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| ESRF | **Experiment title:**<br>Data collection on eye-lens proteins | **Experiment number**:<br>LS-1527 |
| **Beamline**:<br>ID14-3 | **Date of experiment**:<br>from: 15/09/1999 to: 17/09/1999 | **Date of report**:<br>23/02/2000<br>*Received at ESRF:* |
| **Shifts:**<br>6 | **Local contact(s)**:<br>Hassan Berhali | |

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## Report:

During this visit, which was shared with Tracey Barret and Bernard O’ Hara (Dept. of Biochemistry, University College London) a native data set of a truncated form of human βB1 crystallin has been collected at 2.7 Å resolution. The crystals belong to the space group $P4_32_12$ and have cell dimensions a=b=45.2 Å and c=171.0 Å. The completeness of the data is 99.3% and the Rmerge 4.3%. With this data set we were able to solve the structure of human βB1 by molecular replacement using the C-terminal domain of bovine βB2 as a search model.

In addition we collected a native data set of a plant heat shock protein to 2.7 Å resolution. The crystals belong to the space group $R32$ with cell dimensions a=b=171, c=123. The completeness of the data is 94.6% and the Rmerge is 4.0%. Finally we collected a native data set of η-crystallin from the elephant shrew at 2.4 Å resolution. The crystals have the space group $P2_1$ with cell dimensions a=81 Å, b=136.4 Å, c=85 Å and β=102.6º.

The data set is 96.5% complete and has an Rmerge of 6.8%. The structure of η-crystallin has been solved by molecular replacement, using this data set and the structure of aldehyde dehydrogenase from sheep liver (PDB entry code 1bxs) as a search model.