



# DEBP Protein Crystal

**Catalog: CBCRY22**

## PRODUCT INFORMATION

<b>Name</b>	DEBP Protein Crystal
<b>Cat No.</b>	CBCRY22
<b>Fragment</b>	Residues 24-302
<b>Protein Description</b>	Periplasmic Binding Transport Protein
<b>Background</b>	The crystal structure of a periplasmic l-aspartate/l-glutamate binding protein (DEBP) from <i>Shigella flexneri</i> co 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.
<b>Protein Classification</b>	Transport protein
<b>Structure Weight</b>	64851.95 Da
<b>Method</b>	X-Ray Diffraction
<b>Resolution</b>	2.8Å
<b>Ligand Chemical Component</b>	Glutamic acid; 2-amino-2-hydroxymethyl-propane-1,3-diol
<b>Reference</b>	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. <i>J.Mol.Biol.</i> 382: 99-111