



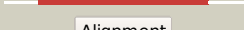

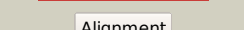

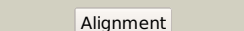





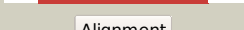

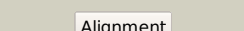

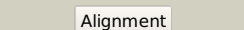





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2833c_ugpB_3139184_3140494
Date	Wed Aug 7 12:50:50 BST 2019
Unique Job ID	786f91a597c903e4

Detailed template information

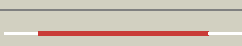
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4mfiA_	 Alignment		100.0	100	PDB header: sugar binding protein Chain: A: PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugpb
2	c4aq4A_	 Alignment		100.0	23	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
3	c6dtqC_	 Alignment		100.0	22	PDB header: sugar binding protein Chain: C: PDB Molecule: maltose-binding protein male3; PDBTitle: maltose bound t. maritima male3
4	c3uorB_	 Alignment		100.0	19	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
5	d1eu8a_	 Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
6	c3osqA_	 Alignment		100.0	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
7	c4r6kA_	 Alignment		100.0	12	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
8	c3k02A_	 Alignment		100.0	20	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.
9	c5azaA_	 Alignment		100.0	16	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
10	c3h4zC_	 Alignment		100.0	16	PDB header: allergen Chain: C: PDB Molecule: maltose-binding periplasmic protein fused with allergen PDBTitle: crystal structure of an mbp-der p 7 fusion protein
11	c6aeoA_	 Alignment		100.0	15	PDB header: protein transport Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,tssl; PDBTitle: tssl periplasmic domain

12	c4qqoC_	Alignment		100.0	16	PDB header: unknown function Chain: C: PDB Molecule: lmo0859 protein; PDBTitle: 2.1 angstrom resolution crystal structure of uncharacterized protein2 lmo0859 from listeria monocytogenes ege
13	c4ry1A_	Alignment		100.0	17	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
14	c4wrnB_	Alignment		100.0	16	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
15	c5i04A_	Alignment		100.0	16	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,endoglin; PDBTitle: crystal structure of the orphan region of human endoglin/cd105
16	c2uvgA_	Alignment		100.0	15	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
17	c4h1gA_	Alignment		100.0	17	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
18	c5gxtA_	Alignment		100.0	16	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pigg
19	c5hzvA_	Alignment		100.0	16	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
20	c5k2xA_	Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter permease; PDBTitle: crystal structure of m. tuberculosis uspc (tetragonal crystal form)
21	c5t0aB_	Alignment	not modelled	100.0	17	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
22	c6dd5B_	Alignment	not modelled	100.0	16	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
23	c3ob4A_	Alignment	not modelled	100.0	17	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
24	c4xa2A_	Alignment	not modelled	100.0	16	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
25	c5fsgA_	Alignment	not modelled	100.0	16	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
26	c4kegA_	Alignment	not modelled	100.0	17	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1
27	c4oviA_	Alignment	not modelled	100.0	13	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

28	c3f5fA		Alignment	not modelled	100.0	17	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.
29	c4ryaA		Alignment	not modelled	100.0	16	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
30	c4egcA		Alignment	not modelled	100.0	17	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
31	c5eduB		Alignment	not modelled	100.0	16	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
32	c5jqeA		Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein,caspase-8 PDBTitle: crystal structure of caspase8 tded
33	c3py7A		Alignment	not modelled	100.0	16	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin ld1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
34	c3waiA		Alignment	not modelled	100.0	17	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
35	c5yseB		Alignment	not modelled	100.0	17	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
36	c5wvmA		Alignment	not modelled	100.0	16	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
37	c3dm0A		Alignment	not modelled	100.0	16	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
38	c5f7vA		Alignment	not modelled	100.0	14	PDB header: cycloalternan binding protein Chain: A: PDB Molecule: lmo0181 protein; PDBTitle: abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloalternan
39	c6anvA		Alignment	not modelled	100.0	16	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
40	c4wgiA		Alignment	not modelled	100.0	17	PDB header: apoptosis/inhibitor Chain: A: PDB Molecule: maltose-binding periplasmic protein,induced myeloid PDBTitle: a single diastereomer of a macrolactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
41	c4r9fA		Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: mbp1; PDBTitle: cpmnbp1 with mannobiose bound
42	c3c4mA		Alignment	not modelled	100.0	16	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)
43	c4qvhA		Alignment	not modelled	100.0	17	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
44	c3d4cA		Alignment	not modelled	100.0	17	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)
45	c5tibA		Alignment	not modelled	100.0	16	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
46	c5ci5B		Alignment	not modelled	100.0	18	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
47	c4r6hA		Alignment	not modelled	100.0	13	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
48	c5dfmB		Alignment	not modelled	100.0	16	PDB header: nuclear protein Chain: B: PDB Molecule: maltose-binding periplasmic protein,telomerase-associated PDBTitle: structure of tetrahymena telomerase p19 fused to mbp

