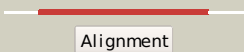

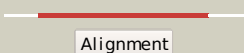

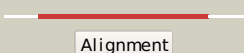

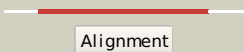

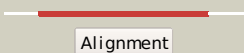

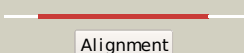

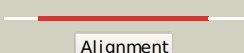

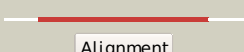

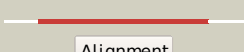

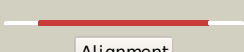

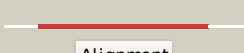




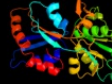





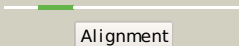
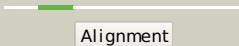
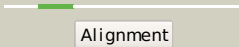
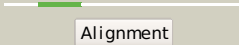
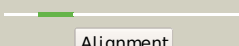

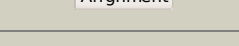
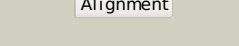
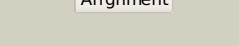




| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">dlixha_</a> |  Alignment   |    | 100.0      | 100    | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 2  | <a href="#">d1pc3a_</a> |  Alignment   |    | 100.0      | 31     | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 3  | <a href="#">d2v3qa1</a> |  Alignment   |    | 100.0      | 24     | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 4  | <a href="#">c1twyG_</a> |  Alignment   |   | 100.0      | 23     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein;<br><b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae |
| 5  | <a href="#">d1twya_</a> |  Alignment |  | 100.0      | 23     | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 6  | <a href="#">c2h5yC_</a> |  Alignment |  | 99.8       | 18     | <b>PDB header:</b> metal transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> molybdate-binding periplasmic protein;<br><b>PDBTitle:</b> crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate |
| 7  | <a href="#">d1atga_</a> |  Alignment |  | 99.7       | 21     | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 8  | <a href="#">d1amfa_</a> |  Alignment |  | 99.7       | 19     | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 9  | <a href="#">c3fj7A_</a> |  Alignment |  | 99.7       | 16     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> major antigenic peptide peb3;<br><b>PDBTitle:</b> crystal structure of l-phospholactate bound peb3  |
| 10 | <a href="#">c3kn3C_</a> |  Alignment |  | 99.7       | 16     | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative periplasmic protein;<br><b>PDBTitle:</b> crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinnella succinogenes             |
| 11 | <a href="#">c3lr1A_</a> |  Alignment |  | 99.6       | 19     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> tungstate abc transporter, periplasmic tungstate-<br><b>PDBTitle:</b> the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens                         |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">c3muqB_</a> | Alignment |    | 99.6 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein;<br><b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633 |
| 13 | <a href="#">d1sbpa_</a> | Alignment |    | 99.5 | 15 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 14 | <a href="#">c3cfxA_</a> | Alignment |    | 98.9 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein ma_0280;<br><b>PDBTitle:</b> crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate  |
| 15 | <a href="#">c3k6wA_</a> | Alignment |    | 98.8 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> solute-binding protein ma_0280;<br><b>PDBTitle:</b> apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans   |
| 16 | <a href="#">d2onsa1</a> | Alignment |    | 98.7 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 17 | <a href="#">d1xvxa_</a> | Alignment |    | 98.7 | 17 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 18 | <a href="#">c3c9hB_</a> | Alignment |  | 98.5 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, substrate binding protein;<br><b>PDBTitle:</b> crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens               |
| 19 | <a href="#">c2pt1A_</a> | Alignment |  | 98.5 | 13 | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> iron transport protein;<br><b>PDBTitle:</b> futa1 synechocystis pcc 6803  |
| 20 | <a href="#">c3cg3A_</a> | Alignment |  | 98.4 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein ph0151;<br><b>PDBTitle:</b> crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate  |
| 21 | <a href="#">d1xc1a_</a> | Alignment | not modelled  | 98.4 | 15 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 22 | <a href="#">d1nnfa_</a> | Alignment | not modelled  | 98.4 | 18 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 23 | <a href="#">d1y4ta_</a> | Alignment | not modelled  | 98.4 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 24 | <a href="#">d1y9ua_</a> | Alignment | not modelled  | 98.4 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 25 | <a href="#">d1xvya_</a> | Alignment | not modelled  | 98.4 | 18 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 26 | <a href="#">d1q35a_</a> | Alignment | not modelled  | 98.2 | 12 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 27 | <a href="#">c3pu5A_</a> | Alignment | not modelled  | 98.0 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein;<br><b>PDBTitle:</b> the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis                       |
| 28 | <a href="#">c3cfzA_</a> | Alignment | not modelled  | 97.9 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein mj1186;<br><b>PDBTitle:</b> crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate  |
| 29 | <a href="#">c2qryD_</a> | Alignment | not modelled  | 97.8 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> thiamine-binding periplasmic protein;   |

