



Experiment title: Crystallographic studies of Staphylococcal exotoxin 1	Experiment number: LS-1672	
Beamline: ID 14-1	Date of experiment: from: 20/02/2000 to: 21/02/2000	Date of report: 18/08/2000 <i>Received at ESRF:</i> 28 AOUT 2000
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Report:

Staphylococcal exotoxin 1 (sET1) is a member of a newly discovered family of superantigen related proteins from *Staphylococcal aureus*. Superantigens in general interact with MHC class II molecules and T-cell receptors in a non-peptide dependent manner, thus eliciting a massive cytokine response from a wide range of T-lymphocytes, resulting in a range of disease. Experiments with sET1 have failed to elicit this response from T-cells to date, and this protein may thus be able to shed light on the evolution of these toxins, and perhaps on the origin of their function, since utility of a large scale immune response for the bacteria's viability is still unclear.

SET1 is a 24 kDa, 230 residue protein which contains no cysteines and only a single methionine, it has, at best, 25% identity to any known structure. Structure solution is being attempted by standard multiple isomorphous replacement methods. Crystals grow readily using PEG-MME 2k as a precipitant, buffered at pH 6.5 with 0.1M MES in the presence of 0.2 M ammonium sulphate. The crystals are in spacegroup $P4_{1/3}$, with cell dimensions $a=b=81.7 \text{ \AA}$, $c=148.0 \text{ \AA}$, there are probably 2 molecules in the asymmetric unit. While at ID14-1, four complete datasets were collected: a native (to 2.7 \AA), and three possible derivatives from crystals that had been soaked in platinum chloride, samarium nitrate and cobalt chloride. The crystals have a tendency to form as near-perfect twins which are not detectable from crystal morphology, and this was the case for two of the derivatives. The last derivative did not reveal any strong peaks in a Patterson map. Since this trip, another

member of this family has become available for crystallisation, this protein contains 5 methionines, and it will now be used for initial structure determination.