



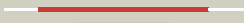




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sbpa_	 Alignment		100.0	45	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	d1y9ua_	 Alignment		100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c2h5yC_	 Alignment		100.0	17	PDB header: metal transport Chain: C: PDB Molecule: molybdate-binding periplasmic protein; PDBTitle: crystallographic structure of the molybdate-binding protein of <i>Xanthomonas citri</i> at 1.7 ang resolution bound to molybdate
4	c3c9hB_	 Alignment		100.0	11	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of the substrate binding protein of the abc2 transporter from <i>Agrobacterium tumefaciens</i>
5	d1atga_	 Alignment		100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
6	c3lr1A_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from <i>Geobacter sulfurreducens</i>
7	c3fj7A_	 Alignment		100.0	13	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide pnb3; PDBTitle: crystal structure of l-phospholactate bound pnb3
8	c2qryD_	 Alignment		100.0	14	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
9	d1amfa_	 Alignment		100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	d1q35a_	 Alignment		100.0	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
11	c3muqB_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from <i>Vibrio parahaemolyticus</i> rimd 2210633

12	d1y4ta_	Alignment		100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
13	c2pt1A_	Alignment		100.0	15	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
14	d1xvya_	Alignment		100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
15	d1xc1a_	Alignment		100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
16	d1xvxa_	Alignment		100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
17	c3rpwA_	Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
18	d1nnfa_	Alignment		100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
19	c3pu5A_	Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein; PDBTitle: the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
20	c2vozA_	Alignment		99.9	14	PDB header: metal-binding protein Chain: A: PDB Molecule: periplasmic iron-binding protein; PDBTitle: apo futa2 from synechocystis pcc6803
21	c3kn3C_	Alignment	not modelled	99.9	18	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
22	c2v84A_	Alignment	not modelled	99.9	13	PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc transporter, periplasmic PDBTitle: crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum
23	d1pota_	Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
24	c3cg3A_	Alignment	not modelled	99.9	14	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ph0151; PDBTitle: crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate
25	d1a99a_	Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	c3k6wA_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
27	c3cfxA_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
28	d2onsa1	Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like

29	c3osrA_	Alignment	not modelled	99.9	15	PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
30	c1ursA_	Alignment	not modelled	99.9	13	PDB header: maltose-binding protein Chain: A: PDB Molecule: maltose-binding protein; PDBTitle: x-ray structures of the maltose-maltodextrin binding2 protein of the thermoacidophilic bacterium alicyclobacillus3 acidocaldarius
31	d1ursa_	Alignment	not modelled	99.9	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
32	c3ob4A_	Alignment	not modelled	99.9	16	PDB header: allergen Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, arah 2; PDBTitle: mbp-fusion protein of the major peanut allergen ara h 2
33	c3f5fA_	Alignment	not modelled	99.9	17	PDB header: transport, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, heparan PDBTitle: crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion.
34	c3cg1A_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein pf0080; PDBTitle: crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate
35	c2xd3A_	Alignment	not modelled	99.9	14	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose.
36	c1twyG_	Alignment	not modelled	99.9	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
37	c1y4cA_	Alignment	not modelled	99.9	15	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
38	c3o3uN_	Alignment	not modelled	99.9	16	PDB header: transport protein, signaling protein Chain: N: PDB Molecule: maltose-binding periplasmic protein, advanced glycosylation PDBTitle: crystal structure of human receptor for advanced glycation endproducts2 (rage)
39	c3mp6A_	Alignment	not modelled	99.9	15	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4
40	c1r6zA_	Alignment	not modelled	99.9	15	PDB header: gene regulation Chain: A: PDB Molecule: chimera of maltose-binding periplasmic protein and PDBTitle: the crystal structure of the argonaute2 paz domain (as a mbp fusion)
41	c2gh9A_	Alignment	not modelled	99.9	15	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
42	d1twya_	Alignment	not modelled	99.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
43	c3py7A_	Alignment	not modelled	99.9	16	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin ld1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
44	c3qufB_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
45	c3d4cA_	Alignment	not modelled	99.9	18	PDB header: cell adhesion Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, zona pellucida PDBTitle: zp-n domain of mammalian sperm receptor zp3 (crystal form i)
46	c2nvuB_	Alignment	not modelled	99.8	17	PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
47	c3oaiB_	Alignment	not modelled	99.8	16	PDB header: membrane protein, cell adhesion Chain: B: PDB Molecule: maltose-binding periplasmic protein, myelin protein p0; PDBTitle: crystal structure of the extra-cellular domain of human myelin protein2 zero
48	c2vgqA_	Alignment	not modelled	99.8	15	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
49	c3uorB_	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: B: PDB Molecule: abc transporter sugar binding protein; PDBTitle: the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
50	c3h4zC_	Alignment	not modelled	99.8	15	PDB header: allergen Chain: C: PDB Molecule: maltose-binding periplasmic protein fused with allergen PDBTitle: crystal structure of an mbp-der p 7 fusion protein
						PDB header: de novo protein, sugar binding protein Chain: A: PDB Molecule: maltose-binding protein monobody ys1

