



Experiment title: Signalling proteins	Experiment number: LS1672	
Beamline: ID14-1	Date of experiment: from: 19/02/2000 to: 21/02/2000	Date of report: 22/08/2000
Shifts: 1	Local contact(s): Hassan Berhali	<i>Received at ESRF:</i> 28 AOUT 2000

Names and affiliations of applicants (* indicates experimentalists):

Dr. Neil McDonald

Department of Crystallography
Birkbeck College
University of London
Malet Street
London WC1E 7HX

Report:

A native dataset was collected to 2.0 Å on crystals of a lipid inositol-phosphatase from *M. Tuberculosis*. This is the highest resolution yet obtained for this project which has previously showed diffraction to Bragg spacings of 3.0Å in-house. We have subsequently determined the crystal structure of this lipid phosphatase by SIRAS using this native dataset.

A native dataset was collected to 2.7 Å resolution on crystals of a MAP kinase phosphatase, again the best native dataset we have recorded at any synchrotron source. This protein selectively inactivates a therapeutically important mitogen-activated protein kinase. A second trip to the ESRF as part of the same BAG gave native diffraction data to 3.3Å on a different crystal form of the same enzyme (collected by Richard Norman on 09-06-00).

Thirdly we screened for crystals of an NO-synthase regulating enzyme in the presence of either substrate or product and monitored the diffraction following soaks. This protein is a key target in cardiovascular disease. Diffraction was observed to Bragg spacing of 3.0Å but this was not deemed to be sufficient quality to record a full dataset. Further efforts to improve these crystals will be made prior to further attempts at recording these data.