

Names and affiliations of applicants (* indicates experimentalists):

Steffi Arzt, Wim Burmeister

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Report:

1

A complete 2.8 \mathring{A} resolution data set was collected using the MRC CCD camera and is currently being processed.

ESRF	Experiment title: Cambridge Block Allocation Group Structure of a chloroplast F1-ATPase	Experiment number: LS1381
Beamline: ID14-4	Date of experiment: from: 1 February 99 to: 3 February 99	Date of report: 24/2/99
Shifts: 1/2	Local contact(s): Sean McSweeney	Received at ESRF: 0 2 MAR. 1999

Names and affiliations of applicants (* indicates experimentalists):

Georg Groth*, Universität Düsseldorf, Germany Daniela Stock*, MRC Laboratory of Molecular Biology, Cambridge, UK A.G.W. Leslie*, MRC Laboratory of Molecular Biology, Cambridge, UK J.E. Walker, MRC Laboratory of Molecular Biology, Cambridge, UK

Report:

Crystals of spinach chloroplast F1-ATPase were tested for the first time at a synchrotron. Currently they diffract to about 5.5 Å resolution. The diffraction pattern showed low mosaicity and sharp single spots. Indexing of the diffraction patterns suggests space group C2 with unit cell dimensions a=260Å, b=150Å, c=155Å, β =123°. The crystals clearly have to be improved in size and quality in order to collect a high-resolution dataset.



Experiment title:

Cambridge Block Allocation Group

Structure of acute myeloid transcription factor 1

(AML1)

Experiment number:
LS1381

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Beamline:	Date of experiment:	Date of report:
ID02B	from: 4 February 99 to: 5 February 99	21/2/99
Shifts:	Local contact(s):	Received at ESRF:
1	Bjarne Rasmussen	

Names and affiliations of applicants (* indicates experimentalists):

Roger Williams*, MRC Laboratory of Molecular Biology, Hills Road, Cambridge, UK Alan Warren*, MRC Laboratory of Molecular Biology, Hills Road, Cambridge, UK Terry Rabbitts, MRC Laboratory of Molecular Biology, Hills Road, Cambridge, UK

Report:

The objective of our project is to determine the structure of the human transcription factor AML1. Crystals of this protein diffract to only low resolution on a rotating anode. We collected a data set (180°) for a putative heavy-atom derivative of the AML1 transcription factor. A low resolution data set (4.2 Å) was obtained using 2 s exposures. Analysis of this derivative is currently in progress.