Master Biologie – UFR Chimie et Biologie

Internship project Master 2 Recherche
Year 2017/2018

Laboratory: Institut de Biologie Structurale
Director: Winfried Weissenhorn
Team: Biomolecular NMR Spectroscopy
Head of team: Jérôme Boisbouvier

Name and status of scientist in charge of the project: Beate Bersch
HDR yes x no ☐
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Specialty MASTER:

☐Neurosciences and Neurobiology ☐mmunology, Microbiology, Infectious Diseases
x Integrative Structural Biology ☐ Physiology Epigenetics Development Differentiation

Title of project: Addressing biological function of proteins involved in protein import into mitochondria by an integrated structural biology approach

Objectives (3 lines max):

The project aims at the characterization of Tim chaperone complexes from the mitochondrial inter-membrane space and their interaction with proteins of import pathways. Solution NMR will be used to address binding site location, changes in dynamics and/or conformation upon complex formation.

Abstract (10 lines max):

Mitochondria perform a wide range of key cellular functions, many of which require the import and export of metabolites through the mitochondrial membranes. This transport is performed by membrane proteins in the inner and outer mitochondrial membranes. These mitochondrial proteins are produced in the cytosol and need to be imported by a sophisticated transport machinery from the cytosol, through the mitochondrial outer membrane to the intermembrane space for eventual insertion into the inner or outer membranes. Two homologous hetero-oligomeric chaperone assemblies are known to protect membrane protein precursors from the aqueous environment in the intermembrane space: TIM9/10 and TIM8/13. The mechanism by which these chaperones transport their substrate proteins is currently poorly understood. We characterized binding of unfolded carrier proteins to TIM9/10 and TIM8/13 assemblies and want to obtain insight on a molecular level on substrate specificity and possible interactions between the two assemblies that are simultaneously present in the intermembrane space.

Methods (3 lines max):

Protein expression and refolding, isotopic labeling, protein purification, chromatography, solution NMR, processing and interpretation of NMR data

Relevant publications of the team (3 max):

- RNA binding and chaperone activity of the E. coli cold-shock protein CspA. Rennella E, Sára T, Juen M, Wunderlich C, Imbert L, Solyom Z, Favier A, Ayala I, Weinhäupl K, **Schanda P**, Konrat R, Kreutz C, Brutscher B. *Nucleic Acids Res.* 2017;45(7):4255-4268.
- Proton-Detected Solid-State NMR Spectroscopy of a Zinc Diffusion Facilitator Protein in Native Nanodiscs. **Bersch B**, Dörr JM, Hessel A, Killian JA, **Schanda P**. *Angew Chem Int Ed Engl.* 2017;56(9):2508-2512.
- Atomic model of a cell-wall cross-linking enzyme in complex with an intact bacterial peptidoglycan. **Schanda P**, et al., *J Am Chem Soc.* 2014;136(51):17852-60

Requested domains of expertise (few keywords):

interest in structural biology, NMR, biophysical characterization of proteins and protein complexes