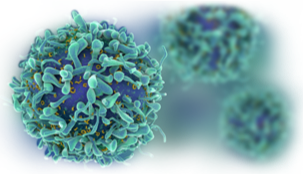

DEBP Protein Crystal

Catalog: CBCRY22

PRODUCT INFORMATION

Name	DEBP Protein Crystal
Cat No.	CBCRY22
Fragment	Residues 24-302
Protein Description	Periplasmic Binding Transport Protein
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 A. 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.
Protein Classification	Transport protein
Structure Weight	64851.95 Da
Method	X-Ray Diffraction
Resolution	2.8Å
Ligand Chemical Component	Glutamic acid; 2-amino-2-hydroxymethyl-propane-1,3-diol
Reference	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