



	<b>Experiment title:</b> BAG - LEBS - 2011-2	<b>Experiment number:</b> MX-1140
<b>Beamline:</b> ID23-2	<b>Date of experiment:</b> from: 6/5/2011 to: 7/5/2011	<b>Date of report:</b>
<b>Shifts: 3</b>	<b>Local contact(s):</b> Gordon Leonard	<i>Received at ESRF:</i>

**Names and affiliations of applicants (\* indicates experimentalists):**

**Agata Nawrotek\*, Ludovic Pecqueur\*, Marcel Knossow\*, Samira Zouhir\*, Sylvie Nessler\* L.E.B.S. (CNRS)**

**Report:**

**Agata Nawrotek, Ludovic Pecqueur and Marcel Knossow :**

- Project: Tubulin-stathmin like domain complex.

During this session, we tested crystals of tubulin in complex with stathmin-like domain proteins in which tubulin was further modified covalently by a peptide derived from stathmin. The crystals belong to the P212121 space group. 5 dataset were collected from 15 tested crystals. They diffracted to 3.7 Ang at best, with the following statistics: I/sig(I)= 7.3 (2.1), Rmeas= 26% (86%), completeness= 99.7 (98.3), multiplicity= 5.4.

The structure was refined using the tubulin-stathmin like domain structure as a starting model. The grafted peptide could not be located in the electron density maps.

We performed also the first tests of crystals of tubulin- CPAP complex stabilized by a darpin. We tested 11 crystals but none diffracted.

In addition, a first attempt to collect data on a tubulin-DARPin complex was made, confirming that the crystals are indeed protein and most likely contain the complex but the quality did not allow us to process a complete data set.

**Samira Zouhir and Sylvie Nessler :**

- Project : Structural study of NprR, a quorum sensing effector from *Bacillus cereus*

We already solved the structure of the binary complex between a truncated form of NprR

deleted from its DNA-binding domain, NprR( $\Delta$ HTH), and its activating peptide NprX. In order to understand the activation mechanism of the peptide, we now want to solve the structure of the apo form of the protein. The first crystals diffracted to 4.2Å resolution and the poor quality of the data did not allow us to solve the structure. In this experiment we tested 30 crystals of apo-NprR( $\Delta$ HTH) obtained in various crystallisation conditions. Unfortunately, the best crystal diffracted only up to 7Å. We did not collect any data. We also tested 10 crystals of the ternary complex NprR/peptide/DNA. However the diffraction pattern did not correspond to protein but salt.