51	c3csqA	Alignment	not modelled	99.8	14	fusion; PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex
52	c3dm0A	Alignment	not modelled	99.8	18	PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein fused with PDBTitle: maltose binding protein fusion with rack1 from a. thaliana
53	c3c4mA	Alignment	not modelled	99.8	15	PDB header: membrane protein Chain: A: PDB Molecule: fusion protein of maltose-binding periplasmic protein and PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
54	c2b3fD	Alignment	not modelled	99.8	10	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein2 bound with galactose
55	c1mh3A	Alignment	not modelled	99.8	14	PDB header: sugar binding, dna binding protein Chain: A: PDB Molecule: maltose binding-a1 homeodomain protein chimera; PDBTitle: maltose binding-a1 homeodomain protein chimera, crystal2 form i
56	c3osqA	Alignment	not modelled	99.8	20	PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 175
57	d1eu8a	Alignment	not modelled	99.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
58	c1hsjA	Alignment	not modelled	99.8	16	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure
59	c2zykA	Alignment	not modelled	99.8	13	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
60	c3k02A	Alignment	not modelled	99.8	13	PDB header: transport protein Chain: A: PDB Molecule: acarbose/maltose binding protein gach; PDBTitle: crystal structures of the gach receptor of streptomyces glaucescens2 gla.o in the unliganded form and in complex with acarbose and an3 acarbose homolog. comparison with acarbose-loaded maltose binding4 protein of salmonella typhimurium.
61	c3oo6A	Alignment	not modelled	99.8	12	PDB header: sugar binding protein Chain: A: PDB Molecule: abc transporter binding protein acbh; PDBTitle: crystal structures and biochemical characterization of the bacterial2 solute receptor acbh reveal an unprecedented exclusive substrate3 preference for b-d-galactopyranose
62	c2fncA	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose.
63	c3ehuA	Alignment	not modelled	99.8	16	PDB header: membrane protein Chain: A: PDB Molecule: fusion protein of crfr1 extracellular domain and mbp; PDBTitle: crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
64	c1mg1A	Alignment	not modelled	99.8	13	PDB header: viral protein Chain: A: PDB Molecule: protein (h1v-1 gp21 ectodomain/maltose-binding protein PDBTitle: h1v-1 gp21 ectodomain/maltose-binding protein chimera
65	d1laxa	Alignment	not modelled	99.8	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
66	c1svxB	Alignment	not modelled	99.8	14	PDB header: de novo protein/sugar binding protein Chain: B: PDB Molecule: maltose-binding periplasmic protein; PDBTitle: crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein
67	c2i58B	Alignment	not modelled	99.8	13	PDB header: sugar binding protein Chain: B: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose
68	c3cfzA	Alignment	not modelled	99.8	15	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
69	d1elja	Alignment	not modelled	99.8	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	c3iouB	Alignment	not modelled	99.8	14	PDB header: signaling protein Chain: B: PDB Molecule: maltose-binding protein, huntingtin fusion PDBTitle: huntingtin amino-terminal region with 17 gln residues -2 crystal c94
71	c2uvgA	Alignment	not modelled	99.8	11	PDB header: sugar-binding protein Chain: A: PDB Molecule: abc type periplasmic sugar-binding protein; PDBTitle: structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
72	c2w7yA	Alignment	not modelled	99.7	11	PDB header: sugar-binding protein Chain: A: PDB Molecule: probable sugar abc transporter, sugar-binding PDBTitle: structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide.
						Fold: Periplasmic binding protein-like II

