



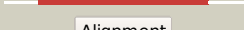

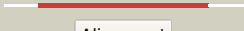
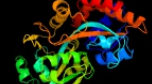








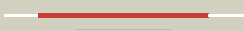







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0928_(pstS3)_1034907_1036019
Date	Fri Jul 26 01:50:52 BST 2019
Unique Job ID	44399a6689c60ca0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4lvqA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphate-binding protein pstS 3; <b>PDBTitle:</b> crystal structure of the m. tuberculosis phosphate binding protein2 pstS3
2	<a href="#">d1pc3a_</a>	 Alignment		100.0	29	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
3	<a href="#">d1ixha_</a>	 Alignment		100.0	29	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
4	<a href="#">c5wnnB_</a>	 Alignment		100.0	29	<b>PDB header:</b> phosphate binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> phosphate-binding protein pstS; <b>PDBTitle:</b> crystal structure of phosphate-binding protein pstS protein from2 burkholderia pseudomallei
5	<a href="#">c5i84H_</a>	 Alignment		100.0	29	<b>PDB header:</b> transport protein <b>Chain:</b> H; <b>PDB Molecule:</b> phosphate-binding protein pstS; <b>PDBTitle:</b> structure of the xanthomonas citri phosphate-binding protein phox
6	<a href="#">d2v3qa1</a>	 Alignment		100.0	23	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
7	<a href="#">c5jk4A_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> phosphate-binding protein from stentrophomonas maltophilia.
8	<a href="#">c4ombB_</a>	 Alignment		99.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> phosphate binding protein; <b>PDBTitle:</b> phosphate binding protein
9	<a href="#">c4jwoA_</a>	 Alignment		99.9	18	<b>PDB header:</b> phosphate binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphate binding protein; <b>PDBTitle:</b> the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776
10	<a href="#">c4ry1A_</a>	 Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> crystal structure of periplasmic solute binding protein eca2210 from2 pectobacterium atrosepticum scri1043, target efi-510858
11	<a href="#">c4aq4A_</a>	 Alignment		99.9	12	<b>PDB header:</b> diester-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> sn-glycerol-3-phosphate-binding periplasmic protein ugpb; <b>PDBTitle:</b> substrate bound sn-glycerol-3-phosphate binding periplasmic protein2 ugpb from escherichia coli

12	<a href="#">c4rk2B_</a>	Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of sugar transporter rhe_pf00321 from rhizobium2 etli, target efi-510806, an open conformation
13	<a href="#">c4r6kA_</a>	Alignment		99.9	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter substrate-binding protein yeso2 from bacillus subtilis, target efi-510761, an open conformation
14	<a href="#">c4gqoC_</a>	Alignment		99.9	11	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> lmo0859 protein; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of uncharacterized protein2 lmo0859 from listeria monocytogenes egd-e
15	<a href="#">c2uvgA_</a>	Alignment		99.9	12	<b>PDB header:</b> sugar-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc type periplasmic sugar-binding protein; <b>PDBTitle:</b> structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
16	<a href="#">c4ovjA_</a>	Alignment		99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein family 1; <b>PDBTitle:</b> extracellular solute-binding protein family 1 from alicyclobacillus2 acidocaldarius subsp. acidocaldarius dsm 446
17	<a href="#">c3uorB_</a>	Alignment		99.9	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter sugar binding protein; <b>PDBTitle:</b> the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
18	<a href="#">c5f7vA_</a>	Alignment		99.9	14	<b>PDB header:</b> cycloaltnan binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0181 protein; <b>PDBTitle:</b> abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloaltnan
19	<a href="#">c4r9fA_</a>	Alignment		99.9	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mbp1; <b>PDBTitle:</b> cpmnbp1 with mannobiose bound
20	<a href="#">c5mkbF_</a>	Alignment		99.9	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> male1; <b>PDBTitle:</b> maltodextrin binding protein male1 from l. casei bl23 without ligand
21	<a href="#">c6ffaA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin transport permease homologue; <b>PDBTitle:</b> maltose/maltodextrin-binding domain male from bdellovibrio2 bacteriovorus bound to maltotriose
22	<a href="#">d1eu8a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
23	<a href="#">c3qufB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein, family 1; <b>PDBTitle:</b> the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
24	<a href="#">c4r6hA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute binding protein msme; <b>PDBTitle:</b> crystal structure of putative binding protein msme from bacillus2 subtilis subsp. subtilis str. 168, target efi-510764, an open3 conformation
25	<a href="#">c5tu0A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2125 protein; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of maltose-binding2 periplasmic protein male from listeria monocytogenes in complex with3 maltose
26	<a href="#">c2xd3A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding protein; <b>PDBTitle:</b> the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose.
27	<a href="#">c4g68A_</a>	Alignment	not modelled	99.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
						<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate abc transporter substrate-

