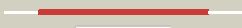









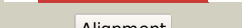

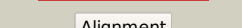

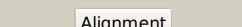

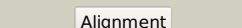

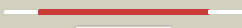





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0932c_(pstS2)_103940_1041052
Date	Fri Jul 26 01:50:52 BST 2019
Unique Job ID	2f7e085cfbd1d329

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4lvqA_	 Alignment		100.0	66	PDB header: transport protein Chain: A; PDB Molecule: phosphate-binding protein psts 3; PDBTitle: crystal structure of the m. tuberculosis phosphate binding protein2 psts3
2	d1ixha_	 Alignment		100.0	30	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c5wnnB_	 Alignment		100.0	30	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	d1pc3a_	 Alignment		100.0	29	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
5	c5i84H_	 Alignment		100.0	28	PDB header: transport protein Chain: H; PDB Molecule: phosphate-binding protein psts; PDBTitle: structure of the xanthomonas citri phosphate-binding protein phox
6	d2v3qa1	 Alignment		100.0	25	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	c5jk4A_	 Alignment		100.0	24	PDB header: transport protein Chain: A; PDB Molecule: alkaline phosphatase; PDBTitle: phosphate-binding protein from stentrophomonas maltophilia.
8	c4ombB_	 Alignment		100.0	18	PDB header: transport protein Chain: B; PDB Molecule: phosphate binding protein; PDBTitle: phosphate binding protein
9	c4jwoA_	 Alignment		100.0	18	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
10	c4n13A_	 Alignment		99.9	21	PDB header: transport protein Chain: A; PDB Molecule: phosphate abc transporter, periplasmic phosphate-binding PDBTitle: crystal structure of psts (bb_0215) from borrelia burgdorferi
11	c4gd5B_	 Alignment		99.9	22	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







12	c4ecfA_	Alignment		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 (Ivis_0633) from lactobacillus brevis atcc 3673 at 1.55 a resolution
13	d1twya_	Alignment		99.9	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
14	c1twyG_	Alignment		99.9	19	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
15	c4exlD_	Alignment		99.9	22	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
16	c4r6kA_	Alignment		99.9	8	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
17	c4ry1A_	Alignment		99.9	11	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
18	c4rk2B_	Alignment		99.9	11	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
19	c2uvqA_	Alignment		99.9	10	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
20	c4ovjA_	Alignment		99.9	11	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
21	c5f7vA_	Alignment	not modelled	99.8	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
22	c4aq4A_	Alignment	not modelled	99.8	12	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
23	d2onsa1	Alignment	not modelled	99.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
24	c3k6wA_	Alignment	not modelled	99.8	12	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
25	c4gqoC_	Alignment	not modelled	99.8	10	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
26	c3cfxA_	Alignment	not modelled	99.8	12	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
27	c3uorB_	Alignment	not modelled	99.8	11	PDB header: sugar binding protein Chain: B: PDB Molecule: abc transporter sugar binding protein; PDBTitle: the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
28	c4g68A_	Alignment	not modelled	99.8	6	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by

