Phyre2

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Description	RVBD1857_(modA)_2104992_2105777
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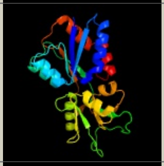
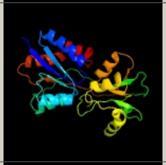
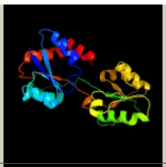
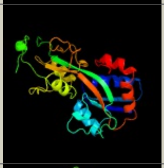
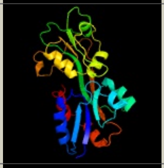
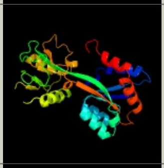
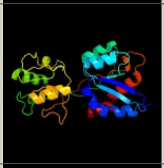
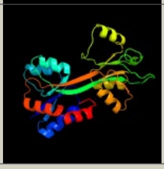
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h5yC_	Alignment		100.0	33	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**molybdate-binding periplasmic protein; **PDBTitle:** crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
2	d1atga_	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
3	c4kd5A_	Alignment		100.0	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type transport system, molybdenum-specific **PDBTitle:** substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
4	d1amfa_	Alignment		100.0	31	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
5	c4rxlA_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**molybdenum abc transporter, periplasmic molybdenum-binding **PDBTitle:** crystal structure of molybdenum abc transporter solute binding protein2 vc_a0726 from vibrio cholerae, target efi-510913, in complex with3 tungstate
6	c4jb7A_	Alignment		100.0	17	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**accessory colonization factor acfc; **PDBTitle:** 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid
7	c6ddnB_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**probable sulfate-binding lipoprotein subi; **PDBTitle:** the sulfate-binding protein subi from mycobacterium tuberculosis h37rv
8	c3fj7A_	Alignment		100.0	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
9	d1sbpa_	Alignment		100.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c6fjlD_	Alignment		100.0	16	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**abc-type fe3+ transport system, periplasmic component; **PDBTitle:** structure of ibps from dickeya dadantii
11	c5um2A_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter sulfate binding protein; **PDBTitle:** functional and structural characterization of a sulfate-binding2 protein (sbp) from xanthomonas citri

12	c3muqB_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
13	c4ecfA_	Alignment		99.9	16	**PDB header:**phosphate-binding protein **Chain:** A: **PDB Molecule:**abc-type phosphate transport system, periplasmic component; **PDBTitle:** crystal structure of an abc-type phosphate transport system,2 periplasmic component (lvis_0633) from lactobacillus brevis atcc 3673 at 1.55 a resolution
14	c2qryD_	Alignment		99.9	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**thiamine-binding periplasmic protein; **PDBTitle:** periplasmic thiamin binding protein
15	c3c9hB_	Alignment		99.9	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
16	c5my5A_	Alignment		99.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic substrate-binding protein; **PDBTitle:** tungstate binding protein - tupa - from desulfovibrio alaskensis g20
17	c3lr1A_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tungstate abc transporter, periplasmic tungstate- **PDBTitle:** the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
18	c4gd5B_	Alignment		99.9	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphate abc transporter, phosphate-binding protein; **PDBTitle:** x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
19	d1y9ua_	Alignment		99.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	c6dgvA_	Alignment		99.9	15	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**fluorescent gaba sensor precursor; **PDBTitle:** igabasnfr fluorescent gaba sensor precursor
21	c4jwoA_	Alignment	not modelled	99.9	14	**PDB header:**phosphate binding protein **Chain:** A: **PDB Molecule:**phosphate binding protein; **PDBTitle:** the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776
22	c4r73B_	Alignment	not modelled	99.9	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc-type fe3+ transport system, periplasmic component; **PDBTitle:** structure of the periplasmic binding protein afua from actinobacillus2 pleuropneumoniae (endogenous glucose-6-phosphate and mannose-6-3 phosphate bound)
23	c4exlD_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**phosphate-binding protein psts 1; **PDBTitle:** crystal structure of phosphate abc transporter, periplasmic phosphate-2 binding protein psts 1 (pbp1) from streptococcus pneumoniae canada3 mdr_19a
24	c3cvgD_	Alignment	not modelled	99.9	11	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**putative metal binding protein; **PDBTitle:** crystal structure of a periplasmic putative metal binding protein
25	c4n13A_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**phosphate abc transporter, periplasmic phosphate-binding **PDBTitle:** crystal structure of psts (bb_0215) from borrelia burgdorferi
26	c6hm2B_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**agropine permease; **PDBTitle:** structure in p1 form of the pbp agtb in complex with agropinic acid2 from a.tumefacien r10
