



Experiment title:
BAG - CNRS gif sur Yvette

Experiment number:
LS 1659

Beamline:
ID14-EH4

Date of experiment:
from: 07/03-00 to: 08/03/00

Date of report:
24/08/00

Shifts: 3

Local contact(s): Sean McSweeney

Received at

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Report:

Protein E1 (fusion protein of Semliki Forest Virus) Space-group $P6_422$. $a=b=78$, $c=338$. Four complete MAD data sets were collected this time from crystals soaked in 1mM $K_3UO_2F_5$, at the L_{III} absorption edge of U. Two Uranyl sites were found, the most highly occupied site lies however on a 2-fold crystallographic axis. i.e. on a special position. The 4 datasets were not isomorphous between them, and electron density maps were calculated to 4 resolution for each of them. These maps were averaged between them and with an older map to yield the map shown in the figure, with a tentative poly-alanine model built in. The ribbon model shown underneath corresponds to the fusion protein of the flavivirus Tick-borne encephalitis virus. The experimental map of E1 shows that these two proteins share very likely the same fold, but they differ enough that molecular replacement fails to find a clear solution. We need to collect now MAD data-sets to higher resolution, from recent crystals that are substantially bigger than the ones we had used that time. Different soaking conditions will also be tried, in an attempt to increase the occupancy of the second Uranyl site.