						the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
29	c4mfiA	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugpb
30	c3qufB	Alignment	not modelled	99.8	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
31	c5mkbF	Alignment	not modelled	99.8	11	PDB header: sugar binding protein Chain: F: PDB Molecule: male1; PDBTitle: maltodextrin binding protein male1 from l. casei bl23 without ligand
32	c6ffiA	Alignment	not modelled	99.8	9	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin transport permease homologue; PDBTitle: maltose/maltodextrin-binding domain male from bdellovibrio2 bacteriovirus bound to maltotriose
33	c4g68C	Alignment	not modelled	99.8	6	PDB header: transport protein Chain: C: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
34	c4ryaA	Alignment	not modelled	99.8	14	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
35	c3cfzA	Alignment	not modelled	99.8	12	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
36	d1eu8a	Alignment	not modelled	99.8	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
37	c3k02A	Alignment	not modelled	99.8	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.
38	c4kd5A	Alignment	not modelled	99.8	14	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
39	c4r6hA	Alignment	not modelled	99.8	10	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
40	c2w7yA	Alignment	not modelled	99.8	10	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.
41	c3woaA	Alignment	not modelled	99.8	11	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
42	c4r2fA	Alignment	not modelled	99.8	11	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of sugar transporter achl_0255 from arthrobacter2 chlorophenolicus a6, target efi-510633, with bound laminaribiose
43	c4ua8A	Alignment	not modelled	99.8	10	PDB header: transport protein Chain: A: PDB Molecule: carbohydrate abc transporter substrate-binding protein, PDBTitle: eur_01830 (maltotriose-binding protein) complexed with maltotriose
44	c2xd3A	Alignment	not modelled	99.8	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.
45	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 xylotetraose
46	c5iaiA	Alignment	not modelled	99.8	12	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
47	c5tu0A	Alignment	not modelled	99.8	8	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	c4r9fA	Alignment	not modelled	99.8	11	PDB header: sugar binding protein Chain: A: PDB Molecule: mbp1; PDBTitle: cpmnbp1 with mannobiose bound
49	c5yseB	Alignment	not modelled	99.8	11	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
50	c6dtqC	Alianment	not modelled	99.8	12	PDB header: sugar binding protein Chain: C: PDB Molecule: maltose-binding protein male3;

						PDBTitle: maltose bound t. maritima male3
51	c6fuvA	Alignment	not modelled	99.8	12	PDB header: transport protein Chain: A: PDB Molecule: solute binding protein, blmbp1 in complex with PDBTitle: structure of a manno-oligosaccharide specific solute binding protein,2 blmbp2 from bifidobacterium animalis subsp. lactis atcc 27673 in3 complex with mannitolose
52	c5dviA	Alignment	not modelled	99.8	13	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 (ppgbp) from p. putida csv86
53	c5k2xA	Alignment	not modelled	99.8	13	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter permease; PDBTitle: crystal structure of m. tuberculosis uspc (tetragonal crystal form)
54	c2z8fB	Alignment	not modelled	99.7	9	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
55	c4wrnB	Alignment	not modelled	99.7	9	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
56	c4h1xA	Alignment	not modelled	99.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphate-binding protein pst5 2; PDBTitle: crystal structure of a phosphate abc transporter, phosphate-binding2 protein (sp_2084) from streptococcus pneumoniae tigr4 at 1.77 a3 resolution
57	c3vxbA	Alignment	not modelled	99.7	11	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxlx from streptomyces thermoviolaceus opc-520
58	c5hzvA	Alignment	not modelled	99.7	9	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
59	c6anvA	Alignment	not modelled	99.7	9	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
60	c5k2yB	Alignment	not modelled	99.7	11	PDB header: transport protein Chain: B: PDB Molecule: probable periplasmic sugar-binding lipoprotein uspc; PDBTitle: crystal structure of m. tuberculosis uspc (monoclinic crystal form)
61	c5ixpA	Alignment	not modelled	99.7	9	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of extracellular solute-binding protein family 1
62	c2b3fD	Alignment	not modelled	99.7	11	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein bound with2 galactose
63	c5ci5B	Alignment	not modelled	99.7	8	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
64	c1y4cA	Alignment	not modelled	99.7	9	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
65	c5i04A	Alignment	not modelled	99.7	9	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,endoglin; PDBTitle: crystal structure of the orphan region of human endoglin/cd105
66	c5k94B	Alignment	not modelled	99.7	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
67	c4rk9B	Alignment	not modelled	99.7	10	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
68	c6h0hB	Alignment	not modelled	99.7	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
69	c6ddnB	Alignment	not modelled	99.7	16	PDB header: transport protein Chain: B: PDB Molecule: probable sulfate-binding lipoprotein subi; PDBTitle: the sulfate-binding protein subi from mycobacterium tuberculosis h37rv
70	c4ozqA	Alignment	not modelled	99.7	9	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
71	c4hs7A	Alignment	not modelled	99.7	11	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. PDB header: metal binding protein

