







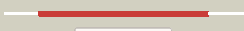















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1235_(lpqY)_1377530_1378936
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	d864052cc59be326

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5i04A_	 Alignment		100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,endoglin; PDBTitle: crystal structure of the orphan region of human endoglin/cd105
2	c6aeoA_	 Alignment		100.0	18	PDB header: protein transport Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,tssl; PDBTitle: tssl periplasmic domain
3	c4wrnB_	 Alignment		100.0	18	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
4	c3osqA_	 Alignment		100.0	21	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
5	c5hzvA_	 Alignment		100.0	18	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
6	c4h1gA_	 Alignment		100.0	18	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
7	c6dd5B_	 Alignment		100.0	19	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
8	c5fsgA_	 Alignment		100.0	19	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
9	c3f5fA_	 Alignment		100.0	18	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.
10	c3h4zC_	 Alignment		100.0	20	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	c5gxtA_	 Alignment		100.0	19	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pig

12	c3py7A_	Alignment		100.0	20	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
13	c3ob4A_	Alignment		100.0	19	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
14	c5azaA_	Alignment		100.0	18	PDB header: sugar binding protein, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein,oligosaccharyl PDBTitle: crystal structure of mbp-sagIb fusion protein with a 20-residue spacer2 in the connector helix
15	c5t0aB_	Alignment		100.0	19	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
16	c5eduB_	Alignment		100.0	19	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
17	d1eu8a_	Alignment		100.0	26	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
18	c5wvmA_	Alignment		100.0	18	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
19	c4qvhA_	Alignment		100.0	18	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
20	c4bl9D_	Alignment		100.0	18	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)
21	c5jqeA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein,caspase-8 PDBTitle: crystal structure of caspase8 tded
22	c3dm0A_	Alignment	not modelled	100.0	19	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
23	c4kegA_	Alignment	not modelled	100.0	18	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1
24	c4b3nA_	Alignment	not modelled	100.0	18	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
25	c4egcA_	Alignment	not modelled	100.0	19	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
26	c5ii5A_	Alignment	not modelled	100.0	18	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
27	c3c4mA_	Alignment	not modelled	100.0	18	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) PDB header: nuclear protein

28	c5dfmB_	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: maltose-binding periplasmic protein,telomerase-associated PDBTitle: structure of tetrahymena telomerase p19 fused to mbp PDB header: lipid binding protein
29	c5tibA_	Alignment	not modelled	100.0	19	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 PDB header: protein transport
30	c4kv3A_	Alignment	not modelled	100.0	18	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 PDB header: cell adhesion
31	c3d4cA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, zona pellucida PDBTitle: zp-n domain of mammalian sperm receptor zp3 (crystal form i) PDB header: immune system
32	c6anvA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: anti-crispr protein acrf1 fused with c-terminal mbp tag; PDBTitle: crystal structure of anti-crispr protein acrf1 PDB header: cell adhesion
33	c4tsmC_	Alignment	not modelled	100.0	19	Chain: C: PDB Molecule: maltose-binding protein, pilin chimera; PDBTitle: mbp-fusion protein of pila1 from c. difficile r20291 residues 26-166 PDB header: membrane protein/hormone
34	c4rwgC_	Alignment	not modelled	100.0	19	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 PDB header: transport protein, signaling protein
35	c3o3uN_	Alignment	not modelled	100.0	18	Chain: N: PDB Molecule: maltose-binding periplasmic protein, advanced glycosylation PDBTitle: crystal structure of human receptor for advanced glycation endproducts2 (rage) PDB header: protein transport
36	c5k94B_	Alignment	not modelled	100.0	18	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 PDB header: cell adhesion
37	c4xa2A_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: maltose-binding periplasmic protein,mbp-pila: c; PDBTitle: structure of the major type iv pilin of acinetobacter baumannii PDB header: histone binding protein
38	c3mp6A_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: maltose-binding periplasmic protein,linker,saga-associated PDBTitle: complex structure of sgf29 and dimethylated h3k4 PDB header: transport protein/contractile protein
39	c4edqA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: maltose-binding periplasmic protein,myosin-binding protein PDBTitle: mbp-fusion protein of myosin-binding protein c residues 149-269 PDB header: transport protein
40	c5jonA_	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd PDB header: transcription
41	c4logA_	Alignment	not modelled	100.0	19	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 PDB header: gene regulation
42	c1r6zA_	Alignment	not modelled	100.0	19	Chain: A: PDB Molecule: chimera of maltose-binding periplasmic protein and PDBTitle: the crystal structure of the argonaute2 paz domain (as a mbp fusion) PDB header: cell adhesion
43	c5tttA_	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: maltose-binding periplasmic protein,pilin isopeptide PDBTitle: minor pilin fctb from s. pyogenes with engineered intramolecular2 isopeptide bond PDB header: transcription/sugar binding protein
44	c1hsiA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: fusion protein consisting of staphylococcus accessory PDBTitle: sarr mbp fusion structure PDB header: transferase, transport protein
45	c3waiA_	Alignment	not modelled	100.0	19	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 PDB header: sugar binding protein,signaling protein
46	c3vd8A_	Alignment	not modelled	100.0	19	Chain: A: PDB Molecule: maltose-binding periplasmic protein, interferon-inducible PDBTitle: crystal structure of human aim2 pyd domain with mbp fusion PDB header: membrane protein, cell adhesion
47	c3oaiB_	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: maltose-binding periplasmic protein, myelin protein p0; PDBTitle: crystal structure of the extra-cellular domain of human myelin protein2 zero PDB header: hydrolase
48	c6apxA_	Alignment	not modelled	100.0	19	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 PDB header: hydrolase

