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: Paul Schanda
HDR yes x no ☐
Address: 71 Avenue des Martyrs, 38044 Grenoble Cedex 9
Phone: 04 57 42 86 59 **e-mail:** paul.schanda@ibs.fr

Specialty MASTER:

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

Title of project: Studies of structure and dynamics of bacteriophage T5 tail by solution- and solid-state NMR spectroscopy

Objectives (3 lines max):

The tail of bacteriophage T5 is formed by a polymeric assembly of a 50 kDa protein, pb6. In this project we want to characterize pb6 in its monomeric form (in solution) and when assembled to large tube structures. We will study the structural changes upon polymerization, and the dynamic switch for polymerization

Abstract (10 lines max):

Bacteriophages, i.e. viruses targeting bacteria possess a tail that allows host recognition, cell wall perforation and safe viral DNA channelling from the capsid to the cytoplasm of the bacterium. The tail is formed by an assembly of a protein, pb6, which forms a tube-like structure, from an assembly of the 50 kDa subunits. Little is known about the structure of the tail, and about the mechanisms that allow the passage from the monomeric state to the assembled state. We want to characterize the structure and dynamics of the phage tail at atomic resolution, by combining NMR spectroscopy in solution of the monomeric state, solid-state NMR of the tubes and cryo-EM data of the assembled tubes. While NMR provides atomic-resolution local information, EM provides lower-resolution data on the overall structure. By combining these methods we aim at deriving a near-atomic structure of the pb6 phage tail assembly. Studying differences in dynamics and structure in the two states may shed light on the mechanisms of assembly.

Methods (3 lines max):

NMR spectroscopy, processing and interpretation of NMR data, integration of EM and NMR data for structure determination.

Relevant publications of the team (3 max):

- Observing the overall rocking motion of a protein in a crystal. Ma P et al and **Schanda P**. *Nat. Commun.* 2015: 6, 8361.
- 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