoshi Kuwana¹, Gen Honda^{1,2}, Satoshi Sawai^{1,3}, Shuii Ishihara^{1,3}

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25P-279 Topography-mediated cell communication

<u>Aleksandra Ardaševa</u>¹, Varun Venkatesh¹, Daiki Matsunaga², Shinji Deguchi², Amin Doostmohammadi¹

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Mathematical & Theoretical biology

25P-280 Latecomer Killing: Elaborate Response in Yeast Communities

<u>Tetsuhiro S. Hatakeyama</u>¹, Kunihiko Kaneko², Kunihiro Ohta³, Miki Tamura³, Arisa Oda³

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Biophysics of disease

25P-281 Reinstating heart rate variability improves cardiac output in heart failure - novel insights from proteomics

<u>David Crossman</u>¹, George Guo¹, Julia Shanks¹, Jizhong Bai¹, Martin Middleditch², Gus Grey¹, Julian Paton¹, Rohit Ramchandra¹

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25P-282 Development of the two-fingered microhand and micro fluidic system for measuring the mechanical properties of cell

Masaru Kojima¹, Masahiro Totani¹, Masahiro Kawakami¹, Toshihiko Ogura², Tatsuo Arai³

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25P-283 Targeting Retinal Angiogenesis: Potential of AT11-L0 Aptamer for Drug Delivery

David Moreira^{1,2}, Jessica Lopes-Nunes², Fátima Santos³, Maria Oliveira^{4,5}, António Paulo^{4,5}, Maria Campello^{4,5}, Carla Cruz^{1,2},

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Wednesday, June 26

Presentation time is organized by whether the last part (suffix) of Poster Session number is odd/even.

Abstracts marked with * in the abstract number eligible for IUPAB2024 Student and Early Career Researcher Poster Award voting

Ex) *25P-999

Protein: Structure

*26P-001 Unravelling Protein Complexity with 3Di-based Structural Entropy

Zecheng Zhang, Qian-Yuan Tang

Hong Kong Bapist University

*26P-002 Frustration-Fluctuation Correspondence in Enzymes

Yuxiang Zheng, Qian-Yuan Tang

Hong Kong Baptist University

*26P-003 Cryo-EM Structure of the hERG Channel Complexed with a K+ Channel Blocker

Yasuomi Miyashita^{1,2}, Toshio Moriya³, Masato Kawasaki³,

Satoshi Ogasawara², Naruhiko Adachi³, Satoshi Yasuda²,

Tetsuichiro Saito¹, Toshiya Senda³, Takeshi Murata²

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Wednesday, June 26

*26P-004 Crystal Structure of Pectocin M1 from Pectobacterium carotovorum: Unveiling Diverse Conformations and Binding Interactions during the Initial Step of Pectocin M Uptake through the Ferredoxin Uptake System

Nawee Jantarit^{1,2}, Hideaki Tanaka¹, Genji Kurisu^{1,2}

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*26P-005 Symmetry Matched Protein – Macrocycle Assembly

<u>Colin Wren</u>¹, Ronan J. Flood¹, Niamh M. Mockler¹, Martin Savko², Qiang Shi³, Peter B. Crowley¹

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*26P-006 Structure of Francisella tularensis subsp. novicida Cas9 in the catalytically poised state

<u>Shinsuke Higashiyama</u>, Ryoya Nakagawa, Hisato Hirano, Osamu Nureki Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo, Japan

*26P-007 Cryo-EM structure of a photosystem I supercomplex from oleaginous green alga Coccomyxa subellipsoidea

Pi-Cheng Tsai, Fusamichi Akita, Jian-Ren Shen

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*26P-008 Structural analysis of the photosystem I-light harvesting I supercomplex from a cryptophyte alga Rhodomonas sp.

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*26P-009 Structural analysis of brain-associated proteins in complex with novel PET radiotracers

Kaede Goto¹, Junta Tomono¹, Shozo Furumoto², Nobuyuki Okamura³, Ryuichi Harada³, Takeshi Yokoyama¹, Yoshikazu Tanaka¹

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26P-010 Cryo-EM structure of the zinc-activated channel (ZAC) in the Cys-loop receptor superfamily

Fei Jin¹, Yi-Yu Lin², Ru-Chun Wang², Yimeng Zhao¹, Cheng Shen¹, Danqi Sheng¹, Muneyoshi Ichikawa¹, Ye Yu², Jin Wang², <u>Motoyuki Hattori</u>¹ Fudan University, Shanghai, China, ²China Pharmaceutical University, Nanjing, China

26P-011 The conformation and its thermal stability of antibiotic peptide alamethic in alcohol solution studied by NMR

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26P-012 A novel blue-carotenoprotein from sponge

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26P-013 Structure-activity Relationship of a novel enzyme derived from marine Streptomyces

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Protein: Structure & Function

*26P-015 Proton conduction mechanism in FO rotary motor studied by quantum molecular dynamics simulation

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*26P-016 Time-resolved crystallography for the study of a B12-dependent photoreceptor using X-ray free-electron lasers

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*26P-017 Heterogeneity of Microtubule Lattices Revealed by Cryo-ET and Non-averaging Structural Analysis

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*26P-018 Structural-dynamics insight of an alligator-derived antimicrobial peptide, AsCATH5, in interaction with membrane mimetics as revealed by solution NMR and MD simulation

<u>Jeremia Oktavian Chrisnanto</u>, Kohei Kano, Mitsuki Shibagaki, Tefera Dessalegn Abeje, Hirai Fumi, Yasuhiro Kumaki, Hiroyuki Kumeta, Tomoyasu Aizawa Hokkaido University

*26P-019 Discovery and structural characterization of novel pore-forming toxins

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*26P-020 Functional annotation of Cysteine Post-Translational Modifications based on protein sequences and structures and development of a consolidated Cysteine database (CysDBase)

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*26P-021 Crystal structure and proton transporting mechanism of viral heliorhodopsin, V2HeR3

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*26P-022 Theoretical study on the photoactivation state of chloride pump NpHR using QM/MM Method

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*26P-023 Investigating allosteric communication with ultrahigh-resolution X-ray crystallography

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*26P-024 Development of supramolecular micelles promoting oxidative protein folding under a crowded environment

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*26P-025 Insights into the Cytochrome c Oxidase proton pumping mechanism from constant-pH MD simulations

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*26P-026 Mass photometry as a novel single molecule approach to study immunoglobulin binding protein (BiP) oligomerization and function

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*26P-027 Catalytic mechanism of the cytosolic θ type carbonic anhydrase from marine diatom Phaeodactylum tricornutum

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*26P-028 Structure of nitric oxide reductase dimer revealed by single particle cryo-electron microscopy

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26P-029 The glycation effect on structure and dynamics of human serum albumin

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26P-030 The crystal structures of Sau3Al with and without bound DNA suggest a self-activation-based DNA cleavage mechanism

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26P-031 Mechanism of Formate Oxidation by NAD-dependent Formate Dehydrogenase: Computational Studies on Near-Attack Conformations

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26P-032 Imaging and inhibition analysis of human serum amyloid A aggregation using quantum dots

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26P-033 Real-time Imaging and Inhibition Analysis of Amylin Aggregations Using Quantum Dot nanoprobes

<u>Xiaoyu Yin</u>, Ziwei Liu, Tuya Gegen, Hayate Sawatari, Keiya Shimamori, Masahiro Kuragano, Kiyotaka Tokuraku Graduate School of Engineering, Muroran Institute of Technology

26P-034 Structural and functional analyses of YeeE/YeeD complex in thiosulfate uptake pathway

Mai Ikei¹, Ryoji Miyazaki¹, Keigo Monden¹, Yusuke Naito¹, Azusa Takeuchi¹, Yutaro S. Takahashi¹, Yoshiki Tanaka¹, Keina Murata², Takaharu Mori², Muneyoshi Ichikawa³, Tomoya Tsukazaki¹

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26P-035 TRANSPLANTATION OF ENZYMATIC FUNCTION BY EXCHANGE OF FUNCTION ELEMENTS

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Protein: Physical property

*26P-037 Thermal Boundary Conductance at the Protein–Water Interface

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*26P-038 Structural Insights into Switching Mechanisms between Spontaneous Folding and Ligand-Induced Folding of Staphylococcal Nuclease

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26P-039 α B-crystallin prevents aging of α -synuclein droplets

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*26P-040 The function of multiple aggregates formed by the tumor suppressor protein p53

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*26P-041 Spatiotemporal formation of a single liquid-like condensate of α-synuclein and subsequent aging by optical trapping

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26P-042 The oligomeric state is essential for fibroin nanofiber formation.

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Protein: Function

*26P-043 pH-gating mechanism of the bacterial inner membrane urea channel HpUrel of Helicobacter pylori

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*26P-044 Yeast complementation assays as a screening tool for urea, water, and ammonia permeability of membrane channels

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*26P-045 Enhanced cell-membrane fluidity mediated by antifreeze proteins mitigates hypothermic injury to cells

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26P-046 Towards longer luminescence lifetime of the minimal luciferase picALuc

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26P-047 High-speed atomic force microscopy reveals functional dynamics of FnCas9

Hideaki Tsukada Mikihiro Shibata

Protein: Measurement & Analysis

*26P-048 Development of Liquid Sample Observation Methods for Pulse-Electron Microscope

Ryoya Katayama, Takeru Yamasaki, Tomoharu Matsumoto, Akihiro Narita Grad. Sch. of Sci., Nagoya Univ.

*26P-049 Light-induced structural changes of heliorhodopsin 48C12 studied by using surface-enhanced infrared absorption spectroscopy

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*26P-050 Nanopore-based peptidome analysis based on the protein-protein interactions.

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26P-051 Protein Acetylation Tracked using UV-Visible Absorption, Luminescence Spectroscopy and TD-DFT calculations

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26P-052 Development of cysteine-specific modification technique for the quantitative analysis

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26P-053 Analysis of membrane translocation of Clostridioides difficile binary toxin using electrophysiologicaltechniques

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26P-054 Simple and Efficient Detection Scheme of Two-Color Fluorescence Correlation Spectroscopy for Protein Dynamics Investigation from Nanoseconds to Milliseconds

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Protein: Design & Engineering

*26P-055 Computational Design of engineered NT-193 antibody with broad activity against SARS-CoV-2 variant.

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*26P-056 In silico/in vitro evolution of peptide nanopore with β -barrel structure

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*26P-057 The molecular basis through which Fv-supercharging affects the physicochemical properties of antibodies

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*26P-058 Dynamics and Evolution of Uniform Substrate Binder

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*26P-059 Tandem artificial nucleocapsid to package longer RNA genome and expand protein architectures

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*26P-060 Exploring the design rules for artificial phase-separating peptides based on natural phase-separating protein sequences

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26P-061 Development of various fluorescence lifetime sensors using mTurquoise2 platform

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26P-062 Darwinian ultrahigh-throughput evolution of biomolecules with in vitro compartmentalized gene amplification races

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26P-063 Magnetic bead-based protein display screening system for quantitative selection and evolution of functional proteins

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Protein: Intrinsic disorder

*26P-064 Improvement of detection ability for amyloid fibril seeds by interaction between ultrasonic cavitation and surfactants

Tomoki Ota, Kichitaro Nakajima, Keiichi Yamaguchi, Yuji Goto, Hirotsugu Ogi

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*26P-065 The role of phase transitions of biopolymers in the formation and functioning of A-bodies

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*26P-066 High-Speed Atomic Force Microscopy Reveals Structural Dynamics of Microtubule-Associated Protein Tau Aggregation.

<u>Tatsuya Kimura</u>¹, Kenjiro Ono², Ken-ichi Umeda¹, Daiki Muramatsu², Hiroki Konno¹, Noriyuki Kodera¹, Toshio Ando¹, Takahiro Nakayama¹ ¹WPI-Nano Life Science Institute, Kanazawa University, Kanazawa, Japan, ²Graduate School of Medical Sciences, Kanazawa University, Kanazawa, Japan

26P-067 From the single-chain behavior to phase behavior of intrinsically disordered proteins

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Heme proteins

*26P-068 Organ-specific probing of mitochondrial and lipid properties in Caenorhabditis elegans with Raman spectroscopy and imaging

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26P-069 Purification and characterization of cholate-free cytochrome c oxidase from bovine heart

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Membrane proteins

***26P-070** Time-resolved FTIR study of light-driven ion pump rhodopsin mutants converted from sodium to chloride pump.

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*26P-071 Detection of TEV protease by pore blockage in Outer Membrane Protein-G Nanopore mutation

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*26P-072 Construction and evaluation of the mutant β -barrel outer membrane protein nanopore

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*26P-073 Detection of Polypeptide Related to Membrane Fusion through Nanopore MscL and Interaction based on Proteins Function

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*26P-074 Time-resolved infrared dual-comb spectroscopy using quantum cascade lasers reveals differences in conformational changes of two heliorhodopsins found from a bacterium and an archaeon

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*26P-075 Exploration of physical properties in streptomyces heliorhodopsin and the physiological function in the native cells

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26P-076 Rottlerin as an aquaporin-3 inhibitor for cancer therapy

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26P-077 An attempt at high-resolution structural analysis of membrane proteins reconstituted into liposomes

Atsuki Nakano, <u>Takaya Kawauchi</u>, Ren Kobayashi, Yuto Muto, Taichi Tsuyama, Ken Yokoyama Kyotosangyo University

26P-078 Reconstitution and nanoscale visualization of cadherin clusters on supported lipid bilayer in solution

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26P-079 Protonophoric function of the 2-oxoglutarate/malate carrier.

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DNA & DNA binding proteins

*26P-080 Dynamic interactions between DNA and a transcription factor, Photozipper, visualized by high-speed atomic force microscopy

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*26P-081 Mechanism of DNAs attraction mediated by low and high valence salts

<u>Hongwei Zuo</u>, Fujia Tian, Liang Dai city university of Hong Kong

26P-082 Encapsulation of cell nucleolus by single-stranded DNA

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RNA & RNA binding proteins

*26P-083 Molecular simulations to investigate the protein-RNA assembly

mechanism of Tetrahymena telomerase

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26P-084 Structural Ensembles of the 5'-UTR of Hepatitis C Virus RNA With and Without MicroRNA Using SIS-RNA Model

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DNA/RNA nanotechnology

*26P-085 Automation of DNA gel generation experiments using machine learning and pipetting robots

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*26P-086 Network formation of enzymes via DNA motif in two types of cascade reactions

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*26P-087 A Hydrogel Biosensor Combining Aptamer Recognition and DNA-Driven Hydrogels

Satofumi Kato¹, Masahiro Takinoue², Hiroaki Onoe¹

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*26P-088 Towards Rotary DNA Motor with Conformational Change

<u>Akihiro Fukuda</u>¹, Yusuke Sato², Takeshi Yokoyama^{1,3}, Yoshikazu Tanaka¹, Shoichi Toyabe¹

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*26P-089 Liquid-liquid phase separation of computational DNA droplets on the gold surface

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Nucleic acid: Others

*26P-090 Molecular Dynamics Simulations to Investigate Interactions Between

Polymers and RNA in Polymer Nanoparticles

<u>James Aaron Robins</u>, Naoto Hori, Cameron Alexander, Keith Spriggs School of Pharmacy, University of Nottingham

*26P-091 Oligonucleotide Assembly enhanced by intrinsically disordered protein droplet

Taiji Ueno, Yoshihiro Minagawa, Hiroyuki Noji

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Chromatin & Chromosomes

*26P-092 Mechanic Properties of Nucleosomes are Key Modulators of the Unwrapping Energy Landscape

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*26P-093 Protein search processes mediated by chromatin topology

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26P-094 Effect of the molecular crowding environment on the structure of poly-nucleosomes

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26P-095 From Sequence to Structure: Refining Chromatin Models with PTM and Contact Frequency Data

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Water & Hydration & Electrolyte

*26P-096 Effect of hydration state polymers on Liquid-Liquid Phase Separation.

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26P-097 Correlation analysis of co-solvation free energies in insulin dissociation

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Molecular genetics & Gene expression

26P-098 PML protein localization and bioinformatic interactome analysis in ageing related diseases.

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Morphogenesis and Development

*26P-099 Nuclear softening triggers a transcriptional burst during early embryogenesis

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Muscle

*26P-100 Cardiac cycle-dependent alterations in redox states revealed by cryo-Raman spectral analysis

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26P-101 Effects of Near-Infrared Laser Irradiation on Circular Cardiomyocyte Network

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Molecular motor

*26P-102 Directionality on kinesin-1 motility can be determined depending on the anchor points

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*26P-103 Three-dimensional motility of myosin IC bound to lipid membrane

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*26P-104 Energetics of engineered FoF1-ATP synthase with high H+/ATP ratio

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*26P-105 Biomolecular motors use two asymmetries to generate unidirectional movement

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26P-107 Nuclear Spin Catalysis in Living Cells and Biomolecular Motors

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26P-108 Mechanical force measurement of F1-ATPase using accurate revolution control by an optical-vortex tweezers.

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26P-109 Flagellar rotation-speed difference observed in the same bacterial cells

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Single Molecule Biophysics

*26P-110 Enhanced Interpretation of STED-FCS Diffusion Law Plot Dependencies

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*26P-111 High sensitivity detection of HBV RNA based on 3D-DNA nanomachine and biological nanopore sensing technology

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*26P-112 NANOSPACER: Optical analysis of biomolecules and nanoparticles in solution using nanofluidic devices

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*26P-113 Single-molecule manipulation of genome integrity guardians

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*26P-114 Interdomain linkers regulate the mechanotransduction in proteins

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26P-115 Single-molecule sensing with aerolysin pore-forming toxins

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26P-116 Live-cell Single-molecule Imaging and Mapping of Human SWI/SNF Chromatin Remodelers Reveal Bromodomain-mediated and Cancer-mutants-specific Landscape of Multi-modal DNA-binding Dynamics

Wilfried Engl, Hendrik Sielaff, Aliz Kunstar-Thomas, Siyi Chen,

Woei Shyuan Ng, Ziqing Winston Zhao

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Cell biology: Adhesion

26P-117 Dynamics and function of adhesion GPCR

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Cell biology: Motility

*26P-118 Sheet-like structure of bacterial actin MreBs driving helicity switching by cryo electron tomography

<u>Haruka Yuasa</u>¹, Yuya Sasajima¹, Hana Kiyama¹, Daichi Takahashi^{1,2}, Takuma Toyonaga^{1,3}, Tomoko Miyata^{4,5}, Fumiaki Makino^{4,5,6}, Keiichi Namba^{4,5}, Makoto Miyata^{1,3}

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*26P-119 Rotation of bacterial cell-bodies in different species capable and incapable of flagellar wrapping

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*26P-120 Viscoelasticity dependence of ciliary beating and the resulting flow Saki Tamura, Misako Otaki, Yoshihiro Murayama Department of Biomedical Engineering, Tokyo University of Agriculture and Technology

*26P-121 Water flow navigates the long journey of surface-associated bacteria living in hot springs

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*26P-122 Analysis of Fluctuations in Measurement Data of Bacterial Flagellar Motors

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*26P-123 Quantitative model of vascular cell motility in angiogenesis

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*26P-124 Suppressing Bacterial Surface Colonization and Motility with Biosurfactants

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*26P-125 Cell Type-Dependent Coordinated Regulation of Rho GTPases in Cell Motility

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26P-126 A highly conserved Arg-391 residue of FlhA is involved in export switching of the flagellar type III secretion system in Salmonella

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26P-128 Cell size variation affects bacterial swimming speed

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26P-129 Atomic model comparison of the L- and R-type straight bacterial flagellar filaments for understanding the supercoiling mechanism

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Cell biology: Cytoskeleton & Membrane skeleton

*26P-130 Deformability cytometry of Jurkat cells for cell immunotherapy

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*26P-131 Development and application of an optogenetic tool to control the actin polymerization

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26P-132 Polymerization of PEG-attached actin

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26P-133 Measurement of intracellular forces using centrifuge polarizing microscope (CPM)

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26P-134 Construction of a mechanical model for C. elegans gastrulation

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Cell biology: Signal transduction & Cell membrane

*26P-135 Cell size feedback mechanism for propagating cell-cell signals in Dictyostelium discoideum

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*26P-136 Cellular Guardianship Symphony by the Dynamic Duo of LL37 and HNP-1

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26P-137 Slow diffusion and signal amplification on membranes regulated by phospholipase D

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26P-138 Small extracellular vesicles trigger integrin-mediated adhesion signal in the recipient cells

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Biological & Artificial membrane: Structure & Property

*26P-139 Membrane tension and its effect on a membrane structure

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*26P-141 Elucidating the Molecular Mechanism of the Dual Cooperative Effect Between antimicrobials LL37 and HNP1: A Study of Peptide-Lipid and Peptide-Peptide Interactions

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26P-142 Dimerization of transmembrane peptides synergistically enhances the lipid scrambling activities

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26P-143 Mechanism of action and lipid-mediated synergistic interactions of antimicrobial peptides: New regulatory mechanisms also for membrane proteins?

