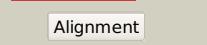
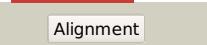
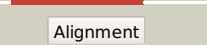
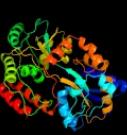
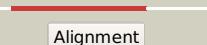
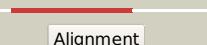
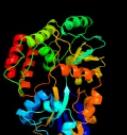
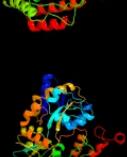
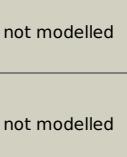


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	multi-dom
Date	Sun Sep 7 16:46:09 BST 2014
Unique Job ID	7563ce6b200bdd4e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4h1gA_			100.0	100	PDB header: motor protein Chain: A: PDB Molecule: maltose binding protein-cakar3 motor domain fusion protein; PDBTitle: structure of candida albicans kar3 motor domain fused to maltose-2 binding protein
2	c3f5fA_			100.0	99	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.
3	c3ob4A_			100.0	98	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
4	c3h4zC_			100.0	95	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
5	c3dm0A_			100.0	99	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
6	c4egcA_			100.0	88	PDB header: transcription/hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein, homeobox protein six1 PDBTitle: crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain
7	c4kegA_			100.0	91	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splnc1
8	c4bl9D_			100.0	100	PDB header: signaling protein Chain: D: PDB Molecule: maltose-binding periplasmic protein, suppressor of fused PDBTitle: crystal structure of full-length human suppressor of fused (2 sufu) mutant lacking a regulatory subdomain (crystal form i)
9	c3py7A_			100.0	98	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
10	c3o3uN_			100.0	100	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)
11	c1hsjA_			100.0	93	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure

12	c3mp6A	Alignment		100.0	99	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4
13	c3d4cA	Alignment		100.0	100	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)
14	c2nvuB	Alignment		100.0	75	PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c11a), a2 trapped ubiquitin-like protein activation complex
15	c4edqA	Alignment		100.0	100	PDB header: transport protein/contractile protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, myosin-binding protein PDBTitle: mbp-fusion protein of myosin-binding protein c residues 149-269
16	c3vd8A	Alignment		100.0	95	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, interferon-inducible PDBTitle: crystal structure of human aim2 pyd domain with mbp fusion
17	c4kv3A	Alignment		100.0	100	PDB header: protein transport Chain: A: PDB Molecule: chimera fusion protein of esx-1 secretion system protein PDBTitle: ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
18	c3c4mA	Alignment		100.0	96	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)
19	c4ozqA	Alignment		100.0	100	PDB header: motor protein Chain: A: PDB Molecule: chimera of maltose-binding periplasmic protein and kinesin PDBTitle: crystal structure of the mouse kif14 motor domain
20	c4logA	Alignment		100.0	99	PDB header: transcription Chain: A: PDB Molecule: maltose abc transporter periplasmic protein and nr2e3 PDBTitle: the crystal structure of the orphan nuclear receptor pnr ligand2 binding domain fused with mbp
21	c4pkqA	Alignment	not modelled	100.0	99	PDB header: dna binding protein Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, truncated PDBTitle: c-terminal domain of dna binding protein
22	c1r6zA	Alignment	not modelled	100.0	99	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)
23	c4ifpC	Alignment	not modelled	100.0	99	PDB header: immune system Chain: C: PDB Molecule: maltose-binding periplasmic protein, nacht, Irr and pyd PDBTitle: x-ray crystal structure of human nlrp1 card domain
24	c3oaiB	Alignment	not modelled	100.0	99	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
25	c4b3nA	Alignment	not modelled	100.0	97	PDB header: sugar binding protein/ligase Chain: A: PDB Molecule: maltose-binding periplasmic protein, tripartite PDBTitle: crystal structure of rhesus trim5alpha pry/spry domain
26	c3waiA	Alignment	not modelled	100.0	99	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of oligosaccharyltransferase (afaglb-1, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
27	c3osqA	Alignment	not modelled	100.0	100	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
28	c2vgqA	Alignment	not modelled	100.0	98	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
29	c4my2A	Alignment	not modelled	100.0	98	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, norrin fusion protein; PDBTitle: crystal structure of norrin in fusion with maltose binding protein
30	c1y4cA	Alignment	not modelled	100.0	98	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
31	c3csgA	Alignment	not modelled	100.0	98	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
32	c3osrA	Alignment	not modelled	100.0	100	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
