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 via the User Portal:

*https://wwws.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.

| ESRF | **Experiment title:** Structural Studies of the Signal Recognition Particle and other Macromolecular Complexes | **Experiment number:** MX-1220 |
|---|---|---|
| **Beamline:** ID23-1 | **Date of experiment:** from: 30 Nov 2010 to: 01 Dez 2010 | **Date of report:** |
| **Shifts:** 3 | **Local contact(s):** Meike Stelter | *Received at ESRF:* |

**Names and affiliations of applicants** (* indicates experimentalists):

Dr. Gitte Merilainen*
Dr. Tobias Hainzl*
Dr Karina Persson*

## Report:

Project I:

**SG07** is the N-terminal part of a large adhesin expressed by the oral bacteria *Streptococcus gordonii*. SAD data from SeMet labeled crystals to 2.2 Å resolution and native data to 2.0 Å resolution were collected at ID-23 (MX/1220). The structure is solved and final refinement and analysis of the structure is underway. A manuscript is in preparation.

Project II:

Acta Crystallogr Sect F Struct Biol Cryst Commun. 2011 Oct 1;67(Pt 10):1207-10. Epub 2011 Sep 24.

# Crystallization of the fimbrial protein FimP from Actinomyces oris and of a triple Ile-to-Met mutant engineered to facilitate selenomethionine labelling.

Persson K.

**Source**

Department of Odontology, Umeå University, SE-901 87 Umeå, Sweden. karina.persson@odont.umu.se

## Abstract

Actinomyces oris is an oral bacterium important for the development of dental plaque. It expresses two forms of fimbriae: type 1 and type 2. FimP, which is the fimbrial protein that is polymerized into the stalk of the type 1 fimbriae, was cloned, overexpressed and crystallized. X-ray data were collected and processed to 2.2 Å resolution. The crystals belonged to space group P2(1)2(1)2, with one molecule in the asymmetric unit. To facilitate structure determination using single anomalous dispersion, three methionines were introduced by site-directed mutagenesis. Crystals of selenomethionine-labelled protein were obtained by streak-seeding and diffracted to 2.0 Å resolution.

PLoS One. 2012;7(10):e48364. doi: 10.1371/journal.pone.0048364. Epub 2012 Oct 31.

# The Pilin Protein FimP from Actinomyces oris: Crystal Structure and Sequence Analyses.

Persson K, Esberg A, Claesson R, Strömberg N.

## Source

Department of Chemistry, Umeå University, Umeå, Sweden.

## Abstract

The Actinomyces oris type-1 pili are important for the initial formation of dental plaque by binding to salivary proteins that adhere to the tooth surface. Here we present the X-ray structure of FimP, the protein that is polymerized into the type-1 pilus stalk, assisted by a pili-specific sortase. FimP consists of three tandem IgG-like domains. The middle and C-terminal domains contain one autocatalyzed intramolecular isopeptide bond each, a feature used by Gram-positive bacteria for stabilization of surface proteins. While the N-terminal domain harbours all the residues necessary for forming an isopeptide bond, no such bond is observed in the crystal structure of this unpolymerized form of FimP. The monomer is further stabilized by one disulfide bond each in the N- and C-terminal domains as well as by a metal-coordinated loop protruding from the C-terminal domain. A lysine, predicted to be crucial for FimP polymerization by covalent attachment to a threonine from another subunit, is located at the rim of a groove lined with conserved residues. The groove may function as a docking site for the sortase-FimP complex. We also present sequence analyses performed on the genes encoding FimP as well as the related FimA, obtained from clinical isolates.

Project III:

Acta Crystallogr Sect F Struct Biol Cryst Commun. 2011 Oct 1;67(Pt 10):1203-6. Epub 2011 Sep 24.

# Expression, purification, crystallization and preliminary X-ray crystallographic studies of alkyl hydroperoxide reductase (AhpC) from the cyanobacterium Anabaena sp. PCC 7120.

Mishra Y, Hall M, Chaurasia N, Rai LC, Jansson S, Schröder WP, Sauer UH.

## Source

Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, SE-901 87 Umeå, Sweden.

## Abstract

Alkyl hydroperoxide reductase (AhpC) is a key component of a large family of thiol-specific antioxidant (TSA) proteins distributed among prokaryotes and eukaryotes. AhpC is involved in the detoxification of reactive oxygen species (ROS) and reactive sulfur species (RSS). Sequence analysis of AhpC from the

cyanobacterium Anabaena sp. PCC 7120 shows that this protein belongs to the 1-Cys class of peroxiredoxins (Prxs). It has recently been reported that enhanced expression of this protein in Escherichia coli offers tolerance to multiple stresses such as heat, salt, copper, cadmium, pesticides and UV-B. However, the structural features and the mechanism behind this process remain unclear. To provide insights into its biochemical function, AhpC was expressed, purified and crystallized by the hanging-drop vapour-diffusion method. Diffraction data were collected to a maximum d-spacing of 2.5 Å using synchrotron radiation. The crystal belonged to space group P2(1)2(1)2(1), with unit-cell parameters a = 80, b = 102, c = 109.6 Å. The structure of AhpC from Anabaena sp. PCC 7120 was determined by molecular-replacement methods using the human Prx enzyme hORF6 (PDB entry 1prx) as the template.