



<b>Experiment title:</b> Crystallographic Studies of Human Growth Hormone	<b>Experiment number:</b> LS1070/LS1071	
<b>Beamline:</b> ID14-4	<b>Date of experiment:</b> from: 15/12/98 to: 17/12/98	<b>Date of report:</b> 27/08/99
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**Report:**

Despite a number of published structures, there is no reliable model of a single, free molecule of human Growth Hormone, which is not mutated or not in complex with its receptor. It is known that the hGH structure is affected by receptor binding and some stable intermediates of the free hormone (dimers) were postulated recently (Kasimova *et al.*, *J. Mol. Biol.* (1998), 277, 409-418). Therefore we reinitiated structural studies of human GH at York. Crystals were obtained by the method described by Clarkson&Korber *et al.*, *J.Mol. Biol* (1998), 208, 719-721.

X-ray data on a flashed frozen crystal (120K) were collected on ID14-4 station at ESRF using Quantum-4 CCD detector. Crystals diffracted well to 2.5 Å with some diffraction observed to 2.3 Å, indicating the anisotropic nature of the crystals.  $R_{merge}$  at 2.5 Å is 0.044 (0.11 in 2.6-2.5 Å shell (0.14 in 2.5-2.3 Å)); completeness is 94% (82% in 2.6-2.5 Å bin (67% in 2.5 - 2.3 Å shell)), average  $I/\sigma(I)$  is 18 with redundancy 12. The structure is currently being refined.