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26P-144 Impact of Acetonitrile Molecules on Miscibility Transition Temperature of Multicomponent Lipid Vesicles

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Biological & Artificial membrane: Dynamics

*26P-145 Effect of actin encapsulation on the behavior of lipid bilayers under osmotic stress

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*26P-146 PORE-FORMING ACTIVITIES OF β -HAIRPIN ANTIMICROBIAL PEPTIDES EVALUATED BY LIPID BILAYER SYSTEM

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*26P-147 Synthesis of fluorescence-derivative of DHA-containing phospholipids and its behavior in lipid bilayers.

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*26P-148 Morphological change in liposomes that encapsulating F-actins with the adjusted length distribution

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26P-149 Membrane viscosity of phase-separated ternary GUVs having Lo domains as the basis for lipid rafts

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Biological & Artificial membrane: Excitation & Channels

26P-150 Development of a high-throughput device for recording channel currents using agarose gel beads

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Biological & Artificial membrane: Transport & Signal transduction

*26P-151 The fusion site of cell penetrating peptide sequences affects the cytoplasmic transport

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Membraneless Organella, autophage, Liquid-liquid phase separation

*26P-152 Phase separation and phase transition of protein mixture on chemically modified glass surfaces

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*26P-153 Quantitative analysis of lipophagy by a small molecule fluorescent reporter

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*26P-154 Quantitative Raman analyses and photo-regulation of nucleic acidpeptide droplets formed by liquid-liquid phase separation

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*26P-155 A new method for structural switching of multiphase coacervates based on rational design of charged polypeptides

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26P-156 Tunable Wetting Properties in Multicomponent Protein Condensates

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26P-157 Super enhancer-derived IncRNA CCAT1-L regulates the condensation of human Mediator

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26P-158 Metastable phase-separated droplet generation and long-time DNA enrichment by laser-induced Soret effect

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Neuroscience & Sensory systems

*26P-159 High-speed AFM reveals activity-dependent stable complexes of kinase domains in CaMKIIβ

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*26P-160 Molecular mechanism of classical conditioning in earthworm

<u>Sukehiro Kabayama</u>, Yoshiichiro Kitamura Kanto-Gakuin University

26P-161 Ion-channel-based complete synchronization between neurons

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26P-162 Models of complex structure-related diffusion anomalies of transport in the brain's extracellular space

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Neuronal circuit & Information processing

*26P-163 Outgrowth order in breaking symmetry of immature neurites is another regulation factor of neuronal polarity formation

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26P-164 Large-scale voltage-sensitive dye imaging of mouse prefrontal cortex: Biophysical mapping of intra- and inter-hemispheric connections

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Behavior

*26P-165 Swimming ciliate, Stentor selects anchoring sites accompanied by extracellular geometries

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Photobiology: Vision & Photoreception

*26P-166 Electrophysiological Study of the Effect of Weak Organic Acids on the Transport Activity of Proton Pumping Rhodopsin of Rhizobacteria

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*26P-167 Structural basis for early proton transfer reaction on a primate bluesensitive pigment

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*26P-168 Time-resolved crystallography uncovering cryptochrome signal transduction mechanism

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*26P-169 Light-induced difference FTIR analysis of xenorhodopsin from Nanosalina at 77 K

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26P-170 Spectroscopic and functional characterization of novel viral rhodopsins

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26P-171 Modulation of intracellular calcium responses using photocyclic vertebrate visual pigments

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Photobiology: Photosynthesis

*26P-172 Carotenoids binding effect of the photoreaction processes on Xanthorhodopsin

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*26P-173 Mobility of protein complexes in plant thylakoid membranes analyzed by high-speed atomic force microscopy

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*26P-174 Excitation energy transfer dynamics among antenna pigments in the ΔpshX-reaction center from Heliomicrobium modesticaldum

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26P-175 Structural Basis for Enabling Photosynthesis with Extremely Lowenergy Near-infrared Light in the LH1–RC Complex of a Thermophilic Purple Nonsulfur Bacterium

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26P-176 Characterization of an LH1–RC photocomplex from a novel Japanese hot spring purple sulfur bacterium, Caldichromatium japonicum

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Photobiology: Optogenetics & Optical control

*26P-177 Channel gating mechanism of K+ selective channelrhodopsin, KCR

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*26P-178 In vivo single-cell 3D optogenetics technology with light-field microscopy

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26P-179 Identification of the important region for photoactivity in photoactivated adenylyl cyclase

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Radiobiology & Active oxygen

26P-180 Verification of the dosimetry techniques using GAFCHROMIC films for the study of the mechanism of the FLASH effect with synchrotron radiation

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Origin of life & Evolution

*26P-181 Observation of Fatty Acid Vesicle Condensation on the Surface of Simulated Hydrothermal Vent Minerals

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*26P-182 Genome reduction increases parasite sensitivity and promotes the evolution of endosymbiotic mutualism

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*26P-183 Proofreading inherited by template-directed ligation

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26P-184 The Relation Between Biology and Physics: Origins of Life Research and its Philosophical Implications

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Synthetic biology & Artificial cells

*26P-185 Control of lipid membrane composition in vesicles by external stimulations

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*26P-186 Construction of enzymatically assembled gel-in-liposome as artificial Cell model

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*26P-187 Creation of cell-sized droplets entrapping DNA or living cells through phase separation under one-dimensional confinement

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*26P-188 TOWARD THE CONSTRUCTION OF A SELF-REPLICATING SYSTEM DRIVEN BY GENE EXPRESSION OF REPLICATION CYCLE REACTION (RCR)

Yuya Yamahishi, Sonoyama Naoki, Kawakami Naoki, Hasebe Tomonori, Su'etsugu Masayuki

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26P-189 Analysis of biochemical reaction in liposomes after terahertz wave irradiation

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26P-190 Cation-selective pores from POSS-decorated amphiphilic diblock copolymers

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Computational biology: Bioinformatics

*26P-191 Learning What AlphaFold2 Learned

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*26P-192 Theoretical Insights into Conformational Changes in SOD1 Involved in the Pathological Mechanism of Amyotrophic Lateral Sclerosis: Residue Interaction Network Analysis

Shun Fujimaki, Norifumi Yamamoto Chiba Tech

26P-193 Analysis of protein-protein interaction search space by ensemble docking

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Computational biology: Molecular simulation

*26P-194 Experimental and Computational Predictions of the Intrinsic Reactivity of Small Molecules with Lipid Membranes

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*26P-195 Multiphase condensate formation of postsynaptic density: a comparative study of protein assembly in 3D and 2D systems

Risa Yamada, Shoji Takada

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*26P-196 Molecular simulations of TMEM16A channel blockers

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*26P-197 Different behavior of dissociation pathways of glutamine and glutamate in complex with Medaka Taste Receptor T1R

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*26P-198 Decoding Peptide Solvation Dynamics: Uncovering the Influence of Hydrophobic Forces and Addressing Solvation Complexity via Multiway Statistical Analysis Techniques.

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*26P-199 Ubiquinone/ubiquinol exchange pathway in the photosynthetic RC-LH1 supercompex

Yosuke Teshirogi, Yoshitaka Moriwaki, Tohru Terada Dept. of Biotechnol., Grad. Sch. of Agri and Life Science., The Univ. of Tokyo

*26P-200 Spectrum analyses on the non-linear response of a red blood cell model

<u>Tetsuya Yamamoto</u>, Hiroshi Watanabe Keio University

*26P-201 Lipid-protein interaction fingerprints for the Kv7 ion channels

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*26P-202 A drug design strategy based on in vitro and in silico studies applied to the development of inhibitors against alpha-glucosidase and alpha-amylase receptors of diabetics from selected Metformin derivatives.

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*26P-203 Molecular Dynamics Study on the Solvent Influence and Stability of the Aspirin-Hydroxypropyl-ß-Cyclodextrin Complex Structure

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*26P-204 Molecular dynamics calculations of peptides self-assembling on boron nitride surfaces

<u>Hiroki Maeda</u>¹, Chishu Homma¹, Eiji Yamamoto², Yuhei Hayamizu¹ Tokyo Tech, ²Keio University

*26P-205 Docking and Molecular Dynamics Simulation Study of BAK1 and BRI1 Proteins in Arabidopsis thaliana Plant

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26P-206 Hydrogen Bond Energies in Helical Secondary Structures Dissected by Negative Fragmentation Approach and Density Functional Theory

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26P-207 Insight into structural propagating mechanism of photoactivated adenylate cyclase OaPAC by microsecond molecular simulation.

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26P-208 Integration of AlphaFold with Molecular Dynamics for Sampling Conformational States of Transporter Proteins

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26P-209 Molecular simulations of cholesterol recognition by SREBP cleavage-activating protein

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26P-210 Development and Application of a Protocol for Predicting Membrane Permeability of Cyclic Peptides Based on Molecular Dynamics Simulations

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26P-211 Impact of glycan shielding on antibody epitopes on viral envelope proteins revealed by molecular dynamics simulations

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26P-212 Hybrid of Manifold Learning and Molecular Simulation to Reconstruct the Protein Conformational Change using Cryo-Electron Microscopy Experiment

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26P-213 Elucidating the Importance of Water Models in Protein-ATP Interactions in High ATP Concentrations

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26P-214 Fast Computational Method for the Hydration Free Energy

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26P-215 Molecular dynamics method for studying a flow on lipid bilayer

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Computational biology: Biological modeling and simulation

*26P-216 Metabolome Analysis in Mice Liver Using Thermodynamics

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*26P-217 INVESTIGATION OF FACTORS AFFECTING THE QUALITY OFSINGLE PHOTON EMISSION COMPUTED TOMOGRAPHY (SPECT) IMAGES: A MONTE CARLO SIMULATION STUDY

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*26P-218 Elucidating the adaptive mechanical behaviors of actomyosin bundles in cells

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*26P-219 Development of a Protein Language Model-Based Thermal Stability Prediction Model for Nanobodies

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*26P-221 Prediction of the mutation effects of Indonesian Protein Nsp3 SARS-Unique domain (SUD)-pyridostatin as a ligand interaction via endpoint binding free energy calculations

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*26P-222 Adhesive Active Brownian Particle Model for Cell Populations

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26P-223 Estimation of biochemical reaction parameters using a mathematical model of the cell-free translation system

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26P-224 Coevolution of functionality and foldability of lattice proteins

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26P-225 Live imaging-based inference of mechanical potential of cell-cell interaction in 3D-multicellular systems

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26P-226 Visualization of protein conformational ensembles using refinement in the information content space: Application to SANXS data

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Computational biology: machine learning for molecules or cell systems

*26P-227 Examining Cell Division Dynamics in Cyanidioschyzon merolae Through High-Resolution 3D Imaging

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*26P-228 Structure changes in the ABC transporter cycle using nonlinear morphing method, MOVE-DM.

Shota Shimogochi¹, Kazuhi Harai², Ryota Kiyooka¹, Naoyuki Miyashita^{1,2} ¹Grad. Sch. BOST, KINDAI Univ., ²BOST. KINDAI Univ.

26P-229 Predicting Novel PLP-binding Proteins Using Transfer Learning of Graph Neural Network-based Ligand-binding Site Prediction

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Mathematical & Theoretical biology

*26P-230 Population dynamics of generalist/specialist strategies in the feastfamine cycle

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*26P-231 Mathematically deriving loop mobility for single protein structures

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*26P-232 Appearance and adaptive properties of bow-tie structures from simple metabolic networks

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26P-233 Reinforcement learning is a common principle for biological control of complex adaptive systems

Tomoyuki Yamaguchi

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26P-234 Evaluation of different machine learning models applied to diagnostics and treatment success at the pulmonary tuberculosis

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Ecology & Environment

*26P-235 Analysis of Alcanivorax borkumensis Biofilm on Binary Oil-mixtures using Microfluidic Devices

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Nonequilibrium state & Biological rhythm

26P-236 Spiral wave and homogeneous cyclic modes on membrane

<u>Hiroshi Noguchi</u>¹, Frédéric van Wijland², Jean-Baptiste Fournier² ¹University of Tokyo, ²Université Paris Cité

Measurements

*26P-237 Hydrogel Colloidosomes from Aqueous Two-Phase Emulsion as New Microreactors for Digital Nucleic Acid Detection

<u>Bicheng Zhang</u>, Kanji Tomohara, Hiroyuki Noji Graduate School of Engineering, The University of Tokyo

*26P-238 Development for the detection of salivary biomarkers by solid-state nanopore

Eiji Kato, Ryo Akita, Sotaro Uemura

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26P-239 3D structural determination of biological ensembles using high-order spatial correlations in single-particle X-ray scattering

Wenyang Zhao¹, Osamu Miyashita¹, Miki Nakano¹, Florence Tama^{1,2,3}
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26P-240 IR measurement of flavin mononucleotide aqueous solution by resonance IR method

Minori Yamakawa, Hirona Takahashi, Konoka Mifune, Makoto Sakai Okayama University of Science

26P-241 Selective IR measurement of fluorescent protein chromophores by resonance IR spectroscopy

Konoka Mifune, Hirona Takahashi, Minori Yamakawa, Makoto Sakai Okayama University of Science

Bioimaging

***26P-242** M

Molecular mechanisms of selective binding of extracellular vesicles to cells as revealed by single particle tracking and super resolution microscopy

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*26P-243 Development of Fluorescent Thermometers Based on Carbon Quantum Dots with Various Detection Modes

<u>Yuki S. Kato</u>¹, Shingo Sotoma^{2,3}, Yukiho Shimazaki^{3,4}, Shunsuke Chuma^{3,4}, Kohki Okabe⁵, Madoka Suzuki³, Yoshie Harada^{3,6,7}

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*26P-244 Nanoendoscopy-AFM Measurements of Live Cells: Impact on Proliferation and Stress Response

Mohammad Mubarak Hosain, Takehiko Ichikawa, Takeshi Fukuma Nano Life Science, Kanazawa University

*26P-245 Miniaturization of the laser spot for cantilever deflection detection to realize ultra-high-speed AFM

<u>Karen Kamoshita</u>², Kenichi Umeda¹, Noriyuki Kodera¹

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*26P-246 Live-cell imaging defines a threshold in CDK activity at the G2/M transition

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*26P-247 Elucidation of various IL-1 α/β release control mechanisms in cellular inflammatory responses by live-cell imaging of secretion activity.

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*26P-248 Cryogenic X-ray Ptychographic Imaging of Cltured Cells toward Visualization of Hierarchical Structures of Chromatin

<u>Yuta Kinami</u>^{1,2}, Kurumi Nishimagi¹, Kosei Harada^{2,3}, Masayoshi Nakasako^{2,3}, Yukako Oma¹, Masahiko Harata^{1,4}, Yuki Takayama^{1,2,4}

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*26P-249 X-ray diffraction imaging tomography at cryogenic temperature is powerful to reveal 3D structures of biological specimens

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*26P-250 Development of nano-endoscopic high-speed atomic force microscopy

<u>Hikaru Ichida</u>¹, Kenichi Umeda², Mohammad Shahidul Alam¹, Risa Omura², Kudo Makiko², Takehiko Ichikawa², Takeshi Fukuma², Takahiro Nakayama², Mikihiro Shibata^{2,3}, Noriyuki Kodera²

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26P-251 CTCF-mediated Chromatin Looping is Coupled to the Formation of Phase-separated Transcriptional Condensate

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26P-252 Mechanical properties of hiPSC derived-cardiomyocytes: investigating beating and non-beating cell's nucleus via Nanoendoscopy-AFM

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26P-253 New mode of intercellular communication: direct vesicle delivery to neighboring cells

<u>Tomohiro Minakawa</u>¹, Fumiyoshi Ishidate², Takahiro K. Fujiwara², Jun K. Yamashita¹

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26P-254 Photonic chips: a versatile platform for super-resolution microscopy

<u>Jean-Claude Tinguely</u>, Vishesh Dubey, Luis Enrique Villegas-Hernandéz, Krishna Agarwal, Balpreet Singh Ahluwalia UiT The Arctic University of Norway

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Bioengineering

*26P-255 Direct and continuous monitoring of multi-component antibiotic gentamicin in blood

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*26P-256 Microalgae- and Cyanobacteria-Mediated Fabrication of Functionalized Gold Nanoparticles for Photothermal Applications

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*26P-257 Iono-chromic control of G-protein Ras by fused with M13 peptide

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*26P-258 Redox-Active Liquid-Liquid Phase Separation Materials Promote Oxidative Protein Folding

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26P-259 SeeDB-Live: minimally invasive optical clearing media for fluorescence imaging of live tissue ex vivo and in vivo

Shigenori Inagaki¹, Nao Tamagawa², Yuki Kambe², Rei Yagasaki³, Aki Teranishi³, Misato Miyagawa³, Hikari Takeshima¹, Shunki Tamura¹, Satoshi Fujimoto¹, Yuki Naito^{1,4}, Keisuke Ito⁵, Hideki Enomoto⁵, Katsuhiko Hayashi^{1,4}, Takashi Sato⁶, Yoshiaki Tagawa², Satoru Okuda³, Tatsuo Sato², Takeshi Imai¹

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Crystal growth & Crystallization technique

*26P-260 Emergence of order from proteins under nucleation

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Virus structure, function, SARS-CoV-2

*26P-261 Complementation of Influenza A virus genome segments by cellular coinfection

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*26P-262 Observation of the compaction process ribonucleoprotein complex formed by SARS-CoV-2 genome RNA and N protein by using fluorescence correlation spectroscopy.

<u>Takuya Katayama</u>^{1,2}, Yuji Itoh^{1,2,3}, Naoya Kaneda^{1,3}, Satoshi Takahashi^{1,2,3} ¹IMRAM, Tohoku Univ., ²Grad. Sch. Life Sci., Tohoku Univ., ³Grad. Sch. Sci., Tohoku Univ.

Wednesday, June 26

26P-263 Pseudo-luciferase activity of the SARS-CoV-2 spike protein

Ryo Nishihara^{1,2}, Hisham M Dokainish^{3,4}, Yoshiki Kihara^{1,5}, Yuji Sugita^{4,6,7}, Ryoji Kurita^{1,5}

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Mechanosensing and Mechanobiology, Biological Temperature

*26P-264 Tracking of adipogenesis process of mesenchymal stem cells cultured in the spherical microwells

You-Hsuan Liu¹, Karen G. Rosal¹, Chon-In Cheong², Feng-Chiao Tsai³, Keng-Hui Lin¹

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*26P-265 Phenotypic Heterogeneity and Cell Orientation in Extracellular Matrix Production of Escherichia coli

Fumiaki Yokoyama, Kazumasa Takeuchi

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26P-266 "DIY Statistical Mechanics" to understand the concepts of Boltzmann distribution and local temperature

<u>Kiyoshi Ohnuma</u>¹, Masayo Inoue², Noritaka Masaki³, Masako Ohtaki⁴, Taro Toyota⁵

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Biophysics of disease

*26P-267 Tissue Repair in Colorectal Cancer Organoids

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*26P-268 Clustering of Progerin Induces Nuclear Deformation By Disrupting Heterochromatin Organization

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26P-269 Fibrinogen-erythrocyte binding and erythrocyte-erythrocyte adhesion as determinants for cardiovascular risk

Catarina Lopes¹, Ryan Gouveia e Melo², Luís Mendes Pedro², Filomena Carvalho¹, Nuno C. Santos¹

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Miscellaneous topics

*26P-270 Immobilization of Liposomes within Porous Aluminum Oxide and Intact Release: Basic Study and Applications to Single Particle Analysis for Exosomes

Masahiro Okada¹, Yusuke Sato¹, Tetsuji Itoh², Seiichi Nishizawa¹ Graduate School of Science, Tohoku University, ²AIST Tohoku

*26P-271 Enhancing Tomato Shelf Life through Nanoparticle-Based Preservation Techniques

Kummari Swathi^{1,2}, CH.Shanthi Devi^{3,4}

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26P-272 NOVEL ANTIBACTERIAL AGENTS IN TREATING MULTIDRUG RESISTANT BACTERIA CAUSING WOUND INFECTIONS IN DIABETIC PATIENTS

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Presentation time is organized by whether the last part (suffix) of Poster Session number is odd/even.

Odd number: 13:50-14:50 Even number: 14:50-15:50

Abstracts marked with * in the abstract number eligible for IUPAB2024 Student and Early Career Researcher Poster Award voting

Ex) *25P-999

Protein: Structure

*27P-001 Structural Basis for the Functional Diversity in Mechanosensitive Channel OSCAs

<u>Kio Horinaka</u>, Tatsuya Hagino, Tsukasa Kusakizako, Osamu Nureki Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Tokyo, Japan

*27P-002 Development of an Oxidative Folding Promoter by Controlling Protein Recognition Properties

<u>Koki Suzuki</u>¹, Ryoya Nojiri¹, Tomohide Saio², Takahiro Muraoka^{1,3}
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*27P-003 How well do Alphafold2 structures perform in Molecular Docking?

Ben Hanks, <u>John Douglas Tanner</u>, Ben Corry Australian National UNiversity

*27P-004 Cryo-EM Structure Analysis of hOCT2, Organic Cation Transporter 2

<u>Haruna Inuzuka</u>, Yongchan Lee, Tomohiro Nishizawa Yokahama City University

*27P-005 Magnetic field effects on structure of iron sulfur protein studied by EPR and SAXS

Shogo Soga¹, Ryoma Kobayashi², Hirokazu Masai³, Shinji Kohara⁴, Kiminori Maeda¹, Mitsuhiro Hirai⁵, Hiroki Nagashima^{1,2}, Shigeki Arai²

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*27P-006 Analysis of the aggregation characteristics of tau droplets under oxidizing and reducing conditions

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*27P-007 Determination of the hemocyanin structure from Concholepas concholepas using an X ray crystallography and Cryo EM combined approach

<u>Sebastian Manuel Muñoz</u>¹, Michelle Salazar², Gabriel Vallejos¹, Augusto Manubens^{2,3}, Mathias Ellena⁴, José Edwin Quesñay⁴, Andre Ambrosio⁴, Maria Inés Becker^{2,3}, Victor Castro-Fernandez¹, Victoria Guixé¹

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*27P-008 Designing Self-assembling Protein Nanoparticle using computational method

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*27P-009 Structure-based discovery of dual pathway inhibitors for SARS-CoV-2 entry

Haofeng Wang

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27P-010 Efficient design of allosteric activators for Rsp5 E3 ligase using machine-learning tool ProteinMPNN

Wei-Lin Lu

Institute of Biological Chemistry, Academia Sinica

27P-011 Structural analysis of dissimilatory sulfate reductase

Rio Hamada, Koji Nishikawa, <u>Hideaki Ogata</u>

University of Hyogo

27P-012 Strucuture analysis of Panx3

Ryuga Teramura, Taiichi Tsuyama, Ken Yokoyama

Kyoto Sangyo University

27P-013 Approach to in situ structural analysis using JEOL's Cryo-FIB-SEM and CRYO ARM

<u>Tomoko Miyata</u>^{1,2}, Miki Kinoshita^{1,2}, Fumiaki Makino^{1,2,3}, Yoshie Kushima^{1,2}, Reiko Yamauchi^{1,2}, Keiichi Namba^{1,2}

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27P-014 Cryo-EM structure of full-length cargo receptor ERGIC-53 in complex with MCFD2

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Protein: Structure & Function

*27P-015 Investigation of structural dynamics of E6AP/E6/p53 complex by using HS-AFM and computational simulation

Yamamoto Sohma¹, Kazusa Takeda², Holger Flechsig³, Hiroki Konno³
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*27P-016 Structural Basis of How MGME1 Processes DNA 5' Ends to Maintain Mitochondrial Genome Integrity

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*27P-017 Unveiling dynamics of Adenosine A2a receptor coupled to G proteins

Sari Hagimoto, Duy Tran, Akio Kitao

Tokyo Institute of Technology

*27P-018 Structural basis for recruitment of peptidoglycan endopeptidase MepS by lipoprotein NlpI

Shen Wang

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*27P-019 Structural and functional analysis of PPL, a lectin from the poisonous mushroom Pleurocybella porrigen

Daisuke Adachi

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*27P-020 ERK1 is a noble topological factor to relax DNA supercoiling

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*27P-021 Reconstruction and Analysis of the Ancestral ATPase

<u>Aya Suzuki</u>¹, Ryutaro Furukawa¹, Meghna Sobti^{2,3}, Hiroshi Ueno¹, Alastair G. Stewart^{2,3}, Satoshi Akanuma⁴, Hiroyuki Noji¹

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*27P-022 In situ structural analysis of Salmonella T3SS within the SCV

<u>Taiga Horii</u>^{1,2}, Hiroko Takazaki², Yukihisa Hayashida³, Yusuke V. Morimoto⁴, Takayuki Kato^{1,2}

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*27P-023 Structural basis of bifunctionality of mimosine synthase in plants

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*27P-024 Revealing KcsA dynamics by single-particle analysis and molecular dynamics

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*27P-025 Molecular Mechanisms of Diverse Chemokine Recognition and Downstream Signaling Selectivity of Chemokine Receptors

<u>Fumiya K. Sano</u>¹, Shirsha Saha², Sharma Saloni², Ramanuj Banerjee², Yoshiaki Kise¹, Wataru Shihoya¹, Osamu Nureki¹, Arun Shukla²

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*27P-027 Deciphering Substrate Selectivity in SWEET Transporters: A Molecular Dynamics Perspective

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*27P-028 Elucidation of Characteristic Cold-Adaptation Mechanism of Pyruvate Kinase from Psychrophilic Bacteria by X-ray Crystallography

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27P-029 Different Dimerization Behavior of Fluorescent Proteins, eGFP and eYFP

Yuna Kinoshita, Haruko Hosoi Toho University

27P-030 Role of actin-binding loops in determining myosin velocity

Hideki Furusawa, Takeshi Haraguchi, Kohji Ito

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27P-031 Investigated the Amino Acid Region That Enables the fastest Movement in the Fastest Myosin

Runa Komoto, Suzune Kato, Kohei Yosimura, Takeshi Haraguchi, Kohji Ito Department of Biology, Graduate School of Science, Chiba University, Chiba 263-8522, Japan

27P-032 Real-Time, Site-Specific Observation of Chaperone-Mediated Protein Folding using Noncanonical Amino Acid Labeling

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27P-033 Search for specific regions of myosin responsible for moving actin through chiral curves

<u>Yoshiki Takayama</u>, Kohei Yoshimura, Taisei Nagai, Takuma Imi, Takeshi Haraguchi, Kohji Ito

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27P-034 Reaction Pathways in DNA Hydrolysis of EcoRV Calculated by QM/ MM Metadynamics

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27P-035 Elucidating the Mechanism Underlying Atypical UBA7-UBE2L6 Disulfide Complex Formation

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27P-036 Molecular mechanisms for smooth rotation of the flagellar rod within the LP ring

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Protein: Physical property

*27P-037 Human antimicrobial peptide LL-37 possesses unique multimerization properties compared to its orthologs in mouse and rat

Mitsuki Shibagaki, Jeremia Chrisnanto, Dessalegn Tefera, Kotaro Tsukioka, Waka Ueda, Kohei Kano, Hao Gu, Fumi Hirai, Yasuhiro Kumaki, Hiroyuki Kumeta, Tomoyasu Aizawa

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*27P-038 A Nanotech methodology of Liquid-liquid phase separated droplet regulation with Butterfly-shaped Gold Nanomaterials

<u>Tomohiro Nobeyama</u>¹, Koji Takata², Megumi Mori³, Yoichi Yamada¹, Tatsuya Murakami², Kentaro Shiraki¹

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*27P-039 Nonionic Amino acid Interactions Evaluated Through Solubility

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*27P-040 Fly-Casting-Like Capture and Translocation of KIF1A by C-Terminal Tail of Tubulin

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*27P-041 α B-crystallin prevents aging of α -synuclein droplets

<u>Kenji Fujitsuka</u>¹, Keisuke Yuzu¹, Yuki Michiue¹, John A. Carver², Eri Chatani¹ Graduate School of Science, Kobe University, Kobe, Japan, ²Research School of Chemistry, Australian National University, Canberra, Australia

27P-042 Differences in microstructural changes during tensile deformation between hair shapes

<u>Hironori Kimura</u>, Kota Yamamoto, Kazuyuki Suzuta Milbon Co., Ltd

Protein: Function

*27P-043 Development of Cell-free Screening Method for Terminal deoxynucleotidyl transferase for Enzymatic DNA synthesis

<u>Takashi Ohmizu</u>, Hiroshi Ueno, Hiroyuki Noji University of Tokyo

*27P-044 Analysis of the physiological significance of dual-localization of Hfd1 in yeast

Yuta Konishi¹, Haruka Sakaue², Hironori Takeda³, Toshiya Endo²

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*27P-045 Identification of multiple responsible genes for abnormal cold acclimation of C. elegans lectin mutants

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27P-046 Reconstitution of ER glutathione transport system

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27P-047 Investigating the catalytic mechanism of Sars-CoV-2 MPro

<u>Stephan Kleine-Doepke</u>, Pedram Mehrabi, Caitlin Hatton Universität Hamburg, Germany

Protein: Measurement & Analysis

*27P-048 Supramolecular chirality in DFNKF amyloid fibrils derived from human calcitonin by VCD

<u>Shinryu Isa</u>¹, Toki Fujino¹, Raja Prema¹, Daisuke Sato¹, Akira Naito¹, Hisako Sato², Izuru Kawamura¹

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*27P-049 Measurement of structural flexibility of enzymes using spin labeling-ESR

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27P-050 Muon in Structural Biology: Visualization of proton and electron transfer by the elementary particle "Muon"

<u>Tamiko Kiyotani</u>¹, Ichiro Tanaka², Masatoshi Hiraishi², Nobuo Niimura² ¹Showa Pharmaceutical University, ²Ibaraki University

27P-051 Optimization of Cryo 3D-CLEM for in situ Structural Analysis

<u>Hiroko Takazaki</u>, Misaki Arie, Taiga Horii, Takayuki Kato Institute for Protein Research, Osaka University, Osaka, Japan.

27P-052 Investigating CRMP2 isoforms multimerization dynamics by High-Speed AFM

Djamel Eddine Chafai, Saho Kitagawa

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27P-053 Designing an alternative protocol to detect the antigen-antibody reaction using EPR and aggregated AuNPs as paramagnetic probes

Luis Celedón Ornelas, Alma Nelly Díaz Herreros,

José Silvestre Figueroa Mendoza, Marco Alonso Arellano Alcántara, Belén Chávez Ramírez, Stephany Natasha Arellano Ahumada,

Daniel Ramírez Rosales

Instituto Politécnico Nacional

Protein: Design & Engineering

*27P-054 De novo design of a protein containing one left-handed $\beta\alpha\beta$ -motif.

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*27P-055 Machine-learning-assisted multiple maturation of antibody fragment: simultaneous improvement of target-binding, bacterial expression, and thermal stability

Tomoyuki Ito¹, Sakiya Kawada¹, Hikaru Nakazawa¹, Akikazu Murakami^{2,3}, Mitsuo Umetsu^{1,4}

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*27P-056 Construction of heptameric de novo peptide nanopore by chimera proteinization

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*27P-057 Library design aiming for the development of covalent binding antibody mimetics

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*27P-058 Miniaturized cyclic peptides derived from CDR-H3 of antibodies exhibit binding activities to SARS-CoV-2 RBD

<u>Yoshiki Yasuda</u>¹, Satoru Nagatoishi², Ryo Matsunaga², Daisuke Kuroda³, Kouhei Tsumoto^{1,2,4}

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*27P-059 De novo nanobody binder design by generative Al models

Hakyung Lee¹, Juyong Lee^{1,2}

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27P-061 Towards further enhancement of the activity of the minimal luciferase picALuc

Tadaomi Furuta¹, Yuki Ohmuro-Matsuyama²

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27P-062 Structural analysis unveils the enhanced stability of Al-designed ubiquitin-fold proteins

<u>Kuen-Phon Wu</u>, Wei-Lin Lu, Wei-Jen Chuang Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan

Protein: Intrinsic disorder

*27P-063 Comprehensive Analysis of Intrinsically Disordered Proteins in the Marsupial

Shiho Aoki¹, Wataru Onodera², Toru Asahi^{3,4}

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*27P-064 Elucidating fusion dynamics of FUS protein droplets using fluorescence microscopy and optical tweezers

<u>Syamil Muharror Ahsanul Husna</u>^{2,3}, Atsumi Hando^{1,2}, Saori Kanbayashi², Satoshi Takahashi^{1,2,3}, Kiyoto Kamagata^{1,2,3}

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*27P-065 Balancing stability, dynamics and kinetics in phase separation of intrinsically disordered proteins

Guoging Zhang, Xiakun Chu

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27P-066 Characterization, regulation, and design of protein droplets

<u>Kiyoto Kamagata</u>¹, Ryo Kusano¹, Atsumi Hando¹, Nanako Iwaki¹, Maulana Ariefai¹, Keisuke Ikeda², Tomoshi Kameda³

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Heme proteins

*27P-067 Two distinct conformations in apo forms of bacterial heme ABC transporter

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27P-068 Dramatic Effects of Chemical Modifications on the Function of a Classical Allosteric Protein by Pin-Point Changes in Hydrophobicity

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Membrane proteins

*27P-069 Vibrational sp

Vibrational spectroscopic study of chemical interaction between κ -opioid receptor (KOR) and ligands having morphinan structure

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*27P-070 Role of ANT1 in proton transport: New insights into the mechanism of fatty acid anion sliding at the protein-lipid interface

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*27P-071 Cryo-EM Structural Analysis of Enterococcus hirae V-ATPase with Improved Resolution

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*27P-072 Solid-state NMR analysis of wild-type and mutant Schizorhodopsin proteins

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*27P-073 Zn2+ Ion Transportation Mechanisms of TRPC6 Channels: All-Atom Molecular Dynamics Simulation

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*27P-074 Structural Basis for Signaling and Drug-Induced Activation of the Trk Receptors

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27P-075 New Lipid-Bilayer Nanodiscs for Membrane-Protein Biophysics

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27P-076 Coupling of ATP reactions with allocrite transport in heme ABC transporter; BhuUV-T, revealed by time-resolved spectroscopy.

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27P-077 Understanding the Structure and Receptor Selectivity of Histamine H4 Receptor

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27P-078 Generation of human TMEM16F-specific affibodies

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DNA & DNA binding proteins

*27P-079 Hi

High-speed AFM analysis of effects of drugs on the dynamic DNA morphologies interacting with MDP1, dormancy induction protein of Mycobacterium tuberculosis

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*27P-080 Single-molecule imaging of MDP1, dormancy induction protein of Mycobacterium tuberculosis, with high-speed AFM

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*27P-081 Template-free oligonucleotide synthesis by Terminal Deoxynucleotidyl Transferase in a microreactor array

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Phosphorylation and histone peptides reduce main- but not sidechain dynamics of N-terminal intrinsically disordered region of HP1 during phase separation, as studied by conventional and TOAC spin labels

Isao Suetake^{1,2}, Toshiki Takei², Tomoaki Sugishiata², Shun Ito², Kazunobu Sato³, Yuichi Mishima², Kohei Muraoka², Toru Kawakami², Yoh Matsuki², Toshimichi Fujiwara², Takeji Takui³, Makoto Miyata³, Hironobu Hojo², Toshiaki Arata^{2,3}

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RNA & RNA binding proteins

27P-083 Short repeat RNA suppresses aggregation of ALS-causative protein TDP-43 and its 25 kDa carboxy-terminal fragment

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DNA/RNA nanotechnology

*27P-084 How to engineer a fast-moving DNA-nanoparticle motor with long run length and high unidirectionality?

