

EMBO
Global Exchange
Lecture Course

Structural and biophysical methods for biological macromolecules in solution

06 – 14 December 2017 | Singapore, Singapore

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REGISTRATION

Application deadline

01 September 2017

Payment deadline

06 November 2017

Student/postdoc fee125 EUR

Academic125 EUR

Industry.....1000 EUR

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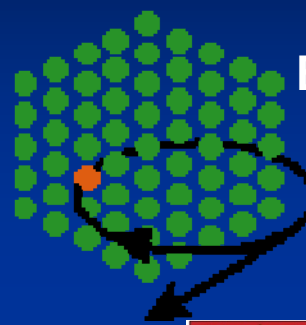
Thorsten Wohland
National University of Singapore, SG

meetings.embo.org/event/17-macromolecule



Co-organizers:

EMBL-Hamburg



Co-sponsors:

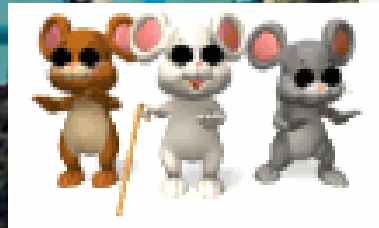
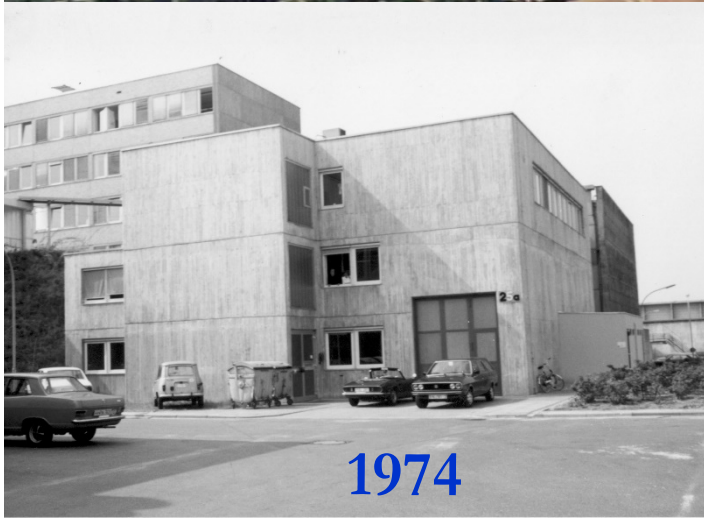
EMBO
reports



EMBOpress



EMBL Outstation at DESY, Hamburg



EMBL integrated facility
at upgraded Petra-3 ring
(in operation from 2012)

