

The 1st Pacific-Rim International Conference on Protein Science

(The 4th Annual Meeting of the Protein Science Society of Japan)



Joint Conference with the Protein Society

14-18 April, 2004

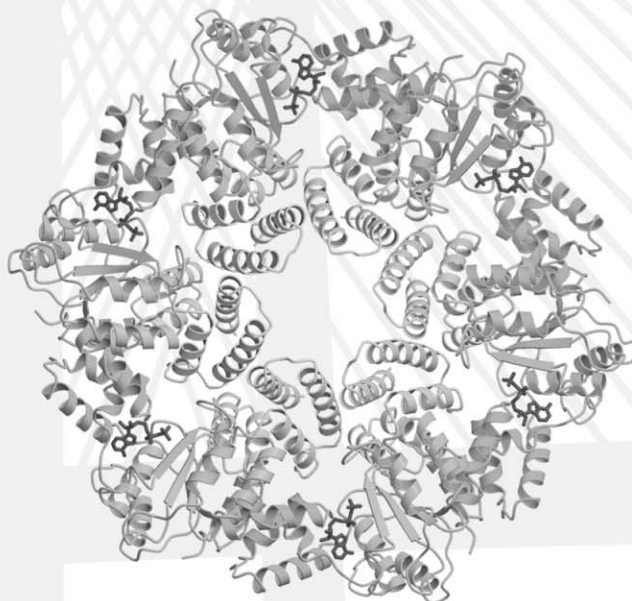
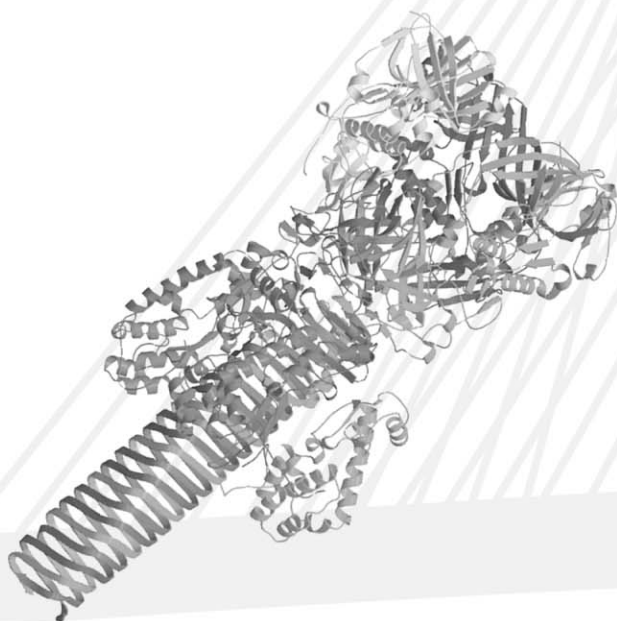
Pacifico Yokohama, Japan

Science Council of Japan / The Protein Science Society of Japan

***"New Approaches to Structure and
Function of Proteins in Pacific-Rim"***



Program & Abstracts



Acknowledgements

This conference was funded in part by

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Yokohama City

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Cooperation

Japan National Tourism Organization



PRICPS2004, the 1st Pacific-Rim International Conference on Protein Science, will be held in Yokohama, Japan on April 14-18 sponsored by the Science Council of Japan and the Protein Science Society of Japan. This is also the first joint conference with the Protein Society. The conference aims at highlighting the current main-stream topics in protein science and also searching for the new direction in the era of post-genome sequencing.

Main Theme

"New Approaches to Structure and Function of Proteins in Pacific-Rim"

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Invitation from Organizing Committee Chair of the PRICPS 2004



A new age is dawning in the field of protein science. The field has rapidly developed in recent years due to the influence of genome projects. The purpose of the First Pacific-Rim International Conference on Protein Science is to announce new findings and analyze future perspectives on the field, as well as to attract young researchers in the post-genome era to this promising field. The conference has been organized by the Protein Science Society of Japan in collaboration with both the Science Council of Japan and the Protein Society. At the conference, young researchers will have the opportunity to hear lectures by world-famous researchers on subjects ranging from structure to function, from new experimental methodology to theoretical calculations, and from physicochemistry to the physiology of proteins. Our hope is that in addition to inspiring young researchers, this conference will contribute to the further development of protein science in Pacific-Rim countries, especially Far Eastern countries.

The conference will be held at Pacifico Yokohama, a well-equipped convention center in the Tokyo-Yokohama region, located on the shore of Tokyo Bay. Due in part to its port, the city of Yokohama is considered a window to foreign countries, and is imbued with an international atmosphere. The city is the second largest city in Japan, second only to Tokyo. Downtown Yokohama has become an attractive destination for young people, and the excellent range of restaurants found there has spurred the growth of tourism.

On behalf of the organizing committee, I would like to welcome all researchers and students in the field of protein science to this conference.

A handwritten signature in cursive script that reads "Tairo Oshima".

Tairo Oshima
Chairperson of the Organizing Committee
Professor of Biochemistry
Tokyo University of Pharmacy and Life Science
Tokyo, Japan

Invitation from the Protein Society



As the President-elect of the Protein Society, I am delighted to support the efforts of the Protein Science Society of Japan and the Science Council of Japan in organizing the PRICPS Meeting in Yokohama, Japan, from April 14th to 18th, 2004. The Protein Society has had a long-standing commitment to international participation in its meetings and to the support of meetings on protein science in other countries around the world. These commitments are made with the realization that discoveries in science know no geographic boundaries and can serve to strengthen the bridges between our cultures and societies.

I am particularly intrigued by the theme of this meeting, "New approaches to structure and function of proteins in the Pacific-Rim". Rapid and dramatic advances in technology have altered the perspective that investigators can bring to problems in protein science. One can begin to think about how our understanding of the structure, function and folding of individual proteins impacts the behavior of cells, organs, and whole organisms. From another perspective, one can consider how the proteome of the various cells in an organism responds to stimuli. From yet another viewpoint, one can survey genomes for insights into similar and different solutions to common problems in catalysis and control mediated by proteins. The opportunities are enormous and exciting.

I encourage the members of the Protein Society and other protein scientists around the world to participate in this meeting. The science shared and the contacts made will enhance the synergy that all meetings hope to achieve.

A handwritten signature in black ink, appearing to read "C. Matthews".

C. Robert Matthews, Ph.D.
Professor and Chair
Biochemistry and Molecular Pharmacology
University of Massachusetts Medical School

Committee Members

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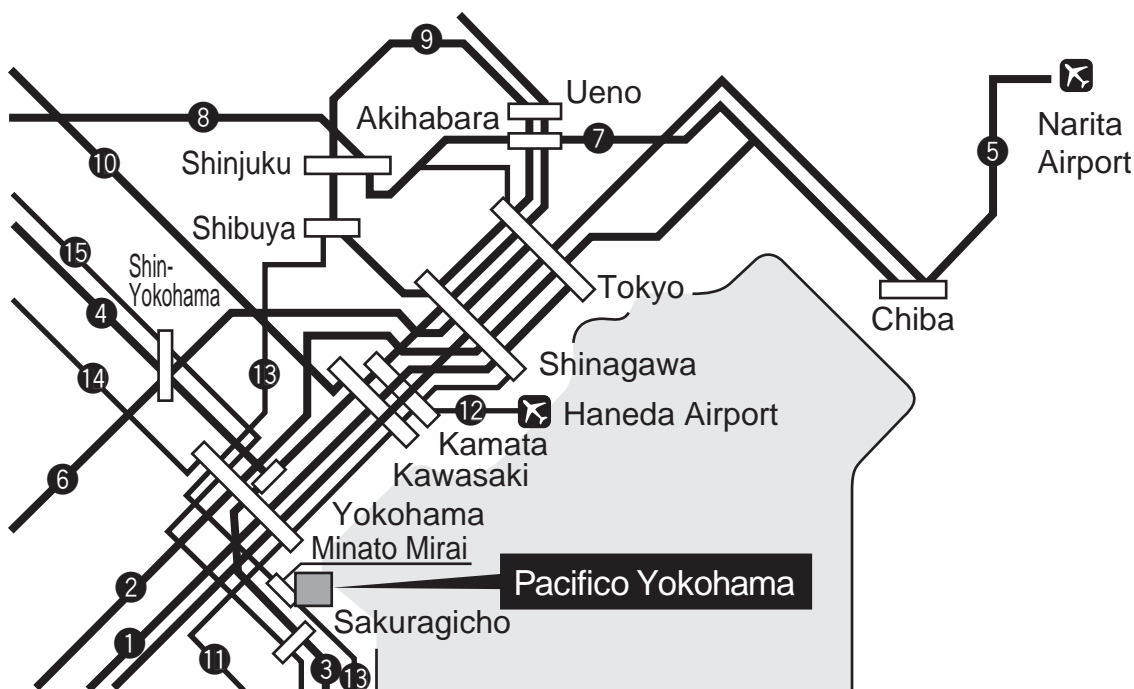
A. Tsugita, *Sci. Univ. of Tokyo*

A. Wada, *RIKEN*

Access Map

Railroad Route Map

- | | |
|--------------|--|
| J R | ① Tokaido Line ② Yokosuka Line ③ Keihin Tohoku Line ④ Yokohama Line ⑤ Narita Express ⑥ Shinkansen (bullet train) ⑦ Soubu Line ⑧ Chuo Line ⑨ Yamanote Line ⑩ Nambu Line |
| Private Line | ⑪ Keihin Kyuko Line ⑫ Keikyu Kuko Line ⑬ Tokyu Toyoko Line & Minato Mirai Line ⑭ Soutetsu Line |
| Subway | ⑮ Yokohama Municipal Subway |



Railway

| | | | |
|---------------------|--|-------------------|--|
| [From Tokyo Area] | | | |
| Tokyo Stn. | 25 min. by JR Tokaido Line, 29min. by JR Yokosuka Line | Yokohama Stn. | |
| | 41 min. by JR Keihin Tohoku Line | Sakuragicho Stn. | |
| Shinagawa Stn. | About 15 min. by Keihin Electric Express Railway | Yokohama Stn. | |
| Shibuya Stn. | About 31 min. by Tokyu Toyoko Line & Minato Mirai Line | Minato Mirai Stn. | |

| | | | |
|-------------------------------|--------------------|-----------------------------|------------------|
| [From Kansai / Chubu areas] | | | |
| Tokaido / Sanyo Shinkansen | Shin-Yokohama Stn. | 15 min. by Municipal Subway | Sakuragicho Stn. |
| | | 15 min. by JR Yokohama Line | Sakuragicho Stn. |
| | | 11 min. by JR Yokohama Line | Yokohama Stn. |

Air plane

| | | | |
|----------------------------|-----------------|------------------------------------|-------------------|
| [From Haneda Airport] | | | |
| 23 min. by monorail | Hamatsuchi Stn. | 38 min. by Keihin Tohoku Line | Sakuragicho Stn. |
| 40 min. by limousine bus | YCAT | 10 min. by Taxi or Bus | Pacifico Yokohama |
| 6 min. by Keikyu Kuko Line | Kamata Stn. | 12 min. by Keihin Electric Express | Yokohama Stn. |

| | | | |
|---------------------------------------|----------------------------|--------------------------|-------------------|
| [From Narita Airport] | | | |
| About 90 minutes by JR Narita Express | | | Yokohama Stn. |
| Limousine Bus 90 minutes | YCAT | Taxi · Bus About 10 min. | Pacifico Yokohama |
| | YOKOHAMA City Air Terminal | | |

Some Limousine Buses travel directly to Pacifico Yokohama via YCAT.

From Minato Mirai Station

| | | |
|----------|-----------------|-------------------|
| [Foot] | About 3 minutes | Pacifico Yokohama |
|----------|-----------------|-------------------|

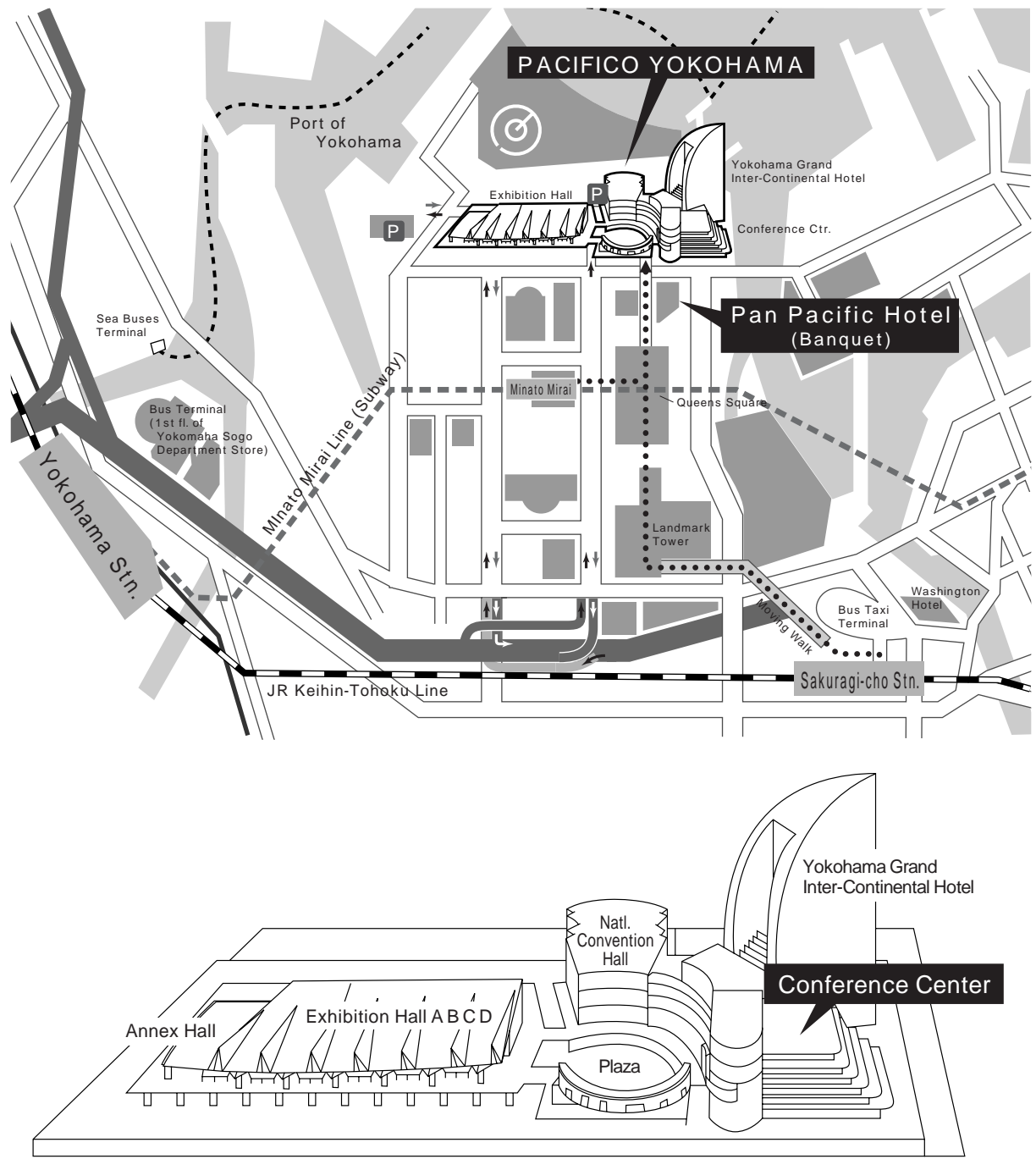
From Sakuragicho Station

| | | |
|----------|---|-------------------|
| [Foot] | About 12 minutes | Pacifico Yokohama |
| [Bus] | Bus Stop No. 4 Route 130, 131, 140 or 141 | Pacifico Yokohama |
| [Taxi] | About 5 minutes | Pacifico Yokohama |

From Yokohama Station

| | | |
|---|---------|-------------------|
| [Railway] | | |
| About 3min. by JR Keihin Tohoku Line or Tokyu Toyoko Line | | Sakuragicho Stn. |
| About 3min. by Minato Mirai Line | | Minato Mirai Stn. |
| [Bus: Yokohama Sogo Bus Terminal] | | |
| Bus stop No. 17 Route 141 | 10 min. | Pacifico Yokohama |
| [Taxi] | | |
| Taxi stand in Porta | 10 min. | Pacifico Yokohama |
| [Sea bus] | | |
| pier adjoining Yokohama Sogo parking garage | 10 min. | Pacifico Yokohama |

Map of Area Around PACIFICO YOKOHAMA



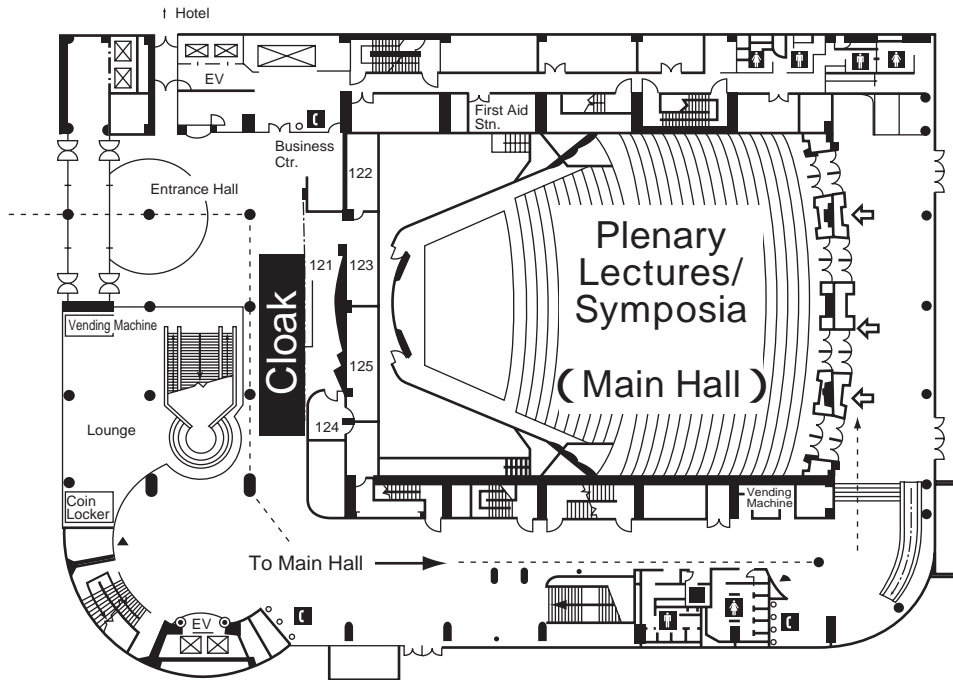
Conference Center

- | | |
|--|---|
| <ul style="list-style-type: none"> 1F Lobby (Cloak) Main Hall (Plenary Lectures / Symposia) 2F Lobby (Registration) 211 (Secretariat) 3F 301 (Workshops / Luncheon Seminars) 302 & Lobby (Scientific Exhibition) 303 (Workshops / Luncheon Seminars) 304 (Workshops / Luncheon Seminars) 311+312 (Posters) 313+314 (Posters) Lounge (Posters) | <ul style="list-style-type: none"> 4F 416+417 (PSSJ General Assembly) 418 (PSSJ Meeting for a Board of Directors, PRICPS International Advisory Committee Meeting) 5F 501+502 (Welcome Reception / Symposia / Luncheon Seminars) 503 (Luncheon Seminar) 511+512 (Satellite Symposium) |
|--|---|

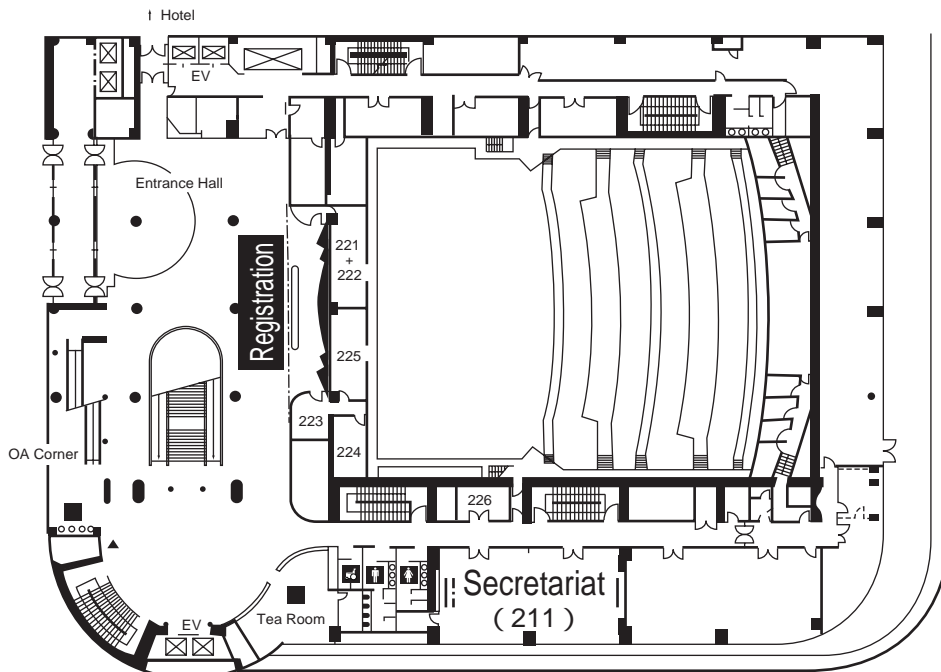
Floor Map (1)

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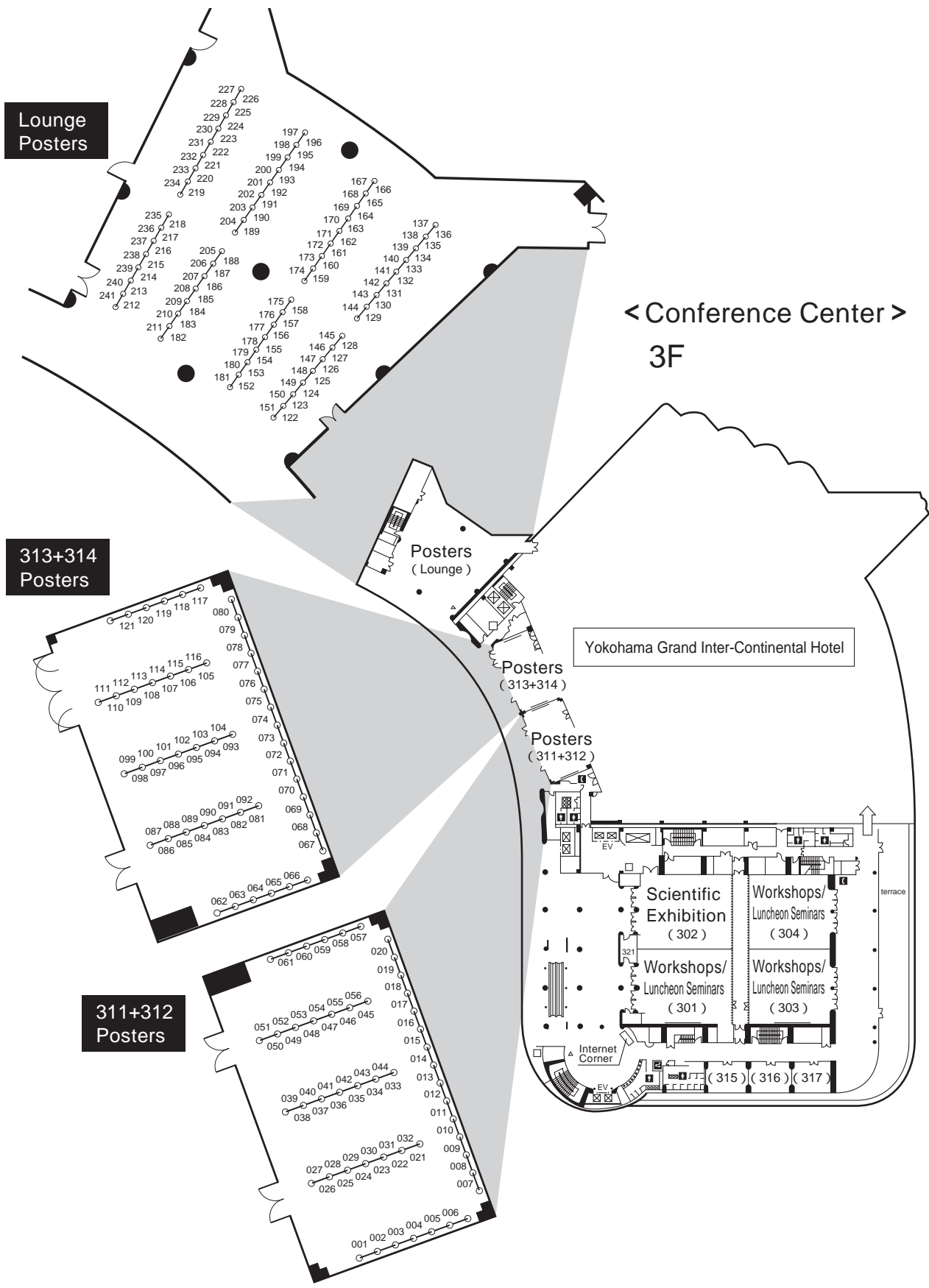
1F



2F

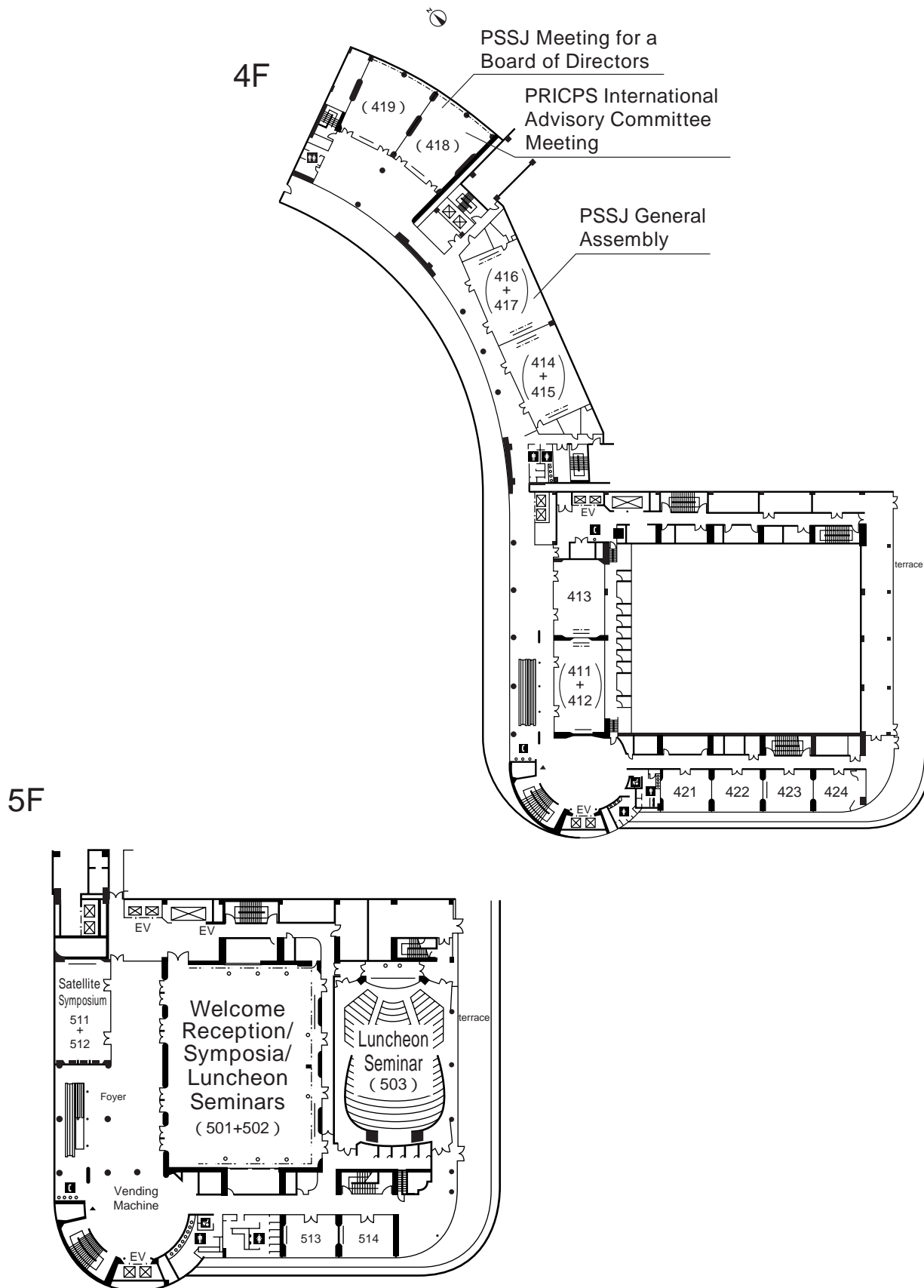


Floor Map (2)



Floor Map (3)

< Conference Center >

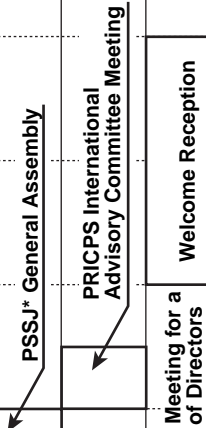


PRICPS 2004 Program at a glance

| | 8:00 | 9:00 | 10:00 | 11:00 | 12:00 | 13:00 | 14:00 | 15:00 | 16:00 | 17:00 | 18:00 | 19:00 | 20:00 | 21:00 |
|-------------------|------|-----------|--|---------------------------|--------------------------------------|--------------------------------------|--------------------------------------|--|--|--|---|--|--|---|
| 14 Apr. Wednesday | | | | | | | | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) | Registration Open (Registration Counter, 2F) |
| 15 Apr. Thursday | | Reg. Open | Workshop on Gender Equality in Protein Science (301) | Open -ing | Plenary Lecture PL-1 (Main Hall, 1F) | Plenary Lecture PL-2 (Main Hall, 1F) | Poster P15/16 (Odd Numbers) | Satellite Symposium (511+512) | PSSJ Meeting for a Board of Directors | PSSJ General Assembly | PRICPS International Advisory Committee Meeting | Workshop W-15f (301) | Workshop W-15g (303) | Workshop W-15h (304) |
| 16 Apr. Friday | | Reg. Open | Symposium S-16a (Main Hall, 1F) | Symposium S-16b (501+502) | | Poster P15/16 (Even Numbers) | Luncheon Seminars | Scientific Exhibition (302 & Lobby) | | | | Workshop W-16f (301) | Workshop W-16g (303) | Workshop W-16h (304) |
| 17 Apr. Saturday | | Reg. Open | Symposium S-17a (Main Hall, 1F) | Symposium S-17b (501+502) | | Poster P17/18 (Odd Numbers) | Luncheon Seminars | Scientific Exhibition (302 & Lobby) | | | | Workshop W-17c (301) | Workshop W-17d (303) | Workshop W-17e (304) |
| 18 Apr. Sunday | | Reg. Open | Symposium S-18a (Main Hall, 1F) | Symposium S-18b (501+502) | Poster P17/18 (Even Numbers) | Scientific Exhibition (302 & Lobby) | Plenary Lecture PL-3 (Main Hall, 1F) | Closing | | | | | | Banquet (Queen's Grand Ball Room, The Pan Pacific Hotel Yokohama) |

Wednesday, April 14

| | 8:00 | 8:30 | 9:00 | 9:30 | 10:00 | 10:30 | 11:00 | 11:30 | 12:00 | 12:30 | 13:00 | 13:30 | 14:00 | 14:30 | 15:00 | 15:30 | 16:00 | 16:30 | 17:00 | 17:30 | 18:00 | 18:30 | 19:00 | 19:30 | 20:00 | 20:30 | 21:00 | |
|----|-------------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--|
| 1F | Main Hall | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 301 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 302 & Lobby | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 303 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 3F | 304 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 311+312 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 313+314 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Lounge | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 416+417 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4F | 418 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 501+502 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5F | 511+512 | | | | | | | | | | | | | | | | | | | | | | | | | | | |



Welcome Reception

Satellite Symposium:
Protein Structure in a Broad Perspective

Satellite Symposium: 13:00 ~ 16:30 PSSJ Meeting for a Board of Directors: 15:30 ~ 16:30 PSSJ General Assembly: 16:30 ~ 17:00
 PRICPS International Advisory Committee Meeting: 17:00 ~ 17:30 Welcome Reception: 18:00 ~ 20:00
 *PSSJ : Protein Science Society of Japan

Thursday, April 15

| | 8:00 | 8:30 | 9:00 | 9:30 | 10:00 | 10:30 | 11:00 | 11:30 | 12:00 | 12:30 | 13:00 | 13:30 | 14:00 | 14:30 | 15:00 | 15:30 | 16:00 | 16:30 | 17:00 | 17:30 | 18:00 | 18:30 | 19:00 | 19:30 | 20:00 | 20:30 | 21:00 |
|----|-------------|------|------|---------|----------------------|----------------------|-------|-------|-------|-------|--|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 1F | Main Hall | | | Opening | Plenary Lecture PL-1 | Plenary Lecture PL-2 | | | | | | | | | | | | | | | | | | | | | |
| | 301 | | | | | | | | | | Luncheon Seminar 1 Merck Ltd., Japan | | | | | | | | | | | | | | | | |
| | 302 & Lobby | | | | | | | | | | Scientific Exhibition | | | | | | | | | | | | | | | | |
| | 303 | | | | | | | | | | Luncheon Seminar 2 Nihon SibirHegner K.K. | | | | | | | | | | | | | | | | |
| | 304 | | | | | | | | | | Luncheon Seminar 3 NIPPON TechnoCluster, Inc. | | | | | | | | | | | | | | | | |
| 3F | 311+312 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 313+314 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Lounge | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4F | 416+417 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 418 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5F | 501+502 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 503 | | | | | | | | | | | | | | | | | | | | | | | | | | |

Workshop on Gender Equality in Protein Science: 8:45 - 9:45 Poster Set-up: 9:00 - 11:00 Scientific Exhibition: 10:00 - 18:00 Opening: 10:00 - 10:30
 Plenary Lectures: 10:30 - 12:30 Luncheon Seminars: 12:40 - 14:10 Poster Presentation: 14:20 - 15:05 Workshops: 15:15 - 17:45 , 18:00 - 20:30

Friday, April 16

| | 8:00 | 8:30 | 9:00 | 9:30 | 10:00 | 10:30 | 11:00 | 11:30 | 12:00 | 12:30 | 13:00 | 13:30 | 14:00 | 14:30 | 15:00 | 15:30 | 16:00 | 16:30 | 17:00 | 17:30 | 18:00 | 18:30 | 19:00 | 19:30 | 20:00 | 20:30 | 21:00 | |
|----|-------------|------|------|---|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--|
| 1F | Main Hall | | | Symposium S-16a: Protein Folding from <i>in vitro</i> to <i>in vivo</i> | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 301 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 3F | 302 & Lobby | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 303 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 304 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 311+312 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4F | 313+314 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Lounge | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 416+417 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5F | 418 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 501+502 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5F | 503 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Scientific Exhibition: 10:00 ~ 18:00 Symposium: 9:00 ~ 12:30 Luncheon Seminars: 12:40 ~ 14:10 Poster Presentation: 14:20 ~ 15:05 Workshops: 15:15 ~ 17:45, 18:00 ~ 20:30 Poster Removal: 17:30 ~ 18:00

Sunday, April 18

| | 8:00 | 8:30 | 9:00 | 9:30 | 10:00 | 10:30 | 11:00 | 11:30 | 12:00 | 12:30 | 13:00 | 13:30 | 14:00 | 14:30 | 15:00 | 15:30 | 16:00 | 16:30 | 17:00 | 17:30 | 18:00 | 18:30 | 19:00 | 19:30 | 20:00 | 20:30 | 21:00 | |
|----|-------------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--|
| 1F | Main Hall | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 301 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 302 & Lobby | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 303 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 304 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 3F | 311+312 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 313+314 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Lounge | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4F | 416+417 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 418 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5F | 501+502 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 503 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Scientific Exhibition: 10:00 ~ 15:00 Symposium: 9:00 ~ 12:30 Poster Presentation: 13:15 ~ 14:00 Plenary Lecture PL-3: 14:10 ~ 15:10 Closing: 15:10 ~ 15:30 Poster Removal: 15:30 ~ 16:00

Registration

Registration

The PRICPS 2004 registration fee includes admission to all sessions, a copy of conference abstracts, admission to welcome reception, exhibition & luncheon seminars, and refreshment breaks each day.

