ESRF	**Experiment title:** NS3 Protease (H strain) complexed with NS4A peptide	**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. Belhrali	*Received at ESRF:*

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Report:

Background: A macromolecular inhibitor of the N-terminal serine protease of the HCV NS3 protein has been affinity selected by phage-display. This inhibitor cVh, a "camelised" variable domain antibody fragment in which the CDR3 was randomised in sequence and length, has a Ki of 150nM. In analytical gel filtration experiments the molecule appears to behave as a dimmer, although it is unknown whether it is functionally active as a dimmer or a monomer. We aim to solve the structure of the complex formed between NS3/4A protease and cVh, to determine the factors influencing the selection of this molecule and its mode of inhibition. For a complete analysis a high resolution structure of the unbound cVh inhibitor must also be known.

*Results:*One data set were collected on a crystal of the cVh protein. Initial processing shows the following results:

Resolution 2.4Å

Cell	74.63	74.63	101.60	90.0	90.0	120.0
Spacegp	P3					

Due to lack of time data were not processed at the beamline. Data has been archived at ESRF and when we receive data it will be processed.