|    |                         |           |              |      |  |
|----|-------------------------|-----------|--------------|------|--|
|    |                         |           |              |      | <b>PDBTitle:</b> periplasmic thiamin binding protein   |
| 30 | <a href="#">d2fyia1</a> | Alignment | not modelled | 97.3 | 13<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 31 | <a href="#">c2hxrA</a>  | Alignment | not modelled | 97.2 | 15<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator cynr;<br><b>PDBTitle:</b> structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism   |
| 32 | <a href="#">c2xd3A</a>  | Alignment | not modelled | 97.1 | 15<br><b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding protein;<br><b>PDBTitle:</b> the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose.  |
| 33 | <a href="#">c2vozA</a>  | Alignment | not modelled | 97.0 | 12<br><b>PDB header:</b> metal-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic iron-binding protein;<br><b>PDBTitle:</b> apo futa2 from synechocystis pcc6803   |
| 34 | <a href="#">d1al3a</a>  | Alignment | not modelled | 96.9 | 14<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 35 | <a href="#">c1al3A</a>  | Alignment | not modelled | 96.9 | 14<br><b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> cys regulon transcriptional activator cysb;<br><b>PDBTitle:</b> cofactor binding fragment of cysb from klebsiella aerogenes   |
| 36 | <a href="#">d1pota</a>  | Alignment | not modelled | 96.5 | 20<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 37 | <a href="#">c3cg1A</a>  | Alignment | not modelled | 96.4 | 16<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein pf0080;<br><b>PDBTitle:</b> crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate   |
| 38 | <a href="#">d1eu8a</a>  | Alignment | not modelled | 96.1 | 14<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 39 | <a href="#">c3cvgC</a>  | Alignment | not modelled | 95.9 | 13<br><b>PDB header:</b> metal binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative metal binding protein;<br><b>PDBTitle:</b> crystal structure of a periplasmic putative metal binding protein  |
| 40 | <a href="#">c3rpwA</a>  | Alignment | not modelled | 95.9 | 17<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter;<br><b>PDBTitle:</b> the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009   |
| 41 | <a href="#">c3ho7A</a>  | Alignment | not modelled | 95.7 | 10<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxyr;<br><b>PDBTitle:</b> crystal structure of oxyr from porphyromonas gingivalis  |
| 42 | <a href="#">c2ql3G</a>  | Alignment | not modelled | 95.7 | 10<br><b>PDB header:</b> transcription<br><b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein;<br><b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1                                       |
| 43 | <a href="#">c3jv9B</a>  | Alignment | not modelled | 95.5 | 16<br><b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family;<br><b>PDBTitle:</b> the structure of a reduced form of oxyr from n. meningitidis   |
| 44 | <a href="#">d1ixca2</a> | Alignment | not modelled | 94.8 | 12<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 45 | <a href="#">c2f7cA</a>  | Alignment | not modelled | 93.6 | 9<br><b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator catm;<br><b>PDBTitle:</b> catm effector binding domain with its effector cis,cis-muconate  |
| 46 | <a href="#">c2h9qC</a>  | Alignment | not modelled | 93.6 | 8<br><b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator catm;<br><b>PDBTitle:</b> crystal structure of the effector binding domain of a catm2 variant (r156h)  |
| 47 | <a href="#">c3oo6A</a>  | Alignment | not modelled | 93.5 | 12<br><b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter binding protein acbh;<br><b>PDBTitle:</b> crystal structures and biochemical characterization of the bacterial2 solute receptor acbh reveal an unprecedented exclusive substrate3 preference for b-d-galactopyranose |
| 48 | <a href="#">d1i6aa</a>  | Alignment | not modelled | 92.7 | 10<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 49 | <a href="#">c3qufB</a>  | Alignment | not modelled | 92.7 | 9<br><b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein, family 1;<br><b>PDBTitle:</b> the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis   |
| 50 | <a href="#">c2gh9A</a>  | Alignment | not modelled | 92.5 | 13<br><b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding protein;<br><b>PDBTitle:</b> thermus thermophilus maltotriose binding protein bound with2 maltotriose   |
| 51 | <a href="#">c2v84A</a>  | Alignment | not modelled | 92.4 | 15<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> spermidine/putrescine abc transporter, periplasmic<br><b>PDBTitle:</b> crystal structure of the tp0655 (tpptod) lipoprotein of2 treponema pallidum   |
| 52 | <a href="#">c2h9bB</a>  | Alignment | not modelled | 92.4 | 11<br><b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm;<br><b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)  |
| 53 | <a href="#">c3n6uA</a>  | Alignment | not modelled | 92.4 | 16<br><b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysr type regulator of tsambcd;<br><b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate   |
