Phyre^2

Email	l.a.kelley@imperial.ac.uk
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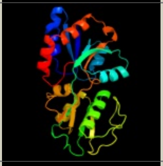
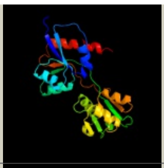
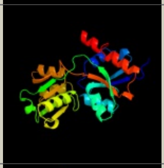
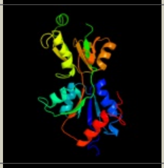
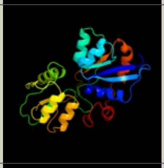
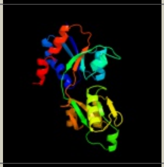
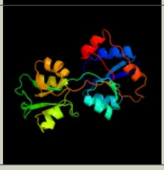
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tqwA_	Alignment		100.0	49	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
2	c3gxaA_	Alignment		100.0	40	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
3	d1xs5a_	Alignment		100.0	33	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
4	c3k2dA_	Alignment		100.0	69	**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
5	c3ir1F_	Alignment		100.0	40	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
6	d1p99a_	Alignment		100.0	40	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
7	c1p99A_	Alignment		100.0	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
8	c3un6A_	Alignment		100.0	18	**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
9	c3e4rA_	Alignment		99.9	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
10	c2x26A_	Alignment		99.9	17	**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
11	c2x7pA_	Alignment		99.9	15	**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

12	c3uifA_	Alignment		99.9	19	**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
13	c2de4B_	Alignment		99.9	15	**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
14	c3qslA_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
15	c2g29A_	Alignment		99.9	15	**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
16	c3ix1B_	Alignment		99.9	17	**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
17	c3ix1A_	Alignment		99.9	17	**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
18	c3hn0A_	Alignment		99.9	13	**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
19	c2i4cA_	Alignment		99.8	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
20	c3n5lA_	Alignment		99.7	17	**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
21	d1zbma1	Alignment	not modelled	99.7	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
22	c3tmgA_	Alignment	not modelled	99.7	17	**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
23	d2nxoa1	Alignment	not modelled	99.6	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
24	d1atga_	Alignment	not modelled	99.6	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
25	c3l6gA_	Alignment	not modelled	99.6	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
26	c2h5yC_	Alignment	not modelled	99.5	12	**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
27	d1amfa_	Alignment	not modelled	99.5	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						Fold: Periplasmic binding protein-like II

28	d2czla1	Alignment	not modelled	99.5	13	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
29	c3fj7A_	Alignment	not modelled	99.4	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
30	c3muqB_	Alignment	not modelled	99.4	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
31	c3lr1A_	Alignment	not modelled	99.4	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
32	c3kn3C_	Alignment	not modelled	99.3	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 wolinella succinogenes
33	d1us5a_	Alignment	not modelled	99.2	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
34	d1sbpa_	Alignment	not modelled	99.2	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
35	c3c9hB_	Alignment	not modelled	99.1	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
36	c2rejA_	Alignment	not modelled	99.1	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
37	d1xvxa_	Alignment	not modelled	98.9	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
38	c2qryD_	Alignment	not modelled	98.9	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**thiamine-binding periplasmic protein; **PDBTitle:** periplasmic thiamin binding protein
39	c3rpwA_	Alignment	not modelled	98.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter; **PDBTitle:** the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
40	d1r9la_	Alignment	not modelled	98.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
41	d1xc1a_	Alignment	not modelled	98.8	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
42	c1twyG_	Alignment	not modelled	98.8	12	**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
43	d1twya_	Alignment	not modelled	98.8	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	c3cfxA_	Alignment	not modelled	98.8	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
45	c3r6uA_	Alignment	not modelled	98.7	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
46	c3pu5A_	Alignment	not modelled	98.7	14	**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
47	d1xvya_	Alignment	not modelled	98.7	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
48	c2v84A_	Alignment	not modelled	98.6	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**spermidine/putrescine abc transporter, periplasmic **PDBTitle:** crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum
49	c3kzgB_	Alignment	not modelled	98.6	11	**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
50	d1y9ua_	Alignment	not modelled	98.6	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
51	c3k6wA_	Alignment	not modelled	98.6	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
52	d1y4ta_	Alignment	not modelled	98.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						PDB header:structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable amino-acid abc transporter

