


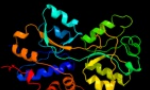
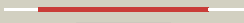




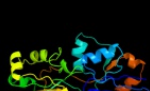











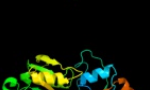
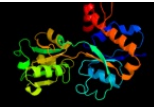










| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">d1r9la_</a> |  Alignment   |    | 100.0      | 100    | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Phosphate binding protein-like   |
| 2  | <a href="#">c2rejA_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> choline-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein;<br><b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation   |
| 3  | <a href="#">c3o66A_</a> |  Alignment   |    | 100.0      | 13     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline abc transporter;<br><b>PDBTitle:</b> crystal structure of glycine betaine/carnitine/choline abc transporter  |
| 4  | <a href="#">c3tmgA_</a> |  Alignment   |    | 100.0      | 22     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter,<br><b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi                              |
| 5  | <a href="#">c3r6uA_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein;<br><b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis  |
| 6  | <a href="#">c3pppA_</a> |  Alignment |  | 100.0      | 13     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline-binding protein;<br><b>PDBTitle:</b> structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc |
| 7  | <a href="#">d1sw5a_</a> |  Alignment |  | 100.0      | 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   |
| 8  | <a href="#">c3l6gA_</a> |  Alignment |  | 100.0      | 22     | <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   |
| 9  | <a href="#">c3chgB_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> ligand binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein;<br><b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa   |
| 10 | <a href="#">c3uifA_</a> |  Alignment |  | 99.8       | 16     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding<br><b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt                      |
| 11 | <a href="#">c3e4rA_</a> |  Alignment |  | 99.7       | 13     | <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   |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c2x26A_</a> | Alignment |     | 99.7 | 18 | <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                                       |
| 13 | <a href="#">c3ix1A_</a> | Alignment |    | 99.7 | 13 | <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                           |
| 14 | <a href="#">c3ix1B_</a> | Alignment |    | 99.7 | 13 | <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                           |
| 15 | <a href="#">c2de4B_</a> | Alignment |    | 99.7 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme b;<br><b>PDBTitle:</b> crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid  |
| 16 | <a href="#">c3un6A_</a> | Alignment |    | 99.6 | 9  | <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                            |
| 17 | <a href="#">c3qslA_</a> | Alignment |    | 99.6 | 17 | <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   |
| 18 | <a href="#">c2x7pA_</a> | Alignment |  | 99.6 | 9  | <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 |
| 19 | <a href="#">c3hn0A_</a> | Alignment |  | 99.5 | 10 | <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 an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution  |
| 20 | <a href="#">c3gxaA_</a> | Alignment |  | 99.5 | 20 | <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   |
| 21 | <a href="#">c3ir1F_</a> | Alignment | not modelled  | 99.4 | 18 | <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  |
| 22 | <a href="#">c3tqwA_</a> | Alignment | not modelled  | 99.4 | 23 | <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  |
| 23 | <a href="#">c2g29A_</a> | Alignment | not modelled  | 99.4 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein nrta;<br><b>PDBTitle:</b> crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803   |
| 24 | <a href="#">c2i4cA_</a> | Alignment | not modelled  | 99.4 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bicarbonate transporter;<br><b>PDBTitle:</b> crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium                                      |
| 25 | <a href="#">c1p99A_</a> | Alignment | not modelled  | 99.4 | 19 | <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  |
| 26 | <a href="#">d1p99a_</a> | Alignment | not modelled  | 99.4 | 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   |
| 27 | <a href="#">c3k2dA_</a> | Alignment | not modelled  | 99.4 | 20 | <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  |
| 28 | <a href="#">d1xs5a_</a> | Alignment | not modelled  | 99.4 | 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   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">d2nxoa1</a> | Alignment | not modelled | 98.9 | 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   |
