



	Experiment title: BAG CBS Montpellier	Experiment number: MX-446
Beamline: ID 14-3	Date of experiment: from: 20th Feb to: 21th Feb 2006	Date of report: 15/06/06
Shifts: 3	Local contact(s): T. Crépin	<i>Received at ESRF:</i>
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1/. NAD

Background: LmNADK1, is a *Listeria monocytogenes* protein involved in the 2' phosphorylation of NAD.

Nine purine derivatives crystals in I222 form soaked on wild-type NAD kinase were tested, and 4 complete datasets were collected (best dataset: max resolution= 2.31 Å, $R_{\text{merge}} = 0.094$ completeness = 100%).

NADK mutant D45N was performed in order to evaluate the role of this residue in the catalysis of NADKs. First mutants data have been collected up to 2.2 Å ($R_{\text{merge}} = 0.090$, completeness = 96%, I222 form).

2/. MOMP85h

Background: MOMP85h is a membrane protein from *Campylobacter jejuni*. with porin-like properties. 30 crystals were tested. Two native datasets were collected with crystals obtained from two different purification batches (best dataset: max resolution= 5.3 Å, $R_{\text{merge}} = 11.3\%$ completeness = 99.2%).

Two Pt derivatives crystals soaked in K₂PtCl₄ were tested. The best one diffracted up to 4.5 Å ($R_{\text{merge}} = 9.3\%$, completeness=98.6%), the other at 5.6 Å ($R_{\text{merge}} = 12.3\%$, completeness=97.9%).

Three Pt sites were located and used to calculate initial phases with Sharp. The phasing power is low and new derivatives are required. Anisotropic diffraction limit is still a serious problem for both native and derivative crystals.

Improvement of stabilizing protocol during freezing and new detergent additives screening in crystallizations are required

3/. Nef

The Nef protein of human immunodeficiency viruses is a critical determinant for the onset of AIDS in infected persons. We attempt to resolve the structural determinants of the complex Nef forms with one of its prime targets, the cytoplasmic tails of CD4.

About ten Nef crystals, soaked with CD4 peptide derivatives, were tested. Two complete datasets were collected, one these diffracted to about 2.9 Å ($R_{\text{merge}}=14.0$). Crystals belonged to space group P6522, with cell parameters of a=b=108 Å and c=220 Å. Data analysis and model building has been hampered by the presence of ice rings.

4/. Phytase (apo and complexed)

3 apo form XL of Phytase were collected at 2.5 Å,
Structure was solved by RM
pdb code 2GFI (on hold, up to publication), one publication in preparation

Around 10 xl soaked with phytic acid were tested with no diffraction.

5/. P3 (1 jeu 6 Å)

First dataset collection at 6Å of P3 protein. Up to now no diffraction were observed, promising.
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