33	c4exkA	Alignment	not modelled	100.0	98	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, uncharacterized PDBTitle: a chimera protein containing mbp fused to the c-terminal domain of the2 uncharacterized protein stm14_2015 from salmonella enterica
34	c3a3cA	Alignment	not modelled	100.0	95	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, mitochondrial PDBTitle: crystal structure of tim40/mia40 fusing mbp, c296s and c298s mutant
35	c3ehuA	Alignment	not modelled	100.0	98	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
36	c1mg1A	Alignment	not modelled	100.0	100	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
37	c4dxbB	Alignment	not modelled	100.0	90	PDB header: sugar binding protein, hydrolase Chain: B: PDB Molecule: maltose-binding periplasmic protein, beta-lactamase tem PDBTitle: 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group
38	c1mh3A	Alignment	not modelled	100.0	99	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	c1svxB	Alignment	not modelled	100.0	98	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
40	c3iouB	Alignment	not modelled	100.0	100	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
41	d1laxa	Alignment	not modelled	100.0	98	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
42	c2zykA	Alignment	not modelled	100.0	29	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
43	c4hs7A	Alignment	not modelled	100.0	28	PDB header: solute-binding protein Chain: A: PDB Molecule: bacterial extracellular solute-binding protein, putative; PDBTitle: 2.6 angstrom structure of the extracellular solute-binding protein2 from staphylococcus aureus in complex with peg.
44	c2fnca	Alignment	not modelled	100.0	33	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose.
45	d1elja	Alignment	not modelled	100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
46	c2gh9A	Alignment	not modelled	100.0	29	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
47	c2xd3A	Alignment	not modelled	100.0	28	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.
48	d1eu8a	Alignment	not modelled	100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
49	c3k02A	Alignment	not modelled	100.0	23	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.
50	c3uorB	Alignment	not modelled	100.0	22	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
51	c2z8fB	Alignment	not modelled	100.0	18	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
52	c4r2fA	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A; PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter achi_0255 from arthrobacter2 chlorophenolicus a6, target efi-510633, with bound laminaribiose
53	c1ursA	Alignment	not modelled	100.0	28	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
54	d1ursa	Alignment	not modelled	100.0	28	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	c4g68C	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: C; PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
56	c4g68A	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A; PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
57	c4aq4A	Alignment	not modelled	100.0	17	PDB header: diester-binding protein Chain: A; PDB Molecule: sn-glycerol-3-phosphate-binding periplasmic protein ugpb; PDBTitle: substrate bound sn-glycerol-3-phosphate binding periplasmic protein2 ugpb from escherichia coli
58	c4ovjA	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A; PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: extracellular solute-binding protein family 1 from alicyclobacillus2 acidocaldarius subsp. acidocaldarius dsm 446
59	c4mfiA	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A; PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugpb
60	c2uvga	Alignment	not modelled	100.0	17	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
61	c3oo6A	Alignment	not modelled	100.0	16	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	c4gqoC	Alignment	not modelled	100.0	18	PDB header: unknown function Chain: C; PDB Molecule: lmo0859 protein; PDBTitle: 2.1 angstrom resolution crystal structure of uncharacterized protein2 lmo0859 from listeria monocytogenes egd-e
63	c3zkkA	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A; PDB Molecule: xos binding protein; PDBTitle: structure of the xylo-oligosaccharide specific solute2 binding protein from bifidobacterium animalis subsp.3 lactis bl-04 in complex with xylotetraose
64	c4r2bB	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: B; PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter oant_3817 from ochrobactrum2 anthropi, target efi-510558, with bound glucose
65	c3vxbA	Alignment	not modelled	100.0	18	PDB header: sugar binding protein Chain: A; PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxle from streptomyces thermophilic opc-520
66	c3qufB	Alignment	not modelled	100.0	20	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
67	c2b3fD	Alignment	not modelled	100.0	18	PDB header: sugar binding protein Chain: D; PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein2 bound with galactose
68	c3i3vC	Alignment	not modelled	100.0	15	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
69	c2w7yA	Alignment	not modelled	100.0	16	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.
70	c2i58B	Alignment	not modelled	100.0	19	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
71	c4kvsA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: thiamine pyridinylase i;

71	c4rysh	Alignment	not modelled	100.0	14	PDBTitle: clostridium botulinum thiaminase i in complex with thiamin
72	d3thia	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	d1j1na	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	d1y3na1	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
75	c4hcwC	Alignment	not modelled	100.0	11	PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i
76	c3ttIB	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: B: PDB Molecule: polyamine transport protein; PDBTitle: crystal structure of apo-spue
77	c3ttkA	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: polyamine transport protein; PDBTitle: crystal structure of apo-spud
78	c4eqbA	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc superfamily atp binding cassette PDBTitle: 1.5 angstrom crystal structure of spermidine/putrescine abc2 transporter substrate-binding protein potd from streptococcus3 pneumoniae strain canada mdr_19a in complex with calcium and hepes
79	c2v84A	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc transporter, periplasmic PDBTitle: crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum
80	d1a99a	Alignment	not modelled	100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
81	d1pota	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
82	c4eq7B	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein (polyamine); PDBTitle: structure of atu4243-gaba receptor
83	c4i1dB	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110
84	c4gl0A	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A: PDB Molecule: lmo0810 protein; PDBTitle: putative spermidine/putrescine abc transporter from listeria2 monocytogenes
85	c3ombA	Alignment	not modelled	100.0	21	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
86	c3rpwA	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
87	c3c9hB	Alignment	not modelled	100.0	15	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
88	c4edpA	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein; PDBTitle: 1.85 angstrom resolution crystal structure of an abc transporter from2 clostridium perfringens atcc 13124
89	d1y4ta	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
90	c3pu5A	Alignment	not modelled	100.0	16	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
91	c2pt1A	Alignment	not modelled	100.0	17	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synchocystis pcc 6803
92	d1q35a	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
93	c4eloD	Alignment	not modelled	100.0	18	PDB header: metal transport Chain: D: PDB Molecule: iron abc transporter, periplasmic iron-binding protein; PDBTitle: ferric binding protein in apo form 1
94	d1xvxa	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
95	d1xc1a	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
96	c2voza	Alignment	not modelled	100.0	16	PDB header: metal-binding protein Chain: A: PDB Molecule: periplasmic iron-binding protein; PDBTitle: apo futa2 from synchocystis pcc6803

97	d1nnfa_	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
98	d1y9ua_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
99	c2qryD_	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
100	d1xvya_	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
101	d2onsa1	Alignment	not modelled	99.9	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
102	c3cfxA_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetylivorans periplasmic binding protein2 moda/wtpa with bound tungstate
103	c3cfzA_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding protein moda/wtpa with bound tungstate
104	c3k6wA_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosaerica acetivorans
105	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
106	c3cg3A_	Alignment	not modelled	99.8	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
107	d1sbpa_	Alignment	not modelled	99.7	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
108	d1atga_	Alignment	not modelled	99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
109	d1lamfa_	Alignment	not modelled	99.6	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
110	c2h5yC_	Alignment	not modelled	99.6	18	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
111	c4kd5A_	Alignment	not modelled	99.5	18	PDB header: transport protein Chain: A: PDB Molecule: abc-type transport system, molybdenum-specific PDBTitle: substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
112	c4jwoA_	Alignment	not modelled	99.4	14	PDB header: phosphate binding protein Chain: A: PDB Molecule: phosphate binding protein; PDBTitle: the crystal structure of a possible phosphate binding protein from2 planctomycetes limnophilus dsm 3776
113	c3fj7A_	Alignment	not modelled	99.4	17	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
114	c4jb7A_	Alignment	not modelled	99.3	13	PDB header: cell invasion Chain: A: PDB Molecule: accessory colonization factor acfc; PDBTitle: 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid
115	c3lr1A_	Alignment	not modelled	99.3	15	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
116	c3mugB_	Alignment	not modelled	99.0	18	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 rimb 2210633
117	c3kn3C_	Alignment	not modelled	99.0	11	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
118	c4gd5B_	Alignment	not modelled	98.7	18	PDB header: transport protein Chain: B: PDB Molecule: phosphate abc transporter, phosphate-binding protein; PDBTitle: x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
119	c1twyG_	Alignment	not modelled	98.7	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
120	d1twya_	Alignment	not modelled	98.7	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like