| 30 | <a href="#">d1us5a</a>  | Alignment | not modelled | 98.7 | 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   |
| 31 | <a href="#">c3n5lA</a>  | Alignment | not modelled | 98.6 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter;<br><b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution |
| 32 | <a href="#">d2czla1</a> | Alignment | not modelled | 98.1 | 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   |
| 33 | <a href="#">d1zbma1</a> | Alignment | not modelled | 97.8 | 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   |
| 34 | <a href="#">c3muqB</a>  | Alignment | not modelled | 97.5 | 13 | <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                                  |
| 35 | <a href="#">c3lr1A</a>  | Alignment | not modelled | 97.4 | 12 | <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  |
| 36 | <a href="#">c2dvzA</a>  | Alignment | not modelled | 97.2 | 14 | <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  |
| 37 | <a href="#">d1sbpa</a>  | Alignment | not modelled | 97.1 | 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   |
| 38 | <a href="#">c2f5xC</a>  | Alignment | not modelled | 97.0 | 11 | <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  |
| 39 | <a href="#">c2qpqC</a>  | Alignment | not modelled | 96.9 | 12 | <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  |
| 40 | <a href="#">c3b50A</a>  | Alignment | not modelled | 96.8 | 15 | <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.   |
| 41 | <a href="#">c2pfyA</a>  | Alignment | not modelled | 96.8 | 11 | <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  |
| 42 | <a href="#">d1amfa</a>  | Alignment | not modelled | 96.7 | 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   |
| 43 | <a href="#">c3fxbB</a>  | Alignment | not modelled | 96.7 | 10 | <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  |
| 44 | <a href="#">c2vpnB</a>  | Alignment | not modelled | 96.7 | 11 | <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  |
| 45 | <a href="#">c3kn3C</a>  | Alignment | not modelled | 96.6 | 11 | <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  |
| 46 | <a href="#">c2hpgB</a>  | Alignment | not modelled | 96.6 | 11 | <b>PDB header:</b> ligand binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding<br><b>PDBTitle:</b> the crystal structure of a thermophilic trap periplasmic2 binding protein  |
| 47 | <a href="#">c2zzxD</a>  | Alignment | not modelled | 96.5 | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> abc transporter, solute-binding protein;<br><b>PDBTitle:</b> crystal structure of a periplasmic substrate binding protein in2 complex with lactate   |
| 48 | <a href="#">c3gyyC</a>  | Alignment | not modelled | 96.5 | 12 | <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   |
| 49 | <a href="#">c2pfzA</a>  | Alignment | not modelled | 96.4 | 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  |
| 50 | <a href="#">c3kzgB</a>  | Alignment | not modelled | 96.3 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> arginine 3rd transport system periplasmic binding<br><b>PDBTitle:</b> crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila                                     |
| 51 | <a href="#">d2fyia1</a> | Alignment | not modelled | 95.8 | 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   |
| 52 | <a href="#">c3c9hB</a>  | Alignment | not modelled | 95.5 | 11 | <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  |
| 53 | <a href="#">c3mmlA</a>  | Alignment | not modelled | 95.3 | 10 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs;   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c3mp1A</a>  | Alignment | not modelled | 93.3 | 10 | <b>PDBTitle:</b> crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)  |
| 54 | <a href="#">d2esna2</a> | Alignment | not modelled | 95.3 | 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  |
| 55 | <a href="#">c2hzbB</a>  | Alignment | not modelled | 94.7 | 13 | <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 |
| 56 | <a href="#">c3fj7A</a>  | Alignment | not modelled | 94.7 | 12 | <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  |
| 57 | <a href="#">d2a5sa1</a> | Alignment | not modelled | 94.5 | 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  |
| 58 | <a href="#">d1xvxa</a>  | Alignment | not modelled | 94.1 | 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  |
| 59 | <a href="#">c2qryD</a>  | Alignment | not modelled | 93.9 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> thiamine-binding periplasmic protein;<br><b>PDBTitle:</b> periplasmic thiamin binding protein   |
| 60 | <a href="#">d1pb7a</a>  | Alignment | not modelled | 93.8 | 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  |
| 61 | <a href="#">c2hxrA</a>  | Alignment | not modelled | 93.6 | 11 | <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                          |
| 62 | <a href="#">c2pt1A</a>  | Alignment | not modelled | 93.2 | 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  |
| 63 | <a href="#">c2h5yC</a>  | Alignment | not modelled | 92.8 | 11 | <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                   |
| 64 | <a href="#">c2rc9A</a>  | Alignment | not modelled | 92.8 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutamate [nmda] receptor subunit 3a;<br><b>PDBTitle:</b> crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution   |
| 65 | <a href="#">c2q89A</a>  | Alignment | not modelled | 92.3 | 15 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter amino acid-binding protein;<br><b>PDBTitle:</b> crystal structure of ehub in complex with hydroxyectoine   |
| 66 | <a href="#">c3o9pA</a>  | Alignment | not modelled | 92.1 | 16 | <b>PDB header:</b> peptide binding protein/peptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic murein peptide-binding protein;<br><b>PDBTitle:</b> the structure of the escherichia coli murein tripeptide binding2 protein mppa   |
| 67 | <a href="#">d1al3a</a>  | Alignment | not modelled | 91.6 | 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  |
| 68 | <a href="#">c1al3A</a>  | Alignment | not modelled | 91.6 | 10 | <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  |
| 69 | <a href="#">d1vr5a1</a> | Alignment | not modelled | 91.5 | 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  |
| 70 | <a href="#">c2h9qC</a>  | Alignment | not modelled | 91.3 | 10 | <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)  |
| 71 | <a href="#">c1ztyA</a>  | Alignment | not modelled | 91.3 | 16 | <b>PDB header:</b> sugar binding protein, signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein;<br><b>PDBTitle:</b> crystal structure of the chitin oligosaccharide binding2 protein   |
| 72 | <a href="#">c3k4uA</a>  | Alignment | not modelled | 91.3 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> binding component of abc transporter;<br><b>PDBTitle:</b> crystal structure of putative binding component of abc transporter2 from wollinella succinogenes dsm 1740 complexed with lysine             |
| 73 | <a href="#">c3pamB</a>  | Alignment | not modelled | 90.9 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein;<br><b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1                  |
| 74 | <a href="#">c2esnC</a>  | Alignment | not modelled | 90.8 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa                           |
| 75 | <a href="#">c3lvuB</a>  | Alignment | not modelled | 90.7 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein;<br><b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi           |
| 76 | <a href="#">c2f7cA</a>  | Alignment | not modelled | 90.5 | 7  | <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  |
| 77 | <a href="#">d1dpea</a>  | Alignment | not modelled | 89.6 | 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  |
|    |                         |           |              |      |    | <b>PDB header:</b> heme binding protein   |

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| 78  | <a href="#">c3tpaA_</a> | Alignment | not modelled | 88.9 | 12 | <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a;<br><b>PDBTitle:</b> structure of hbpa2 from haemophilus parasuis   |
| 79  | <a href="#">c2h9bB_</a> | Alignment | not modelled | 88.9 | 8  | <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)  |
| 80  | <a href="#">d1jeta_</a> | Alignment | not modelled | 88.9 | 16 | <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="#">c2f78A_</a> | Alignment | not modelled | 88.3 | 7  | <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   |
| 82  | <a href="#">c3ho7A_</a> | Alignment | not modelled | 88.0 | 14 | <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  |
| 83  | <a href="#">c3m8uA_</a> | Alignment | not modelled | 87.4 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a;<br><b>PDBTitle:</b> crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)  |
| 84  | <a href="#">c3n6uA_</a> | Alignment | not modelled | 87.4 | 17 | <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   |
| 85  | <a href="#">d1ixca2</a> | Alignment | not modelled | 87.2 | 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   |
| 86  | <a href="#">d1i6aa_</a> | Alignment | not modelled | 87.2 | 6  | <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   |
| 87  | <a href="#">c2o1mB_</a> | Alignment | not modelled | 86.7 | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable amino-acid abc transporter<br><b>PDBTitle:</b> crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572     |
| 88  | <a href="#">d1b1xa1</a> | Alignment | not modelled | 86.4 | 15 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |
| 89  | <a href="#">c2ql3G_</a> | Alignment | not modelled | 86.1 | 11 | <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   |
| 90  | <a href="#">d1ii5a_</a> | Alignment | not modelled | 84.9 | 9  | <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   |
| 91  | <a href="#">c2o7jA_</a> | Alignment | not modelled | 84.5 | 16 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic<br><b>PDBTitle:</b> the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose   |
| 92  | <a href="#">d1y4ta_</a> | Alignment | not modelled | 84.3 | 16 | <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   |