49	c4g68A	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
50	c1hsjA	Alignment	not modelled	100.0	16	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus accessory PDBTitle: sarr mbp fusion structure
51	c4g68C	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: C: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
52	c5ii5A	Alignment	not modelled	100.0	16	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
53	c2z8fB	Alignment	not modelled	100.0	15	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
54	c1r6zA	Alignment	not modelled	100.0	17	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)
55	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 achl_0255 from arthrobacter2 chlorophenolicus a6, target efi-510633, with bound laminaribiose
56	c5k94B	Alignment	not modelled	100.0	18	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
57	c3vd8A	Alignment	not modelled	100.0	17	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
58	c5iaiA	Alignment	not modelled	100.0	18	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
59	c4b3nA	Alignment	not modelled	100.0	16	PDB header: sugar binding protein/ligase Chain: A: PDB Molecule: maltose-binding periplasmic protein, tripartite motif- PDBTitle: crystal structure of rhesus trim5alpha pry/spry domain
60	c3o3uN	Alignment	not modelled	100.0	17	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)
61	c4tsmC	Alignment	not modelled	100.0	17	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
62	c4kv3A	Alignment	not modelled	100.0	17	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
63	c3qufB	Alignment	not modelled	100.0	16	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
64	c4edqA	Alignment	not modelled	100.0	17	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
65	c4qsZB	Alignment	not modelled	100.0	15	PDB header: transcription Chain: B: PDB Molecule: maltose-binding periplasmic protein, jmjc domain-containing PDBTitle: crystal structure of mouse jmjd7 fused with maltose-binding protein
66	c5jonA	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd
67	c6ffIA	Alignment	not modelled	100.0	17	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
68	c4pqkA	Alignment	not modelled	100.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, truncated PDBTitle: c-terminal domain of dna binding protein
69	c3mp6A	Alignment	not modelled	100.0	16	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,linker,saga-associated PDBTitle: complex structure of sgf29 and dimethylated h3k4
70	c5y2gA	Alignment	not modelled	100.0	16	PDB header: toxin Chain: A: PDB Molecule: maltose-binding periplasmic protein,protein b;

71	c3oaiB_	Alignment	not modelled	100.0	16	PDBTitle: structure of mbp tagged gbs camp 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
72	c4bl9D_	Alignment	not modelled	100.0	16	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)
73	c4logA_	Alignment	not modelled	100.0	16	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
74	c2vgqA_	Alignment	not modelled	100.0	16	PDB header: immune system/transport Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein, PDBTitle: crystal structure of human ips-1 card
75	c3woaA_	Alignment	not modelled	100.0	16	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
76	c4rwcC_	Alignment	not modelled	100.0	16	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 cgpr analog
77	c6apxA_	Alignment	not modelled	100.0	16	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 monobody ysx1
78	c5tttA_	Alignment	not modelled	100.0	15	PDB header: cell adhesion Chain: A: PDB Molecule: maltose-binding periplasmic protein,pilin isopeptide PDBTitle: minor pilin fctb from s. pyogenes with engineered intramolecular2 isopeptide bond
79	c4my2A_	Alignment	not modelled	100.0	16	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
80	c4exkA_	Alignment	not modelled	100.0	15	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
81	c6h0hB_	Alignment	not modelled	100.0	15	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
82	c5hz7A_	Alignment	not modelled	100.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: comp; PDBTitle: high-resolution crystal structure of the minor dna-binding pilin comp2 from neisseria meningitidis in fusion with mbp
83	c2zykA_	Alignment	not modelled	100.0	13	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
84	c5ixpA_	Alignment	not modelled	100.0	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
85	c2nvuB_	Alignment	not modelled	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
86	c3csgA_	Alignment	not modelled	100.0	17	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 binding protein2 fusion complex
87	c5k2yB_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: B: PDB Molecule: probable periplasmic sugar-binding lipoprotein uspc; PDBTitle: crystal structure of m. tuberculosis uspc (monoclinic crystal form)
88	c1y4cA_	Alignment	not modelled	100.0	16	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
89	c4wviA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein,signal peptidase ib; PDBTitle: crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2).
90	c5yevB_	Alignment	not modelled	100.0	16	PDB header: apoptosis Chain: B: PDB Molecule: tnfrsf25 death domain; PDBTitle: murine dr3 death domain
91	c4ozqA_	Alignment	not modelled	100.0	16	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

