EUROPEAN SYNCHROTRON RADIATION FACILITY

INSTALLATION EUROPEENNE DE RAYONNEMENT SYNCHROTRON

ESRF

Experiment Report Form

The double page inside this form is to be filled in by all users or groups of users who have had access to beam time for measurements at the ESRF.

Once completed, the report should be submitted electronically to the User Office using the **Electronic Report Submission Application:**

http://193.49.43.2:8080/smis/servlet/UserUtils?start

Reports supporting requests for additional beam time

Reports can now be submitted independently of new proposals – it is necessary simply to indicate the number of the report(s) supporting a new proposal on the proposal form.

The Review Committees reserve the right to reject new proposals from groups who have not reported on the use of beam time allocated previously.

Reports on experiments relating to long term projects

Proposers awarded beam time for a long term project are required to submit an interim report at the end of each year, irrespective of the number of shifts of beam time they have used.

Published papers

All users must give proper credit to ESRF staff members and proper mention to ESRF facilities which were essential for the results described in any ensuing publication. Further, they are obliged to send to the Joint ESRF/ ILL library the complete reference and the abstract of all papers appearing in print, and resulting from the use of the ESRF.

Should you wish to make more general comments on the experiment, please note them on the User Evaluation Form, and send both the Report and the Evaluation Form to the User Office.

Deadlines for submission of Experimental Reports

- 1st March for experiments carried out up until June of the previous year;
- 1st September for experiments carried out up until January of the same year.

Instructions for preparing your Report

- fill in a separate form for each project or series of measurements.
- type your report, in English.
- include the reference number of the proposal to which the report refers.
- make sure that the text, tables and figures fit into the space available.
- if your work is published or is in press, you may prefer to paste in the abstract, and add full reference details. If the abstract is in a language other than English, please include an English translation.

ESRF	**Experiment title:** BAG-LEBS-2004-1	**Experiment number:** 30-01-665
Beamline: BM30A	**Date of experiment:** from: 24/04/2004 to: 26/04/2004	**Date of report:** 08/12/2003
Shifts: 6	**Local contact(s):** Philippe Carpentier.	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Lionel Trésaugues (Orsay University; PhD student), Marc Graille (CNRS; LEBS ; Post-doc), Institut de Biochimie et de Biophysique Moleculaire et Cellulaire (IBBMC), CNRS UMR8619 Bat 430 Universite Paris Sud, 91405 Orsay Cedex and LEBS, Laboratoire d'Enzymologie et de Biochimie Structurales, CNRS UPR 9063, 91198 Gif-sur-Yvette, France

Stephane Mouilleron (PhD student), ICSN, CNRS, 91198 Gif-sur-Yvette, France

Report:

Lionel Trésaugues, M. Graille (3 shifts): yeast *Saccharomyces cerevisiae* Structural Genomics project

The systematic names of the genes are used. More details on every orf can be found on http://genomics.eu.org:targets.html

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1) YIL020c (target 69).
Spacegroup C2 a=100A; b=72A;c=40A.
Resolution 2A
Completion: 100 %.

This protein contains 261 residues but only one methionine. During this session, we have collected a 3 wavelengths MAD dataset from crystal soaked overnight with sodium tungstate. A second 3 wavelength MAD dataset from a crystal grown in the presence of 0.5M NaBr was also collected. Unfortunately, both datasets did not allow to solve the structure.

2) YPL152157w (target 228).
Spacegroup C2221 a=157A; b=172A; c=53A.

Resolution 3.2A
Completion 100 %

This protein is an activator of the phosphotyrosyl phosphatase activity of protein phosphatase 2A (PP2A) in *S. cerevisiae* and hence is important for cell cycle progression and microtubule dynamics. Rod shaped crystals grown from a SeMet labeled protein have been obtained just before this run and have diffracted to 3.2A. This protein contains 12 methionine out of 358 residues. We have collected a 3 wavelength dataset at the Selenium edge. Although the presence of selenium as observed during the edge, we were not able to solve the structure. Further analysis of these crystals by mass spectrometry revealed that the crystals were made from a mix of 2 protein species: one fully labeled and one unlabelled, thus explaining the problems encountered for phasing. A new labeling has been successfully realized and new crystals have been obtained.

3) RRM. (SET-1 domain)
Spacegroup $P4_132$
Resolution 4A.
Completion 100%.
This domain from the Set1 protein of *S. cerevisiae* plays a key role in methylation of histones thus in chromatin remodeling. It contains 129 residues and one methionine. During this session, we have collected a 3 wavelengths MAD dataset from a SeMet crystal. Phasing is under process.

Stephane Mouilleron (3 shifts): Structural study of glucosamine-6-P synthase from *E. coli*

We have previously determined the structure at 2.4 Å resolution of glucosamine-6-P synthase from *E. coli* in complex with fructose-6-P and a glutamine analogue. In order to better visualize the channel between the glutamine and the fructose-6-P sites, we have infiltrated crystals of the enzyme with xenon in different conditions. The infiltrated crystals were tested for diffraction but most of them did not diffract beyond 6 Å resolution. These trials have however allowed to determine the best conditions for infiltrating crystals with xenon. We expect to collect a higher data set on ID14 beamline in the next future.