

**Experiment title:**Structure determination of Alloose-binding Protein from *E. coli***Experiment number:**

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

The alloose-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).