28	<a href="#">c4ua8A_</a>	Alignment	not modelled	99.9	12	binding protein, <b>PDBTitle:</b> eur_01830 (maltotriose-binding protein) complexed with maltotriose
29	<a href="#">c5iaiA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter; <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein arad_98872 from agrobacterium radiobacter k84, target efi-510945 in complex with3 ribitol
30	<a href="#">c6dtqC_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> maltose-binding protein male3; <b>PDBTitle:</b> maltose bound t. maritima male3
31	<a href="#">c2z8fB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> galacto-n-biose/lacto-n-biose i transporter substrate- <b>PDBTitle:</b> 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
32	<a href="#">c3woaA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> dna binding protein, sugar binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci, maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
33	<a href="#">c5k2xA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter permease; <b>PDBTitle:</b> crystal structure of m. tuberculosis uspc (tetragonal crystal form)
34	<a href="#">c4ryaA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter substrate binding protein (sorbitol); <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein avi_35672 from agrobacterium vitis s4, target efi-510645, with bound d-mannitol
35	<a href="#">c5ixpA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein family 1; <b>PDBTitle:</b> crystal structure of extracellular solute-binding protein family 1
36	<a href="#">c5yseB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lin1841 protein; <b>PDBTitle:</b> crystal structure of beta-1,2-glucooligosaccharide binding protein in2 complex with sophorotetraose
37	<a href="#">c5k2yB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable periplasmic sugar-binding lipoprotein uspc; <b>PDBTitle:</b> crystal structure of m. tuberculosis uspc (monoclinic crystal form)
38	<a href="#">c3zkKA_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> xos binding protein; <b>PDBTitle:</b> structure of the xylo-oligosaccharide specific solute binding protein2 from bifidobacterium animalis subsp. lactis bl-04 in complex with3 xylotetraose
39	<a href="#">c4mfIA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn-glycerol-3-phosphate abc transporter substrate-binding <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ugpb
40	<a href="#">c2zykA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute-binding protein; <b>PDBTitle:</b> crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
41	<a href="#">c6fuvA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute binding protein, blmnbp1 in complex with <b>PDBTitle:</b> structure of a manno-oligosaccharide specific solute binding protein,2 blmnbp2 from bifidobacterium animalis subsp. lactis atcc 27673 in3 complex with mannitol
42	<a href="#">c4rk9B_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate abc transporter substrate-binding protein <b>PDBTitle:</b> crystal structure of sugar transporter bl01359 from bacillus2 licheniformis, target efi-510856, in complex with stachyose
43	<a href="#">c4g68C_</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
44	<a href="#">c4wrnB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein,uromodulin; <b>PDBTitle:</b> crystal structure of the polymerization region of human2 uromodulin/tamm-horsfall protein
45	<a href="#">d2onsa1</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
46	<a href="#">c4hs7A_</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial extracellular solute-binding protein, putative; <b>PDBTitle:</b> 2.6 angstrom structure of the extracellular solute-binding protein2 from staphylococcus aureus in complex with peg.
47	<a href="#">c2w7yA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> sugar-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar abc transporter, sugar-binding <b>PDBTitle:</b> structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide.
48	<a href="#">c4kysA_</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine pyridinylase i; <b>PDBTitle:</b> clostridium botulinum thiaminase i in complex with thiamin
49	<a href="#">c3k02A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acarbose/maltose binding protein gach; <b>PDBTitle:</b> crystal structures of the gach receptor of streptomyces glaucescens2 gla.o in the unliganded form and in complex with acarbose and an3 acarbose homolog. comparison with acarbose-loaded maltose binding4 protein of salmonella typhimurium.

