## EUROPEAN SYNCHROTRON RADIATION FACILITY

INSTALLATION EUROPEENNE DE RAYONNEMENT SYNCHROTRON



## **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: Cocksfoot mottle virus	<b>Experiment</b> <b>number</b> : LS-2187
<b>Beamline</b> :	Date of experiment:	Date of report:
ID14-EH1	from: 13 July 2002 to: 14 July 2002	30-Aug-04
Shifts:1	Local contact(s): Dr. Sigrid KOZIELSKI	Received at ESRF:
Names and affiliations of applicants (* indicates experimentalists):   T. Alwyn Jones, Uppsala University, alwyn@xray.bmc.uu.se   Kaspars Tars, Uppsala University, kaspars@xray.bmc.uu.se   Lars Liljas, Uppsala University, lars@xray.bmc.uu.se   * Gunnar Berglund, Uppsala University, gunnar@xray.bmc.uu.se		

### **Report:**

A 2.7 Å dataset of Cocksfoot Mottle virus has been collected. The structure has been solved and published. The abstract of paper is attached below.

Tars K., Zeltins A., Liljas L. The three-dimensional structure of cocksfoot mottle virus at 2.7Å resolution. *Virology* 310 (2003), 287-297.

Cocksfoot Mottle virus is a plant virus that belongs to the genus sobemovirus. The structure of the virus has been determined at 2.7Å resolution. The icosahedral capsid has T=3 quasi-symmetry and 180 copies of the coat protein. Except for a couple of stacked bases, the viral RNA is not visible in the electron density map. The coat protein has a jelly-roll  $\beta$ -sandwich fold and its conformation is very similar to that of other sobemoviruses and tobacco necrosis virus. The N-terminal arm of one of the three quasi-equivalent subunits is partly ordered and follows the same path in the capsid as the arm in rice yellow mottle virus, another sobemovirus. In other sobemoviruses, the ordered arm follows a different path, but in both cases the arms from three subunits meet and form a similar structure at a three-fold axis. A comparison of the structures and sequences of viruses in this family shows that the only conserved parts of the protein-protein interfaces are those that form binding sites for calcium ions. Still, the relative orientations and position of the subunits are maintained.