



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

**Experiment number:**  
LS1669

**Beamline:**

ID14-2

**Date of experiment:**

from: 5/3/00 to: 8/3/00

**Date of report:**

25/8/00

**Shifts:**

3

**Local contact(s):**

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*Received at ESRF:*

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**Report:**

The structure of the truncated HepB capsid (aa 1-149) with T=4 icosahedral symmetry has been determined previously using data collected on ID2 at ESRF. Crystals of the full length capsid (aa 1-183), which includes an arginine rich C-terminal region involved in binding nucleic acid have been obtained using four different cryoprotectants. The diffraction qualities of these crystals using different cryomounting procedures have been assessed. Those grown in the presence of butane diol as the cryoprotectant diffract to about 3.6Å resolution. In spite of the cryocooling, the crystal lifetime in the beam is quite short, and long exposure times are required (90-120 seconds on station ID14-2 for an 0.3 degree oscillation). Approximately 5 degrees of data can be collected from each crystal. This preliminary screening, which used approximately 12 hours beamtime, is essential prior to attempting to collect a full dataset.