



	Experiment title: Structure determination of Allose-binding Protein from <i>E. coli</i> . BAG: Uppsala (II)	Experiment number: LS-1520 f
Beamline: ID14:4	Date of experiment: from: 10 December, 1999 to: 12 December, 1999	Date of report: 24 August, 2000
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Report:

After diffusion through the bacterial outer membrane, allose may be recognized by a specific periplasmic receptor, the allose-binding protein. The resulting activation of this protein allows it to interact with membrane proteins that convey the nutrient into the cell.

The allose-binding protein (ALBP) consists of two domains where each domain consists of a parallel beta-sheet flanked by alpha-helices on both sides. The domains are joined by a three-stranded hinge region. In the closed form the domains come together to form the binding cleft of the sugar.

A closed ligand-bound structure has been solved previously. Data collected at ESRF (resolution 1.7 Å, R-merge 9.3 (36)%, multiplicity 7.2) allowed us to solve the structures of two open, ligand-free forms by molecular replacement using the ligand-complex structure. We are in the final stages of the refinement of models at 1.7 Å resolution (R-factor 22%, R-free 27%). Together, these structures will provide a description of the molecular details of the opening and closing process that is so crucial in transport (manuscript in preparation).