53	c2o1mB_	Alignment	not modelled	98.6	13	**PDBTitle:** crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
54	d1q35a_	Alignment	not modelled	98.6	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
55	c2q2aD_	Alignment	not modelled	98.6	14	**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
56	c3mplA_	Alignment	not modelled	98.6	14	**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)
57	c3osrA_	Alignment	not modelled	98.6	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
58	c3cg3A_	Alignment	not modelled	98.6	13	**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
59	d2onsa1	Alignment	not modelled	98.5	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
60	d1nnfa_	Alignment	not modelled	98.5	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
61	c3k4uA_	Alignment	not modelled	98.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding component of abc transporter; **PDBTitle:** crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
62	c3cg1A_	Alignment	not modelled	98.5	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
63	c3r39A_	Alignment	not modelled	98.5	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative periplasmic binding protein; **PDBTitle:** crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
64	d2a5sa1	Alignment	not modelled	98.5	7	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
65	d2ozza1	Alignment	not modelled	98.4	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
66	c2hpgB_	Alignment	not modelled	98.4	19	**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
67	c2pt1A_	Alignment	not modelled	98.4	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
68	d1hsla_	Alignment	not modelled	98.4	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
69	d1pota_	Alignment	not modelled	98.4	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
70	c3gyyC_	Alignment	not modelled	98.4	11	**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
71	c2ylnA_	Alignment	not modelled	98.4	11	**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
72	c3pppA_	Alignment	not modelled	98.4	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
73	c3g41A_	Alignment	not modelled	98.3	14	**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
74	c2pfyA_	Alignment	not modelled	98.3	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
75	d1a99a_	Alignment	not modelled	98.3	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
76	c2vpnB_	Alignment	not modelled	98.3	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
						PDB header:transport protein

77	c2pfzA_	Alignment	not modelled	98.3	16	**Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
78	d1lsta_	Alignment	not modelled	98.3	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
79	d1ii5a_	Alignment	not modelled	98.3	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
80	c3fxbB_	Alignment	not modelled	98.3	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
81	d1sw5a_	Alignment	not modelled	98.2	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
82	c3delC_	Alignment	not modelled	98.2	12	**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
83	c3b50A_	Alignment	not modelled	98.2	18	**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.
84	c3o66A_	Alignment	not modelled	98.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
85	c2ieeB_	Alignment	not modelled	98.2	15	**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.
86	c3hv1A_	Alignment	not modelled	98.2	16	**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
87	c3h7mA_	Alignment	not modelled	98.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
88	c3ob4A_	Alignment	not modelled	98.1	14	**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
89	c2q89A_	Alignment	not modelled	98.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter amino acid-binding protein; **PDBTitle:** crystal structure of ehub in complex with hydroxyectoine
90	c3cfzA_	Alignment	not modelled	98.1	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
91	c3py7A_	Alignment	not modelled	98.0	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
92	c2rc9A_	Alignment	not modelled	98.0	11	**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
93	d1pb7a_	Alignment	not modelled	98.0	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
94	c2nvuB_	Alignment	not modelled	98.0	15	**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
95	c3f5fA_	Alignment	not modelled	98.0	16	**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.
96	c2y7iB_	Alignment	not modelled	98.0	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.
97	d1wdna_	Alignment	not modelled	98.0	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
98	c3o3uN_	Alignment	not modelled	97.9	14	**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)
99	c3i6vA_	Alignment	not modelled	97.9	14	**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
						PDB header:sugar binding protein,signaling protein

100	c3dm0A_	Alignment	not modelled	97.9	16	**Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
101	c2pyyB_	Alignment	not modelled	97.9	8	**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
102	c3h4zC_	Alignment	not modelled	97.9	16	**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
103	c2xx7B_	Alignment	not modelled	97.9	11	**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.
104	c3oaiB_	Alignment	not modelled	97.9	15	**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
105	d1dtza1	Alignment	not modelled	97.8	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
106	c3mp6A_	Alignment	not modelled	97.8	14	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, saga- **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
107	c2zzxD_	Alignment	not modelled	97.8	13	**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	d1b1xa1	Alignment	not modelled	97.8	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
109	d1eh3a_	Alignment	not modelled	97.7	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
110	d1mqia_	Alignment	not modelled	97.7	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
111	c3kbrA_	Alignment	not modelled	97.7	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
112	c2hzkB_	Alignment	not modelled	97.7	11	**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
113	c1xt8B_	Alignment	not modelled	97.7	13	**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
114	d2fyia1	Alignment	not modelled	97.7	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
115	c1mh3A_	Alignment	not modelled	97.6	15	**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
116	d1ryoa_	Alignment	not modelled	97.6	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
117	d1ursa_	Alignment	not modelled	97.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
118	c1ursA_	Alignment	not modelled	97.6	14	**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
119	c3d4cA_	Alignment	not modelled	97.6	16	**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)
120	c2xd3A_	Alignment	not modelled	97.5	18	**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.