



Experiment title: Cambridge MRC Block Allocation Group
Structure of full length human Hepatitis B viral capsid

Experiment number:
LS1669

Beamline:
ID14-4

Date of experiment:
from: 12/07/00 to: 14/07/00

Date of report:
25/8/00

Shifts:
3

Local contact(s):
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Report:

The structure of the Hepatitis B capsid assembled from truncated capsid protein (aa 1-149) with T=4 icosahedral symmetry has been determined previously using data collected on ID2 at ESRF. Crystals of capsids of the full length capsid protein (aa 1-183), which includes an arginine rich C-terminal region involved in binding nucleic acid, have been obtained. These capsids package RNA (probably the mRNA for the capsid protein), and this structure may provide information on how the RNA interacts with the capsid protein. Optimal cryoprotection conditions were established in a previous trip to ID14-2.

High resolution data were collected from 10 crystals (two positions per crystal) and a low resolution dataset from a further crystal to be able to measure the strongest reflections. Exposure times of up to 90 seconds for an 0.25 degree oscillation were required for the high resolution data. Data collection time was just less than 24 hours. The data have been merged to give an Rmerge of 10.7% to 3.6Å (94% complete, mean I/σ of 5.6) with an average multiplicity of 2.

Phase extension using the 7.5Å resolution cryo EM model and exploiting the 30-fold non-crystallographic symmetry is in progress.