92	c3zkA		Alignment	not modelled	100.0	15	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
93	c3vxbA		Alignment	not modelled	100.0	14	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxle from streptomyces thermoviolaceus opc-520
94	c4r0yA		Alignment	not modelled	100.0	15	PDB header: protein binding Chain: A: PDB Molecule: maltose-binding periplasmic protein, disks large-associated PDBTitle: structure of maltose-binding protein fusion with the c-terminal gh12 domain of guanylate kinase-associated protein from rattus norvegicus
95	c4ifpC		Alignment	not modelled	100.0	17	PDB header: immune system Chain: C: PDB Molecule: maltose-binding periplasmic protein,nacht, lrr and pyd PDBTitle: x-ray crystal structure of human nlrp1 card domain
96	c4r2bB		Alignment	not modelled	100.0	14	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
97	c5tu0A		Alignment	not modelled	100.0	15	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
98	c4hs7A		Alignment	not modelled	100.0	14	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.
99	c6eg3A		Alignment	not modelled	100.0	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,probable PDBTitle: crystal structure of human brm in complex with compound 15
100	c2gh9A		Alignment	not modelled	100.0	18	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
101	c5dviA		Alignment	not modelled	100.0	14	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
102	c3ehuA		Alignment	not modelled	100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: fusion protein of crf1 extracellular domain and mbp; PDBTitle: crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crf1) in complex with crf
103	c3oo6A		Alignment	not modelled	100.0	15	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
104	d1elja		Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
105	c4rk9B		Alignment	not modelled	100.0	12	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
106	c5az6A		Alignment	not modelled	100.0	15	PDB header: sugar binding protein, peptide binding p Chain: A: PDB Molecule: maltose-binding periplasmic protein,mitochondrial import PDBTitle: crystal structure of mbp-tom20 fusion protein with a 2-residue spacer2 in the connector helix
107	c4rk2B		Alignment	not modelled	100.0	18	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
108	c3a3cA		Alignment	not modelled	100.0	15	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
109	c2b3fD		Alignment	not modelled	100.0	13	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein bound with2 galactose
110	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.
111	c5c7rA		Alignment	not modelled	100.0	16	PDB header: antifreeze protein Chain: A: PDB Molecule: fusion protein of maltose-binding periplasmic protein and PDBTitle: revealing surface waters on an antifreeze protein by fusion protein2 crystallography
112	c1mg1A		Alignment	not modelled	100.0	16	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
113	c4o2yA		Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, atp-

113	c40z8A_	Alignment	not modelled	100.0	17	dependent clp PDBTitle: structure of a malarial protein PDB header: sugar binding protein
114	c2fncA_	Alignment	not modelled	100.0	17	maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose. PDB header: sugar binding protein
115	c2xd3A_	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose.
116	c5b3zB_	Alignment	not modelled	100.0	14	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
117	c4ua8A_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: carbohydrate abc transporter substrate-binding protein, PDBTitle: eur_01830 (maltotriose-binding protein) complexed with maltotriose
118	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
119	c1mh3A_	Alignment	not modelled	100.0	16	PDB header: sugar binding, dna binding protein Chain: A: PDB Molecule: maltose binding-a1 homeodomain protein chimera; PDBTitle: maltose binding-a1 homeodomain protein chimera, crystal form i
120	c1ursA_	Alignment	not modelled	100.0	18	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