| 93  | <a href="#">c3jv9B_</a> | Alignment | not modelled | 84.2 | 12 | <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   |
| 94  | <a href="#">d1eh3a_</a> | Alignment | not modelled | 84.2 | 15 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |
| 95  | <a href="#">d1dtza1</a> | Alignment | not modelled | 84.1 | 16 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |
| 96  | <a href="#">d1zlqa1</a> | Alignment | not modelled | 83.8 | 9  | <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   |
| 97  | <a href="#">c2xx7B_</a> | Alignment | not modelled | 83.7 | 22 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor 2;<br><b>PDBTitle:</b> crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution. |
| 98  | <a href="#">c2uyeA_</a> | Alignment | not modelled | 81.5 | 9  | <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   |
| 99  | <a href="#">c2pyyB_</a> | Alignment | not modelled | 81.3 | 6  | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ionotropic glutamate receptor bacterial homologue;<br><b>PDBTitle:</b> crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate   |
| 100 | <a href="#">c3fd3A_</a> | Alignment | not modelled | 81.2 | 16 | <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.  |
| 101 | <a href="#">c2v25B_</a> | Alignment | not modelled | 80.5 | 16 | <b>PDB header:</b> receptor<br><b>Chain:</b> B: <b>PDB Molecule:</b> major cell-binding factor;<br><b>PDBTitle:</b> structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate   |
| 102 | <a href="#">d1atga_</a> | Alignment | not modelled | 79.8 | 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   |



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| 103 | <a href="#">dlxvya_</a> | Alignment | not modelled | 79.7 | 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   |
| 104 | <a href="#">dlutha_</a> | Alignment | not modelled | 78.5 | 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   |
| 105 | <a href="#">c3t66A_</a> | Alignment | not modelled | 77.7 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nickel abc transporter (nickel-binding protein);<br><b>PDBTitle:</b> crystal structure of nickel abc transporter from bacillus halodurans  |
| 106 | <a href="#">clq1kA_</a> | Alignment | not modelled | 73.1 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase;<br><b>PDBTitle:</b> structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp  |
| 107 | <a href="#">dly9ua_</a> | Alignment | not modelled | 72.0 | 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   |
| 108 | <a href="#">d1pdaa1</a> | Alignment | not modelled | 70.4 | 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   |
| 109 | <a href="#">c2q2aD_</a> | Alignment | not modelled | 70.4 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> artj;<br><b>PDBTitle:</b> crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus                         |
| 110 | <a href="#">c3crnA_</a> | Alignment | not modelled | 70.1 | 15 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like;<br><b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1     |
| 111 | <a href="#">dlryoa_</a> | Alignment | not modelled | 70.0 | 15 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |
| 112 | <a href="#">c3eq1A_</a> | Alignment | not modelled | 69.9 | 9  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase;<br><b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at2 2.8a resolution  |
| 113 | <a href="#">c3ftoA_</a> | Alignment | not modelled | 68.7 | 13 | <b>PDB header:</b> peptide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide-binding protein oppa;<br><b>PDBTitle:</b> crystal structure of oppa in a open conformation  |
| 114 | <a href="#">dlieja_</a> | Alignment | not modelled | 68.0 | 11 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |
| 115 | <a href="#">clvfgB_</a> | Alignment | not modelled | 67.2 | 9  | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase;<br><b>PDBTitle:</b> crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog   |
| 116 | <a href="#">d1xoca1</a> | Alignment | not modelled | 64.7 | 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   |
| 117 | <a href="#">c2y7iB_</a> | Alignment | not modelled | 64.3 | 6  | <b>PDB header:</b> arginine-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> stm4351;<br><b>PDBTitle:</b> structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.   |
| 118 | <a href="#">c3r39A_</a> | Alignment | not modelled | 64.3 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic binding protein;<br><b>PDBTitle:</b> crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica   |
| 119 | <a href="#">c3hv1A_</a> | Alignment | not modelled | 63.6 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> polar amino acid abc uptake transporter substrate<br><b>PDBTitle:</b> crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus |
| 120 | <a href="#">d1h76a1</a> | Alignment | not modelled | 63.3 | 14 | <b>Fold:</b> Periplasmic binding protein-like II<br><b>Superfamily:</b> Periplasmic binding protein-like II<br><b>Family:</b> Transferrin  |