REPORT ON VISIT TO MAJOR RESEARCH FACILITY

DATE OF REPORT: 23/9/99	FACILITY: ESRF	BEAMLINE/INSTRUMENT (if applicable) BM30/FIP
EXPERIMENT NO: 30.01.1		

TITLE:	DATE OF EXPERIMENT from 15/07/99 to 18/07/99
APPLICANTS + EXPERIMENTALISTS (name + affiliation/contact phone number) Dr Paul D Carr, RSC, ANU Dr Denis Verger, RSC, ANU Prof Ian G Young, JCSMR, ANU	CONTACT AT THE FACILITY: Dr Michel Roth (to be filled in by ANSTO) Received on:

ABSTRACT (200 words in plain English):

High quality datasets were collected from native and six mercurial derivatives of the cytokine receptor protein il5rβ. The resulting electron density maps have been used to fully trace the polypeptide chain of this important molecule. Structural refinement of the resulting model is currently underway.

Has this work been published (references)? Submitted

EXPERIMENTAL REPORT

The cytokine receptor IL5R is an important protein that has been implicated in the pathogensis of asthma and host response to certain parasite infections. The extracellular β chain of this receptor has been crystallised and is the study of a major research effort in our home laboratory. The β chain has been shown to play a key signalling role in response to the binding of IL5 and also to the closely related cytokines IL3 and GM-CSF. This receptor is approximately twice the size of any other cytokine receptor whose three dimensional structure has been elucidated to date, and it represents a separate class of receptor. International efforts to solve cytokine receptors of this class are intense.

X-ray data were collected from a native crystal and mercurial derivatives of six genetically engineered cyteine mutants. The wavelength used for the experiments (1.0085Å) selected to maximize the anomalous signal contained in the data. In excess of 1000 frames of useful data were collected on a MAR345 imaging plate detector. These included a triple wavelength MAD experiment and a dataset from a native activated mutant in addition to the data required for MIR phasing.

The electron density maps calculated from the MIR phases have allowed us to almost completely trace the polypeptide chain of the molecule. This confirmed our initial positioning of domains obtained from in-house data and clearly defined the connectivity.

Refinement of this exciting structure is currently underway.

Acknowledgement:

We would like to gratefully acknowledge the help and support of Dr Michel Roth whilst at the facility