

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 via the User Portal:

<https://www.esrf.fr/misapps/SMISWebClient/protected/welcome.do>

Reports supporting requests for additional beam time

Reports can 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.



	Experiment title: Structural Studies of proteins and RNA involved in bacterial and viral virulence and amyloid formation	Experiment number: MX 1758
Beamline: ID 29	Date of experiment: from: 22 juli 2015 17.00 to: 23 juli 2015 08.00	Date of report: 10-11-2015
Shifts: 2	Local contact(s): LEONARD Gordon	<i>Received at ESRF:</i>
Names and affiliations of applicants (* indicates experimentalists): *HAINZL Tobias, Laboratory Umea University, Sweden *PERSSON Karina, Laboratory Umea University, Sweden SAUER-ERIKSSON Elisabeth, Laboratory Umea University, Sweden		

Report:

Following results were achieved from data collected during MX-1758:

Data were collected of several fimbrial proteins (Mfa1, Mfa2 and Mfa3) from the periodontal pathogen *Porphyromonas gingivalis*. Data from SeMet labelled crystals of Mfa1, the main fimbrial protein, were collected to 1.8 Å and the structure was solved. Native data were also collected.

Native data to 1.9 Å from the accessory protein Mfa3 were collected. (The structure was previously solved using Bromide SAD from data collected at beam time MX-1705).

Data of the accessory protein Mfa2 were collected to 2.5 Å.

Data of the SeMet labelled adhesin domain of the *Streptococcus pyogenes* surface protein AspA, were collected to 2.0 Å and the structure was determined.

Approximately 22 high resolution data sets between 1.9-2.4 Å resolution were collected and structures solved of the *Listeria* master regulatory transcription factor PrfA in complex with various virulence inhibitors. Manuscript in preparation.

A number of crystals of different RNA constructs containing the conserved and essential Dengue virus promoter have been evaluated on the beam line ID 29 (MX-1705). So far, none

of the collected data sets was of quality high enough for structure solving. However, analysis of the different crystals and data sets clearly allowed us to identify the most promising constructs which we are currently optimizing to yield better diffracting crystals.

In addition 13 data sets diffracting between 1.6 – 2 Å were collected from crystals of DmpR, a ATP dependent transcription factor from *P. aeruginosa* belonging to the AAA+ family. Crystals of DmpR contained different ATP analogues.

About 8 data sets to about 2 Å resolution were collected from crystals of AnPrx6, a peroxiredoxin from *Anabaena* sp. PCC 7120 in different oxidation states (manuscript in preparation).

Four test data sets (2.5 – 3.0 Å resolution) were collected from crystals containing a truncated filamentous protein FilP.