73	d3thia_	Alignment	not modelled	99.7	16	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c2z8fB_	Alignment	not modelled	99.7	10	PDB header: sugar binding protein Chain: B: PDB Molecule: galacto-n-biose/lacto-n-biose i transporter substrate- PDBTitle: the galacto-n-biose-/lacto-n-biose i-binding protein (gl-bp) of the2 abc transporter from bifidobacterium longum in complex with lacto-n-3 tetraose
75	d1pc3a_	Alignment	not modelled	99.7	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
76	c3i3vC_	Alignment	not modelled	99.6	12	PDB header: transport protein Chain: C: PDB Molecule: probable secreted solute-binding lipoprotein; PDBTitle: crystal structure of probable secreted solute-binding2 lipoprotein from streptomyces coelicolor
77	d1ixha_	Alignment	not modelled	99.4	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
78	d1j1na_	Alignment	not modelled	99.3	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
79	d1y3na1	Alignment	not modelled	99.2	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
80	c3ombA_	Alignment	not modelled	99.0	12	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: crystal structure of extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
81	c3n5lA_	Alignment	not modelled	98.0	12	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
82	c1p99A_	Alignment	not modelled	97.9	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
83	d1p99a_	Alignment	not modelled	97.9	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
84	c3k2dA_	Alignment	not modelled	97.9	10	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
85	c3cvqC_	Alignment	not modelled	97.8	13	PDB header: metal binding protein Chain: C: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
86	d2v3qa1	Alignment	not modelled	97.8	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
87	c3ir1F_	Alignment	not modelled	97.6	10	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
88	c2dvzA_	Alignment	not modelled	97.5	11	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
89	c3gxaA_	Alignment	not modelled	97.4	10	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
90	c3tqwA_	Alignment	not modelled	97.3	12	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
91	c2qpqC_	Alignment	not modelled	97.3	11	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
92	d1xs5a_	Alignment	not modelled	97.3	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
93	c2f5xC_	Alignment	not modelled	97.0	8	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
94	c3l6gA_	Alignment	not modelled	96.6	12	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
95	c3e4rA_	Alignment	not modelled	96.1	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
96	d1us5a_	Alignment	not modelled	96.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
97	c2x26A_	Alignment	not modelled	95.7	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein;

						PDBTitle: crystal structure of the periplasmic aliphatic sulphate2 binding protein ssua from escherichia coli
98	c3ix1B_	Alignment	not modelled	94.6	12	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
99	c3ix1A_	Alignment	not modelled	94.6	12	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
100	c3tmgA_	Alignment	not modelled	93.3	12	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
101	c2x7pA_	Alignment	not modelled	92.5	8	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
102	c2rejA_	Alignment	not modelled	92.4	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
103	c3uifA_	Alignment	not modelled	92.0	12	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
104	c3hn0A_	Alignment	not modelled	92.0	11	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
105	c3qslA_	Alignment	not modelled	90.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
106	c2ql3G_	Alignment	not modelled	86.9	14	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
107	d2fyia1	Alignment	not modelled	84.3	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
108	c3un6A_	Alignment	not modelled	80.2	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
109	d1sw5a_	Alignment	not modelled	80.2	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
110	c3r6uA_	Alignment	not modelled	75.8	12	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
111	d1al3a_	Alignment	not modelled	66.2	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
112	c1al3A_	Alignment	not modelled	66.2	9	PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
113	c3ho7A_	Alignment	not modelled	64.4	16	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
114	c2hxrA_	Alignment	not modelled	63.0	13	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
115	c3pppA_	Alignment	not modelled	54.9	11	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
116	c3kzgB_	Alignment	not modelled	52.7	10	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
117	d1h76a1	Alignment	not modelled	47.1	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
118	d1r9la_	Alignment	not modelled	45.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
119	c1d0rA_	Alignment	not modelled	39.3	42	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water PDB header: hormone/growth factor

120	c1jrjA_	Alignment	not modelled	38.8	25	Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
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