ESRF	**Experiment title:** HCV non-structural protein 3 protease domain (NS3) bound to a X inhibitor	**Experiment number:** LS-1517
Beamline: ID14 EH1	**Date of experiment:** from: 20/11/99 to: 21/11/99	**Date of report:** 29.02.00
Shifts: 1	**Local contact(s):** H.Belrhali	*Received at ESRF:*

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Report:

Background: Hepatitis C virus (HCV) currently infects approximately 3% of the world's population. The HCV protease domain of NS3 is a serine protease with a chymotrypsin-like fold and is a potential antiviral target. Reversible covalent inhibitors have been designed. The crystal structures of these inhibitors will shed light on the mode of binding of these compounds allowing a structure-directed approach to the design of more potent inhibitors.

Results: A 2.2 Å resolution data set of the NS3 protease with a covalent peptide inhibitor was collected on beamline ID14-EH1. Data were 96.5% complete in the 20-2.2 Å rang e with an overall R_{merge} of 6.2%.