2 MX beamlines
1 BioSAXS beamline



Biological SAXS @ EMBL-HH

Group leader: D. Svergun

**Staff : C.Jeffries,
C.Blanchet, D.Franke,
A.Kikhney, H.Mertens,
C.Borges**

**Postdocs: D.Molodenskiy,
M.Graewert, T.Graewert,
A.Panjovich, M.Schroer,
A.Gruzinov, S. da Vela**

**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



Course aims



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)**

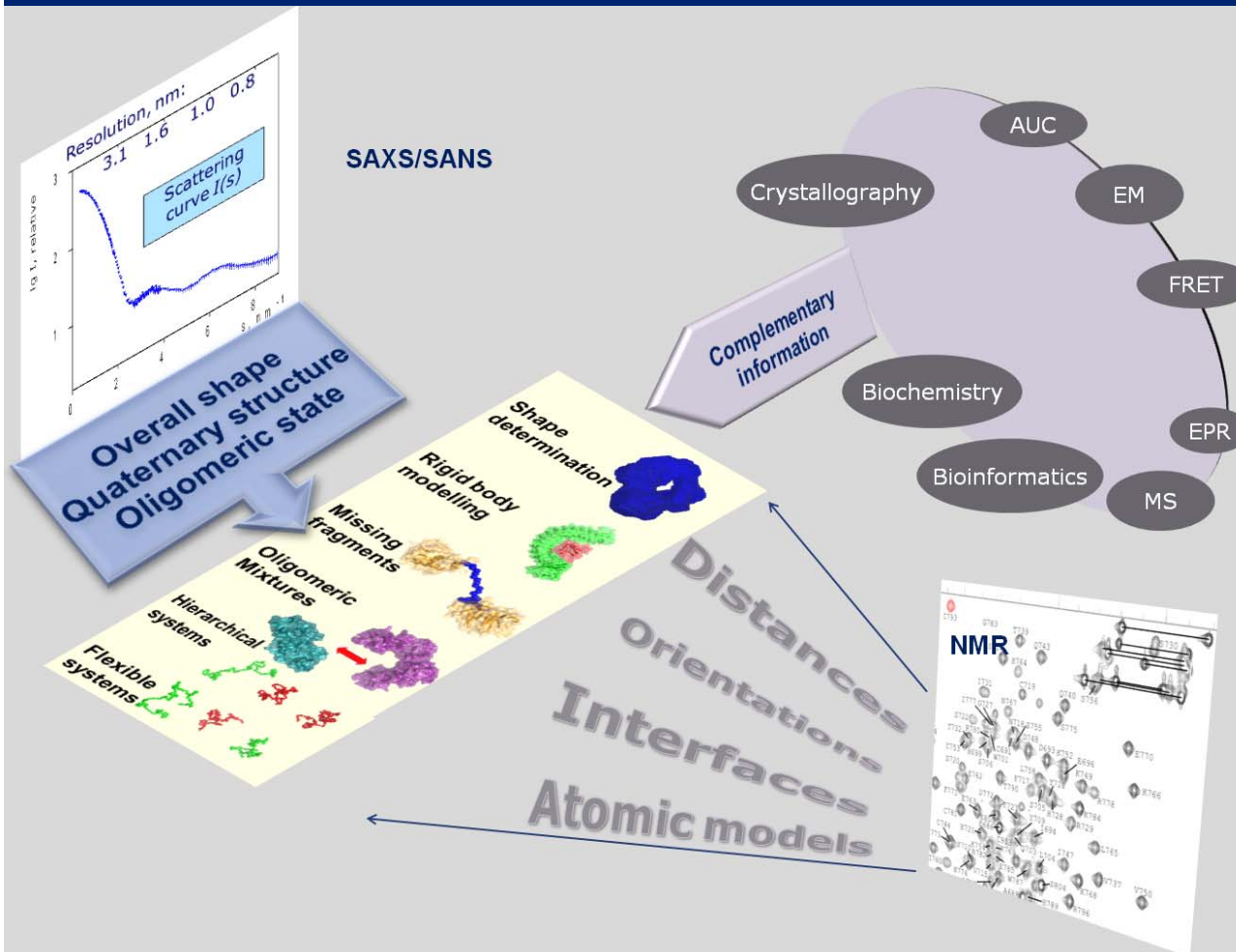
However, attention will be paid to interdisciplinary approaches where SAS, NMR and cryo-EM are employed together with these and other non-solution methods.

SAS Play Station VI (anti-sleeping pills)

- SAS Quest



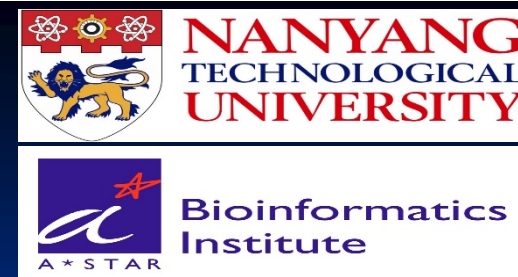
Joint use of SAS and NMR



- 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

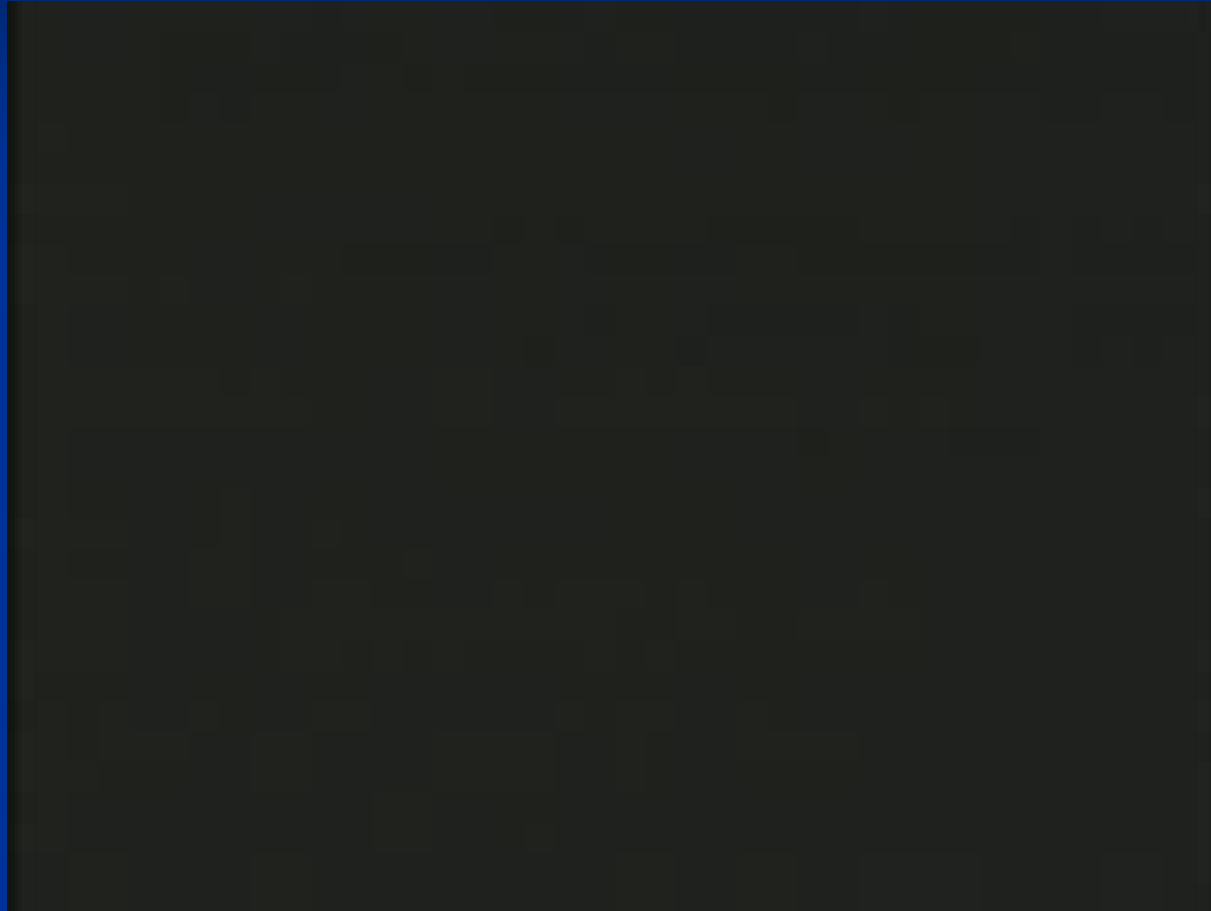
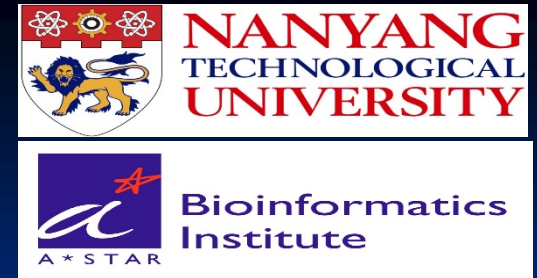


Day 1, 06.12	Introduction, Basics of SAXS/SANS, Poster Session
Day 2, 07.12	SAXS/SANS Data Collection and Analysis
Day 3, 08.12	Biophysical techniques (light scattering, spectroscopy)
Day 4, 09.12	Biomolecular NMR basics and bioinformatics
Day 5, 10.12	Biophysical techniques (AUC), city tour
Day 6, 11.12	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)₉