27	d1twya_	Alignment	not modelled	99.9	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						PDB header:structural genomics, unknown function

28	c1twyG_	Alignment	not modelled	99.9	13	**Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
29	d1xvxa_	Alignment	not modelled	99.9	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	c5t1pB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of the putative periplasmic solute-binding protein2 from campylobacter jejuni
31	c3kn3C_	Alignment	not modelled	99.9	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
32	d1xc1a_	Alignment	not modelled	99.9	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
33	c3cfxA_	Alignment	not modelled	99.9	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein ma_0280; **PDBTitle:** crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
34	d1y4ta_	Alignment	not modelled	99.9	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
35	c4edpA_	Alignment	not modelled	99.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate-binding protein; **PDBTitle:** 1.85 angstrom resolution crystal structure of an abc transporter from2 clostridium perfringens atcc 13124
36	d1xvya_	Alignment	not modelled	99.9	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
37	c4eq7B_	Alignment	not modelled	99.9	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein (polyamine); **PDBTitle:** structure of atu4243-gaba receptor
38	c2pt1A_	Alignment	not modelled	99.9	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
39	c5l9pA_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein; **PDBTitle:** crystal structure of the pbp mota from a. tumefaciens b6
40	c4ombB_	Alignment	not modelled	99.9	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphate binding protein; **PDBTitle:** phosphate binding protein
41	d1nnfa_	Alignment	not modelled	99.9	24	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
42	c4r6yA_	Alignment	not modelled	99.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative 2-aminoethylphosphonate-binding periplasmic **PDBTitle:** crystal structure of solute-binding protein stm0429 from salmonella2 enterica subsp. enterica serovar typhimurium str. lt2, target efi-3 510776, a closed conformation, in complex with glycerol and acetate
43	c3k6wA_	Alignment	not modelled	99.9	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute-binding protein ma_0280; **PDBTitle:** apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
44	c6g7qB_	Alignment	not modelled	99.9	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**extracellular solute-binding protein, family 1; **PDBTitle:** trichodesmium tery_3377 (idia) (futa) in complex with iron and citrate2 ligands.
45	d2onsa1	Alignment	not modelled	99.9	26	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
46	c4eloD_	Alignment	not modelled	99.9	16	**PDB header:**metal transport **Chain:** D: **PDB Molecule:**iron abc transporter, periplasmic iron-binding protein; **PDBTitle:** ferric binding protein in apo form 1
47	c4i1dB_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter substrate-binding protein; **PDBTitle:** the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110
48	c2v84A_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**spermidine/putrescine abc transporter, periplasmic binding **PDBTitle:** crystal structure of the tp0655 (tppotd) lipoprotein of treponema2 pallidum
49	c3rpwA_	Alignment	not modelled	99.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter; **PDBTitle:** the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
50	c4gl0A_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lmo0810 protein; **PDBTitle:** putative spermidine/putrescine abc transporter from listeria2 monocytogenes
51	c4eqbA_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**spermidine/putrescine abc superfamily atp binding cassette **PDBTitle:** 1.5 angstrom crystal structure of spermidine/putrescine abc2 transporter substrate-binding protein potd from streptococcus3 pneumoniae strain canada mdr_19a in complex with calcium and hepes

52	d1q35a_	Alignment	not modelled	99.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
53	c3cg1A_	Alignment	not modelled	99.9	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein pf0080; **PDBTitle:** crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate
54	c3cg3A_	Alignment	not modelled	99.9	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein ph0151; **PDBTitle:** crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate
55	c5l9sA_	Alignment	not modelled	99.9	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein (mannopine); **PDBTitle:** structure of agrobacterium tumefaciens c58 strain pbp attc in open2 unliganded conformation
56	c3osrA_	Alignment	not modelled	99.8	12	**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
57	d1pota_	Alignment	not modelled	99.8	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
58	c6nlpA_	Alignment	not modelled	99.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bacterial extracellular solute-binding family protein; **PDBTitle:** the crystal structure of an abc transporter periplasmic binding2 protein ydcs from escherichia coli bw25113
