

## 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.

	<b>Experiment title:</b> Structural studies of Human Foamy Virus (HFV) Integrase	<b>Experiment number:</b> MX-630
<b>Beamline:</b> ID23-1	<b>Date of experiment:</b> from: 14/12/06                      to: 15/12/06	<b>Date of report:</b> 31/10/2007
<b>Shifts:</b> 2	<b>Local contact(s):</b> Mr Didier NURIZZO	<i>Received at ESRF:</i>
<b>Names and affiliations of applicants (* indicates experimentalists):</b>  *Lewit-Bentley Anita, LBPA, CNRS UMR8113, Cachan, France Mouscadet Jean-François, LBPA, CNRS UMR8113, Cachan, France *Réty Stéphane, LBPA, CNRS UMR8113, Cachan, France Delelis Olivier, LBPA, CNRS UMR8113, Cachan, France		

## Report:

The experiment in December 2006 was a MAD experiment on crystals of the HFV integrase catalytic core prepared with Se-Met containing protein. The crystals diffracted to 3Å on a laboratory source and we had selected the best ones that appeared single for the ESRF experiment.

Most of our crystals diffracted to around 2.5Å on ID23-1 and gave a good fluorescence signal at the Se absorption edge. Unfortunately, none of them turned out to be single crystals. We nevertheless collected three MAD and 2 SAD data sets.

Careful data treatment using MOSFLM gave only three datasets that were good enough for further use. The anomalous signal is, however, weak and not always reliable, due to the problem of multiple lattices overlapping. Furthermore, with only two methionines for a 200 residue protein, the signal was intrinsically weak. We have therefore not been able to obtain reliable phasing for the structure determination.

We have since managed to improve the crystallisation protocol such that we now do obtain single crystals reproducibly. We have also learned to diagnose the problem of subtly multiple crystals.

Recently we have obtained one native data set of excellent quality which we have used for phasing by molecular replacement, using coordinates of the HIV and ASV integrase catalytic core as search models. Unfortunately, we have been unable to find a solution that would give a satisfactory refinement.