

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3osqA_	 Alignment		100.0	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 175
2	c3ob4A_	 Alignment		100.0	12	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
3	c3f5fA_	 Alignment		100.0	12	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.
4	c3o3uN_	 Alignment		100.0	12	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)
5	c3h4zC_	 Alignment		100.0	13	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
6	c3dm0A_	 Alignment		100.0	12	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
7	c3d4cA_	 Alignment		100.0	12	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)
8	c3py7A_	 Alignment		100.0	12	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
9	c3c4mA_	 Alignment		100.0	12	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)
10	c1y4cA_	 Alignment		100.0	12	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
11	c1r6zA_	 Alignment		100.0	12	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)

12	c3csgA	Alignment		100.0	12	PDB header: de novo protein, sugar binding protein Chain: A: PDB Molecule: maltose-binding protein monobody ys1 fusion; PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex
13	c2nvuB	Alignment		100.0	13	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
14	c3osrA	Alignment		100.0	13	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
15	c3oaiB	Alignment		100.0	12	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
16	c3mp6A	Alignment		100.0	12	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4
17	c2vgqA	Alignment		100.0	12	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
18	c1hsjA	Alignment		100.0	12	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure
19	c3ehuA	Alignment		100.0	12	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
20	c2qh9A	Alignment		100.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
21	d1elja	Alignment	not modelled	100.0	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
22	c3k02A	Alignment	not modelled	100.0	9	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.
23	c3oo6A	Alignment	not modelled	100.0	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
24	c3qufB	Alignment	not modelled	100.0	14	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
25	c2zykA	Alignment	not modelled	100.0	14	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
26	d1eu8a	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c3uorB	Alignment	not modelled	100.0	16	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
28	d1a99a	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
29	c1mg1A_	Alignment	not modelled	100.0	12	PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein) PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
30	c3iouB_	Alignment	not modelled	100.0	12	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
31	c2xd3A_	Alignment	not modelled	100.0	10	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.
32	c3rpwA_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
33	c2uvgA_	Alignment	not modelled	100.0	12	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
34	c1svxB_	Alignment	not modelled	100.0	12	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
35	c2z8fB_	Alignment	not modelled	100.0	12	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
36	c3pu5A_	Alignment	not modelled	100.0	12	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
37	d1pota_	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
38	c2b3fD_	Alignment	not modelled	100.0	10	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein2 bound with galactose
39	c3c9hB_	Alignment	not modelled	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 agrobacterium tumefaciens
40	c2fncA_	Alignment	not modelled	100.0	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.
41	c2qryD_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
42	d1laxa_	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
43	c2v84A_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc transporter, periplasmic PDBTitle: crystal structure of the tp0655 (tpptd) lipoprotein of2 treponema pallidum
44	c1mh3A_	Alignment	not modelled	100.0	12	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
45	c3i3vC_	Alignment	not modelled	100.0	11	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
46	c2i58B_	Alignment	not modelled	100.0	10	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
47	d1lursa_	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
48	c1lursA_	Alignment	not modelled	100.0	15	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
49	d3thia_	Alignment	not modelled	100.0	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
50	c2w7yA_	Alignment	not modelled	100.0	8	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.
51	d1y4ta_	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like

52	c2pt1A	Alignment	not modelled	100.0	14	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
53	d1xvxa	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	d1j1na	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	d1q35a	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
56	d1y3na1	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
57	d1y9ua	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
58	d1xvya	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
59	c3ombA	Alignment	not modelled	100.0	9	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
60	d1xc1a	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
61	c2vozA	Alignment	not modelled	100.0	16	PDB header: metal-binding protein Chain: A: PDB Molecule: periplasmic iron-binding protein; PDBTitle: apo futa2 from synechocystis pcc6803
62	d1nnfa	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
63	d2onsa1	Alignment	not modelled	99.9	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
64	c3k6wA	Alignment	not modelled	99.9	12	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
65	c3cfxA	Alignment	not modelled	99.9	14	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
66	c3cfzA	Alignment	not modelled	99.9	11	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
67	c3cg3A	Alignment	not modelled	99.9	12	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
68	c3cg1A	Alignment	not modelled	99.9	12	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
69	d1amfa	Alignment	not modelled	99.8	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	d1atga	Alignment	not modelled	99.8	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
71	d1sbpa	Alignment	not modelled	99.8	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
72	c2h5yC	Alignment	not modelled	99.8	15	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
73	c3fj7A	Alignment	not modelled	99.8	10	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
74	c3lr1A	Alignment	not modelled	99.7	10	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
75	c3muqB	Alignment	not modelled	99.6	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
76	c3kn3C	Alignment	not modelled	99.5	12	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
77	c1twyG	Alignment	not modelled	99.2	10	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
78	d1twya_	Alignment	not modelled	99.2	10 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
79	d1pc3a_	Alignment	not modelled	97.2	12 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
80	d1ixha_	Alignment	not modelled	96.1	15 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
81	c3tqwA_	Alignment	not modelled	94.2	13 PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
82	c3k2dA_	Alignment	not modelled	94.0	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
83	c3cvqC_	Alignment	not modelled	93.3	21 PDB header: metal binding protein Chain: C: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
84	c2rejA_	Alignment	not modelled	93.2	17 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
85	c3e4rA_	Alignment	not modelled	91.4	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
86	c3tmgA_	Alignment	not modelled	91.3	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
87	c3n5lA_	Alignment	not modelled	90.8	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
88	c2qpqC_	Alignment	not modelled	90.1	13 PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
89	c2f5xC_	Alignment	not modelled	89.8	17 PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
90	c3l6gA_	Alignment	not modelled	87.6	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
91	c3gxaA_	Alignment	not modelled	87.2	13 PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
92	c3ir1F_	Alignment	not modelled	87.2	13 PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
93	c2x26A_	Alignment	not modelled	82.8	13 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
94	c3ix1B_	Alignment	not modelled	81.2	11 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
95	c3un6A_	Alignment	not modelled	80.5	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
96	c2dvzA_	Alignment	not modelled	78.8	12 PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
97	d1xs5a_	Alignment	not modelled	77.8	11 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
98	c2hpgB_	Alignment	not modelled	70.1	11 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
99	c2g29A_	Alignment	not modelled	67.1	12 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
100	c3ix1A_	Alignment	not modelled	63.6	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
101	c1p99A_	Alignment	not modelled	56.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
102	d1p99a_	Alignment	not modelled	56.7	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
103	c3b50A_	Alignment	not modelled	56.5	9	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.
104	c2pfyA_	Alignment	not modelled	55.6	11	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
105	c2vpnB_	Alignment	not modelled	46.9	8	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
106	d2v3qa1	Alignment	not modelled	46.0	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
107	c2zzxD_	Alignment	not modelled	45.1	12	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
108	c3fxbB_	Alignment	not modelled	45.0	9	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
109	c2pfzA_	Alignment	not modelled	41.1	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
110	d1r9la_	Alignment	not modelled	36.9	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
111	c1jrjA_	Alignment	not modelled	32.8	17	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
112	d1dtza1	Alignment	not modelled	31.3	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
113	d1bwlA_	Alignment	not modelled	30.1	18	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
114	c3r6uA_	Alignment	not modelled	29.3	10	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
115	c1d0rA_	Alignment	not modelled	27.1	33	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
116	d1us5a_	Alignment	not modelled	26.2	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
117	d1eh3a_	Alignment	not modelled	26.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
118	d1whqa_	Alignment	not modelled	22.1	38	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)