On-site Registration Hours

The registration desk will be open during the following hours.

| | |
|----------------------|-------------|
| 14 April (Wednesday) | 15:00-18:00 |
| 15 April (Thursday) | 08:00-18:00 |
| 16 April (Friday) | 08:00-18:00 |
| 17 April (Saturday) | 08:00-18:00 |
| 18 April (Sunday) | 08:00-16:00 |

Registration Fee (in Japanese yen)

| | Pre-Registration (Before Feb. 29, 2004) | On-site Registration (After Mar. 1, 2004 & On-site) |
|---------------------|--|--|
| Regular | ¥ 25,000 | ¥ 30,000 |
| Student | ¥ 10,000 | ¥ 15,000 |
| Accompanying Guest* | ¥ 10,000 | ¥ 10,000 |
| Banquet** | ¥ 5,000 | ¥ 5,000 |

*Accompanying Guests are spouses, family members and non-professional friends who wish to participate in all conference activities except the technical sessions.

**The limited number of on-site banquet tickets are available at the registration desk.

Payments

Payments can be made by cash or credit card. (American Express, MasterCard, VISA, or Diners Club). For our convenience, payment by credit card is accepted only from overseas participants. Japanese participants (residents) please pay the registration fees by cash. Only Japanese yen is acceptable.

Cancellation & Refunds

Due to advance financial commitments, refunds of registration fees requested after March 1, 2004, cannot be guaranteed. ¥ 5,000 processing fee will be withheld from all refunds. No refunds can be made in respect of the charges for social events.

Instructions for Speakers

Plenary Lectures, Symposia & Workshops

- (1) The allocated time for a speaker differs from each session. Please ask the session organizers.
- (2) The session rooms are equipped with a data projector. Speakers are required to bring their own PC with mini D-sub 15-pin compatible. (Personal computers are not provided by the conference organizer. Overhead projectors, slides etc. are not available.)

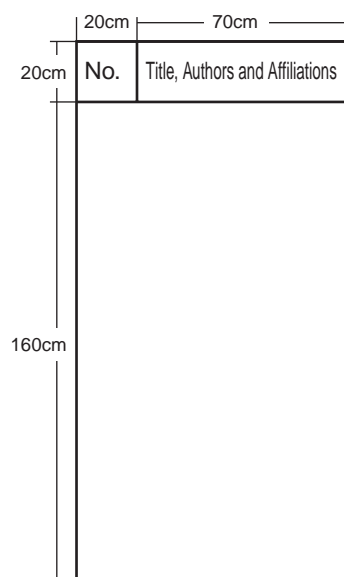
For presentation preview, speakers are requested to drop by the speaker's desk at the front of the session room at least 20 minutes before the presentation to test the projection. After the preview, please remain at the front of the room and wait your turn.

Poster Sessions

- (1) Posters should be displayed for 2 days, 15/16 April or 17/18 April according to the presentation ID.
- (2) Presenters must set-up and remove posters during the assigned time.
- (3) During the presentation time, presenters are requested to remain in front of their poster boards and discuss with other attendees.

| Presentation ID. | | Set-up | Presentation time | Removal |
|------------------|--------------|----------------------|-----------------------|-----------------------|
| P15/16 | Odd Numbers | 9:00-11:00, 15 April | 14:20-15:05, 15 April | 17:30-18:00, 16 April |
| | Even Numbers | | 14:20-15:05, 16 April | |
| P17/18 | Odd Numbers | 9:00-11:00, 17 April | 14:20-15:05, 17 April | 15:30-16:00, 18 April |
| | Even Numbers | | 13:15-14:00, 18 April | |

- (4) The secretariat will provide a poster board (W:90cm x H:180cm) with a poster number (W:20cm x H:20cm). Other than posters, please prepare a header (W:70cm x H:20cm) including a title, authors and affiliations. Chess-pins will be prepared to attach posters.



PRICPS2004

Scientific Events

Luncheon Seminars

Luncheon Seminars organized by the following up-coming scientific companies will be held at lunch time (12:40 ~ 14:10) on 15, 16 and 17 April. The PRICPS 2004 participants are invited to the seminars. (See P.32)

Exhibition

During the Conference, a scientific exhibition will be held at Room 302 & Lobby, 3F. It will offer great opportunity for delegates and exhibitors to meet. The exhibition is opened for 10:00 ~ 18:00 on 15, 16 and 17 and 10:00 ~ 15:00 on 18 April. (See P.255)

Social Events

Welcome Reception

The PRICPS 2004 participants and registered accompanying guests are invited to the welcome reception.

18:00~, Wednesday, 14 April, 2004

Room 501 & 502, 5F, Pacifico Yokohama

Banquet

The banquet will be held in the last evening of the conference. The limited number of on-site banquet tickets are available for ¥ 5,000 per person.

Registered accompanying guests are invited.

Saturday, 17 April, 2004

Queen's Grand Ball Room, The Pan Pacific Hotel Yokohama

19:00~ Welcome Drink

19:30~ Opening Attraction "Wadaiko" (The Japanese drums band)

Banquet



General Information

Hotel Accommodation & Excursion

Kinki Nippon Tourist Co., Ltd. is the official travel agent of PRICPS 2004.

The travel desk is opened by the registration counter during the conference.

Inquiries about hotel reservations, travel and pre- and post-conference sightseeing tours should be directed to Kinki Nippon Tourist Co., Ltd. as follows.

Kinki Nippon Tourist Co., Ltd.

Event, Convention & Congress Dept.

6F, Kyodo Bldg. 2-2 Kanda-Jimbocho, Chiyoda-ku, Tokyo, Japan

TEL: +81-3-3263-5581 FAX: +81-3-3263-5961

E-mail: pricps-ecc@or.knt.co.jp

Secretariat

If you require further information about PRICPS 2004, please contact the conference secretariat.

The secretariat is opened at room 211, 2F.

PRICPS 2004 Secretariat

c/o Center for Academic Societies Japan, Osaka (CASJO)

13F Senri Asahi Hankyu Bldg.,

1-5-3 Shinsenrihigashimachi, Toyonaka, Osaka 560-0082, Japan

TEL. +81-6-6873-2730 FAX. +81-6-6873-2750

E-mail: pricps2004@bcasj.or.jp

Cloak

The cloak room is located on the 1F of the conference center.

Baggages cannot be kept over night. Also, valuables cannot be kept in the cloak room.

Announcement

The message board is located beside the registration counter, 2F. Please write messages and post on the board. (Announcement by microphone or sub-screen is not available.)

Lunch & Refreshment

Luncheon seminars will be held on 15, 16 and 17 April. The participants are invited to the seminars.

There are cafeterias on 6F of the conference center and 2F of the Exhibition Hall. A lot of restaurants and cafes are around the Pacifico Yokohama.

Self-service coffee will be available during the morning session and before the evening session at the lobby of the 3F.

Internet Corner

Internet corner is located on the 3F. A few desktop PCs and free LAN cables are prepared.

Parking Lot

Pacifico Yokohama Underground Parking garage is available for 24 hours.

Related Events

PSSJ Meeting for a Board of Directors

15:30-16:30, 14 April Room 418, 4F

PSSJ General Assembly

16:30-17:00, 14 April Room 416+417, 4F

PRICPS International Advisory Committee Meeting

17:00-17:30, 14 April Room 418, 4F

Satellite Symposium

Protein Structure in a Broad Perspective

Organized by Akinori Kidera, *Yokohama City Univ.*

13:00-16:30, 14 April, 2004

Rm. 511+512 (5F), Pacifico Yokohama

13:00-14:00 **Overview of Protein Folding**

Harold A. Scheraga (*Cornell Univ.*)

14:00-14:45 **Conformational Dynamics of Native Proteins**

Nobuhiro Go (*Japan Atomic Energy Research Inst.*)

15:00-15:45 **A Study of Comparative Genomics based on Domain Structures of Proteins**

Ken Nishikawa (*National Inst. of Genetics*)

15:45-16:30 **Studies on Cooperative Formation, Transformation, and Collapse of Hydrogen-Bonds in Poly (aminoacid ester) s**

Akihiro Abe (*Tokyo Polytechnic Univ.*)

Workshop on Gender Equality in Protein Science

(This session will be held in Japanese.)

“Factors promoting and suppressing the status of female researchers: Comparison with the situation of other countries”

Organized by Working Group on Gender Equality

Yuji Goto (*Osaka Univ.*), Yuriko Yamagata (*Kumamoto Univ.*), Hideki Taguchi (*Tokyo Univ.*), Nozomi Nagano (*AIST*)

8:45 - 9:45, 15 April 2004

Rm. 301 (3F), Pacifico Yokohama

8:45-8:55 **Overview**

Yuji Goto (*Osaka Univ.*)

8:55-9:35 **Comparison of Japan and other countries**

Tomoko Ohnishi (*Univ. of Pennsylvania*) (not confirmed)

Yoko Kimura (*Tokyo Metropolitan Inst. of Medical Science*)

9:35-9:45 **Address to the future**

Mitiko Go (*Nagahama Inst. of Bioscience and Technology*)

Scientific Programme

Opening

15 April

10:00-10:30 Main Hall, 1F

Plenary Lectures

15 April

10:30-11:30 Main Hall, 1F

PL-1 Protein Misfolding and its Links with Human Disease

Christopher M. Dobson (*University of Cambridge, UK*)

Chaired by **Yuji Goto**, *Osaka Univ.*

11:30-12:30 Main Hall, 1F

PL-2 Apoptosis and phagocytosis

Shigekazu Nagata (*Osaka University, Japan*)

Chaired by **Kin-ichiro Miura**, *Proteios Res., Inc.*

18 April

14:10-15:10 Main Hall, 1F

PL-3 Structural and Functional Mapping of the Protein Structure Universe

Sung-Hou Kim (*University of California, Berkeley, USA*)

Chaired by **Masaru Tanokura**, *Univ. of Tokyo*

Symposia

16 April

9:00-12:30 Main Hall, 1F

S-16a: Protein Folding from *in vitro* to *in vivo*

Organizers: **Y. Goto**, *Osaka Univ., Japan*

K. Kuwajima, *Univ. of Tokyo, Japan*

K. Y. Choi, *Pohang Univ. of Science and Technology, Korea*

S-16a-1 Folding Mechanism of Ketosteroid Isomerases

Kwan Yong Choi (*PF & E Lab, Div. of Mol. and Life Sci., POSTECH, Republic of Korea*)

S-16a-2 Order out of chaos: does the ubiquitous TIM barrel motif have a common folding mechanism?

C. Robert Matthews (*Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, United States of America*)

S-16a-3 Mechanical Unfolding of Globular Proteins by Atomic Force Microscopy

Atsushi Ikai (*Laboratory of Biodynamics, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, Japan*)

S-16a-4 The molecular chaperone function of the *Escherichia coli* chaperonin GroEL

Kunihiro Kuwajima (*Department of Physics, School of Science, University of Tokyo, Japan*)

S-16a-5 ALPHA B-CRYSTALLIN, A SMALL HEAT SHOCK PROTEIN WITH CHAPERONE ACTIVITY : INTRACELLULAR LOCALIZATION

Mohan C Rao (*Centre for Cellular and Molecular Biology, Hyderabad, India*)

S-16a-6 Refolding of Recombinant Human Endostatin from *in vitro* to *in vivo*

Qingxin Lei¹, Zhuanglin Li², Hongmei Wang², Guiyong Yuan², Huadong Tang¹, Hao Zhou¹, Yongzhang Luo¹ (*¹Department of Biological Sciences & Biotechnology, Tsinghua University, ²Medgenn Ltd., People's Republic of China*)

S-16a-7 Folding and amyloid fibril formation of β 2-microglobulin

Yuji Goto (*Institute for Protein Research, Osaka University, and CREST, JST, Japan*)

PRICPS2004

9:00-12:30 Rm. 501+502, 5F

S-16b: Proteins for Regeneration and Stem Cells

Organizers: T. Nakano, *Osaka Univ., Japan*

T. Yokota, *Kanazawa Univ., Japan*

- S-16b-1 The homeodomain protein Nanog in mouse embryonic stem cell self-renewal**
Ian P. Chambers, Austin G Smith (*Institute for Stem Cell Research, United Kingdom of Great Britain and Northern Ireland*)
- S-16b-2 Quantitative effects of transcription factors governing cell fate determination of mouse ES cells**
Hitoshi Niwa (*Lab. Pluripotent Cell Studies, RIKEN CDB, Japan*)
- S-16b-3 Self-renewal mechanism of embryonic stem cells**
Takashi Yokota¹, Takahiko Matsuda², Tadayuki Akagi¹, Masayuki Usuda¹, Urara Yoshida-Koide¹, S.A. Jaradat³, Minoru Ko³, Hitoshi Niwa⁴, Hiroshi Koide¹ (¹*Division of Stem Cell Biology, Graduate School of Med. Sci., Kanazawa University*, ²*Dept. of Genetics, Harvard Med. School*, ³*Natl. Inst. of Aging, NIH*, ⁴*Lab. Pluripotent Cell Studies, CDB, RIKEN, Japan*)
- S-16b-4 Systematic analysis of mouse stem cells and early embryos**
Minoru S.H. Ko (*Developmental Genomics & Aging Section, Laboratory of Genetics, National Institute on Aging, National Institutes of Health, United States of America*)
- S-16b-5 Human Embryonic Stem Cells: Development for the Treatment of Degenerative Diseases**
Joseph Gold (*Geron Corporation, United States of America*)
- S-16b-6 Tumor Suppressor, PTEN, as a stem cell regulator**
Toru Nakano¹, Tohru Kimura¹, Akira Suzuki² (¹*DMCB, BIKEN, Osaka University*, ²*Department of Biochemistry, Faculty of Medicine, Akita University, Japan*)
- S-16b-7 Protein expression profiles of liver regeneration-associated cells**
Katsutoshi Yoshizato (*Dept. of Biological Science Grad. Sch. of Science, Hiroshima Univ., JST Innovation Plaza Hiroshima, and Cluster Hiroshima*)
- S-16b-8 THE PROMISE OF STEM CELLS FOR THE TREATMENT OF DIABETES.**
Alan Colman (*ES Cell International, Republic of Singapore*)

17 April

9:00-12:30 Main Hall, 1F

S-17a: Three-dimensional Structural View of DNA Transaction

Organizers: K. Morikawa, *BERI, Japan*

M. Shirakawa, *Yokohama City Univ., Japan*

- S-17a-1 Structure and mechanism of archaeal replication factor C**
Dale B. Wigley (*Cancer Research UK Clare Hall Laboratories, United Kingdom of Great Britain and Northern Ireland*)
- S-17a-2 Three-dimensional structural view of branch migration in DNA homologous recombination**
Kosuke Morikawa (*Biomolecular Engineering Research Institute (BERI), Japan*)
- S-17a-3 PROMISCUITY IN TRANSCRIPTIONAL COREPRESSOR INTERACTIONS**
Ishwar Radhakrishnan (*Department of Biochemistry, Molecular Biology and Cell Biology, Northwestern University, United States of America*)
- S-17a-4 Structure and function of CRSP/Mediator2: a promoter-selective transcriptional co-activator complex.**
Dylan J. Taatjes¹, Tilman Schneider-Poetsch², Robert Tjian² (¹*University of Colorado, Dept. of Chemistry and Biochemistry*, ²*Howard Hughes Medical Institute, Dept. of Molecular and Cell Biology, United States of America*)
- S-17a-5 Chemical modifications of DNA and proteins, which regulate nuclear functions**
Masahiro Shirakawa (*Graduate School of Integrated Science, Yokohama City University, Japan*)

- S-17a-6** **A Dynamic Interplay Between H1 And HMG Proteins In Chromatin Modulates The Histone Code.**
Michael Bustin, Jae-Hwan Lim, Frederic Catez, Yuri V. Postnikov (*Protein Section, National Cancer Institute, NIH, United States of America*)

9:00-12:30 Rm. 501+502, 5F

S-17b: Functional Proteomics: Novel Method and Its Application to Disease-related Proteome Analysis

Organizers: H. Hirano, *Yokohama City Univ., Japan*

T. Isobe, *Tokyo Metropol. Univ., Japan*

- S-17b-1** **Quantitative proteomics to diagnose and study human disease**
Ruedi H. Aebersold, Xiao-Jun Li, Eugene Yi, Parag Mallick, Hui Zhang (*Institute for Systems Biology, United States of America*)
- S-17b-2** **Large-scale analysis of the human ubiquitin-related proteome**
Masaki Matsumoto^{1,2}, Shigetsugu Hatakeyama^{1,2}, Koji Oyamada^{1,2}, Yoshiya Oda^{3,4}, Toshihide Nishimura^{3,5}, Keiichi Nakayama^{1,2} (¹*Dept. Mol. Cell. Biol., Med. Inst. Bioreg., Kyushu Univ.*, ²*CREST, JST*, ³*Div. Mol. Design, Med. Inst. Bioreg., Kyushu Univ.*, ⁴*Lab. Seeds Finding Tech., Eisai Co., Ltd.*, ⁵*Clin. Proteome Ctr., Tokyo Med. Univ., Japan*)
- S-17b-3** **Possible involvement of the nucleolar protein treacle, which is responsible for Treacher Collins syndrome, in human ribosome biogenesis**
Toshiya Hayano^{1,2}, Yoshio Yamauchi^{2,3}, Toshiaki Isobe^{2,3}, Nobuhiro Takahashi^{1,2} (¹*Tokyo Univ. of Agri. & Technol.*, ²*MEXT Integrated Proteomics System Project*, ³*Tokyo Metropolitan Univ., Japan*)
- S-17b-4** **Comprehensive analysis of post-translational modifications of yeast 26S proteasome**
Hisashi Hirano, Yuko Iwafune, Tomoe Nishimura, Yayoi Kimura, Hiroshi Kawasaki (*Yokohama City University, Kihara Institute for Biological Research/Graduate School of Integrated Science, Japan*)
- S-17b-5** **Proteomic analysis of colorectal cancer: strategies for novel biomarker discovery**
Richard J. Simpson, Robert L. Moritz (*Joint ProteomicS Laboratory (JPSSL), Ludwig Institute for Cancer Research & The Walter and Eliza Hall Institute of Medical Research, Australia*)
- S-17b-6** **The application of proteomics to cancer biomarker discovery**
Samir Hanash (*Dept. of Pediatrics, Sch. of Medicine, Univ. of Michigan, United States of America*)

18 April

9:00-12:30 Main Hall, 1F

S-18a: Coupling Mechanism between Electron and Proton Transfers in Respiration System

Organizers: T. Kitagawa, *Okazaki Natl. Res. Inst., Japan*

S. Yoshikawa, *Himeji Inst. Tech., Japan*

- S-18a-1** **The reaction mechanism of proton-translocating NADH-quinone oxidoreductase (complex I)**
Tomoko Ohnishi¹, T. Yano¹, J. J. Johnson², W. R. Dunham³, R. LoBrutto⁴, W. R. Widger² (¹*Johnson Res. Fdn., Dept. Biochem. & Biophys., Univ. Penn.*, ²*Dept. Biol. Biochem., Houston*, ³*Univ. Mich. Medical School*, ⁴*Dept. Plant Biol., Arizona State Univ., United States of America*)
- S-18a-2** **X-ray structure of cytochrome $b_6 f$, the surprising half-brother of the bc_1 complex**
Daniel Picot, David Stroebel, Jean-Luc Popot (*CNRS /Universite Paris-7 UMR 7099, Institut de Biologie Physico-Chimique, French Republic*)
- S-18a-3** **Electron Equilibrium between the Two bL Hemes in the Dimeric Cytochrome bc_1 Complex Facilitates Ubiquinol Oxidation and Retards Superoxide Formation**
Chang-An Yu, Linda Yu (*Department of Biochemistry and Molecular Biology, Oklahoma State University, United States of America*)
- S-18a-4** **Oxygen Activation by Cytochrome c Oxidase as Studied with Resonance Raman Spectroscopy: Implication for Proton Transfer in the Protein**
Takashi Ogura (*Grad. Sch. Sci., Himeji Inst. Tech., Japan*)

S-18a-5 **A Cytochrome c Oxidase Proton Pumping Mechanism that Excludes the O₂ Reduction Site**
Shinya Yoshikawa¹, Tomitake Tsukihara², Hideo Shimada³ (¹*Department of Life Science, Himeji Institute of Technology*, ²*Institute for Protein Research, Osaka University*, ³*Department of Biochemistry, School of Medicine, Keio University, Japan*)

S-18a-6 **Proton and water exit in Cytochrome c Oxidase: specific, reversible paths?**
Denise Mills, Bryan Schmidt, Carrie Hiser, Ling Qin, Yasmin Hilmi, Steve Siebold, Robert Cukier, John McCracken, Shelagh Ferguson-Miller (*Depts of Chemistry and Biochemistry & Molecular Biology, Michigan State Univ., United States of America*)

9:00-12:30 Rm. 501+502, 5F

S-18b: Structural Genomics and Proteomics from the Viewpoint of Structural Biology

Organizers: **K. Miki**, *Kyoto Univ., Japan*

M. Tanokura, *Univ. of Tokyo, Japan*

S-18b-1 **Structural Genomics and Proteomics in Japanese University Community**
Kunio Miki (*Graduate School of Science, Kyoto University, Japan*)

S-18b-2 **Integration of Technologies for Structural Genomics.**
Bi-Cheng Wang (*Southeast Collaboratory for Structural Genomics, Dept. of Biochemistry and Molecular Biology, Univ. of Georgia, United States of America*)

S-18b-3 **Structural Biology as a Partner in Canadian Proteomics Projects.**
Emil F. Pai^{1,2} (¹*Division of Molecular & Structural Biology, Ontario Cancer Institute/University Health Network*, ²*Departments of Biochemistry, Medical Biophysics, and Molecular & Medical Genetics, University of Toronto, Canada*)

S-18b-4 **Structural investigation of antibacterial target proteins**
Se Won Suh (*Department of Chemistry, Seoul National University, Republic of Korea*)

S-18b-5 **SARS Structural Genomics: The First Crystal Structures of SARS Virus Main Protease M^{pro} and Its Complex with an Inhibitor**
Zihe Rao (*Lab. of Structural Biology, Tsinghua Univ. & National Lab. of Biomacromolecules, Inst. of Biophysics, Chinese Academy of Science, People's Republic of China*)

S-18b-6 **Structural Biology on Lipid related proteins: toward the medical and medicinal applications**
Masashi Miyano¹, Hideo Ago¹, Tetsuya Hori¹, Takashi Kumasaka^{1,2}, Tsuyoshi Inoue⁴, Yuko Hisanaga^{1,3}, Daisuke Irikura⁵, Takehiko Yokomizo⁶, Yoshihiro Urade⁵, Takao Shimizu⁶, Osamu Hayaishi⁵ (¹*Structural Biophysics Laboratory, RIKEN Harima Insitute at SPring-8*, ²*Tokyo Institute Technology*, ³*National Cardiovascular Center Research Institute*, ⁴*Osaka University*, ⁵*Osaka BioScience Institute*, ⁶*The University of Tokyo, Japan*)

S-18b-7 **Structural genomics on development and differentiation of organisms and replication and repair of DNA**
Masaru Tanokura (*Dept. of Applied Biological Chemistry, Grad. Sch. of Agricultural and Life Sciences, Univ. of Tokyo, Japan*)

Workshops

15 April

15:15-17:45 Rm. 301, 3F

W-15c: Structural and Functional Networks in the Membrane Interface Area

Organizers: H. Akutsu, *Osaka Univ., Japan*

B.-J. Lee, *Seoul Natl. Univ., Korea*

- W-15c-1 Structural biology of the phagocyte NADPH oxidase**
Fuyuhiko Inagaki (*Division of Structural Biology, Graduate School of Pharmaceutical Sciences, Hokkaido University, Japan*)
- W-15c-2 The M2 Proton Channel from Influenza A Virus: Structural and Functional Studies by Solid-State NMR**
Timothy A. Cross (*Dept. of Chemistry and Biochemistry, Florida State Univ., United States of America*)
- W-15c-3 Structural Analysis of Membrane Peptide and Protein by Multi-Dimensional High-Resolution Solid-State NMR**
Toshimichi Fujiwara (*Institute for Protein Research, Osaka University, Japan*)
- W-15c-4 Structure-activity relationship study of membrane-active antimicrobial peptides from an Asian frog**
Hyung-Sik Won¹, Sang-Ho Park², Seo-Jeong Jung¹, Hyung-Eun Kim¹, Min-Duk Seo¹, Bong-Jin Lee¹
(¹Nat'l Res. Lab. of Membr. Prot. Struct., Col. of Pharm., Seoul Nat'l Univ., Korea, ²Dept. of Chem. and Biochem., Univ. of California, USA, Republic of Korea)
- W-15c-5 Organization of signaling complexes by PDZ-domain scaffold proteins**
Mingjie Zhang, Wei Feng, Jia-fu Long (*Department of Biochemistry, Hong Kong University of Science and Technology, Hong Kong*)

15:15-17:45 Rm. 303, 3F

W-15d: Protein Expression

Organizers: Y. Endo, *Ehime Univ., Japan*

D. A. Vinarov, *Univ. of Wisconsin-Madison, USA*

- W-15d-1 Cell-free protein production in structural proteomics**
Takanori Kigawa¹, Shigeyuki Yokoyama^{1,2,3,4} (*¹Protein Research Group, RIKEN Genomic Sciences Center, ²Cellular Signaling Laboratory, RIKEN Harima Institute at SPring-8, ³Structurome Research Group, RIKEN Harima Institute at SPring-8, ⁴Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo,)*)
- W-15d-2 Systematic Cloning, Expression, and Protein Purification Efforts Applied to Arabidopsis thaliana**
Brian G. Fox (*Department of Biochemistry and Center for Eukaryotic Structural Genomics, United States of America*)
- W-15d-3 High-Throughput, Genome-Scale Protein Production Method Based on the Wheat Germ Cell-Free Expression System**
Yaeta Endo, Tatsuya Sawasaki (*Cell-Free Sciences and Technology Research Center, and Venture Business Laboratory, Ehime University, Japan*)
- W-15d-4 High-Throughput Protein Production for Structural Investigations from a Cell-Free Wheat Germ Expression System**
Dmitriy A. Vinarov, Ejan M. Tyler, John L. Markley (*Center for Eukaryotic Structural Genomics, University of Wisconsin-Madison, USA, United States of America*)
- W-15d-5 Wheat-embryo cell-free protein expression system for protein engineering**
Yuzuru Tozawa¹, Takuya Kanno¹, Nobutaka Hirano², Kazuyuki Takai^{1,2} (*¹Cell-Free Sciences and Technology Research Center, Ehime University, ²Venture Business Laboratory, Ehime University, Japan*)

PRICPS2004

15:15-17:45 Rm. 304, 3F

W-15e: Computer Simulation Enlarging the Protein Landscape

Organizers: A. Kidera, *Yokohama City Univ., Japan*

J. Lee, *KIAS, Korea*

- W-15e-1 Ab initio prediction of protein structure with both all-atom and simplified force fields**
Harold A. Scheraga (*Chemistry & Chemical Biology, Cornell University, United States of America*)
- W-15e-2 Folding of small proteins using a single continuous potential**
Seung-Yeon Kim¹, Julian Lee^{1,2}, Jooyoung Lee¹ (¹*School of Computational Sciences, Korea Institute for Advanced Study,* ²*Department of Bioinformatics and Life Sciences, Soongsil University, Republic of Korea*)
- W-15e-3 Modeling the initial steps of the Zn-assisted folding of zinc-finger proteins**
Todor Dudev, Dimitri Sakharov, Carmay Lim (*Institute of Biomedical Sciences, Academia Sinica, Taiwan*)
- W-15e-4 Theoretical Study of Structural Changes in Proteins Associated with Ligand Binding**
Mitsunori Ikeguchi, Jiro Ueno, Miwa Sato, Akinori Kidera (*Graduate School of Integrated Science, Yokohama City University, Japan*)

18:00-20:30 Rm. 301, 3F

W-15f: Higher Order Structural Dynamics and Their Functional Significance in Sensory Proteins

Organizers: Y. Shiro, *RIKEN Harima Inst. / SPring-8, Japan*

T. Shimizu, *Tohoku Univ., Japan*

- W-15f-1 PAS domains: A versatile way to build a biological switch**
Paul B. Card, Paul J.A. Erbel, Shannon M. Harper, James Lee, Qiong Wu, Kevin H. Gardner (*Department of Biochemistry, University of Texas Southwestern Medical Center, United States of America*)
- W-15f-2 Sensing Mechanism by Heme-based Oxygen Sensor FixL/FixJ System**
Yoshitsugu Shiro, Hiro Nakamura (*RIKEN Harima Institute / SPring-8, Japan*)
- W-15f-3 Structure and Function Relationships of A Heme-regulated Phosphodiesterase from *Escherichia coli* (Ec DOS)**
Hirofumi Kurokawa, Tokiko Yoshimura, Satoshi Hirata, Miki Watanabe, Sue Taguchi, Jotaro Igarashi, Yukie Sasakura, Toshitaka Matsui, Ikuko Sagami, Toru Shimizu (*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, Japan*)
- W-15f-4 Redox Sensing by Human Cystathionine β -Synthase**
Ruma Banerjee (*Dept. of Biochemistry, Univ. of Nebraska, Lincoln, United States of America*)
- W-15f-5 Resonance Raman Investigation on the Sensing and Signaling Mechanisms of the Oxygen Sensing Signal Transducer Protein HemAT-Bs from *Bacillus subtilis***
Takehiro Ohta¹, Hideaki Yoshimura¹, Toshiyuki Kato², Mayumi Matsuki², Hiroshi Nakajima³, Shigetoshi Aono¹, Teizo Kitagawa¹ (¹*Center for Integrative Bioscience, Okazaki National Research Institutes,* ²*School of Materials Science, Japan Advanced Institute of Science and Technology,* ³*Department of Chemistry, Nagoya University, Japan*)
- W-15f-6 Structure and function of the CO-sensing transcriptional activator CoxA**
Shigetoshi Aono (*Center for Integ. Biosci., Okazaki Natl. Res. Inst., Japan*)

18:00-20:30 Rm. 303, 3F

W-15g: G Protein-coupled Receptor and Its Signaling

Organizers: Y. Shichida, *Kyoto Univ., Japan*

Y. Fukada, *Univ. of Tokyo, Japan*

- W-15g-1 Ligand-Protein Interaction Changes in Rhodopsin Revealed by X-ray Crystallography**
Tetsuji Okada^{1,2} (¹*Biological Information Research Center, National Institute of Advanced Industrial Science and Technology,* ²*CREST, JST, Japan*)

- W-15g-2 Insights into Structural Factors Controlling Rhodopsin Stability and Activation.**
David L. Farrens, Jay Janz, Steven E. Mansoor (*Biochemistry and Molecular Biology, Oregon Health and Science Univ., United States of America*)
- W-15g-3 Comparative investigation of G protein activation mechanisms between rhodopsin and mGluR**
Akihisa Terakita^{1,2} (¹*Department of Biophysics, Graduate School of Science, Kyoto University,* ²*Core Research for Evolutional Science and Technology (CREST), Japan Science and Technology Agency, Japan*)
- W-15g-4 Regulation of G β Signaling**
Chang-Seon Myung (*Laboratory in Pharmacology, College of Pharmacy, Chungnam National University, Republic of Korea*)
- W-15g-5 Transgenic Approach to Non-Classical Opsin of Zebrafish Brain**
Daisuke Kojima (*Molecular and Cellular Biology, Harvard University, United States of America*)

18:00-20:30 Rm. 304, 3F

W-15h: Modeling Protein and Domain Interactions toward Understanding Biological Functions

Organizers: M. Go, *Nagahama Inst. Bio-Sci. Tech., Japan*
K. Yura, *JAERI, Japan*

- W-15h-1 Protein complexes and functional pathways in *Saccharomyces cerevisiae***
Nevan J. Krogan¹, Nira Datta¹, Jeffrey Pootoolal¹, Gerard Cagney¹, Guaqing Zhong¹, Grace Guo¹, Huiming Ding¹, Amy Tong¹, Veronica Canadien², Dawn Richards², Bryan Beattie², Jonathan Weissman³, Erin O'Shea³, Charles Boone¹, Andrew Emili¹, Timothy Hughes¹, Jack Greenblatt¹ (¹*Banting and Best Dept. of Medical Research, University of Toronto,* ²*Affinium Pharmaceuticals,* ³*Howard Hughes Medical Institute, University of California, San Francisco, Canada*)
- W-15h-2 Assembly and activities of macromolecular tRNA synthetase complex: Molecular reservoir for signaling network**
Sunghoon Kim (*Center for ARS Network, College of Pharmacy, Seoul National University, Republic of Korea*)
- W-15h-3 Applications of transferred cross-saturation method to larger protein-protein complexes**
Ichio Shimada^{1,2} (¹*Graduate School of Pharmaceutical Sciences, the University of Tokyo,* ²*Biological Information Research Center (BIRC), National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- W-15h-4 Characterization of transient long-range conformational substructure in disordered prion protein repeat peptides probed by combined use of FRET measurements and MD simulations**
Jill E. Gready, Marsia Gustiananda, John R. Liggins, Peter L. Cummins (*Computational Proteomics Group, JCSMR, ANU, Canberra, Australia*)
- W-15h-5 Assessing predictions of protein-protein interaction: The CAPRI experiment**
Joel Janin (*Laboratoire d'Enzymologie et Biochimie Structurales, CNRS, French Republic*)
- W-15h-6 Alternative splicing, protein structure and interaction in human genome**
Mitiko Go (*Department of Bio-Science, Faculty of Bio-Science, Nagahama Institute of Bio-Science and Technology, Japan*)

16 April

15:15-17:45 Rm. 301, 3F

W-16c: *In vivo* Folding, Transport, and Quality Control

Organizers: T. Endo, *Nagoya Univ., Japan*
K. Nagata, *Kyoto Univ., Japan*

- W-16c-1 Cutting into pieces of yeast Sup35 fibers by Hsp104 and heat-aggregates by ClpB**
Masasuke Yoshida^{1,2}, Hideki Taguchi², Yuji Inoue¹, Aiko Kishimoto¹, Shigeko Noma¹, Yo-hei Watanabe¹ (¹*Tokyo Inst. Tech.,* ²*Univ. of Tokyo, Japan*)

- W-16c-2 Protein import into chloroplasts**
Hsou-min Li, Ming-Lun Chou, Shu-Long Tu, Yi-Shan Teng, Yi-Shin Su, Lih-Jen Chen (*Institute of Molecular Biology, Academia Sinica, Taiwan*)
- W-16c-3 Cooperation of translocators in unfolding and import of mitochondrial proteins**
Toshiya Endo (*Dept. of Chemistry, Grad. School of Sci., Nagoya Univ., Japan*)
- W-16c-4 ER-associate degradation: EDEM, soluble EDEM and more...**
Kazuhiro Nagata, Nobuko Hosokawa (*Dept. of Molecular Cellular Biology, Institute for Frontier Medical Sciences, Kyoto Univ. and CREST, JST, Japan*)
- W-16c-5 Roles and regulation of YaeL, a RIP protease involved in the extracytoplasmic stress response in *E. coli*.**
Yoshinori Akiyama, Kazue Kanehara (*Institute for Virus Research, Kyoto University*)

15:15-17:45 Rm. 303, 3F

W-16d: Glycoproteins: Structure-based Functions

Organizers: N. Taniguchi, Osaka Univ., Japan

T. Kawasaki, Kyoto Univ., Japan

- W-16d-1 X-Ray Crystal Structure of the Core 2 beta1,6-N-acetylglucosaminyltransferase in the Presence and Absence of Acceptor Disaccharide**
John E. Pak, Pascal Arnoux, Dengbo Ma, Prashanth Sivarajah, Sihong Zhou, Xuekun Xing¹, Malathy Satkunarajah, James M. Rini (*Dept of Med. Genetics & Microbiology and Biochem., Univ. of Toronto, Canada*)
- W-16d-2 Structure of a human glucuronyltransferase, GlcAT-P, an enzyme critical in the biosynthesis of a neural specific carbohydrate epitope, HNK-1**
Toshisuke Kawasaki¹, Shogo Oka¹, Shinako Kakud¹, Ryuichi Kato², Soichi Wakatsuki², Tomoo Shiba², Masaji Ishiguro³ (*¹Department of Biological Chemistry, Graduate School of Pharmaceutical Sciences, Kyoto University, ²Structural Biology Research Center, Photon Factory, Institute of Materials Structure Science, High Energy Acceleration Research Organization (KEK), ³Suntory Institute for Bioorganic Research*)
- W-16d-3 Molecular dance of Galactosyltransferase: X-ray Snapshots of the conformational changes induced by substrate binding and design of novel glycosyltransferases.**
B. Ramakrishnan^{1,2}, Elizabeth Boeggeman^{1,2}, Velavan Ramasamy¹, Pradman K. Qasba¹ (*¹Structural Glycobiology Section, LECB, CCR, NCI, ²IRSP-SAIC, LECB, CCR, NCI, United States of America*)
- W-16d-4 Structural basis of human α 1,6-Fucosyltransferase**
Hideyuki Ihara¹, Sachiko Toma², Atsushi Nakagawa², Eiji Miyoshi¹, Jianguo Gu¹, Tomitake Tsukihara³, Naoyuki Taniguchi¹ (*¹Department of Biochemistry, Osaka University Medical School, ²Laboratory of Supramolecular Crystallography, ³Division of Protein Crystallography, Institute for Protein Research, Osaka University, Japan*)

