


























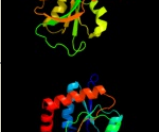
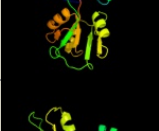




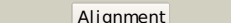

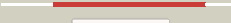
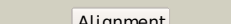
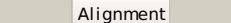
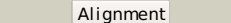

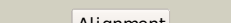
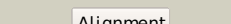
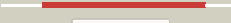

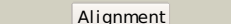
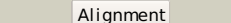
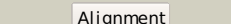
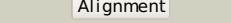
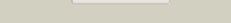


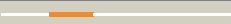
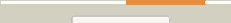
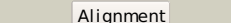
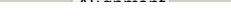



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2y7iB_</a>	 Alignment		100.0	58	<b>PDB header:</b> arginine-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> stm4351; <b>PDBTitle:</b> structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
2	<a href="#">c3g41A_</a>	 Alignment		100.0	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
3	<a href="#">c2ylnA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, periplasmic binding protein, <b>PDBTitle:</b> crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
4	<a href="#">d1hsla_</a>	 Alignment		100.0	39	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
5	<a href="#">c3hv1A_</a>	 Alignment		100.0	30	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polar amino acid abc uptake transporter substrate <b>PDBTitle:</b> crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
6	<a href="#">c3k4uA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding component of abc transporter; <b>PDBTitle:</b> crystal structure of putative binding component of abc transporter2 from wolfinella succinogenes dsm 1740 complexed with lysine
7	<a href="#">c3kzgB_</a>	 Alignment		100.0	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> arginine 3rd transport system periplasmic binding <b>PDBTitle:</b> crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
8	<a href="#">c3delC_</a>	 Alignment		100.0	30	<b>PDB header:</b> protein binding, transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine binding protein; <b>PDBTitle:</b> the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
9	<a href="#">c2o1mB_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable amino-acid abc transporter <b>PDBTitle:</b> crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
10	<a href="#">d1lsta_</a>	 Alignment		100.0	35	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
11	<a href="#">c3i6vA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic his/glu/gln/arg/opine family-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine

12	<a href="#">c2ieeB_</a>	Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable abc transporter extracellular-binding <b>PDBTitle:</b> crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
13	<a href="#">c2q2aD_</a>	Alignment		100.0	29	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> artj; <b>PDBTitle:</b> crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
14	<a href="#">c3h7mA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
15	<a href="#">d1wdna_</a>	Alignment		100.0	28	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
16	<a href="#">c3r39A_</a>	Alignment		100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic binding protein; <b>PDBTitle:</b> crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
17	<a href="#">c3kbrA_</a>	Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexadienyl dehydratase; <b>PDBTitle:</b> the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
18	<a href="#">c2q89A_</a>	Alignment		100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter amino acid-binding protein; <b>PDBTitle:</b> crystal structure of ehuh in complex with hydroxyectoine
19	<a href="#">c2vhaB_</a>	Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic binding transport protein; <b>PDBTitle:</b> debp
20	<a href="#">c1xt8B_</a>	Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative amino-acid transporter periplasmic solute-binding <b>PDBTitle:</b> crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution
21	<a href="#">c3mplA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
22	<a href="#">c2yjpB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter, periplasmic binding protein, <b>PDBTitle:</b> crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
23	<a href="#">d2a5sa1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
24	<a href="#">d1xt8a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
25	<a href="#">c2v25B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> receptor <b>Chain:</b> B: <b>PDB Molecule:</b> major cell-binding factor; <b>PDBTitle:</b> structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
26	<a href="#">d1mqia_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
27	<a href="#">d1ii5a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
28	<a href="#">c2xx7B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor 2; <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.

29	<a href="#">c2pyyB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ionotropic glutamate receptor bacterial homologue; <b>PDBTitle:</b> crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
30	<a href="#">d1pb7a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
31	<a href="#">c2rc9A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate [nmda] receptor subunit 3a; <b>PDBTitle:</b> crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
32	<a href="#">d1s50a1</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
33	<a href="#">d2f34a1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
34	<a href="#">c2v3tA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor delta-2 subunit synonym <b>PDBTitle:</b> structure of the ligand-binding core of the ionotropic2 glutamate receptor-like glurdelta2 in the apo form
35	<a href="#">c1yaeB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor, ionotropic kainate 2; <b>PDBTitle:</b> structure of the kainate receptor subunit glur6 agonist binding domain2 complexed with domoic acid
36	<a href="#">c3kg2A</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2; <b>PDBTitle:</b> ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
37	<a href="#">c3n5lA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter; <b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
38	<a href="#">c3ix1B</a>	Alignment	not modelled	98.3	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
39	<a href="#">c3ix1A</a>	Alignment	not modelled	98.3	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
40	<a href="#">c3k2dA</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type metal ion transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of immunogenic lipoprotein a from vibrio vulnificus
41	<a href="#">c2x26A</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic aliphatic sulphonates-binding protein; <b>PDBTitle:</b> crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
42	<a href="#">c3e4rA</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
43	<a href="#">c3uifA</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
44	<a href="#">d1xs5a</a>	Alignment	not modelled	97.8	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
45	<a href="#">c1p99A</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg110; <b>PDBTitle:</b> 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
46	<a href="#">d1p99a</a>	Alignment	not modelled	97.8	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
47	<a href="#">c3tqwA</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding protein; <b>PDBTitle:</b> structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
48	<a href="#">c2x7pA</a>	Alignment	not modelled	97.7	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme; <b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
49	<a href="#">c3gxaA</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of gna1946
50	<a href="#">c3qslA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of cae31940 from bordetella bronchiseptica rb50
51	<a href="#">c3l6gA</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation

52	<a href="#">c3un6A</a>	 Alignment	not modelled	97.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein saouhsc_00137; <b>PDBTitle:</b> 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
53	<a href="#">c3hn0A</a>	 Alignment	not modelled	97.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
54	<a href="#">d1zbma1</a>	 Alignment	not modelled	97.4	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
55	<a href="#">c3tmgA</a>	 Alignment	not modelled	97.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter, <b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
56	<a href="#">d2czla1</a>	 Alignment	not modelled	97.3	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
57	<a href="#">c2g29A</a>	 Alignment	not modelled	97.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein nrtA; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate-binding2 protein nrtA from synechocystis pcc 6803
58	<a href="#">c3ir1F</a>	 Alignment	not modelled	97.1	12	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
59	<a href="#">c2i4cA</a>	 Alignment	not modelled	95.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bicarbonate transporter; <b>PDBTitle:</b> crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
60	<a href="#">c2rejA</a>	 Alignment	not modelled	95.5	19	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein; <b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation
61	<a href="#">d1us5a</a>	 Alignment	not modelled	95.1	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
62	<a href="#">c2de4B</a>	 Alignment	not modelled	94.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme b; <b>PDBTitle:</b> crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
63	<a href="#">c3lr1A</a>	 Alignment	not modelled	93.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tungstate abc transporter, periplasmic tungstate- <b>PDBTitle:</b> the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
64	<a href="#">d2nxoa1</a>	 Alignment	not modelled	92.4	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
65	<a href="#">d1pdaa1</a>	 Alignment	not modelled	90.7	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
66	<a href="#">c3b50A</a>	 Alignment	not modelled	88.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid-binding periplasmic protein siap; <b>PDBTitle:</b> structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
67	<a href="#">c3muqB</a>	 Alignment	not modelled	88.3	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
68	<a href="#">c2f5xC</a>	 Alignment	not modelled	87.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> bugd; <b>PDBTitle:</b> structure of periplasmic binding protein bugd
69	<a href="#">c2ypnA</a>	 Alignment	not modelled	86.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hydroxymethylbilane synthase); <b>PDBTitle:</b> hydroxymethylbilane synthase
70	<a href="#">c2vd3B</a>	 Alignment	not modelled	86.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
71	<a href="#">c2pfzA</a>	 Alignment	not modelled	85.6	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
72	<a href="#">c1nh7A</a>	 Alignment	not modelled	85.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
73	<a href="#">c3chgB</a>	 Alignment	not modelled	85.3	12	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein; <b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
74	<a href="#">c2qpqC</a>	 Alignment	not modelled	84.1	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein bug27; <b>PDBTitle:</b> structure of bug27 from bordetella pertussis
75	<a href="#">d1h3da1</a>	 Alignment	not modelled	83.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
76	<a href="#">c3ag1A</a>	 Alignment	not modelled	83.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase;

