	Experiment title: BAG - LEBS - 2011-2	**Experiment number**: MX-1292
Beamline: ID14eh1	**Date of experiment**: 12/11/2011 from: 9h30 to: 8h00	**Date of report**: 13/02/2012
Shifts: 3	**Local contact(s)**: P. Carpentier	*Received at ESRF:*

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Report:

1) Project 1: Tubulin in complex with an engineered stathmin-like domain

Stathmin-like domain proteins from vertebrates bind two tubulin molecules in a T_2SLD complex. We have designed a stathmin-like domain that binds efficiently only one tubulin. Crystals of this assembly further complexed by an anti-tubulin DARPin have been obtained and about 10 crystals have been tested during this session. The diffraction is highly variable. Most crystals diffract to low resolution (about 7 Ang). We collected data from two crystals. One of them diffracted to around 4 Ang and was not pursued further. The second crystal diffracted to 3.2 Ang resolution. Data have been processed in the P1 space group with the following statistics:

Cell dimensions a=58.72, b=59.13, c=155.93, α=84.73, β=86.62, γ=71.70
I/sig = 9.8 (2.0), Rsym 9.1% (50%), completeness 96.8% (95.3%), multiplicity 2.5 (2.5)

There are two complexes per asymmetric unit. The structure was solved by molecular replacement and is being refined.

1) Project 2: Tubulin modified with a stathmin-derived peptide

Tubulin redeally oligomerizes to protofilament-like assemblies, which makes its structural study difficult by crystallography. We have covalently linked a stahtmin-derived peptide at what is termed the longitudinal interface, which prevents this autoassembly. We co-crystallized the modified heterodimer with an anti-tubulin DARPin. 10 crystals of this complex have been tested during the session MX-1292. Most of them diffracted at low resolution (around 7 Å) but some diffracted to better resolution. The best dataset reached (3.7 Å resolution) displayed the following statistics:

Space group $P2_12_12_1$ (a=58.9 Å, b=67.9 Å, c=308.3 A).
I/sig = 13.9 (1.6), Rmerge 6.8 % (73.6 %), completness 98.8 % (96.4 %), multiplicity 4.7 (4.6).

There is one complex per asymmetric unit. The structure was solved by molecular replacement and the preliminary electron density maps show the positionning of the bound peptide.