15:15-17:45 Rm. 304, 3F

W-16e: Structure and Dynamics of Motor Proteins

Organizers: K. Namba, Osaka Univ., Japan

T. Yanagida, Osaka Univ., Japan

- W-16e-1 An actomyosin motor moves by biased Brownian motion.**
H. Tanaka (*Formation of soft nano-machines, CREST, JST, Japan*)
- W-16e-2 Structural and in vivo analysis of the microtubule tip binding proteins EB1 and Clip-170**
Kevin C. Slep¹, Ronald D. Vale^{1,2} (*¹Department of Cellular and Molecular Pharmacology, University of California San Francisco, ²Howard Hughes Medical Institute, United States of America*)
- W-16e-3 Electron cryomicroscopy of bacterial flagellar structures**
Koji Yonekura^{1,2,3}, Saori Maki-Yonekura³, Keiichi Namba^{2,3} (*¹Department of Biochemistry and Biophysics, University of California, San Francisco, ²Graduate School of Frontier Biosciences, Osaka University, ³Dynamic NanoMachine Project, ICORP, JST, United States of America*)

W-16e-4 The rotary motor in F- and V-type ATPases
 Ricardo A. Bernal, Daniela Stock (*MRC Laboratory of Molecular Biology, United Kingdom of Great Britain and Northern Ireland*)

W-16e-5 Single molecule dynamics of F1-ATPase: Mechanical synthesis of ATP by F1-ATPase
 Hiroyasu Itoh^{1,2}, Kengo Adachi³, Kazuhiko Kinosita, Jr.³ (¹*Tsukuba Research Laboratory, Hamamatsu Photonics*, ²*CREST Formation of Soft Nano-machines Team13**, ³*Center for Integrative Bioscience, Okazaki National Research Institutes, Japan*)

18:00-20:30 Rm. 301, 3F

W-16f: Directed Evolution

Organizers: T. Yomo, Osaka Univ., Japan

W-16f-1 Directed Evolution of Biofunctional Molecules in Phage-displayed Combinatorial Libraries
 Ikuo Fujii^{1,2} (¹*Res. Inst. of Advanced Science and Technology, Osaka Prefecture Univ.*, ²*Biomolecular Engineering Research Institute (BERI), Japan*)

W-16f-2 In vitro selection for biophysical properties of proteins
 Greg Winter, Lutz Riechmann, Stephanie de Bono, Oliver Schon, Kristoffer Famm, Laurent Jespers (*MRC Laboratory of Molecular Biology, United Kingdom of Great Britain and Northern Ireland*)

W-16f-3 Protein evolution - the theory and the practice
 Dan S. Tawfik (*Department of Biological Chemistry, The Weizmann Institute of Science, State of Israel*)

W-16f-4 Experimental molecular evolution from random sequences
 Tetsuya Yomo (*Department of Bioinformatic Engineering, Graduate School of Information Science and Technology, Osaka University, Japan*)

W-16f-5 Evolutionary perspectives on protein stability and robustness
 Richard A. Goldstein (*Department of Mathematical Biology, National Institute for Medical Research, United Kingdom of Great Britain and Northern Ireland*)

18:00-20:30 Rm. 303, 3F

W-16g: Drug Discovery in the Proteome Era

Organizers: M. Ishiguro, Suntory Bioorg. Inst., Japan

T. Matsuzaki, ZOEGENE Corp., Japan

W-16g-1 Structural Mechanism for Transmembrane Signaling by the Atrial Natriuretic Peptide Receptor
 Kunio Misono¹, Haruo Ogawa¹, Yue Qiu¹, Craig M. Ogata² (¹*Department of Molecular Cardiology, Lerner Research Institute, Cleveland Clinic Foundation*, ²*Advanced Photon Source, Argonne National Laboratory, United States of America*)

W-16g-2 Crystal Structure of Bacterial Multidrug Efflux Transporter AcrB
 Akihito Yamaguchi^{1,3}, Satoshi Murakami^{1,3,4}, Ryoichi Nakashima^{1,3}, Eiki Yamashita^{2,3} (¹*Dept. of Cell Membrane Biology, Inst. Sci. Indu. Res., Osaka Univ.*, ²*Inst. Protein Res., Osaka Univ.*, ³*CREST*, ⁴*PRESTO, Japan*)

W-16g-3 Systematic analysis of protein interactions using human full length cDNA
 Tohru Natsume (*AIST, BIRC, Japan*)

W-16g-4 Proteomics and drug target discovery using ProteomIQ™
 Rebecca Harcourt, Jenny Harry (*Proteome Systems, Australia*)

W-16g-5 Accelerating structure based drug design at ActiveSight
 Duncan E. McRee, Mark W. Knuth, Ron V. Swanson, Leslie W. Tari, Michael Wester (*ActiveSight, United States of America*)

PRICPS2004

18:00-20:30 Rm. 304, 3F

W-16h: Molecular Strategy for Designing Robust Proteins

Organizers: K. Yutani, *RIKEN Harima Inst., Japan*

T. Oshima, *Tokyo Univ. Pharm. & Life Sci., Japan*

- W-16h-1** **Structure-Stability-Function Relationships of Thermophile Isopropylmalate Dehydrogenase**
Tairo Oshima (*Dept. of Molecular Biology, Tokyo Univ. of Pharmacy and Life Science, Japan*)
- W-16h-2** **Generating stable ($\beta\alpha$)₈-barrel proteins from half-barrels**
Birte Hocker, Reinhard Sterner (*Univ. of Cologne, Inst. of Biochemistry, Federal Republic of Germany*)
- W-16h-3** **Unusually slow unfolding and refolding rates of pyrrolidone carboxyl peptidase from a hyperthermophile, *Pyrococcus furiosus***
Katsuhide Yutani (*RIKEN Harima Institute, HTPF, Japan*)
- W-16h-4** **Engineering Proteins for Thermostability**
George I. Makhatadze (*Dept. of Biochemistry and Molecular Biology, Pennsylvania State Univ., Coll. of Medicine, United States of America*)
- W-16h-5** **Genome-wide compositional changes of DNA and proteins in thermophilic bacteria for adaptation to higher temperatures**
Ken Nishikawa (*National Institute of Genetics, Japan*)

17 April

15:15-17:45 Rm. 301, 3F

W-17c: Molecular Imaging of Cell Dynamics

Organizers: Y. Yoneda, *Osaka Univ., Japan*

Y. Hiraoka, *Comm. Res. Lab., Japan*

- W-17c-1** **Live imaging of GFP-tagged cohesin and condensin in mammalian cells**
Daniel Gerlich¹, Florine Dupeux², Jan-Michael Peters², Jan Ellenberg¹ (¹*Gene Expression and Cell Biology/Biophysics Programmes, EMBL, Meyerhofstr. 1, D-69117 Heidelberg, Germany*, ²*Research Institute of Molecular Pathology (IMP), Dr. Bohr-Gasse 7, A-1030, Vienna, Austria, Federal Republic of Germany*)
- W-17c-2** **Kinetics of histones in living human cells: roles of H2A variants and factors that regulate histone exchange**
Hiroshi Kimura (*HMRO, School of Medicine, Kyoto University, Japan*)
- W-17c-3** **Interactions of nuclear membrane protein emerin: roles in gene regulation, chromatin structure and actin dynamics**
Katherine L. Wilson², James M. Holaska¹, Rocio Montes de Oca¹, Kathryn Tifft¹, Luiza Bengtsson¹, Michael Zastrow¹, Miriam Segura-Totten² (¹*Dept. of Cell Biology, Johns Hopkins University School of Medicine*, ²*Dept. of Science and Technology, Universidad Metropolitana, Puerto Rico, United States of America*)
- W-17c-4** **Direct visualization of molecular interaction between the nuclear envelope proteins and BAF, a DNA binding protein, in living cells**
Tokuko Haraguchi^{1,2}, Takeshi Shimi^{1,2}, Takako Koujin¹, Yasushi Hiraoka^{1,2} (¹*CREST of JST and Kansai Advanced Research Center*, ²*Graduate School of Science, Osaka University, Japan*)
- W-17c-5** **Single Molecule Imaging and Quantitative Analysis of Molecular Interactions Inside Cells**
Makio Tokunaga^{1,2,3} (¹*Struct. Biol. Ctr., Natl. Inst. of Genetics*, ²*Grad. Univ. for Advanced Studies*, ³*Res. Ctr. for Allergy and Immunology, RIKEN, Japan*)

15:15-17:45 Rm. 303, 3F

W-17d: Ca²⁺ Signalling and Protein Activation Mechanisms

Organizers: M. Ikura, *Univ. Toronto, Canada*

P. L. Davies, *Queen's Univ., Canada*

- W-17d-1 Structure-function of IP3 receptor and its role in cell function**
Katsuhiko Mikoshiba^{1,2,3} (¹*Div. Mol. Neurobiol., Inst. Med. Sci., Univ. Tokyo,* ²*The Brain Science Institute, RIKEN,* ³*Calcium Oscillation Project, JST, Japan*)
- W-17d-2 Structural basis for Ca²⁺ and IP3 signalling**
Mitsu Ikura (*Ontario Cancer Institute and Department of Medical Biophysics, University of Toronto, Canada*)
- W-17d-3 Mechanism of Calcium Dependent Inactivation of Kinesin at Atomic Resolution**
Maia V. Vinogradova¹, Vaka S. Reddy², Anireddy S.N. Reddy², Elena P. Sablin¹, Robert J. Fletterick¹ (¹*Department of Biochemistry/Biophysics, University of California, San Francisco, California, USA,* ²*Department of Biology and Program in Cell and Molecular Biology, Colorado State University, Fort Collins, Colorado, USA*)
- W-17d-4 Photo-induced peptide cleavage for the green-to-red conversion of a fluorescent protein**
Atsushi Miyawaki¹, Hideaki Mizuno¹, Ryoko Ando¹, Satoshi Karasawa¹, Toshiaki Furuta³, Mitsuhiko Ikura² (¹*Brain Science Institute, RIKEN, Japan,* ²*Ontario Cancer Institute, University of Toronto, Canada,* ³*Dept. of Biomolecular Science, Toho University, Japan*)
- W-17d-5 Calcium-dependent regulation of the cysteine protease, calpain**
Peter L. Davies¹, Beatriz Garcia-Diaz¹, Dominic Cuerrier¹, Robert L. Campbell¹, Michael Osbourne², Tudor Moldoveanu², Kalle Gehring² (¹*Department of Biochemistry, Queen's University, Kingston, Ontario, Canada,* ²*Department of Biochemistry, McGill University, Montreal, Quebec, Canada, Canada*)

15:15-17:45 Rm. 304, 3F

W-17e: ABRF Workshop: Recent Technological Advances in Proteomics

Organizers: R. Aebersold, *Inst. for Systems Biol., U.S.A.*

K. Nagai, *Osaka Univ., Japan*

- W-17e-1 The Current Status of Mass Spectrometry Based Proteomics Technology: An Overview**
Ruedi H. Aebersold (*Institute for Systems Biology, United States of America*)
- W-17e-2 Comparative Studies of Gel-based vs. Non gel-based 2-Dimensional Electrophoresis**
Young-Ki Paik (*Yonsei Proteome Research Ctr., and Biomedical Proteome Research Ctr., Yonsei Univ., Republic of Korea*)
- W-17e-3 Identification of gel-separated proteins by mass spectrometry**
Toshifumi Takao¹, Yoshinori Satomi¹, Satoshi Fujita², Yoshinori Tamura² (¹*Institute for Protein Research, Osaka Univ.,* ²*Asahi Technion Co. Ltd., Japan*)
- W-17e-4 LC-MS/MS and LC/LC-MS/MS for large-scale protein analysis**
T. Isobe^{1,2}, Y. Yamauchi^{1,2}, T. Shinkawa^{1,2}, M. Taoka^{1,2}, H. Kaji^{1,2}, T. Hayano^{1,3}, N. Takahashi^{1,3} (¹*Integrated Proteomics System Project, Pioneer Research on Genome the Frontier, MEXT,* ²*Dept. Chemistry, Grad. Science, Tokyo Metropolitan Univ.,* ³*Dept. Biotechnology, United Grad. Agriculture, Tokyo Univ. Agriculture & Technology, Japan*)
- W-17e-5 Protein identification using MS/MS spectra: sequence database searching and data validation**
Alexey I. Nesvizhskii (*Institute for Systems Biology, United States of America*)

Closing

18 April

15:10-15:30 Main Hall, 1F

PRICPS2004

Luncheon Seminars

15 April

12:40-14:10 Rm. 301, 3F

Luncheon Seminar 1

Solving Problems in Protein Expression

Merck Ltd., Japan

メルク株式会社

Chairperson: Ryuta Kaneko (*Life Science Department, Merck Ltd., Japan*)

1. **Solving Problems in Protein Expression** (*Held in Japanese*)

Keiko Kawaguchi, Kumiko Yashiro (*Life Science Department, Merck Ltd., Japan*)

12:40-14:10 Rm. 303, 3F

Luncheon Seminar 2

MicroCalorimetry for Protein Sciences

Nihon SiberHegner K.K.

日本シイベルヘグナー株式会社

Chairperson: Junji Nakamura (*Laboratory Instruments Dept., Nihon SiberHegner K.K.*)

1. **MicroCalorimetry for Protein Sciences** (*Held in English*)

William Gelb (*MicroCal LLC.*)

12:40-14:10 Rm. 304, 3F

Luncheon Seminar 3

蛋白質結晶化システムと観察・解析システムの最前線

NIPPON TechnoCluster, Inc.

ニッポンテクノクラスタ株式会社

1. **The Advantages and Features of the Rombix Vision System**

– **Crystal Imaging Requirements, Software Developments** – (*Held in English*)

David Lorenz (*VP Sales & Marketing, DCA/DataCentric Automation*)

2. **Complete Dispensing Solutions for Protein Crystallization** (*Held in English*)

Barbara McIntosh (*Cartesian Dispensing System, Genomic Solutions, Inc.*)

3. **Cartesian Hummingbird System**を利用した結晶化試薬ならびに蛋白質のナノリッター分注 (*Held in Japanese*)

三城 明 (*プロテインウエーブ株式会社*)

16 April

12:40-14:10 Rm. 301, 3F

Luncheon Seminar 4

Cold-Shock Vector System and RNAi: New Tools for Post-Genomic Research

ポストゲノムを切り拓く2つのツール - コールドショック発現とRNAi -

TAKARA BIO INC.

タカラバイオ株式会社

1. **Tool-1**

Protein production by cold-shock vector (*Held in Japanese*)

大腸菌コールドショック発現系の開発と応用 (*日本語講演*)

高蔵 晃 (*タカラバイオ(株)製品開発センター*)

2. **Tool-2**

RNAi with viral vector and its application (*Held in Japanese*)

ウイルスベクターを用いたRNA干渉とその応用 (*日本語講演*)

峰野純一 (*タカラバイオ(株)細胞・遺伝子治療センター、DNA機能解析センター*)

12:40-14:10 Rm. 303, 3F

Luncheon Seminar 5

Progressive Solutions on Proteomics Research Process by Preparative/Analytical Ultra Centrifugation, 2D-LC and Capillary Electrophoresis

Beckman Coulter K.K.
ベックマン・コールター株式会社

1. Analysis of protein-protein interactions in solution -Feature and advantage of several techniques-

(Held in Japanese)

Susumu Uchiyama *(Department of Biotechnology, Graduate School of Engineering, Osaka University)*

2. Protein differential display by 2D-LC and peptides/carbohydrate conformation analysis by CE-MS

(Held in Japanese)

Etsuo Arai *(Biological Automation, Biomedical Research, Beckman Coulter K.K.)*

12:40-14:10 Rm. 304, 3F

Luncheon Seminar 6

Agilent Technologies "Proteomics Solution Seminar"

Yokogawa Analytical Systems, Inc.
横河アナリティカルシステムズ株式会社

Chairpersons: Rudolf Grimm & Yasushi Konno *(Agilent Technologies, Inc.)*

1. Title-1

Expanding Dynamic Range of Human Serum Protein Detection and Identification by Affinity Removal of Multiple High-Abundant Proteins *(Held in English)*

Rudolf Grimm *(Agilent Technologies Inc., Proteomics Solution Unit)*

2. Titel-2

Mass Spectrometry-based Proteomics: Present and Future *(Held in English)*

Hisaaki Taniguchi *(Inst. Enzyme Reserch. The Univ. of Tokushima)*

12:40-14:10 Rm. 501+502, 5F

Luncheon Seminar 7

Next Generation Technology for Protein Crystallization

Fluidigm Corporation

1. The Topaz™ Screen-to-Beam Solution for Protein Crystallization *(Held in English)*

Kyle Self *(Fluidigm Corporation)*

2. Integrated Fluidic Circuits: The New Paradigm for Protein Crystallization *(Held in English)*

Andrew May *(Fluidigm Corporation)*

PRICPS2004

12:40-14:10 Rm. 503, 5F

Luncheon Seminar 8

Exploring Protein Function by Surface Plasmon Resonance Sensor

-Sail over Functional Proteomics Ocean from Yokohama with Biacore system-

Biacore K.K.
ピアコア株式会社

Chairperson: Setsuko Hashimoto (Biacore K.K.)

1. SPR in functional proteomics. (Held in English)

Robert Karlson (R&D Division Biacore AB, Sweden)

2. Exploiting Biacore® S51 technology in the screening of interactions between human proteins and commonly used drugs. (Held in English)

Yorimasa Suwa (Proteomics Department. REVERSE PROTEOMICS RESEARCH INSTITUTE CO., LTD.)

17 April

12:40-14:10 Rm. 301, 3F

Luncheon Seminar 9

最新プロテオミクステクノロジー「臨床プロテオミクスとFT-ICRMSによるトップダウンプロテオミクス」

Bruker Daltonics K.K.
ブルカー・ダルトニクス株式会社

司会：弦巻誠一郎（ブルカー・ダルトニクス株式会社）

1. The ClinProt System: 質量分析による臨床プロテオミクス（英語講演）

Dagmer Niemeyer (Bruker Daltonik GmbH)

2. FT-ICRMSによるタンパク質翻訳後修飾の同定とトップダウン解析へのアプローチ（日本語講演）

高橋勝利（産業技術総合研究所生命情報科学研究センター）

12:40-14:10 Rm. 303, 3F

Luncheon Seminar 10

Revolution in Highthroughput Protein Purification

~ Introduction of the latest technology in the functional, structural and differential expression analysis ~

タンパク質ハイスループット精製革命

~ 飛躍的な機能・構造解析および発現ディファレンシャル解析の最新事情の紹介 ~

Amersham Biosciences K.K.
アマシャム バイオサイエンス株式会社

Chairperson: Joe Hirano (Amersham Biosciences K.K. Proteomics)
司会：平野 穰（アマシャムバイオサイエンス株式会社プロテオミクス部）

1. -Session1-

The Most Current Tools for Optimized Purification of His-tagged and GST-tagged Proteins (Held in English)

Fredrik Calais (Amersham Biosciences AB, Uppsala, Sweden)

2. -Session2-

Automated multistep purification using ÄKTExpress (Held in English)

Tuomo Frigard (Amersham Biosciences AB, Uppsala, Sweden)

3. -Session3-

Ettan DIGE system: detection of difference in protein abundance and its application to the Post-Translation Modification (PTM) analysis (Held in Japanese)

Junichi Inagawa (Amersham Biosciences K.K. Proteomics)

12:40-14:10 Rm. 304, 3F

Luncheon Seminar 11

State of the art technology for Proteomics Research

Tecan Japan Co., Ltd.
テカン ジャパン株式会社

Chairperson: Tomoyuki Ueno (*Tecan Japan Co., Ltd.*)

- 1. Proteomic characterization of tumors: Identification of metastasis-related markers by statistical analysis of LC/MS peptide profiles** (*Held in Japanese*)
Takao Kawakami (*Clinical Proteome Center, Tokyo Medical University*)
- 2. FFE a perfect complementary separation technique for various approaches in Proteomics** (*Held in English*)
Gerhard Weber (*FFEWeber GmbH, Germany*)
- 3. Automated Protein Crystallization on the Tecan Freedom EVO** (*Held in English*)
Roland Durner (*Tecan Schwiz AG, Switzerland*)

12:40-14:10 Rm. 501+502, 5F

Luncheon Seminar 12

An expansion of application for Single-Molecule Fluorescence Detection System

OLYMPUS CORPORATION K.K.
オリンパス株式会社

Chairperson: Naoaki Okamoto (*Bioscience Division, Life Science Group, OLYMPUS CORPORATION*)

- 1. HT-biochemical analyses of gene products from a cell-free wheat germ translation system** (*Held in Japanese*)
Yaeta Endo (*Ehime University*)
- 2. Application for screening of expressed protein using Single-Molecule Fluorescence Detection System** (*Held in Japanese*)
Tamiyo Kobayashi (*Bioscience Division, Life Science Group, OLYMPUS CORPORATION*)

Poster Sessions

15 & 16 April

Presentation time: Odd Numbers 14:20-15:05, 15 April
Even Numbers 14:20-15:05, 16 April

- P15/16-001 Can an Arbitrary Sequence Evolve Towards Acquiring a Biological Function?**
Yuuki Hayashi¹, Hiroshi Sakata², Yoshihide Makino², Itaru Urabe², Tetsuya Yomo^{1,2,3,4} (¹The Dept. of Bioinfo. Eng., Univ. of Osaka, ²The Dept. of Biotech., Univ. of Osaka, ³Intelligent Cooperation and Control Project, PRESTO, JST, ⁴The Dept. of Pure and Applied Sci., Univ. of Tokyo, Japan)
- P15/16-002 Directed evolution of subtilisin from a hyperthermophilic archaeon by *in vitro* random mutagenesis**
Marian A. Pulido, Kenji Saito, Kazufumi Takano, Masaaki Morikawa, Shigenori Kanaya (Department of Material and Life Science, Graduate School of Engineering, Osaka University, Japan)
- P15/16-003 Evolutionary correlation between foldability and functionality of proteins: Molecular evolution simulation of zinc-binding proteins**
Sotaro Fuchigami¹, Shoji Takada^{1,2} (¹ACT-JST, ²Dept. of Chem., Fac. of Sci., Kobe Univ., Japan)
- P15/16-004 Evolution of proteins of leucine biosynthesis and their related proteins**
Shin-ichi Yokobori¹, Chie Motono², Masatada Tamakoshi¹, Tairo Oshima¹, Akihiko Yamagishi¹ (¹Dept. Mol. Biol., Sch. of Life Sci., Tokyo Univ. Pharm. Life Sci., ²Comput. Biol. Res. Cen., Natl. Inst. Adv. Indust. Sci. Tech., Japan)
- P15/16-005 Cold adaptation of 3-isopropylmalate dehydrogenase of the hyperthermophile *Sulfolobus tokodaii* by evolutionary molecular engineering**
Mayumi Uno, Tairo Oshima, Akihiko Yamagishi (Department of Molecular Biology, School of Life Science, Tokyo University of Pharmacy and Life Science, Japan)
- P15/16-006 X-Ray Structure of Family 8 Chitosanase Suggests a Paradigm of Structural Prosperity from Different Ancestors in Molecular Evolution**
W. Adachi, S. Shimizu, T. Sunami, T. Fukazawa, Y. Sakiyama, M. Suzuki, R. Yatsunami, S. Nakamura, A. Takenaka¹ (Grad. Schl. Biosci. Biotech., Tokyo Institute of Technology, Japan)
- P15/16-007 Generation of functional intrabodies, using phage display**
JungMin Kim¹, Boris Steipe^{1,2} (¹Department of Molecular and Medical Genetics, University of Toronto, ²Department of Biochemistry, University of Toronto, Canada)
- P15/16-008 Functional and folded proteins selected with ribosome display**
Tomoaki Matsuura^{1,3}, Nobuhiko Tokuriki², Testuya Yomo^{1,2}, Andreas Plueckthun⁴ (¹Department of Bioinformatic Engineering, Osaka University, ²Department of Biotechnology, Osaka University, ³PRESTO, JSTA, ⁴Department of Biochemistry, University of Zurich, Switzerland, Japan)
- P15/16-009 Improvement of *in vivo* DNA shuffling system**
Yoshiko Uesugi, Koichi Mori, Masaki Iwabuchi, Tadashi Hatanaka (Research Institute for Biological Sciences, Okayama, Japan)
- P15/16-010 In vitro selection of GTP-binding proteins from the artificial alternative splicing library of estrogen receptor**
Toru Tsuji, Michiko Onimaru, Hideaki Takashima, Yumi Ikeda, Hiroshi Yanagawa (Dept. of Biosciences and Informatics, Faculty of Science and Technology, Keio Univ.)
- P15/16-011 Two-cistronic high-level expression of porcine liver cytochrome P450 reductase solubilized domain in *Escherichia coli***
Shigenobu Kimura, Tomoka Umemura, Yoshikazu Emi, Shin-ichi Ikushiro, Takashi Iyanagi (Dept. of Life Sci., Grad. Sch. of Sci., Himeji Inst. of Tech., Japan)
- P15/16-012 Protein expression system using silkworm pupae**
Akio Shimamura¹, Teruyuki Koyama¹, Mutsumi Futatsumori¹, Mineko Yamaguchi¹, Rie Itoh¹, Shin-ichi Naya¹, Ryohei Satoh^{4,5}, Shigeo Tanaka^{3,4}, Kei-ichi Kanehori^{2,3}, Sumio Sugano⁸, Takao Isogai⁷, Naoki Goshima⁶, Nobuo Nomura⁶ (¹Katakura Industries, ²Hitachi Science Systems, ³JBIC, ⁴Invitrogen Japan, ⁵JBIRC, ⁶BIRC, ⁷REPRORI, ⁸IMS, University of Tokyo, Japan)

- P15/16-013 Genome-wide screening of novel malaria vaccine candidates using wheat-germ cell-free protein synthesis system**
Takafumi Tsuboi¹, Satoru Takeo¹, Osamu Kaneko², Motomi Torii², Yaeta Endo¹ (¹*Cell-free Sci. and Tech. Res. Center, Ehime Univ.*, ²*Dept. of Mol. Parasitol., Ehime Univ. Sch. of Med., Japan*)
- P15/16-014 Synthesis of interleukin [IL]-2 with the wheat germ cell-free *in vitro* translation system.**
Akikazu Asada¹, Shigemichi Nishikawa¹, Takehiro Kokuho², Shigeki Inumaru² (¹*Wakenyaku CO., LTD.*, ²*National Institute of Animal Health, Japan*)
- P15/16-015 Functional expression of *Paracoccus denitrificans* cytochrome c oxidase in an *Eschericia coli* cell-free transcription/translation system**
Yukie Katayama^{1,2}, Takashi Ogura³, Tomitake Tsukihara⁴, Shinya Yoshikawa³, Hideo Shimada¹ (¹*Dept. of Biochem., Sch. of Med. Keio Univ.*, ²*JBIC*, ³*Dept. of Life Science, Himeji Inst. of Tech.*, ⁴*Inst. for Protein Res. Osaka Univ., Japan*)
- P15/16-016 The emerging role of chaperonin in a cell-free translation system**
Bei-Wen Ying¹, Mayumi Kondo², Hideki Taguchi¹, Takuya Ueda¹ (¹*Grad. Sch. Frontier Sci., Univ. Tokyo*, ²*Grad. Sch. Eng., Univ. Tokyo, Japan*)
- P15/16-017 Efficient mass-production of porcine IL-2 by baculovirus/insect cell culture and baculovirus/silkworm gene expression systems**
Shigeki Inumaru¹, Shinji Suegami², Takehiro Kokuho¹, Masaharu Yamamoto², Shigemichi Nishikawa², Satoko Watanabe¹, Takayuki Kubota¹, Keiji Kurata³, Mitsuhiro Miyazawa³ (¹*National Institute of Animal Health*, ²*Wakenyaku Co. Ltd.*, ³*National Institute of Agrobiological Sciences, Japan*)
- P15/16-018 Biotechnological Innovation for Cell-free Based Functional Proteomics**
Tatsuya Sawasaki, Yaeta Endo (*Cell-Free Sciences and Technology Research Center, and Venture Business Laboratory, Ehime University, Japan*)
- P15/16-019 Direct solubilization of active green fluorescence protein and hyperthermophilic archaeon proteins from inclusion bodies**
Mitsuo Umetsu², Kouhei Tsumoto¹, Mitsutaka Terada¹, Yoshikazu Tanaka¹, Tsutomu Arakawa³, Tadafumi Adschiri², Izumi Kumagai¹ (¹*Dept. Biomol. Eng., Grad. Sch. Eng., Tohoku Univ.*, ²*Inst. Mult. Res. Adv. Mat., Tohoku Univ.*, ³*Alliance Protein Lab., Inc., Japan*)
- P15/16-020 Soluble Transition of mammalian TIMP-2 in E. Coli using the modified StEP**
Dong Soon Choi¹, Chunkyu Lee², Sung Soo Kim¹, Churl K. Min², Hyun Joo^{1,2} (¹*Department of Molecular Science and Technology, Ajou University*, ²*Department of Biological Science, Ajou University, Republic of Korea*)
- P15/16-021 Maltose-binding protein promotes effective folding and soluble expression of both high GC and AT-rich coding genes**
Lihuh Ling Goh, Chiah Yian Yo, Tiow-Suan Sim (*Department of Microbiology, Faculty of Medicine, National University of Singapore, Republic of Singapore*)
- P15/16-022 Cloning and expression of three polypeptide release factor genes from *Desulfovibrio vulgaris* (Miyazaki F)**
Masaya Kitamura, Shuko Numata, Hideo Inoue (*Department of Applied and Bioapplied Chemistry, Graduate School of Engineering, Osaka City University, Japan*)
- P15/16-023 Structure analysis of ribosome-RRF complex by cryo-EM**
Takayuki Kato¹, Koji Yonekura^{2,3}, Hitomi Mastuo¹, Masato Yamazaki¹, Takuya Yoshida¹, Tadayasu Ohkubo¹, Keiichi Namba^{2,3}, Yuji Kobayashi¹ (¹*Graduate School of Pharmaceutical Sciences, Osaka university*, ²*Graduate School of Frontier Biosciences, Osaka university*, ³*ICORP, JST, Japan*)
- P15/16-024 The isolation and characterization of transcriptional activator NifA from photosynthetic bacteria, *Ectothiorhodospira halophila***
Hisayoshi Tsuihiji, Hironari Kamikubo, Yoichi Yamazaki, Mikio Kataoka (*Graduate School of Materials Science, Nara Institute of Science and Technology, Japan*)
- P15/16-025 Regulation of gene expression using artificial α -helical coiled-coil motives induced by metal-ion**
Jun Miyata, Yukari Takeshima, Toshihisa Mizuno, Jun-ichi Oku, Toshiki Tanaka (*Graduate School of Material Science, Nagoya Institute of Technology, Japan*)

- P15/16-026 A Statistical Mechanical Model for Protein Folding: A Study on Three-Dimensional Lattice Proteins**
Haruo Abe¹, Hiroshi Wako² (¹*Department of Natural Sciences, Nishinippon Institute of Technology,* ²*School of Social Sciences, Waseda University, Japan*)
- P15/16-027 Thermal unfolding of a (β/α)₈-barrel protein studied by a molecular dynamic simulation**
Satoshi Akanuma^{1,3}, Hiroh Miyagawa^{2,3}, Kunihiro Kitamura^{2,3}, Akihiko Yamagishi^{1,3} (¹*Dept. Mol. Biol., Tokyo Univ. Pharm. Life Sci.,* ²*Taisho Pharm. Co., Ltd.,* ³*JST, BIRD, Japan*)
- P15/16-028 Biological Immune Algorithm for the Protein Folding Problem**
Jing Huang¹, Feng Shi^{2,3} (¹*School of Computer, Wuhan University,* ²*School of Science, Huazhong Agricultural University,* ³*School of Mathematics and Statistics, Wuhan University, People's Republic of China*)
- P15/16-029 A transition state exhibited by a charge-neutralized all-atom protein model.**
Daisuke Mitomo^{1,2}, Keiichiro Maruyama^{1,2}, Junichi Higo^{1,2} (¹*Bioinformatics Labo, Tokyo University of Pharmacy and Life Science,* ²*JST, BIRD, Japan*)
- P15/16-030 Folding simulation of a β -hairpin peptide from the disordered conformations in explicit water**
Narutoshi Kamiya¹, Junichi Higo², Haruki Nakamura³ (¹*Biomolecular Engineering Research Institute,* ²*School of Life Science, Tokyo University of Pharmacy and Life Science,* ³*Institute for Protein Research, Osaka University, Japan*)
- P15/16-031 Correlation between folding rate and contact order studied by a traditional Go lattice model**
Hironori K. Nakamura^{1,2}, Mitsunori Takano¹ (¹*Grad. Sch. of Arts & Sci., Univ. of Tokyo,* ²*ACT-JST, JST, Japan*)
- P15/16-032 Testing protein folding simulations by experiments**
Satoshi Sato, Tomasz Religa, Alan R. Fersht (*MRC Centre for Protein Engineering, United Kingdom of Great Britain and Northern Ireland*)
- P15/16-033 The Storage of Refolding Buffer on the Renaturation Efficiency of Lysozyme**
Hwai-Shen Liu, Steven S.-S. Wang, Che-Kuei Chang, Huei-Mei Liao (*National Taiwan University, Taiwan*)
- P15/16-034 Folding Mechanism of Small Proteins**
Seung-Yeon Kim¹, Julian Lee^{1,2}, Jooyoung Lee¹ (¹*Sch. of Computational Sciences, Korea Inst. for Advanced Study,* ²*Dept. of Bioinformatics and Life Sciences, Soongsil Univ., Republic of Korea*)
- P15/16-035 Characterization of the Folding Intermediate of Ketosteroid Isomerase Modified at the Dimeric Interface**
Bee Hak Hong, Hyung Jin Cha, Chang Wook Park, DoSoo Jang, Kwan Yong Choi (*PF & E Lab, Div. of Mol. and Life Sci., POSTECH, Republic of Korea*)
- P15/16-036 Early folding events of wild type staphylococcal nuclease and a single-tryptophan variant studied by ultrarapid mixing**
Kosuke Maki¹, Hong Cheng², Dmitry Dolgikh², M. C. Ramachandra Shastry², Heinrich Roder² (¹*Department of physics, Graduate school of science, the University of Tokyo,* ²*Institute for Cancer Research, Fox Chase Cancer Center, Japan*)
- P15/16-037 Collapse and search dynamics of apomyoglobin folding revealed by submillisecond observations of α -helical content and compactness**
Takanori Uzawa¹, Shuji Akiyama², Tetsunari Kimura¹, Satoshi Takahashi^{1,3,4}, Koichiro Ishimori¹, Isao Morishima¹, Tetsuro Fujisawa² (¹*Dept. of Mol. Eng., Grad. Sch. of Eng., Kyoto Univ.,* ²*RIKEN Harima Inst./SPRING-8, Struct. Bio. Lab.,* ³*PREST,* ⁴*Inst. for Protein Res., Osaka Univ., Japan*)
- P15/16-038 ϕ value analysis of an allosteric transition of GroEL based on a single-pathway model**
Tomonao Inobe^{1,2}, Kunihiro Kuwajima^{1,2} (¹*Dept. of Physics, Univ. of Tokyo,* ²*CREST, JST, Japan*)
- P15/16-039 Early folding events of dihydrofolate reductase revealed by systematic sequence perturbation analysis**
Munehito Arai, Masahiro Iwakura (*Institute for Biological Resources and Functions, National Institute of Advanced Industrial Science and Technology (AIST), Japan*)

