Structural and biophysical methods for biological macromolecules in solution

06 – 14 December 2017 | Singapore, Singapore

Co-organizers:
EMBL-Hamburg

Co-sponsors:
Nanyang Technological University
Bioinformatics Institute

Organizers:
Dmitrii Svergun
EMBL, Hamburg, DE
Haydyn Mertens
EMBL, Hamburg, DE

Co-organizers:
Gerhard Gruber
Nanyang Technological University, SG
Chandra Verma
A*STAR, SG

Registration:
Application deadline: 01 September 2017
Payment deadline: 06 November 2017
Student/postdoc fee: 125 EUR
Academic: 15 EUR
Industry: 1000 EUR

Speakers:
Lucia Banci
University of Perugia, IT
Shashi Bhushan
Nanyang Technological University, SG
Peter Bond
A*STAR, SG
Alexandre Bonvin
Utrecht University, NL
Ollwyn Byron
Glasgow University, UK
Kristina Djuricic-Barugo
University of Vienna, AT
Daniel Franke
EMBL, Hamburg, DE
Gerhard Gruber
Nanyang Technological University, SG

Cy Jeffries
EMBL, Hamburg, DE
Sheemei Lok
Duke-National University of Singapore, SG

Haydyn Mertens
EMBL, Hamburg, DE
Alejandro Panjikovic
EMBL, Hamburg, DE
Konstantin Pervushin
Nanyang Technological University, SG
Dmitrii Svergun
EMBL, Hamburg, DE
Jill Trewhella
University of Sydney, AU
Jaume Torres
Nanyang Technological University, SG
Bente Vestergaard
University of Copenhagen, DK
Thorsten Wohland
National University of Singapore, SG

meetings.embo.org/event/17-macromolecule
EMBL Outstation at DESY, Hamburg

1974

EMBL-Paradise

43 years later

EMBL integrated facility
at upgraded Petra-3 ring
2 MX beamlines
1 BioSAXS beamline
(in operation from 2012)
Biological SAXS @ EMBL-HH

Group leader: D. Svergun


Predocs: N. Hajizadeh, K. Malanastas

Trainee: D. Rastenyte

Major tasks:

- Development of data analysis methods
- Running and developing SAXS beamlines
- User support and collaborative projects
- Interactions, education and training
The main objective of the EMBO Global Exchange Lecture Course is to teach the young PhD students and postdocs from all areas of biology the methods applicable to study biological macromolecules in solution. We aim at a comprehensive coverage of the field including the major structural and biophysical techniques employed for the characterization of high and low resolution structure and structural transitions, macromolecular complex formation, protein folding and stability, protein-protein interactions and enzymatic mechanisms.
What will (and what will not) be covered

The three major structural methods covered are:
- small-angle X-ray and neutron scattering (SAXS/SANS)
- nuclear magnetic resonance (NMR)
- cryo-electron microscopy (cryo-EM)

The other methods applicable to solutions including analytical ultracentrifugation (AUC), light scattering, fluorescence and absorption, spectroscopic approaches, bioinformatic tools etc.

The structural methods, which will NOT be directly covered:
- macromolecular crystallography (MX)
- mass spectrometry (MS)

However, attention will be paid to interdisciplinary approaches where SAS, NMR and cryo-EM are employed together with these and other non-solution methods.
SAS Play Station VI
(anti-sleeping pills)

- SAS Quest
Joint use of SAS and NMR

- Cross-validation of structural models
- The use of mutual constrains, especially for rigid body modeling
- Comprehensive quantitative analysis of flexible systems and mixtures
- Dynamic (including short-lived and encounter) complexes
Overall Course schedule

Day 1, 06.12  Introduction, Basics of SAXS/SANS, Poster Session
Day 2, 07.12  SAXS/SANS Data Collection and Analysis
Day 3, 08.12  Biophysical techniques (light scattering, spectroscopy)
Day 4, 09.12  Biomolecular NMR basics and bioinformatics
Day 5, 10.12  Biophysical techniques (AUC), city tour
Day 6, 11.12  Studies of evolving systems, mixtures and processes
Day 7, 12.12  Cryo-EM, circular dichroism, databases
Day 8, 13.12  Hybrid methods, applications, conclusions

Plus remote SAXS data collection, demonstrations, tutorials, practicals, SAS Quest, etc
So, let us slowly start

A practical issue: all tutors will be asked to provide PDFs of the talks to the students (after removal of sensitive information, if any)