

大阪大学蛋白質研究所セミナー IPR Seminar  
**Analysis and prediction of  
protein assembly structures by bioinformatics**

**Date: 6 March 2015**

Place: Institute for Protein Research (IPR), Osaka Univ., Lecture Hall on First Floor  
Organizers: Haruki Nakamura (IPR, Osaka Univ.) & Kei Yura (Ochanomizu Univ.)

**6 March (Friday)**

- 9:55 **Opening by Haruki Nakamura** (IPR, Osaka Univ.)
- 10:00 **Tsuyoshi Shirai** (Nagahama Inst. BioScience and Tech.)  
Knowledge-based protein complex modeling in supporting structure analyses
- 10:30 **Sotaro Fuchigami** (Yokohama City Univ.)  
A combined approach of mass spectrometry and simulation for characterizing the histone multimers with flexible tails
- 11:00 **Atsushi Matsumoto** (JAEA)  
2D hybrid analysis: A new approach to build 3D atomic model from 2D EM image
- 11:30 **Takeshi Kawabata & Hirofumi Suzuki** (IPR, Osaka Univ.)  
Shape similarity search of EMDB and PDB: Omokage search
- 12:00 Lunch
- 13:30 **Dongsup Kim** (KAIST)  
Computational design of specific protein binders
- 14:00 **Yoichi Murakami** (Tohoku Univ.)  
A machine learning approach for predicting protein-protein interactions
- 14:30 **Kazuo Yamashita** (iFReC, Osaka Univ.) & **Daron M. Standley** (Kyoto Univ.)  
NGS data-driven docking of protein-RNA complexes
- 15:00 Coffee break
- 15:30 **Bhaskar Dasgupta & Akira R. Kinjo** (IPR, Osaka Univ.)  
Dynamic roles of Ubiquitin structures in multispecificity
- 16:00 **Kei Yura** (Ochanomizu Univ.)  
A simple statistical potential for protein complex structure prediction and its application to protein-docking problems
- 16:30 **Hafumi Nishi** (Tohoku Univ.)  
Disease and non-disease mutations on protein-protein interface
- 17:00 **Closing by Kei Yura** (Ochanomizu Univ.)
- 17:10 Gathering

事前登録不要・聴講無料

Access to IPR:

<http://www.protein.osaka-u.ac.jp/eng/access/>  
<http://www.protein.osaka-u.ac.jp/jpn/access/>

連絡先 中村 春木

〒565-0871 大阪府吹田市山田丘 3-2

大阪大学 蛋白質研究所

Tel & Fax : 06-6879-4310

E-mail: harukin@protein.osaka-u.ac.jp