

Periplasmic Binding Transport Protein

Shigella flexneri, DEBP

Expressed in *E.Coli*

Cat. No. CBCRY22

Lot. No. (See product label)

BACKGROUND

The crystal structure of a periplasmic l-aspartate/l-glutamate binding protein (DEBP) from *Shigella flexneri* complexed with an l-glutamate molecule has been determined and refined to an atomic resolution of 1.0 Å. There are two DEBP molecules in the asymmetric unit. The refined model contains 4462 non-hydrogen protein atoms, 730 water molecules, 2 bound glutamate molecules, and 2 Tris molecules from the buffer used in crystallization. The final R (cryst) and R(free) factors are 13.61% and 16.89%, respectively.

MOLECULAR DESCRIPTION

Protein classification: Transport protein

Structure Weight: 64851.95 Da

Polymer: 1

Molecule: Periplasmic Binding Transport Protein

Chains: A, B

Type: polypeptide (L)

Chain Length: 287 amino acids

CRYSTAL INFORMATION

PDB ID: [2VHA](#)

MMDB ID: [70491](#)

Source: *E.Coli*

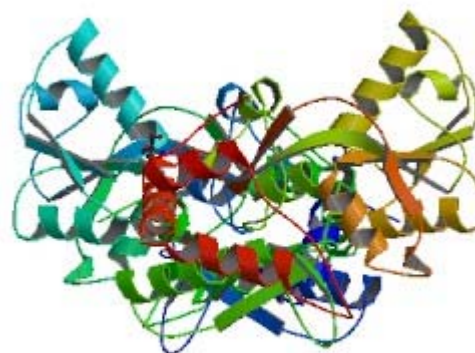
Method: X-Ray Diffraction

Resolution: 2.8 Å

Ligand Chemical Component: Glutamic acid; 2-amino-2-hydroxymethyl-propane-1,3-diol

FOR RESEARCH USE ONLY

CRYSTAL STRUCTURE



GENE INFORMATION

Gene Name: [livJ](#)

Synonyms: S4285; high-affinity amino acid transport protein, periplasmic binding protein

GeneID: [1080493](#)

Function: Transport activity

PRIMARY CITATION

Hu, Y.L., Fan, C.-P., Fu, G.S., Zhu, D.Y., Jin, Q., Wang, D.-C. (2008) Crystal Structure of a Glutamate/Aspartate Binding Protein Complexed with a Glutamate Molecule: Structural Basis of Ligand Specificity at Atomic Resolution. *J.Mol.Biol.* 382: 99-111