59	c3cfzA_	Alignment	not modelled	99.8	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein mj1186; **PDBTitle:** crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
60	c2vozA_	Alignment	not modelled	99.8	18	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**periplasmic iron-binding protein; **PDBTitle:** apo futa2 from synechocystis pcc6803
61	c3woaA_	Alignment	not modelled	99.8	12	**PDB header:**dna binding protein, sugar binding prote **Chain:** A: **PDB Molecule:**repressor protein ci, maltose-binding periplasmic protein; **PDBTitle:** crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
62	d1ursa_	Alignment	not modelled	99.8	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
63	c1ursA_	Alignment	not modelled	99.8	14	**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
64	c5fsgA_	Alignment	not modelled	99.8	11	**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
65	c4dxbB_	Alignment	not modelled	99.8	12	**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
66	c5eduB_	Alignment	not modelled	99.8	12	**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
67	c4wrnB_	Alignment	not modelled	99.8	12	**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
68	c5i04A_	Alignment	not modelled	99.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,endoglin; **PDBTitle:** crystal structure of the orphan region of human endoglin/cd105
69	c3ttkA_	Alignment	not modelled	99.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polyamine transport protein; **PDBTitle:** crystal structure of apo-spud
70	c3pu5A_	Alignment	not modelled	99.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular solute-binding protein; **PDBTitle:** the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
71	c4r0yA_	Alignment	not modelled	99.8	12	**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
72	c3ttlB_	Alignment	not modelled	99.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**polyamine transport protein; **PDBTitle:** crystal structure of apo-spue
73	c3py7A_	Alignment	not modelled	99.8	12	**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
						PDB header:gene regulation

74	c1r6zA_	Alignment	not modelled	99.8	12	**Chain:** A: **PDB Molecule:**chimera of maltose-binding periplasmic protein and **PDBTitle:** the crystal structure of the argonaute2 paz domain (as a mbp fusion)
75	c3ob4A_	Alignment	not modelled	99.8	12	**PDB header:**allergen **Chain:** A: **PDB Molecule:**maltose abc transporter periplasmic protein, arah 2; **PDBTitle:** mbp-fusion protein of the major peanut allergen ara h 2
76	c4h1gA_	Alignment	not modelled	99.8	12	**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
77	c3h4zC_	Alignment	not modelled	99.8	12	**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
78	c6dd5B_	Alignment	not modelled	99.8	12	**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
79	c5hzvA_	Alignment	not modelled	99.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,endoglin; **PDBTitle:** crystal structure of the zona pellucida module of human endoglin/cd105
80	c5f7vA_	Alignment	not modelled	99.8	17	**PDB header:**cycloalternan binding protein **Chain:** A: **PDB Molecule:**lmo0181 protein; **PDBTitle:** abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloalternan
81	c4qvhA_	Alignment	not modelled	99.8	12	**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
82	d1a99a_	Alignment	not modelled	99.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
83	c2gh9A_	Alignment	not modelled	99.8	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding protein; **PDBTitle:** thermus thermophilus maltotriose binding protein bound with2 maltotriose
84	c3o3uN_	Alignment	not modelled	99.8	12	**PDB header:**transport protein, signaling protein **Chain:** N: **PDB Molecule:**maltose-binding periplasmic protein, advanced glycosylation **PDBTitle:** crystal structure of human receptor for advanced glycation endproducts2 (rage)
85	c5tu0A_	Alignment	not modelled	99.8	19	**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
86	c3mp6A_	Alignment	not modelled	99.8	12	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,linker,saga-associated **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
87	c4egcA_	Alignment	not modelled	99.8	12	**PDB header:**transcription/hydrolase **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, homeobox protein six1 **PDBTitle:** crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain
88	c4rwgC_	Alignment	not modelled	99.8	12	**PDB header:**membrane protein/hormone **Chain:** C: **PDB Molecule:**maltose-binding periplasmic protein, receptor activity- **PDBTitle:** crystal structure of the clr:ramp1 extracellular domain heterodimer2 with bound high affinity cgrp analog
89	c5t0aB_	Alignment	not modelled	99.8	12	**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
90	c4kegA_	Alignment	not modelled	99.8	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic/palate lung and nasal **PDBTitle:** crystal structure of mbp fused human splunc1
91	c5mkbF_	Alignment	not modelled	99.8	16	**PDB header:**sugar binding protein **Chain:** F: **PDB Molecule:**male1; **PDBTitle:** maltodextrin binding protein male1 from l. casei bl23 without ligand
92	c4hs7A_	Alignment	not modelled	99.8	8	**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.
