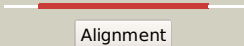

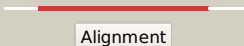

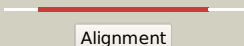







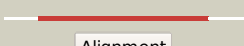




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0934_(pstS1)_1042119_1043243
Date	Fri Jul 26 01:50:53 BST 2019
Unique Job ID	d4dee729ef9c28de

Detailed template information

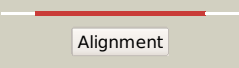
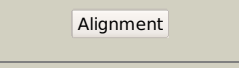
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pc3a_	 Alignment		100.0	100	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	d1ixha_	 Alignment		100.0	32	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c5wnnB_	 Alignment		100.0	31	PDB header: phosphate binding protein Chain: B: PDB Molecule: phosphate-binding protein pstS; PDBTitle: crystal structure of phosphate-binding protein pstS protein from2 burkholderia pseudomallei
4	c5i84H_	 Alignment		100.0	32	PDB header: transport protein Chain: H: PDB Molecule: phosphate-binding protein pstS; PDBTitle: structure of the xanthomonas citri phosphate-binding protein phox
5	c4lvqA_	 Alignment		100.0	28	PDB header: transport protein Chain: A: PDB Molecule: phosphate-binding protein pstS 3; PDBTitle: crystal structure of the m. tuberculosis phosphate binding protein2 pstS3
6	d2v3qa1	 Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	c5jk4A_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: phosphate-binding protein from stentrophomonas maltophilia.
8	c4jwoA_	 Alignment		100.0	15	PDB header: phosphate binding protein Chain: A: PDB Molecule: phosphate binding protein; PDBTitle: the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776
9	c4ombB_	 Alignment		100.0	18	PDB header: transport protein Chain: B: PDB Molecule: phosphate binding protein; PDBTitle: phosphate binding protein
10	c4ry1A_	 Alignment		99.9	10	PDB header: transport protein Chain: A: PDB Molecule: periplasmic solute binding protein; PDBTitle: crystal structure of periplasmic solute binding protein eca2210 from2 pectobacterium atrosepticum scri1043, target efi-510858
11	c4r6kA_	 Alignment		99.9	10	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of abc transporter substrate-binding protein yeso2 from bacillus subtilis, target efi-510761, an open conformation

12	c4aq4A_	Alignment		99.9	17	PDB header: diester-binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate-binding periplasmic protein ugbp; PDBTitle: substrate bound sn-glycerol-3-phosphate binding periplasmic protein2 ugbp from escherichia coli
13	c4ovjA_	Alignment		99.9	12	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
14	c3k02A_	Alignment		99.9	16	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.
15	c2uvgA_	Alignment		99.9	11	PDB header: sugar-binding protein Chain: A: PDB Molecule: abc type periplasmic sugar-binding protein; PDBTitle: structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
16	c4rk2B_	Alignment		99.9	9	PDB header: transport protein Chain: B: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of sugar transporter rhe_pf00321 from rhizobium2 etli, target efi-510806, an open conformation
17	c5mkbF_	Alignment		99.9	12	PDB header: sugar binding protein Chain: F: PDB Molecule: male1; PDBTitle: maltodextrin binding protein male1 from l. casei bl23 without ligand
18	c3uorB_	Alignment		99.9	8	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
19	c4gqoC_	Alignment		99.9	12	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
20	c4g68A_	Alignment		99.9	10	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
21	c4mfiA_	Alignment	not modelled	99.9	13	PDB header: sugar binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugbp
22	c6dtqC_	Alignment	not modelled	99.9	9	PDB header: sugar binding protein Chain: C: PDB Molecule: maltose-binding protein male3; PDBTitle: maltose bound t. maritima male3
23	c2w7yA_	Alignment	not modelled	99.9	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.
24	d1eu8a_	Alignment	not modelled	99.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
25	c4ecfA_	Alignment	not modelled	99.9	22	PDB header: phosphate-binding protein Chain: A: PDB Molecule: abc-type phosphate transport system, periplasmic component; PDBTitle: crystal structure of an abc-type phosphate transport system,2 periplasmic component (lvis_0633) from lactobacillus brevis atcc 3673 at 1.55 a resolution
26	c4g68C_	Alignment	not modelled	99.9	10	PDB header: transport protein Chain: C: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
27	c5k2xA_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter permease; PDBTitle: crystal structure of m. tuberculosis uspc (tetragonal crystal form)
28	c4r9fA_	Alignment	not modelled	99.9	13	PDB header: sugar binding protein Chain: A: PDB Molecule: mbp1; PDBTitle: cpmnbp1 with mannobiose bound

29	c5f7vA_	Alignment	not modelled	99.9	10	PDB header: cycloalternan binding protein Chain: A: PDB Molecule: lmo0181 protein; PDBTitle: abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloalternan
30	c4exlD_	Alignment	not modelled	99.9	23	PDB header: transport protein Chain: D: PDB Molecule: phosphate-binding protein psts 1; PDBTitle: crystal structure of phosphate abc transporter, periplasmic phosphate-2 binding protein psts 1 (ppb1) from streptococcus pneumoniae canada3 mdr_19a
31	c5k2yB_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: B: PDB Molecule: probable periplasmic sugar-binding lipoprotein uspc; PDBTitle: crystal structure of m. tuberculosis uspc (monoclinic crystal form)
32	c4r6hA_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: solute binding protein msme; PDBTitle: crystal structure of putative binding protein msme from bacillus2 subtilis subsp. subtilis str. 168, target efi-510764, an open3 conformation
33	c5ixpA_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of extracellular solute-binding protein family 1
34	c6fflA_	Alignment	not modelled	99.9	7	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin transport permease homologue; PDBTitle: maltose/maltodextrin-binding domain male from bdellovibrio2 bacteriovorus bound to maltotriose
35	c4ryaA_	Alignment	not modelled	99.9	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate binding protein (sorbitol); PDBTitle: crystal structure of abc transporter solute binding protein avi_35672 from agrobacterium vitis s4, target efi-510645, with bound d-mannitol
36	c4ua8A_	Alignment	not modelled	99.9	10	PDB header: transport protein Chain: A: PDB Molecule: carbohydrate abc transporter substrate-binding protein, PDBTitle: eur_01830 (maltotriose-binding protein) complexed with maltotriose
37	c3qufB_	Alignment	not modelled	99.9	9	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
38	c4n13A_	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: A: PDB Molecule: phosphate abc transporter, periplasmic phosphate-binding PDBTitle: crystal structure of psts (bb_0215) from borrelia burgdorferi
39	c3woaA_	Alignment	not modelled	99.9	12	PDB header: dna binding protein, sugar binding prote Chain: A: PDB Molecule: repressor protein ci, maltose-binding periplasmic protein; PDBTitle: crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
40	c4r2fA_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter achl_0255 from arthrobacter2 chlorophenicus a6, target efi-510633, with bound laminaribiose
41	c2gh9A_	Alignment	not modelled	99.9	13	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
42	c5yseB_	Alignment	not modelled	99.9	9	PDB header: sugar binding protein Chain: B: PDB Molecule: lin1841 protein; PDBTitle: crystal structure of beta-1,2-glucooligosaccharide binding protein in2 complex with sophorotetraose
43	c5iaiA_	Alignment	not modelled	99.9	10	PDB header: solute-binding protein Chain: A: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of abc transporter solute binding protein arad_98872 from agrobacterium radiobacter k84, target efi-510945 in complex with3 ribitol
44	d2onsa1	Alignment	not modelled	99.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
45	c4rk9B_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: B: PDB Molecule: carbohydrate abc transporter substrate-binding protein PDBTitle: crystal structure of sugar transporter bl01359 from bacillus2 licheniformis, target efi-510856, in complex with stachyose
46	c4gd5B_	Alignment	not modelled	99.9	19	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
47	c5tu0A_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: lmo2125 protein; PDBTitle: 1.9 angstrom resolution crystal structure of maltose-binding2 periplasmic protein male from listeria monocytogenes in complex with3 maltose
48	c6fuvA_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: solute binding protein, blmnbp1 in complex with PDBTitle: structure of a manno-oligosaccharide specific solute binding protein,2 blmnbp2 from bifidobacterium animalis subsp. lactis atcc 27673 in3 complex with mannose
49	c4hcwC_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i

