

SFB 960-/BZR – Colloquium

Thursday, 2 March, 14.00

H 53



Barbara Steigenberger, Ph.D.

Mass Spectrometry Core Facility

MPI of Biochemistry, Martinsried

“State of the art crosslinking mass spectrometry approaches for structural biologists”

You are interested in how protein complexes are assembled and how variations in their stoichiometry or post-translational modifications alters their function? Mass spectrometry-based proteomics techniques provide unique insights into protein sequences, protein stoichiometry, interaction interfaces, and post-translational modifications involved in protein function. Specifically, **Crosslinking mass spectrometry (XL-MS)** provides valuable information on the binding interfaces between interacting proteins. Novel developments in data acquisition, data interpretation and crosslinker design make this technique an easy-to-use tool to gain information that is highly complementary to classical structural biology techniques. Combined with other structural proteomics techniques, details of protein structures can be discovered that are not always accessible with classical structural determination approaches.

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