- P15/16-040** **Cancelled**
- P15/16-041** **The inhomogeneous collapse as the initial event of the cytochrome c folding studied by microsecond-resolved near-ultraviolet circular dichroism**
Akira Yane^{1,2}, Takanori Uzawa¹, Yuji Goto², Satoshi Takahashi², Koichiro Ishimori¹, Isao Morishima¹
(¹Dept. of Mol. Eng., Grad. Sch. of Eng., Kyoto Univ., ²Inst. for Protein Res., Osaka Univ., Japan)
- P15/16-042** **Localized Nature of the Transition-State Structure in Goat α -Lactalbumin Folding**
Kimiko Saeki¹, Munehito Arai^{1,2}, Takao Yoda^{1,3}, Masaharu Nakao¹, Kunihiro Kuwajima¹ (¹Department of Physics, Graduate School of Science, University of Tokyo, ²Institute for Biological Resources and Functions, National Institute of Advanced Industrial Science and Technology, ³School of Bioscience, Nagahama Institute of Bio-Science and Technology, Japan)
- P15/16-043** **Construction of an expression system of canine milk lysozyme in the methylotrophic yeast *Pichia pastoris***
Masanori Yasui¹, Yutaka Sasaki¹, Yasuhiro Nonaka¹, Masahiro Watanabe¹, Tomoyasu Aizawa¹, Makoto Demura¹, Keiichi Kawano², Katsutoshi Nitta¹ (¹Div. Biol. Sci., Grad. Sch. Sci., Hokkaido Univ., ²Fac. Pharm. Sci., Toyama Med. Pharm. Univ., Japan)
- P15/16-044** **Volumetric Behavior of the Molten Globule State of Canine Milk Lysozyme**
Masahiro Watanabe¹, Yoshihiro Kobashigawa^{1,2}, Tomoyasu Aizawa¹, Makoto Demura¹, Katsutoshi Nitta¹
(¹Division of Biological Sciences, Graduate School of Science, Hokkaido University, ²Department of Structural Biology, Graduate School of Pharmaceutical Sciences, Hokkaido University, Japan)
- P15/16-045** **Inhibitor-assisted refolding of protease --A protease inhibitor as an intramolecular chaperone**
Shuichi Kojima, Akane Iwahara, Yuri Hisano, Hideyuki Yanai (*Institute for Biomolecular Science, Gakushuin University, Japan*)
- P15/16-046** **Substrate-induced folding of Staphylococcal nuclease**
Masayoshi Onitsuka, Hironari Kamikubo, Yoichi Yamazaki, Yasushi Imamoto, Mikio Kataoka (*Graduate School of Materials Science, Nara Institute of Science and Technology, Japan*)
- P15/16-047** **Influence of experimental conditions and Trp mutations on the folding characteristics of goat α -lactalbumin**
Herman P. Van Dael, Allel Chedad (*Interdisciplinary Research Centre, K.U.Leuven Campus Kortrijk, Kingdom of Belgium*)
- P15/16-048** **Thermal unfolding mechanism of lipocalin-type prostaglandin D synthase**
Takashi Inui^{1,4}, Tsukimi Iida¹, Akiyoshi Tanaka², Tadayasu Ohkubo³, Yoshihiro Urade⁴ (¹Dept. of Food and Nutri., Tsu City Coll., ²Fac. of Bioresources, Mie Univ., ³Fac. of Pharmaceu. Sci., Osaka Univ., ⁴Dept. of Mol. Behav. Biol., Osaka Biosci. Inst., Japan)
- P15/16-049** **Effect of anion species and pH on stability of halorhodopsin**
Megumi Kubo¹, Maki Sato¹, Naoki Kamo², Tomoyasu Aizawa¹, Makoto Demura¹, Katsutoshi Nitta¹ (¹Grad. School Sci., Hokkaido Univ., ²Grad. School Pharma. Sci., Hokkaido Univ., Japan)
- P15/16-050** **Detecting conformational fluctuation of ubiquitin with variable-pressure NMR**
Ryo Kitahara¹, Shigeyuki Yokoyama^{1,2,3}, Kazuyuki Akasaka^{1,4} (¹RIKEN Harima, ²RIKEN GSC, ³Dept. of Biophys. and Biochem., Univ. of Tokyo, ⁴Dept. of Biotech. Sci., Kinki Univ., Japan)
- P15/16-051** **Mechanical Unfolding of Single Green Fluorescent Protein with Atomic Force Microscopy**
Tong Wang^{1,2}, Ken Nakajima³, Atsushi Miyawaki⁴, Masahiko Hara^{1,2} (¹Department of Electronic Chemistry, Tokyo Institute of Technology, ²Frontier Research System, RIKEN, ³Department of Organic and Polymeric Materials, Tokyo Institute of Technology, ⁴Brain Science Institute, RIKEN, Japan)
- P15/16-052** **Mechanical Unfolding of Single Filamin A Molecules and Its Role in the Actin/Filamin A Gel**
Ryoko Sano¹, Tadanao Ito², Kazuyo Ohashi³, Masahito Yamazaki¹ (¹Dept. Physics, Fac. Science, Shizuoka University, ² Dept. Biophysics, Graduate School of Science, Kyoto University, ³Dept. Biology, Fac. Science, Chiba University, Japan)

- P15/16-053** **Detection of Hydrophobic Interactions During RNase A Folding**
Tetsunari Kimura¹, Shuji Akiyama^{1,2}, Satoshi Takahashi^{1,3}, Koichiro Ishimori¹, Isao Morishima¹ (¹*Dept. of Mol. Eng., Kyoto Univ.*, ²*Riken Harima*, ³*Inst. of Protein Res., Osaka Univ., Japan*)
- P15/16-054** **Structural characterization of two-disulfide variants of lysozyme**
Keiko Sakamoto¹, Kouta Yamasaki¹, Kunihiko Okamoto¹, Masaya Kimura¹, Yasuo Noda¹, Hideki Tachibana², Shin-ichi Segawa¹ (¹*School of Science and Technology, Kwansai Gakuin University*, ²*Faculty of Science and Graduate School of Science and Technology, Kobe University, Japan*)
- P15/16-055** **The Stabilization Mechanism of the Extremely Stable Molten Globule State of Canine Milk Lysozyme**
Haruka Miyakita¹, Yasuhiro Nonaka¹, Tomoyasu Aizawa¹, Yoshihiro Kobashigawa^{1,2}, Min Yao¹, Nobuhisa Watanabe¹, Isao Tanaka¹, Makoto Demura¹, Katsutoshi Nitta¹ (¹*Div. of Biol. Sci., Graduate School of Sci., Hokkaido Univ.*, ²*Dept. of Struct. Biol., Graduate School of Pharm. Sci., Hokkaido Univ., Japan*)
- P15/16-056** **What determines the folding rates of non-two-state and two-state proteins?**
Kiyoto Kamagata¹, Munehito Arai², Kunihiro Kuwajima¹ (¹*Department of Physics, School of Science, University of Tokyo*, ²*Institute for Biological Resources and Functions, National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- P15/16-057** **Reversible unfolding of bovine β -lactoglobulin mutants without a free thiol group**
Masanori Yagi, Kazumasa Sakurai, Satoshi Takahashi, Yuji Goto (*Inst. for Prot. Res., Osaka Univ. and CREST, JST, Japan*)
- P15/16-058** **Partially Folded Structures of Equine β -Lactoglobulin Probed by Proline Substitutions**
Kanakano Nakagawa, Akihito Tokushima, Yoshiteru Yamada, Masamichi Ikeguchi (*Department of Bioengineering, Soka University, Japan*)
- P15/16-059** **Cold denaturation of equine β -lactoglobulin**
Yoshiteru Yamada¹, Takeo Yajima¹, Kazuo Fujiwara¹, Munehito Arai², Kazuki Ito³, Kanako Nakagawa¹, Akio Shimizu¹, Hiroshi Kihara⁴, Kunihiro Kuwajima⁵, Yoshiyuki Amemiya⁶, Masamichi Ikeguchi¹ (¹*Dept. of Bioeng., Soka Univ.*, ²*Inst. Bio. Res. Func., AIST*, ³*SSRL/SLAC, Stanford Univ.*, ⁴*Dept. of Phys., Kansai Med. Univ.*, ⁵*Dept. of Phys., Sch. Sci., Univ. of Tokyo*, ⁶*Grad. Sch. of Frontier Sci., Univ. of Tokyo, Japan*)
- P15/16-060** **Amino acid pairs substituted for S-S bond in immunoglobulin fold proteins**
Yoshihisa Hagihara, Noboru Yumoto (*National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- P15/16-061** **Behavior of Hydrated Water in Protein-Protein Interaction**
Teikichi Ikura^{1,2} (¹*School of Biomedical Science, Tokyo Medical and Dental University*, ²*PRESTO, JST, Japan*)
- P15/16-062** **Titration experiment of bovine β -lactoglobulin by using NMR**
Kazumasa Sakurai¹, Masaru Hoshino¹, Yuji Goto^{1,2} (¹*Inst. Protein Res., Osaka Univ.*, ²*CREST/JST, Japan*)
- P15/16-063** **Identification and disruption of a weak protein association: NMR studies on the cytoplasmic Rac1 Binding Domain of Plexin B1**
Yufeng Tong, Matthias Buck (*Department of Physiology & Biophysics, Case Medical School, United States of America*)
- P15/16-064** **Physicochemical Characterization of the Reassembled Dimer of an Oligomeric Integral Membrane Protein OmpF Porin**
Yasushi Watanabe (*Protein Lab., National Food Research Institute, Japan*)
- P15/16-065** **Solution Interactions of Two Baseplate Wedge Components, Gp10 and Gp11, of Bacteriophage T4**
Said A. Ali¹, Allen P. Minton², Fumio Arisaka¹ (¹*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology*, ²*National Institute of Diabetes, Digestive, and Kidney Diseases, National Institutes of Health, Japan*)
- P15/16-066** **Design of a hetero-trimeric α -helical coiled-coil using a cation- π interaction**
Masataka Kawaguchi, Toshihisa Mizuno, Jun-ichi Oku, Toshiki Tanaka (*Dep. of Material Sci., Graduate School of Engineering, Nagoya Inst. of Technology, Japan*)

- P15/16-067** **Experimental and simulation studies of the unfolding of recombinant and authentic α -lactalbumin: Effect of an N-terminal methionine residue.**
Tomotaka Oroguchi¹, Mitunori Ikeguchi², Kimiko Saeki¹, Akinori Kidera², Kunihiro Kuwajima¹ (¹*Department of Physics, University of Tokyo*, ²*Graduate School of Integrated Science, Yokohama City University, Japan*)
- P15/16-068** **ACID INDUCED UNFOLDING AND REFOLDING OF FATTED AND DEFATTED HUMAN SERUM ALBUMIN**
Parveen Salahuddin (*DISC, Interdisciplinary Biotechnology Unit, A.M.U, Aligarh 202002, India, Republic of India*)
- P15/16-069** **pH-induced Conformational Transition of *H. pylori* Acyl Carrier Protein; Insight into the unfolding of Local Structure**
Sun-Bok Jang, Sung-Jean Park, Ji-Sun Kim, Woo-Sung Son, Kyung-Doo Han, Bong-Jin Lee (*Natl. Res. Lab. (MPS), Res. Inst. of Pharmaceutical Sciences, Coll. of Pharmacy, Seoul Natl. Univ., Republic of Korea*)
- P15/16-070** **Non-native structure in the alkaline-denatured pepsin and its implication for folding of the zymogen-derived protein**
Yuji O. Kamatari¹, Chris M. Dobson², Takashi Konno³ (¹*Cellular Signaling Lab., RIKEN Harima Inst., ²Dept. of Chem., Univ. of Cambridge*, ³*Dept. of Mol. Phys. and Biophys., Faculty of Med., Univ. of Fukui, Japan*)
- P15/16-071** **Tissue characterization of protein aggregates or associates in living systems studied by proton NMR spectroscopy ---- protein model system and rat living tissues**
Seiichi Era¹, Masaru Sogami², Kazuo Kato³ (¹*Dept. of Biochem. and Biophys., Gifu Univ. Sch. of Med.*, ²*Gifu Univ.*, ³*Dept. of Pathol., Sch. of Health Sci., Fujita Health Univ., Japan*)
- P15/16-072** **Stabilizing mechanism of collagen triple helical structure**
Yoshinori Nishi¹, Masamitsu Doi², Susumu Uchiyama¹, Yuji Nishiuchi³, Takashi Nakazawa⁴, Tadayasu Ohkubo¹, Yuji Kobayashi¹ (¹*Grad. Sch. of Pharm. Sci., Osaka Univ.*, ²*Dep. of Mat. Sci., Wakayama Nat. Coll. of Tech.*, ³*Peptide Inst. Inc.*, ⁴*Dep. of Chem., Nara Women's Univ., Japan*)
- P15/16-073** **Molecular orientation and protein secondary structure of spider silk and silkworm silk**
Mitsuhiro Miyazawa¹, Norihisa Katayama², Hidetoshi Teramoto¹ (¹*Natl. Inst. of Agrobiol. Sci.*, ²*Graduate School of Natl. Sci., Nagoya City Univ., Japan*)
- P15/16-074** **Analysis of atelocollagen fibril formation by using thioflavin T**
Koichi Morimoto, Kaori Hamano, Kazuyuki Akasaka (*Department of Biotechnological Science, Kinki University, Japan*)
- P15/16-075** **Morphological analysis and hemostatic efficacy of actinidain-processed atelocollagen**
Koichi Morimoto¹, Saori Kunii¹, Takuya Saito¹, Takafumi Yoshikawa², Ben'ichiro Tonomura¹ (¹*Department of Biotechnological Science, Kinki University*, ²*First Department of Pathology, Nara Medical University, Japan*)
- P15/16-076** **Amyloid Database: Toward an Understanding of Amyloid Fibril Formation**
Nami Hirota, Christopher M. Dobson (*Department of Chemistry, University of Cambridge, United Kingdom of Great Britain and Northern Ireland*)
- P15/16-077** **Amyloid Fibril Formation of Human α -Synuclein by Other Amyloid Nuclei Seed**
Hisashi Yagi, Isao Sakane, Kunihiro Hongo, Tomohiro Mizobata, Yasushi Kawata (*Dept. of Biotech., Faculty of Eng. and Graduate School of Med. Sci., Tottori Univ., Japan*)
- P15/16-078** **Temperature dependent conformational changes of α -synuclein observed by CD and NMR spectroscopy**
Yuji O. Kamatari¹, Hiroshi Sawano², Hua Li³, Hiroaki Yamada⁴, Shigeyuki Yokoyama^{1,3,5}, Kazuyuki Akasaka⁶, Makoto Yoshimoto² (¹*Cellular Signaling Lab., RIKEN Harima Inst.*, ²*Molecular Biology Lab., Taisho Pharmaceutical Co., Ltd.*, ³*Genomic Sciences Center, RIKEN Yokohama Inst.*, ⁴*Graduate School of Sci. and Tech., Kobe Univ.*, ⁵*Graduate School of Sci., Univ. of Tokyo*, ⁶*Dept of Biotech. Sci., School of Biology-Oriented Sci. and Tech., Kinki Univ., Japan*)

- P15/16-079** **Effects of the amino acid substitutions in the DE loop of transthyretin on the protein structure and amyloid fibril formation.**
Makoto Takeuchi, Mineyuki Mizuguchi, Atsushi Matsuura, Kimiaki Matsubara, Keiichi Kawano (*Faculty of Pharmaceutical Sciences, Toyama Medical and Pharmaceutical University, Japan*)
- P15/16-080** **Structure, Stability and Cytotoxicity of Transthyretin Variants, Ser23Asn, Pro24Ser, Ile84Thr and Ile84Asn**
Kouhei Igarashi, Kimiaki Matsubara, Mineyuki Mizuguchi, Yoshinori Shinohara, Takahiro Aoki, Yasuhisa Kawaguchi, Keiichi Kawano (*Faculty of Pharmaceutical Sciences, Toyama Medical and Pharmaceutical University, Japan*)
- P15/16-081** **Loss of global cooperativity is a common feature underlying the amyloidogenicity of lysozyme mutations**
Mireille Dumoulin¹, Lode Wyns², David Archer³, Andre Matagne⁴, Christina Redfield⁵, Carol V. Robinson¹, Christopher M. Dobson¹ (¹*Dept of Chemistry, Univ. of Cambridge, Cambridge, UK*, ²*Dept Ultrastructure, VUB, Brussel, Belgium*, ³*School of Life and Environmental Sciences, Univ. of Nottingham, Nottingham, UK*, ⁴*Institut de Chimie B6, Univ. de Liege, Liege, Belgium*, ⁵*OCMS, Univ. of Oxford, Oxford, U.K, United Kingdom of Great Britain and Northern Ireland*)
- P15/16-082** **Amyloid Formation by Bovine beta-Lactoglobulin**
Daizo Hamada¹, Toshiki Tanaka², Naoki Tanaka³, Kentaro Shiraki⁴, Masahiro Takagi⁴, Itaru Yanagihara¹ (¹*Dept of Develop Infect Dis, Res Inst, Osaka Med Cent for Mat and Child Health*, ²*Dept of Mater Sci and Eng, Omohi College, Grad Schl of Eng, Nagoya Inst of Tech*, ³*Dept of Polymer Sci & Eng, Kyoto Inst of Tech*, ⁴*Schl of Mater Sci, Jp Adv Inst of Sci and Tech, Japan*)
- P15/16-083** **Expression and solid-state NMR studies of GST/KSI-fused Yeast prion like protein fragment, supN.**
Jung-Hyun Hwang, Jae-Joon Park, Tae-Joon Park, Yongae Kim (*Dept. of Chemistry, HanKuk Univ. of Foreign Studies, Republic of Korea*)
- P15/16-084** **Amyloid nucleation and hierarchical assembly of Ure2p fibrils: Role of Asn/Gln repeat and non-repeat regions of the prion domain**
Yi Jiang¹, Hui Li², Li Zhu¹, Jun-Mei Zhou¹, Sarah Perrett¹ (¹*Institute of Biophysics, Chinese Academy of Sciences*, ²*Institute of Physics, Chinese Academy of Sciences, People's Republic of China*)
- P15/16-085** **Amyloid fibril formation of β_2 -microglobulin fragment K3 -Effect of pH and disulfide bond-**
Yumiko Ohhashi¹, Kazuhiro Hasegawa², Hironobu Naiki^{2,3}, Yuji Goto^{1,3} (¹*Inst. Protein Res., Osaka Univ.*, ²*Faculty of Med. Sci., Fukui Univ.*, ³*CREST/JST, Japan*)
- P15/16-086** **Amyloid fibril formation and structural stability of β_2 -microglobulin mutants**
Miho Kihara¹, Yoshihisa Hagihara², Kazuhiro Hasegawa³, Hironobu Naiki^{3,4}, Yuji Goto^{1,4} (¹*Inst. Protein Res., Osaka Univ.*, ²*AIST, Special Division for Human Life Technology*, ³*Faculty of Med.Sci., Fukui Univ.*, ⁴*CREST/JST, Japan*)
- P15/16-087** **Folding of β_2 -microglobulin monitored by real-time NMR**
Atsushi Kameda¹, Masaru Hoshino¹, Takashi Higurashi^{1,2,4}, Hironobu Naiki^{3,4}, Yuji Goto^{1,4} (¹*Inst. Protein Res., Osaka Univ.*, ²*SPring-8/JASRI*, ³*Faculty of Med. Sci., Fukui Univ.*, ⁴*CREST/JST, Japan*)
- P15/16-088** **Calorimetric Analysis of the Amyloid Fibril Extension Reaction**
Kaori Yamamoto¹, Jozsef Kardos¹, Kazuhiro Hasegawa², Hironobu Naiki^{2,3}, Yuji Goto^{1,3} (¹*Inst. Protein Res., Osaka Univ.*, ²*Dept. Pathol., Fukui Univ.*, ³*CREST/JST, Japan*)
- P15/16-089** **Beta2-microglobulin amyloidosis: a comparative study of aggregates with different morphologies**
Jozsef Kardos¹, D. Okuno², T. Nakamura³, M. Sakai¹, T. Kawai³, Y. Schimizu⁴, Y. Yumoto⁴, T. Kitagawa², H. Naiki⁵, Yuji Goto¹ (¹*Inst Prot Res, Osaka Univ.*, ²*Inst Mol Sci Okazaki Nat Res Inst*, ³*Inst of Sci and Ind Res, Osaka Univ.*, ⁴*Nat Inst of Adv Industrial Sci and Tech, Ikeda*, ⁵*Dept Pathol, Fukui Med Univ, Japan*)
- P15/16-090** **Alcohol induced-amyloid fibril formation of a peptide fragment of β_2 -microglobulin**
Keiichi Yamaguchi¹, Takashi Kanno², Tomoji Kawai², Hironobu Naiki^{3,4}, Yuji Goto^{1,4} (¹*Inst. Protein Res., Univ. of Osaka*, ²*Inst. Sci. Ind. Res., Univ. of Osaka*, ³*Dept. Pathology 2, Univ. of Fukui Med.*, ⁴*CREST, Japan*)

- P15/16-091 Mutation analysis of CAD domain and its fibril formation**
 Tsutomu Nakamura, Atsuko Kobayashi, Yoshihisa Hagihara, Noboru Yumoto, Koichi Uegaki (*Special Division for Human Life Technology, National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- P15/16-092 Stereospecific inhibition of A β (25-35) amyloid fibril formation**
 Tadato Ban¹, Kazuhiro Hasegawa², Hironobu Naiki^{2,3}, Yuji Goto^{1,3} (*¹Institute for Protein Research, Osaka University, ²Department of Pathology, Fukui University, ³CREST/JST, Japan*)
- P15/16-093 Fibrous assembly of the amphipathic α -helix forming polypeptides**
 Toshiaki Takei¹, Kazuya Hasegawa², Keiichi Namba³, Shuhei Tanaka⁴, Atsuo Tamura⁴, Tetsuo Oikawa⁵, Kazumori Yazaki^{1,6}, Shuichi Kojima¹, Kin-ichiro Miura^{1,7} (*¹Inst. for Biomol. Sci. Gakushuin Univ., ²Spring-8/JASRI, ³Grad. Sch. Front. Biosci., Osaka Univ., ⁴Grad. Sch. of Sci. and Tec., Kobe Univ., ⁵JEOL Ltd., ⁶Tokyo Metropol. Inst. of Med. Sci., ⁷Proteios Research Inc., Japan*)
- P15/16-094 Creation of a new biomaterial by the self-assembled peptide nanofiber**
 Masanori Kiyozono¹, Shuhei Tanaka¹, Yasuko Mukai¹, Masanori Kawabata¹, Atsuo Tamura^{1,2} (*¹Grad. Sch. of Sci. and Tech., Kobe Univ., ²PRESTO, Japan Sci. and Tech. Co., Japan*)
- P15/16-095 Interactions between amino-acid residues responsible for forming amyloid-like fibrils**
 Masatoshi Saiki^{1,2}, Kazunori Kawasaki², Deshan Zhou^{2,3}, Shinya Honda², Takeo Konakahara¹, Hisayuki Morii² (*¹Dept. of Ind. Chem., Tokyo Univ. of Science, ²Natl. Inst. of Adv. Ind. Sci. Technol., ³Chongqing Res. Inst. of Neurosci., Japan*)
- P15/16-096 Depolymerization of β_2 -microglobulin amyloid fibril induced by high pressure**
 Eri Chatani¹, Azusa Okamoto¹, Michiko Kato², Hironobu Naiki^{3,4}, Yuji Goto^{1,4} (*¹Institute for Protein Research, Osaka University, ²Department of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, ³Department of Pathological Sciences, University of Fukui, ⁴CREST, Japan Science and Technology Corporation, Japan*)
- P15/16-097 Calorimetric Determination of the Thermal Stability of β 2-Microglobulin Amyloid Fibrils**
 Kenji Sasahara^{1,2}, Jozsef Kardos^{1,2}, Hironobu Naiki^{1,3}, Yuji Goto^{1,2} (*¹CREST, Japan Science and Technology Corporation, ²Institute for Protein Research, Osaka University, ³Department of Pathological Sciences, Faculty of Medical Sciences, University of Fukui, Japan*)
- P15/16-098 The effect of hydrophobic groups on the surface of protein molecule toward the thermodynamic stability: DSC analysis of hen egg-white lysozymes with completely acylated amino groups**
 Yoshiya Matsuhashi, Shigeyoshi Nakamura, Shun-ichi Kidokoro (*Dept. Bionegineer., Nagaoka Univ. Tech., Japan*)
- P15/16-099 Solvent-Exposed Hydrophobic Cluster Contributes to Conformational Stability and Steroid Binding in Ketosteroid Isomerase from *Pseudomonas putida* Biotype B**
 Young Sung Yun, Gyu Hyun Nam, Yeon-Gil Kim, Byung-Ha Oh, Kwan Yong Choi (*Division of Molecular and Life Sciences, Pohang University of Science & Technology, Republic of Korea*)
- P15/16-100 Mutational and Structural-based Analyses of Osmolyte Effect on Protein Stability**
 Kazufumi Takano^{1,2}, Minoru Saito³, Masaaki Morikawa¹, Shigenori Kanaya¹ (*¹Department of Material and Life Science, Osaka University, ²PRESTO, JST, ³Faculty of Science and Technology, Hirosaki University, Japan*)
- P15/16-101 Thermostability of ancestral mutant 3-isopropylmaltose dehydrogenases of a thermophilic bacteria designed by using a phylogenetic tree**
 Keiko Watanabe¹, Takatoshi Ohkuri^{1,2}, Shin-ichi Yokobori¹, Tairo Oshima¹, Akihiko Yamagishi^{1,3} (*¹Dept. Mol. Biol., Tokyo Univ. Pharm. and Life Sci., ²Grad. Sch. Pharm. Sci. Kyush. Univ, ³JST-BIRD, Japan*)
- P15/16-102 The pH dependence of the enthalpy and the heat capacity of molten globule state of cytochrome c evaluated by isothermal acid-titration calorimetry**
 Shigeyoshi Nakamura, Shun-ichi Kidokoro (*Dept. Bioengineer., Nagaoka Univ. Tech., Japan*)
- P15/16-103 Protein thermodynamic structure and protein properties**
 Qinyi Zhao (*China rehabilitation research center, People's Republic of China*)

- P15/16-104 Mechanism of Thermostabilization in a Designed Cold Shock Protein with Optimized Surface Electrostatic Interactions.**
Alexey V. Gribenko, Vakhtang V. Loladze, Marimar Lopez, Jessica L. Wolgemuth, Samantha S. Strickler, George I. Makhatadze (*Pennsylvania State University College of Medicine, United States of America*)
- P15/16-105 Stability of Ribonuclease HII from Hyperthermophile, *Thermococcus kodakaraensis***
Atsushi Mukaiyama¹, Kazufumi Takano¹, Mitsuru Haruki^{1,2}, Masaaki Morikawa¹, Shigenori Kanaya¹ (¹*Department of Material and Life Science, Osaka University,* ²*Department of Material Chemistry and Engineering, Nihon University, Japan*)
- P15/16-106 An Experimental And Computational Approach Applied To Cancer Associated Variants Of A DNA Repair Enzyme Ape1- Mutations That Affect Protein Stability**
Masood Z. Hadi¹, Peter T. Beernink², Daniel Barsky², David M. Wilson³ (¹*Biosystems Research Department, Sandia National Laboratory,* ²*Biology and Biotechnology Research Program, Lawrence Livermore National Laboratory,* ³*Laboratory of Molecular Gerontology, National Institute on Aging, IRP, NIH, United States of America*)
- P15/16-107 Origins of protein stability revealed by comparing crystal structures of TATA-binding proteins**
Hideaki Koike¹, Yoshie Kawashima Ohya¹, Tomoko Yamasaki¹, Lester Clowney¹, Yoshio Katsuya², Masashi Suzuki¹ (¹*National Institute of Advanced Industrial Science and Technology (AIST),* ²*Hyogo Prefectural Institute of Industrial Research, Japan*)
- P15/16-108 Molecular Dynamics Study of a Hyperthermophilic, a Thermophilic, and Mesophilic Cold Shock Proteins**
Chie Motono, Makiko Suwa (*Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- P15/16-109 Molecular Mechanism of the Arrhenius effect by Thermostable direct hemolysin of *Vibrio parahaemolyticus*.**
Itaru Yanagihara¹, Kentaro Shiraki², Daizo Hamada¹ (¹*Dept of Develop Infect Dis, Res Inst, Osaka Med Cent for Mat and Child Health,* ²*Schl of Mater Sci, Jp Adv Inst of Sci and Tech, Japan*)
- P15/16-110 Stabilization mechanism of pyrrolidone carboxyl peptidase from a hyperthermophile, *Pyrococcus furiosus*, focusing on its denatured state**
Satoshi Iimura¹, Hiromasa Yagi², Kyoko Ogasahara², Hideo Akutsu², Yasuo Noda¹, Shin-ichi Segawa¹, Katsuhide Yutani^{1,3} (¹*Sch. of Sci. & Tech. Kwansai Gakuin Univ.,* ²*Inst. Protein Res. Osaka Univ. ,* ³*RIKEN Harima Inst. HTPF, Japan*)
- P15/16-111 Role of salt bridges in the stabilization of tryptophan synthase α subunit from a hyperthermophile**
Kyoko Ogasahara¹, Soo J. Lee¹, Jai Kaushik¹, Yusaku Hioki¹, Masami Ishida², Masayuki Miyazawa³, Yuriko Yamagata³, Katsuhide Yutani⁴ (¹*Inst. Protein Res., Osaka Univ.,* ²*Tokyo Univ. of Marine Sci. Tech.,* ³*Graduate Sch. of Pharmaceutical Sci., Kumamoto Univ.,* ⁴*RIKEN Harima Inst., HTPF, Japan*)
- P15/16-112 Studies on dihydrofolate reductase from a deep-sea bacterium *Moritella yayanosii* strain DB21MT-5**
Chiho Murakami¹, Eiji Ohmae¹, Kunihiko Gekko¹, Kaoru Nakasone², Fumiyoshi Abe³, Chiaki Kato³ (¹*Grad. Sch. of Sci., Hiroshima Univ. ,* ²*Sch. of Eng., Kinki Univ. ,* ³*JAMSTEC, Japan*)
- P15/16-113 Studies on a cold-adaptation mechanism of RNase HI from a Psychrotrophic bacterium**
Takashi Tadokoro, Yasuo Tsunaka, Kazufumi Takano, Masaaki Morikawa, Shigenori Kanaya (*Kanaya Lab., Dept. Material and Lifescience, Osaka Univ., Japan*)
- P15/16-114 Higher specific activity of a recombinant *Streptomyces thermovulgaris* Fumarase C at high temperatures**
Wenjie Lin, Lih Ling Goh, Maurice Chan, Tiow-Suan Sim (*Department of Microbiology, Faculty of Medicine, National University of Singapore, Republic of Singapore*)
- P15/16-115 Relating Thermodynamics to Protein Function: Understanding TyrR-Mediated Activation**
Jarrod P. Belcher, Geoffrey J. Howlett, Barrie E. Davidson, Matthew A. Perugini, Richard N. Pau (*Grimwade School of Biochemistry and Molecular Biology, The University of Melbourne, Australia*)
- P15/16-116 Amino acid residues involved in the activity of uroporphyrinogen III synthase**
Yoshiaki Omata, Hiroshi Sakamoto, Yuichiro Higashimoto, Shunsuke Hayashi, Saori Harada, Masato Noguchi (*Dept. of Med. Biochem., Kurume Univ. Schl. of Med., Japan*)

- P15/16-117 Analyzing the Specific Role of Chaperonin Apical Domain Movements Using a Temperature-sensitive Mutant**
Tatsunari Yoshimi, Masaaki Taniguchi, Kunihiro Hongo, Tomohiro Mizobata, Yasushi Kawata (*The Dept. of Biotech., Faculty of Eng. and Graduate School of Med. Sci., Tottori Univ., Japan*)
- P15/16-118 A novel contact between GroEL and GroES that is critical to encapsulate substrate protein into the cis-cavity.**
Ayumi Koike¹, Tatsuro Shimamura², Ken Yokoyama³, So Iwata², Masasuke Yoshida^{1,3}, Hideki Taguchi^{4,5} (¹*Chem. Res. Lab., Tokyo Inst. of Tech.*, ²*Imperial College*, ³*ERATO, JST*, ⁴*Grad. Sch. Frontier Sci., Univ. of Tokyo*, ⁵*PRESTO, JST, Japan*)
- P15/16-119 Analysis of conformational changes in the GroEL apical domain induced by ATP binding**
Masaaki Taniguchi, Tatsunari Yoshimi, Kunihiro Hongo, Tomohiro Mizobata, Yasushi Kawata (*The Dept. of Biotech., Faculty of Eng. and Graduate School of Med. Sci., Tottori Univ., Japan*)
- P15/16-120 Mechanical Stability of Co-chaperonin GroES Studied by Atomic Force Microscopy**
Isao Sakane^{1,2}, Kunihiro Hongo^{1,2}, Tomohiro Mizobata^{1,2}, Yasushi Kawata^{1,2} (¹*Department of Biotechnology, Faculty of Engineering, Tottori University*, ²*Institute of Regenerative Medicine and Biofunction, Graduate School of Medical Science, Tottori University, Japan*)
- P15/16-121 Effect of Chaperonin GroEL Fluctuation by Nucleotide**
Takuya Miyazaki¹, Yasuaki Okumura¹, Yasushi Kawata², Yuji C. Sasaki¹ (¹*SPRING-8/JASRI JST/CREST (Sasaki Team)*, ²*Tottori University, Japan*)
- P15/16-122 Structure and functional characterization of the group II chaperonin from hyperthermophilic archaeum, Thermococcus strain KS-1.**
Takao Yoshida¹, Ryo Iizuka¹, Yasuhito Shomura², Kunio Miki², Tadashi Maruyama³, Masafumi Yohda¹ (¹*Dpt. of Biotech. and Life Sci., Tokyo Univ. of Agr. and Tech.*, ²*Dpt. of Chem. Grad. School of Sci., Kyoto Univ.*, ³*JAMSTC., Japan*)
- P15/16-123 Physical interaction and functional cooperation between group II chaperonin and prefoldin from the hyperthermophilic archaea**
Masafumi Yohda¹, Mina Okochi¹, Tomoko Nomura¹, Ryo Iizuka¹, Tamotsu Zako¹, Takashi Funatsu² (¹*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, ²*Department of Physics, Waseda University, Japan*)
- P15/16-124 The mechanism of ATP-driven conformational change of the helical protrusion region of the archaeal group II chaperonin**
Ryo IIZUKA¹, Takao YOSHIDA¹, Tomonao INOBE², Kunihiro KUWAJIMA², Masafumi YOHDA¹ (¹*Tokyo Univ. of Agric. & Technol.*, ²*Univ. of Tokyo, Japan*)
- P15/16-125 Fluorescence detection and kinetic analysis of interaction between Pyrococcus prefoldin and substrate protein**
Tamotsu Zako¹, Ryo Iizuka¹, Taro Ueno², Takashi Funatsu², Masafumi Yohda¹ (¹*Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology*, ²*Department of Physics, School of Science and Technology, Waseda University, Japan*)
- P15/16-126 Structure and function of the N-terminal domain of E. Coli HSP100 ClpB**
Naoki Tanaka, Yasushi Tani (*Department of Polymer Science and Engineering, Kyoto Institute of Technology, Japan*)
- P15/16-127 Characterization of small heat shock proteins from the thermoacidophilic crenarchaeon**
Keisuke Usui¹, Omer Faruk Hatipoglu¹, Noriyuki Ishii², Masafumi Yohda¹ (¹*Dept. of Biotech. & Life Sci., Tokyo Univ. of Agric. & Technol.*, ²*Biol. Info. Res. Center, Natl. Inst. of Adv. Ind. Sci. & Tech., Japan*)
- P15/16-128 Mammalian Hsp22 Exhibits Molecular Chaperone-like Activity**
Tirumala Kumar Chowdary¹, Raman Bakthisaran^{1,2}, Ramakrishna Tangirala¹, Mohan Rao Chinthlagiri¹ (¹*Centre for Cellular and Molecular Biology, Hyderabad 500 007, India*, ²*Institute for Protein Research, Osaka University, Osaka, Japan, Japan*)
- P15/16-129 Reticulocalbin-3 : A novel protein which regulates biosynthesis of subtilisin-like proprotein convertase**
Akihiko Tsuji, Yayoi Kikuchi, Yoshiko Matsuda (*The Department of Biological Science and Technology, The Faculty of Engineering, The University of Tokushima, Japan*)