50	c5ci5B_	Alignment	not modelled	99.9	10	PDB header: sugar binding protein Chain: B: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of an abc transporter solute binding protein from2 thermotoga lettingae tmo (tlet_1705, target efi-510544) bound with3 alpha-d-tagatose
51	c3zkkA_	Alignment	not modelled	99.8	9	PDB header: transport protein Chain: A: PDB Molecule: xos binding protein; PDBTitle: structure of the xylo-oligosaccharide specific solute binding protein2 from bifidobacterium animalis subsp. lactis bl-04 in complex with3 xylo-tetraose
52	c5dvjA_	Alignment	not modelled	99.8	12	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc sugar transporter; PDBTitle: crystal structure of galactose complexed periplasmic glucose binding2 protein (ppgpb) from p. putida csv86
53	d1ursa_	Alignment	not modelled	99.8	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	c1ursaA_	Alignment	not modelled	99.8	12	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
55	c2b3fD_	Alignment	not modelled	99.8	12	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein bound with2 galactose
56	c4r2bB_	Alignment	not modelled	99.8	11	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-510528, with bound glucose
57	c2zykA_	Alignment	not modelled	99.8	10	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
58	c2xd3A_	Alignment	not modelled	99.8	12	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.
59	c4wrnB_	Alignment	not modelled	99.8	14	PDB header: structural protein Chain: B: PDB Molecule: maltose-binding periplasmic protein, uromodulin; PDBTitle: crystal structure of the polymerization region of human2 uromodulin/tamm-horsfall protein
60	d1twya_	Alignment	not modelled	99.8	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
61	c1twyG_	Alignment	not modelled	99.8	20	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
62	c4kysA_	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: thiamine pyridinylase i; PDBTitle: clostridium botulinum thiaminase i in complex with thiamin
63	c4hs7A_	Alignment	not modelled	99.8	7	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.
64	c5k94B_	Alignment	not modelled	99.8	12	PDB header: protein transport Chain: B: PDB Molecule: maltose-binding periplasmic protein, protein translocase PDBTitle: deletion-insertion chimera of mbp with the preprotein cross-linking2 domain of the seca atpase
65	c6h0hB_	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: B: PDB Molecule: probable solute binding protein of abc transporter system PDBTitle: the abc transporter associated binding protein from b. animalis subsp.2 lactis bl-04 in complex with beta-1,6-galactobiose
66	c3c9hB_	Alignment	not modelled	99.8	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
67	c2i58B_	Alignment	not modelled	99.8	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
68	c5i04A_	Alignment	not modelled	99.8	14	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, endoglin; PDBTitle: crystal structure of the orphan region of human endoglin/cd105
69	d1elja_	Alignment	not modelled	99.8	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	c3k6wA_	Alignment	not modelled	99.8	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
71	c2z8fB_	Alignment	not modelled	99.8	11	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 PDB header: sugar binding protein

72	c3oo6A	Alignment	not modelled	99.8	14	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
73	c5hzvA	Alignment	not modelled	99.8	12	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,endoglin; PDBTitle: crystal structure of the zona pellucida module of human endoglin/cd105
74	c3ob4A	Alignment	not modelled	99.8	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
75	c3f5fA	Alignment	not modelled	99.8	13	PDB header: transport, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, heparan sulfate 2-o- PDBTitle: crystal structure of heparan sulfate 2-o-sulfotransferase from gallus2 gallus as a maltose binding protein fusion.
76	c3vxbA	Alignment	not modelled	99.8	10	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxl from streptomyces thermoviolaceus opc-520
77	c5eduB	Alignment	not modelled	99.8	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: maltose-binding periplasmic protein, histone deacetylase 6 PDBTitle: crystal structure of human histone deacetylase 6 catalytic domain 2 in2 complex with trichostatin a
78	c5azaA	Alignment	not modelled	99.8	14	PDB header: sugar binding protein, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein,oligosaccharyl PDBTitle: crystal structure of mbp-saglb fusion protein with a 20-residue spacer2 in the connector helix
79	c3osqA	Alignment	not modelled	99.8	17	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
80	c4qvhA	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, 4'-phosphopantetheinyl PDBTitle: crystal structure of the essential mycobacterium tuberculosis2 phosphopantetheinyl transferase pptt, solved as a fusion protein with3 maltose binding protein
81	c5t0aB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: maltose binding protein - heparan sulfate 6-o- PDBTitle: crystal structure of heparan sulfate 6-o-sulfotransferase with bound2 pap and heptasaccharide substrate
82	c4h1gA	Alignment	not modelled	99.8	13	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
83	c6dd5B	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: mmb-1 cas6 fused to maltose binding protein,crispr- PDBTitle: crystal structure of the cas6 domain of marinomonas mediterranea mmb-12 cas6-rt-cas1 fusion protein
84	c3cfxA	Alignment	not modelled	99.8	11	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
85	c4tsmC	Alignment	not modelled	99.8	15	PDB header: cell adhesion Chain: C: PDB Molecule: maltose-binding protein, pilin chimera; PDBTitle: mbp-fusion protein of pila1 from c. difficile r20291 residues 26-166
86	c6anvA	Alignment	not modelled	99.8	13	PDB header: immune system Chain: A: PDB Molecule: anti-crispr protein acrf1 fused with c-terminal mbp tag; PDBTitle: crystal structure of anti-crispr protein acrf1
87	c4egcA	Alignment	not modelled	99.8	12	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
88	c5gxtA	Alignment	not modelled	99.8	11	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pigg
89	c3i3vC	Alignment	not modelled	99.8	13	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
90	c4ozqA	Alignment	not modelled	99.8	13	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
91	c5jqeA	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein,caspase-8 PDBTitle: crystal structure of caspase8 tded
92	c4xa2A	Alignment	not modelled	99.8	12	PDB header: cell adhesion Chain: A: PDB Molecule: maltose-binding periplasmic protein,mbp-pila: c; PDBTitle: structure of the major type iv pilin of acinetobacter baumannii
93	c2fncA	Alignment	not modelled	99.8	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.