50	<a href="#">c6h0hB</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable solute binding protein of abc transporter system <b>PDBTitle:</b> the abc transporter associated binding protein from b. animalis subsp.2 lactis bl-04 in complex with beta-1,6-galactobiose
51	<a href="#">c5ci5B</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein family 1; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein from2 thermotoga lettingae tmo (tlet_1705, target efi-510544) bound with3 alpha-d-tagatose
52	<a href="#">c1ursa</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> maltose-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding protein; <b>PDBTitle:</b> x-ray structures of the maltose-maltodextrin binding2 protein of the thermoacidophilic bacterium alicyclobacillus3 acidocaldarius
53	<a href="#">d1ursa</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
54	<a href="#">c2gh9A</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding protein; <b>PDBTitle:</b> thermus thermophilus maltotriose binding protein bound with2 maltotriose
55	<a href="#">c3k6wA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute-binding protein ma_0280; <b>PDBTitle:</b> apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
56	<a href="#">c5dviA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc sugar transporter; <b>PDBTitle:</b> crystal structure of galactose complexed periplasmic glucose binding2 protein (ppgbp) from p. putida csv86
57	<a href="#">c5hzvA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,endoglin; <b>PDBTitle:</b> crystal structure of the zona pellucida module of human endoglin/cd105
58	<a href="#">c2i58B</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> sugar abc transporter, sugar-binding protein; <b>PDBTitle:</b> crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose
59	<a href="#">c4r2fA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein family 1; <b>PDBTitle:</b> crystal structure of sugar transporter achl_0255 from arthrobacter2 chlorophenicus a6, target efi-510633, with bound laminaribiose
60	<a href="#">c3cfxA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein ma_0280; <b>PDBTitle:</b> crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
61	<a href="#">c3cfzA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0100 protein mj1186; <b>PDBTitle:</b> crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
62	<a href="#">c2b3fD</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-binding protein; <b>PDBTitle:</b> thermus thermophilus glucose/galactose binding protein bound with2 galactose
63	<a href="#">c3ob4A</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein, arah 2; <b>PDBTitle:</b> mbp-fusion protein of the major peanut allergen ara h 2
64	<a href="#">c3osrA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> fluorescent protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,green fluorescent <b>PDBTitle:</b> maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
65	<a href="#">c6anvA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> anti-crispr protein acrf1 fused with c-terminal mbp tag; <b>PDBTitle:</b> crystal structure of anti-crispr protein acrf1
66	<a href="#">c1y4cA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
67	<a href="#">c4qvhA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, 4'-phosphopantetheinyl <b>PDBTitle:</b> crystal structure of the essential mycobacterium tuberculosis2 phosphopantetheinyl transferase pptt, solved as a fusion protein with3 maltose binding protein
68	<a href="#">c5i04A</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,endoglin; <b>PDBTitle:</b> crystal structure of the orphan region of human endoglin/cd105
69	<a href="#">c4egcA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transcription/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, homeobox protein six1 <b>PDBTitle:</b> crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain
70	<a href="#">c6aeoA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding periplasmic protein,tssl; <b>PDBTitle:</b> tssl periplasmic domain
71	<a href="#">c4r2bB</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein family 1; <b>PDBTitle:</b> crystal structure of sugar transporter oant_3817 from

					ochrobactrum2 anthropi, target efi-510528, with bound glucose <b>PDB header:</b> transport protein, signaling protein <b>Chain:</b> N: <b>PDB Molecule:</b> maltose-binding periplasmic protein, advanced glycosylation <b>PDBTitle:</b> crystal structure of human receptor for advanced glycation endproducts2 (rage)
72	<a href="#">c3o3uN_</a>	Alignment	not modelled	99.8	13
73	<a href="#">c4hwcC_</a>	Alignment	not modelled	99.8	11
74	<a href="#">c4h1gA_</a>	Alignment	not modelled	99.8	13
75	<a href="#">c5k94B_</a>	Alignment	not modelled	99.8	14
76	<a href="#">c4tsmC_</a>	Alignment	not modelled	99.8	14
77	<a href="#">c5jqeA_</a>	Alignment	not modelled	99.8	12
78	<a href="#">c4xa2A_</a>	Alignment	not modelled	99.8	15
79	<a href="#">c3osqA_</a>	Alignment	not modelled	99.8	15
80	<a href="#">c5fsgA_</a>	Alignment	not modelled	99.8	13
81	<a href="#">c4kegA_</a>	Alignment	not modelled	99.8	13
82	<a href="#">c5gxtA_</a>	Alignment	not modelled	99.8	12
83	<a href="#">c4dxbB_</a>	Alignment	not modelled	99.8	13
84	<a href="#">c3oo6A_</a>	Alignment	not modelled	99.8	12
85	<a href="#">c4kv3A_</a>	Alignment	not modelled	99.8	13
86	<a href="#">c3d4cA_</a>	Alignment	not modelled	99.8	14
87	<a href="#">c3mp6A_</a>	Alignment	not modelled	99.8	13
88	<a href="#">c2fncA_</a>	Alignment	not modelled	99.8	14
89	<a href="#">c6dd5B_</a>	Alignment	not modelled	99.8	13
90	<a href="#">c4n13A_</a>	Alignment	not modelled	99.8	22
91	<a href="#">c4ecfA_</a>	Alignment	not modelled	99.8	25
92	<a href="#">d1elja_</a>	Alignment	not modelled	99.8	13
					<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like <b>PDB header:</b> sugar binding protein