93	c5azaA_	Alignment	not modelled	99.8	12	**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
94	c4logA_	Alignment	not modelled	99.8	12	**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
95	c3waiA_	Alignment	not modelled	99.8	12	**PDB header:**transferase, transport protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, transmembrane **PDBTitle:** crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion

96	c5dfmB_	Alignment	not modelled	99.8	12	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**maltose-binding periplasmic protein,telomerase-associated **PDBTitle:** structure of tetrahymena telomerase p19 fused to mbp
97	c5b3zB_	Alignment	not modelled	99.8	11	**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
98	c6anvA_	Alignment	not modelled	99.8	12	**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
99	c5ii5A_	Alignment	not modelled	99.8	12	**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
100	c5jonA_	Alignment	not modelled	99.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,potassium/sodium **PDBTitle:** crystal structure of the unliganded form of hcn2 cnbd
101	c3f5fA_	Alignment	not modelled	99.8	13	**PDB header:**transport, transferase **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, heparan sulfate 2-o- **PDBTitle:** crystal structure of heparan sulfate 2-o-sulfotransferase from gallus2 gallus as a maltose binding protein fusion.
102	c4kv3A_	Alignment	not modelled	99.8	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chimera fusion protein of esx-1 secretion system protein **PDBTitle:** ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
103	c3oaiB_	Alignment	not modelled	99.8	12	**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
104	c1y4cA_	Alignment	not modelled	99.8	12	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
105	c5wvmA_	Alignment	not modelled	99.8	12	**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
106	c4pqkA_	Alignment	not modelled	99.8	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**maltose abc transporter periplasmic protein, truncated **PDBTitle:** c-terminal domain of dna binding protein
107	c5ttdA_	Alignment	not modelled	99.8	12	**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
108	c4wgiA_	Alignment	not modelled	99.8	13	**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)
109	c3c4mA_	Alignment	not modelled	99.8	12	**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)
110	c4my2A_	Alignment	not modelled	99.8	12	**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
111	c5tibA_	Alignment	not modelled	99.8	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**sugar abc transporter substrate-binding protein,gasdermin- **PDBTitle:** gasdermin-b c-terminal domain containing the polymorphism residues2 arg299:ser306 fused to maltose binding protein
112	c6aeoA_	Alignment	not modelled	99.8	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding periplasmic protein,tssl; **PDBTitle:** tssl periplasmic domain
113	c4b3nA_	Alignment	not modelled	99.8	11	**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
114	c4edqA_	Alignment	not modelled	99.8	12	**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
115	c2vgqA_	Alignment	not modelled	99.8	12	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**sugar abc transporter substrate-binding protein, **PDBTitle:** crystal structure of human ips-1 card
116	c4rk2B_	Alignment	not modelled	99.8	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
117	c3k02A_	Alignment	not modelled	99.8	17	**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.
118	d1eu8a_	Alignment	not modelled	99.8	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
119	c4wviA_	Alignment	not modelled	99.8	11	**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).
120	c4xa2A_	Alignment	not modelled	99.8	13	**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