



| | | |
|----------------------------|---|--|
| | Experiment title: Ribokinase and Xylose binding protein from <i>E. coli</i> . | Experiment number: LS-1164 |
| Beamline: ID14-4 | Date of experiment: from: 20 Nov 1998 to: 23 Nov 1998 | Date of report: 1 March 1999 |
| Shifts: 1 | Local contact(s): Sean McSweeney | <i>Received at ESRF:</i> |

Names and affiliations of applicants (* indicates experimentalists):

Sherry L. Mowbray, Swedish Univ. Agric. Sciences, mowbray@alpha2.bmc.uu.se

T. Alwyn Jones, Uppsala University, alwyn@xray.bmc.uu.se

* Joakim Björkman, Swedish Univ. Agric. Sciences, joakim@alpha2.bmc.uu.se

* Alexander Cameron, Uppsala University, alex@alpha2.bmc.uu.se

* Mark Harris, Uppsala University, markh@alpha2.bmc.uu.se

* Mats Sandgren, Uppsala University, mats@alpha2.bmc.uu.se

Report:

This was our first visit and our first opportunity to use the beamlines at ESRF. The two days allocated were shared with two other projects from our department. Due to machine problems only about 4 shifts (of 6 scheduled) could be used for data collection and of these about 1 shift was used for this project. Crystals that had been tested for good diffraction on our local rotating anode x-ray source were brought frozen to ESRF for data collection. For some of the crystals, however, the strong diffraction at ID14-4 revealed defects that were not evident from the diffraction pattern obtained at home. Out of 9 crystals tried, only 3 were found to be useful for data collection:

- 1) RK: *E. coli* Ribokinase, in the presence of ribose, magnesium and AMP-PCP (an ATP analog). 2.1 Å. The crystal turned out to be a twin crystal showing two distinct diffraction patterns overlaid. The spots were however enough separated to allow indexing and data processing. Actually both patterns could be indexed and were merged together with an Rmerge of 7.7% (23.4%). Structure refinement has been started and current R-factor and R-free are 26.4% and 30.7%, respectively.
- 2) XBP: *E. coli* Xylose binding protein, no ligand. 2.7 Å. Structure being refined.
- 3) XBP: *E. coli* Xylose binding protein, no ligand. 2.3 Å. Structure being refined.