EUROPEAN **S**YNCHROTRON **R**ADIATION **F**ACILITY

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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 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:** EMBL Grenoble Outstation BAG (Protein-DNA group of Christoph Muller)	**Experiment number**: LS 1814/1945
Beamline: various	**Date of experiment**: from: September 2000 to: August 2001	**Date of report**: 31/8/01
Shifts:	**Local contact(s)**: various	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Dr. Christoph Muller, EMBL Grenoble Outstation

Dr. Fabrice Michel, Dr. Carlo Petosa, Dr. M. Soler-Lopez,

Mr. Serge Cohen

Report:

a) Structure of the ankyrin repeat domain of Bcl-3 at 1.9 Å resolution

Bcl-3 is a member of the IκB protein family. IκB proteins associate via their ankyrin (ANK) repeat domain with the transcription factor NF-κB. Bcl-3 is an unusual IκB protein because it is primarily nucleoplasmic and can associate with DNA-bound homodimers. Using data collected at ID14-1 we have solved the crystal structure of the ANK repeat domain of human Bcl-3 at 1.9 Å resolution. The structure contains 7 ankyrin repeats and it is the first structure of an IκB protein in its unbound form. The structure provides a basis for understanding the functional diversity of IκB proteins.

Publication: Crystal structure of the ankyrin repeat domain of Bcl-3. F. Michel, M. Soler-Lopez, C. Petosa, P. Cramer, U. Siebenlist & C.W. Müller (submitted).

b) GCM1:DNA complex

The transcriptional regulator GCM1 (glia cells missing) directs differentiation of neuron precursor cells into glia cells. GCM1 contains a 150 amino acid residues DNA-binding domain of unknown structure. We have crystallized GCM1 in complex with its target site in different crystal forms. The best crystals diffract to 2.8 Å resolution. In June 2000 an initial MIR elctron density was obtained using iodo-substituted oligonucleotides. This electron density allowed tracing of about 80% of the model. More recently on different bromine-derivatives helped to improve the experimental phases. At the same time we tried to extend the resolution of the native data. Furthermore data were collected from two other crystal forms with DNA and the quality of crystals without DNA were tested. At this stage refinement of the GCM/DNA complex at 2.8Å is almost completed.

Manuscript in preparation.