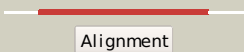

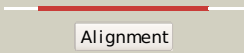


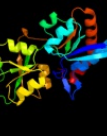




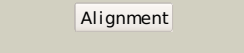

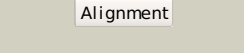

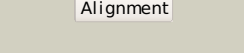



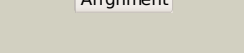

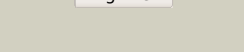



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wdna_	 Alignment		100.0	100	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	c2q2aD_	 Alignment		100.0	37	PDB header: transport protein Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
3	c3g41A_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
4	c2ieeB_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable abc transporter extracellular-binding PDBTitle: crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
5	c3k4uA_	 Alignment		100.0	28	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinetella succinogenes dsm 1740 complexed with lysine
6	c2ylnA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
7	d1hsla_	 Alignment		100.0	28	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
8	c3i6vA_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
9	c3h7mA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
10	c3delC_	 Alignment		100.0	22	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
11	c3hv1A_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus

12	d1lsta_	Alignment		100.0	29	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
13	c2o1mB_	Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter PDBTitle: crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
14	c3kzqB_	Alignment		100.0	26	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
15	c2y7iB_	Alignment		100.0	28	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
16	c3r39A_	Alignment		100.0	24	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
17	c3mplA_	Alignment		100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
18	c3kbrA_	Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
19	c2q89A_	Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter amino acid-binding protein; PDBTitle: crystal structure of ehuh in complex with hydroxyectoine
20	c2vhaB_	Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
21	d1ii5a_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
22	c2xx7B_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: 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.
23	d1mqia_	Alignment	not modelled	100.0	26	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
24	c2yjpB_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
25	c1xt8B_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution
26	d2a5sa1	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c2v25B_	Alignment	not modelled	100.0	24	PDB header: receptor Chain: B: PDB Molecule: major cell-binding factor; PDBTitle: structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
						Fold: Periplasmic binding protein-like II

28	d1xt8a1	Alignment	not modelled	100.0	22	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
29	c2pyyB	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: B: PDB Molecule: ionotropic glutamate receptor bacterial homologue; PDBTitle: crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
30	d1pb7a	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
31	c2rc9A	Alignment	not modelled	100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit 3a; PDBTitle: crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
32	d1s50a1	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
33	c2v3tA	Alignment	not modelled	99.9	18	PDB header: receptor Chain: A: PDB Molecule: glutamate receptor delta-2 subunit synonym PDBTitle: structure of the ligand-binding core of the ionotropic2 glutamate receptor-like glurdelta2 in the apo form
34	d2f34a1	Alignment	not modelled	99.9	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	c1yaeB	Alignment	not modelled	99.9	25	PDB header: membrane protein Chain: B: PDB Molecule: glutamate receptor, ionotropic kainate 2; PDBTitle: structure of the kainate receptor subunit glur6 agonist binding domain2 complexed with domoic acid
36	c3kg2A	Alignment	not modelled	99.8	26	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
37	c3n5lA	Alignment	not modelled	98.6	13	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc phosphonate transporter; PDBTitle: crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
38	c2x26A	Alignment	not modelled	98.2	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
39	c3l6gA	Alignment	not modelled	98.2	15	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
40	c3e4rA	Alignment	not modelled	98.1	12	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
41	c3ix1B	Alignment	not modelled	98.0	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
42	c3ix1A	Alignment	not modelled	98.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
43	d1xs5a	Alignment	not modelled	98.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
44	c3uifA	Alignment	not modelled	97.9	15	PDB header: transport protein Chain: A: PDB Molecule: sulfonate abc transporter, periplasmic sulfonate-binding PDBTitle: crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
45	c3un6A	Alignment	not modelled	97.8	10	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein saouhsc_00137; PDBTitle: 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
46	c2x7pA	Alignment	not modelled	97.8	14	PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
47	c3k2dA	Alignment	not modelled	97.6	15	PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus
48	c3qslA	Alignment	not modelled	97.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
49	c3hn0A	Alignment	not modelled	97.6	10	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
50	c3tqwA	Alignment	not modelled	97.3	15	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii

51	c3tmgA	Alignment	not modelled	97.3	9	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
52	c2g29A	Alignment	not modelled	97.1	11	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrta; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
53	c3gxaA	Alignment	not modelled	96.7	13	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
54	c1p99A	Alignment	not modelled	96.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
55	d1p99a	Alignment	not modelled	96.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
56	d1zbma1	Alignment	not modelled	96.6	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
57	c3ir1F	Alignment	not modelled	96.4	13	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
58	d1atga	Alignment	not modelled	95.9	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
59	d2czla1	Alignment	not modelled	95.6	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
60	c2de4B	Alignment	not modelled	95.5	11	PDB header: hydrolase Chain: B: PDB Molecule: di-benzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfonic acid
61	c2rejA	Alignment	not modelled	95.3	14	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
62	c2i4cA	Alignment	not modelled	95.0	8	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
63	c2dvzA	Alignment	not modelled	94.0	15	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
64	c3jv9B	Alignment	not modelled	93.9	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
65	d2nxoa1	Alignment	not modelled	93.5	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
66	c3ho7A	Alignment	not modelled	93.5	11	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
67	c2qpqC	Alignment	not modelled	93.4	10	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
68	c2f5xC	Alignment	not modelled	93.0	18	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
69	c3fj7A	Alignment	not modelled	92.3	16	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
70	c3oxnD	Alignment	not modelled	92.2	14	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
71	c2ql3G	Alignment	not modelled	90.8	12	PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
72	d1us5a	Alignment	not modelled	89.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	d1i6aa	Alignment	not modelled	89.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c3r6uA	Alignment	not modelled	88.9	17	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
75	c2hpgB	Alignment	not modelled	87.9	12	PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic2

						binding protein
76	c2uyeA	Alignment	not modelled	86.7	11	PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dntR from burkholderia sp. strain2 dnt in complex with thiocyanate
77	d2ozza1	Alignment	not modelled	86.1	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
78	c3lr1A	Alignment	not modelled	85.9	12	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
79	d1amfa	Alignment	not modelled	84.2	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
80	d1lutha	Alignment	not modelled	82.4	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
81	c3chgB	Alignment	not modelled	79.0	13	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
82	d2esna2	Alignment	not modelled	77.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
83	c3fxbB	Alignment	not modelled	76.6	17	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
84	c3pppA	Alignment	not modelled	74.6	17	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
85	c2hxrA	Alignment	not modelled	73.4	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
86	c2vpnB	Alignment	not modelled	73.2	14	PDB header: transport Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
87	c2h5yC	Alignment	not modelled	71.6	11	PDB header: metal transport Chain: C: PDB Molecule: molybdate-binding periplasmic protein; PDBTitle: crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
88	c3b50A	Alignment	not modelled	70.8	14	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
89	c3eq1A	Alignment	not modelled	69.6	15	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
90	d1sw5a	Alignment	not modelled	67.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
91	c2vd3B	Alignment	not modelled	65.8	13	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
92	c2h9bB	Alignment	not modelled	63.1	13	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
93	d1pdaa1	Alignment	not modelled	63.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	c2pfzA	Alignment	not modelled	61.1	11	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
95	c2h9qC	Alignment	not modelled	59.6	13	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
96	c3n6uA	Alignment	not modelled	59.5	8	PDB header: transcription regulator Chain: A: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
97	c3gyyC	Alignment	not modelled	59.2	14	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
98	c2f7cA	Alignment	not modelled	55.9	13	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
99	c3muqB	Alignment	not modelled	55.9	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
						PDB header: gene regulation

100	c2f78A_	Alignment	not modelled	54.8	13	Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
101	dlixca2	Alignment	not modelled	54.3	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
102	d1z7me1	Alignment	not modelled	46.5	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
103	c2pfyA_	Alignment	not modelled	46.2	13	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
104	c3dtfB_	Alignment	not modelled	45.7	15	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
105	c3kn3C_	Alignment	not modelled	44.9	11	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of 2 putative periplasmic protein from wolinnella succinogenes
106	c1nh7A_	Alignment	not modelled	43.7	12	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
107	c3fd3A_	Alignment	not modelled	35.9	7	PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
108	c2ypnA_	Alignment	not modelled	33.8	10	PDB header: transferase Chain: A: PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
109	d1r9la_	Alignment	not modelled	32.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
110	c2abjG_	Alignment	not modelled	32.1	15	PDB header: transferase Chain: G: PDB Molecule: branched-chain-amino-acid aminotransferase, cytosolic; PDBTitle: crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
111	d1twya_	Alignment	not modelled	30.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
112	c1twyG_	Alignment	not modelled	30.9	14	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
113	d2a1ha1	Alignment	not modelled	28.9	14	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
114	c3pamB_	Alignment	not modelled	28.5	16	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
115	d2fyia1	Alignment	not modelled	28.5	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
116	d1al3a_	Alignment	not modelled	27.9	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
117	c1al3A_	Alignment	not modelled	27.9	8	PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
118	c3lvuB_	Alignment	not modelled	26.3	9	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
119	d1h3da1	Alignment	not modelled	25.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
120	d1vr5a1	Alignment	not modelled	25.2	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like