- P15/16-130** **JPDI, a novel endoplasmic reticulum-resident protein containing both a BiP-interacting J domain and thioredoxin-like motifs**
Akira Hosoda, Kenji Kohno (*Lab. of Mol. and Cell Genet., Res. and Edu. Ctr. for Genet. Info., Nara Inst. of Sci. and Tech., Japan*)
- P15/16-131** **Different contribution of the three CXXC motifs of human protein disulfide isomerase-related protein (hPDIR) to isomerase activity and oxidative refolding**
Tomohisa Horibe¹, Mitsuhiro Gomi^{1,2}, Daisuke Iguchi¹, Hideaki Ito¹, Yukiko Kitamura¹, Toshio Masuoka¹, Ryo Ushioda¹, Ikuo Tsujimoto^{1,3}, Taiji Kimura¹, Masakazu Kikuchi¹ (¹*Dept. of Biosci. & Tech., Ritsumeikan Univ.*, ²*Present address: Kobayashi Pharm. Co.,Ltd. R&D COMPANY.*, ³*Present address: Fujisawa Pharm. Co.,Ltd., Japan*)
- P15/16-132** **Phage Antibodies that Cross-react with Protein Disulfide Isomerase Family Proteins:Isolation and Application in the Functional Analysis of the CXXC motif**
Taiji Kimura, Ai Nishida, Nobutoshi Ohara, Daisuke Yamagishi, Fuyuki Fujihara, Tomohisa Horibe, Masakazu Kikuchi (*Department of Bioscience & Technology, Faculty of Science & Engineering, Ritsumeikan University, Japan*)
- P15/16-133** **A peptidyl-prolyl cis-trans isomerase from a psychrotrophic bacterium *Shewanella* sp. SIB1**
Yutaka Suzuki¹, Mitsuru Haruki², Kazufumi Takano¹, Masaaki Morikawa¹, Shigenori Kanaya¹ (¹*Department of Material and Life Science, Graduate School of Engineering, Osaka University*, ²*Department of Materials Chemistry and Engineering, College of Engineering, Nihon University, Japan*)
- P15/16-134** **Three-dimensional structure of rice calreticulin P-domain by NMR spectroscopy**
Yasuhisa Kawaguchi¹, Takahide Kouno¹, Setsuko Komatsu², Jun Miura³, Etsuko Katoh³, Toshimasa Yamazaki³, Mineyuki Mizuguchi¹, Keiichi Kawano¹ (¹*Faculty of Pharmaceutical Sciences, Toyama Medical and Pharmaceutical University*, ²*Department of Molecular Biology, National Institute of Agrobiological Sciences*, ³*Biochemistry Department, National Institute of Agrobiological Sciences, Japan*)
- P15/16-135** **The C-terminal Sequence (Residues 331-376) Is Essential for Dimerization and Chaperone Activity of *Escherichia coli* DnaJ.**
Yuan-yuan Shi, Chih-chen Wang (*National Laboratory of Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences., People's Republic of China*)
- P15/16-136** **The in vivo conformational changes of mutant SOD1 and its implications for motor neuron death in fALS**
Fujian Zhang, Kei Fukada, Haining Zhu (*Department of Molecular and Cellular Biochemistry, College of Medicine, University of Kentucky, United States of America*)
- P15/16-137** **Receptor-Mediated Protein Import: A Complex of the Colicin E3 Coiled-Coil with the Cobalamin Transporter BtuB**
Genji Kurisu¹, Stanislav D. Zakharov², Mariya V. Zhalnina², Sufiya Bano², William A. Cramer² (¹*Institute for Protein Research, Osaka University*, ²*Department of Biological Sciences, Purdue University, Japan*)
- P15/16-138** **Relationship between local/global structures and import rates of mitochondrial precursor proteins**
Takehiro Satoh¹, Masatoshi Esaki¹, Julio M. Fernandez², Toshiya Endo¹ (¹*Dept. Chem., Grad. Sch. Sci., Nagoya Univ.*, ²*Dept. Biol. Sci., Columbia Univ., Japan*)
- P15/16-139** **Research on function analysis of mFis1, a mitochondrial fission protein, based on its 3D structure**
Wakana Ohashi, Toshio Yamazaki, Ryoichi Arai, Eiko Matsumoto, Mikako Shirouzu, Shigeyuki Yokoyama, Hiroshi Hirota (*Genomic Sciences Center, RIKEN Yokohama Institute, Japan*)
- P15/16-140** **Structural basis of the decoding of the mitochondrial targeting signals by Tom20**
Takayuki Obita¹, Mayumi Igura¹, Toshiya Endo², Katsumi Maenaka¹, Daisuke Kohda¹ (¹*Division of Structural Biology, Medical Institute of Bioregulation, Kyushu University*, ²*Department of Chemistry, Graduate School of Science, Nagoya University, Japan*)
- P15/16-141** **ATP dependent protease FtsH degrades flavodoxin in vitro : spectroscopic monitoring system of substrate protein degradation**
Takashi Okuno, Satomi Fukunaga, Kunitoshi Yamanaka, Teru Ogura (*Division of Molecular Cell Biology, Institute of Molecular Embryology and Genetics, Kumamoto University, Japan*)

- P15/16-142 Function of the N-terminal propeptide from bacterial metallo aminopeptidases**
Satoru Nirasawa, Kiyoshi Hayashi (*National Food Research Institute, Japan*)
- P15/16-143 Intra or Inter Molecular Interactions of the GGA1 GAE domain in the vesicle transport**
Michio Inoue^{1,2}, Tomoo Shiba², Masato Kawasaki², Yusuke Yamada^{1,2}, Ryuichi Kato^{1,2}, Kazuhisa Nakayama³, Soichi Wakatsuki^{1,2} (¹*The Graduate University for Advanced Studies, PF, KEK, PF, 3Grad. Sch. of Pharmaceutical Sciences, Kyoto University, Japan*)
- P15/16-144 γ 1-Adaptin Recognizes an [F/W]xx ϕ Motif of Accessory Proteins and GGA1**
Yusuke Yamada^{1,2}, Masato Kawasaki¹, Ryuichi Kato^{1,2}, Kazuhisa Nakayama³, Soichi Wakatsuki^{1,2} (¹*Struct. Biol. Res. Center, PF, KEK, 2The Dept. Mater. Struct. Sci., The Grad. Univ. for Adv. Stud., 3Grad. Sch. Pharm. Sci., Kyoto Univ., Japan*)
- P15/16-145 Conformational Changes and Bound State Conformation of Maltose Binding Protein (MBP) Upon Interaction with the Chaperone SecB: ESR and Fluorescence Studies**
Wolfgang E. Trommer², K. Beena², Vikram G. Panse², M.V.L. Narasimha Raju¹, Raghavan Varadarajan² (¹*Department of Chemistry, Technical University Kaiserslautern, Germany, 2Molecular Biophysics Unit, Indian Institute of Science, bangalore, India, Federal Republic of Germany*)
- P15/16-146 Application of mutant precursors for the analysis of interaction between precursors and protein translocation machinery during protein import into chloroplasts**
Mitsuru Akita, Hisashi Inoue (*Faculty of Agriculture, Ehime University, Japan*)
- P15/16-147 Molecular Dissection of the Ire1 Luminal Region to Understand its Stress-Sensing Mechanism in the Unfolded Protein Response**
Daisuke Oikawa, Yusuke Shimizu, Yukio Kimata, Yuki Kimata, Kenji Kohno (*Lab. of Mol. and Cell Genet., Res. and Edu. Ctr. for Genet. Info., Nara Inst. of Sci. and Tech, Japan*)
- P15/16-148 Simulation of Solute Diffusion Inside the Cell**
Damien R. Hall, Christopher M. Dobson (*Chemistry Dept. University of Cambridge., United Kingdom of Great Britain and Northern Ireland*)
- P15/16-149 Expression of peroxiredoxin proteins in rat olfactory epithelium at a single cell level.**
Marina F. Bystrova, Stanislav S. Kolesnikov (*Institute of Cell Biophysics RAS, Russian Federation*)
- P15/16-150 Prediction of interfaces for the class A GPCR oligomerization**
Wataru Nemoto^{1,2}, Hiroyuki Toh¹ (¹*Institute for Chemical Research, Kyoto University, 2Graduate School of Information Science, Nara Institute for Science and Technology, Japan*)
- P15/16-151 Expression, purification and NMR analysis of isotopically labeled PACAP**
Yukihiro Tateishi, Hidehito Tochio, Masahiro Shirakawa (*Grad. Sch. of Integrated Sci. Yokohama City Univ., Japan*)
- P15/16-152 In vivo anti-tumor activity and humanization of an anti-EGFR x anti-CD3 bispecific diabody**
Ryutarō Asano^{1,2}, Yukiko Sone¹, Kouhei Tsumoto¹, Hiroki Hayashi³, Koki Makabe¹, Yu Katayose³, Michiaki Unno³, Toshio Kudo², Izumi Kumagai¹ (¹*Dept. Biomol. Eng., Grad. Sch. Eng., Tohoku Univ., 2Inst. Dev., Aging and Cancer, Tohoku Univ., 3First Dep. Surgery, Tohoku Univ. Sch. of Med., Japan*)
- P15/16-153 Thermodynamics analysis of the activation mechanism of GCSF-R receptor induced by ligand binding**
Shouhei Mine^{1,2}, Takumi Koshiba³, Eijiro Honjo¹, Tomoyuki Okamoto¹, Taro Tamada¹, Yoshitake Maeda¹, Yasuko Matsukura¹, Akane Horie¹, Matsujiro Ishibashi⁴, Miharū Sato¹, Mizue Azuma¹, Masao Tokunaga⁴, Katsuhiko Nitta³ (¹*Kirin Brewery Co.Ltd., 2Univ. of Osaka, 3Univ. of Hokkaido, 4Univ. of Kagoshima, Japan*)
- P15/16-154 The involvement of β -arrestin in signaling transduction of protease-activated receptor 1**
Fang-Ting Kuo¹, Sung-Baul Lee², Hua-Wen Fu^{1,2} (¹*Institute of Molecular and Cellular Biology, National Tsing Hua University, 2Department of Life Science, National Tsing Hua University, Taiwan*)
- P15/16-155 Heterogeneity of structural stability of bacteriorhodopsin in purple membrane upon irreversible photobleaching at high temperature**
Yasunori Yokoyama, Masashi Sonoyama, Shigeki Mitaku (*Department of Applied Physics, Graduate School of Engineering, Nagoya University, Japan*)

- P15/16-156 Chloride ion promotes retinal binding to halo-opsin in Triton X-100**
Takanori Sasaki, Makoto Demura, Tomoyasu Aizawa, Katsutoshi Nitta (*Div. Biol Sci., Grad. Sch. of Sci., Hokkaido Univ, Japan*)
- P15/16-157 Direct measure of functional importance visualized atom-by-atom for photoactive yellow protein: Application to photoisomerization reaction**
Atushi Yamada¹, Takakazu Ishikura², Takahisa Yamato² (¹*Research Center for Computational Science, Institute for Molecular Science, ²Graduate School of Science, Nagoya University, Japan*)
- P15/16-158 Molecular Mechanics of a Heme-Redox Switch Revealed by the Crystal Structure of a Bacterial PAS Sensor**
Hirofumi Kurokawa¹, Don-Sun Lee², Miki Watanabe¹, Ikuko Sagami¹, Bunzo Mikami³, C. S. Raman², Toru Shimizu¹ (¹*Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, ²Department of Biochemistry and Structural Biology, University of Texas Medical School, ³Graduate School of Agriculture, Kyoto University, Japan*)
- P15/16-159 Crystal structure of Puruvate oxidase (POPG) from *Aerococcus viridans***
M. Tofazzal Hossain¹, Kaoru Suzuki², Tamotsu Yamamoto³, Shigeyuki Imamura³, Takeshi Sekiguchi², Akio Takenaka¹ (¹*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, ²College of Science and Engineering, Iwaki Meisei University, ³Asahi Kasei Corporation, Japan*)
- P15/16-160 Crystal Structure of *Escherichia coli* Lipoate-protein Ligase A**
Kazuko Fujiwara¹, Sachiko Toma², Kazuko Okamura-Ikeda¹, Yutaro Motokawa¹, Atsushi Nakagawa³, Hisaaki Taniguchi¹ (¹*Inst. Enzyme Res., Univ. of Tokushima, ²Grad. Sch. Pharm. Sci., Kumamoto Univ., ³Inst. Protein Res., Osaka Univ., Japan*)
- P15/16-161 Conformational Stability as a Probe for Ligand Specificity**
Tobias H. Elgan^{1,2}, Kerstin Nordstrand¹, Kurt D. Berndt^{1,2} (¹*Department of Biosciences, Karolinska Institutet, ²Department of Natural Sciences, Sodertorns Hogskola, Kingdom of Sweden*)
- P15/16-162 Mass spectrometry on hydrogen/deuterium exchange of dihydrofolate reductase**
Tatsuya Yamamoto, Shunsuke Izumi, Eiji Ohmae, Kunihiko Gekko (*Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, Japan*)
- P15/16-163 ATOMIC-SCALE PROPAGATED BROWNIAN FLUCTUATIONS FROM ACTIN FILAMENTS TO SINGLE NANOPARTICLES**
Yuji C. Sasaki¹, Yasuaki Okumura¹, Noboru Oishi² (¹*Biomedical Group, SPring-8/JASRI, Sasaki-team, JST/CREST, ²Biotechnology Research Center, Teikyo University, Japan*)
- P15/16-164 Calculation of potential of mean force between two actin molecules through excluded volume effect by using extended scaled particle theory**
Masayuki Irida (*Department of Bioscience and Bioinformatics, Kyushu Institute of Technology, Japan*)
- P15/16-165 α B-crystallin and tubulin decreases in atrophied soleus muscle with hindlimb suspension**
Takashi Sakurai, Yoriko Atomi (*Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo, Japan*)
- P15/16-166 Single molecule measurement of elasticity of Serine-, Glutamate- and Lysine-rich repeats of invertebrate connectin: its elasticity is caused entropically by random coil structure.**
Michio Hiroshima^{1,2}, Atsushi Fukuzawa³, Sumiko Kimura³, Makio Tokunaga^{1,2,4}, Kosaku Maruyama³ (¹*Research Center for Allergy and Immunology, RIKEN, ²Structural Biology Center, National Institute of Genetics, ³Dept. of Biology, Faculty of Science, Chiba University, ⁴Dept. of Genetics, Graduate University for Advanced Studies, Japan*)
- P15/16-167 Structure of the hook-filament junction of the bacterial flagellum**
Katsumi Imada^{1,2}, Hideyuki Matsunami², Midori Yamane¹, Fadel Samatey², Shigehiro Nagashima², Keiichi Namba^{1,2} (¹*Department of Frontier Biosciences, Osaka University, ²Dynamic NanoMachine Project, ICORP, JST, Japan*)
- P15/16-168 Prostaglandin E2 protects cells via activation of Akt and induction of HO-1 in preconditioned rat brain**
Ki Churl Chang, Min Kyu Park, Han Geuk Seo, Jae Heun Lee (*Department of Pharmacology, Colege of Medicine, Gyeongsang National University, Republic of Korea*)

- P15/16-169 The Biological Chemistry Mechanism of Type I Collagen Inhibition of Hydroxyl Radical Induced HeLa Cell Apoptosis**
Helan Xiao¹, Isao Noda², Guoping Cai¹ (¹*Dep. Bio. Tsinghua Univ.*, ²*The P&G Company, People's Republic of China*)
- P15/16-170 Proteome analysis of boar sperm and changes of proteins with sperm maturation in epididymis**
Michiko Sugaya¹, Tomonobu Sunaga¹, Tosifusa Toda², Kuniko Akama¹ (¹*Graduate School of Science and Technology, Chiba University*, ²*Proteomic Collaboration Center, Tokyo Metropolitan Institute of Gerontology, Japan*)
- P15/16-171 A Database for Computing of the Molecular Interaction between Proteins and Chemicals (KiBank)**
Junwei Zhang¹, Masahiro Aizawa¹, Kenji Onodera¹, Shinji Amari¹, Yoshio Iwasawa², Tatsuya Nakano³, Kotoko Nakata³ (¹*Collaborative Research Center of Frontier Simulation Software for Industrial Science, Institute of Industrial Science, University of Tokyo*, ²*AdvanceSoft Corporation*, ³*Division of Safety Information on Drug, Food and Chemicals, National Institute of Health Sciences, Japan*)
- P15/16-172 RETROSPECT STUDY BY BIOSIMULATED BINDING TO RATIONALIZE SELECTIVITY OF PHENYLAMINOPYRIMIDINE (PAP) DERIVATIVES TO INACTIVE AND ACTIVE ABELSON KINASE ONCOPROTEIN**
Amor A. San Juan, Eva Marie A. Ratilla (*Institute of Chemistry, College of Science, University of the Philippines Diliman, Republic of the Philippines*)
- P15/16-173 SPR assays for lead optimization in drug discovery**
Asa Frostell-Karlsson¹, Robert Karlsson¹, Helena Widegren¹, Helena Nordin¹, Annie Naslund², Setsuko Hashimoto³ (¹*Dept. of Biochemistry & Chemistry, Biacore AB*, ²*Dept. of Systems, Biacore AB*, ³*Business Development, Biacore KK, Kingdom of Sweden*)
- P15/16-174 A surface plasmon resonance approach to screening and characterizing small molecule inhibitors of protein kinases**
Helena Nordin¹, Robert Karlsson¹, Olof Karlsson¹, Setsuko Hashimoto², Maria Karlsson¹ (¹*Dept. of Biochemistry & Chemistry, Biacore AB*, ²*Business Development, Biacore KK, Kingdom of Sweden*)
- P15/16-175 Rapid characterization of 200 compounds binding to estrogen receptors alpha and beta**
Karl Andersson², Helena Widegren³, Setsuko Hashimoto¹, Diana Martik⁴, Sheree Long⁴, Lisa A. Orband-Miller⁵, Thomas B. Stanley⁵, Julie B. Stimmel⁵ (¹*Business Development, Biacore KK*, ²*Dept. of Systems, Biacore AB*, ³*Dept. of Biochemistry & Chemistry, Biacore AB*, ⁴*Biacore Research Contract Services, Biacore Inc.*, ⁵*GlaxoSmithKline, Research Triangle Park, NC, USA, Japan*)
- P15/16-176 QSAR Studies and ligand specificity of kinases and proteases**
Shandar Ahmad, Koji Kitajima, Akinori Sarai (*Department of Biochemical Science and Engg., Kyuhsu Institute of Technology, Japan*)
- P15/16-177 HUMAN PRORENIN HAS "GATE AND HANDLE" REGIONS CRITICAL FOR ITS NON-PROTEOLYTIC ACTIVATION BY PROTEIN-PROTEIN INTERACTION.**
Fumiaki Suzuki^{1,2}, Makoto Hayakawa¹, Tsutomu Nakagawa^{1,2}, Nasir M. Uddin¹, Nurun A.H.M. Nabi², Atsushi Iwasawa^{1,2}, Yukio Nakamura^{1,2} (¹*Fac. Appl. Biol. Sci., Gifu University*, ²*United Graduate School of Agric. Sci., Gifu University, Japan*)
- P15/16-178 Detailed structure of L-Methionine γ -Lyase from Pseudomonas putida as an effective anti-tumor agent.**
Shintaro Misaki³, Tomoaki Takakura¹, Takayuki Yoshioka¹, Robert M Hofman², Shigeo Yagi², Kenji Inagaki³, Akio Takimoto¹ (¹*SHIONOGI & Co., LTD*, ²*AntiCancer Inc*, ³*Department of Bioresources Chemistry, Faculty of Agriculture, Okayama University,)*
- P15/16-179 Crystal structure analysis Uricase from *Arthrobacter globiformis***
M. Tofazzal Hossain¹, Kaoru Suzuki², Tamotsu Yamamoto³, Shigeyuki Imamura³, Takeshi Sekiguchi², Akio Takenaka¹ (¹*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology*, ²*College of Science and Engineering, Iwaki Meisei University*, ³*Asahi Kasei Corporation, Japan*)

- P15/16-180** **Quaternary Structure of DPP-IV Studied by the Mutations at the Dimer Interface**
Li-Hao Huang¹, Chia-Hui Chien¹, Chi-Yuan Chou², Yu-Shan Han¹, Yuan-Shou Chen¹, Gu-Gang Chang², Po-Huang Liang³, Xin Chen¹ (¹*Division of Biotechnology and Pharmaceutical Research, National Health Research Institutes*, ²*Faculty of Biological Science, Institute of Biochemistry, National Yang-ming University*, ³*Institute of Biological Chemistry, Academia Sinica, Taiwan*)
- P15/16-181** **The cloning and characterization of glyoxylate cycle genes in Burkholderia pseudomallei to facilitate the development of antimicrobials targeting the glyoxylate cycle**
Yu Min Lye, Maurice Chan, Lih Ling Goh, Tiow-Suan Sim (*Department of Microbiology, Faculty of Medicine, National University of Singapore, Republic of Singapore*)
- P15/16-182** **Cloning and Heterologous Expression of Glycerol Kinase from Plasmodium falciparum**
Siew Li Goh, Maurice Chan, Mulkit Singh, Tiow-Suan Sim (*Department of Microbiology, Faculty of Medicine, National University of Singapore, Republic of Singapore*)
- P15/16-183** **Monte Carlo Simulation of Short Polypeptide Molecules Using a Single Amino Acid Potential (SAAP) Force Field**
Michio Iwaoka, Daisuke Yosida (*Department of Chemistry, School of Science, Tokai University, Japan*)
- P15/16-184** **Energy Landscape of the chameleon sequence**
Kazuyoshi Ikeda^{1,2,3}, Junichi Higo^{1,2} (¹*Tokyo Univ. of Pharmacy and Life Science*, ²*JST, BIRD*, ³*Computational Biology Research Center (CBRC), AIST, Japan*)
- P15/16-185** **Folding Energy Landscape of Two Model Peptides: α -Helical and β -Hairpin Peptides Explored with Brownian Dynamics Simulation**
Tadashi Ando, Toshiyuki Meguro, Ichiro Yamato (*Department of Biological Science and Technology, Tokyo University of Science, Japan*)
- P15/16-186** **Structural Analysis of Acid-unfolded Myoglobin by a Molecular Modeling Method**
Yasutaka Seki¹, Kunitsugu Soda² (¹*Nagahama Institute of Bio-Science and Technology*, ²*Department of Bioengineering, Nagaoka University of Technology, Japan*)
- P15/16-187** **An Analysis Software For Protein Folding**
Wang Longhui, Zhou Huaibei (*Advanced Research Centre of Science and Technology, Wuhan University, People's Republic of China*)
- P15/16-188** **Stochastic formulation of sampling dynamics in generalized ensemble methods: Multicanonical sampling and Average energy guided simulated tempering.**
Jae-Gil Kim¹, Yoshifumi Fukunishi², Akinori Kidera³, Haruki Nakamura⁴ (¹*Japan Biological Information Research Center (JBIRC), Japan Biological Informatics Consortium (JBIC)*, ²*Biological Information Research Center (BIRC), National Institute of Advanced Industrial Science and Technology (AIST)*, ³*Graduate School of Integrated Science, Yokohama City University*, ⁴*Laboratory of Protein Informatics, Research Center for Structural Biology, Institute for Protein Research, Osaka University, Japan*)
- P15/16-189** **Relationship between protein folding and structure prediction studied by the reversible fragment assembly method**
George Chikenji¹, Yoshimi Fujitsuka², Shoji Takada¹ (¹*Department of Chemistry, Faculty of Science, Kobe University*, ²*Graduate School of Science and Technology, Kobe University, Japan*)
- P15/16-190** **Molecular Dynamics Simulation of Wild-Type and Mutant Human Prion Protein: Effect of Pro102Leu**
Masakazu Sekijima¹, Chie Motono¹, Tamotsu Noguchi¹, Kiyotoshi Kaneko^{2,3}, Yutaka Akiyama¹ (¹*Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)*, ²*Department of Cortical Function Disorders, National Institute of Neuroscience (NIN), National Center of Neurology and Psychiatry (NCNP)*, ³*Japan Science and Technology Corporation (CREST), Japan*)
- P15/16-191** **Physical properties of transmembrane helices which are targeted to mitochondria**
Toshiyuki Tsuji, Shigeki Mitaku (*Department of Applied Physics, Graduate School of Engineering, Nagoya University, Japan*)

- P15/16-192 MD simulations of excited vibrations in myosin head due to a disturbance given to ATPase pocket**
 Tatsuyuki Kawakubo¹, Okimasa Okada², Tomoyuki Minami³ (¹Faculty of Engineering, Toin University of Yokohama, ²Optical System Business Development, Fuji Xerox Co., Ltd., ³Science Systems, Industrial Materials & Products Div., Fuji Photo Film Co., Ltd., Japan)
- P15/16-193 Theory of Domain Motions of Proteins**
 Mitsunori Ikeguchi, Miwa Sato, Jiro Ueno, Akinori Kidera (*Grad. Sch. of Integrated Sci., Yokohama City Univ., Japan*)
- P15/16-194 Computation of the field potentials around a DNA molecule.**
 Hirohumi Hirayama (*The Department of Health Science, Asahikawa Medical College., Japan*)
- P15/16-195 Volume Fluctuation and Compressibility of Proteins by Molecular Dynamics Simulation**
 Kazuki Mori¹, Yasutaka Seki², Keitaro Tsugika¹, Kunitsugu Soda¹ (¹Department of Bioengineering, Nagaoka University of Technology, ²Nagahama Institute of Bio-Science and Technology, Japan)
- P15/16-196 Reevaluation of Atomic Packing Density of Protein Interior**
 Yutaka Yamada¹, Hiroki Matsumoto¹, Yasutaka Seki², Kunitsugu Soda¹ (¹Department of Bioengineering, Nagaoka University of Technology, ²Nagahama Institute of Bio-Science and Technology, Japan)
- P15/16-197 Development of energy-minimization and molecular simulation algorithm considering solvation effects in dihedral angle space**
 Takuya Takahashi¹, Hiroshi Wako², Shigeru Endo³ (¹Faculty of Science and Engineering, Ritsumeikan University, ²School of Social Sciences, Waseda University, ³School of Science, Kitasato University, Japan)
- P15/16-198 The molecular design of thioredoxin reduction based on the semiempirical molecular orbital calculation, WinMOPAC**
 Takashi Tamura¹, Keiichi Horie¹, Keiichiro Sameshima², Kenji Inagaki¹ (¹Faculty of Agriculture, Okayama University, ²Fujitsu co., Japan)
- P15/16-199 Study on the Hydrogen Bond with the π -electron Cloud as an Acceptor Using a Hybrid-QM/MM Molecular Dynamics Simulation.**
 Yasushige Yonezawa¹, Toshihiro Sakuma², Kazuto Nakata³, Toshikazu Takada⁴, Shusuke Yamanaka⁵, Kizashi Yamaguchi⁵, Haruki Nakamura¹ (¹Institute for Protein Research, Osaka University, ²NEC Informatel Systems, Ltd, ³NEC Software, Ltd, ⁴NEC Laboratories, Ltd, ⁵Department of Chemistry, Graduate School of Science, Osaka University, Japan)
- P15/16-200 Proton wire breakage in Aquaporin1 channel protein:A Hybrid-QM/MM Computer Simulation**
 Rossen Apostolov, Yasushige Yonezawa, Haruki Nakamura (*Institute for Protein Research, Osaka University, Japan*)
- P15/16-201 Binding Conformation of SMPI to Thermolysin and Pseudolysin using MM/PBSA as a tool.**
 Olayiwola Adekoya¹, Ingebrigt Sylte¹, Nils P. Willasen² (¹Pharmacology Department, IMB, University of Tromsø, Tromsø, Norway, ²Department of Molecular Biotechnology, IMB, University of Tromsø, Tromsø, Norway,)
- P15/16-202 Molecular dynamics on biotin carboxylase**
 Satoshi Fujii¹, Shigeori Takenaka¹, Yuko Ito², Shinji Sueda², Hiroki Kondo² (¹Dept. of Appl. Chem., Kyushu Univ., ²Dept. of Biochem. Eng. & Sci., Kyushu Inst. of Tech., Japan)
- P15/16-203 Molecular dynamic simulation of Escherichia coli adenylate kinase in its free form as well as complexed with its substrates MgATP and AMP**
 Harini Krishnamurthy¹, Hongfeng Lou¹, Adam Kimple¹, Claire Vieille¹, Greg Zeikus¹, Robert Cukier¹ (¹Dept of Chemistry, MSU, USA, ²Dept of Chemistry, MSU, USA, ³Dept of Biochemistry, MSU, USA, ⁴Dept of Biochemistry, MSU, USA, ⁵Dept of Chemistry, MSU, USA, United States of America)
- P15/16-204 Molecular dynamics and SPR analysis of interactions between the SH2 domain of p85 and phosphotyrosyl peptides**
 Naoki Takada¹, Atsushi Suenaga¹, Mio Ichikawa², Xiaomei Yu¹, Mariko Hatakeyama¹, Noriyuki Futatsugi¹, Makoto Taiji¹, Mikako Shirouzu³, Shigeyuki Yokoyama^{3,4,5}, Akihiko Konagaya¹ (¹GSC Bioinformatics Group, RIKEN, ²School of Medicine, KEIO Univ., ³GSC Protein Research Group, RIKEN, ⁴Harima Inst., RIKEN, ⁵Dept. of Biophys. and Biochem, Grad. school of Sci., Univ. of Tokyo, Japan)

- P15/16-205 Flexible docking multicanonical molecular dynamics simulation between enzyme and inhibitor in explicit water**
Narutoshi Kamiya¹, Junichi Higo² (¹*Biomolecular Engineering Research Institute*, ²*School of Life Science, Tokyo University of Pharmacy and Life Science, Japan*)
- P15/16-206 Investigation of Nuclear Factor-kappa beta and DNA Interactions Using Macromolecular Docking and Simulation Experiments**
Mahmud Tareq Hassan Khan, M. Iqbal Choudhary, Atta-ur Rahman (*H.E.J. Research Institute of Chemistry, International Center for Chemical Sciences, University of Karachi, Karachi-75270, Pakistan, Islamic Republic of Pakistan*)
- P15/16-207 Molecular dynamics simulation for investigation the structural impact of Shc phosphorylation**
Atsushi Suenaga¹, Anatoly B. Kiyatkin², Mariko Hatakeyama¹, Noriyuki Futatsugi¹, Tetsu Narumi¹, Naoki Takada¹, Yousuke Ohno¹, Jan B. Hoek², Makoto Taiji¹, Boris N. Kholodenko², Akihiko Konagaya¹ (¹*Bioinformatics Group, RIKEN GSC*, ²*Dept. Path. Anatomy and Cell Biol., Thomas Jefferson Univ., Japan*)
- P15/16-208 Molecular dynamics simulation of Aquaporin-1.**
Masanori Hashido, Mitsunori Ikeguchi, Akinori Kidera (*Graduate School of Integrated Science, Yokohama City University, Japan*)
- P15/16-209 Evaluation of Robustness property of ribosomal progression on the mRNA by the H infinity control.**
Hirohumi Hirayama (*The department of health science, Asahikawa medical college., Japan*)
- P15/16-210 Helical parameters of 3₁₀-helices in proteins**
Purejav Enkhbayar^{1,2}, Mitsuru Osaki¹, Norio Matsushima² (¹*Grad. Sch. of Agri., Hokkaido Univ.*, ²*Sch. of Hlth Sci., Sapporo Med. Univ, Japan*)
- P15/16-211 Novel assignment method of protein secondary structure from circular dichroism spectrum**
Kazuyasu Konko¹, Hiroya Osoegawa², Misa Nakamura², Shokichi Ohuchi^{1,2} (¹*Department of Biochemical Engineering and Science, Faculty of Computer Science and Systems Engineering, Kyushu Institute of Technology*, ²*Department of Biological Functions and Engineering, Graduate School of Life Science and Systems Engineering, Kyushu Institute of Technology, Japan*)
- P15/16-212 Conserved cavities at protein interiors**
Ken-ichi Takahashi, Mitiko Go (*Fac. of Bio-Sci., Nagahama Inst. Bio-Sci. Tech., Japan*)
- P15/16-213 Developing Physical Energy Functions for Protein Structure Prediction**
Yoshimi Fujitsuka, Shoji Takada (*Graduated School of Science and Technology, Kobe University, Japan*)
- P15/16-214 Modeling protein-protein interaction: Ras-Raf and Ras-RaIGDS complexes**
Noriyuki Futatsugi¹, Mikako Shirouzu², Atsushi Suenaga¹, Noriaki Okimoto³, Tetsu Narumi¹, Toshikazu Ebisuzaki³, Makoto Taiji¹, Akihiko Konagaya¹, Shigeyuki Yokoyama² (¹*Bioinformatics Group, RIKEN Genomic Sciences Center*, ²*Protein Research Group, RIKEN Genomic Sciences Center*, ³*Computational Astrophysics Lab., RIKEN, Japan*)
- P15/16-215 Theoretical implications of PPAR γ impairment in type 2 diabetes mellitus**
Takuma Shiraki, Narutoshi Kamiya, Takashi S. Kodama¹, Hisato Jingami (*Biomolecular Engineering Research Institute, Japan*)
- P15/16-216 Transcapsidation between Rice dwarf virus and Rice gall dwarf virus suggested by the three dimensional homology analysis**
Naoyuki Miyazaki¹, Kyoji Hagiwara², Hisashi Naitow³, R. Holland Cheng⁴, Toshihiro Omura², Atsushi Nakagawa¹ (¹*Laboratory of Supramolecular Crystallography, Institute for Protein Research, Osaka University*, ²*National Agricultural Research Center*, ³*RIKEN Harima Institute*, ⁴*Department of Biosciences at Novum Karolinska Institute, Japan*)
- P15/16-217 Folding and Stability of Proteins: Structural Analysis Based on Inter-residue Contacts**
Michael Gromiha¹, Samuel Selvaraj² (¹*Computational Biology Research Center, AIST, Japan*, ²*Department of Physics, Bharathidasan University, Tiruchirapalli, Tamil Nadu, India*)

- P15/16-218** **Is RMSD-criterion good enough for an identification of native structures from the structural ensembles of protein in NMR experiment?**
 Suhkmann Kim, Muyoung Heo, Mookyung Cheon, Kwanghoon Chung, Eun-Joung Moon¹, Iksoo Chang
(Department of Physics, Pusan National University, Republic of Korea)
- P15/16-219** **Detecting Local Structural Similarity in Proteins by Maximizing the Number of Equivalent Residues**
 Daron M. Standley¹, Hiroyuki Toh², Haruki Nakamura¹ (¹*Institute for Protein Research, Osaka University,*
²*Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan)*
- P15/16-220** **A New Protein Structural Comparison Approach: Aligning Encoded Sequences of Protein Structures**
 Shuang-Ping Chen¹, Hao-Ran Zheng¹, Hai-Yan Liu², Xu-Fa Wang¹ (¹*Department of Computer Science and Technology, University of Science and Technology of China,* ²*School of Life Sciences, University of Science and Technology of China, People's Republic of China)*
- P15/16-221** **Probabilistic Alignment for Protein Sequences and Structures**
 Ryotaro Koike^{1,2}, Kengo Kinoshita², Akinori Kidera² (¹*Institute for Protein Research, Osaka University,*
²*Graduate School of Integrated Science, Yokohama City University, Japan)*
- P15/16-222** **Long- and short-range interactions in native protein structures are consistent/minimally-frustrated in sequence space**
 Sanzo Miyazawa¹, Robert L. Jernigan² (¹*Faculty of Technology, Gunma University,* ²*L. H. Baker Center for Bioinformatics and Biological Statistics, Iowa State University, USA, Japan)*
- P15/16-223** **Prediction of Protein-Protein Interaction Sites using Residue Interface Propensity**
 Naoshi Fukuhara, Takeshi Kawabata, Nobuhiro Go (*Graduate School of Information Science, Nara Institute of Science and Technology, Japan)*
- P15/16-224** **The novel algorithm for finding pockets on protein surface using small and large probe spheres**
 Takeshi Kawabata¹, Nobuhiro Go^{1,2} (¹*Grad. School of Information Science, Nara Institute of Science and Technology,* ²*CCSE, Japan Atomic Energy Research Institute, Japan)*
- P15/16-225** **Binding Surface Mapping of Intra and Inter Domain Interactions Among hHR23B, Ubiquitin and Poly Ubiquitin Binding Site 2 of S5a**
 Kyoung-Seok Ryu, Sung-Hun Bae, Byong-Seok Choi (*Department of Chemistry, Korea Advanced Institute of Science and Technology, Republic of Korea)*
- P15/16-226** **An empirical approach for structure-based prediction of carbohydrate-binding sites on proteins**
 Clara Shionyu-Mitsuyama¹, Hirokazu Ishida², Tomohisa Ogawa³, Koji Muramoto³, Tsuyoshi Shirai¹ (¹*Dept. of Comput. Bio., BERI,* ²*Advanced IT Develop. Dept., CTI Co., Ltd,* ³*Dept. of Biol. Sci., Univ. of Tohoku, Japan)*
- P15/16-227** **Analyses of RNA-binding site properties and development of a method to predict RNA interfaces on proteins**
 Oanh T. P. Kim¹, Kei Yura¹, Nobuhiro Go^{1,2} (¹*Quantum Bioinformatics Group, Japan Atomic Energy Research Institute,* ²*Bioinformatics Unit, Nara Institute of Science and Technology, Japan)*
- P15/16-228** **Potential binding sites in Synechocystis genome predicted by using the mutation matrices derived from systematic binding data for SYCRP1 and CRP**
 Katsumi Omagari¹, Hidehisa Yoshimura¹, Mitsunori Takano¹, Masayuki Ohmori¹, Akinori Sarai², Akira Suyama¹ (¹*The Dept. of Life Sci., Univ. of Tokyo,* ²*The Dept. of Biochem. Eng. and Sci., Kyushu Inst. of Tech., Japan)*
- P15/16-229** **Development of an empirical prediction method for nucleotide-binding site**
 Mihoko Saito¹, Hirokazu Ishida⁴, Mitiko Go³, Tsuyoshi Shirai² (¹*Dept. of Biology, Grad. Sch. of Science, Nagoya Univ.,* ²*Dept. of Compute. Bio., BERI,* ³*Fac. of Bio-Sci, Nagahama Inst. Bio-Sci Tech., Japan,* ⁴*Advanced IT Develop. Dept., CTI Co., Ltd, Japan)*
- P15/16-230** **Identification of protein biochemical functions by similarity search using the molecular surface database, eF-site.**
 Kengo Kinoshita^{1,2}, Haruki Nakamura³ (¹*Graduate School of Integrated Science, Yokohama City Univ.,*
²*PRESTO, JST,* ³*Protein Research Institute, Osaka Univ., Japan)*