93	<a href="#">c5wvma_</a>	Alignment	not modelled	99.8	13	<b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, two-component system <b>PDBTitle:</b> crystal structure of baes cocrystallized with 2 mm indole
94	<a href="#">c3ehuA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of crfr1 extracellular domain and mbp; <b>PDBTitle:</b> crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
95	<a href="#">c3f5fA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transport, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, heparan sulfate 2-o- <b>PDBTitle:</b> crystal structure of heparan sulfate 2-o-sulfotransferase from gallus2 gallus as a maltose binding protein fusion.
96	<a href="#">c3py7A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, paxillin ld1, protein e6 <b>PDBTitle:</b> crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
97	<a href="#">c4gd5B_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate abc transporter, phosphate-binding protein; <b>PDBTitle:</b> x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
98	<a href="#">c3vxbA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar-binding lipoprotein; <b>PDBTitle:</b> crystal structure of bxlx from streptomyces thermoviolaceus opc-520
99	<a href="#">c5azaA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> sugar binding protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, oligosaccharyl <b>PDBTitle:</b> crystal structure of mbp-saglb fusion protein with a 20-residue spacer2 in the connector helix
100	<a href="#">c4logA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein and nr2e3 <b>PDBTitle:</b> the crystal structure of the orphan nuclear receptor pnr ligand2 binding domain fused with mbp
101	<a href="#">c4wgiA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> apoptosis/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, induced myeloid <b>PDBTitle:</b> a single diastereomer of a macrolactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
102	<a href="#">c5tibA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter substrate-binding protein, gasdermin- <b>PDBTitle:</b> gasdermin-b c-terminal domain containing the polymorphism residues2 arg299:ser306 fused to maltose binding protein
103	<a href="#">c4exlD_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphate-binding protein psts 1; <b>PDBTitle:</b> crystal structure of phosphate abc transporter, periplasmic phosphate-2 binding protein psts 1 (pbp1) from streptococcus pneumoniae canada3 mdr_19a
104	<a href="#">c5y2gA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, protein b; <b>PDBTitle:</b> structure of mbp tagged gbs camp
105	<a href="#">c3oaiB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> membrane protein, cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, myelin protein p0; <b>PDBTitle:</b> crystal structure of the extra-cellular domain of human myelin protein2 zero
106	<a href="#">c5t0aB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein - heparan sulfate 6-o- <b>PDBTitle:</b> crystal structure of heparan sulfate 6-o-sulfotransferase with bound2 pap and heptasaccharide substrate
107	<a href="#">c4my2A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, norrin fusion protein; <b>PDBTitle:</b> crystal structure of norrin in fusion with maltose binding protein
108	<a href="#">c2nvuB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> protein turnover, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein/nedd8-activating enzyme <b>PDBTitle:</b> structure of appbp1-uba3--nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
109	<a href="#">c1hsiA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transcription/sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein consisting of staphylococcus accessory <b>PDBTitle:</b> sarr mbp fusion structure
110	<a href="#">c4edqA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein/contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, myosin-binding protein <b>PDBTitle:</b> mbp-fusion protein of myosin-binding protein c residues 149-269
111	<a href="#">c5b3zB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> isomerase, sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase nima-interacting 1, <b>PDBTitle:</b> crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein
112	<a href="#">c5eduB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, histone deacetylase 6 <b>PDBTitle:</b> crystal structure of human histone deacetylase 6 catalytic domain 2 in2 complex with trichostatin a
113	<a href="#">c5ii5A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, vitelline envelope <b>PDBTitle:</b> crystal structure of red abalone verl repeat 1 at 1.8 a

						resolution
114	<a href="#">c5dfmB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein,telomerase-associated <b>PDBTitle:</b> structure of tetrahymena telomerase p19 fused to mbp
115	<a href="#">c4bl9D_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> maltose-binding periplasmic protein, suppressor of fused <b>PDBTitle:</b> crystal structure of full-length human suppressor of fused (sufu)2 mutant lacking a regulatory subdomain (crystal form i)
116	<a href="#">c3h4zC_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> allergen <b>Chain:</b> C: <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with allergen <b>PDBTitle:</b> crystal structure of an mbp-der p 7 fusion protein
117	<a href="#">c1r6zA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of maltose-binding periplasmic protein and <b>PDBTitle:</b> the crystal structure of the argonaute2 paz domain (as a mbp fusion)
118	<a href="#">c5jonA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,potassium/sodium <b>PDBTitle:</b> crystal structure of the unliganded form of hcn2 cnbd
119	<a href="#">c3waiA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, transmembrane <b>PDBTitle:</b> crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
120	<a href="#">c6fjID_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc-type fe3+ transport system, periplasmic component; <b>PDBTitle:</b> structure of ibps from dickeya dadantii