



Universität Leipzig | Institut für Biochemie | Prof. Beck-Sickinger | Brüderstr. 34 | 04103 Leipzig

## Exploring Biomolecules in 3D: Principles and Applications of Computational Structural Biology

Dr. Georg Künze | Dr. Jens Meiler | Dr. Jarrod Smith | Dr. Rocco Moretti

13.-20. August 2021 | virtually via Zoom | Lecture: 3-6pm CEST | Lab: 7-10pm CEST

### Program

Date	Program	
13.08.2021	Computer setup • introduction to the Linux command line • shells • Linux filesystem • text editors • data processing tools	Lab
16.08.2021	Fundamentals of protein structure and protein structure determination • data representation and databases • visualization of protein structures	Lecture
	<i>De novo</i> protein structure prediction with ROSETTA • scoring and analysis of protein structures with ROSETTA • protein structure prediction with EPR data	Lab
17.08.2021	Prediction of protein structure in 1D (secondary structure, membrane regions, solvent accessibility) • Homology modeling • <i>De novo</i> protein structure prediction • Loop closure problem	Lecture
	Sequence alignment • structure-based alignment • threading • comparative modeling of membrane proteins with ROSETTACM • ROSETTA membrane scoring function	Lab
18.08.2021	The ROSETTA scoring function • Comparison and evolution of protein structures • Protein-protein docking	Lecture
	Protein-protein docking with ROSETTADOCK • low-resolution docking and high-resolution refinement • experimental restraints	Lab
19.08.2021	Protein-ligand docking • structure-based virtual screening	Lecture
	Protein-ligand docking with ROSETTALIGAND • generation of small molecule conformers and ROSETTA parameter files	Lab
20.08.2021	Protein engineering • Antibody and immunogen design	Lecture
	Protein design with ROSETTA • single-state and multi-state design	Lab