ESRF	**Experiment title:** The structural basis of the escape of influenza virus mutants for neutralization of their infectivity.	**Experiment number:** LS-652
Beamline: ID02	**Date of experiment:** from: 23/04/97 to:25/04/97	**Date of report:** 23/12/97
Shifts: 5	**Local contact(s):J.** Grimes	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

M. Knossow, Laboratoire d'Enzymologie et Biochimie Structurales (L.E.B.S), CNRS, Gif-sur-Yvette, FRANCE

T. Bizebard*, L.E.B.S, CNRS, Gif-sur-Yvette, FRANCE

D. Fleury*, L.E.B.S, CNRS, Gif-sur-Yvette, FRANCE

B. Gigant*, L.E.B.S, CNRS, Gif-sur-Yvette, FRANCE

Report:

We collected a dataset at cryogenic temperature (110 K) on crystals of a complex between an influenza virus hemagglutinin (BHA X31) and the Fab of a neutralizing antibody (Hc63). The crystals were very thin plates with dimensions 0. lmm x 0.05 mm x 0.01 mm. In fact, the diffraction pattern showed they were only poorly diffracting crystals, with very weak diffraction above 4.0 Å resolution. Futhermore, as often seen in cryogenic conditions, the crystals displayed a high mosaic spread (0.8°). The presence of a 315 Å long unit cell parameter enforced us to collect the data using three different oscillation ranges (1.0°, 0.6° and 0.3°) as this very long unit cell axis was coming parallel to the beam. The data characteristics after processing with the HKL suite (Otwinowsky, Z. Minor, W.(1997) "Processing of X-Ray Diffraction Data Collected in Oscillation Mode" in Methods in Enzymology vol 276) are as follows:

space group P21212
unit cell a= 142.1, b= 3 13.6, c= 96.2 and $\alpha=\beta=\gamma=90°$
maximun resolution : 4.0 Å
completness : 80%
Rsym : 0.12

space group P21212
unit cell a= 142.1, b= 3 13.6, c= 96.2 and $\alpha=\beta=\gamma=90°$
maximun resolution : 4.0 A
completness : 80%
Rsym : 0.12
Average redundancy : 2.5

We are currently solving the structure of this complex by the molecular replacement method. The hemagglutinin part of the complex has already been located in the unit cell. As far as the antibody is concerned, its amino-acid sequence is just becoming available now. This will allow us to perform further molecular replacement searches using as a model the Fab deposited in the PDB that displays the higher sequence identity with Fab Hc63. New crystallization trials have produced bigger and better shaped crystals, which may enable higher resolution data collection.