Phyre2

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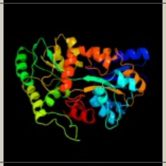
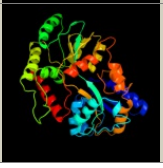
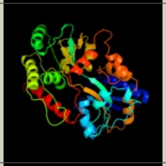
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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	15	**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	15	**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	c3py7A_	Alignment		100.0	15	**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
5	c3h4zC_	Alignment		100.0	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
6	c3dm0A_	Alignment		100.0	15	**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	c3o3uN_	Alignment		100.0	15	**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)
8	c1y4cA_	Alignment		100.0	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
9	c3d4cA_	Alignment		100.0	15	**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)
10	c3mp6A_	Alignment		100.0	15	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, saga- **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
11	c1r6zA_	Alignment		100.0	14	**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	c3osrA_	Alignment		100.0	16	**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
13	c1hsjA_	Alignment		100.0	15	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
14	c3c4mA_	Alignment		100.0	14	**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)
15	d1a99a_	Alignment		100.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
16	c2vgqA_	Alignment		100.0	14	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
17	c2nvuB_	Alignment		100.0	16	**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
18	c3oaiB_	Alignment		100.0	14	**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
19	d1elja_	Alignment		100.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	c3csgA_	Alignment		100.0	14	**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
21	d1pota_	Alignment	not modelled	100.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
22	c2zykA_	Alignment	not modelled	100.0	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**solute-binding protein; **PDBTitle:** crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
23	c2v84A_	Alignment	not modelled	100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**spermidine/putrescine abc transporter, periplasmic **PDBTitle:** crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum
24	c3ehuA_	Alignment	not modelled	100.0	15	**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
25	c3k02A_	Alignment	not modelled	100.0	12	**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.
26	c1mg1A_	Alignment	not modelled	100.0	14	**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
27	c2gh9A_	Alignment	not modelled	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

28	c2xd3A_	Alignment	not modelled	100.0	13	**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.
29	c3oo6A_	Alignment	not modelled	100.0	13	**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
30	c3uorB_	Alignment	not modelled	100.0	15	**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
31	d1eu8a_	Alignment	not modelled	100.0	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
32	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
33	c2fncA_	Alignment	not modelled	100.0	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose abc transporter, periplasmic maltose-binding **PDBTitle:** thermotoga maritima maltotriose binding protein bound with2 maltotriose.
34	c3iouB_	Alignment	not modelled	100.0	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
35	c1svxB_	Alignment	not modelled	100.0	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
36	d1laxa_	Alignment	not modelled	100.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
37	c3rpwA_	Alignment	not modelled	100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter; **PDBTitle:** the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
38	c1mh3A_	Alignment	not modelled	100.0	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
39	c2z8fB_	Alignment	not modelled	100.0	13	**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
40	c3qufB_	Alignment	not modelled	100.0	13	**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
41	c2b3fD_	Alignment	not modelled	100.0	11	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**glucose-binding protein; **PDBTitle:** thermus thermophilus glucose/galactose binding protein2 bound with galactose
42	c2uvgA_	Alignment	not modelled	100.0	13	**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
43	c1ursA_	Alignment	not modelled	100.0	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
44	d1ursa_	Alignment	not modelled	100.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
45	c2w7yA_	Alignment	not modelled	100.0	13	**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.
46	c2i58B_	Alignment	not modelled	100.0	15	**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	c3c9hB_	Alignment	not modelled	100.0	13	**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
48	c2qryD_	Alignment	not modelled	100.0	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**thiamine-binding periplasmic protein; **PDBTitle:** periplasmic thiamin binding protein
49	d3thia_	Alignment	not modelled	100.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
50	c3i3vC_	Alignment	not modelled	100.0	10	**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

