Registration

Deadline for registration: May 28th 2019 eva.huber@tum.de Participation is free of charge but limited to 30 persons.

Organization

Eva M. Huber is a habilitation candidate at the Technical University of Munich and member of the Young Scholars' Program of the Bavarian Academy of Sciences and Humanities since 2017.

jungeskolleg.badw.de

BAVARIAN ACADEMY OF SCIENCES AND HUMANITIES

Alfons-Goppel-Straße 11 (Residenz) 80539 München Sitzungssäle, first floor Phone +49 89 23031-0, www.badw.de

Directions U3/U6, U4/U5 Odeonsplatz Tram 19 Nationaltheater No car park available







Structural Biology of Proteins

workshop

8.45 A.M. - 17.00 P.M.

Program

8.45 Uhr	Reception DR. E. M. HUBER (Technical University of Munich)
	Session 1: X-ray crystallography
9.00 Uhr	Crystallization and diffraction data collection DR. A. BRACHER (Max Planck Institute of Biochemistry, Martinsried)
9.30 Uhr	The phase problem in X-ray crystallography DR.E.M.HUBER (Technical University of Munich)
10.00 Uhr	Refinement, validation and ligand building DR. J. KÖHNKE (Helmholtz Institute for Pharmaceutical Research, Saarbrücken)
10.30 Uhr	Coffee break
	Session 2: SAXS
11.00 Uhr	Biological SAXS DR. M. GRÄWERT (EMBL, Hamburg)
	Session 3: NMR and homology modeling
11.30 Uhr	Solution-state NMR for probing structure and dynamics of proteins PROF. DR. F. HAGN (Technical University of Munich and Helmholtz Zentrum München)
12.00 Uhr	Combining X-ray crystallography, NMR and homology modeling DR. S. WIESNER (University of Regensburg)
12.30 Uhr	Lunch

Structural Biology of Proteins

Structural biology serves to decipher the molecular architecture of biomolecules, especially of proteins. Knowledge about the structure of proteins is essential for understanding how they fulfill their biological function and how disease-associated modifications affect their functioning. To visualize the atomic details of proteins, researchers apply sophisticated methods that examine a vast number of identical molecules at the same time. This workshop will cover the most popular techniques of structural biology, X-ray crystallography, cryo-electron microscopy, nuclear magnetic resonance spectroscopy and small angle X-ray scattering. Advantages and limitations as well as latest developments will be discussed. The course primarily addresses (PhD) students and postdocs.

Session 4: Cryo-electron microscopy

14.00 Uhr	Single particle reconstruction
	PROF. DR. P. WENDLER
	(University of Potsdam)

14.30 Uhr Cryo-electron tomography PROF. DR. J. PLITZKO (Max Planck Institute for Biochemistry, Martinsried)

Session 5: Visualization and analysis of protein structures

- 15.00 Uhr Programs and online-Tools DR. S. SCHNEIDER (Technical University of Munich)
- 15.30 Uhr Coffee break

Key note lecture

16.00 Uhr The century of vision: Protein structures in basic science and pharma research PROF. DR. R. HUBER (Max Planck Institute of Biochemistry, Martinsried