

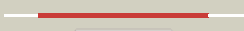






























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n5lA_	 Alignment		100.0	61	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc phosphonate transporter; PDBTitle: crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
2	c3e4rA_	 Alignment		99.9	15	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
3	c2x26A_	 Alignment		99.9	14	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
4	c3uifA_	 Alignment		99.9	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
5	c3qslA_	 Alignment		99.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
6	d1b1xa1	 Alignment		99.8	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
7	d1dtza1	 Alignment		99.8	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
8	d1eh3a_	 Alignment		99.8	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
9	c3k2dA_	 Alignment		99.8	11	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
10	c3un6A_	 Alignment		99.8	16	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
11	c3ix1B_	 Alignment		99.8	9	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

12	c3ix1A_	Alignment		99.8	9	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
13	dlce2a1	Alignment		99.8	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
14	c2x7pA_	Alignment		99.8	10	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
15	dlryoa_	Alignment		99.8	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
16	dlh76a1	Alignment		99.8	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
17	dlxs5a_	Alignment		99.8	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
18	c2de4B_	Alignment		99.8	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
19	dlieja_	Alignment		99.7	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
20	c3gxaA_	Alignment		99.7	16	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
21	c3hn0A_	Alignment	not modelled	99.7	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
22	dljnfal	Alignment	not modelled	99.7	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
23	c3tqwA_	Alignment	not modelled	99.7	14	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
24	c2g29A_	Alignment	not modelled	99.7	10	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
25	d2hava1	Alignment	not modelled	99.7	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
26	c3ir1F_	Alignment	not modelled	99.7	17	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
27	dlus5a_	Alignment	not modelled	99.6	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
28	c3l6gA_	Alignment	not modelled	99.6	16	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
						PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter;

29	c2i4cA_	Alignment	not modelled	99.6	11	PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
30	c2qpqC_	Alignment	not modelled	99.6	13	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
31	c3tmgA_	Alignment	not modelled	99.6	13	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
32	d1tfda_	Alignment	not modelled	99.6	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
33	c1p99A_	Alignment	not modelled	99.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
34	d1p99a_	Alignment	not modelled	99.6	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	d2b6da1	Alignment	not modelled	99.5	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
36	c2dvzA_	Alignment	not modelled	99.5	14	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
37	c2f5xC_	Alignment	not modelled	99.5	15	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
38	d2czla1	Alignment	not modelled	99.5	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
39	d2nxoa1	Alignment	not modelled	99.4	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
40	d1cb6a2	Alignment	not modelled	99.4	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
41	d1jw1a1	Alignment	not modelled	99.4	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
42	d1jnfa2	Alignment	not modelled	99.4	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
43	d1zbma1	Alignment	not modelled	99.3	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
44	d1dota1	Alignment	not modelled	99.3	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
45	d2d3ia2	Alignment	not modelled	99.2	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
46	d1b1xa2	Alignment	not modelled	99.2	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
47	c1lfgA_	Alignment	not modelled	99.2	18	PDB header: transferrin Chain: A: PDB Molecule: lactoferrin; PDBTitle: molecular replacement solution of the structure of apolactoferrin, a2 protein displaying large-scale conformational change
48	c3mplA_	Alignment	not modelled	99.0	13	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)
49	c2hauA_	Alignment	not modelled	99.0	16	PDB header: metal transport Chain: A: PDB Molecule: serotransferrin; PDBTitle: apo-human serum transferrin (non-glycosylated)
50	d1pb7a_	Alignment	not modelled	99.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	d1dtza2	Alignment	not modelled	99.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
52	d1amfa_	Alignment	not modelled	99.0	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
53	c2q2aD_	Alignment	not modelled	98.9	15	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
54	d1h76a2	Alignment	not modelled	98.9	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
						PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic

55	c3g41A_	Alignment	not modelled	98.9	9	amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
56	c3kzgB_	Alignment	not modelled	98.9	16	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
57	c1ce2A_	Alignment	not modelled	98.9	15	PDB header: metal transport Chain: A: PDB Molecule: protein (lactoferrin); PDBTitle: structure of diferric buffalo lactoferrin at 2.5a resolution
58	c2pfzA_	Alignment	not modelled	98.9	18	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
59	d1dota2	Alignment	not modelled	98.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
60	c2hpgB_	Alignment	not modelled	98.9	18	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
61	c2rejA_	Alignment	not modelled	98.9	10	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	d2a5sa1	Alignment	not modelled	98.9	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
63	c3gyyC_	Alignment	not modelled	98.9	12	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
64	c2zzxD_	Alignment	not modelled	98.9	16	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
65	c2q89A_	Alignment	not modelled	98.8	15	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter amino acid-binding protein; PDBTitle: crystal structure of ehub in complex with hydroxyectoine
66	c2h5yC_	Alignment	not modelled	98.8	14	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
67	c2pfyA_	Alignment	not modelled	98.8	14	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
68	d1atga_	Alignment	not modelled	98.8	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	d1lsta_	Alignment	not modelled	98.8	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	c2ylnA_	Alignment	not modelled	98.8	15	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
71	c3delC_	Alignment	not modelled	98.8	11	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
72	c3k4uA_	Alignment	not modelled	98.7	17	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinnella succinogenes dsm 1740 complexed with lysine
73	d1hsla_	Alignment	not modelled	98.7	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c2rc9A_	Alignment	not modelled	98.7	15	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
75	c3r6uA_	Alignment	not modelled	98.7	12	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
76	c2hzkB_	Alignment	not modelled	98.7	13	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
77	c2vpnB_	Alignment	not modelled	98.7	12	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
78	c3hv1A_	Alignment	not modelled	98.7	14	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

79	c3kn3C	Alignment	not modelled	98.6	9	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 wolinnella succinogenes
80	c3b50A	Alignment	not modelled	98.6	17	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.
81	c3fxbB	Alignment	not modelled	98.6	10	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
82	c3h7mA	Alignment	not modelled	98.6	12	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
83	c3fj7A	Alignment	not modelled	98.6	15	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
84	c3e79A	Alignment	not modelled	98.5	15	PDB header: tpb binding protein Chain: A: PDB Molecule: high affinity transport system protein p37; PDBTitle: structure determination of the cancer-associated mycoplasma2 hyorhinis protein mh-p37
85	c2o1mB	Alignment	not modelled	98.5	15	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
86	c3muqB	Alignment	not modelled	98.5	13	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
87	c2vhaB	Alignment	not modelled	98.5	12	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
88	c3pppA	Alignment	not modelled	98.5	13	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
89	c3lr1A	Alignment	not modelled	98.5	15	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
90	d1sbpa	Alignment	not modelled	98.5	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
91	c2pyyB	Alignment	not modelled	98.5	13	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
92	c3mc2C	Alignment	not modelled	98.4	14	PDB header: lyase inhibitor Chain: C: PDB Molecule: inhibitor of carbonic anhydrase; PDBTitle: crystal structure of the murine inhibitor of carbonic anhydrase
93	c3r39A	Alignment	not modelled	98.4	14	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
94	d1jw1a2	Alignment	not modelled	98.4	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
95	c3i6vA	Alignment	not modelled	98.4	15	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
96	d1r9la	Alignment	not modelled	98.3	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
97	c2v25B	Alignment	not modelled	98.3	16	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
98	c2y7iB	Alignment	not modelled	98.3	11	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
99	d1mqia	Alignment	not modelled	98.3	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
100	d1ii5a	Alignment	not modelled	98.2	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
101	d1wdna	Alignment	not modelled	98.2	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
102	c1ryxA	Alignment	not modelled	98.2	20	PDB header: metal transport Chain: A: PDB Molecule: ovotransferrin; PDBTitle: crystal structure of hen serum transferrin in apo- form
						PDB header: structural genomics, unknown function

103	c2ieeB_	Alignment	not modelled	98.1	17	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.
104	c2xx7B_	Alignment	not modelled	98.1	12	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.
105	d2i6ea1	Alignment	not modelled	97.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
106	c3kbrA_	Alignment	not modelled	97.9	13	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
107	c2qryD_	Alignment	not modelled	97.8	11	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
108	c3o66A_	Alignment	not modelled	97.8	11	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter; PDBTitle: crystal structure of glycine betaine/carnitine/choline abc transporter
109	c2i6eG_	Alignment	not modelled	97.8	16	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein dr0370 from deinococcus radiodurans, pfam2 duf178
110	d1sw5a_	Alignment	not modelled	97.6	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
111	d2ozza1	Alignment	not modelled	97.6	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
112	c3chgB_	Alignment	not modelled	97.6	18	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
113	d1y9ua_	Alignment	not modelled	97.4	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
114	d1xt8a1	Alignment	not modelled	97.3	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
115	c1xt8B_	Alignment	not modelled	97.2	20	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
116	c1twyG_	Alignment	not modelled	97.1	13	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
117	d1twya_	Alignment	not modelled	97.1	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
118	d1qv8a_	Alignment	not modelled	97.1	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
119	c1q1kA_	Alignment	not modelled	96.8	16	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
120	c1yaeB_	Alignment	not modelled	96.8	14	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