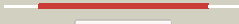



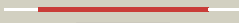




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2400c_(subl)_2696654_2697724
Date	Mon Aug 5 13:25:56 BST 2019
Unique Job ID	ead5edc049bba9c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ddnB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable sulfate-binding lipoprotein subi; <b>PDBTitle:</b> the sulfate-binding protein subi from mycobacterium tuberculosis h37rv
2	<a href="#">d1sbpa_</a>	 Alignment		100.0	32	<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="#">c5um2A_</a>	 Alignment		100.0	30	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter sulfate binding protein; <b>PDBTitle:</b> functional and structural characterization of a sulfate-binding2 protein (sbp) from xanthomonas citri
4	<a href="#">c6fjID_</a>	 Alignment		100.0	15	<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
5	<a href="#">c4wrnB_</a>	 Alignment		100.0	15	<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
6	<a href="#">c5i04A_</a>	 Alignment		100.0	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
7	<a href="#">d1y9ua_</a>	 Alignment		100.0	19	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
8	<a href="#">c5hzvA_</a>	 Alignment		100.0	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 zona pellucida module of human endoglin/cd105
9	<a href="#">c3woaA_</a>	 Alignment		100.0	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
10	<a href="#">c4h1gA_</a>	 Alignment		100.0	13	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein-cakar3 motor domain fusion protein; <b>PDBTitle:</b> structure of candida albicans kar3 motor domain fused to maltose-2 binding protein
11	<a href="#">c5jqeA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter substrate-binding protein,caspase-8 <b>PDBTitle:</b> crystal structure of caspase8 tded

12	<a href="#">c5eduB</a>	Alignment		100.0	14	<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
13	<a href="#">c6dd5B</a>	Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mmb-1 cas6 fused to maltose binding protein,crispr- <b>PDBTitle:</b> crystal structure of the cas6 domain of marinomonas mediterranea mmb-12 cas6-rt-cas1 fusion protein
14	<a href="#">c6dgvA</a>	Alignment		100.0	14	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> fluorescent gaba sensor precursor; <b>PDBTitle:</b> igabasnfr fluorescent gaba sensor precursor
15	<a href="#">c4egcA</a>	Alignment		100.0	14	<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
16	<a href="#">c5t1pB</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of the putative periplasmic solute-binding protein2 from campylobacter jejuni
17	<a href="#">c3py7A</a>	Alignment		100.0	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
18	<a href="#">c3ob4A</a>	Alignment		100.0	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
19	<a href="#">c5t0aB</a>	Alignment		100.0	12	<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
20	<a href="#">c5fsgA</a>	Alignment		100.0	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, hantavirus <b>PDBTitle:</b> structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design
21	<a href="#">c4kegA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic/palate lung and nasal <b>PDBTitle:</b> crystal structure of mbp fused human splunc1
22	<a href="#">c4r0yA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, disks large-associated <b>PDBTitle:</b> structure of maltose-binding protein fusion with the c-terminal gh12 domain of guanylate kinase-associated protein from rattus norvegicus
23	<a href="#">c3waiA</a>	Alignment	not modelled	100.0	13	<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
24	<a href="#">c3h4zC</a>	Alignment	not modelled	100.0	13	<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
25	<a href="#">c3osrA</a>	Alignment	not modelled	100.0	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
26	<a href="#">c3o3uN</a>	Alignment	not modelled	100.0	14	<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)
27	<a href="#">c3f5fA</a>	Alignment	not modelled	100.0	15	<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.
28	<a href="#">c4edpA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate-binding protein; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of an abc transporter from2 clostridium perfringens atcc 13124
29	<a href="#">c6anvA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> anti-crispr protein acr1 fused with c-terminal mbp tag; <b>PDBTitle:</b> crystal structure of anti-crispr protein acr1
30	<a href="#">c4logA</a>	Alignment	not modelled	100.0	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
31	<a href="#">c4rwgC</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> membrane protein/hormone <b>Chain:</b> C: <b>PDB Molecule:</b> maltose-binding periplasmic protein, receptor activity- <b>PDBTitle:</b> crystal structure of the clr:ramp1 extracellular domain heterodimer2 with bound high affinity cgrp analog
32	<a href="#">c4bl9D</a>	Alignment	not modelled	100.0	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)
33	<a href="#">c4qvhA</a>	Alignment	not modelled	100.0	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
34	<a href="#">c3dm0A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with rack1; <b>PDBTitle:</b> maltose binding protein fusion with rack1 from a. thaliana
35	<a href="#">d1ursa</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
36	<a href="#">c1ursa</a>	Alignment	not modelled	100.0	13	<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
37	<a href="#">c4edqA</a>	Alignment	not modelled	100.0	13	<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
38	<a href="#">c5ii5A</a>	Alignment	not modelled	100.0	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
39	<a href="#">c3osqA</a>	Alignment	not modelled	100.0	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 175
40	<a href="#">c4i1dB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter substrate-binding protein; <b>PDBTitle:</b> the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110
41	<a href="#">c4kv3A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chimera fusion protein of esx-1 secretion system protein <b>PDBTitle:</b> ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
42	<a href="#">c4xa2A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,mbp-pila: c; <b>PDBTitle:</b> structure of the major type iv pilin of acinetobacter baumannii
43	<a href="#">c3d4cA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, linker, zona pellucida <b>PDBTitle:</b> zp-n domain of mammalian sperm receptor zp3 (crystal form i)
44	<a href="#">c4pqkA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein, truncated <b>PDBTitle:</b> c-terminal domain of dna binding protein
45	<a href="#">c6aeoA</a>	Alignment	not modelled	100.0	11	<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
46	<a href="#">c5qxtA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,pigg; <b>PDBTitle:</b> crystal structure of pigg
47	<a href="#">c5tibA</a>	Alignment	not modelled	100.0	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
48	<a href="#">c3mp6A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> histone binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,linker,saga-associated <b>PDBTitle:</b> complex structure of sgf29 and dimethylated h3k4
						<b>PDB header:</b> nuclear protein

49	<a href="#">c5dfmB_</a>	Alignment	not modelled	100.0	13	<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
50	<a href="#">c5azaA_</a>	Alignment	not modelled	100.0	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
51	<a href="#">c5b3zB_</a>	Alignment	not modelled	100.0	11	<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
52	<a href="#">c4dxbB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> sugar binding protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, beta-lactamase tem <b>PDBTitle:</b> 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group
53	<a href="#">c5wvmA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> sugar binding protein <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
54	<a href="#">c3oaiB_</a>	Alignment	not modelled	100.0	12	<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
55	<a href="#">c4tsmC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> maltose-binding protein, pilin chimera; <b>PDBTitle:</b> mbp-fusion protein of pila1 from c. difficile r20291 residues 26-166
56	<a href="#">c6apxA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,dual specificity <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the monobody ysx1
57	<a href="#">c1r6zA_</a>	Alignment	not modelled	100.0	13	<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)
58	<a href="#">c1hsjA_</a>	Alignment	not modelled	100.0	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
59	<a href="#">c5jonA_</a>	Alignment	not modelled	100.0	12	<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
60	<a href="#">c2nvuB_</a>	Alignment	not modelled	100.0	14	<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
61	<a href="#">c1y4cA_</a>	Alignment	not modelled	100.0	14	<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
62	<a href="#">c5ttDA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,pilin isopeptide <b>PDBTitle:</b> minor pilin fctb from s. pyogenes with engineered intramolecular2 isopeptide bond
63	<a href="#">c4b3nA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein/ligase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, tripartite motif- <b>PDBTitle:</b> crystal structure of rhesus trim5alpha pry/spry domain
64	<a href="#">c3c9hB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, substrate binding protein; <b>PDBTitle:</b> crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
65	<a href="#">c6hm2B_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> agropine permease; <b>PDBTitle:</b> structure in p1 form of the pbp agtb in complex with agropinic acid2 from a.tumefacien r10
66	<a href="#">c3vd8A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> sugar binding protein,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, interferon-inducible <b>PDBTitle:</b> crystal structure of human aim2 pyd domain with mbp fusion
67	<a href="#">c3c4mA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of maltose-binding periplasmic protein and <b>PDBTitle:</b> structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
68	<a href="#">c2qrvD_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine-binding periplasmic protein; <b>PDBTitle:</b> periplasmic thiamin binding protein
69	<a href="#">c5y2gA_</a>	Alignment	not modelled	100.0	14	<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
70	<a href="#">c5l9pA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein; <b>PDBTitle:</b> crystal structure of the pbp mota from a. tumefaciens b6
71	<a href="#">c5hz7A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> comp; <b>PDBTitle:</b> high-resolution crystal structure of the minor dna-binding pilin comp2 from neisseria meningitidis in fusion with mbp
72	<a href="#">c4n10A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0810 protein;

