

Summer School “EPR spectroscopy”

Lecturer: Professor Dr. Hassane Mchaourab (Vanderbilt University)

Location: Medical Faculty, Medicine Institute of Medical Physics and Biophysics, Room S018,
Härtelstr. 16-18, 04107 Leipzig

Date: 15. – 18. July 2013

Course description

This is an advanced, intensive course directed at graduate students. It is intended to provide an overview of the EPR spectroscopy and its application to protein biophysics. Electron paramagnetic resonance is a magnetic resonance technique for the analysis of naturally occurring or introduced free radicals. In protein spin labeling, a stable free radical, spin label, is introduced specifically into the protein sequence via site-directed mutagenesis. The lectures will describe the technical and biochemical aspects of protein spin labeling, discuss the spectral parameters that are determined from EPR analysis of spin labeled proteins and their structural and dynamic interpretation. The lectures will end with an examination.

Dr. Hassane S. Mchaourab is professor of molecular physiology, biophysics, physics and chemistry at the Vanderbilt University. He has a life-long interest in the application of EPR spectroscopy to protein dynamics. The laboratory is engaged in method developments and applications on a variety of systems including kinases, transporters and chaperones.

Schedule

15.07.2013	Program
09:00 – 09:30	Welcome
09:30 – 12:30	Principles of magnetic resonance & “what is EPR”
13:30 – 15:00	Spin labels & site-directed spin labeling EPR sample requirements

16.07.2013	Program
09:00 – 15:00	continuous wave EPR instrumentation spectral parameters from spin labeled proteins structural interpretation of spin label mobility and accessibility

17.07.2013	Program
09:00 – 15:00	Dipolar coupling distance measurements in doubly labeled proteins Pulse EPR Double Electron Electron Resonance (DEER) membrane protein conformational dynamics

18.07.2013	Program
09:00 – 12:30	Membrane protein conformational dynamics from EPR
13:30 – 17:00	Computational tools to model protein structure from EPR data