ESRF	**Experiment title:** University College London BAG – Preliminary Report.	**Experiment number**: LS-1334
Beamline: ID14-4	**Date of experiment**: from: 20/2/99 to: 22/2/99	**Date of report**: 2/3/99
Shifts: 6	**Local contact(s)**: Raymond Ravelli	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

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Report:

Project: DNA Polymerase.

This batch of crystals grew as rods, rather than the plates previously seen. The cell appeared to be the same, but all crystals proved to be intimately twinned along the rod axis. This also appeared to reduce the diffraction limit to a poor 4.0Å. The twinning was not detected previous to the trip due to the rather weak diffraction seen on home sources. After analysis of all crystals, the project was abandoned – a further day on BM14 to be used for a MAD experiment on SeMet crystals was returned to ESRF User Office.

Project: RuvABC

The diffraction limit of our RuvA-Holliday junction crystals was extended from 3.0Å to 2.5Å in spacegroup $P3_1$. A further dataset was recorded to lower resolution (3.0Å) in spacegroup P1 to study the effect of the spacegroup symmetry on the image of multiply disordered Holliday junction present in the complex. Refinement is in progress.

Project: Hsp26.

None of these crystals were taken. None of the five types of crystal grown diffract beyond ~10-15Å. This is due to the presence of inseparable 24mer and 26mers in the crystallisation sample, as discovered by EM.

Project: 7,8-dihydro-8-oxo-guanine N-glycosylase.

Due to problems with protein preparation, no native crystals could be grown before the trip. Data collection was attempted on crystals of a mutant protein complexed with DNA, but these crystals were very small and none could be found that diffracted past 6Å.

Non Listed Project: HSP90 N-terminus with ATP analogue AMPNP bound.

A high resolution (1.7Å) data set was collected from these crystals, using two sweeps – low res (2.4Å, 0.1sec/1º) and high res (1.7Å, 1sec/1º). Previous low resolution (2.6Å) data sets indicated some change had occurred compared to bound ADP. Refinement is in progress.

Non Listed Project: GU mismatch specific DNA N-glycosylase.

Data was collected on these extremely small crystals (0.05 x 0.015 x 0.015mm) to a resolution of 2.3Å, 10secs/1º. Refinement is in progress.