72	c3cvgD	Alignment	not modelled	99.7	13	Chain: D: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
73	d1ursa	Alignment	not modelled	99.7	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c1ursA	Alignment	not modelled	99.7	11	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
75	c3ob4A	Alignment	not modelled	99.7	11	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
76	c4egcA	Alignment	not modelled	99.7	9	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
77	c4h1gA	Alignment	not modelled	99.7	11	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
78	c4kegA	Alignment	not modelled	99.7	9	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1
79	c3o3uN	Alignment	not modelled	99.7	9	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)
80	c4tsmC	Alignment	not modelled	99.7	9	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
81	c2i58B	Alignment	not modelled	99.7	7	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
82	c5gxtA	Alignment	not modelled	99.7	9	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pigg
83	c3osrA	Alignment	not modelled	99.7	9	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
84	c4r2bB	Alignment	not modelled	99.7	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
85	c5jqeA	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein,caspase-8 PDBTitle: crystal structure of caspase8 tded
86	c2gh9A	Alignment	not modelled	99.7	12	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
87	c4kysA	Alignment	not modelled	99.7	8	PDB header: transferase Chain: A: PDB Molecule: thiamine pyridinylase i; PDBTitle: clostridium botulinum thiaminase i in complex with thiamin
88	c3oo6A	Alignment	not modelled	99.7	12	PDB header: sugar binding protein Chain: A: PDB Molecule: abc transporter binding protein acbh; PDBTitle: crystal structures and biochemical characterization of the bacterial2 solute receptor acbh reveal an unprecedented exclusive substrate3 preference for b-d-galactopyranose
89	c5azaA	Alignment	not modelled	99.7	9	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
90	c2zykA	Alignment	not modelled	99.7	9	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
91	c6g7qB	Alignment	not modelled	99.7	7	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.
92	c2fncA	Alignment	not modelled	99.7	8	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose.
93	c4hwcC	Alignment	not modelled	99.7	10	PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i
94	c3d4cA	Alignment	not modelled	99.7	9	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)

95	c6dd5B	 Alignment	not modelled	99.7	9	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
96	c3f5fA	 Alignment	not modelled	99.7	10	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.
97	c4r73B	 Alignment	not modelled	99.7	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)
98	c4qvhA	 Alignment	not modelled	99.7	10	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
99	c4xa2A	 Alignment	not modelled	99.7	10	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
100	c6aeoA	 Alignment	not modelled	99.7	10	PDB header: protein transport Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,tssl; PDBTitle: tssl periplasmic domain
101	c4kv3A	 Alignment	not modelled	99.7	10	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	c4dxbB	 Alignment	not modelled	99.7	9	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
103	c4my2A	 Alignment	not modelled	99.7	10	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
104	c5tibA	 Alignment	not modelled	99.7	10	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
105	c3ehuA	 Alignment	not modelled	99.7	10	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
106	c3py7A	 Alignment	not modelled	99.7	9	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
107	c5b3zB	 Alignment	not modelled	99.7	10	PDB header: isomerase,sugar binding protein Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1, PDBTitle: crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein
108	c2pt1A	 Alignment	not modelled	99.7	10	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
109	c4logA	 Alignment	not modelled	99.7	10	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
110	c5ii5A	 Alignment	not modelled	99.7	9	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
111	c2nvuB	 Alignment	not modelled	99.7	10	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
112	c4exkA	 Alignment	not modelled	99.7	9	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
113	c3mp6A	 Alignment	not modelled	99.7	10	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,linker,saga-associated PDBTitle: complex structure of sgf29 and dimethylated h3k4
114	c5jonA	 Alignment	not modelled	99.7	9	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd

115	c3dm0A_	 Alignment	not modelled	99.7	9	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
116	c3osqA_	 Alignment	not modelled	99.7	19	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
117	c3waiA_	 Alignment	not modelled	99.7	12	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
118	c5y2gA_	 Alignment	not modelled	99.7	11	PDB header: toxin Chain: A: PDB Molecule: maltose-binding periplasmic protein,protein b; PDBTitle: structure of mbp tagged gbs camp
119	c1r6zA_	 Alignment	not modelled	99.7	10	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)
120	c1hsjA_	 Alignment	not modelled	99.7	9	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus accessory PDBTitle: sarr mbp fusion structure