| 54 | <a href="#">c3n6rA</a>  | Alignment | not modelled | 91.9 | 13<br><b>PDB header:</b> fluorescent protein, transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, green fluorescent  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 54 | <a href="#">c5usiA</a>  | Alignment | not modelled | 91.9 | 15 | <b>PDBTitle:</b> maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311   |
| 55 | <a href="#">c2f78A</a>  | Alignment | not modelled | 91.6 | 10 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm;<br><b>PDBTitle:</b> benm effector binding domain with its effector benzoate  |
| 56 | <a href="#">c2zykA</a>  | Alignment | not modelled | 89.8 | 15 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> solute-binding protein;<br><b>PDBTitle:</b> crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin  |
| 57 | <a href="#">c3fd3A</a>  | Alignment | not modelled | 89.3 | 8  | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> chromosome replication initiation inhibitor protein;<br><b>PDBTitle:</b> structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.   |
| 58 | <a href="#">c2w7yA</a>  | Alignment | not modelled | 86.4 | 11 | <b>PDB header:</b> sugar-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar abc transporter, sugar-binding<br><b>PDBTitle:</b> structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide.  |
| 59 | <a href="#">d2esna2</a> | Alignment | not modelled | 84.8 | 8  | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 60 | <a href="#">c3oxnD</a>  | Alignment | not modelled | 83.6 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family;<br><b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus  |
| 61 | <a href="#">c1y4cA</a>  | Alignment | not modelled | 82.5 | 13 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed<br><b>PDBTitle:</b> designed helical protein fusion mbp   |
| 62 | <a href="#">d1a99a</a>  | Alignment | not modelled | 82.0 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 63 | <a href="#">c2b3fD</a>  | Alignment | not modelled | 79.3 | 10 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> glucose-binding protein;<br><b>PDBTitle:</b> thermus thermophilus glucose/galactose binding protein2 bound with galactose   |
| 64 | <a href="#">c3uorB</a>  | Alignment | not modelled | 77.5 | 10 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter sugar binding protein;<br><b>PDBTitle:</b> the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri  |
| 65 | <a href="#">d1us5a</a>  | Alignment | not modelled | 75.8 | 23 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 66 | <a href="#">c3k02A</a>  | Alignment | not modelled | 75.3 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> acarbose/maltose binding protein gach;<br><b>PDBTitle:</b> crystal structures of the gach receptor of streptomyces glaucescens2 gla.o in the unliganded form and in complex with acarbose and an3 acarbose homolog. comparison with acarbose-loaded maltose binding4 protein of salmonella typhimurium. |
| 67 | <a href="#">c2vpnB</a>  | Alignment | not modelled | 71.2 | 10 | <b>PDB header:</b> transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic substrate binding protein;<br><b>PDBTitle:</b> high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata   |
| 68 | <a href="#">d3thia</a>  | Alignment | not modelled | 67.0 | 10 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 69 | <a href="#">c3gyyC</a>  | Alignment | not modelled | 63.4 | 10 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein;<br><b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state  |
| 70 | <a href="#">c2x26A</a>  | Alignment | not modelled | 61.6 | 7  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic aliphatic sulphonates-binding protein;<br><b>PDBTitle:</b> crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli  |
| 71 | <a href="#">c1ursA</a>  | Alignment | not modelled | 60.8 | 14 | <b>PDB header:</b> maltose-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding protein;<br><b>PDBTitle:</b> x-ray structures of the maltose-maltodextrin binding2 protein of the thermoacidophilic bacterium alicyclobacillus3 acidocaldarius  |
| 72 | <a href="#">d1ursa</a>  | Alignment | not modelled | 60.8 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 73 | <a href="#">c2uvvA</a>  | Alignment | not modelled | 60.8 | 13 | <b>PDB header:</b> sugar-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc type periplasmic sugar-binding protein;<br><b>PDBTitle:</b> structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica   |
| 74 | <a href="#">c2qpqC</a>  | Alignment | not modelled | 60.3 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein bug27;<br><b>PDBTitle:</b> structure of bug27 from bordetella pertussis   |
| 75 | <a href="#">d1elja</a>  | Alignment | not modelled | 59.6 | 12 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 76 | <a href="#">c2i58B</a>  | Alignment | not modelled | 58.7 | 14 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> sugar abc transporter, sugar-binding protein;<br><b>PDBTitle:</b> crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose   |
| 77 | <a href="#">c3tqwA</a>  | Alignment | not modelled | 58.5 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding protein;<br><b>PDBTitle:</b> structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii   |

|     |                         |   |              |      |    |  |
|-----|-------------------------|---|--------------|------|----|--|
| 78  | <a href="#">c3qslA</a>  |  Alignment    | not modelled | 57.0 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein;<br><b>PDBTitle:</b> structure of cae31940 from bordetella bronchiseptica rb50   |
| 79  | <a href="#">c1p99A</a>  |  Alignment   | not modelled | 56.6 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg110;<br><b>PDBTitle:</b> 1.7a crystal structure of protein pg110 from staphylococcus2 aureus  |
| 80  | <a href="#">d1p99a</a>  |  Alignment   | not modelled | 56.6 | 13 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 81  | <a href="#">c2uyeA</a>  |  Alignment   | not modelled | 56.6 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein;<br><b>PDBTitle:</b> double mutant y110s,f111v dntR from burkholderia sp. strain2 dnt in complex with thiocyanate   |
| 82  | <a href="#">c3gxaA</a>  |  Alignment   | not modelled | 55.1 | 7  | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946;<br><b>PDBTitle:</b> crystal structure of gna1946   |
| 83  | <a href="#">c2pfzA</a>  |  Alignment   | not modelled | 53.2 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein;<br><b>PDBTitle:</b> crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid  |
| 84  | <a href="#">c2dvzA</a>  |  Alignment   | not modelled | 50.9 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein;<br><b>PDBTitle:</b> structure of a periplasmic transporter  |
| 85  | <a href="#">c3l6gA</a>  |  Alignment   | not modelled | 50.9 | 13 | <b>PDB header:</b> glycine betaine-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding<br><b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation   |
| 86  | <a href="#">c1mh3A</a>  |  Alignment   | not modelled | 49.9 | 17 | <b>PDB header:</b> sugar binding, dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding-a1 homeodomain protein chimera;<br><b>PDBTitle:</b> maltose binding-a1 homeodomain protein chimera, crystal2 form i   |
| 87  | <a href="#">c2f5xC</a>  |  Alignment   | not modelled | 49.1 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> bugd;<br><b>PDBTitle:</b> structure of periplasmic binding protein bugd  |
| 88  | <a href="#">c3lr1F</a>  |  Alignment   | not modelled | 49.1 | 8  | <b>PDB header:</b> protein binding<br><b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946;<br><b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria2 meningitidis  |
| 89  | <a href="#">d2ozza1</a> |  Alignment   | not modelled | 49.1 | 12 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 90  | <a href="#">c2x7pA</a>  |  Alignment | not modelled | 48.6 | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme;<br><b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold |
| 91  | <a href="#">c3un6A</a>  |  Alignment | not modelled | 48.1 | 7  | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein saouhsc_00137;<br><b>PDBTitle:</b> 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound                            |
| 92  | <a href="#">c3ix1B</a>  |  Alignment | not modelled | 38.0 | 11 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding<br><b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans                           |
| 93  | <a href="#">c2pfyA</a>  |  Alignment | not modelled | 36.1 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein;<br><b>PDBTitle:</b> crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid  |
| 94  | <a href="#">c3kg2A</a>  |  Alignment | not modelled | 36.1 | 15 | <b>PDB header:</b> membrane protein, transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2;<br><b>PDBTitle:</b> ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775   |
| 95  | <a href="#">c2fncA</a>  |  Alignment | not modelled | 35.5 | 13 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter, periplasmic maltose-binding<br><b>PDBTitle:</b> thermotoga maritima maltotriose binding protein bound with2 maltotriose.  |
| 96  | <a href="#">c2qsxB</a>  |  Alignment | not modelled | 34.7 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family;<br><b>PDBTitle:</b> crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus  |
| 97  | <a href="#">d1lutha</a> |  Alignment | not modelled | 34.1 | 11 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 98  | <a href="#">c3d4cA</a>  |  Alignment | not modelled | 31.8 | 17 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, linker, zona pellucida<br><b>PDBTitle:</b> zp-n domain of mammalian sperm receptor zp3 (crystal form i)   |
| 99  | <a href="#">c3ix1A</a>  |  Alignment | not modelled | 31.7 | 8  | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding<br><b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans                           |
| 100 | <a href="#">d2a5sa1</a> |  Alignment | not modelled | 30.4 | 11 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 101 | <a href="#">c3k2dA</a>  |  Alignment | not modelled | 28.1 | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc-type metal ion transport system, periplasmic component;<br><b>PDBTitle:</b> crystal structure of immunogenic lipoprotein a from  |



|     |                         |           |              |      |   |
|-----|-------------------------|-----------|--------------|------|---|
|     |                         |           |              |      | vibrio vulnificus   |
| 102 | <a href="#">c2hzkB_</a> | Alignment | not modelled | 27.6 | 10<br><b>PDB header:</b> ligand binding, transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> trap-t family sorbitol/mannitol transporter, periplasmic<br><b>PDBTitle:</b> crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form |
| 103 | <a href="#">d1laxa_</a> | Alignment | not modelled | 26.5 | 17<br><b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like  |
| 104 | <a href="#">c3fxbB_</a> | Alignment | not modelled | 26.5 | 11<br><b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit;<br><b>PDBTitle:</b> crystal structure of the ectoine-binding protein ueha   |
| 105 | <a href="#">c3e4rA_</a> | Alignment | not modelled | 25.6 | 8<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein;<br><b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes     |
| 106 | <a href="#">c3ns5B_</a> | Alignment | not modelled | 25.6 | 18<br><b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b;<br><b>PDBTitle:</b> crystal structure of the rna recognition motif of yeast eif3b residues2 76-161  |
| 107 | <a href="#">c3f5fA_</a> | Alignment | not modelled | 24.2 | 17<br><b>PDB header:</b> transport, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, heparan<br><b>PDBTitle:</b> crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion.              |
| 108 | <a href="#">c3ob4A_</a> | Alignment | not modelled | 23.8 | 17<br><b>PDB header:</b> allergen<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein, arah 2;<br><b>PDBTitle:</b> mbp-fusion protein of the major peanut allergen ara h 2   |
| 109 | <a href="#">c3mp6A_</a> | Alignment | not modelled | 23.0 | 17<br><b>PDB header:</b> histone binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, linker, saga-<br><b>PDBTitle:</b> complex structure of sgf29 and dimethylated h3k4   |
| 110 | <a href="#">c3b50A_</a> | Alignment | not modelled | 22.5 | 15<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid-binding periplasmic protein siap;<br><b>PDBTitle:</b> structure of h. influenzae sialic acid binding protein2 bound to neu5ac.  |