	Experiment title: BAG-LEBS-2007-2	Experiment number: MX-669
Beamline: ID14-1	**Date of experiment**: from **23/2/08-8:30 to 25/2/08-8:00**	**Date of report**: 21/2/08
Shifts: 3	**Local contact(s)**: Dr Matthew BOWLER	*Received at ESRF:*

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Report:

Sonia Fieulaine*: Structural study of the N-terminal methionine excision pathway (1 shift)

Project aPDFm : With this project, we study mutants of the Arabidopsis thaliana PDF1B, and look at the effects of mutations on ligand binding (according to the results previously obtained on BM30A) Two data sets were collected (one native and one soaked ligand). Data are under refinement.

Project sPDF2a: Four data sets were collected from crystals of *Streptococcus agalactiae* PDF2a soaked with four distinct ligands. Data are under refinement.

Nicolas Leulliot*, Toufic EL ARNAOUT*: yeast multi-protein complexes involved in DNA replication, ribosome biogenesis, mRNA quality control pathway and cell signalling and archeophage structural genomics project (2 shifts)

1) Cgi121
Spacegroup $P2_12_12_1$ a= 76 Å, b=77 Å and c=81Å.
Resolution 1.90A.
Completion= 98.4%
Rsym=3.9%

EKC/KEOPS complex has recently been identified in *Saccharomyces cerevisiae* as being involved in the transcription of galactose induced genes and maintenance of telomere homeostasis. It contains the 5

following proteins: Bud32, Kae1, Gon7, Cgi121 and Pcc1 and is widely conserved among eukaryotic genomes. We have obtained crystals of Cgi121 and these have been tested during this session. We have collected several datasets from crystals of native Cgi121. Among the three datasets collected, one is of high quality (1.9A resolution). We have also collected a 1000° dataset from a crystal soaked with $NaWO_4$. This 3.5A dataset exhibit some anomalous signal but attempts to phase were unsuccessful for the moment.

2) *S. cerevisiae* Dcs1-Dcs2.

In yeast, the heterodimer Dcs1-Dcs2 catalyses cleavage of 5′end m^7G-oligoribonucleotide fragments generated by 3′→5′ exonucleolytic decay, and cleavage of m^7GDP generated by Dcp1/Dcp2-mediated decapping in the 5′→3′ decay pathway. We have obtained small crystals of this heterodimer that were tested for diffraction during this run. Spots could be observed beyond 3A resolution but diffraction was weak between 7 and 3A. We have collected a 180° section and tried to process it but the quality of the resulting dataset is too low (4A with Rsym=25%). More optimisation is needed.

3) *S. cerevisiae* Tpa1

Spacegroup: $P2_12_12_1$ with a= 105 Å, b=160 Å and c=210Å.
Resolution: 2.9A.
Completion= 97%
Rsym=14%

The deletion of the gene encoding for yeast Tpa1 protein strongly affects translation termination, deadenylation and mRNA stability, suggesting a role in the control of gene expression at the level of translation. The Tpa1 protein is a component of a ribonucleotidic complex bound to the 3'-end of mRNAs. The knowledge of its 3D structure might help to decipher the precise function of Tpa1. Crystals of native and selenomethionlylated protein have been grown and diffract to 3Å. However, they suffer from serious anisotropy and weak anomalous signal. During this run we collected two native datasets to 2.9A and 3.1A, respectively. We still need to obtain experimental phases on this project

Moreover, during this session, diffraction tests have been performed on other proteins studied in our group but the crystals diffracted only weakly.

3 shifts with no users