51	d1y4ta_	Alignment	not modelled	100.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
52	d1q35a_	Alignment	not modelled	100.0	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
53	d1y9ua_	Alignment	not modelled	100.0	14	**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	c2pt1A_	Alignment	not modelled	100.0	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
56	d1y3na1	Alignment	not modelled	100.0	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
57	d1xc1a_	Alignment	not modelled	100.0	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
58	d1xvxa_	Alignment	not modelled	100.0	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
59	d1xvya_	Alignment	not modelled	100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
60	d1nnfa_	Alignment	not modelled	100.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
61	c2vozA_	Alignment	not modelled	100.0	11	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**periplasmic iron-binding protein; **PDBTitle:** apo futa2 from synechocystis pcc6803
62	c3ombA_	Alignment	not modelled	100.0	13	**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
63	d2onsa1	Alignment	not modelled	100.0	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
64	c3k6wA_	Alignment	not modelled	100.0	10	**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	c3cfzA_	Alignment	not modelled	99.9	10	**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
66	c3cfxA_	Alignment	not modelled	99.9	10	**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
67	d1atga_	Alignment	not modelled	99.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
68	d1sbpa_	Alignment	not modelled	99.9	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
69	c3cg3A_	Alignment	not modelled	99.9	9	**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
70	c3cg1A_	Alignment	not modelled	99.9	7	**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
71	d1amfa_	Alignment	not modelled	99.9	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
72	c2h5yC_	Alignment	not modelled	99.9	16	**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	99.9	13	**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	99.8	13	**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	99.7	11	**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	99.6	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 wolinella succinogenes
						PDB header:structural genomics, unknown function

77	c1twyG_	Alignment	not modelled	99.4	10	**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	99.4	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
79	d1pc3a_	Alignment	not modelled	98.0	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
80	d1ixha_	Alignment	not modelled	97.5	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
81	c3tqwA_	Alignment	not modelled	97.4	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
82	c3k2dA_	Alignment	not modelled	96.5	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
83	c3ir1F_	Alignment	not modelled	95.2	11	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
84	c3gxaA_	Alignment	not modelled	94.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
85	d1xs5a_	Alignment	not modelled	93.7	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c3n5lA_	Alignment	not modelled	93.3	8	**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
87	c3cvgC_	Alignment	not modelled	92.9	7	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**putative metal binding protein; **PDBTitle:** crystal structure of a periplasmic putative metal binding protein
88	d1p99a_	Alignment	not modelled	88.9	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
89	c1p99A_	Alignment	not modelled	88.9	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
90	c2de4B_	Alignment	not modelled	88.8	10	**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
91	c2dvzA_	Alignment	not modelled	84.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
92	c2rejA_	Alignment	not modelled	83.7	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
93	c3hn0A_	Alignment	not modelled	79.1	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
94	c3un6A_	Alignment	not modelled	74.4	7	**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
95	c3l6gA_	Alignment	not modelled	69.6	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
96	c3ix1A_	Alignment	not modelled	68.0	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
97	c2x26A_	Alignment	not modelled	64.7	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
98	c3ix1B_	Alignment	not modelled	64.4	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
99	c3e4rA_	Alignment	not modelled	64.2	13	**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
						PDB header:transport protein **Chain:** A: **PDB Molecule:**sulfonate abc transporter, periplasmic

100	c3uifA_	Alignment	not modelled	63.7	11	sulfonate-binding **PDBTitle:** crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
101	c2f78A_	Alignment	not modelled	61.6	7	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** benm effector binding domain with its effector benzoate
102	c2h9bB_	Alignment	not modelled	54.6	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
103	c2qpqC_	Alignment	not modelled	52.3	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
104	d2fyia1	Alignment	not modelled	49.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
105	c3ho7A_	Alignment	not modelled	49.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
106	c2f7cA_	Alignment	not modelled	49.1	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
107	c3qslA_	Alignment	not modelled	48.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
108	d2v3qa1	Alignment	not modelled	48.3	4	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
109	c3n6uA_	Alignment	not modelled	46.6	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
110	c2h9qC_	Alignment	not modelled	46.2	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** crystal structure of the effector binding domain of a catm2 variant (r156h)
111	c3jv9B_	Alignment	not modelled	46.2	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
112	c2ql3G_	Alignment	not modelled	43.7	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
113	c3tmgA_	Alignment	not modelled	40.3	11	**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
114	d1i6aa_	Alignment	not modelled	38.9	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
115	c2x7pA_	Alignment	not modelled	38.2	14	**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
116	d1ixca2	Alignment	not modelled	34.2	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
117	c3b50A_	Alignment	not modelled	33.7	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.
118	c2f5xC_	Alignment	not modelled	30.6	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
119	c2yuiA_	Alignment	not modelled	30.4	11	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**anamorsin; **PDBTitle:** solution structure of the n-terminal domain in human2 cytokine-induced apoptosis inhibitor anamorsin
120	c1jrjA_	Alignment	not modelled	27.7	8	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol