



Experiment title: E1, the fusion protein of Semliki Forest Virus

(Data collected in part as part of the BAG CNRS -Gif sur Yvette coordinated by M. Knossow)

Experiment number:
LS 1798

<p>Beamline: ID14-EH4 ID14-EH1</p>	<p>Date of experiment: from: 03/11/00, 08.00 to: 04/11/00, 07.30 from: 15/11/00, 08.00 to: 16/11/00, 07.30</p>	<p>Date of report: 27/02/01</p>
<p>Shifts: 3 (EH4) 1.5 (EH1)</p>	<p>Local contact(s): Julien Lescar, Stephanie Monaco, Hassan Belrhali</p>	<p><i>Received at ESRF:</i></p>

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Report: Semliki Forest Virus has been used as a model system for viruses that enter cells through receptor-mediated endocytosis. The viral nucleocapsid is released into the cytoplasm of the target cell by fusion of the viral and endosomal membranes in a process that is triggered by the acidic pH of the endosome. Protein E1, which is part of the viral spike, undergoes an irreversible fusogenic conformational change to expose a "fusion peptide" that is kept buried in the viral spike under conditions of neutral pH..

Using crystals of the ectodomain of E1 that diffract X-ray anisotropically (Res. 2.3 Å along c^* and only 3.5 Å along a^*), we have been able to solve its 3D structure by averaging different experimental electron density maps. These maps were obtained either by multiple isomorphous replacement or multiple anomalous diffraction using essentially two heavy-atom derivatives: $K_3UO_2F_5$ and K_2PtCl_4 .

A preliminary account of the structure together with its placement in the electron microscopy reconstruction has been accepted for publication (Lescar et al., 2001, Cell, in the press).

Data collected on eh4 have yielded one native, one osmium data set at three wavelengths (resolution: 3.5 Å, 95.3% complete, $R_{merge}=7.8\%$ for f'' maximum) two platinum MAD data sets (three wavelengths) (resolution: 3.5 Å, 96.4% complete, $R_{merge}=5.7\%$, for f'' maximum), one native data set resolution 3.5 Å, (98.4% complete, $R_{merge}=6.7\%$)

-Data collected on eh1 have yielded one native 3.0 Å, (96.7% complete, $R_{merge}=5.7\%$) and several putative derivatives (Ir, 3.0 Å, 97.2% complete, $R_{merge}=5.5\%$); (Os, 3.6 Å, 99.7% complete, $R_{merge}=8.4\%$) (Re, 3.2 Å, 96.0% complete, $R_{merge}=8.9\%$).