



DEBP Protein Crystal

Catalog: CBCRY22

PRODUCT INFORMATION

| Name | DEBP Protein Crystal |
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| 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 co mplexed 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 atom s, 730 water molecules, 2 bound glutamate molecules, and 2 Tris molecules from the buffer used in crystallizat ion. 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, CP., Fu, G.S., Zhu, D.Y., Jin, Q., Wang, DC. (2008) Crystal Structure of a Glutamate/Aspart ate Binding Protein Complexed with a Glutamate Molecule: Structural Basis of Ligand Specificity at Atomic R esolution. J.Mol.Biol. 382: 99-111 |