49	c4wviA	Alignment	not modelled	100.0	18	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).
50	c4pqkA	Alignment	not modelled	100.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, truncated PDBTitle: c-terminal domain of dna binding protein
51	c4exkA	Alignment	not modelled	100.0	17	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
52	c6dtqC	Alignment	not modelled	100.0	24	PDB header: sugar binding protein Chain: C: PDB Molecule: maltose-binding protein male3; PDBTitle: maltose bound t. maritima male3
53	c2vgqA	Alignment	not modelled	100.0	18	PDB header: immune system/transport Chain: A: PDB Molecule: sugar abc transporter substrate-binding protein, PDBTitle: crystal structure of human ips-1 card
54	c4ozqA	Alignment	not modelled	100.0	17	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
55	c5hz7A	Alignment	not modelled	100.0	19	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
56	c1y4cA	Alignment	not modelled	100.0	17	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
57	c3csgA	Alignment	not modelled	100.0	19	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
58	c4qszB	Alignment	not modelled	100.0	19	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
59	c5y2gA	Alignment	not modelled	100.0	19	PDB header: toxin Chain: A: PDB Molecule: maltose-binding periplasmic protein, protein b; PDBTitle: structure of mbp tagged gbs camp
60	c4my2A	Alignment	not modelled	100.0	17	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
61	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
62	c4wgiA	Alignment	not modelled	100.0	18	PDB header: apoptosis/inhibitor Chain: A: PDB Molecule: maltose-binding periplasmic protein, induced myeloid PDBTitle: a single diastereomer of a macro lactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
63	c2nvuB	Alignment	not modelled	100.0	17	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
64	c3uorB	Alignment	not modelled	100.0	18	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
65	c5f7vA	Alignment	not modelled	100.0	14	PDB header: cycloaltermann binding protein Chain: A: PDB Molecule: lmo0181 protein; PDBTitle: abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloaltermann
66	c5yevB	Alignment	not modelled	100.0	17	PDB header: apoptosis Chain: B: PDB Molecule: tnfrsf25 death domain; PDBTitle: murine dr3 death domain
67	c4r0yA	Alignment	not modelled	100.0	19	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
68	c3k02A	Alignment	not modelled	100.0	24	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.
69	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
70	c3woaA	Alignment	not modelled	100.0	15	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 PDB header: sugar binding protein

