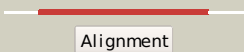

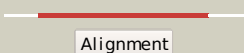

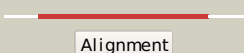

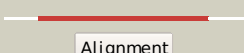



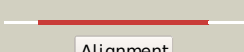

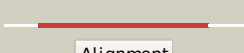

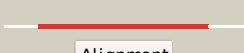






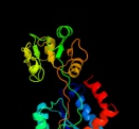



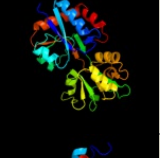
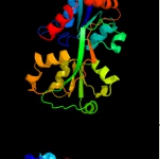
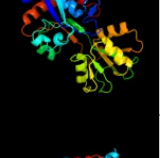
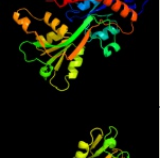
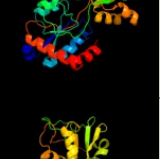
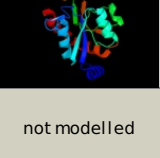


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hsla_	 Alignment		100.0	69	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	d1lsta_	 Alignment		100.0	93	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c2ylnA_	 Alignment		100.0	23	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
4	c3g41A_	 Alignment		100.0	25	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
5	c3k4uA_	 Alignment		100.0	24	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	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
7	c3delC_	 Alignment		100.0	27	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
8	c3i6vA_	 Alignment		100.0	29	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	c2q2aD_	 Alignment		100.0	29	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
10	c2ieeB_	 Alignment		100.0	19	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.
11	c2o1mB_	 Alignment		100.0	21	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 ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572

12	d1wdna_	Alignment		100.0	29	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
13	c3kzgB_	Alignment		100.0	30	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
14	c2y7iB_	Alignment		100.0	32	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
15	c3h7mA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
16	c3r39A_	Alignment		100.0	19	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	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
18	c2vhaB_	Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
19	c3kbrA_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
20	c3mplA_	Alignment		100.0	17	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)
21	c2v25B_	Alignment	not modelled	100.0	20	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
22	d2a5sa1	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
23	d1mqia_	Alignment	not modelled	100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
24	c2yjpB_	Alignment	not modelled	100.0	16	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	21	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	d1xt8a1	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c2xx7B_	Alignment	not modelled	100.0	22	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.
						Fold: Periplasmic binding protein-like II

28	d1ii5a_	Alignment	not modelled	100.0	14	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
29	d1pb7a_	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
30	c2ppyB_	Alignment	not modelled	100.0	15	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
31	c2rc9A_	Alignment	not modelled	100.0	18	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	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
33	c2v3tA_	Alignment	not modelled	100.0	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	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	c1yaeB_	Alignment	not modelled	99.9	17	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	98.8	11	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	c3e4rA_	Alignment	not modelled	98.3	17	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
39	c2x26A_	Alignment	not modelled	98.3	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
40	d1xs5a_	Alignment	not modelled	98.1	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
41	c3ix1A_	Alignment	not modelled	98.1	14	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
42	c3ix1B_	Alignment	not modelled	98.1	14	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
43	c3uifA_	Alignment	not modelled	98.0	18	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
44	c3l6gA_	Alignment	not modelled	97.9	11	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
45	c2x7pA_	Alignment	not modelled	97.9	13	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
46	c3un6A_	Alignment	not modelled	97.9	12	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
47	c3hn0A_	Alignment	not modelled	97.8	16	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
48	c3k2dA_	Alignment	not modelled	97.8	18	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
49	c3tqwA_	Alignment	not modelled	97.5	16	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
50	c2g29A_	Alignment	not modelled	97.5	14	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