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*27P-085 Timing-controlled dynamics of DNA droplet-based artificial cell

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*27P-086 Regulation of molecular distribution in lipid vesicles based on artificial DNA cortex

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*27P-087 Mechanical properties of artificial cells with DNA cytoskeleton

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*27P-088 Lipid nanoparticle fusion with a phospholipid membrane

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*27P-089 Spontaneous film-like DNA structure formation at the oil-air interface

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Nucleic acid: Others

*27P-090 The effect of Temperature and Pressure on the structural transition

from the quadruplex to random coil of VEGF

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27P-091 Modelling complex and large RNA structures to advance RNA biology

and therapeutics

Naoto Hori, James A. Robins, Huong T. Vu School of Pharmacy, University of Nottingham

Chromatin & Chromosomes

*27P-092 DNA Unwinding analysis of N-terminal tailless nucleosomes using nanopore measurements

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27P-093 Effect of RNA expression on chromatin phase separation : Molecular Dynamics simulation

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Electronic

*27P-095 Electrochemical activity of catalytic amyloids: self-assembly of (XH)4 peptides and hemin on graphite electrodes

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Water & Hydration & Electrolyte

*27P-096 Prediction of hydration structures over membrane proteins using deep learning in combination with the emprical hydration distribution

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27P-097 Hydration and Fluctuation Dynamics of a Membrane Transport Protein-Glucose Complex

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Molecular genetics & Gene expression

27P-098 Nine-banded armadillo tr

Nine-banded armadillo transcriptome and chromatin accessibility at single-cell reveal persistent identity signatures in concordance with cell population variations

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Morphogenesis and Development

***27P-099** Deep learning approach to investigate tissue hydraulics during ovarian follicle development.

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Muscle

27P-100 Morphological discrimination of isolated sarcoplasmic reticulum vesicles in different Ca2+ concentrations using deep learning

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Molecular motor

*27P-101

Microscopic Choreography: Unraveling Molecular Properties of Cytoplasmic Dynein Shaping Collective Motion of Microtubules in vitro

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*27P-102 Biochemical Characterization of C. elegans Kinesin Bmk-1

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*27P-103 Rejuvenating actin filaments: Direct observation of nucleotide exchange in actin filaments enhanced by myosin II

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*27P-104 Molecular dynamics observation of rotational motion in the stator unit of the flagellar motor

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*27P-105 Negative differential resistance of bio-molecular motor F1-ATPase

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27P-106 V-ATPase rotation probed by Janus nanoparticle

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27P-107 Detecting conformations of F1-ATPase to elucidate the rotation mechanism

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27P-108 Cooperation among c-subunits of FoF1-ATP synthase in rotation-coupled proton translocation by hetero-mutated c-ring

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27P-109 DNA Hybridization kinetics in Active Matter self-assembly

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Single Molecule Biophysics

*27P-110 Microsecond single molecule dynamics measurement of SARS-CoV-2 Spike protein using Diffracted X-ray Tracking

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*27P-111 REGULATORY MECHANISMS OF KINESIN FUNCTION AT VARYING PH

Suvranta Tripathy, <u>Fawaz Baig</u>, Hassan Bazzi University of Michigan Dearborn

*27P-112 Impact of mutations on cadherin 23 functions and leads to hearing-loss disease

<u>Gaurav Kumar Bhati</u>, Surbhi Garg, Pritam Saha, Sabyasachi Rakshit Department of Chemical sciences, Indian Institute of Science Education and Research Mohali, India

*27P-113 Direct observation of a single DNA molecule responding for the AC electric field and different physical environment.

<u>Yunosuke Fuji</u>, Shin Tkano, Takuma Yoshinaga, Yuuta Moriyama, Toshiyuki Mitsui

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*27P-114 Photothermal assisted ultra-low concentration detection using nanopore sensing

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27P-115 Single-molecule analysis of the behavioral dynamics of EGFR cancer mutants with resistance to anticancer drugs

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27P-116 Mechanistic insight into the mechanical unfolding of integral membrane proteins

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Cell biology: Adhesion

27P-117 Study of adhesion factor in Acanthamoeba bunch formation caused by Hokutovirus infection

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Cell biology: Motility

*27P-118 The mechanical properties of fibroblasts in co-culture system

Arata Nagai, Kaito Kojima, Hiromu Kuwabara, Yuuta Moriyama, Toshiyuki Mitsui

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*27P-119 Mechanism of bacterial actin driven motility reconstituted in a minimal synthetic bacterium

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*27P-120 Light-Induced Control of Archaellum Rotation in Haloacterium salinarum

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*27P-121 Haloplasma motility reconstituted in a minimal synthetic bacterium, JCVI-syn3B

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*27P-122 Gliding machinery of Mycoplasma mobile observed by electron cryotomography

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*27P-123 Rapid response of bacterial motility with pressure change

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*27P-124 Visualization and analysis of MreBs driving Spiroplasma motility in minimal synthetic bacterium

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*27P-125 In vitro analysis of the bacterial actin MreB molecule that gives swimming motility to the minimal synthetic bacterium JCVI-syn3B.

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27P-126 CryoEM structures of the growing end of the bacterial flagellar hook.

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27P-127 Activation of the PomA/B flagellar stator by a site-specific chemical modification in the plug segment

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27P-128 Analysis of the Virio alginolyticus lateral flagellar motor genes, lafT and lafU

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27P-129 Structural change of ATPase ring complex of the flagellar type III export apparatus revealed by cryoEM analysis and high-speed AFM

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Cell biology: Cytoskeleton & Membrane skeleton

*27P-130 Cryo-ET of vertebrate cilia revealed that Calaxin stabilizes the docking of outer arm dyneins onto ciliary doublet microtubule

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*27P-131 Capping and severing mechanisms of Cytochalasin D to actin filament by TIRF observation

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*27P-132 Physically specific domain at the plasma membrane induced by transmembrane phospholipid movement during myoblast cytokinesis

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*27P-133 Elucidating the Role of Spiroplasma fibril protein using synthetic bacterium, JCVI syn3

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Osaka Metropolitan University, Graduate School of Science

27P-134 Domain characterization of Archaea gelsolin for inhibiting actin polymerization by TIRF and crystal structure observations

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27P-135 Thermodynamic Analysis of Cofilin–F-actin Interaction

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²Department of Applied Chemistry, Kyushu Institute of Technology

27P-136 The phase separation of EB and TEN2 promotes inhibitory synapse formation

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Cell biology: Signal transduction & Cell membrane

*27P-137 Aquaporin-3 and aquaporin-5 differentially modulate cell stiffness and cell-cell adhesion and promote cell migration

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*27P-138 Aquaporin-3 is involved in inflammasome activation contributing to the settings of inflammatory response in THP-1 cells

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*27P-139 Positive feedback regulation of excitable Ras by RasGEFX for spontaneous signal generation in cell migration

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27P-140 Phosphatidylserine enhances membrane localization and lateral diffusion of active form of Ras for excitability

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Biological & Artificial membrane: Structure & Property

*27P-141 Nanofluidic model cell membrane platform for molecular analysis of membrane-bound proteins

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*27P-142 Integrated model membrane arrays generated by self-spreading of lipid bilayers

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*27P-143 Field model for multistate lateral diffusion of various transmembrane proteins observed in living Dictyostelium cells

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*27P-144 Membrane shapes, liquid-liquid interfaces, and elastocapillarity

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27P-145 Study on the mechanism of double cooperative effect of antimicrobial peptide LL-37 with HNP1 by leakage assay

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27P-146 Induction of Apoptosis by Ceramide Derivatives and Its Potential Mechanisms through Domain Formation

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27P-147 Structural effects of Cholesterol, Lanosterol, and Oxysterol on Model Biomembranes

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Biological & Artificial membrane: Dynamics

*27P-148 Generation of autonomous rotors

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*27P-149 Molecular dynamics investigation of the dynamical response of the interfacial waters near DPPC bilayer to Hyaluronic acid

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*27P-150 Optical Trapping of Membrane Proteins on the Supported Lipid Bilayers

<u>Yasushi Tanimoto</u>, Shunya Moriyama, Kyoko Masui, Chie Hosokawa Graduate School of Science, Osaka Metropolitan University

27P-151 Structurally Stable Phospholipid Membrane Tube Developed by Self-assembly of Peptide Receptors

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Biological & Artificial membrane: Transport & Signal transduction

27P-153 Reconstituting G protein-coupled receptors into a supported lipid bilayer using meta-stable peptide nanodiscs

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Membraneless Organella, autophage, Liquid-liquid phase separation

*27P-155 TMAO and urea effects on liquid-liquid phase separation of fused in sarcoma

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*27P-156 Coarse-Grained Molecular Dynamics Study of Coacervate Formation using Elastin-like Polypeptides with Varying Hydrophobicity

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*27P-157 Raman spectroscopic study of liquid-liquid phase separation in Lysozyme/Ovalbumin mixture system

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27P-158 Liquid-liquid phase separation of the P53 core domain

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27P-159 Theoretical studies of protein accumulation during mitosis with Flory-Huggins free energy

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27P-160 Quantitative Analytical Method Based on Machine Learning by Classification of Condensate Forming Cells by Glycolytic Enzymes in Saccharomyces cerevisiae

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Neuroscience & Sensory systems

*27P-161 Controlling Tau Aggregation Using Light-Induced Cellular Models of Tau Oligomers

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27P-162 Specification of Smallest Neural Cell Colony Size for Measurement of Firing or Burst Firing

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Neuronal circuit & Information processing

27P-164 Classifying Dynamics of Ising Interaction Networks by Structure of Traffic Diagrams

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Behavior

*27P-165 Quantitative Description and Investigation into the Mechanism of Gravitactic Swimming Behavior in Coral Larvae

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Photobiology: Vision & Photoreception

*27P-166 The structural dynamics study of green-cone pigment by using spectroscopies

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*27P-167 FTIR study of mutants of primate red and green pigments

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*27P-168 Activation mechanism of light-sensitive Gs protein-coupled receptor, jellyfish rhodopsin

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*27P-169 Spectroscopic analysis of the photoreaction of TAT rhodopsin in the presence of calcium ion

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27P-170 Free energy profile analysis of natural anion channelrhodopsin GtACR1 in each state of the photocycle

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27P-171 Production of a light-driven Cl--dependent Na+ pump: Implications for the binding and transport of distinctive ions

<u>Manami Hashimoto</u>¹, Kano Suzuki², Marie Kurihara¹, Taiki Nakamura³, Keiichi Kojima⁴, Susumu Yoshizawa⁵, Yasuhisa Mizutani³, Takeshi Murata², Yuki Sudo⁴

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Photobiology: Photosynthesis

*27P-172 Light factor-dependent Growth of Yellow Chlamydomonas

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*27P-173 Robustness of photosynthetic light-harvesting antenna chlorosome against structural heterogeneity

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*27P-174 Energy Transfer Pathway in Chlorophyll-f Containing Photosystem I Revealed by Single-Molecule Spectroscopy

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27P-175 Post-translational conversion of amino acids in the O2-evolving complex of photosystem II: Formation of carboxylate ligands from aliphatic amino acids

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27P-176 Modification of chlorophyll pigments in photosynthetic light-harvesting proteins

Yoshitaka Saga, Shota Kawato, Kohei Hamanishi, Moe Sumura Kindai University

Photobiology: Optogenetics & Optical control

*27P-177 Effect of photoactivated adenylyl cyclase expression in Salmonella

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*27P-178 Novel Optogenetic Strategy for Regulating Insulin Signaling in the Deep Tissues of Living Mice

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27P-179 Relationship between Responsiveness of Cardiomyocytes Stimulated by Laser Irradiation and Cell Population Status

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27P-180 The "fifth" color switch of microbial rhodopsin

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Radiobiology & Active oxygen

27P-181 Cell-killing caused by direct and indirect actions of high-LET particles in Boron Neutron Capture Therapy (BNCT)

Ryoichi Hirayama¹, Yu Sanada², Akiko Uzawa¹, Yoshitaka Matsumoto³, Atsushi Ito⁴, Shin-ichiro Masunaga⁵, Hiroki Tanaka², Yoshinori Sakurai², Minoru Suzuki², Sumitaka Hasegawa¹

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Origin of life & Evolution

*27P-182 Droplets in PEG / salt solution as primitive compartments at the origin of life

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*27P-183 Adaptive Laboratory Evolution of Minimal Genome Bacterium to Low Temperature

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*27P-184 Stability, structure, and interactions of prebiotic fatty acid membranes

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Synthetic biology & Artificial cells

*27P-185 Induction of Dynamic Formation of ATPS-based membrane-less Artificial Cell Compartment by Thermal Control

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*27P-186 Microtubule/kinesin complexes spontaneously emerge vortices in cell-sized droplet generated by water/water phase separation

<u>Hiroki Sakuta</u>^{1,2}, Naoki Nakatani³, Takayuki Torisawa⁴, Yutaka Sumino⁵, Kanta Tsumoto⁶, Kazuhiro Oiwa^{7,8}, Kenichi Yoshikawa³

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*27P-187 Regulation of Stochastic Cell Re-differentiation Ratio of Genetic Toggle Switch with Minute Expression Balancing Control of Repressor Proteins

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*27P-188 Zombie cells produced from the minimal synthetic bacterium JCVI-syn3B

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*27P-189 Large coiled-coil protein of Mycoplasma pneumoniae induces morphological changes in a minimal synthetic bacterium by inhibiting septum formation

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27P-190 Efficient Proliferation of Synthetic Minimal Cells with Low Energy Costs

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Computational biology: Bioinformatics

*27P-191 Elucidation of mechanistic details of copper chaperoning to Superoxide Dismutase (SOD) using a novel free-energy computation technique and cross-validated with Molecular Dynamics Simulations

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27P-192 Computational analysis of OPRD1-OPRM1 heterodimer ligands

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Computational biology: Molecular simulation

*27P-193 A Gradient-Based Approach for Optimizing Molecular Structures using Atomic Force Microscopy Images and Normal Mode Analysis

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*27P-194 PINning down the elevator-type mechanism of auxin transport

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*27P-195 The Effect of Tricaprylin Surface on The Lid Region Dynamics of Candida antarctica Lipase B

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*27P-196 Development of drug discovery platform technology based on a generalized-ensemble simulation method -Evaluation of SARS CoV-2 PLpro candidate inhibitors-

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*27P-197 Unraveling the Catalytic Mechanism of EPS1 in Salicylic Acid Biosynthesis Using Computational Modeling

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*27P-198 Complementary Analysis between 4D Crystallography and Extensive MD Simulation Captures Transient IF1-Ribosome Dynamics in Translation Initiation

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*27P-199 The Regulatory Role of p53 C-Terminal Domain Acetylation in Modulating the Dynamics of SIR2's NAD+ Binding Pocket

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*27P-200 An Open Source de novo Drug Design Workflow with Active Learning and Enamine REAL

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*27P-201 Studying the role of protonation in the (de)activation mechanism of class A GPCRs

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*27P-202 Molecular Dynamics simulation of the complex of the multiple distinctive structurral regions in the WNV envelope and human monoclonal antibody.

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*27P-203 Identifying and Characterizing Ligands for Mutant p53 as Potential Breast Cancer Therapy

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*27P-204 Molecular Docking, Molecular Dynamics, And MM-PBSA Analysis of Quinolone Antibiotics Againts FmtA of Staphylococcus aureus

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*27P-205 Computational analysis on binding structure of limonin to a bitter taste receptor TAS2R38

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27P-206 Molecular Dynamics Study of the Unfolding Processes of Proteins with Highly Similar Native Structure

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27P-207 Dynamic structure analysis of superoxide dismutase 1 protein upon Cys111 oxidation using molecular dynamics simulation

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27P-208 Investigation of the effect of the 2-OH group of in Arabidopsis thaliana ceramide on plant cell membranes using MD simulation

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27P-209 Dynamin-1 membrane tubule constriction mechanism revealed by coarse-grained MD simulations

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27P-210 Heterogeneous organization in phase-separated transcription factors: Residue-revel molecular simulations

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27P-211 Molecular dynamics simulation of the PWW domain of LEDGF protein and histone tail H3K36

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27P-212 MD-based in silico screening using supercomputer Fugaku

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27P-213 Effects of sodium ions on conformational changes of the adenosine A2A receptor by molecular simulations

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27P-214 Optimal transport maps for targeted free energy estimation

Tsuyoshi Kawai, Yasuhiro Matsunaga

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27P-215 Surface oleophilicity induced by UV-hydroxylation of titanium

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Computational biology: Biological modeling and simulation

*27P-216 Looking for non-opioid analgesics using stochastic titration CpHMD with AMBER14SB

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*27P-217 Prediction of cross-fitness for adaptive evolution to different environmental conditions: Consequence of phenotypic dimensional reduction.

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*27P-218 Theoretical model of cell shape control by cytoskeleton

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*27P-219 Universally conserved Mg-pinch motif in NTP processing enzymes

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*27P-220 A binding site for phosphoinositide modulation of voltage gated sodium channels described by multiscale simulations

<u>Yiechang Lin</u>, Elaine Tao, James Champion, Ben Corry Australian National University

27P-221 Development of an Efficient Estimation Method for Maximum Tolerated Dose by Reinforcement Learning

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*27P-222 Study of the Allosteric Mechanism of Human Mitochondrial Phenylalanyl-tRNA Synthetase by Transfer Entropy via an Improved Gaussian Network Model and Co-evolution Analyses

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27P-223 Nucleosome-resolution modeling and simulation of singlegene level chromatin organization mechanisms

<u>Gu Chenyang</u>, Shoji Takada, Giovanni Brandani Grad. Sch. Sci., Kyoto university, Kyoto, Japan

27P-224 Allosteric drugs: new principles and design approaches

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27P-225 Study of Liquid-liquid Phase Separation of Tau fragment K18 via Coarse-grained Simulation

Zhuqing Zhang, Qinglin Yan

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27P-226 Design principles of microtubule-associated proteins: exploring the role of lever arms and linker regions under directional loads

Ilya B. Kovalenko¹, Vladimir A. Fedorov¹, Ekaterina G. Kholina¹, Philipp S. Orekhov³, Egor M. Pozdnyakov¹, Fazoil I. Ataullakhanov^{2,4}, Nikita Gudimchuk^{1,2}

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Computational biology: machine learning for molecules or cell systems

*27P-227 A Machine Learning Approach to Classify Force Curves of Nuclear Elasticity Measurements.