71	c2zykA_	Alignment	not modelled	100.0	16	Chain: A; PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
72	c4mfiA_	Alignment	not modelled	100.0	20	PDB header: sugar binding protein Chain: A; PDB Molecule: sn-glycerol-3-phosphate abc transporter substrate-binding PDBTitle: crystal structure of mycobacterium tuberculosis ugpb
73	c1mg1A_	Alignment	not modelled	100.0	17	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
74	c5yseB_	Alignment	not modelled	100.0	18	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
75	c3ehuA_	Alignment	not modelled	100.0	17	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
76	c6eg3A_	Alignment	not modelled	100.0	19	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
77	c4ry1A_	Alignment	not modelled	100.0	14	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
78	c2z8fB_	Alignment	not modelled	100.0	14	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
79	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
80	c4r2fA_	Alignment	not modelled	100.0	17	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
81	c4aq4A_	Alignment	not modelled	100.0	16	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
82	c4o2xA_	Alignment	not modelled	100.0	18	PDB header: transport protein Chain: A; PDB Molecule: maltose-binding periplasmic protein, atp-dependent clp PDBTitle: structure of a malarial protein
83	c2xd3A_	Alignment	not modelled	100.0	14	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.
84	c4hs7A_	Alignment	not modelled	100.0	16	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.
85	c3a3cA_	Alignment	not modelled	100.0	18	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
86	c5iaiA_	Alignment	not modelled	100.0	19	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
87	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
88	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
89	c2fncA_	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A; PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose.
90	c5c7rA_	Alignment	not modelled	100.0	17	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
91	c4r9fA_	Alignment	not modelled	100.0	16	PDB header: sugar binding protein Chain: A; PDB Molecule: mbp1; PDBTitle: cpmbnp1 with mannobiose bound
						PDB header: sugar binding protein, peptide binding p Chain: A; PDB Molecule: maltose-binding periplasmic

92	c5az6A_	Alignment	not modelled	100.0	16	protein,mitochondrial import PDBTitle: crystal structure of mbp-tom20 fusion protein with a 2-residue spacer2 in the connector helix
93	c2gh9A_	Alignment	not modelled	100.0	19	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
94	c6ffaA_	Alignment	not modelled	100.0	16	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
95	c4ovjA_	Alignment	not modelled	100.0	15	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
96	d1elja_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
97	c4r6kA_	Alignment	not modelled	100.0	14	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
98	c5b3zB_	Alignment	not modelled	100.0	17	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
99	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
100	c2uvgA_	Alignment	not modelled	100.0	14	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
101	c4gqoC_	Alignment	not modelled	100.0	14	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
102	c4g68C_	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: C: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
103	c4g68A_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
104	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
105	c5dviA_	Alignment	not modelled	100.0	15	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
106	c3zkkA_	Alignment	not modelled	100.0	16	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 xyloetraose
107	c5ixpA_	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein family 1; PDBTitle: crystal structure of extracellular solute-binding protein family 1
108	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
109	c1ursA_	Alignment	not modelled	100.0	19	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
110	d1ursa_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
111	c4r6hA_	Alignment	not modelled	100.0	14	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
112	c4dxbB_	Alignment	not modelled	100.0	19	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
113	c1mh3A_	Alignment	not modelled	100.0	18	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
						PDB header: signaling protein

114	c3iouB_	Alignment	not modelled	100.0	17	Chain: B: PDB Molecule: maltose-binding periplasmic protein, huntingtin; PDBTitle: huntingtin amino-terminal region with 17 gln residues - crystal c94
115	c1svxB_	Alignment	not modelled	100.0	17	PDB header: de novo protein/sugar binding protein Chain: B: PDB Molecule: maltose-binding periplasmic protein; PDBTitle: crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein
116	c2b3fD_	Alignment	not modelled	100.0	15	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein bound with 2 galactose
117	c5k2xA_	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter permease; PDBTitle: crystal structure of m. tuberculosis uspc (tetragonal crystal form)
118	c5mkbF_	Alignment	not modelled	100.0	16	PDB header: sugar binding protein Chain: F: PDB Molecule: male1; PDBTitle: maltodextrin binding protein male1 from l. casei bl23 without ligand
119	c3vxB_	Alignment	not modelled	100.0	16	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxlE from streptomyces thermoviolaceus opc-520
120	c3osrA_	Alignment	not modelled	100.0	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 311