76	<a href="#">c3eq1A</a>	Alignment	not modelled	83.4	18	<b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at2.8a resolution <b>PDB header:</b> transport protein
77	<a href="#">c3fxbB</a>	Alignment	not modelled	80.5	14	<b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of the ectoine-binding protein ueha
78	<a href="#">c2vpnB</a>	Alignment	not modelled	78.2	12	<b>PDB header:</b> transport <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
79	<a href="#">c2dvzA</a>	Alignment	not modelled	76.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of a periplasmic transporter
80	<a href="#">d1atga</a>	Alignment	not modelled	73.4	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
81	<a href="#">c3gyyC</a>	Alignment	not modelled	72.6	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
82	<a href="#">c3fj7A</a>	Alignment	not modelled	71.2	7	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> major antigenic peptide peb3; <b>PDBTitle:</b> crystal structure of l-phospholactate bound peb3
83	<a href="#">d1z7me1</a>	Alignment	not modelled	66.7	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
84	<a href="#">d1i6aa</a>	Alignment	not modelled	65.8	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
85	<a href="#">c3r6uA</a>	Alignment	not modelled	64.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
86	<a href="#">d1twya</a>	Alignment	not modelled	64.0	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
87	<a href="#">c1twyG</a>	Alignment	not modelled	64.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
88	<a href="#">c2hpgB</a>	Alignment	not modelled	63.1	14	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding <b>PDBTitle:</b> the crystal structure of a thermophilic trap periplasmic2 binding protein
89	<a href="#">d1nh8a1</a>	Alignment	not modelled	62.4	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
90	<a href="#">c2pfyA</a>	Alignment	not modelled	59.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
91	<a href="#">c2ql3G</a>	Alignment	not modelled	59.1	14	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
92	<a href="#">c3mstA</a>	Alignment	not modelled	57.3	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrate transport protein; <b>PDBTitle:</b> crystal structure of a putative nitrate transport protein (tn0104)2 from thermoplasma volcanium at 1.35 a resolution
93	<a href="#">d2ozza1</a>	Alignment	not modelled	57.2	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
94	<a href="#">c1q1kA</a>	Alignment	not modelled	57.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
95	<a href="#">c3kn3C</a>	Alignment	not modelled	57.0	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinetella succinogenes
96	<a href="#">c2zzxD</a>	Alignment	not modelled	55.1	15	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc transporter, solute-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic substrate binding protein in2 complex with lactate
97	<a href="#">d1ve4a1</a>	Alignment	not modelled	49.9	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
98	<a href="#">c2hzkB</a>	Alignment	not modelled	48.0	11	<b>PDB header:</b> ligand binding, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap-t family sorbitol/mannitol transporter, periplasmic <b>PDBTitle:</b> crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
99	<a href="#">c3lvuB</a>	Alignment	not modelled	48.0	3	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
100	<a href="#">c3jv9B</a>	Alignment	not modelled	47.6	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> the structure of a reduced form of oxyr from n. meningitidis
						<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein;



101	<a href="#">c3pamB_</a>	Alignment	not modelled	47.1	9	<b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
102	<a href="#">c1jvnB_</a>	Alignment	not modelled	44.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
103	<a href="#">d1r9la_</a>	Alignment	not modelled	43.6	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
104	<a href="#">c3dtfB_</a>	Alignment	not modelled	42.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain amino acid aminotransferase; <b>PDBTitle:</b> structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
105	<a href="#">d1eh3a_</a>	Alignment	not modelled	42.0	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
106	<a href="#">d1o63a_</a>	Alignment	not modelled	40.2	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
107	<a href="#">d2esna2</a>	Alignment	not modelled	36.6	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
108	<a href="#">d1vr5a1</a>	Alignment	not modelled	36.1	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
109	<a href="#">d1sw5a_</a>	Alignment	not modelled	36.0	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
110	<a href="#">d1amfa_</a>	Alignment	not modelled	35.3	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
111	<a href="#">c1ztyA_</a>	Alignment	not modelled	34.9	11	<b>PDB header:</b> sugar binding protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein; <b>PDBTitle:</b> crystal structure of the chitin oligosaccharide binding2 protein
112	<a href="#">c2o7jA_</a>	Alignment	not modelled	34.0	9	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic <b>PDBTitle:</b> the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
113	<a href="#">c3tpaA_</a>	Alignment	not modelled	33.4	10	<b>PDB header:</b> heme binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> structure of hbpa2 from haemophilus parasuis
114	<a href="#">c3o9pA_</a>	Alignment	not modelled	32.5	14	<b>PDB header:</b> peptide binding protein/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic murein peptide-binding protein; <b>PDBTitle:</b> the structure of the escherichia coli murein tripeptide binding2 protein mppa
115	<a href="#">d2a1ha1</a>	Alignment	not modelled	31.7	11	<b>Fold:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Superfamily:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Family:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes
116	<a href="#">c2h5yC_</a>	Alignment	not modelled	31.6	10	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> molybdate-binding periplasmic protein; <b>PDBTitle:</b> crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
117	<a href="#">d1b1xa1</a>	Alignment	not modelled	30.8	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
118	<a href="#">d1dpea_</a>	Alignment	not modelled	29.1	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
119	<a href="#">c2abjG_</a>	Alignment	not modelled	29.1	17	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> branched-chain-amino-acid aminotransferase, cytosolic; <b>PDBTitle:</b> crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
120	<a href="#">d1dtza1</a>	Alignment	not modelled	28.3	19	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin