



## 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.

**Experiment title:**Structure of the *quorum sensing* regulatory protein EsaR bound to the 3-oxo-hexanoyl homoserine lactone**Experiment number:**

MX-394

<b>Beamline:</b> BM30A	<b>Date of experiment:</b> from: June 30 <sup>th</sup> to: July 1 <sup>st</sup>	<b>Date of report:</b> 26 July 2005
<b>Shifts:</b> 1	<b>Local contact(s):</b> Dr Sonia FIEULAINÉ	<i>Received at ESRF:</i>

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

Matt Bottomley\* and Andrea Carfí\*

*Dept. of Biochemistry, IRBM P. Angeletti, Pomezia (RM) 00040, Italy***Report:****Introduction**

Virulence in the plant pathogenic bacterium *Pantoea stewartii* requires the *quorum sensing* regulatory protein EsaR and its ligand, the diffusible inducer 3-oxo-hexanoyl homoserine lactone. There is currently only one known structure of an EsaR homologue, namely the TraR protein from *Agrobacterium tumefaciens*. TraR is representative of most quorum sensing R (regulatory) proteins insofar as the binding of its homoserine lactone ligand induces dimerization, DNA binding and transcriptional activation. In contrast, the EsaR protein appears to be one of only a few proteins where homoserine lactone binding induces a dimer to monomer transition, thereby relieving gene repression mediated by apo-EsaR. To gain further insight into the mechanisms of gene regulation by quorum sensing and to understand the molecular basis for the dimer to monomer transition in EsaR, we have expressed and crystallized the EsaR ligand binding domain (EsaR-LBD) in presence of 3-oxo-hexanoyl homoserine lactone.

**Data collected**

One data set has been collected from native crystals. The crystals belong to the orthorhombic space group  $P2_12_12$  with  $a = 67.7\text{\AA}$ ,  $b = 120.2\text{\AA}$ ,  $c = 163.0\text{\AA}$  and diffract to at least  $2.6\text{\AA}$  resolution. The selenomethionine protein has been prepared and the structure will be solved by the SAD/MAD method.