- P15/16-231 A Bioinformatics Approach for the Prediction of RNAi Functions in Controlling Gene Expression**
Taeho Kim¹, Young C. Chung², Sun J. Kim¹, Hanjip Kim², Churl K. Min², Hyun Joo^{1,2} (¹*Department of Molecular Science & Technology, Ajou University,* ²*Department of Biological Science, Ajou University, Republic of Korea*)
- P15/16-232 Analysis for the structural diversity of proteins by a clustering of short segments**
Yoshito Z Sawada, Shinya Honda (*National Institute of Advanced Industrial Science and Technology (AIST), Japan*)
- P15/16-233 Evolutionary analysis of membrane-associated proteins**
Hiroyuki Toh, Hisako Ichihara, Hiromi Daiyasu (*Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan*)
- P15/16-234 Computational Analyses on Functional Diversification by Alternative Splicing of Heterotrimeric G Protein Signal Transduction Pathway**
Kei Yura¹, Mitiko Go² (¹*Quantum Bioinformatics Group, Japan Atomic Energy Research Institute,* ²*Department of Bio-Science, Faculty of Bio-Science, Nagahama Institute of Bio-Science and Technology, Japan*)
- P15/16-235 Prediction of Protein Disordered Region using Support Vector Machine**
Takashi Ishida, Tohru Terada, Shugo Nakamura, Kentaro Shimizu (*Dept. of Biotech., The Univ. of Tokyo, Japan*)
- P15/16-236 In silico study of the C-type lectin superfamily**
Alex N. Zelensky, Jill E. Gready (*Computational Proteomics and Therapy Design Group, Department of Molecular Bioscience, John Curtin School of Medical Research, Australian National University, Australia*)
- P15/16-237 PDB-XML: The XML-based Protein Data Bank**
Nobutoshi Ito¹, Kaori Kobayashi^{2,3}, Hisashi Sakamoto^{2,3}, Haruki Nakamura³ (¹*School of Biomedical Science, Tokyo Medical and Dental University,* ²*BIRD, Japan Science and Technology Corporation,* ³*Institute for Protein Research, Osaka University, Japan*)
- P15/16-238 ProMode: a collection and comparison of normal mode analysis results of protein molecules**
Hiroshi Wako¹, Masaki Kato², Mikiko Tada³, Shigeru Endo³ (¹*Sch. of Soc. Sci., Waseda Univ.,* ²*Dept. of Sci. of Biol. Supramol. Systems, Yokohama City Univ.,* ³*Dept. of Phys., Sch. of Sci., Kitasato Univ., Japan*)
- P15/16-239 Protherm: Thermodynamic Database for Proteins and Mutants**
Abdulla Bava K. ¹, Michael, M. Gromiha², Hatsuho Uedaira³, Koji Kitajima¹, Akinori Sarai¹ (¹*Dept of Biochemical Engg. & Sci., Kyushu Institute of Technology,* ²*Computational Biology Research Center, AIST,* ³*Research Center for Glycoscience, AIST Tsukuba Central 6, Japan*)
- P15/16-240 Analysis of the sugar-protein interaction using whole PDB data in structural and evolutionary view point toward rational design of sugar recognizing protein**
Taku Nakahara, Nobuaki Miura, Shin-Ichiro Nishimura (*Division of Biological Sciences, Graduate School of Science, Hokkaido University, Japan*)
- P15/16-241 Protein swerving on threadsomes, swervent binds to interface between threadsomal assembly units**
Tsukasa Sakai (*Nifty Institute of Bioscience and Human-technology, Japan*)

17 & 18 April

Presentation time: Odd Numbers 14:20-15:05, 17 April
Even Numbers 13:15-14:00, 18 April

- P17/18-001 Copper binding to plant glycine-rich proteins**
Masakatsu Kamiya^{1,3}, Yasuhiro Kumaki², Katsutoshi Nitta¹, Norio Matsushima³ (¹*Div. of Biol. Sci., Grad Sch. of Sci., Hokkaido Univ.*, ²*High-Resolution NMR Lab., Grad Sch. of Sci., Hokkaido Univ.*, ³*Sch. of Hlth. Sci., Sapporo Med. Univ., Japan*)
- P17/18-002 Functional analysis of the flexible N-terminal region in biological activity of the insect cytokine, GBP**
Masanobu Yoshida¹, Tomoyasu Aizawa², Kunio Shitara¹, Kimiaki Matsubara¹, Takahide Kouno¹, Yoichi Hayakawa³, Yasuhiro Kumaki², Mineyuki Mizuguchi¹, Makoto Demura², Katsutoshi Nitta², Keiichi Kawano¹ (¹*Fac. Pharm. Sci., Toyama Med. Pharm. Univ.*, ²*Div. Biol. Sci., Grad. Sch. Sci., Hokkaido Univ.*, ³*Inst. Low Temp. Sci., Hokkaido Univ., Japan*)
- P17/18-003 Structural variety of the tail-lysozymes in T4-related phages**
Mai Nemoto, Shuji Kanamaru, Fumio Arisaka (*Grad. Sch. of Biosci & Biotech, Tokyo Institute of Technology, Japan*)
- P17/18-004 Characterization of α Gln90 mutants of nitrile hydratase from *Rhodococcus* sp. N-771**
Hiromi Yamagishi^{1,2}, Masafumi Odaka^{1,3}, Hiroshi Nakayama¹, Shunsaku Ueda², Masafumi Yohda³, Mizuo Maeda¹ (¹*RIKEN*, ²*United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology*, ³*Faculty of Technology, Tokyo University of Agriculture and Technology, Japan*)
- P17/18-005 Characterization of protease III from *E. coli*: a homologue of human insulin degrading enzyme**
Joel C. Cornista, Kazufumi Takano, Masaaki Morikawa, Shigenori Kanaya (*Department of Material and Life Science, Graduate School of Engineering, Osaka University, Japan*)
- P17/18-006 Cloning, expression, purification and characterization of phosphatase C from *M. moganii***
Woong Kim¹, Yooni Choi¹, Young Sung Yoon² (¹*School of Environmental Engineering, Pohang University of Science and Technology*, ²*Division of Molecular and Life Sciences, Pohang University of Science and Technology, Republic of Korea*)
- P17/18-007 Activation of prophenol oxidase in *Drosophila*.**
Nobuhiko Asada¹, Masayoshi Namba² (¹*Biological Laboratory, Faculty of Science, Okayama University of Science*, ²*Niimi College (President), Japan*)
- P17/18-008 An N-terminal Region of Chromogranin A Binds Copper, Eliciting Ascorbate Oxidase Activity**
In Sook Matsui Lee, Morimitsu Nishikimi (*Department of Biochemistry, Wakayama Medical University, Japan*)
- P17/18-009 Characterization and preliminary structural study of thiocyanate hydrolase**
Takatoshi Arakawa¹, Shingo Kataoka^{1,4}, Yoshiaki Kawano⁵, Masafumi Odaka^{1,4}, Yoko Katayama², Hiroshi Nyunoya³, Nobuo Kamiya⁵, Mizuo Maeda⁴, Masafumi Yohda¹ (¹*Dept. of Tech.*, ²*Agric.*, ³*and Gene Res. Center, Tokyo Univ. of Agric. and Tech.*, ⁴*RIKEN Wako*, ⁵*and Harima Inst., Japan*)
- P17/18-010 The cloning, expression and characterization of phenylacetic acid hydroxylase from a thermophilic archaeon *Pyrococcus horikoshii* OT3**
Jong-Uk Koh¹, Kwang-Hoon Kong¹, Masaru Tanokura² (¹*Department of Chemistry, College of Natural Sciences, Chung-Ang University*, ²*Graduate School of Agricultural and Life Science, University of Tokyo, Republic of Korea*)
- P17/18-011 Molecular cloning, expression, and characterization of putative dihydrolipoamide dehydrogenase from the silkworm, *Bombyx mori***
Yoichi Aso¹, Toshiro Irie¹, Kohji Yamamoto², Ningjia He², Takeshi Yamagami¹, Banno Yutaka², Yoshizumi Ishino¹, Hiroshi Fujii² (¹*Laboratory of Protein Chemistry & Engineering, Kyushu University*, ²*Laboratory of Insect Genetic Resources, Kyushu University, Japan*)
- P17/18-012 Novel dye-linked L-proline dehydrogenases from anaerobic hyperthermophilic archaea, *Thermococcus profundus* and *Pyrococcus horikoshii* OT-3**
Ryushi Kawakami¹, Hideaki Tsuge², Shuichiro Goda¹, Haruhiko Sakuraba¹, Nobuhiko Katunuma², Toshihisa Ohshima¹ (¹*Dept. of Biol. Sci. and Tech., Fac. of Engi., Univ. of Tokushima*, ²*Inst. for Health Sci., Tokushima Bunri Univ., Japan*)

- P17/18-013 Binding study of heme oxygenase with NADPH-cytochrome P450 reductase by surface plasmon resonance measurements**
Yuichiro Higashimoto¹, Hiroshi Sakamoto¹, Masakazu Sugishima², Keiichi Fukuyama^{2,3}, Masato Noguchi¹
(¹Dept. of Med. Biochem., Kurume Univ. Sch. of Med., ²Dept. of Biol., Grd Sch. of Sci., Osaka Univ., ³RIKEN Harima Inst. at SPring-8, Japan)
- P17/18-014 Activity and structural changes of Horseradish peroxidase: Effects of modification and pH variations**
Kourosh Bamdad, Masoumeh Khazaei, Minoo Akbari, Bijan Ranjbar (Tarbiat Modarres University, Faculty of Sciences,, Islamic Republic of Iran)
- P17/18-015 Functional analysis of tyrosine 108 residue in human glutathione S-transferase P1-1**
Kyung-Hun Kim, Hyun-Young Cho, Kwang-Hoon Kong (Department of Chemistry, College of Natural Sciences, Chung-Ang University, Republic of Korea)
- P17/18-016 Tau class glutathione S-transferase from *Oryza sativa*: Molecular cloning, expression and characterization**
Sun-Young Yoo, Jong-Uk Koh, Kwang-Hoon Kong (Department of Chemistry, College of Natural Sciences, Chung-Ang University, Republic of Korea)
- P17/18-017 Molecular analysis of *Agaricus blazei* polyphenoloxidase gene**
Akiko M. Akanuma^{1,2}, Tairo Oshima², Naohito Ohno^{1,2} (¹School of Pharm., Tokyo Univ. of Pharm. & Life Sci., ²School of Life Sci., Tokyo Univ. of Pharm. & Life Sci., Japan)
- P17/18-018 Analysis of catalytic mechanism of Ndx4, a nudix protein from *Thermus thermophilus* HB8**
Takushi Ooga¹, Sachiko Yoshida¹, Takayoshi Iwai¹, Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2} (¹Grad. Sch. Sci, Osaka Univ., ²RIKEN Harima Inst., Japan)
- P17/18-019 Characterization of the tail-knob protein (gp9) from bacteriophage ϕ 29**
Shuji Kanamaru¹, Marc C. Morais², Megan Fisher², Michael G. Rossmann², Fumio Arisaka¹ (¹Department of Biomolecular Engineering, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, Japan, ²Department of Biological Sciences, Purdue University, The United States of America)
- P17/18-020 Expression and purification of Bacteriophage Mu subunits**
Shigeki Takeda¹, Yasuhiro Kageyama¹, Masashi Tomihara¹, Daisuke Kitazawa¹ (¹Dep. of Nano-Material Systems, Gunma Univ., ²Dep. of Nano-Material Systems, Gunma Univ., ³Dep. of Nano-Material Systems, Gunma Univ., ⁴Dep. of Nano-Material Systems, Gunma Univ., ⁵Gunma Univ., Japan)
- P17/18-021 Dissection of the Interactions between Anti-Ciguatoxin Antibodies and the antigen: SPR analyses and crystallization of the complex**
Akiko Yokota¹, Yoko Nagumo², Hiroki Oguri², Shin-ya Sasaki², Kohei Tsumoto¹, Takeshi Tsumuraya³, Ikuo Fujii⁴, Hidemasa Kondo⁵, Masahiro Hiramata², Kumagai Izumi¹ (¹Dept. of Biochem. and Eng., Grad. Sch. of Eng., Tohoku Univ., ²Depart. of Chem., Grad. Sch. of Sci., Tohoku Univ., ³Biomol. Eng. Res. Inst., ⁴Osaka Prefect. Univ., ⁵AIST, Japan)
- P17/18-022 Selection and characterization of anti-biodegradable poly-hydroxybutylate antibody**
Hideki Watanabe¹, Kouhei Tsumoto¹, Seiichi Taguchi², Koichi Yamashita², Tadahisa Iwata², Yoshiharu Doi², Hidemasa Kondo³, Yoshiyuki Nishimiya³, Izumi Kumagai¹ (¹Department of Biomolecular Engineering, Graduate School of Engineering, Tohoku University, ²RIKEN, ³National Institute of Advanced Industrial Science and Technology, Japan)
- P17/18-023 A Linear Correlation Between Allosteric Behavior and Flexibility in *E. coli* Cyclic AMP Receptor Revealed by Mutation-Induced Changes in Compressibility and Amide Hydrogen/Deuterium Exchange**
Kunihiko Gekko¹, Norihiro Obu¹, Jianquan Li², J. Ching Lee² (¹Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, ²University of Texas Medical Branch, Japan)
- P17/18-024 Strategy for the Control of Enzymatic Activity Using Designed Coiled-Coil**
Satoshi Yuzawa, Toshihisa Mizuno, Toshiki Tanaka (Graduate School of Material Science, Nagoya Institute of Technology, Japan)

- P17/18-025** **Designing stable β -sheet peptides based on the single layer β -sheet**
Hidetsugu Okamoto¹, Hiroaki Sasakawa², Tomoko Nakagawa¹, Atsuo Tamura^{1,2} (¹Grad. Sch. of Sci. and Tech., Kobe Univ., ²PRESTO, Japan Sci. and Tech. Co., Japan)
- P17/18-026** **Design and synthesis of *de novo* cytochrome c**
Manabu Ishida^{1,2}, Naoshi Dohmae³, Yoshitsugu Shiro^{1,2}, Yasuhiro Isogai^{2,3} (¹Dept. of Life Sci., Fac. of Sci., Himeji Inst. of Technol., ²Biophysical Chemistry Lab., RIKEN, Harima Inst., ³Biomolecular Characterization Team, RIKEN, Japan)
- P17/18-027** **Cancelled**
- P17/18-028** **Reactive Amino Acid Residues Involved in Glutamate-Binding of Human Glutamate Dehydrogenase Isozymes**
Sung-Woo Cho¹, Seung-Ju Yang¹, Jae-Wan Huh¹, Hea-Nam Hong², Hyun Jin Choi¹ (¹Dep. of Biochemistry and Molecular Biology, Univ. of Ulsan College of Med., ²Dep. of Anatomy, Univ. of Ulsan College of Med., Republic of Korea)
- P17/18-029** **Effect of mutations within nine-residue sequence motifs on secretion and enzymatic activity of *Pseudomonas* MIS38 lipase**
Clement Angkawidjaja¹, Aditya Paul¹, Kazufumi Takano¹, Kenji Omori², Masaaki Morikawa¹, Shigenori Kanaya¹ (¹Dept. of Material and Life Science, Osaka Univ., ²Discovery Research Lab., Tanabe Seiyaku Co. Ltd., Japan)
- P17/18-030** **Identification of the catalytic residues involved in the carboxyl transfer of pyruvate carboxylase**
Shinji Sueda, Md. Nurul Islam, Jin Yong-Biao, Hiroki Kondo (*Dept. of Biochem. Eng. & Sci., Kyushu Inst. of Tech., Japan*)
- P17/18-031** **Investigation of catalytic function of phospholipase D enzyme by site directed mutagenesis**
Chiaki Ogino, Mariko Izumi, Takako Oishi, Nobuaki Shimizu (*Department of Chemistry and Chemical Engineering, Kanazawa University, Japan*)
- P17/18-032** **Studies on the structure and function of mouse Alcohol Dehydrogenase by chimera construction**
Seiichi Tsukamoto¹, Akio Simizu¹, Norio Kurosawa¹, Takeshi Haseba², Masamichi Ikeguchi¹ (¹The Department of Bioengineering, Faculty of Technology, Soka University, ²The Department of Forensic Medicine, Medical Department, Nippon Medical School, Japan)
- P17/18-033** **Application of Self-splicing Inteins in Protein Engineering and Peptide Array**
Luo Sun, Inca Ghosh, Ming-Qun Xu (*New England Biolabs, Inc., United States of America*)
- P17/18-034** **A capture approach to SPR analysis of receptors expressed on cell surfaces. Analysis of the EGF receptor expressed on A431 cells.**
Robert Karlsson², Pascale Richalet Secordel¹, Stephen Mulholland¹, Setsuko Hashimoto² (¹Dept. of Biochemistry & Chemistry, Biacore AB, ²Business Development, Biacore KK, Kingdom of Sweden)
- P17/18-035** **Development of SPR imaging protein chip system to study Cdk-Cyclin interaction**
Hyeon S. Ro, Byung Kho, Sun Ok Jung, Min G. Kim, Yong B. Shin, Bong H. Chung (*Laboratory of Integrative Biotechnology, KRIBB, Republic of Korea*)
- P17/18-036** **Automated on-column tag cleavage and multi-step purification of (His)₆- and GST-tagged proteins**
Par Eklund, Thomas Stromqvist, Tuomo Frigard, Markus Galin, Hans O. Andersson, Lotta Hedkvist, Christine Markeland-Johansson, Pia Liljedahl, Anna Sjoberg, Elisabeth Linde, Niklas Pettersson, Mats Nilsson, Jill A. Simon (*R&D, Amersham Biosciences, Kingdom of Sweden*)
- P17/18-037** **Automated Multi-step Purification of (His)₆- and GST-Tagged Proteins**
Par Eklund, Markus Galin, Lotta Hedkvist, Pia Liljedahl, Elisabeth Linde, Christine Markeland-Johansson, Mats Nilsson, Niklas Pettersson, Jill A. Simon, Anna Sjoberg, Tuomo Frigard (*R&D, Amersham Biosciences, Kingdom of Sweden*)

- P17/18-038 Optimizing Protocols for Automated Multi-step Purification of (His)₆- and GST- Tagged Proteins Using AKTExpress™**
Lotta Hedkvist, Markus Galin, Pia Liljedahl, Anna Sjoberg, Christine Markeland-Johansson, Par Eklund, Tuomo Frigard, Elisabeth Linde, Niklas Pettersson, Mats Nilsson, Jill A. Simon (*R&D, Amersham Biosciences, Kingdom of Sweden*)
- P17/18-039 Sensitive and precise method to evaluate the glycosidase activity using bicinchoninic acid**
Satoshi Souma, Nurul Karim, Hiroshi Arikawa, Shun-ichi Kidokoro (*Dept. Bioengineer., Nagaoka Univ. Tech., Japan*)
- P17/18-040 Secondary Structure Analysis of Proteins by Vacuum Ultraviolet Circular Dichroism Spectroscopy**
Koichi Matsuo¹, Ryota Yonehara¹, Kunihiro Gekko^{1,2} (*¹Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, ²Hiroshima Synchrotron Radiation Center, Hiroshima University, Japan*)
- P17/18-041 Crystal structure of parasporin-1, a cancer-cell-recognizing toxin from *Bacillus thuringiensis***
Toshihiko Akiba¹, Tokio Ichimatsu², Hideki Katayama², Tetsuyuki Aka², Eiichi Mizuki², Michio Ohba³, Kazuaki Harata¹ (*¹Biological Information Research Center, National Institute of Advanced Industrial Science and Technology, ²Biotechnology and Food Research Institute, Fukuoka Industrial Technology Center, ³Bioresources and Management Laboratory, Graduate School of Agriculture, Kyushu University, Japan*)
- P17/18-042 Crystal structure of ubiquitin:Hrs-UIM complex**
Satoshi Hirano¹, Masato Kawasaki¹, Hideaki Ura¹, Ryuichi Kato¹, Harald Stenmark², Soichi Wakatsuki¹ (*¹Structural Biology Research Center, Photon Factory, High Energy Accelerator Organization, Japan, ²Department of Biochemistry, Institute for Cancer Research, the Norwegian Radium Hospital, Norway*)
- P17/18-043 A bound water molecule is crucial in initiating auto-catalytic precursor activation in a Nterminal Hydrolase**
Kyunggon Kim, Jongchul Yoon, Bora Oh, Jungeun Park¹, Dohyun Han, Youngsoo Kim (*Division of Molecular Genomic Medicine, College of Medicine, Seoul National University, Republic of Korea*)
- P17/18-044 Crystal Structure and Metal-Binding Properties of CutA from *Pyrococcus horikoshii***
Yoshikazu Tanaka¹, Kouhei Tsumoto¹, Takeshi Nakanishi¹, Yoshiaki Yasutake², Naoki Sakai², Min Yao², Isao Tanaka², Izumi Kumagai¹ (*¹Dept. of Biomol. Eng., Grad. Sch. of Eng., Tohoku Univ., ²Div. of Biol. Sci., Grad. Sch. of Sci., Hokkaido Univ., Japan*)
- P17/18-045 The X-ray crystallography of the complex of Metallo- β -lactamase (IMP-1) with thiol compound and the investigation on binding mode of inhibitors with IMP-1.**
Yoshihiro Yamaguchi¹, Hisami Yasuzawa¹, Hiromasa Kurosaki¹, Yuriko Yamagata², Yoshichika Arakawa³, Masafumi Goto¹ (*¹The Dept. of Phys. Chem., the Grad. Sch. of Pharm. Sci., Univ. of Kumamoto., ²The Dept. of Struct. Biol., the Grad. Sch. of Pharm. Sci., Univ. of Kumamoto., ³NIID, Japan*)
- P17/18-046 The crystal structure of sulerythrin, a rubrerythrin-like protein from a strictly aerobic archaeon, *Sulfolobus tokodaii* strain 7**
Shinya Fushinobu, Hirofumi Shoun, Takayoshi Wakagi (*Department of Biotechnology, The University of Tokyo, Japan*)
- P17/18-047 Crystal structure of ABC-ATPase SufC**
Satoshi Watanabe¹, Akiko Kita¹, Kunio Miki^{1,2} (*¹Department of Chemistry, Graduate school of Science, Kyoto University, ²Riken Harima Institute /Spring-8, Japan*)
- P17/18-048 Crystallographic analysis of the reaction mechanism of G6-amylose from alkalophilic *Bacillus* sp.707**
Ryuta Kanai^{1,2}, Keiko Haga¹, Toshihiko Akiba², Kunio Yamane¹, Kazuaki Harata² (*¹Inst. of Biol. Sci., Univ. of Tsukuba, ²BIRC, AIST, Japan*)
- P17/18-049 Structure of β -glucosidase at atomic resolution and complex with glucose**
Neratur K. Lokanath, Ikuya Shiromizu, Emiko Matsunaga, Tomoyuki Tanaka, Naoki Kunishima (*Highthroughput Factory, RIKEN Harima Institute, Japan*)

- P17/18-050** **Reaction mechanism of GTP cyclohydrolase I**
Yoko Tanaka¹, Noriko Nakagawa^{1,2}, Ryoji Masui^{1,2}, Seiki Kyramitsu^{1,2} (¹Grad. Sch. Sci., Osaka Univ., ²RIKEN Harima Inst., Japan)
- P17/18-051** **Crystal structures of the carbohydrate recognition domain of glycoprotein cargo receptors, Emp46p and Emp47p, from *Saccharomyces cerevisiae***
Tadashi Satoh¹, Ken Sato², Tomoo Shiba¹, Masato Kawasaki¹, Ryuichi Kato¹, Akihiko Nakano², Soichi Wakatsuki¹ (¹Photon Factory, KEK, ²Molecular Membrane Biology Laboratory, RIKEN, Japan)
- P17/18-052** **Mutational and structural studies of RNase HIII from *Bacillus stearothermophilus***
Hyongi Chon¹, Kazufumi Takano¹, Hiroyoshi Matsumura², Tsuyoshi Inoue², Yasushi Kai², Masaaki Morikawa¹, Shigenori Kanaya¹ (¹Dept. Material&Life Science, Osaka Univ., ²Dept. Materials Chemistry, Osaka Univ., Japan)
- P17/18-053** **Crystal Structure of Archaeal Ribonuclease P Protein Ph1771p from *Pyrococcus horikoshii* OT3**
Tomoyuki Numata, Kazumi Kimura, Yoshimitsu Kakuta, Makoto Kimura (Laboratory of Biochemistry, Department of Bioscience and Biotechnology, Faculty of Agriculture, Graduate School, Kyushu University, Japan)
- P17/18-054** **Crystal structure of carboxypeptidase 1 from *Thermus thermophilus***
Shiho Tsutsui¹, Woo Cheol Lee¹, Kosuke Ito¹, Yumiko Inoue², Koji Nagata¹, Masaru Tanokura^{1,3} (¹Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, The University of Tokyo, ²Structurome Research Group, RIKEN Harima Institute, ³Theoretical Structural Biology Laboratory, RIKEN Harima Institute, Japan)
- P17/18-055** **Crystal Structure of human T-protein of Glycine Cleavage System**
Kazuko Okamura-Ikeda¹, Masato Yoshimura², Harumi Hosaka², Eiki Yamashita², Sachiko Toma³, Atsushi Nakagawa², Kazuko Fujiwara¹, Yutaro Motokawa¹, Hisaaki Taniguchi¹ (¹Inst. Enz. Res., Univ. of Tokushima, ²Inst. Prot. Res., Osaka Univ., ³Grad. Sch. Pharm. Sci., Kumamoto Univ., Japan)
- P17/18-056** **Structural investigation of the reaction catalyzed by ODCase**
Masahiro Fujihashi¹, Subhash C. Annedi², Angelica M. Bello², Lakshmi P. Kotra^{2,3}, Emil F. Pai^{1,4} (¹Ontario Cancer Inst., ²Facul. of Pharmacy, Univ. of Toronto, ³MDIT Center, Univ. of Toronto, ⁴Dept. of Biochemistry, Univ. of Toronto, Canada)
- P17/18-057** **Crystal structure of the biotin carboxylase subunit of *Aquifex aeolicus* pyruvate carboxylase**
Shin Kondo¹, Yoshitaka Nakajima¹, Shigetoshi Sugio¹, Shinji Sueda², Hiroki Kondo² (¹Sci. & Tech. Res. Cent., Mitsubishi Chem. Co., ²Dept. of Biochem. Eng. & Sci., Kyushu Inst. of Tech., Japan)
- P17/18-058** **Purification, characterization and crystallization of two giant hemoglobins from vestimentiferan worm, *Lamellibrachia satsuma***
Seiko Onoda¹, Tomoyuki Miura², Yoshihiro Fukumori¹ (¹Faculty of Science, Kanazawa University, ²Faculty of Agriculture, Miyazaki University, Japan)
- P17/18-059** **Crystallographic Study of Multi Hemoglobin System from *Oligobrachia mashikoi***
Nobutaka Numoto¹, Taro Nakagawa², Akiko Kita¹, Yoshihiro Fukumori², Kunio Miki^{1,3} (¹Department of Chemistry, Graduate School of Science, Kyoto University, ²Department of Biology, Faculty of Science, Kanazawa University, ³RIKEN Harima Institute / SPring-8, Japan)
- P17/18-060** **Structural Basis for Discrimination between CO and O₂ in Heme Oxygenase**
Masakazu Sugishima¹, Hiroshi Sakamoto², Masato Noguchi², Keiichi Fukuyama^{1,3} (¹Dept. of Biol., Grad. Sch. of Sci., Osaka Univ., ²Dept. of Med. Biochem., Kurume Univ. Sch. of Med., ³RIKEN Harima Inst., Japan)
- P17/18-061** **Crystal Structure of rat heme oxygenase-1 in complex with biliverdin-iron chelate: implications for product release**
Masakazu Sugishima¹, Hiroshi Sakamoto², Yuichiro Higashimoto², Masato Noguchi², Keiichi Fukuyama^{1,3} (¹Dept. of Biol., Grd. Sch. of Sci., Osaka Univ., ²Dept. of Med. Biochem., Kurume Univ. Sch. of Med., ³RIKEN Harima Inst./SPring-8, Japan)
- P17/18-062** **Crystal structure of heme uptake protein, p44 from *Bacteroides fragilis***
Atsushi Izumi¹, Ben R. Otto², Jonathan Heddle¹, Sam-Yong Park¹, Jeremy R. H. Tame¹ (¹Protein Design Laboratory, Graduate School of Integrated Science, Yokohama City University, ²Department of Molecular Microbiology, Institute of Molecular Biological Sciences, Japan)

- P17/18-063** **X-ray structural and mutagenetic analysis to elucidate the mechanism for determining substrate specificity in homoisocitrate dehydrogenase from an extreme thermophile, *Thermus thermophilus***
Junichi Miyazaki¹, Shinya Fushinobu², Makoto Nishiyama¹ (¹*Biotechnol. Res. Center, Univ. of Tokyo, Dept. of Biotechnol., Univ. of Tokyo, Japan*)
- P17/18-064** **Crystallographic analysis of coenzyme specificity of malate dehydrogenase**
Takeo Tomita¹, Shinya Fushinobu², Makoto Nishiyama¹ (¹*Biotechnology Research Center, The University of Tokyo, Dept. of Biotechnology, The University of Tokyo, Japan*)
- P17/18-065** **Structure of hyperthermostable NAD-specific glutamate dehydrogenase of *Pyrobaculum islandicum***
Mohammad Wadud Bhuiya¹, Haruhiko Sakuraba¹, Toshihisa Ohshima¹, Takahito Imagawa², Nobuhiko Katunuma², Hideaki Tsuge² (¹*Department of Biological Science and Technology, Tokushima University, Institute for Health Science, Japan*)
- P17/18-066** **Cancelled**
- P17/18-067** **Crystal structure of an unique FAD and FMN containing enzyme; Dye-linked L-proline dehydrogenase from *Pyrococcus horikoshii***
Hideaki Tsuge^{1,4}, Ryushi Kawakami², Haruhiko Sakuraba², Kazunari Yoneda², Hideo Ago³, Masashi Miyano³, Kenji Aki¹, Nobuhiko Katunuma¹, Toshihisa Ohshima² (¹*Tokushima Bunri University, Institute for Health Sciences, The University of Tokushima, Faculty of Engineering, RIKEN Harima Inst., Structural Biophysics Laboratory, The University of Tokushima, Institute for Enzyme Research, Japan*)
- P17/18-068** **X-ray Structure of RadB from *Thermococcus kodakaraensis*, a hyperthermophilic Archaeon**
Kazuaki Harata¹, Toshihiko Akiba¹, Masaaki Morikawa², Tadayuki Imanaka³ (¹*Biological Information Research Center, National Institute of Advanced Industrial Science and Technology, Graduate School of Engineering, Osaka University, Graduate School of Engineering, Kyoto University, Japan*)
- P17/18-069** **Structure of putative alanyl-tRNA synthetase from *Pyrococcus horikoshii* OT3**
Jun Ishijima, Yumiko Uchida, Chizu Kuroishi, Chizuru Tuzuki, Nobuo Okazaki, Katsuhide Yutani (*Highthroughput Factory, Riken Harima Institute, Japan*)
- P17/18-070** **Structure of Rat Monoamine Oxidase A and Its Specific Recognitions for Substrates and Inhibitors**
Jichun Ma¹, Masato Yoshimura¹, Eiki Yamashita¹, Atsushi Nakagawa¹, Akio Ito², Tomitake Tsukihara¹ (¹*Institute for Protein Research, Osaka University, Dept. of Chemistry, Faculty of Science, Kyushu University, Japan*)
- P17/18-071** **Structural Double-Mutant Cycle Analysis of a Hydrogen Bond Network In Ketosteroid Isomerase from *Pseudomonas putida* biotype B**
Do Soo Jang¹, Hyung Jin Cha, Bee Hak Hong, Kwan Yong Choi (*Division of Molecular Life Sciences, Pohang University of Science and Technology, Republic of Korea*)
- P17/18-072** **The Structure and Function of the Most Prevalent Mutant Form of Aldolase B Associated with Hereditary Fructose Intolerance**
A.D. Malay¹, K.N. Allen², D.R. Tolan¹ (¹*Dept. of Biology, Boston Univ., Dept. of Physiology and Biophysics, Boston Univ., Sch. of Medicine, United States of America*)
- P17/18-073** **Crystal Structure of Dihydroneopterin Aldolase from *Thermus thermophilus* HB8**
Tamao Hisano¹, Hideyuki Miyatake¹, Kunio Miaki^{1,2} (¹*RIKEN Harima Inst., Grad. Sch. Sci., Kyoto Univ., Japan*)
- P17/18-074** **Creation and Crystallographic Study of a Hyper-active Cysteine- and Methionine-Free Mutant of *Escherichia coli* Dihydrofolate Reductase**
Masahiro Iwakura¹, Kosuke Maki^{1,2}, Hisashi Takahashi¹, Tatsuyuki Takenawa¹, Katsuo Katayanagi³, Kunihiko Gekko³ (¹*National Institute of Advanced Industrial Science and Technology, Department of Physics, Graduate School of Science, University of Tokyo, Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, Japan*)
- P17/18-075** **Crystal structure of *m*-hydroxybenzoate 4-hydroxylase from *Comamonas testosteroni* KH122-3**
Takeshi Hiromoto¹, Keiichi Hosokawa², Shinsuke Fujiwara¹, Hiroshi Yamaguchi¹ (¹*Sch. of Sci. and Technol., Kwansai Gakuin Univ., Inst. of Bio-microbiol., Japan*)