MD Fahim Newaz

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*27P-228 Development of an Efficient Estimation Method for Maximum Tolerated Dose by Reinforcement Learning

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*27P-229 RVINN: Inference of gene regulation dynamics in the mRNA life cycle using Physics-Informed Neural Networks

Osamu Muto^{1,2}, Zhongliang Guo², Rui Yamaguchi^{1,2}
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Mathematical & Theoretical biology

*27P-230 Active thermodynamic force drives mitochondrial equidistant distribution in axons

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*27P-231 Global propagation of single-gene deletion effects through stoichiometry conservation relations

<u>Genta Chiba</u>¹, Ken-ichiro F. Kamei¹, Arisa Oda^{1,2}, Kunihiro Ohta^{1,2,3}, Yuichi Wakamoto^{1,2,3}

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*27P-232 Pattern propagation driven by surface curvature

Ryosuke Nishide, Shuji Ishihara

The University of Tokyo

27P-233 Entangled gene regulatory networks with cooperative expression endow responses to unforeseen environmental changes

Masayo Inoue

Graduate School of Engineering, Kyushu Institute of Technology

Nonequilibrium state & Biological rhythm

*27P-234 Exploring dense active dynamics in suspension of ciliate Tetrahymena based on all cell tracking

Kohei Okuyama, Masatoshi Ichikawa

Department of Physics, Kyoto University

27P-235 Emergence of spontaneous oscillations in a liquid film of bacterial swimmers

Lei-Han Tang

Hong Kong Baptist University, Hong Kong, China

Measurements

*27P-236 Single EVs detection and analysis using a glass nanopore

Izumi Shibayama, Kohei Hayashi, Ryuji Kawano

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*27P-237 Ultra-low-noise and wide-bandwidth current detection for enhanced scanning ion conductance imaging rate in scanning ion conductance microscopy

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27P-238 Aptamer-based Al-driven nanopore measurement for the simultaneous detection of biomarkers for the cancer diagnosis

Ryo Akita, Lysenko Artem, Shunsuke Ono, Hikaru Nozawa,

Tatsuhiko Tsunoda, Sotaro Uemura

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27P-239 Analysis of the conformational dynamics of oligosaccharides using ion mobility spectrometry

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Bioimaging

*27P-240 A bright and highly-response Ca2+ biosensor based on mScarlet: Progress toward fluorescence lifetime imaging

Shosei Imai¹, Ryan Fink², Takuya Terai¹, Olivia A. Masseck², Robert E. Campbell¹

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*27P-241 Hydroxyquinoline-derived Multifunctional Small Molecule Turn-On Fluorescent Probe as a Theranostic Agent for Alzheimer's Disease

Priyam Ghosh, Parameswar Iyer

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*27P-242 Precision-enhanced 1,000-fold faster 3D quantum thermometry in vivo

<u>Yurina Nakane</u>¹, Haruka Maeoka¹, Ryuki Imamura¹, Ryuji Igarashi², Shin Usuki³, Takuma Sugi¹

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*27P-243 Elucidation of neuronal differentiation mechanisms by thermal signaling through control of intracellular local temperature

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*27P-244 Imaging and modeling of glycolytic oscillations

<u>Saaya Hario</u>¹, Shosei Imai¹, Yudai Iyoda², Hikaru Sugimoto³, Takuya Terai¹, Shinya Kuroda⁴, Robert E. Campbell¹

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*27P-245 Development of selective plane activation structured illumination microscopy

Kenta Temma^{1,2,9}, Ryosuke Oketani^{1,3}, Toshiki Kubo¹, Kazuki Bando¹, Shunsuke Maeda¹, Kazunori Sugiura⁴, Tomoki Matsuda⁴, Rainer Heintzmann^{5,6}, Tatsuya Kaminishi^{7,9}, Koki Fukuda^{8,9}, Maho Hamasaki^{7,8}, Takeharu Nagai⁴, Katsumasa Fujita^{1,2,9}

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*27P-246 High-speed, high-resolution computational phase microscopy visualizing organelles

Yugo Inutsuka^{1,2}, Yasushi Okada^{1,2}
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27P-247 Extraction of dependent spatial or spectral features from different disease states in Raman images

Ryoya Kondo¹, Yuta Mizuno^{1,2,3}, Jean-Emmanuel Clement^{2,3}, Kentaro Mochizuki⁴, Katsumasa Fujita⁵, Yoshinori Harada⁴, Tamiki Komatsuzaki^{1,2,3}

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*27P-248 Quantification of Spatial and Spectral Information Dependent on Measurement Methods and Disease States in Raman Images

Ryoya Kondo¹, Yuta Mizuno^{1,2,3}, Jean-Emmanuel Clement^{2,3}, Kentaro Mochizuki⁴, Katsumasa Fujita⁵, Yoshinori Harada⁴, Tamiki Komatsuzaki^{1,2,3}

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27P-249 Simultaneous measurement of average size and number of biomolecular condensates using spatial image correlation spectroscopy (SICS)

Yuta Hamada¹, Akita Kitamura^{2,3}

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27P-250 Imaging of Biomolecules by Constant Thermal Fluctuation Mode Atomic Force Microscopy

Daisuke Yamamoto

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27P-251 Development of small nanodiamonds that can be observed by optically detected magnetic resonance inside cells.

<u>Hirotaka Okita</u>¹, Shingo Sotoma², Yuki S Kato³, Yukiho Shimazaki^{1,4}, Hiroshi Abe⁵, Seiichi Saiki⁵, Madoka Suzuki¹, Yoshie Harada^{1,5,6}

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27P-252 Volumetric imaging of micrometer-scale cellular dynamics in centimeter-scale multicellular systems

<u>Taro Ichimura</u>¹, Taishi Kakizuka², Keiko Itano², Kaoru Seiriki³, Hitoshi Hashimoto^{1,3}, Yuki Sato⁴, Hiroya Itoga⁵, Shuichi Onami^{1,5}, Takeharu Nagai^{1,2}

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27P-253 Multi-color fluorescence lifetime biosensors for quantifying Ca2+, ATP, and GTP/GDP ratio in live cells

Cong Quang Vu

WPI-NanoLSI, Kanazawa University

Bioengineering

*27P-254 Cell-free synthesis of hydrophobic peptides that form nanopores in bilayer lipid membranes

Shoko Fujita¹, Izuru Kawamura², Ryuji Kawano¹

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27P-255 Morphological Difference in Hydrogel Induced Cancer Stem Cell in Synovial Sarcoma Model Cells

Zannatul Ferdous¹, Jean-Emmanuel Clément¹, Jian Ping Gong^{1,3}, Shinya Tanaka^{1,2}, Masumi Tsuda^{1,2,3}, Tamiki Komatsuzaki^{1,4}

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*27P-256 Novel approach for anticancer peptides carried by nanoparticles

Roberta Moisa

Horia Hulubei National Institute for Physics and Nuclear Engineering

*27P-257 Stereo 3D reconstruction of a dragonfly flapping motion and its quantification using fine grid spotlight

Natsuki Yamamoto Akita Prefectural University

27P-258 Microscopic toxicity assay of human organoids in microfluidic devices advanced by quantum beam technologies

Kotaro Oyama¹, Tomoko G Oyama¹, Hiroki Hamaguchi¹, Yusuke Kimura¹, Atsushi Kimura¹, Kimio Yoshimura¹, Masaaki Omichi¹, Yuuji Ueki¹, Akihiro Hiroki¹, Hiroyuki Hoshina¹, Yasuhiro Oshima¹, Michiyo Suzuki¹, Shinichiro Mori², Noriaki Seko¹, Noriko Ishioka¹, Mitsumasa Taguchi¹

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Crystal growth & Crystallization technique

*27P-259 High-Speed AFM investigation of structured fats' crystallization dynamics

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27P-260 Advancing Structural Biology: Innovations and Applications of In Vivo Macromolecular Crystallography at Nagoya University

Etsuko Tokunaga¹, Swagatha Ghosh², Hiroki Onoda¹, Yasufumi Umena¹, Leonard M.G. Chavas^{1,2}

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Virus structure, function, SARS-CoV-2

*27P-261 Cryo-EM structure of infectious and non-infectious Human Astrovirus and insights into its maturation process

<u>Kentaro Hiraka^{1,2}</u>, Raymond Burton-Smith^{1,2}, Chihong Song^{1,2}, Kana Miyamoto³, Kei Haga³, Reiko Todaka³, Kazuhiko Katayama³, Kazuyoshi Murata^{1,2}

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*27P-262 Structural basis for antiviral activity of a nucleoside analogue targeting dengue virus RNA-dependent RNA polymerase

Shiori Ito¹, Shunsuke Kita¹, Kentaro Uemura^{1,2,3,4}, Yuki Iwama¹, Takashi Tadokoro⁵, Hirofumi Sawa^{2,6}, Akihiko Sato^{2,3,6}, Akira Matsuda¹, Katsumi Maenaka^{1,2,6}

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27P-263 DEVELOPING BROAD SPECTRUM ANTIVIRALS: PEPTIDE-PORPHYRIN CONJUGATES ACTION, FROM MOLECULAR SCALE TO IN VIVO

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27P-264 Conformational dynamics of SARS-CoV-2 spike protein investigated by single molecule fluorescence spectroscopy

<u>Yuji Itoh</u>^{1,2}, Taisei Mori^{1,2}, Tateki Suzuki³, Takao Hashiguchi³, Satoshi Takahashi^{1,2}

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Mechanosensing and Mechanobiology, Biological Temperature

*27P-265 Investigation of the mechanism of neurite outgrowth using nuclear heating

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Japan, ⁵Premium Research Institute for Human Metaverse Medicine (WPI-PRIMe),
Osaka University, Osaka, Japan

*27P-266 Small-molecule FLIM sensors for visualization of temperature in calcium cycling of sarcoplasmic reticulum

<u>Takeru Yamazaki</u>¹, Kayoko Nomura¹, Toshiko Yamazawa², Satoshi Arai¹ ¹WPI Nano Life Science Institute (WPI-NanoLSI), Kanazawa Univ., Ishikawa, Japan, ²Core Research Facilities, The Jikei Univ. Sch. of Med., Tokyo, Japan

27P-267 Differential roles of a periplasmic tension sensor and a cytoplasmic one in the channel opening of MscL

Takeshi Nomura¹, Yasuyuki Sawada², Masahiro Sokabe³

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Biophysics of disease

*27P-268 Tau Inclusions in Soma Induce Neuronal Death in Human iPSC-derived Neurons

<u>Naoki Kato</u>¹, Sumihiro Maeda², Hideyuki Okano², Hiroko Bannai¹ ¹School of Advanced Science and Engineering, Waseda University, ²School of Medicine, Keio University

*27P-269 Reversible tangle formation of Alzheimer's disease-fold Tau filaments by conformational changes of the fuzzy coat region

Shingo Tamai^{1,2}, Takashi Nomura¹, Ryohei Kojima³, John Burke¹, Atsushi Yamagata⁴, Mikako Shirouzu⁴, Takeshi Fukuma³, Motomasa Tanaka^{1,2}

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27P-270 Lead and Mercury poisoning promote cardiac dysfunction in isolated hearts affecting cardiac ion channels and intracellular calcium homeostasis.

Gonzalo R. Ferreira¹, Romina Cardozo¹, Axel Santander¹, Luisina Chavarria¹, Santiago Sastre¹, Milagros Benitez¹, Nicolas Mujica¹, Lucia Dominguez¹, Garth Lamb Nicolson²

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Miscellaneous topics

*27P-271 Novel antibacterial agents to treat Multidrug resistant bacteria causing wound infections in diabetic patients

Mithali Raj Marla², Shailaja Raj Marla¹, Maria Shajan¹

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27P-272 An Interactive 3-D Graph Tool to Visualize Electromagnetic Waves on Web Browsers for Physics Education

Satoshi Yamaguchi, Masayuki Irisa Comp. Sci. and Sys. Eng., Kyushu Inst. Tech., Japan

Friday, June 28

Presentation time is organized by whether the last part (suffix) of Poster Session number is odd/even.

Odd number: 13:50-14:50 Even number: 14:50-15:50

Abstracts marked with * in the abstract number eligible for IUPAB2024 Student and Early Career Researcher Poster Award voting

Ex) *25P-999

Protein: Structure

28P-001 Cryo-EM analysis of human GLUT9

<u>Daiki Matsushita</u>¹, Yongchan Lee¹, Yu Toyoda^{2,3}, Teppei Takada³, Tomohiro Nishizawa¹

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28P-002 Molecular basis of substrate recognition in human y+LAT1-CD98hc complex

<u>Juntaro Nakahara</u>¹, Yongchang Lee¹, Natsumi Yoshida¹, Pattama Wiriyasermkul², Ryo Ekimoto¹, Mitsunori Ikeguchi¹, Sushi Nagamori², Tomohiro Nishizawa¹

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28P-003 Particle formation for nanofiber elongation in Fibroin artificial sequence

Kento Yonezawa^{1,2}, Chan Kok Sim², Takehiro Sato³, Haruya Kajimoto², Kiichi Hayashi², Takuya Sawai², Yusuke Okamoto², Rakuri Aiba², Yuki Nakatani², Kenta Kimura², Yoichi Yamazaki², Sachiko Toma-Fukai², Yugo Hayashi², Hironari Kamikubo^{1,2}
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28P-004 Cryo-EM analysis of mouse b0,+AT-rBAT complex

Aoi Maeda¹, Yongchan Lee¹, Pattama Wiriyasermkul², Sushi Nagamori², Tomohiro Nishizawa¹

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28P-005 Cryo-EM Structure of MexB-MexY Chimera Protein MexBYB Multidrug Efflux Pump

<u>Jiye Wang</u>¹, Kenta Tsutsumi¹, Ryosuke Nakashima², Kunihiko Nishino², Eiki Yamashita¹, Atsushi Nakagawa¹

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28P-006 Investigation of the effect of ATP/ADP for formation of 2-Cys peroxiredoxin (Prx2) high molecular weight complex

Trang Ngoc Tran¹, Ryusei Yamada², Hiroki Konno³

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28P-007 Comprehensive analysis of different fold proteins with similar interfaces

<u>Takumi Sekine</u>, Kazuo Fujiwara, Masamichi Ikeguchi Department of Biosciences, Soka University, Hochioji, Japan

28P-008 Solution structure of clock protein complex KaiA-KaiC

<u>Ken Morishima</u>¹, Masahiro Shimizu¹, Ritsuki Sakamoto², Yasuhiro Yunoki¹, Rintarao Inoue¹, Masaaki Sugiyama¹

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28P-010 The brain metabolites, betaine and dimethyl glycine disrupt acetylcholinesterase activity and enhance the inhibitory effect of Donepezil, Rivastigmine, and Galantamine

Laishram Rajendrakumar Singh, Kritika Kumari

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Friday, June 28

28P-011 Towards serial femtosecond crystallography of metalloproteins with sub-ångström details

<u>Faisal Koua</u>¹, Tiankun Zhou², Jay-How Yang³, Marcin Sikorski¹, Jayanath Koliyadu¹, Mohammed Vakili¹, Johan Bielecki¹, Richard Bean¹, Tokushi Sato¹, Adrian Mancuso^{1,2,4}

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28P-012 Structural basis of main proteases of HCoV-229E bound to inhibitor PF-07304814 and PF-07321332

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Protein: Structure & Function

28P-014 Evidence for an alternative YidC-assisted insertion mode - Exploring a putative parallel YidC dimer.

Denis Knyazev¹, Lukas Winter¹, Andreas Vogt^{2,3,4}, Sandra Posch¹, Yavuz Öztürk², Christine Siligan¹, Nikolaus Goessweiner-Mohr¹, Nora Hagleitner-Ertugrul¹, Hans-Georg Koch^{2,3}, Peter Pohl¹

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28P-015 Modeling of Photoswitchable Ligands Linked to Physiology

Wieslaw A Nowak

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28P-016 Identifying functional hotspot residues for activation in M2 muscarinic receptor

Yuya Sugiura¹, Tatsuya Ikuta³, Yuji Sumii¹, Hirokazu Tsujimoto⁵, Ryoji Suno^{4,5}, Putri Nur Arina Binti Mohd Ariff¹, So Iwata⁵, Norio Shibata¹, Asuka Inoue³, Takuya Kobayashi^{4,5}, Hideki Kandori^{1,2}, <u>Kota Katayama^{1,2}</u>

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28P-017 Aqp5 mutations in patients suffering from palmoplantar keratoderma (Bothnian type)

<u>Christine Siligan</u>, Helena Zich, Nikolaus Gössweiner-Mohr, Anna Stoib, Peter Pohl

Institute of Biophysics, Johannes Kepler University, Linz, Austria

28P-018 pH-Induced Conformational Dynamics and Oligomeric Assembly of Peroxiredoxin 6: Insights into Catalytic Mechanisms

<u>Hamidur Rahaman</u>, Shahnaj Sharifun, Kakchingtabam Pushpa Department of Biotechnology, Manipur University, Indo Myanmar Road, Canchipur, Imphal, India-795003

28P-019 Exploring Covalent Bond Electron Densities in the Active Site of the EcoRV-DNA Complex through QM/MM Metadynamics

<u>Hiroki Sato</u>, Itaru Onishi, Mika Mitsumatsu, Ryotarou Matsuda, Masayuki Irisa

Comp. Sci. and Sys. Eng., Kyushu Inst. Tech., Japan

28P-020 Fantastic Enzymes and where to find them

Ehmke Pohl¹, Katy Cornish¹, Stefanie Freitag-Pohl¹, Arnthór Aevarsson² ¹Department of Chemistry, Durham University, Durham, DH1 3LE, UK, ²Matis ohf, Vinlandsleid 12, Reykjavik 113, Iceland

28P-021 Theoretical study on allosteric control mechanism of a luminescent reaction of bioluminescent protein Aequorin

Tomohiro Ando¹, Toshiya Funahashi², Toru Nakatsu³, Shigehiko Hayashi¹ Grad. Sch. of Sci. Kyoto Univ., ²Grad. Sch. of Pharm. Sci. Kyoto Univ., ³Sch. of Pharm. Sci. Wakayama Med. Univ.

Friday, June 28

28P-022 Correlating single molecule studies with Cryo-EM structures to understand the inner workings of ATP synthase.

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28P-023 Molecular basis for heat-hypersensitive mutants of ryanodine receptor type 1

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28P-024 Proton-coupled electron transfer dynamics and ligand binding in the mycobacterial respiratory supercomplex III2IV2

Ana Patricia Gamiz-Hernandez, Daniel Riepl, Terezia Kovalova, Sylwia M. Król, Dan Sjöstrand, Martin Högbom, Peter Brzezinski, Ville R. I. Kaila

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28P-025 High-speed AFM observation of collagen degradation process by Grimontia hollisae collagenase

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28P-026 Structural basis for the pH-dependent functional regulation of cytochrome b6f complex from Chlamydomonas reinhardtii

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28P-027 Structural insights into the elongation complex of RNA polymerase II paused at the +1 nucleosome entrance

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28P-028 Positive allosteric modulation of cytochrome c oxidase activity

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28P-029 The structure and function of the ghrelin receptor coding for drug actions

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28P-030 Cracking the code: A computational expedition into neurodegenerative polypeptides and innovative therapies

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28P-031 Structural and Functional Elucidations of Druggable Viral Macrodomains

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National Taiwan University, Taipei, Taiwan

28P-032 Synthesis of versatile neuromodulatory molecules by a gut microbial glutamate decarboxylase

Pavani Dadi^{1,2}, Clint Pauling^{1,3}, Abhishek Shrivastava^{1,2}, <u>Dhara D. Shah</u>^{1,3} ¹Biodesign Center for Fundamental and Applied Microbiomics, Arizona State University, Tempe, AZ, USA., ²School of Life Sciences, Arizona State University, Tempe, AZ, USA., ³School of Mathematical and Natural Sciences, Arizona State University, Glendale, AZ, USA.

28P-033 An integrated approach using sequential and structural features for precise prediction of protein-protein binding affinity

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28P-034 Structure of the human 80S ribosome at 1.9 Å resolution – the molecular role of chemical modifications and ions in RNA

<u>Charles Barchet</u>^{1,2,3,4}, Samuel Holvec^{1,2,3,4}, Antony Lechner^{1,2,3,4,5}, Léo Fréchin^{1,2,3,4}, Nimali De Silva^{1,2,3,4}, Isabelle Hazemann^{1,2,3,4}, Philippe Wolff⁵, Ottilie von Loeffelholz^{1,2,3}, Bruno Klaholz^{1,2,3,4}

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Protein: Physical property

28P-035 Amyloid formation of the β 2-microglobulin variants, D76N and V27M: Diverse diseases via a common assembly mechanism

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28P-036 Negative Charge Increment during Evolution of Ferritin

Takumi Kuwata, Yusuke Murakami, Kazuo Fujiwara, <u>Masamichi Ikeguchi</u> Department of Biosciences, Soka University

28P-037 Prediction of detailed structures over the entire free energy landscape of protein folding using extended statistical mechanical models and restrained simulations

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28P-038 Structural studies of protein condensates prepared by ultracentrifugation/air-drying

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Protein: Function

28P-039 SsUrel is a pH-gated urea channel from Streptococcus salivarius

Anna Stoib, Xenia Fischer, Sandra Posch, Felix Wolkenstein, Sahar Shojaei, Christine Siligan, Nikolaus Goessweiner-Mohr, <u>Andreas Horner</u> Institute of Biophysics, Johannes Kepler University Linz, Gruberstr. 40, 4020 Linz, Austria

28P-040 Effect of the inorganic phosphate on the iron oxidation/mineralization activity of Escherichia coli non-heme ferritin A

<u>Takumi Kuwata</u>, Kazuo Fujiwara, Masamichi Ikeguchi Dept. of Biosci. Grad. Sch. of Sci. and Eng. Soka Univ., Tokyo, Japan,

28P-041 Structural Changes of Poly(ethylene terephthalate) undergoing Enzymatic Degradation

<u>Daisuke Tadokoro</u>, Tomoya Imai

Reserch Institute of Sustainable Humanosphere, Kyoto University

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28P-042 Mode of action of virulence factors of intracellular pathogens studied with time-resolved and high-resolution atomic force microscopy

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Protein: Measurement & Analysis

28P-043 BioSAXS for solution protein structure analysis at SPring-8

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28P-044 Biomolecular Interactions with the NanoTemper Dianthus

Stefanie Freitag-Pohl, Dorata Gasparikova, Kate V. Sowerby, Abbey M. Butler, Ehmke Pohl
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28P-045 Easy and fast LLPS size estimation using microplate reader

Enomoto Mayu¹, Suai Anzawa¹, Tadashi Kodama², Kyoko Furuita², Wataru Togawa¹, Ryoga Kobayashi³, Naotaka Sekiyama³, Yohei Miyanoiri², Toshimichi Fujiwara², Hidehito Toshio³, Chojiro Kojima^{1,2}

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28P-046 Spatiotemporal and global profiling of DNA-protein interactions and substrates of lysine-modifying enzymes in living cells

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28P-047 EPR Spectroscopy Combined with Rapid Freeze-Quenching Reveals Relationship Between Temperature Dependence of Active Site Rearrangement and of Activity in Inorganic Pyrophosphatase

Masaki Horitani¹, Hiroshi Sugimoto², Yuri Kasu¹ Saga University, ²RIKEN

Protein: Design & Engineering

28P-048 DNA replication triggered by small-molecule for in vitro auto-selection of enzymes

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28P-049 Generation of antibodies to an extracellular region of the transporters Glut1/Glut4 by immunization with a designed antigen

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28P-050 Heterocomponent protein tube formation via "Nature Inspired Protein Assembly Design (NIPAD)"

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28P-051 Understanding the tussle between aggregation-prone proteins and chaperons; toward the development of an enzyme immobilization platform

Nilanjana Bose INDIAN INSTITUTE OF TECHNOLOGY, DELHI

28P-052 De Novo Design of P-loop Harboring Protein

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Friday, June 28

28P-053 De novo design of helical peptide binders targeting the KIX domain of CBP

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28P-054 Red fluorescent proteins engineered from green fluorescent proteins

<u>Hiromi Imamura</u>¹, Shiho Otsubo², Mizuho Nishida¹, Norihiro Takekawa², Katsumi Imada²

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28P-055 A "Protein Structure Transformer" for integrative structural biology and molecular design

<u>Lucien Fabrice Krapp</u>, Fernando Meireles, Luciano Abriata, Matteo Dal Peraro

Laboratory for Biomolecular Modeling, EPFL

28P-056 Genetically encoded fluorescent biosensors for cellular metabolism

Yusuke Nasu^{1,2}, Yuki Kamijo¹, Robert Campbell¹

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28P-057 Role of "relaxed" peptide bond in protein structure and function

<u>Kaori Chiba</u>¹, Masaru Hoshino², Hiromu Ohshima¹, Manami Suwa¹ ¹National Institute of Technology, Ibaraki college, ²Kyoto University

Protein: Intrinsic disorder

28P-058 Deciphering the Role of GM1 Ganglioside-Bound A β Species in Alzheimer's Disease: Insights from Monoclonal Antibody 4396C and Advanced Biophysical Techniques

Maho Yagi-Utsumi^{1,2}, Satoru G. Itoh^{2,3}, Yui Kanaoka⁴, Shogo Miyajima⁴, Katsuhiko Yanagisawa⁵, Katsuyuki Nishimura³, Hisashi Okumura^{2,3}, Takayuki Uchihashi^{2,4}, Koichi Kato^{1,2,3}

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Membrane proteins

28P-060 Strategies for Cancer Therapy by Regulating Intracellular Dynamics of Antibody Drugs

Kazuya Kabayama^{1,2,3}, Yoshiyuki Manabe^{2,3}, Atsushi Toyoshima^{1,3},

Kazuko Kaneda^{2,3}, Tadashi Watabe⁴, Koichi Fukase^{1,2,3}

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28P-061 Differential molecular responses of PIEZO1 to membrane tension and ligand binding observed with diffracted X-ray tracking

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28P-062 Thermodynamic Analysis of pH-Dependent Substrate Binding in the Multidrug Transporter, EmrE

<u>Kazumi Shimono</u>^{1,2}, Keisuke Matsuda², Shoko Suzuki², Shuichi Miyamoto¹, Seiji Miyauchi²

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28P-063 INTRAMOLECULAR DOMAIN DYNAMICS OF LIGHT-HARVESTING PROTEIN LH1-RC OBSERVED BY THE DIFFRACTED X-RAY TRACKING METHOD

<u>Tatsunari Ohkubo</u>^{1,2}, Tatsuya Arai^{2,3}, Hiroshi Sekiguchi⁴, Kazuhiro Mio^{1,2}, Yuji C. Sasaki^{2,3}

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28P-064 NMR and modelling study of interaction of spider Cys-knot toxins with membrane and cationic ion-channels of P-loop superfamily

Zakhar Shenkarev^{1,2}, Pavel Mironov^{2,3}, Eugene Kovalenko^{2,3}, Dmitrii Kulbatskii^{2,3}, Alexander Paramonov^{2,3}, Mikhail Shulepko¹,

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28P-066 Diffusion and Oligomerization of GPCRs in Live Cells – The Impact of Ligands and Membrane Disruptors

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28P-067 Usability of the novel detergent NDT-C11 in cryoEM

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28P-068 The functional role of the pleckstrin homology domains of dynamins in evolution and disease

Isabel Pérez-Jover^{1,2}, Javier Espadas^{1,2}, Irune Ornos^{1,2}, Julene Ormaetxea Guisasola^{1,2}, Isaac Santos-Pérez³, Vadim Frolov^{1,4}, <u>Anna Shnyrova</u>^{1,2}

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DNA & DNA binding proteins

28P-069 The conformational analysis of DNA and nucleosome with doxorubicin analyzed by molecular dynamics simulation

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28P-070 DNA-binding and -unwinding Dynamics of the nonhexameric Escherichia coli UvrD helicase lacking C-terminal amino acids

Hiroaki Yokota

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28P-071 Role of Long-range Interactions in Protein-DNA Recognition

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28P-072 In-cell NMR analysis on base-pair opening dynamics and interactions with ligands of nucleic acids in living human cells

<u>Yudai Yamaoki</u>^{1,2}, Takashi Nagata^{1,2}, Tomoki Sakamoto², Omar Eladl², Keiko Kondo¹, Masato Katahira^{1,2}

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RNA & RNA binding proteins

28P-073 Theoretical study on an enzymatic reaction of the hammerhead ribozyme

<u>Ayaka Matsuyama</u>¹, Masahiko Taguchi², Shigehiko Hayashi¹ Kyoto University, Kyoto, Japan, ²Tohoku University, Miyagi, Japan

DNA/RNA nanotechnology

28P-074 RNA droplets perform 'AND' logic operation upon an input of targeted microRNAs

<u>Hirotake Udono</u>¹, Minzhi Fan¹, Yoko Saito¹, Hirohisa Ohno², Shin-ichiro M. Nomura³, Yoshihiro Shimizu⁴, Hirohide Saito², Masahiro Takinoue¹

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28P-075 Use of aptamers to control nucleic acid phase separation

Samuel Hauf, Yohei Yokobayashi

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28P-077 Experimental investigation of a modified Whiplash PCR driven by successive primer extension for massively parallel Implementation of DNA-based state machines

Ken Komiya, Koji Sakamoto

Japan Agency for Marine-Earth Science and Technology (JAMSTEC)

28P-078 Construction of giant unilamellar vesicle type molecular robots that

uses cargo/component-holding DNA hydrogel

Shoji Iwabuchi, Ryuji Kawano

Tokyo University of Agriculture and Technology

28P-079 Dimeric DNA origami nanocapsules for controllable cargo accessibility

Yusuke Sakai, Joanna Markiewicz, Martyna Adamiak, Dmitry Ghilarov,

Piotr Stepien, Jonathan G Heddle

Malopolska Centre of Biotehonology, Jagiellonian University, Poland

Chromatin & Chromosomes

28P-080 Brownian dynamics with exact solutions of diffusion in 3D for chromatin dynamics

Yukitaka Ishimoto

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Water & Hydration & Electrolyte

28P-081 Nonthermal excitation effects of sub-terahertz radiation on

transcription by RNA polymerase

Masahiko Imashimizu

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28P-082 Role of hydration water on the stability of proteins

Mafumi Hishida

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28P-083 Liquid water structure by means of molecular dynamic simulation and machine-learning

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Morphogenesis and Development

28P-084 Epithelial Morphogenesis Analysis Using Texture Tensor

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Molecular motor

28P-085 KIF6 is essential for male fertility through the ATP production pathway within sperm flagella

Tsukasa Makino¹, Chizuru Ito², Takeshi Masuda³, Kazuho Ikeda¹,

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28P-086 Exploring Efficient Control of F1-ATPase

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28P-087 Product inhibition slow down the moving velocity of processive chitinase and sliding-intermediate state blocks re-binding of product

Yoshiko Tanaka¹, Takayuki Uchihashi², <u>Akihiko Nakamura</u>^{1,3}
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28P-088 Decoding Volvox Swimming: Out-of-Phase Metachronal Waves Drive Oscillating Speed and Rotational Steering

<u>Katsuya Shimabukuro</u>, Natsume Takeda, Tatsuya Suehiro, Naoki Uemura National Institute of Technology, Ube College

28P-090 The Force-Generating State of Myosin Detected by Quasielastic Neutron Scattering

<u>Satoru Fujiwara</u>¹, Shinsaku Maruta², Yasunobu Sugimoto³, Kai Nishikubo¹, Taiki Tominaga⁴, Akio Inoue⁵, Hidetaka Furuya⁶, Katsuzo Wakabayashi⁶, Toshiaki Arata⁷

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28P-091 Rotation-dependent inhibition and activation mechanism of ATPase inhibitory factor 1 for mitochondrial ATP synthase from atomistic simulation

Ryohei Kobayashi, Kei-ichi Okazaki

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28P-092 CryoEM structure of dimeric F1-like ATPase in Mycoplasma mobile suggests a rotary catalytic mechanism for the gliding motility

<u>Takuma Toyonaga</u>^{1,2,3,4}, Takayuki Kato⁵, Akihiro Kawamoto⁵, Tomoko Miyata^{6,7}, Keisuke Kawakami⁸, Junso Fujita^{6,7,9,10}, Tasuku Hamaguchi^{3,4}, Keiichi Namba^{6,7}, Makoto Miyata^{1,2}

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28P-093 Processive movement of myosin II HMM oligomers along actin filaments

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Single Molecule Biophysics

28P-094 CHEMICAL FRICTION ALONG THE MINOR GROOVE OF DNA FACILITATES ENZYMATIC TRANSLOCATION OF λ EXONUCLEASE VIA ELECTROSTATIC RATCHET

<u>Gwangrog Lee</u>¹, Jungmin Yoo¹, HyeokJin Cho¹, Jejoong Yoo²

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28P-095 Single-molecule level tracking of the CCT/TRiC chaperonine mediated functional cycle

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28P-097 Multidisciplinary Platforms to Study Biological Questions

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28P-098 deepFLUOR: Deep Learning Classification of Single-Molecule Signals

<u>Jinseob Lee</u>¹, Byungju Kim², Yeongkyoung Park^{3,4}, Yoonki Kim^{3,4}, Jongbong Lee^{1,2}

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Cell biology: Adhesion

28P-099 Stress propagation in a living cell

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28P-101 S100A11 promotes focal adhesion disassembly via myosin II-driven contractility and Piezo1-mediated Ca2+ entry

Tareg Omer Mohammed¹, You-Rong Lin¹, Kai Weissenbruch², Kien Xuan Ngo¹, Yanjun Zhang¹, Noriyuki Kodera¹, Martin Bastmeyer^{2,3}, Yusuke Miyanari^{1,4}, Azuma Taoka^{1,5}, <u>Clemens M. Franz</u>¹

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Cell biology: Motility

28P-102 Wave dynamics and collective behavior of swimming flagellar apparatus isolated from the green algae C. reinhardtii

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28P-103 Symbiotic bacteria break through narrow passage by flagellar wrapping

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28P-104 The effect of TGF- β -induced EMT on the establishment of epithelial collective migration

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28P-106 Characteristics and mechanics of the crawling of the tested amoeba Arcella sp.

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28P-107 Shape coupled bifurcation of an amoeba cell brings ballistic movement in amoeboid migration

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28P-108 Ciliary waveform conversion is induced by the shape change of doublet microtubule accompanied by the modification of outer-arm dynein motor activity

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28P-109 Viewing the swimming motion of a unicellular organism in extreme environmental conditions.

Masayoshi Nishiyama

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28P-110 The Calcium Sensitive Helical Arrangement of Axonemal Components in Chlamydomonas Flagella

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28P-111 Utilizing Wavelet Analysis Features for the Simplified Prediction of Enhanced Cellular Stress Fluctuations on the Matrix with Stiffness Heterogeneity

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28P-112 Gliding direction of Mycoplasma mobile correlates with the curved configuration of its cell shape

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28P-113 Functional exploration of Candidatus Izimaplasma MreB using the minimal synthetic bacterium JCVI-syn3B.

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Cell biology: Cytoskeleton & Membrane skeleton

28P-114 Preparation of Dictyostelium discoideum NAA80 knockout strain

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28P-115 Visualization of intracellular structure of D. discoideum during unicellular and multicellular phases

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28P-116 Direct measurement of the physical properties of ER

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28P-117 Visualization of GTP hydrolysis in microtubules

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28P-118 Void space around microtubules

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Cell biology: Signal transduction & Cell membrane

28P-120 Application of Single-Molecule Tracking to Drug Discovery

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28P-121 Investigation of cellular localization of opioid receptors: A combined biochemical assay and microscopy study

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28P-122 Quantification of repellent response of single E. coli cell through the change in polar localization of adaptation enzyme CheB and flagellar motor rotation

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28P-123 Lamellipodia-like membrane protrusions maintain the integrity of epithelial cell-cell junctions

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28P-124 Unilateral-bidirectional regulation of electrical synapse formation in C. elegans

Zan Wu, Lin Pang, Mei Ding

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Biological & Artificial membrane: Structure & Property

28P-125 Curcumin Exerts the Membrane Raft Modulating Activity via Phase Separation and Induces CD44 Shedding in Tumor Cells

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28P-126 The effect of different lateral packing stress in acyl chains on KcsA orientation and structure in lipid bilayer

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28P-127 Probing the supramolecular aggregation state of bacterial endotoxin to reveal the basis of biological recognition and endotoxin masking in drug formulations

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Biological & Artificial membrane: Dynamics

28P-128 Non-equilibrium patterns in phase-separated lipid membranes under shear flow

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Biological & Artificial membrane: Excitation & Channels

28P-129 Towards elucidating the tension effects on water flux across lipid bilayers and aquaporins: An attempt using water-in-oil microdroplets

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28P-130 Light-evoked channel activity using photolipids

Rohit Yadav, Juergen Pfeffermann, Nikolaus Goessweiner-Mohr, <u>Peter Pohl</u> Johannes Kepler University, Linz, Austria

Membraneless Organella, autophage, Liquid-liquid phase separation

28P-131 The role of promyelocytic leukemia protein (PML) in the regulation of calcium homeostasis in HeLa cells

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28P-132 Effect of F-actin, myosin and its fragments on the morphology and stability of PEG/DEX droplets

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28P-133 Translation-coupled genomic RNA replication in fibril-stabilized all-aqueous droplet colonies

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28P-134 PRESSURE AND TEMPERATURE EFFECTS ON FUS LIQUID DROPLET OF AMYOTROPHIC LATERAL SCLEROSIS PATHOLOGICAL VARIANT, R495X

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28P-136 Micropolarity governs the structural organization of biomolecular condensates

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Chemoreception

28P-137 Structural and biochemical analyses of SatA, a periplasmic binding protein involved in chemotactic response to serine with Mlp3 in Vibrio cholerae.

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Neuroscience & Sensory systems

28P-138 Post-synaptic Effects of CPTX on Excitatory Synapses

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28P-139 Regulation of intracellular tau dynamics using optogenetic tools

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Neuronal circuit & Information processing

28P-141 Fast Intrinsic Optical Signal (FIOS) measurements of brain slices: no-stain, label-free and non-invasive fast optical signal measurements

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28P-142 Visualizing demyelination effects on interhemispheric communication with voltage-sensitive dye imaging in cuprizone-induced multiple sclerosis model mice

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Behavior

28P-143 The Implications of microRNA, CaMK2A, and MeCP2 Signaling on Adolescent Cognitive Ability

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Photobiology: Vision & Photoreception

28P-144 The importance of water in membrane receptor function

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28P-145 Time-resolved detections of substrate release and uptake reactions of the light-driven chloride pump halorhodopsin

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28P-146 Molecular characterization of opsins from a nematode

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28P-147 Study on the Mechanisms of High Fluorescence of Archaearhodopsin-3 (AR3) Mutants

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28P-148 Analysis of the mechanism of photoreceptor RcPYP complex formation

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28P-149 Driving force of proton pump rhodopsins revealed by electrophysiological study

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28P-150 Solid-state NMR characterization of histidine residues in Themoplasmatales archaeon heliorhodopsin

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28P-151 Characterization of the magnetic and geometrical structure of radical pairs in Serum Albumin by electron spin resonance

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28P-152 Novel green/red light-sensing mechanism in the phytochrome-superfamily protein

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Photobiology: Photosynthesis

28P-153 Molecular Docking Simulations at Quinone Binding Site in Photosynthetic Reaction Centers

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28P-154 Fluorescence spectra of a photosynthetic carbonyl carotenoid, siphonaxanthin: Dual fluorescence observed only at ambient temperature in polar solvents

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28P-155 Cryo-EM structure of marine green algal LHCII utilizing blue-green light

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28P-156 Biohydrogen production from whiskey waste liquid by two-stage fermentation

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28P-157 Energy gradient of the β 82 chromophores established by the linker proteins in Synechocystis PCC 6803 Phycobilisome Rod

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28P-158 Estimation of Local Antenna Sizes of Photosystem I in Chlamydomonas Cells

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Photobiology: Optogenetics & Optical control

28P-159 The effect of blue light on the proliferation of E. coli cells

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28P-160 Photocontrol of small GTPase Ras fused with a photoresponsive protein

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28P-161 Electrophysiological characterization of light-activated proton-transporting heliorhodopsins

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28P-162 Reconstitution of a light-activatable transcription factor, Photozipper, with extrinsic chromophores

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Radiobiology & Active oxygen

28P-163 YAP/Aurora A-mediated ciliogenesis regulates ionizing radiation-induced senescence via Hedgehog pathway in tumor cells

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28P-164 Cadmium tolerance, accumulation and translocation in sweet sorghum irradiated by carbon beam

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Origin of life & Evolution

28P-165 Analysis of evolutionary constraints using bacterial experimental evolution

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28P-166 Mega-phylogenetic evolution of complex adaptive traits in thousands of bacterial species

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28P-167 Quantum evolution form electronic state of macro-biomolecules

Masanori Yamanaka

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28P-168 The Relation Between Biology and Physics: Origins of Life Research and its Philosophical Implications

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Synthetic biology & Artificial cells

28P-169 Spatially separated transcription and translation in the artificial cell with the artificial organelle

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28P-170 Synthetic minimal cells with various vesicle-polymer compositions: Toward implementing evolution

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28P-171 Molecular tools aiming at arbitrary manipulation of micro-structures in living cells

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28P-172 Phase separation-induced actin bundle elongates filopodia-like tube on giant liposome from inside

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28P-173 Pattern diversity emerges from a simple gene network

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Genome biology

28P-174 Insights into chromatin organization obtained by a rapid classification of A/B compartments from Hi-C data

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Computational biology: Bioinformatics

28P-175 Computational Evaluation of the Human Health Effects of the Main Compounds Found in Artemisia dracunculus

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28P-178 Development of Prediction Methods for Class A GPCR and G-protein Coupling Selectivity Using Deep Learning

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28P-179 Consortium of "Consistent substitutions" on Influenza A(H1N1) viral proteome and its possible consequences on human host-viral interactions: A study using Multiple Sequence Alignments, text mining, and Molecular Dynamics Simulations

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28P-180 Analysis of Partial Structural Similarity of ribonuclease and chymotrypsin based on their amino acid sequences

<u>Takeshi Kikuchi</u>, Ahasanul Kabir, Takuya Takahashi Ritsumeikan University

Computational biology: Molecular simulation

28P-181 Gas-phase Structural Analysis of Biomolecules using Coarse-grained Molecular Dynamics Simulation

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28P-183 2D-replica exchange simulation of membrane permeation process of cyclic hexapeptides

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28P-184 Classification of conformational dynamics of high mannose- type oligosaccharides by molecular simulation and data clustering

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28P-185 The role of water and cholesterols in APP cleavage by gamma-secretase

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28P-186 Decoupling processes of the Adenosine A2A receptor from G-proteins through the lens of dPaCS-MD simulations

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28P-187 PROTAC-mediated ternary complex structure distribution profiles using enhanced sampling methods

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28P-188 3D Structure Prediction of the Odorant-bound Olfactory Receptor

Takumi Hirao¹, Yusuke Ihara², Chiori Ijichi², Genki Kudo³,

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28P-189 Quantitative Evaluation of Protein-Compound Substructure Interaction with Inverse Mixed-Solvent Molecular Dynamics Simulation

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28P-190 Binding Free Energy Shifts of Protein Complexes due to Amino Acid Mutations

Kazutomo Kawaguchi, Hidemi Nagao

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28P-191 Computational estimation of the free energy change of peptide- bond rotation induced by reduction of "plant-type" ferredoxin

Tomoki Nakayoshi^{1,2}, Yusuke Ohnishi³, Hideaki Tanaka³, Genji Kurisu³, Yu Takano¹

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28P-192 Dependence of the abnormal open states patterns in the ATXN2 gen on the number of CAG repeats

<u>Stepan Dzhimak</u>^{1,2}, Mikhail Drobotenko², Oksana Lyasota¹, Jose Luis Hernandez-Caceres³, Yuriy Nechipurenko⁴, Alexandr Svidlov¹, Anna Dorohova¹

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28P-193 GPU-accelerated coarse-grained MD simulator and its application to postsynaptic density

Yutaka Murata, Shoji Takada

Dept. Biophysics, Div. Biology, Grad. Sch. of Science, Kyoto University

28P-195 Vibrational Dynamics of Water Molecules in FUS Protein Condensates: Molecular Interpretation

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28P-196 Collagen-collagen interactions: Triple helix to helix-helix to fibrils.

George Anthony Pantelopulos, Robert Best

National Institutes of Health

28P-197 Analysis of Antigen-Antibody Interface Based on MD Simulations: Toward Antibody Design

Takefumi Yamashita^{1,2}

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28P-198 Simulation-based prediction and elucidation of the pathogenic mechanism of deafness in GJB2-encoded Cx26 channel protein

<u>Cheng-Yu Tsai</u>^{1,2}, Ying-Chang Lu², Yen-Hui Chan^{2,3}, Chuan-Jen Hsu^{2,3}, Pei-Lung Chen^{1,4}, Chen-Chi Wu², Lee-Wei Yang^{5,6}

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28P-199 Applications of Tree-Search-MD to drug target proteins: conformational changes between inactive and active structures of a kinase and a ligand binding to a GPCR

Yukina Nakai¹, <u>Toru Ekimoto</u>¹, Tsutomu Yamane², Masao Inoue¹, Naoki Ogawa¹, Sun-Yong Park¹, Kei Terayama¹, Mitsunori Ikeguchi^{1,2} ¹Yokohama City University, ²RIKEN R-CCS

28P-200 Theoretical Insights into Drug Resistance Mechanisms of HIV-1 Protease: Residue Interaction Network Analysis

Keidai Yamase

Chiba Institute of Technology

28P-201 Molecular dynamics simulations of lipid adsorption by PLA2 of snake venom.

Tatsuhiro Kawashima, Ryuta Imayoshi, Kazutomo Kawaguchi,

Hidemi Nagao Graduate School of Natural Science and Technology, Kanazawa University, Japan

28P-202 Analysis of Protein Simulations Using Relaxation Mode Analysis

Ayori Mitsutake Meiji University

28P-203 How the Membranes Fuse: From Spontaneous to Induced

Hongxia Guo

Institute of Chemistry, Chinese Academy of Sciences

28P-204 Impact of glycosylation on the structural features and hydration effects of glycoproteins

Haeri Im¹, Song-Ho Chong², Isseki Yu³, Yuji Sugita^{1,4,5}

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28P-205 Developing an IDP-Specific Force Field by Optimizing CMAP Parameters

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28P-206 Coarse-Grained Co-transcriptional Folding Simulation of RNA Switch

Akito Taneda

Hirosaki University

Computational biology: Biological modeling and simulation

28P-207 Dynamic transitions in microtubules: role of flared ends and lattice repair in catastrophes and rescues

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28P-208 Analysis of fracture patterns in a vertex model including detachment of cells

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28P-210 Learning force field parameters from ensemble-averaged data with a differentiable approach

Yohei Sako, Yasuhiro Matsunaga

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28P-211 Controlled Drug Delivery from Polymeric Surfaces: Harnessing Sonochemical Methods for Fluorouracil Nanoparticle Synthesis

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28P-212 Molecular modelling, homo-oligomerisation and membrane interactions of hepatitis E virus pORF1 replication polyprotein

Thibault Tubiana, Sonia Fieulaine, Stéphane Bressanelli

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28P-213 Improving Structure-Based Virtual Screening using AlphaFold2 with Multi-State Modeling

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28P-214 Flexible Fitting of Coarse-Grained Models to AFM Images of Intrinsically Disordered Proteins

<u>Sakura Homma</u>, Yasuhiro Matsunaga Saitama University

28P-215 Structure formations induced by a non-reciprocal cell-cell interactions in a multicellular system.

<u>Biplab Bhattacherjee</u>, Masayuki Hayakawa, Tatsuo Shibata Laboratory for Physical Biology, RIKEN Center for Biosystems Dynamics Research, Kobe, Japan.

28P-216 Universal existence of power-law correlations in homogeneous states of anisotropic active matter models

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28P-217 Searching for the BET interactome through AI and Molecular dynamics simulations

Alberto Perez^{1,2}

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28P-219 Membrane fusion as a pathway to fission

Russell k w Spencer, Marcus Müller Georg-August Universitat Goettingen

Computational biology: machine learning for molecules or cell systems

28P-220 Optimization of In Vitro Glycolytic Pathway Using Machine Learning

Naosato Takagi, Daisuke Kiga Waseda University, Tokyo, Japan

28P-221 Development of the super-resolution Cryo-EM based on the Generative Adversarial Networks

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28P-222 Deep Learning-Based Water Molecule Displacement Prediction Method for Improving the Accuracy of Drug Discovery Docking Software

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28P-223 Construction of a physical reservoir computing device using active matter made from a swarm of biomolecular motors

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Mathematical & Theoretical biology

28P-224 Spatial point processes with molecular density-dependent

association-dissociation and cluster formation in signal transduction

on the plasma membrane

Hiroaki Takagi

Nara Medical University, Nara, Japan

28P-226 Professor

Chanho Park, Junil Kim, Julian Lee

Department of Bioinformatics and Life Science, Soongsil University

Data Sharing and Open Science

28P-227 Crafting an Individual-Centric Genomics Platform

Senkei Umehara, Atsushi lida, Ken Yagi

GENEX, Inc. (Tokyo, Japan)

28P-228 Serious accumulation of sequence errors in international public

database searched by analyzing deposited plasmids in RIKEN-BRC

Gene bank with high-throughput sequencing

Yoshihiro Miwa, Tetsushi lida, Junko Kijima, Shingo Nozaki,

Shotaro Kishikawa

Gene-Eng-Div, BRC, RIKEN

Ecology & Environment

28P-229 Ionic-strength and pH dependent reactivities of ascorbic acid and cysteine toward ozone in microdroplets studied by aerosol optical

tweezers

Yuan-Pin Chang

Department of Chemistry, National Sun Yat-sen University, Kaohsiung, Taiwan.

Nonequilibrium state & Biological rhythm

28P-230 From cellular chirality to large-scale chirality: Emergence of chiral spiral in migrating cellular system

Masayuki Hayakawa¹, Biplab Bhattacherjee¹, Lihao Guo¹,

Hidekazu Kuwayama², Tatsuo Shibata¹

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28P-231 Integrated Analysis of Circadian Clock in cyanobacteria

Masaaki Sugiyama, Ken Morishima, Yasuhiro Yunoki, Rintaro Inoue Institute for Integrated Radiation and Nuclear Science, Kyoto University

28P-232 Computational Study of Peak Position in One Dimensional Mesoscopic Reaction Diffusion System

Ryuta Imayoshi, Kazutomo Kawaguchi, Hidemi Nagao Graduate School of Natural Science and Technology, Kanazawa University

28P-233 Density-dependent state transitions and periodic advective flow in an active actomyosin system

Tomoka Kashiwabara, Yusuke T. Maeda Dept. of Phys. Kyushu Univ., Fukuoka, Japan

Measurements

28P-234 Extracellular Potential Measurement of Cardiomyocytes in Hyperkalemic Conditions

Kentaro Kito, Masahito Hayashi, <u>Tomoyuki Kaneko</u> LaRC, FB, Grad. Sch. Sci. & Eng., Hosei Univ., Tokyo, Japan

28P-235 Single Molecule Analysis of Perforin Dynamics Using Nanopore Measurements.

Sotaro Nakamura, Kazuhiro Kobayashi, Ryo lizuka, Hideaki Kato, Sotaro Uemura

The University of Tokyo

28P-236 IR super-resolution micro-spectroscopy of keratin proteins in human nails

<u>Ayaka Nagaoka</u>, Hirona Takahashi, Tetsuya Ida, Makoto Sakai Okayama University of Science

28P-237 Measurement of photocatalytic hydrogen production in titanium/ manganese oxide film/hydrogenated amorphous silicon thin film stack using flavan molecules

<u>Yutaka Tsujiuchi</u>^{1,2}, Kohei Saito¹, Kazunori Takada¹, Koyu Akiyama¹, Hiroshi Masumoto²

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28P-238 Current control using external blue-green light in an amino acidcontaining gel stacked device in contact with a hydrogenated amorphous silicon thin film

Kohei Saito¹, Yutaka Tsujiuchi^{1,2}, Hiroshi Masumoto² ¹Akita UNIV, ²Tohoku UNIV

Bioimaging

28P-240 Coupling between vinculin and retrograde actin flow visualized by live-cell single-molecule imaging

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28P-241 Data-Driven Approaches in Single-Molecule Trajectory Analysis of Protein Mobility in Live Cells

Yuma Ito, Makio Tokunaga

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28P-242 Monitoring the biofilm development of Escherichia coli BL21

Alexander Karl Bullen, Tomohiro Shima

University of Tokyo

28P-243 Label-free direct screening of "spectral biomarkers" of colorectal tumour-specific P. anaerobius via Raman mapping in combination

with data mining

<u>Pooja Manik Badgujar</u>, Yu-Chung Yu-Chung Lin, Zhe-Rui Zhe-Rui Lin, Kuan-Ting Wu, Chia-Liang Cheng

Department of Physics, National Dong Hwa University, Hualien 97401, Taiwan

28P-244 Revisiting the 105 gap issue in cellular thermal biology by label-free mid-infrared photothermal microscopy

<u>Keiichiro Toda</u>¹, Masaharu Takarada², Genki Ishigane¹, Hiroyuki Shimada¹, Venkata Ramaiah Badarla¹, Kohki Okabe², Takuro Ideguchi¹

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28P-245 Visualization of exocytosis using video-rate bioluminescence imaging

<u>Satoru Yokawa</u>¹, Shinji Fukuda², Takahiro Suzuki², Tadahide Furuno¹
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28P-246 Topography considerations for high-speed atomic force microscopy based force mapping on bacteria

<u>Christian Ganser</u>¹, Shigetaka Nishiguchi², Takayuki Uchihashi^{1,3}
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28P-247 Optical Freshness Evaluation Method of Raw Fish Meat

<u>Yasuhiro Maeda</u>, Go Shioi, Tomonobu Watanabe Laboratory for Comprehensive Bioimaging, RIKEN, BDR, Japan

28P-248 Nanopipette-based single-cell stimulation with non-thermal atmospheric pressure plasma

<u>Han Gia Nguyen</u>¹, Linhao Sun², Shinya Kumagai³, Shinji Watanabe² ¹Grad. Sch. Nano Life Sci., Kanazawa University, Japan, ²WPI-NanoLSI, Kanazawa University, Japan, ³Meijo University, Japan

28P-249 The role of receptor oligomerization in signal transduction investigated through single-molecule analysis

<u>Hideaki Yoshimura</u>, Takeaki Ozawa Department of Chemistry, School of Science, The University of Tokyo, Tokyo, Japan

28P-250 Real-Time Imaging of Granzyme Secretion During CTL Assault on Cancer Cells

Zhuohao Yang¹, Yuto Kurisu², Koji Nagaoka³, Kazuhiro Kakimi⁴, Takashi Funatsu², Yoshitaka Shirasaki¹

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28P-251 Advancing Severe Asthma Research through Live-Cell Imaging of Secretion Activity

Yoshitaka Shirasaki¹, Mai Yamagishi², Kaede Miyata³, Yumiko Tanaka³, Hiroki Kabata⁴, Misato Irie⁴, Rie Baba⁴, Takashi Kamatani^{4,5,6}, Kazuyo Moro⁷, Koichi Fukunaga⁴, Sotaro Uemura³

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28P-252 Imaging of mitochondrial ATP in mouse sperm before and after capacitation using AMPK activators and inhibitors

<u>Takashi W Ijiri</u>¹, Yuika Asanuma¹, Masamichi Yamamoto²
¹Setsunan University, ²National Cerebral Cardiovascular Center

28P-253 Numerous-color simultaneous imaging with dozens of bioluminescence colors

Mitsuru Hattori¹, Yuki Hiruta², Takeharu Nagai¹
¹SANKEN, Osaka University, Japan, ²Department of Applied Chemistry Faculty of Science and Technology, Keio University, Japan

Bioengineering

28P-255 Spiral Formation of Microtubules Driven by Kinesin Motors

<u>Douglas Ng'ang'a</u>, Takahiro Nitta Applied Physics Course, Faculty of Engineering, Gifu University

28P-256 Sensitive detection of Salmonella with CRISPR–Cas13a system

Svitlana Kovalchuk2, Yoshihiro Minagawa1, Hiroyuki Noji1

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28P-257 Spectroscopic signature responsible for the life activity of regenerating worm A. viride studied using Raman spectroscopy and Two-Photon Fluorescence Lifetime Imaging

<u>Chia-Liang Cheng</u>¹, Pooja Badgujar¹, Pei-Yang Huang¹, Artashes Karmenyan¹, Viktor Nikolayev², Jiun-Hong Chen³

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³Department of Life Sciences, National Taiwan University, Taipei, Taiwan

28P-258 Anticancer peptides delivery systems effects on model and natural lipid membranes

Bogdan Zorila, Diana Lavinia Stan, Roberta (Stoica) Moisa, Mihaela Bacalum

Department of Life and Environmental Physics, Horia Hulubei National Institute for Physics and Nuclear Engineering

28P-259 Spatiotemporal changes in single cell rheology of developing embryos unveiled by atomic force microscopy

<u>Takahiro Kotani</u>¹, Yuki Miyata¹, Yosuke Tsuboyama¹, Yuki Fujii¹, Takaharu Okajima²

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Crystal growth & Crystallization technique

28P-260 Assembly of Cage-Shaped Protein Dps Using Functional Peptides

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Virus structure, function, SARS-CoV-2

28P-261 Rational in silico design and structure analysis of SARS-CoV-2 neutralizing antibody UT28K

Shunsuke Kita¹, Tatsuhiko Ozawa^{2,3}, Kouki Ikeda⁴, Liuan Chen¹, Yuki Anraku¹, Hideo Fukuhara¹, Emiko Igarashi⁵, Yumiko Saga⁵, Noriko Inasaki⁵, Jiei Sasaki⁶, Yuhei Kirita⁷, Takao Hashiguchi⁶, Hideki Tani⁵, Hiroyuki Kishi^{2,3}, Hideki Niimi^{2,3}, Katsumi Maenaka¹