51	c3qslA	Alignment	not modelled	97.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
52	c1p99A	Alignment	not modelled	97.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
53	d1p99a	Alignment	not modelled	97.3	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	c3gxaA	Alignment	not modelled	97.2	14	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
55	c2i4cA	Alignment	not modelled	96.9	14	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
56	c3tmgA	Alignment	not modelled	96.9	14	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
57	c2f5xC	Alignment	not modelled	96.5	13	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
58	c3ir1F	Alignment	not modelled	96.0	10	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
59	d1zbma1	Alignment	not modelled	95.9	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
60	d2ozza1	Alignment	not modelled	95.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
61	d1us5a	Alignment	not modelled	95.7	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	d2czla1	Alignment	not modelled	95.0	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
63	c2de4B	Alignment	not modelled	94.7	11	PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
64	c2dvzA	Alignment	not modelled	94.1	9	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
65	c2qpqC	Alignment	not modelled	94.0	8	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
66	c2rejA	Alignment	not modelled	93.1	13	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
67	c3lr1A	Alignment	not modelled	91.3	11	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
68	d1atga	Alignment	not modelled	90.4	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	d2nxoa1	Alignment	not modelled	87.3	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	c3fxbB	Alignment	not modelled	87.2	12	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
71	c3kn3C	Alignment	not modelled	87.1	10	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
72	c3chgB	Alignment	not modelled	84.3	8	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 dnsa
73	d1amfa	Alignment	not modelled	83.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c3eq1A	Alignment	not modelled	83.4	12	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
75	c2zzxD	Alignment	not modelled	83.2	15	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
						PDB header: transport protein

76	c3b50A_	Alignment	not modelled	82.6	16	Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
77	c2h5yC_	Alignment	not modelled	81.9	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
78	c3jv9B_	Alignment	not modelled	81.2	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
79	c3pppA_	Alignment	not modelled	80.0	16	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
80	c3r6uA_	Alignment	not modelled	76.6	12	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
81	c3muqB_	Alignment	not modelled	75.8	9	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
82	c2vpnB_	Alignment	not modelled	75.1	10	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
83	c3fj7A_	Alignment	not modelled	74.6	14	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
84	c2pfzA_	Alignment	not modelled	74.5	12	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
85	c2pfyA_	Alignment	not modelled	74.4	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
86	c3ho7A_	Alignment	not modelled	71.7	9	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
87	d1pdaa1	Alignment	not modelled	71.4	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
88	c3gyyC_	Alignment	not modelled	71.0	10	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
89	c2ql3G_	Alignment	not modelled	59.8	10	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
90	d1b1xa1	Alignment	not modelled	50.8	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
91	c2ypnA_	Alignment	not modelled	48.4	11	PDB header: transferase Chain: A: PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
92	d1eh3a_	Alignment	not modelled	47.7	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
93	d2esna2	Alignment	not modelled	46.3	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	c2hzkB_	Alignment	not modelled	36.9	10	PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
95	c3fd3A_	Alignment	not modelled	35.6	10	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.
96	d1ce2a1	Alignment	not modelled	33.3	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
97	c1twyG_	Alignment	not modelled	33.3	16	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
98	d1twya_	Alignment	not modelled	33.3	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
99	c2q5cA_	Alignment	not modelled	33.3	13	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
						PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-

100	c2hpgB_	Alignment	not modelled	32.8	9	binding PDBTitle: the crystal structure of a thermophilic trap periplasmic2 binding protein
101	c1jvnB_	Alignment	not modelled	32.0	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
102	d1h76a1	Alignment	not modelled	30.6	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
103	c2f7cA_	Alignment	not modelled	30.6	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
104	c3lvuB_	Alignment	not modelled	30.2	7	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
105	c3dtfB_	Alignment	not modelled	30.2	11	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
106	d1mb3a_	Alignment	not modelled	29.9	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
107	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
108	d1i6aa_	Alignment	not modelled	28.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
109	c2hxrA_	Alignment	not modelled	27.7	15	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
110	d1zcca1	Alignment	not modelled	27.5	10	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
111	d2qmw1	Alignment	not modelled	27.4	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
112	d1r9la_	Alignment	not modelled	27.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
113	d1dtza1	Alignment	not modelled	25.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
114	d1ryoa_	Alignment	not modelled	25.4	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
115	d1ieja_	Alignment	not modelled	25.4	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
116	d1jnfa1	Alignment	not modelled	21.2	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
117	c3n6uA_	Alignment	not modelled	20.7	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
118	c3mwbA_	Alignment	not modelled	20.5	22	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureus to 2.0a
119	d2pjua1	Alignment	not modelled	20.3	13	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like