- P17/18-076 X-ray structure analysis of long-chain fatty acyl-CoA synthetase from *Thermus thermophilus* (HB8).**
Yuko Hisanaga¹, Hideo Ago², Hidezo Mori¹, Seiki Kuramitsu^{3,4}, Shigeyuki Yokoyama^{5,6,7}, Masashi Miyano²
(¹Dept. of Cardiac. Phys., NCVC, ²Structural Biophys. Lab., RIKEN Harima Inst., ³Dept. of Biol., Grad. Sch. of Sci., Osaka Univ., ⁴Structurome Re., Group, RIKEN Harima Inst., ⁵Dept. of Biophys. and Biochem., Grad. Sch. of Sci., Univ. of Tokyo, ⁶GSC, RIKEN Yokohama Inst., ⁷Cellular Signaling Lab., RIKEN Harima Inst., Japan)
- P17/18-077 Crystallographic and Kinetic Analysis of the Osmotically Inducible Protein C from *Thermus Thermophilus* HB8**
Peter H. Rehse, Noriyasu Oshima, Yuichi Nodake, Tahir Tahirov (*High ThroughPut Factory, Harima Institute, RIKEN, Japan*)
- P17/18-078 On the Construction of a Model Signaling System with Structural Information: Crystallographic Studies of *Bacillus subtilis* Stress Response Regulators**
Tomonori Kaneko, Hiroyuki Koyama, Daigo Aketa, Nobuo Tanaka, Takashi Kumasaka (*Dept. of Life Science, Grad. School of Bioscience and Biotechnology, Tokyo Institute of Technology, Japan*)
- P17/18-079 The crystal structure of glycosyl transferase family 36 chitobiose phosphorylase from *Vibrio proteolyticus* in complex with GlcNAc and sulfate**
Masafumi Hidaka¹, Yuji Honda², Satoru Nirasawa², Motomitsu Kitaoka², Kiyoshi Hayashi², Takayoshi Wakagi¹, Hirofumi Shoun¹, Shinya Fushinobu¹ (¹Depart. of Biotech., The Univ. of Tokyo, ²NFRI, Japan)
- P17/18-080 Structure and function of *Thermus thermophilus* 2-keto-3-deoxygluconate kinase**
Noriyasu Ohshima¹, Eiji Inagaki¹, Yasuhiro Kajihara², Kiyonori Yasuie², Koji Takio¹, Tahir H. Tahirov¹
(¹Highthroughput Factory, RIKEN Harima Institute, ²Graduate School of Integrated Sciences, Yokohama City University, Japan)
- P17/18-081 Crystal structure of Alginate lyase from *Pseudoalteromonas sp.No.272***
Hiroyuki Motoshima¹, Yoshiko Iwamoto², Tatsuya Oda², Tsuyoshi Muramatsu³, Keiichi Watanabe¹
(¹Department of Applied Biological Sciences, Saga University, ²Division of Biochemistry, Faculty of Fisheries, Nagasaki University, ³Department of Food and Nutrition, Faculty of Food and Nutrition, Beppu University, Japan)
- P17/18-082 Crystal Structure of polyamine Aminopropyltransferase from *Thermus thermophilus***
Tadashi Ganbe¹, Mio Ohnuma², Takao Sato¹, Takashi Kumasaka¹, Tairo Oshima², Nobuo Tanaka¹
(¹Grad. Sch. of Biosci. and Biotech., Tokyo Inst. of Tech., ²Dept. of Mol. Biol., Tokyo Univ. of Pharm. and Life Sci., Japan)
- P17/18-083 Structural comparison between human glucuronyltransferases, GlcAT-P and GlcAT-S, which are involved in the biosynthesis of a neural specific carbohydrate epitope, HNK-1**
Tomoo Shiba¹, Shinako Kakuda², Shogo Oka², Toshisuke Kawasaki², Soichi Wakatsuki¹, Ryuichi Kato¹
(¹Struct. Biol. Res. Cent., PF, IMSS, KEK, ²Dep. of Biol. Chem., Grad. School of Pharma. Sci., Kyoto Univ., Japan)
- P17/18-084 Interaction between Thrombopoietin (TPO) and soluble c-Mpl(TPO-receptor) Explored using Neutralizing Antibody Fragment**
Taro Tamada¹, Michael D. Feese², Yoichi Kato², Yoshitake Maeda¹, Masako Hirose², Yasuko Matsukura², Hideki Shigematsu¹, Takanori Muto¹, Atsushi Matsumoto¹, Hiroshi Watarai¹, Kinya Ogami¹, Tomoyuki Tahara¹, Takashi Kato¹, Hiroshi Miyazaki¹, Ryota Kuroki¹ (¹Pharmaceutical Research Laboratories, Kirin Brewery Co., Ltd., ²Central Laboratories for Key Technology, Kirin Brewery Co. Ltd., Japan)
- P17/18-085 Purification, crystallization and preliminary X-ray analysis of G-CSF/G-CSF receptor (Ig-CRH) complex**
Eijiro Honjo¹, Shouhei Mine¹, Takumi Koshiba³, Tomoyuki Okamoto², Taro Tamada¹, Yoshitake Maeda¹, Yasuko Matsukura¹, Akane Horie¹, Matsujiro Ishibashi⁴, Miharu Sato², Mizue Azuma², Masao Tokunaga⁴, Katsutoshi Nitta³, Ryota Kuroki¹ (¹Pharmaceutical Research Laboratories, Kirin Brewery Co. Ltd., ²Central Laboratories for Key Technology, Kirin Brewer Co. Ltd., ³Division of Biological Sciences, Graduate School of Science, Hokkaido University, ⁴Laboratory of Applied Microbiology, Faculty of Agriculture, Kagoshima University, Japan)

- P17/18-086 Humanization of anti-human EGF receptor antibody variable region: Functional and structural characterization**
Koki Makabe¹, Ryutaro Asano¹, Yukiko Sone¹, Kouhei Tsumoto¹, Hidemasa Kondo², Izumi Kumagai¹
(¹Dept. Biomol. Eng., Grad. Sch. Eng., Tohoku Univ., ²Institute for Biological Researches and Functions, AIST, Japan)
- P17/18-087 Structure and function of the BRCA2-interacting protein EMSY**
Caroline M.S. Ekblad¹, Piku B. Basu², Gayatri Chavali², Aidan J. Doherty², Laura S. Itzhaki¹
(¹Hutchison/MRC Research Centre, Cambridge University, ²Cambridge Institute for Medical Research, Cambridge University, United Kingdom of Great Britain and Northern Ireland)
- P17/18-088 Crystal Structures of the CP1 Domain from Thermus thermophilus Isoleucyl-tRNA Synthetase and Its Complex with L-Valine**
Ryuya Fukunaga¹, Shuya Fukai^{1,5}, Ryuichiro Ishitani¹, Osamu Nureki^{1,2,5}, Shigeyuki Yokoyama^{1,3,4}
(¹Dept. of Biophys. and Biochem., Univ. of Tokyo, ²PREST, ³RIKEN GSC, ⁴RIKEN Harima, ⁵Dept. of Biological Info., TITECH, Japan)
- P17/18-089 De novo structure determination by sulphur (S) and iodine (I) SAD phasing using laboratory Cr K α X-ray equipment**
Hideyuki Miyatake¹, Akihito Yamano^{3,4}, Tomokazu Hasegawa^{3,4}, Kunio Miki^{1,2}
(¹RIKEN Harima Institute, ²Grad. Sch. Sci., Kyoto Univ., ³RIGAKU Corp. X-Ray Research Lab., ⁴PharmAxess, Inc., Japan)
- P17/18-090 Crystal structure determination using Cr X-rays**
Zhi-Jie Liu, John Rose, Bi-Cheng Wang
(Southeast Collaboratory for Structural Genomics, Department of Biochemistry and Molecular Biology, University of Georgia, United States of America)
- P17/18-091 Structural basis of replication origin recognition by the DnaA protein.**
Norie Fujikawa⁵, Hitoshi Kurumizaka⁴, Osamu Nureki³, Takaho Terada¹, Mikako Shirouzu¹, Tsutomu Katayama⁵, Shigeyuki Yokoyama^{1,2,3}
(¹RIKEN GSC, ²RIKEN Harima Institute, ³University of Tokyo, ⁴Waseda Univ., ⁵Kyushu Univ., Japan)
- P17/18-092 Specificities of three PCNAs for the effect on DNA synthesis activities of Poll and Pol II in the hyperthermophilic archaeon, *Aeropyrum pernix*.**
Kaori Imamura¹, Katsuya Daimon², Sonoko Ishino², Ryosuke Fujikane¹, Yoshihiko Sako³, Yutaka Kawarabayashi⁴, Yoshizumi Ishino¹
(¹Dept. of Genetic Resources Technology Faculty of Agriculture, Kyushu University, ²Department of Molecular Biology, Biomolecular Engineering Research Institute, ³Kyoto University, ⁴AIST, Japan)
- P17/18-093 Three-dimensional structure of the clamp loading complex from *Pyrococcus furiosus* : Formation of clamp loading complex**
Tomoko Miyata¹, Kouta Mayanagi¹, Takuji Oyama¹, Yoshizumi Ishino², Kosuke Morikawa¹
(¹Biomolecular Engineering Research Institute, ²Dept. of Genetic Resources Tech., Kyushu Univ, Japan)
- P17/18-094 Three-dimensional structure of an archaeal DNA sliding clamp and Holliday junction resolvase complex**
Shigeki Matsumiya¹, Sonoko Ishino², Yoshizumi Ishino², Kosuke Morikawa¹
(¹Department of Structural Biology, Biomolecular Engineering Research Institute, ²Department of Molecular Biology, Biomolecular Engineering Research Institute, Japan)
- P17/18-095 Role of N-terminal domain of RecA for its filament formation on ssDNA**
Tsutomu Mikawa^{1,2}, Yutaka Ito^{1,2}, Takehiko Shibata^{1,2}
(¹Cellular & Molecular Biology Laboratory, RIKEN, ²CREST, JST, Japan)
- P17/18-096 Structural Basis for Homologous Pairing by the Human Dmc1 Octameric Ring**
Takashi Kinebuchi¹, Wataru Kagawa¹, Rima Enomoto¹, Takehiko Shibata², Hitoshi Kurumizaka^{1,3}, Shigeyuki Yokoyama^{1,4,5}
(¹RIKEN GSC, ²RIKEN CMBL, ³Waseda Univ., ⁴RIKEN Harima at Spring-8, ⁵Univ. of Tokyo, Japan)
- P17/18-097 Crystal structure of the homologous-pairing domain of the human Rad52 protein**
Wataru Kagawa¹, Ako Kagawa¹, Shukuko Ikawa³, Takehiko Shibata³, Hitoshi Kurumizaka⁵, Shigeyuki Yokoyama^{1,2,4}
(¹RIKEN GSC, ²RIKEN Harima at Spring-8, ³RIKEN CMBL, ⁴Univ. of Tokyo, ⁵Waseda Univ., Japan)

- P17/18-098 Functional domains of mouse TBPIP**
Rima Enomoto¹, Hitoshi Kurumizaka^{1,2}, Makoto Sato³, Shigeyuki Yokoyama^{1,4,5} (¹RIKEN,GSC, ²Waseda Univ., Sch. Sci. Eng., ³Fukui Univ., Sch. Med., ⁴RIKEN, Harima Institute at SPring8, ⁵Univ. of Tokyo, Grad. Sch. Sci., Japan)
- P17/18-099 Structure and function of heat-stable homing endonuclease I-Tsp061I, which is encoded by a gene within an archaeal intron**
Hitoshi Nakayama¹, Takahito Imagawa², Hideaki Tsuge^{2,3}, Norimichi Nomura¹, Yoshihiko Sako¹ (¹Division of Applied Biosciences, Graduate School of Agriculture, Kyoto University, ²Tokushima Bunri University, Institute for Health Sciences, ³The University of Tokushima, The Institute for Enzyme Research, Japan)
- P17/18-100 Thermus thermophilus MutS2, a MutS homologue, possesses an endonuclease activity effected by MutL and MutS**
Kenji Fukui¹, Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2} (¹Grad. Sch. Sci., Osaka Univ., ²RIKEN Harima Inst., Japan)
- P17/18-101 Recognition and cleavage of an identical 22-bp target DNA by two structurally distinct endonucleases**
Yayoi Morinaga, Norimichi Nomura, Yoshihiko Sako (*Division of Applied Biosciences, Graduate School of Agriculture, Kyoto University, Japan*)
- P17/18-102 Structural and functional analyses of the nuclease domain of the archaeal structure-specific endonuclease Hef**
Yoshizumi Ishino^{1,3}, Tatsuya Nishino², Kayoko Komori¹, Kosuke Morikawa² (¹Department of Molecular Biology, Biomolecular Engineering Research Institute, ²Department of Structure Biology, Biomolecular Engineering Research Institute, ³Department of Genetic Resources Technology, Faculty of Agriculture, Kyushu University, Japan)
- P17/18-103 Structural insights into substrate recognition and hydrolysis by the MutT protein from Escherichia coli**
Teruya Nakamura¹, Yuki Kitaguchi², Takefumi Doi¹, Mutsuo Sekiguchi³, Yuriko Yamagata² (¹Grad. School of Pharmaceut. Sci., Osaka Univ., ²Grad. School of Pharmaceut. Sci., Kumamoto Univ., ³BERI, Japan)
- P17/18-104 Roles of active site residues in Thermus thermophilus MutM**
Naoko Akiyama¹, Noriko Nakagawa², Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2} (¹Grad. Sch. Sci., Osaka Univ., ²RIKEN Harima Inst./SPring-8)
- P17/18-105 Nucleotide excision repair system of Thermus thermophilus HB8**
Ikumi Saito¹, Noriko Nakagawa^{1,2}, Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2} (¹Dept. Biol., Grad. Sch. Sci., Osaka Univ., ²RIKEN/Harima Inst., Japan)
- P17/18-106 The Solution Structure and the Switch Mechanism of the DNA repair protein Ada from Escherichia coli**
Hiroto Takinowaki, Yasuhiro Matsuda, Takuya Yoshida, Yuji Kobayashi, Tadayasu Ohkubo (*Graduate School of Pharmaceutical Sciences, Osaka University, Japan*)
- P17/18-107 Crystal structure of the human centromere protein B (CENP-B) dimerization domain at 1.65angstrom-resolution**
Maki S. Tawaramoto¹, Sam-Yong Park², Yoshinori Tanaka^{1,3}, Osamu Nureki³, Hitoshi Kurumizaka^{1,4}, Shigeyuki Yokoyama^{1,3,5} (¹Genomic Science Center, RIKEN Yokohama Institute, ²Protein Design Laboratory, Yokohama City University, ³Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo, ⁴Waseda University School of Science and Engineering, ⁵RIKEN Harima Institute at SPring8, Japan)
- P17/18-108 Resonance Raman Characterization of the Heme A Domain of the Newly Discovered CO-dependent Gene Regulatory Protein, NPAS2**
Takeshi Uchida¹, Emiko Sato², Akira Sato¹, Ikuko Sagami², Toru Shimidzu², Teizo Kitagawa¹ (¹Center for Integrative Bioscience, ²Institute of Multidisciplinary Research for Advanced Materials, Tohoku Univ., Japan)
- P17/18-109 Structure of Transcription Factor Sp1 DNA Binding Domain**
Shinichiro Oka¹, Yasuhisa Shiraishi², Takuya Yoshida¹, Tadayasu Ohkubo¹, Yukio Sugiura², Yuji Kobayashi¹ (¹Graduate School of Pharmaceutical Sciences, Osaka University, ²Institute for Chemical Research, Kyoto University, Japan)

- P17/18-110** **in vitro SUMOylation of p53 tumor suppressor**
Daichi Baba¹, Tetsuya Ohta¹, Yasuhiro Uchimura², Hisato Saitoh², Masahiro Shirakawa¹ (¹Grad. Sch. of Integrated Sci. Yokohama City Univ., ²Inst. of Embryol. and Genetics, Dept. of Regeneration Med., Kumamoto Univ., Japan)
- P17/18-111** **The mechanism of transcriptional stimulation by HMGB1 on chromatin structure**
Tetsuya Ueda, Hiroyasu Chou, Toshifumi Kawase, Michiteru Yoshida (Department of Biological Science and Technology, Science University of Tokyo, Japan)
- P17/18-112** **Solution structure of DNA binding domain composed of tandem repeat sequence**
Takeshi Yamaki¹, Kyosuke Kawaguchi¹, Tomoyasu Aizawa¹, Yasuhiro Kumaki¹, Shigeharu Takiya², Makoto Demura¹, Katsutoshi Nitta¹ (¹Graduate School of Science, Hokkaido University, ²Center for Advanced Science and Technology, Hokkaido University, Japan)
- P17/18-113** **Solution structure of the SAND domain of mouse 5830484A20Rik protein**
Naoya Tochio¹, Seizo Koshiba¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Eiko Seki¹, Takayoshi Matsuda¹, Mikako Shirouzu¹, Takaho Terada¹, Mayumi Yoshida¹, Hiroshi Hirota¹, Takashi Osanai¹, Akiko Tanaka¹, Takahiro Arakawa¹, Piero Carninci¹, Jun Kawai¹, Yoshihide Hayashizaki¹, Takanori Kigawa¹, Shigeyuki Yokoyama^{1,2,3} (¹RIKEN Genomic Sciences Center, ²RIKEN Harima Institute., ³Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo, Japan)
- P17/18-114** **Acceptor-Donor-Acceptor protein motifs recognize the Watson-Crick, Hoogsteen and Sugar edges of adenine and adenosine containing ligands in proteins with different folds and functions**
Konstantin A. Denessiouk, Mark S. Johnson (Department of Biochemistry and Pharmacy, Abo Akademi University, Republic of Finland)
- P17/18-115** **Structure-based prediction of DNA-binding sites on proteins using the empirical preference of electrostatic potential and the shape of molecular surfaces**
Yuko Tsuchiya¹, Kengo Kinoshita^{2,3}, Haruki Nakamura¹ (¹Institute for Protein Research, Osaka University, ²Graduate School of Integrated Science, Yokohama City University, ³Structure and Function of Biomolecules, PRESTO, JST, Japan)
- P17/18-116** **Thermodynamic Database for Protein-Nucleic Acid Interactions (ProNIT): New Developments**
Shaji Kumar Mattathil Damodaran¹, Prabakaran Ponraj², Hatsuho Uedaira¹, Gromiha Michael³, Kouji Kitajima¹, Akinori Sarai¹ (¹Dept. of Biochemical Engineering & Science, Kyushu Institute of Technology (KIT), ²NIH, USA, ³CBRC, AIST, Tokyo, Japan)
- P17/18-117** **Contracted Inchworm Structure of Vasa DEAD-box RNA Helicase in the RNA- and ATP-bound Form**
Toru Sengoku¹, Osamu Nureki², Akira Nakamura³, Satoru Kobayashi⁴, Shigeyuki Yokoyama^{1,5,6} (¹Grad. Sch. Sci., Univ. of Tokyo, ²Grad. Sch. Biosci. and Biotechnol., Tokyo Inst. Technol., ³CDB, RIKEN, ⁴Ctr. Integrat. Biosci., Okazaki Natl. Res. Inst., ⁵Cellular Signaling Lab., RIKEN, ⁶GSC, RIKEN, Japan)
- P17/18-118** **Origin of high affinity to RNA of Musashi, structure of hnRNP D complexed with telomere DNA, and DNA chaperon activity**
Youhei Miyanoiri¹, Yoshiaki Enokizono¹, Yuki Konishi¹, Kayoko Marumoto¹, Seiichi Uesugi¹, Takao Imai², Hideyuki Okano², Fuyuki Ishikawa³, Hirokazu Fukuda⁴, Naoto Tsuchiya⁴, Takashi Sugimura⁴, Minako Nagao⁴, Hitoshi Nakagama⁴, Masato Katahira¹ (¹Yokohama National University, ²Keio University School of Medicine, ³Kyoto University, ⁴National Cancer Center Research Institute, Japan)
- P17/18-119** **Domain architecture of an RNA binding protein, TLS/FUS**
Yuko Iko¹, Takashi S. Kodama², Eugene H. Morita³, Mika Okumura¹, Takanori Muto¹, Ritsuko Fujii⁴, Toru Takumi⁴, Hisato Jingami¹, Kosuke Morikawa¹ (¹Biomolecular Engineering Research Institute, ²Japan Biological Information Research Center, JBiC, ³INCS, Ehime Univ., ⁴Osaka Bioscience Institute, Japan)
- P17/18-120** **Development of the method for detecting RNA-binding proteins with OB-fold**
Shingo Kikugawa, Makoto Kimura (Laboratory of Biochemistry, Department of Bioscience and Biotechnology, Faculty of Agriculture, Graduate School, Kyushu University, Japan)
- P17/18-121** **Bimodal nickel-binding mode mediated by the C-terminal tail of Bacillus pasteurii UreE**
Ji-hun Kim, Hyung-Sik Won, Yeon-Hee Lee, Sung-Jean Park, Seo-Jeong Jung, Bong-Jin Lee (Natl. Res. Lab. (MPS), Coll. of Pharmacy, Seoul Natl. Univ., Republic of Korea)

- P17/18-122 Structure-function relationship of gaegurin 5, an antimicrobial peptide isolated from a Korean frog**
 Su-Jin Kang, Seo-Jeong Jung, Hyung-Sik Won, Sang-Ho Park, Bong-Jin Lee (*Natl. Res. Lab. (MPS), Res. Inst. of Pharmaceutical Sciences, Coll. of Pharmacy, Seoul Natl. Univ., Republic of Korea*)
- P17/18-123 Structure-function relationship of peptide analogues of gaegurin 4, an antimicrobial peptide isolated from a Korean frog**
 Yong-Jin Kim, Hyung-Sik Won, Bong-Jin Lee (*Natl. Res. Lab. (MPS), Coll. of Pharmacy, Seoul Natl. Univ., Republic of Korea*)
- P17/18-124 Solution structure and structure-activity relationship of the crustacean molt-inhibiting hormone**
 Hidekazu Katayama¹, Tsuyoshi Ohira², Shinji Nagata¹, Koji Nagata¹, Masaru Tanokura¹, Hiromichi Nagasawa¹ (¹*Dept. of Applied Biological Chemistry, Grad. School of of Agricultural and Life Sciences, The Univ. of Tokyo*, ²*Grad. School of Marine Science and Technology, Tokyo Univ. of Marine Science and Technology, Japan*)
- P17/18-125 Purification, characterization and structure elucidation of two toxins and a comparison between the toxic properties of the toxins and a glycoprotein purified from puffer fish**
 Nurul Absar, Md. Sohel Hasan (*Department of Biochemistry and Molecular Biology, University of Rajshahi, People's Republic of Bangladesh*)
- P17/18-126 Solution Structure of a Ubiquitin-like Domain in Mouse Tubulin-specific Chaperone B**
 Chenhua Zhao¹, Takanori Kigawa¹, Kohei Saito¹, Sheizo Koshiba¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Eiko Seki¹, Takayoshi Matsuda¹, Mikako Shirouzu¹, Takaho Terada¹, Mayumi Yoshida¹, Hiroshi Hirota¹, Takashi Osanai¹, Akiko Tanaka¹, Takahiro Arakawa¹, Piero Carninci¹, Jun Kawai¹, Yoshihide Hayashizaki¹, Shigeyuki Yakoyama^{1,2,3} (¹*GSC, RIKEN*, ²*Harima, RIKEN*, ³*University of Tokyo, Japan*)
- P17/18-127 Structure of the ubiquitin-interacting motif of S5a bound to the ubiquitin-like domain of HR23B**
 Kenichiro Fujiwara¹, Takeshi Tenno^{1,2}, Kaoru Sugawara³, Jun-Goo Jee^{1,4}, Izuru Ohki⁵, Chojiro Kojima⁶, Hidehito Tochio¹, Hidekazu Hiroaki¹, Fumio Hanaoka³, Masahiro Shirakawa^{1,4} (¹*Graduate School of Integrated Science, Yokohama City University*, ²*Graduate School of Science and Engineering, Ehime University*, ³*Cellular Physiology Laboratory, Discovery Research Institute, RIKEN*, ⁴*Genomic Sciences Center, RIKEN*, ⁵*Department of Structural Biology, Biomolecular Engineering Research Institute*, ⁶*Graduate School of Biological Sciences, Nara Institute of Science and Technology*, ⁷*Graduate School of Frontier Biosciences, Osaka University, Japan*)
- P17/18-128 The higher order structures of polyubiquitin chains in solution**
 Takeshi Tenno¹, Kenichiro Fujiwara¹, Hidehito Tochio¹, Kazuhiro Iwai², Shigeo Murata³, Hidekazu Hiroaki¹, Mamoru Sato¹, Keiji Tanaka³, Masahiro Shirakawa¹ (¹*Grad. Sch. of Integrated Sci., Yokohama City Univ.*, ²*Grad. Sch. of Med., Osaka City Univ.*, ³*Dept. of Mol. Oncol., Tokyo Metro. Inst. of Med. Sci., Japan*)
- P17/18-129 NMR study on the interaction between the UBA domain of budding yeast DSK2p and the ubiquitin.**
 Ayako Ohno^{1,2}, Hidekazu Hiroaki², Kenichiro Fujiwara², Jee JunGoo^{2,3}, Takeshi Tenno^{2,4}, Hidehito Tochio², Hideki Kobayashi⁵, Masahiro Shirakawa² (¹*Kihara Memorial Yokohama Foundation for the Advancement of Life Science*, ²*Yokohama City Univ., Graduate School of Integrated Sci.*, ³*RIKEN GSC*, ⁴*Ehime Univ., Graduate School Sci. Eng.*, ⁵*Kyushu Univ., Graduate School Med. Sci., Japan*)
- P17/18-130 Solution structure of ribosomal protein L16 from *Thermus thermophilus***
 Mitsuhiro Nishimura¹, Takuya Yoshida¹, Mikako Shirouzu^{2,3}, Takaho Terada^{2,3}, Seiki Kuramitsu^{4,5}, Shigeyuki Yokoyama^{2,3,5,6}, Tadayasu Ohkubo¹, Yuji Kobayashi¹ (¹*Grad. Sch. of Pharm. Sci., Osaka Univ.*, ²*GSC, RIKEN Yokohama Inst.*, ³*Cellular Signaling Lab., RIKEN Harima Inst.*, ⁴*Structurome Project, RIKEN Harima Inst.*, ⁵*Grad. Sch. of Sci., Osaka Univ.*, ⁶*Dept. of Biophys. and Biochem., Grad. Sch. of Sci., Univ. of Tokyo, Japan*)
- P17/18-131 Solution Structure of the Pleckstrin Homology (PH) Domain of Sbf1 from Mouse**
 Hua Li¹, Seizo Koshiba¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Eiko Seki¹, Takayoshi Matsuda¹, Mikako Shirouzu¹, Takaho Terada¹, Mayumi Yoshida¹, Hiroshi Hirota¹, Takashi Osanai¹, Akiko Tanaka¹, Takahiro Arakawa¹, Piero Carninci¹, Jun Kawai¹, Yoshihide Hayashizaki¹, Takanori Kigawa¹, Shigeyuki Yokoyama^{1,2,3} (¹*GSC, RIKEN Yokohama*, ²*RIKEN Harima*, ³*Graduate School of Sci., Univ. of Tokyo, Japan*)

- P17/18-132 Tandem PDZ repeats in glutamate receptor-interacting proteins have a novel mode of PDZ domain-mediated target binding**
Wei Feng, Yawei Shi, Ming Li, Mingjie Zhang (*Department of Biochemistry, Hong Kong University of Science and Technology, Hong Kong*)
- P17/18-133 The structural characterization of TRADD death domain**
Yun M. Ko¹, Chi H. Park², Si M. Byun², Key S. Kim¹ (¹*Biomedical Research Center, Life Sciences Division, Korea Institute of Science and Technology,* ²*Biochemistry/Molecular Biology Lab, Dep. of Biological Sciences, Korea Advanced Institute of Science and Technology, Republic of Korea*)
- P17/18-134 Solution structure of the RWD domain of the mouse GCN2 protein**
Nobukazu Nameki¹, Misao Yoneyama¹, Seizo Koshiba¹, Naoya Tochio¹, Makoto Inoue¹, Eiko Seki¹, Takayoshi Matsuda¹, Yasuko Tomo¹, Kohei Saito¹, Naohiro Kobayashi¹, Takashi Yabuki¹, Masaaki Aoki¹, Emi Nunokawa¹, Natsuko Matsuda¹, Noriko Sakagami¹, Takaho Terada¹, Mikako Shirouzu¹, Mayumi Yoshida¹, Hiroshi Hirota¹, Takashi Osanai¹, Akiko Tanaka¹, Takahiro Arakawa¹, Piero Carninci¹, Jun Kawai¹, Yoshihide Hayashizaki¹, Kengo Kinoshita^{1,2,3}, Peter Güntert¹, Takanori Kigawa¹, Shigeyuki Yokoyama^{1,4,5} (¹*RIKEN Genomic Sci. Center,* ²*Grad. Sch. of Integrated Sci., Yokohama City Univ.,* ³*PRESTO, Japan Sci. and Tech. Corp.,* ⁴*RIKEN Harima Inst.,* ⁵*Grad. Sch. of Sci., Univ. of Tokyo, Japan*)
- P17/18-135 The structure of yeast TFA2 C-terminal domain**
Nobuyuki Kasai, Izuru Ohki, Shin-ichi Tate (*The Dept. of Structural Biology, BERI, Japan*)
- P17/18-136 Solution Structure of a General Transcription Factor 2I Domain in Mouse TFII-I Protein Short Form**
Yukiko Doi-Katayama¹, Fumiaki Hayashi¹, Satoru Kubo², Kazuhito Sato¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Eiko Seki¹, Takayoshi Matsuda¹, Mayumi Yoshida¹, Mikako Shirouzu¹, Takaho Terada¹, Takahiro Arakawa¹, Piero Carninci¹, Jun Kawai¹, Yoshihide Hayashizaki¹, Takashi Osanai¹, Akiko Tanaka¹, Shigeyuki Yokoyama^{1,3,4}, Hiroshi Hirota^{1,2} (¹*RIKEN Genomic Sciences Center,* ²*Graduate School of Integrated Science, Yokohama City University,* ³*Cellular Signaling Laboratory, RIKEN Harima Institute at SPring-8,* ⁴*Department of Biochemistry, Graduate School of Science, The University of Tokyo, Japan*)
- P17/18-137 SOLUTION STRUCTURE OF HBS1-LIKE DOMAIN IN HYPOTHETICAL PROTEIN BAB28515**
F. He^{1,2,3}, Y. Muto¹, M. Hayami¹, M. Shirouzu¹, T. Terada¹, T. Kigawa¹, M. Inoue¹, T. Yabuki¹, M. Aoki¹, E. Seki¹, T. Matsuda¹, H. Hirota¹, M. Yoshida¹, N. Kabayashi¹, A. Tanaka¹, T. Osanai², Y. Matsuo², Y. Hayashizaki¹, S. Yokoyama^{1,2,3} (¹*RIKEN Genomic Sciences Center,* ²*RIKEN Harima Institute at SPring-8,* ³*Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo, Japan*)
- P17/18-138 Structure of the TSR-1 domain of F-spondin**
Kimmo Paakkonen¹, Ilkka Kilpelainen², Harri Rakkolainen², Erkki Raulo², Heikki Rauvala², Peter Guentert¹ (¹*RIKEN Genomic Sciences Center,* ²*Institute of Biotechnology, University of Helsinki, Japan*)
- P17/18-139 NMR studies on the 56kDa *Escherichia coli* nickel-binding protein NikA**
Yutaka Ito^{1,2,3}, Sundareshan Rajesh^{1,4}, Jonathan Heddle⁴, Kaori Kurashima^{1,2}, Daniel Nietlispach⁵, Masahiro Shirakawa⁶, Jeremy Tame⁴ (¹*Research Group for Bio-supramolecular Structure-Function, RIKEN,* ²*Molecular and Cellular Physiology Lab., Yokohama City Univ.,* ³*CREST/JST,* ⁴*Protein Design Lab., Yokohama City Univ.,* ⁵*Dept. of Biochemistry, Univ. of Cambridge,* ⁶*Molecular Biophysics Lab., Yokohama City Univ., Japan*)
- P17/18-140 Solution structure of CwlCr, a peptidoglycan binding domain of a cell wall lytic amidase**
Masaki Mishima¹, Ken-ichi Kato¹, Toshio Shida², Junichi Sekiguchi², Chojiro Kojima¹ (¹*Graduate School of Biological Sciences, Nara Institute of Science and Technology,* ²*Department of Applied Biology, Faculty of Textile Science and Technology, Shinshu University, Japan*)
- P17/18-141 NMR studies on the conformational ferredoxin-NADP+ reductase and insight into the role of N-terminal region**
Young H. Lee¹, Masahiro Maeda¹, Kohsuke Tamura¹, Takahisa Ikegami¹, Masaru Hoshino¹, Toshio Yamazaki³, Toshiharu Hase¹, Yuji Goto^{1,2} (¹*Institute for Protein Research, Osaka University,* ²*CREST, JST,* ³*Genomics Sciences Center, RIKEN, Japan*)
- P17/18-142 Domain-domain interaction of protein disulfide isomerase as revealed by NMR spectroscopy**
Michiko Nakano^{1,2}, Yoshiki Yamaguchi^{1,2}, Chiho Murakami¹, Takushi Harada¹, Eiji Kurimoto^{1,2}, Osamu Asami³, Tsutomu Kajino³, Kenji Inaba⁴, Koichi Kato^{1,2} (¹*Dept. Struct. Biol. Biomol. Engin., Grad. Sch. of Pharm. Sci., Nagoya City Univ.,* ²*CREST/JST,* ³*Toyota Central Research & Development Labs., Inc.,* ⁴*Inst. for Virus Research, Kyoto Univ., Japan*)

- P17/18-143 Structure-activity relationships of HIV-2 Nucleocapsid Protein**
Takashi Matsui¹, Takeshi Tanaka², Hiroshi Endoh¹, Misa Nagai¹, Hiroyoshi Komatsu³, Toshiyuki Kohno², Kazuki Sato^{2,4}, Yoshio Kodera¹, Tadakazu Maeda¹ (¹*Dept. of Physics, Sch. of Sci., Kitasato Univ.*, ²*Mitsubishi Kagaku Inst. of Life Sci. (MITILS)*, ³*Dept. of Immunol., Sch. of AHS., Kitasato Univ.*, ⁴*Sch. of Human Environmental Sci., Fukuoka Women's Univ., Japan*)
- P17/18-144 Evidence of intradomain interaction in FADD**
Jong hui Hong^{1,2}, Kyeong-Ae Kim¹, Bong-Jin Lee², Key-Sun Kim¹ (¹*Biomedical Research Center, Korea Institute of Science and Tehcnology*, ²*Department of Physical Pharmacy, College of Pharmacy, Seoul National University Republic of Korea*)
- P17/18-145 Solution structure of the N-terminal DCX domain of doublecortin-like kinase**
Kohei Saito¹, Seizo Koshiba¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Eiko Seki¹, Takayoshi Matsuda¹, Yoko Motoda¹, Hajime Inamochi¹, Takaho Terada¹, Mikako Shirouzu¹, Hiroshi Hirota¹, Mayumi Yoshida¹, Takahiro Nagase², Reiko Kikuno², Manabu Nakayama², Osamu Ohara^{2,3}, Akiko Tanaka¹, Takanori Kigawa¹, Shigeyuki Yokoyama^{1,4,5} (¹*RIKEN Genomic Sciences Center*, ²*Facility for Genome Structure Analysis, Kazusa DNA Research Institute*, ³*RIKEN Research Center for Allergy and Immunology*, ⁴*RIKEN Harima Institute at SPring-8*, ⁵*Department of Biophysics and Biochemistry, Graduate School of Science, the University of Tokyo, Japan*)
- P17/18-146 A new paramagnetic NMR agent, Cu²⁺-IDA, to obtain long-range distance information**
Makoto Nomura¹, Toshitsatu Kobayashi¹, Toshiyuki Kohno², Masaki Mishima¹, Chojiro Kojima¹ (¹*Graduate School of Biological Science, Nara Institute of Science and Technology*, ²*Mitsubishi Kagaku Institute of Life Sciences, Japan*)
- P17/18-147 Automated NMR Structure Calculation with CYANA 2.0**
Blanca Lopez-Mendez, Jee Jun-Goo, David Pantoja-Uceda, Peter Guentert (*Protein Research Group, RIKEN Genomic Sciences Center, Japan*)
- P17/18-148 Modelbuilding of a Protein-Protein complex structures using NMR information of saturation transfer and residual dipolar coupling**
Tomoki Matsuda, Takahisa Ikegami, Nobuyuki Nakajima, Haruki Nakamura (*Institute for Protein Research, Osaka University, Japan*)
- P17/18-149 A new algorithm for NMR protein structure determination without chemical shift assignment**
JunGoo Jee, Blanca Lopez-Mendez, Peter Guntert (*Genomic Sciences Center, RIKEN, Japan*)
- P17/18-150 Length-dependent characteristics of domain linker loops in multi-domain proteins**
Takanori Tanaka, Yutaka Kuroda, Shigeyuki Yokoyama (*Protein Research Group, Genomic Sciences Center, RIKEN, Japan*)
- P17/18-151 The PRESAT-Vector. Asymmetric T-vector for expression and screening of soluble protein domains for structural proteomics.**
Hidekazu Hiroaki¹, Takeshi Tenno^{1,2}, Natsuko Goda¹, Masahiro Shirakawa¹ (¹*Graduate School of Integrated Science, Yokohama City University*, ²*Graduate School of Science, Ehime University, Japan*)
- P17/18-152 Large scale protein crystallization system**
Masahiko Hiraki¹, Ryuichi Kato¹, Minoru Nagai², Soichi Wakatsuki¹ (¹*Structural Biology Research Center, Photon Factory, KEK*, ²*Mechanical Engineering Center, KEK, Japan*)
- P17/18-153 Integrated Fluidic Circuits: The New Paradigm for Protein Crystallization**
Andrew May (*Fluidigm Corporation, United States of America*)
- P17/18-154 High Speed and High Reliably Protein Crystal Imaging**
Matt Thompson (*Veeco Instruments, Japan*)
- P17/18-155 Effective Protein Crystal Growth by Solution Stirring**
Mari Yaoi¹, Hiroaki Adachi^{1,2,3}, Hiroyoshi Matsumura^{1,2,3}, Kazufumi Takano^{1,2,3}, Tsuyoshi Inoue^{1,2,3}, Yusuke Mori^{1,2,3}, Takatomo Sasaki^{1,2} (¹*Graduate School of Engineering, Osaka University*, ²*SOSHO project (Crystal Design Project)*, ³*NEDO, Japan*)
- P17/18-156 Protein Crystallization Using Novel Stirring Technique**
Ai Niino¹, Hiroaki Adachi^{1,2,3}, Hiroyoshi Matsumura^{1,2,3}, Kazufumi Takano^{1,2,3}, Tsuyoshi Inoue^{1,2,3}, Yusuke Mori^{1,2,3}, Takatomo Sasaki^{1,2} (¹*SOSHO project (Crystal Design Project), Osaka University*, ²*Graduate School of Engineering, Osaka University*, ³*NEDO, Japan*)