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28P-262 Verification of the effect of ligand and receptor flexibility on inhibitory activity by MD simulation

<u>Suzuka Saito</u>¹, Masashi Muramoto¹, Simon Hikiri², Junichi Higo³, Takuya Takahashi²

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28P-263 N-substituted anthranilic acid derivatives as PPI inhibitors between Syntenin-1 PDZ domain and SARS-CoV-2 Env protein

<u>Hidekazu Hiroaki</u>^{1,4,5}, Ryusei Hamajima¹, Youichi Suzuki², Eiji Morita³, Hong Wu², Yoshihiko Fujioka², Takeshi Tenno^{1,5}

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28P-264 Molecular mechanisms of SARS-CoV-2 resistance to nirmatrelvir and the countermeasures

Haitao Yang

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Mechanosensing and Mechanobiology, Biological Temperature

28P-265 Analysis on the Role of the Periplasmic Loop of the Bacterial Mechanosensitive Channel MscL

Yasuyuki Sawada¹, Takeshi Nomura², Masahiro Sokabe³

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28P-266 Activation of chloride ion channel CLIC1 by mechanical external force using AFM in breast cancer cell

<u>Ayana Yamagishi</u>^{1,2}, Samrat Mukherjee^{1,2}, Chikashi Nakamura^{1,2}
¹National Institute of Advanced Industrial Science and Technology (AIST), ²Tokyo University of Agriculture and Technology

28P-267 Mechanical properties of nestin tail domain analyzed by tensile test using AFM

Ayana Yamagishi^{1,2}, Rina Tokuoka^{1,2}, Daijiro Takeshita¹, Chiaki Yoshikawa³, Tomohiko Yamazaki³, Taro Uyeda⁴, <u>Chikashi Nakamura</u>^{1,2}

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28P-268 Elucidation of the mechanism of intracellular temperature variation by high-speed temperature mapping

Masaharu Takarada, Takashi Funatsu, <u>Kohki Okabe</u> Graduate School of Pharmaceutical Sciences, The University of Tokyo

Biophysics of disease

28P-269 Changes in the properties of rbcs in the process of extracorporeal membrane oxygenation by scanning flow cytometry

Ekaterina Yastrebova¹, Valeri Maltsev¹, Gleb Moroz²

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28P-270 Morphology of Cancer Organoids Reproduced by 3D Phase-Field Model

Kotaro Kawamura¹, Toshikaze Chiba¹, Keita Yanagiya¹, Yutaka Oya², Toshihiro Kawakatsu¹, Tatsuaki Tsuruyama¹, Masayuki Imai¹

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Miscellaneous topics

28P-271 Investigation of boson peak like behaviors appeared in cysteine and related amino acids

<u>Hirofumi Nema</u>, Yasuhiro Fujii, Akitoshi Koreeda Ritsumeikan University

28P-272 Interactions of Model Antimicrobial Peptides with Lipid Membranes

Normand Voyer¹, Pierre-Alexandre Paquet-Côté¹, François Otis¹, Jochen Bürck², Patrick Lagüe³, Anne S. Ulrich²

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Tuesday, June 25

Morning Seminar 1 (Avanti Polar Lipids)		Room A
8:00-8:50	Delicious Molecules: A Primer on Lipids and Membrane Bio	physics
Chairs Roberto Covino (Frankfurt Institute for Advanced Studies, Germany)		
	Chiho Watanabe (Hiroshima University, Japan)	
MS1-1	Roberto Covino ¹ , Chiho Watanabe ²	
	¹ Frankfurt Institute for Advanced Studies, Frankfurt am Main, Germany,	
	School of Integrated Life Sciences, Hiroshima University, Hiroshima, Japa	an

BP Seminar 1 (JEOL Ltd.)		
12:35-13:35	Microscope Technology that Realizes Structural Biology	
Chair	Akio Sekigawa (JEOL Ltd.)	
BP1-1	Introduction of high throughput and high flexible workflows of cryo- TEM Naoki Hosogi JEOL Ltd., Tokyo, Japan	
BP1-2	Introduction of newly developed cryo-FIB for cryo-TEM Noriaki Mizuno ¹ , Wataru Shigeyama, Naoki Hosogi, Hideki Matsushima JEOL Ltd., Kyoto, Japan	

BP Seminar 2	2 (Carl Zeiss Co., Ltd.)	Room B-1
12:35-13:35	Investigate Molecular Dynamics in Live Cells and Organis	sms using
	Fluorescence Correlation-based Microscopy Methods	
Chair	Akira Sato (ZEISS Research Microscopy Solutions, Japan)	
BP2-1	Xianke Shi	
	ZEISS Research Microscopy Solutions, APAC, Singapore	

Tuesday, June 25

BP Seminar 3 (Leica Microsystems K.K.)		Room B-2
12:35-13:35	To The Future of Microscopy Imaging	
Chair	Shintaro Tanaka (Leica Microsystems K.K.)	
BP3-1	Intracellular temperature mapping using high-speed fluore lifetime imaging microscopy	escence
	Kohki Okabe ¹ , Suguru Osari ²	
	¹ Graduate School of Pharmaceutical Sciences, The University of Tokyo	, Tokyo, Japan,
	² Leica Microsystems K.K., Tokyo, Japan	

BP Seminar	4 (Nakatani Foundation)	Room C-2
12:35-13:35	Unveil the Spark: Explore the Decision Moment to become Biophysicists!	ie
Chairs	Satoshi Takahashi (Tohoku University) Seiji Kojima (Nagoya University) Ikuko Fujiwara (Nagaoka Univresity of Technology)	
BP4-1	Elizabeth Hinde ¹ , Yoshie Harada ² , Heeyoun Bunch ³ ¹ Sch. Phys., Univ. Melbourne, ² Institute of Protein Res., Osaka Univ, National Univ	³Kyungpook

BP Seminar 5	BP Seminar 5 (SIGMAKOKI CO., LTD.) Room D		
12:35-13:35	A New World from Single Cells to Cell Populations Revealed by the Ultra-wide-field Microscope "AMATERAS"		
Chair	Nobutoyo Oguni (SIGMAKOKI CO., LTD.)		
BP5-1	Development of trans-scale scope "AMATERAS" and direct observation of millions of cellular dynamics Taro Ichimura Osaka University, Osaka, Japan		
BP5-2	Introducing a new product of wide-field microscope "CUS-WF" that can be installed in each laboratory Yuichi Inoue SIGMAKOKI CO., LTD., Tokyo, Japan		

BP Seminar 6	6 (On-chip Biotechnologies Co., Ltd)	Room E
12:35-13:35	BarBIQ: a novel method for single-cell-based quantitative a of bacterial microbiota using droplets	analysis
Chair	Kageyasu Takanashi (On-chip Biotechnologies Co., Ltd.)	
BP6-1	BarBIQ: accurate identification and quantification of bacter the microbiota using droplets and cellular barcoding Katsuyuki Shiroguchi RIKEN Center for Biosystems Dynamics Research (BDR), Japan	rial cells in

Sponsored States	ymposium 1: Physics and Mechanobiology in Cellular and Systems Room D
16:00-18:20	Physics and Mechanobiology in Cellular and Extracellular Systems
	Sponsor: MEXT KAKENHI Grant-in-Aid for Transformative Research Area (A) "Material properties determine body shapes and their constructions" MEXT KAKENHI Grant-in-Aid for Transformative Research Area (A) "Integration of Extracellular Information by Multimodal ECM Activity"
Chairs	Shinji Deguchi (Osaka University)
	Yasuhiro Inoue (Kyoto University)

\$\$-1-1 Molecular mechanisms regulating mechanotransduction at cell adhesions

Cristina Bertocchi^{1,2}

¹Pontificia Universidad Católica de Chile, Chile, ²Osaka University, Japan

SS-1-2 Dissecting the Mechanical and Dynamic Behaviors of Cells in Silico

Makito Miyazaki², June Hyung Kim¹, <u>Taeyoon Kim</u>¹

¹Weldon School of Biomedical Engineering, Purdue University, West Lafayette, USA, ²RIKEN Center for Biosystems Dynamics Research, Yokohama, Japan

SS-1-3 Statistical mechanics approach to cell-substrate interactions

Shinji Deguchi, Yuika Ueda

Osaka University

SS-1-4 The Role of Environmental Asymmetry in Epithelial Tissue

Yasuhiro Inoue, Kentaro Morikawa

Department of Micro Engineering, Graduate School of Engineering, Kyoto University, Kyoto, Japan

Wednesday, June 26

Morning Som	ninar 2 (GeneFrontier)	Room A
	•	
8:00-8:50	Introduction of the reconstituted cell-free protein synthesis	system,
	the PURE system, for synthetic biology research	
Chair	Takashi Kanamori (GeneFrontier Corporation)	
MS2-1	A reconstituted cell-free protein synthesis for synthetic bio	logy
	research: gene regulation to artificial cell synthesis	
	Tomoaki Matsuura	
	Earth-Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan	

BP Seminar 7 (Refeyn)		' (Refeyn)	Room A	
	12:35-13:35	Mass Photometry - Revolutionary Biophysical Characterization	tion of	
		Single Molecules		
	Chair	Kohei Shiba (Refeyn Japan, K.K.)		
	BP7-1	Tomás de Garay		
		Refeyn Ltd.		

BP Seminar 8	Room B-1	
12:35-13:35	Nanoscale Quantum Biosensors: Imaging Techniques for	
	Measurement	
BP8-1	Ryuji Igarashi ^{1,2,3}	
	¹ Institute for Quantum Life Science, National Institutes for Quantum Science	cience and
Technology, Chiba, Japan, ² School of Life Science and Technology, To		okyo Institute of
Technology, Tokyo, Japan, ³ Graduate School of Science and Engineering, Chib		ring, Chiba
University, Chiba, Japan		

	Room D		
	12:35-13:35	The Story behind the Invention of the Confocal Scanner CS	U
	Chairs	Toshiaki Endou (Yokogawa Electric Corporation)	
		Yoshitaka Sekizawa (Yokogawa Electric Corporation)	
,	BP9-1	The story behind the invention of the confocal scanner CSU	 J
		Takeo Tanaami	

BP Seminar 10 (Digital Bioassay Laboratory, The University of Tokyo and TOPPAN Holdings Inc.)		
12:35-13:35	Digital Bioassay Laboratory in Univ. Tokyo	
Chair	Yoichi Makino (Technical Research Institute, TOPPAN Holdings Inc.)	
BP10-1	Digital bioassay for analyzing Alzheimer's amyloid β-bound extracellular vesicles Kohei Yuyama ¹ , Hui Sun ¹ , Yoichi Makino ² ¹ Faculty of Advanced Life Science, Hokkaido University, Sapporo, Japan, ² Technical Research Institute, TOPPAN Holdings Inc., Saitama, Japan	
BP10-2	Applications of Digital Bioassay Yoshihiro Minagawa ^{1,2} , Hiroshi Ueno ^{1,2} , Hiroyuki Noji ^{1,2} Department of Applied Chemistry, Graduate School of Engineering, The University of Tokyo, Tokyo, Japan, ² Digital Bioanalysis Laboratory, The University of Tokyo, Tokyo, Japan	

Thursday, June 27

Morning Seminar 3 (Avanti Polar Lipids) Room		
8:00-8:50	PROTEIN AGGREGATION AND DISEASES	
Chair	Motomasa Tanaka (RIKEN Center for Brain Science)	
MS3-1	Motomasa Tanaka ¹ , Lukasz A. Joachimiak ² , Eri Chatani ³ ¹ RIKEN Center for Brain Science, Wako, Japan, ² University of Texas Sol Medical Center, Dallas, Texas, USA, ³ Graduate School of Science, Kobe Kobe, Japan	

BP Seminar 1	11 (NIKON SOLUTIONS CO.,LTD.)	Room A
12:35-13:35	From VAAS to NSPARC: 15 Years of Super-Resolution Conf Microscopy	ocal
Chair	Tatsuo Fukui (NIKON SOLUTIONS CO.,LTD.)	
BP11-1	Yasushi Okada ^{1,2,3} ¹ RIKEN Center for Biosystems Dynamics Research (BDR), Osaka, Japan ² Department of Cell Biology, Graduate School of Medicine, the University Tokyo, Japan, ³ Department of Physics, Universal Biology Institute (UBI) a International Research Center for Neurointelligence (WPI-IRCN), the Univ Tokyo, Tokyo, Japan	of Tokyo, and

BP Seminar 12 (Refeyn) Room B-		
12:35-13:35	Mass Photometry - Revolutionary Biophysical Characterization of	
	Single Molecules	
Chair	Kohei Shiba (Refeyn Japan, K.K.)	
BP12-1	Kohei Shiba	
	Refevn Japan K K	

BP Seminar 13 (Evident Corporation) Room D		
12:35-13:35	Reconstitution of actin cytoskeletal dynamics and functions	
BP13-1	Makito Miyazaki ^{1,2}	
	¹ RIKEN Center for Biosystems Dynamics Research, Kanagawa, Japan, ² G	iraduate
	School of Medicine, Science, and Technology, Shinshu University, Nagano,	Japan

BP Seminar 1	BP Seminar 14 (Twist Bioscience) Room E		
12:35-13:35	WeMakeDNA - Approaches to Optogenetics Using Synthetic	ic Genes	
Chair	Masanori Noguchi (Twist Bioscience)		
BP14-1	Structural and Functional Analysis of Light-Gated Ion Chan Assisted by Rapid DNA Synthesis Services Hideaki Kato The University of Tokyo, Tokyo, Japan	nels	

Sponsored Sy Assemblies	ymposium 2: Exploring the Dynamics of Biomolecular Supra- Room A
16:00-18:20	Exploring the Dynamics of Biomolecular Supra-Assemblies:
	Sponsor: JST PRESTO, Dynamic supra-assembly of biomolecular systems
Chairs	Hideki Nakamura (Kyoto University)
	Shunsuke Shimobayashi (Kyoto University)
	Eiji Yamamoto (Keio University)
SS-2-1	Challenging the frontiers of single-molecule or super-resolution live-cell Imaging. Yasushi Okada ^{1,2}
	¹ Dept Cell Biol, Grad Sch Med, Univ Tokyo, ² RIKEN BDR
SS-2-2	Liquid-liquid phase separation and synaptic plasticity Yasunori Hayashi
	Kyoto University Graduate School of Medicine
SS-2-3	Dynamics of phase separated protein condensate materials Yongwon Jung
	Department of Chemistry, Korea Advanced Institute of Science and Technology, Daejon, Korea
SS-2-4	Mega-scale experimental analysis of protein folding stability in
	biology and design
	Kotaro Tsuboyama ¹ , Gabriel Rocklin ²
	¹ IIS, UTokyo, ² Feinberg Medical School, Northwestern University

Thursday, June 27

\$\$-2-5 Manipulating and elucidating nucleation principles of biomolecular condensates in living cells

Shunsuke Shimobayashi Kyoto University, CiRA

\$\$-2-6 Molecular dynamics of intrinsically disordered proteins within protein condensates

Eiji Yamamoto

Department of System Design Engineering, Keio University

Friday, June 28

BP Seminar	BP Seminar 15 (The Biophysical Society of Japan & Acaric.co.ltd.) Room A		
12:35-13:35	Beyond Borders: Insights into International Employment Opportunities		
Chairs	Takayuki Nishizaka (Committee for Gender Equality and Support for Young Researchers, The Biophysical Society of Japan)		
	Daisuke Nakane (Committee for Gender Equality and Support for Young Researchers, The Biophysical Society of Japan)		
BP15-1	Global Employment Trends and Application Tips <u>Toshiaki Kaminaka</u> ¹ , <u>Junko Tamaki</u> ¹ , Daisuke Nakane ² , Takayuki Nishizaka ² ¹ Acaric co. Itd., Tokyo Japan, ² Committee for Gender Equality and Support for Young Researchers, The Biophysical Society of Japan		

BP Seminar 16 (Nagoya Institute of Technology & SHIMADZU CORPORATION) Room B-2		
12:35-13:35	Introduction of Mass Spectrometry Imaging Technology	
Chair	Kota Katayama (Graduate School of Engineering Nagoya Institute of Technology)	
BP16-1	Introduction of Mass Spectrometry Imaging Technology Eiichi Matsuo Analytical & Measuring Instruments Division Shimadzu Corporation, Japan	

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Awards

The following awards will be offered by IUPAB, IUPAB2024 and Biophysical Society of Japan (BSJ).

Awards and Awardees

1. The Avanti Prize Lecture

Location: Room A

Date & time: Monday, June 24 17:00-17:40

Chairs: Manuel Prieto (University of Lisbon, Portugal)

Anthony Watts (University of Oxford, UK)

Awardee: Massimo Olivucci (University of Siena)

2. The Young Investigator Award Lecture

Location: Room A

Date & time: Wednesday, June 26 16:00-16:40

Chairs: Manuel Prieto (University of Lisbon, Portugal)

Anthony Watts (University of Oxford, UK)

Awardee: Hideaki Kato (The University of Tokyo)

3. The Bei Lecture

Location: Room A

Date & time: Thursday, June 27 18:30-19:10

Chair: Tao Xu (National Laboratory of Biomacromolecules, Guangzhou)

Awardee: Xiyun Yan (Institute of Biophysics, Chinese Academy of Sciences)

4. BPS Award Lecture

Location: Room B-1

Date & time: Wednesday, June 26 16:40-17:30

Chair: Kumiko Hayashi (The University of Tokyo)
Presenter: Jennifer Pesanelli (Biophysical Society)
Awardee: Jerelle A. Joseph (Princeton University)

5. ABA Young Investigator Award Lecture

Location: Room E

Date & time: Thursday, June 27 16:00-18:20

Awards

Chairs: Shang-Te Danny Hsu (President of ABA, member of Biophysical Society of

R.O.C, Academia Sinica)

Haibin Su (Member of The Biophysical Society of Hong Kong, Hong Kong

University of Science and Technology)

Awardee: Tetsuhiro S. Hatakeyama (Tokyo Institute of Technology)

6. The 20th Early Career Award in Biophysics Candidate Presentations

Location: Room A

Date & time: Tuesday, June 25 10:00-12:20

Up to five awardees of the Early Career Award in Biophysics will be selected from the candidates, and the rest of the candidates will be given the Early Career Presentation Award. The awardees will be announced at the Conference Dinner.

7. IUPAB2024 Student and Early Career Researcher Poster Award

The awardees will be selected by voting. Please access your "My Page" to vote. You can choose up to 10 nominees.

Names, titles and affiliations of the awardees as well as their presentation title will be announced at the Closing Ceremony of IUPAB2024.

Voting period: Monday, June 24 12:00 – Thursday, June 27 18:30

8. Nakatani Foundation Award

The awardee(s) will be announced at the Conference Dinner.

9. BPS-IUPAB Student Presentation Award

The awardee(s) will be announced at the Conference Dinner.

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