94	c4edqA		Alignment	not modelled	99.8	14	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
95	c3d4cA		Alignment	not modelled	99.8	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)
96	c6aeoA		Alignment	not modelled	99.8	13	PDB header: protein transport Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,tssl; PDBTitle: tssl periplasmic domain
97	c1y4cA		Alignment	not modelled	99.8	14	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
98	c5fsgA		Alignment	not modelled	99.8	14	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, hantavirus PDBTitle: structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design
99	c3o3uN		Alignment	not modelled	99.8	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)
100	c3osrA		Alignment	not modelled	99.8	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
101	c4kv3A		Alignment	not modelled	99.8	12	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
102	c5ii5A		Alignment	not modelled	99.8	13	PDB header: cell adhesion Chain: A: PDB Molecule: maltose-binding periplasmic protein,vitelline envelope PDBTitle: crystal structure of red abalone verl repeat 1 at 1.8 a resolution
103	c3mp6A		Alignment	not modelled	99.8	14	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,linker,saga-associated PDBTitle: complex structure of sgf29 and dimethylated h3k4
104	c5dfmB		Alignment	not modelled	99.8	14	PDB header: nuclear protein Chain: B: PDB Molecule: maltose-binding periplasmic protein,telomerase-associated PDBTitle: structure of tetrahymena telomerase p19 fused to mbp
105	c4bI9D		Alignment	not modelled	99.8	14	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 (sufu)2 mutant lacking a regulatory subdomain (crystal form i)
106	c4kegA		Alignment	not modelled	99.8	12	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1
107	c5wvmA		Alignment	not modelled	99.8	13	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,two-component system PDBTitle: crystal structure of baes cocrystallized with 2 mm indole
108	c4r73B		Alignment	not modelled	99.8	11	PDB header: transport protein Chain: B: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of the periplasmic binding protein afua from actinobacillus2 pleuropneumoniae (endogenous glucose-6-phosphate and mannose-6-3 phosphate bound)
109	c6g7qB		Alignment	not modelled	99.8	12	PDB header: metal binding protein Chain: B: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: trichodesmium tery_3377 (idia) (futa) in complex with iron and citrate2 ligands.
110	c6apxA		Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein,dual specificity PDBTitle: crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the antibody ysx1
111	c4edpA		Alignment	not modelled	99.8	9	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
112	c5tibA		Alignment	not modelled	99.8	12	PDB header: lipid binding protein Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein,gasdermin- PDBTitle: gasdermin-b c-terminal domain containing the polymorphism residues2 arg299:ser306 fused to maltose binding protein
113	c3cfzA		Alignment	not modelled	99.8	10	PDB header: transport protein Chain: A: PDB Molecule: supf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
114	d3thia		Alignment	not modelled	99.8	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
							PDB header: viral protein

115	c3py7A_	Alignment	not modelled	99.8	12	Chain: A; PDB Molecule: maltose-binding periplasmic protein, paxillin Id1, protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with Id1 motif of paxillin at 2.3a resolution
116	c3dm0A_	Alignment	not modelled	99.8	14	PDB header: sugar binding protein, signaling protein Chain: A; PDB Molecule: maltose-binding periplasmic protein fused with rack1; PDBTitle: maltose binding protein fusion with rack1 from a. thaliana
117	c4logA_	Alignment	not modelled	99.8	15	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
118	c4rwgC_	Alignment	not modelled	99.8	15	PDB header: membrane protein/hormone Chain: C; PDB Molecule: maltose-binding periplasmic protein, receptor activity- PDBTitle: crystal structure of the clr:ramp1 extracellular domain heterodimer2 with bound high affinity cgrp analog
119	c5yevB_	Alignment	not modelled	99.8	11	PDB header: apoptosis Chain: B; PDB Molecule: tnfrsf25 death domain; PDBTitle: murine dr3 death domain
120	c3wajA_	Alignment	not modelled	99.8	13	PDB header: transferase, transport protein Chain: A; PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of 2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion