



	Experiment title: BAG CBS Montpellier	Experiment number: MX-536
Beamline: ID 14-4	Date of experiment: from: 13th to: 14 th September 2006	Date of report:
Shifts: 3	Local contact(s): John MCGEEHAN	<i>Received at ESRF:</i>
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p32

- 12 crystals were tested
- 1 data set was collected at 4.5 Å resolution.
- Molecular replacement failed
- Refining crystallization conditions

RXR in complex with different ligands

- 17 crystals were tested
- 7 data sets were collected
- 2 structures were solved at 2.2 Å resolution by molecular replacement. The refinement process is almost complete.
- The PDB files should be deposited soon at the PDB

nadk

10 datasets collected with 10 different ligands

MOMP

20 xl of native and heavy metals derivatives (KptCl4 and TELA) were tested with very poor diffraction. 5 datasets were collected (6-8 Å) for the derivatives form.

P14-AKT2 complex

15 xl were tested with no diffraction

Phytase

- 7 xl of Phyt-6sulfate-inositol complexes were tested and 2 datasets collected at 2.4 and 2.9 Å. After resolution by MR and refinement, no ligand was visible.
- 15 xl of Phyt-Mono phosphate -inositol complexes were tested and 2 datasets collected at 2 and 2.5 Å. After resolution by MR and refinement, no ligand was visible

P3

4 xl were tested. Either no or very low (10 Å) diffraction.

BCL-inhibitor

18 xl of complexes with 4 different inhibitors tested. A total of 9 datasets of the different complexes were collected (resolution around 2 – 2.5 Å). After resolution by MR and refinement, no inhibitor was visible.