- P17/18-157** **A high-throughput protein structure analysis system of the Structural Genomics Consortium for research on Gene Expression System (SGCGES)**
Naoki Sakai, Min Yao, Nobuhisa Watanabe, Isao Tanaka (*Division of Biological Sciences, Graduate School of Science, Hokkaido University, Japan*)
- P17/18-158** **Ligand Screening for the Comprehensive Structural and Functional Analyses of Proteins**
Naoei Yoshitani, Kazuhito Satou, Kazuki Saito, Hiroshi Hirota, Shigeyuki Yokoyama (*Protein Research Group, RIKEN Genomic Sciences Center, Japan*)
- P17/18-159** **Structural genomics on C2 domain of synaptotagmin IV and RIM2 related to neurotransmitter release at presynaptic membrane**
Toshio Nagashima¹, Fumiaki Hayashi¹, Mikako Shirouzu¹, Takaho Terada¹, Takanori Kigawa¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Takayoshi Matsuo¹, Takahiro Nagase², Reiko Kikuno², Manabu Nakayama², Osamu Ohara^{2,3}, Shigeyuki Yokoyama^{1,4,5} (*¹RIKEN Genomic Sciences Center, ²Kazusa DNA Research Institute, ³RIKEN Research Center for Allergy and Immunology, ⁴RIKEN Harima Institute, ⁵Graduate School of Science, University of Tokyo, Japan*)
- P17/18-160** **Crystal structure determination by phasing with anomalous signal measured using in-house X-ray radiation**
Yu Kitago, Nobuhisa Watanabe, Isao Tanaka (*Graduate School of Science, Hokkaido University, Japan*)
- P17/18-161** **Whole Cell Project of *Thermus thermophilus* HB8 toward Atomic-Resolution Biology: Prediction of the coding sequences**
Ryoji Masui^{1,2}, Ken Kurokawa³, Noriko Nakagawa², Takaho Terada⁴, Mikako Shirouzu⁴, Yoshinori Koyama⁵, Fumio Tokunaga¹, Tairo Oshima⁶, Takehiko Shibata⁴, Yorinao Inoue⁴, Teruo Yasunaga³, Kunio Miki⁴, Shigeyuki Yokoyama^{2,4}, Seiki Kuramitsu^{1,2,4} (*¹Grad. Sch. Sci., Osaka Univ., ²RIKEN Harima Inst., ³Genomic Information Res. Cent., Osaka Univ., ⁴RIKEN Genomic Sciences Center, ⁵Nat. Inst. Biosci. Human Tech., MITI, ⁶Dept. Mol. Biol., Tokyo Univ. Pharm. Life Sci., Japan*)
- P17/18-162** **Whole Cell Project of *Thermus thermophilus* HB8 toward Atomic-Resolution Biology: Protein Expression and Purification**
Akio Ebihara¹, Noriko Nakagawa^{1,2}, Yukihide Kousumi¹, Shinya Satoh¹, Yoshihiro Agari¹, Nobuko Maoka¹, Kazuko Agari¹, Hitoshi Iino¹, Aiko Kashihara¹, Yumiko Inoue¹, Ryoji Masui^{1,2}, Mikako Shirouzu^{1,3}, Takaho Terada^{1,3}, Kunio Miki^{1,4}, Shigeyuki Yokoyama^{1,3,5}, Seiki Kuramitsu^{1,2,3} (*¹RIKEN Harima Inst./SPRING-8, ²Grad. Sch. of Sci., Osaka Univ., ³RIKEN Genomic Sciences Center, ⁴Grad. Sch. of Sci., Kyoto Univ., ⁵Grad. Sch. of Sci., Univ. of Tokyo, Japan*)
- P17/18-163** **Whole Cell Project of *Thermus thermophilus* HB8 toward atomic-resolution biology: protein crystallization and structural determination**
Noriko Nakagawa¹, Akio Ebihara¹, Yukihide Kousumi¹, Shinya Satoh¹, Yoshihiro Agari¹, Nobuko Maoka¹, Kazuko Agari¹, Hitoshi Iino¹, Aiko Kashihara¹, Yumiko Inoue¹, Takaho Terada², Mikako Shirouzu², Ryoji Masui³, Kunio Miki^{1,4}, Shigeyuki Yokoyama^{1,2,5}, Seiki Kuramitsu^{1,2,3} (*¹RIKEN Harima Inst./SPRING-8, ²Genomic Sciences Center, RIKEN Yokohama Inst., ³Grad. Sch. of Sci., Osaka Univ., ⁴Grad. Sch. of Sci., Kyoto Univ., ⁵Grad. Sch. of Sci., Univ. of Tokyo, Japan*)
- P17/18-164** **Whole Cell Project of *Thermus thermophilus* HB8 toward Atomic-Resolution Biology: Development of collaborative annotation system for *Thermus thermophilus* HB8 on OBIGrid**
Akinobu Fukuzaki^{1,3}, Fumikazu Konishi^{1,3}, Takeshi Nagashima¹, Kaori Ide^{1,3}, Mariko Hatakeyama^{1,3}, Shigeyuki Yokoyama^{3,4,5}, Seiki Kuramitsu^{2,3}, Akihiko Konagaya^{1,3} (*¹Bioinformatics Group, RIKEN GSC, ²Grad. Sch. of Sci., Osaka Univ., ³Harima Inst./Spring-8, ⁴Grad. Sch. of Sci., Univ. of Tokyo, ⁵Protein Res. Group, RIKEN GSC, Japan*)
- P17/18-165** **Whole cell project of *Thermus thermophilus* HB8 toward Atomic-Resolution Biology: Towards a metabolic simulation of tryptophan operon regulation in *Thermus thermophilus* HB8**
Kaori Ide^{1,5}, Takuji Kawasaki², Mariko Hatakeyama^{1,5}, Keiichiro Tanaka³, Mitsutoshi Toyama⁴, Mikako Shirouzu^{4,5}, Shigeyuki Yokoyama^{3,4,5}, Seiki Kuramitsu^{5,6}, Akihiko Konagaya^{1,5} (*¹RIKEN GSC Bioinformatics Group, ²Fuji Res. Corp., ³Univ. of Tokyo, ⁴RIKEN GSC Protein Research Group, ⁵RIKEN Harima, ⁶Osaka Univ., Japan*)
- P17/18-166** **Identification of *Thermus thermophilus* TT1383 revealed a novel dNTP triphosphohydrolase activity stimulated by dATP and dTTP**
Naoyuki Kondo¹, Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2} (*¹Dept. of Biol., Grad. Sch. of Sci., Osaka Univ., ²RIKEN, Harima Inst., Japan*)

- P17/18-167 Functional inference of a hypothetical protein: a cofactor binding predicted from the structural analysis**
 Akio Ebihara¹, Akihiro Okamoto^{1,2}, Yukihide Kousumi¹, Hitoshi Yamamoto³, Ryoji Masui^{1,4}, Norikazu Ueyama³, Shigeyuki Yokoyama^{1,5,6}, Seiki Kuramitsu^{1,4,6} (¹RIKEN Harima Inst./SPRING-8, ²Dept. of Biochem., Osaka Medical College, ³Dept. of Chem., Grad. Sch. of Sci., Osaka Univ., ⁴Dept. of Biol., Grad. Sch. of Sci., Osaka Univ., ⁵Dept. of Biophys. and Biochem., Grad. Sch. of Sci., Univ. of Tokyo, ⁶RIKEN Genomic Sciences Center, Japan)
- P17/18-168 Comprehensive structure-based functional analysis of transcription factors**
 Hiroshi Itou, Ui Okada, Min Yao, Nobuhisa Watanabe, Isao Tanaka (*Division of Biological Sciences, Graduate School of Science, Hokkaido University, Japan*)
- P17/18-169 The Extra C-terminal Fragment of Cytochrome b Is Required for Structural Integrity of the cytochrome bc₁ Complex from Rhodobacter sphaeroides.**
 Linda Yu, Xiaoying Liu, Chang-An Yu (*Department of Biochemistry and Molecular Biology, Oklahoma State University, United States of America*)
- P17/18-170 Effect of chemical modification on energy-transducing reactions in the mitochondrial cytochrome bc₁ complex**
 Toshiaki Miki, Yoshie Harada (*Depart. Mol. Physiol., Tokyo Metropolitan Institute of Medical Science, Japan*)
- P17/18-171 Resonance Raman Characterization of the P Intermediate in the Reaction of Mixed-Valence Cytochrome c Oxidase with Dioxide**
 Kenji Oda¹, Takashi Ogura¹, Evan H. Appelman², Shinya Yoshikawa¹ (¹Himeji Institute of Technology, ²Chemistry Division, Argonne National Laboratory, Japan)
- P17/18-172 Oxygen activation by cytochrome c oxidase in intact mitochondria as probed by time-resolved resonance Raman spectroscopy**
 Toshinari Takahashi^{1,2}, Takashi Ogura², Shinya Yoshikawa² (¹Grad. Sch. Arts Sci., Univ. of Tokyo, ²Fac. of Sci., Himeji Inst. Tech., Japan)
- P17/18-173 A Model Study of CH=O (Heme a)-Arg³⁸ Hydrogen Bond of Cytochrome c Oxidase with Resonance Raman Spectroscopy**
 Shigeki Kuroiwa¹, Shintaro Kitaoka¹, Hiroshi Fujii², Takashi Ogura^{1,3}, Shinya Yoshikawa³ (¹Department of Life Science, Graduate School of Arts and Sciences, The University of Tokyo, ²Institute for Molecular Science, Okazaki National Research Institutes, ³Department of Life Science, Graduate School of Science, Himeji Institute of Technology, Japan)
- P17/18-174 Expression of extramembrane subunit Vb of bovine cytochrome c oxidase as a soluble protein in *E. coli***
 Kazuhiro Yamanoi¹, Kunitoshi Shimokata^{1,2}, Aya Hosokawa³, Yukie Katayama^{1,2}, Haruka Murayama¹, Takako Hishiki¹, Tomitake Tsukihara⁴, Hideo Shimada¹ (¹Dept. of Biochem., Sch. of Med., Keio Univ., ²JBIC, ³Tamagawa Univ., ⁴Inst. of Protein Res. Osaka Univ., Japan)
- P17/18-175 FTIR Study of Proton Pumping Mechanism of Bovine Cytochrome c Oxidase**
 Daichi Okuno¹, Tadashi Iwase², Kyouko Shinzawa-Itoh³, Shinya Yoshikawa³, Teizo Kitagawa² (¹Dept. of Photosci., The Grad. Univ. for Advanced Studies, ²Center for Integrative Bioscience, Okazaki Natl. Res. Inst., ³Dept. of Life Sci. Himeji Inst. Tech., Japan)
- P17/18-176 Role of aromatic rings in cytochrome c₃ from *Desulfovibrio vulgaris* Miyazaki F**
 Yuki Takayama¹, Erisa Harada^{1,2}, Rie Kobayashi³, Kiyoshi Ozawa³, Hideo Akutsu¹ (¹Institute for Protein Research, Osaka University, ²Japan Biological Informatics Consortium, ³Yokohama National University, Japan)
- P17/18-177 Characterization of the pH-dependent transitions of archaeal high- and low-potential Rieske-type Proteins**
 Toshio Iwasaki¹, Asako Kounosu¹, Sergei A. Dikanov², Daijiro Ohmori³, Yoko Hayashi-Iwasaki⁴, Akihisa Jin⁵, Takeo Imai⁵, Akio Urushiyama⁵ (¹Dept. of Biochem. and Mol. Biol., Nippon Med. Sch., Japan, ²Dept. of Veterinary Clinical Med., Univ. of Illinois at Urbana-Champaign, The United States of America, ³Dept. of Chemistry, Juntendo Univ., ⁴Dept. of Bioengineering, Nagaoka Univ. of Tech., ⁵Dept. of Chemistry, Rikkyo (St Paul's) Univ., Japan)

- P17/18-178 Biochemical Characterization of the Menaquinone-driven Disulfide Bond Formation Pathway of *Escherichia coli***
Yoh-hei Takahashi¹, Kenji Inaba^{1,2}, Koreaki Ito^{1,3} (¹*Inst. for Virus Res., Kyoto Univ.*, ²*JST PRESTO*, ³*JST CREST, Japan*)
- P17/18-179 Local structures and dynamics of bacteriorhodopsin as revealed by solid state ¹³C NMR spectroscopy**
Akira Naito, Izuru Kawamura, Masato Ohmine, Katsuyuki Nishimura (*Graduate School of Engineering, Yokohama National University, Japan*)
- P17/18-180 NMR Characterization of Subcomplexes of TF₁-ATPase**
Masumi Kobayashi¹, Hiromasa Yagi¹, Takuya Tsujimoto¹, Toshio Yamazaki², Masasuke Yoshida³, Hideo Akutsu¹ (¹*Institute for Protein Research, Osaka University*, ²*Genome Sciences Center, RIKEN Yokohama Institute*, ³*Chemical Resources Laboratory, Tokyo Institute of Technology, Japan*)
- P17/18-181 Structural Analysis of Transmembrane Halobacterial Transducer pHtrII by High-Resolution Two-Dimensional Solid-State ¹³C NMR**
Yoh Matsuki^{1,4}, Yuki Sudo², Chojiro Kojima³, Naoki Kamo², Toshimichi Fujiwara¹, Hideo Akutsu¹ (¹*Institute for Protein Research, Osaka University*, ²*Graduate School of Pharmaceutical Science, Hokkaido University*, ³*Graduate School of Biological Science, Nara Institute for Science and Technology*, ⁴*Japan Science and Technology Agency (JST), Japan*)
- P17/18-182 Solution structure of the third PDZ domain of synapse-associated protein (SAP) 102.**
Xu-rong Qin¹, Fumiaki Hayashi¹, Toshio Nakashima¹, Mikako Shirouzu¹, Takaho Terada¹, Takanori Kigawa¹, Makoto Inoue¹, Takashi Yabuki¹, Masaaki Aoki¹, Takayoshi Matsuo¹, Takahiro Nagase², Reiko Kikuno², Manabu Nakayama², Osamu Ohara^{2,4}, Shigeyuki Yokoyama^{1,3,5} (¹*RIKEN Genomic Sciences Center*, ²*Kazusa DNA Research Institute*, ³*RIKEN Harima Institute*, ⁴*RIKEN Research Center for Allergy and Immunology*, ⁵*Graduate School of Science, University of Tokyo, Japan*)
- P17/18-183 Conformational resemblance between the structures of integrin-activating pentapeptides derived from β ig-h3 and RGD peptide analogues in a membrane environment.**
Yoo-Sun Jung, Sung-Jean Park, Sang-ho Park, Hee-Chul Ahn, In-San Kim¹, Bong-Jin Lee¹ (*Natl. Res. Lab. (MPS), Coll. of Pharmacy, Seoul Natl. Univ., Republic of Korea*)
- P17/18-184 Structural basis for the phosphoregulation of β -secretase sorting signal by the VHS domain of GGA1**
Tomoo Shiba¹, Satoshi Kametaka², Masato Kawasaki¹, Masahiro Shibata², Satoshi Waguri², Yasuo Uchiyama², Soichi Wakatsuki¹ (¹*Struct. Biol. Res. Center, PF, KEK*, ²*Dept. of Cell Biol. and Neuroscience, Osaka Univ. Grad. Sch. of Med., Japan*)
- P17/18-185 Detailed binding analyses of human immunoglobulin-like transcript (ILT) 2 and 4 receptors for their ligands MHC class I molecules.**
Mitsunori Shiroishi¹, Linda Rasubala¹, Kohei Tsumoto², Izumi Kumagai², Kimie Amano³, Yasuo Shirakihara³, Eiji Kurimoto⁴, Koichi Kato⁴, Daisuke Kohda¹, Katsumi Maenaka¹ (¹*Div. of Struct. Biol., Med. Inst. of Bioreg., Kyushu Univ.*, ²*Dept. of Biomol. Eng., Grad. Sch. of Eng., Tohoku Univ.*, ³*Struct. Biol. Cent., Natl. Inst. of Genet.*, ⁴*Dept. of Struct. Biol and Biomol. Eng., Nagoya City Univ., Japan*)
- P17/18-186 Functional domains of a pore-forming cardiotoxic protein, volvatoxin A2**
Yui-Ping Weng, Ya-Ping Lin, Jung-Yaw Lin (*Institute of Biochemistry and Molecular Biology, College of Medicine, National Taiwan University, Taiwan*)
- P17/18-187 Effect of de novo Designed Peptides Interacting with Electrically Neutral Lipid Membrane Interface on Stability of Cubic Phases of Monoolein Membrane**
Shah Masum, Tarek Awad, Yukihiko Tamba, Masahito Yamazaki (*Dept. of Physics, Faculty of Science, Shizuoka University,)*
- P17/18-188 Stable-isotope-assisted NMR analyses of the interactions of the Sugar-binding domain of SCF^{Fbs1} with glycopeptides**
Takeshi Hirao^{1,2}, Yoshiki Yamaguchi^{1,2}, Yukiko Yoshida^{2,3}, Keiji Tanaka³, Koichi Kato^{1,2} (¹*Dept. Struc. Biol. Biomol. Engin., Grad. Sch. Pharm., Nagoya City Univ.*, ²*CREST / JST*, ³*Tokyo Metro. Inst. Med. Sci., Japan*)

- P17/18-189 Crystal Structures of Alkaline α -Amylase, AmyK38 and Its Complexes with Oligosaccharides**
 Tsuyoshi Nonaka¹, Masahiro Fujihashi¹, Akiko Kita¹, Hiroshi Hagihara², Katsuya Ozaki², Susumu Ito³, Kunio Miki^{1,4} (¹*Grad. Sch. of Sci., Kyoto Univ.*, ²*Biol. Sci. Lab., Kao Corp.*, ³*Japan Marine Sci. and Technol. Center*, ⁴*RIKEN Harima Inst. / SPring-8, Japan*)
- P17/18-190 Novel Crystal Structure of the Hemolytic Lectin CEL-III from Marine Invertebrate at 1.7 Å resolution**
 Tatsuya Uchida¹, Tomomitsu Hatakeyama², Takayuki Yamasaki², Seiichiro Eto², Genji Kurisu¹, Atsushi Nakagawa¹, Hajime Sugawara³, Masami Kusunoki¹ (¹*Institute for Protein Research, Osaka Univ.*, ²*Faculty of Engineering, Nagasaki Univ.*, ³*Plant Science Center, RIKEN, Japan*)
- P17/18-191 Crystal structure of lectin from algae, which belongs to a new lectin family**
 Yasunori Kamiya¹, Kanji Hori², Kunihiko Gekko¹, Katsuo Katayanagi¹ (¹*Grad. Sch. of Sci, Hiroshima Univ.*, ²*Grad. Sch. of Biosphere Sci, Hiroshima Univ., Japan*)
- P17/18-192 Mutational and gene shuffling analysis of specificity and calcium requirement of barley α -amylase**
 Sophie Bozonnet¹, Kenji Fukuda¹, Birte Kramhoeft¹, Tae-jip Kim¹, Birte Svensson^{1,2} (¹*Department of Chemistry, Carlsberg Laboratory*, ²*Biochemistry and Nutrition Group, BioCentrum-DTU, Kingdom of Denmark*)
- P17/18-193 Characterization of Carbohydrate binding of mouse Macrophage C-type lectin and Dendritic cell immunoreceptor**
 Youngmin Hyun^{1,2}, Mark Hulett¹, Nick Dixon², Jill Gready¹ (¹*The John Curtin School of Medical Research, Australian National Univ.*, ²*Research School of Chemistry, Australian National Univ., Australia*)
- P17/18-194 Effects of alternative splicing on protein structure and function**
 Masafumi Shionyu¹, Yoshinori Hirashima², Kei Yura³, Atsushi Hijikata², Mitiko Go⁴ (¹*Dept. Sci. Biol. Supramol. Sys., Grad. Sch. Int. Sci., Yokohama City Univ.*, ²*Div. Biol. Sci., Grad. Sch. Sci., Nagoya Univ.*, ³*Quantum Bioinformatics Group, Japan Atomic Energy Research Institute*, ⁴*Fac. Bio-Sci., Nagahama Inst. Bio-Sci. Tech., Japan*)
- P17/18-195 Cancelled**
- P17/18-196 Molecular weight determination of protein-carbohydrate complexes by low-angle laser light scattering technique**
 Yasushi Watanabe, Masato Shiraishi (*Protein Lab., National Food Research Institute, Japan*)
- P17/18-197 Purification and some properties of a cobalt dependent α -mannosidase from *Ginkgo biloba* seeds**
 Kwan Kit Woo¹, Yoshinobu Kimura^{1,2} (¹*The Grad. School of Natural Sci. and Tech., Okayama Univ.*, ²*Dept. of Bioresource Chem., Fac. of Agric., Okayama Univ., Japan*)
- P17/18-198 Plant endo- β -N-acetylglucosaminidase: enzymatic property, subcellular localization, and functional feature.**
 Megumi Maeda¹, Masashi Suzuki¹, Mariko Kimura³, Yoshinobu Kimura^{1,2} (¹*Grad. School Natural Sci. Technol., Okayama Univ.*, ²*Dept. Biores. Chem., Okayama Univ.*, ³*Dept. Food Sys., Kurashiki Sakuyo Univ., Japan*)
- P17/18-199 Expression and purification of functional human Saposin A in *Pichia pastoris*.**
 Minoru Yamada, Daizo Hamada, Kumiko Nakahira, Itaru Yanagihara (*Department of Developmental Infectious Diseases, Research Institute, Osaka Medical Center for Maternal and Child Health, Japan*)
- P17/18-200 Proteomic Analysis Of Proteins Specifically Binding To Potential LTR HERV-K Regulatory Element**
 Dmitrii Trubetskoy, Lev Nikolaev, Sergey Akopov, Ludmila Zavalova (*Institute of Bioorganic Chemistry, Russian Federation*)
- P17/18-201 Epigenetic Modification of Histones in Liver**
 Keiichi Hosokawa¹, Gao Jialing¹, Akira Tsugita^{1,2}, Kenichi Kamijo² (¹*Proteomics Research Laboratory TOKYO RIKAKIKAI CO., LTD.*, ²*Proteomics Research Center, NEC Fundamental & Environmental Research Laboratories, Japan*)

- P17/18-202 Cross-talk of signaling pathways regulated by myristoylation, a multifunctional posttranslational protein modification**
Nobuhiro Hayashi¹, Sebastian Maurer-Stroh², Masaki Gouda¹, Naomi Mori¹, Naoshi Shimojo¹, Yuji Jinbo³, Keiichiro Hashimoto¹, Yoshinobu Izumi³, Norio Matsushima⁴, Frank Eisenhaber² (¹*Inst. for Comprehensive Medical Sci., Fujita Health Univ., Japan*, ²*Bioinformatics Grp., Inst. of Mol. Pathology, Austria*, ³*Grad. Sch. of Sci. and Eng., Yamagata Univ.*, ⁴*Sch. of Hlth. Sci., Sapporo Med. Univ., Japan*)
- P17/18-203 Proteomic analysis of human intrahepatic calcuolosis**
Akira Tsugita^{1,2}, Takuji Nabetani², Yo Tabuse¹, Junichi Shoda³ (¹*NEC Laboratories Proteomics Research Center*, ²*Proteomics Research Laboratory TOKYO RIKAKIKAI CO., LTD*, ³*Med. School, Tsukuba Univ., Japan*)
- P17/18-204 The definition and prediction of ionization flux of peptides for protein identification using mass spectrometry.**
Takashi Nishikaze, Mitsuo Takayama (*Graduate School of Integrated Science, Yokohama City University, Japan*)
- P17/18-205 Identification of activation-dependent gene expression profiling of human peripheral CD8 T cells by proteomic tools**
Jung-hui Koo¹, Wook-Jin Chae², Je-Min Choi², Hyung-Wook Nam¹, Yu-sam Kim¹, Sang-Kyou Lee² (¹*Department of Biochemistry, Yonsei University*, ²*Department of Biotechnology, Yonsei University, Republic of Korea*)
- P17/18-206 Proteomic analysis of H₂O₂-resistant Chinese hamster V79 cells**
Masaya Sano¹, Manami Kato¹, Hiroataka Naitou², Norio Ohashi², Kayoko Shimoi², Shigenori Kumazawa¹, Tsutomu Nakayama¹ (¹*Dept. of Food and Nutritional Sci., Univ. of Shizuoka*, ²*Dept. of Environmental Health Sci., Univ. of Shizuoka, Japan*)
- P17/18-207 Proteomic analysis of the established U-87MG human glioblastoma cell lines for tumor suppressor PTENs protein network**
Jung Hye Shim, Jung Wook Park, Young Yil Bahk, Yu Sam Kim (*Dept. of Biochemistry & Protein Network Research Center, Yonsei University, Republic of Korea*)
- P17/18-208 Proteomic analysis of imatinib mesylate effects on chronic myelogenous leukemia cells**
Jungeun Park, Sangmi Kim, Youngsoo Kim (*Division of Genomics Medicine, Seoul National University, College of Medicine, Republic of Korea*)
- P17/18-209 Kinase Trapping: A Novel Strategy for the Identification of Kinase-Substrate Pairs.**
Dustin J Maly, Jasmina A Allen, Kevan M Shokat (*Department of Molecular and Cellular Pharmacology, University of California, San Francisco, United States of America*)
- P17/18-210 Total net charge distribution of proteomes**
Ke Runcong, Shigeki Mitaku (*Department of Applied Physics, School of Engineering, Nagoya University, Japan*)
- P17/18-211 Analysis of proteins interacted with gel-resolved proteins by a novel protein chip**
Jian-Zhong Tan¹, Nobutake Suzuki², Mikiko Arima³, Hiroshi Okamura⁴, Shuichi Kamei⁴, Michifumi Tanga⁴, Takeshi Okada⁵, Hisashi Hirano³ (¹*Univ. of Suzhou, People's Republic of China*, ²*Kazusa DNA Inst.*, ³*Yokohama City Univ.*, ⁴*Toyokohan Co.*, ⁵*SUS Co., Japan*)
- P17/18-212 Protein function prediction through gene positional information - Application for discovery of DNA repair related proteins -**
Kei Yura¹, Hidetoshi Kono¹, Nobuhiro Go^{1,2} (¹*Quantum Bioinformatics Group, Japan Atomic Energy Research Institute*, ²*Bioinformatics Unit, Nara Institute of Science and Technology, Japan*)
- P17/18-213 ProteoMix: An integrated system for interactively analyzing and annotating proteomes.**
Atsushi Kurotani¹, Eisuke Chikayama¹, Yutaka Kuroda¹, Shigeyuki Yokoyama^{1,2,3} (¹*RIKEN Genomic Science Center (GSC)*, ²*Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo*, ³*RIKEN Harima Institute at SPring-8, Japan*)
- P17/18-214 Mitochondrial Proteome Analysis of Motor Neurons Expressing SOD1 Mutations**
Kei Fukada, Fujian Zhang, Haining Zhu (*Department of Molecular and Cellular Biochemistry, University of Kentucky, United States of America*)

- P17/18-215** **Tags for oxidized proteins, TOP, useful for assessing the effect of reactive oxygen species on disease proteomics**
Yoshio Kodera², Mamoru Satoh¹, Yusuke Kawashima¹, Jae Il Kim², Tadakazu Maeda¹ (¹*Dept. of Physics, Sch. of Sci., Kitasato Univ., Japan*, ²*Dept. of Life Sci., Kwangju Inst. of Sci. and Tech., Korea*)
- P17/18-216** **Dissection and preparation of SARS-CoV surface protein**
Shuang Li, Zhen Cai, Zhanglin Lin (*Department of Chemical Engineering, Tsinghua University, People's Republic of China*)
- P17/18-217** **Effects of using highly diverged sequences in profile-profile comparisons**
Kentaro Tomii (*CBRC, AIST, Japan*)
- P17/18-218** **Methods for Predicting Transcription Factors and Their Targets**
Akinori Sarai¹, Shandar Ahmad¹, Michael M. Gromiha², Hidetoshi Kono³ (¹*Dept. Biochem. Eng. & Sci., Kyushu Institute of Technology*, ²*CBRC, AIST*, ³*Neutron Science Research Center and Center for Promotion of Computational Science and Engineering JAERI, Japan*)
- P17/18-219** **New candidates for protein markers of diabetes found in kidney proteomes of the diabetic model Otsuka Long-Evans Tokushima fatty (OLETF) rat**
Kaori Dobashi, Masamichi Oh-Ishi, Yoshio Kodera, Tadakazu Maeda (*Dept. of Physics, Kitasato Univ. Sch. of Sci., Japan*)
- P17/18-220** **Proteomic analysis of human metaphase chromosomes**
Susumu Uchiyama, Shouhei Kobayashi, Hideaki Takata, Takeshi Ishihara, Sachihito Matsunaga, Kiichi Fukui (*Dept. of Biotechnol., Grad. Sch. of Eng., Osaka Univ., Japan*)
- P17/18-221** **Proteomic analysis of human metaphase chromosomes by using RFHR-PAGE**
Hideaki Takata, Susumu Uchiyama, Shouhei Kobayashi, Sachihito Matsunaga, Kiichi Fukui (*Department of Biotechnol., Grad. Sch. of Eng. Osaka Univ., Japan*)
- P17/18-222** **A novel approach for comprehensive search of nucleocytoplasmic signaling molecules in neurons**
Masahiro Fukumoto, Toshihiro Sekimoto, Yoshihiro Yoneda (*Dept. Frontier Biosci., Grad. Sch. Frontier Biosci., Osaka Univ., Japan*)
- P17/18-223** **Functional analysis of unknown-function proteins/domains: Identification of binding partners**
Ryoichi Arai^{1,2}, Eiko Matsumoto¹, Keiko Tsuganezawa¹, Kaori Tajima-Ito¹, Ayako Sakamoto¹, Yumiko Terazawa¹, Madoka Nishimoto¹, Yuuka Etou¹, Yumi Saito¹, Seiko Yoshikawa¹, Mikako Shirouzu^{1,2}, Shigeyuki Yokoyama^{1,2,3} (¹*Genomic Sciences Center, RIKEN Yokohama Inst.*, ²*RIKEN Harima Inst./SPRING-8*, ³*Dept. of Biophys. and Biochem., Grad. Sch. of Sci., Univ. of Tokyo, Japan*)
- P17/18-224** **Enhanced responses in MALDI-MS of peptides derivatized with arginine through the C-terminal oxazolone**
Takashi Nakazawa¹, Minoru Yamaguchi², Kimiko Nishida¹, Hiroki Kuyama², Takashi Obama², Eiji Ando², Taka-aki Okamura³, Norikazu Ueyama³, Shigemi Norioka⁴ (¹*Department of Chemistry, Nara Women's University*, ²*Life Science Laboratory, Shimadzu Corporation*, ³*Graduate School of Science, Osaka University*, ⁴*Graduate School of Frontier Biosciences, Osaka University, Japan*)
- P17/18-225** **A new method for N-terminal *de novo* sequencing of protein by mass spectrometry coupled with affinity tag and chemically assisted fragmentation methods**
Shigemi Norioka¹, Minoru Yamaguchi², Takashi Obama², Hiroki Kuyama², Eiji Ando², Masami Ichikawa², Taka-aki Okamura³, Norikazu Ueyama³, Makiko Kondo¹, Takashi Nakazawa⁴ (¹*Grad. School of Frontier Biosciences, Osaka Univ.*, ²*Shimadzu Corp.*, ³*Grad. School of Science, Osaka Univ.*, ⁴*Dept. of Chemistry, Nara Women's Univ., Japan*)
- P17/18-226** **Application of FTICR-MS equipped with metal NanoESI emitter for identification of protein complex interface and Topdown Proteomics.**
Naoyuki Yamada, Ei-ichiro Suzuki, Kazuo Hirayama (*Institute of Life Sciences, Ajinomoto Co., Inc., Japan*)
- P17/18-227** **C-terminal sequencing method for proteins based on truncation reaction by acetic anhydride**
Kenji Miyazaki¹, Ken'ichi Kamijo¹, Akira Tsugita^{1,2} (¹*Proteomics Research Center, Fundamental Research Laboratories, NEC corp.*, ²*Proteomics Research Laboratories, Tokyo Rika Kikai, Japan*)

- P17/18-228** **A new proteomic method using molecular probes detects simultaneously protein carbonyls and protein ubiquitination in muscles of a diabetic model rat**
Masamichi Oh-Ishi¹, Yoriko Watai², Hisayuki Matsui³, Takanori Kurouzu³, Tadakazu Maeda¹ (¹*Dept. of Physics, Kitasato Univ. Sch. of Sci.*, ²*Yokohama Lab., SC BioSciences Corp.*, ³*Electron Tube Center, Hamamatsu Photonics Corp., Japan*)
- P17/18-229** **Comprehensive analysis of posttranslationally modified proteins enriched by immunoaffinity chromatography**
Masaki Matsumoto, Koji Oyamada, Shigetsugu Hatakeyama, Keiichi I. Nakayama (*Dept. of Mol. and Cellular Biol., Med. Inst. of Bioreg. Kyushu Univ., Japan*)
- P17/18-230** **Dynamics of lipid rafts revealed by molecular imaging**
Kumiko Sakata-Sogawa¹, Sho Yamasaki², Takashi Saito^{1,2}, Makio Tokunaga^{1,3} (¹*Res. Ctr. for Allergy and Immunology, RIKEN*, ²*Dep. of Mol. Genetics, Chiba Univ. Grad. Sch. Med.*, ³*Struct. Biol. Ctr, Natl. Inst. of Genetics, Japan*)
- P17/18-231** **Development and Biological Application of Novel Fluorescent Probes for Ratiometric Imaging of Protein Tyrosine Phosphatase Activity**
Hideo Takakusa¹, Kazuya Kikuchi^{1,2}, Asako Sawano-Sakae^{3,4}, Atsushi Miyawaki³, Tetsuo Nagano¹ (¹*Graduate School of Pharmaceutical Sciences, Univ. of Tokyo*, ²*Presto, JST Corporation*, ³*Brain Science Institute, RIKEN*, ⁴*Brain Science and Life Technology Research Foundation, Japan*)
- P17/18-232** **Noncompetitive homogeneous immunodetection of phosphotyrosine for facile imaging of intracellular signal transduction**
Yoshiyuki Sasajima¹, Kenzo Sakamoto², Takahide Aburatani², Hiroshi Ueda^{1,2} (¹*Dept. of Integ. Biosci., Grad. Sch. of Frontier Sci., University of Tokyo*, ²*Dept. of Chem. & Biotech., Sch. of Eng., University of Tokyo, Japan*)
- P17/18-233** **Localization of calreticulin on human metaphase chromosomes**
Shouhei Kobayashi, Susumu Uchiyama, Sachihito Matsunaga, Kiichi Fukui (*Dept. of Biotechnol., Grad. Sch. of Eng., Osaka Univ., Japan*)
- P17/18-234** **FT-IR Spectroscopy Study of Metal Ion Binding of S100B Brain Protein**
Koichi Murayama¹, Sadayuki Matsuda² (¹*Department of Biochemistry and Biophysics, Gifu University School of Medicine*, ²*School of Natural Science, Engineering and Agriculture, Hokkaido University of Education at Asahikawa, Japan*)
- P17/18-235** **Dimer in a new crystal form of CPB40, Calcium-binding protein from *Physarum polycephalum***
Victor Gritsenko¹, Toshimitsu Tanaka¹, Kosuke Ito¹, Masayuki Kamo¹, Tsukasa Makino¹, Akio Nakamura², Kazuhiro Kohama², Masaru Tanokura¹ (¹*Dept. of Applied Biological Chemistry, Grad. Sch. of Agricultural and Life Sciences, Univ. of Tokyo*, ²*Dept. of Pharmacology, Gunma Univ. Sch. of Medicine, Japan*)
- P17/18-236** **The calcium modulation system of *Streptomyces* aminopeptidase**
Jiro Arima, Masaki Iwabuchi, Tadashi Hatanaka (*Research Institute for Biological Science, Okayama, Japan*)
- P17/18-237** **Optimum Solubility (OS) Screening: an efficient screen to optimize buffer conditions for stability and crystallization of proteins**
Ramona Pufan, Jarmila Jancarik, Connie Hong, Rosalind Kim (*Berkeley Structural Genomics Center, Lawrence Berkeley National Laboratory, United States of America*)