72	<a href="#">c4gi0A</a>	Alignment	not modelled	100.0	12	<b>PDBTitle:</b> putative spermidine/putrescine abc transporter from listeria2 monocytogenes <b>PDB header:</b> immune system/transport <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter substrate-binding protein, <b>PDBTitle:</b> crystal structure of human ips-1 card
73	<a href="#">c2vgqA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, linker, mitochondrial <b>PDBTitle:</b> crystal structure of tim40/mia40 fusing mbp, c296s and c298s mutant
74	<a href="#">c3a3cA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine/putrescine abc superfamily atp binding cassette <b>PDBTitle:</b> 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
75	<a href="#">c4eqbA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, substrate binding protein (polyamine); <b>PDBTitle:</b> structure of atu4243-gaba receptor
76	<a href="#">c4eq7B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> de novo protein, sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding protein monobody ys1 fusion; <b>PDBTitle:</b> crystal structure of monobody ys1(mbp-74)/maltose binding protein2 fusion complex
77	<a href="#">c3csgA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc-type fe3+ transport system, periplasmic component; <b>PDBTitle:</b> structure of the periplasmic binding protein afua from actinobacillus2 pleuropneumoniae (endogenous glucose-6-phosphate and mannose-6-3 phosphate bound)
78	<a href="#">c4r73B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,signal peptidase ib; <b>PDBTitle:</b> crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2).
79	<a href="#">c4wviA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> the crystal structure of an abc transporter from rhodospseudomonas2 palustris cga009
80	<a href="#">c3rpwA</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, jmjc domain-containing <b>PDBTitle:</b> crystal structure of mouse jmjd7 fused with maltose-binding protein
81	<a href="#">c4qszB</a>	Alignment	not modelled	100.0	12	<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
82	<a href="#">c3ehuA</a>	Alignment	not modelled	100.0	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)
83	<a href="#">c4wgiA</a>	Alignment	not modelled	100.0	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
84	<a href="#">c4my2A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of maltose-binding periplasmic protein and <b>PDBTitle:</b> revealing surface waters on an antifreeze protein by fusion protein2 crystallography
85	<a href="#">c5c7rA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine/putrescine abc transporter, periplasmic binding <b>PDBTitle:</b> crystal structure of the tp0655 (tppotd) lipoprotein of treponema2 pallidum
86	<a href="#">c2v84A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular solute-binding protein; <b>PDBTitle:</b> the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
87	<a href="#">c3pu5A</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
88	<a href="#">d1atga</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of maltose-binding periplasmic protein and kinesin <b>PDBTitle:</b> crystal structure of the mouse kif14 motor domain
89	<a href="#">c4ozqA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2-aminoethylphosphonate-binding periplasmic <b>PDBTitle:</b> 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
90	<a href="#">c4r6yA</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
91	<a href="#">d1y4ta</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> iron transport protein; <b>PDBTitle:</b> futa1 synechocystis pcc 6803
92	<a href="#">c2pt1A</a>	Alignment	not modelled	100.0	18	<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
93	<a href="#">c3uorB</a>	Alignment	not modelled	100.0	11	

						phytopathogen2 xanthomonas citri
94	<a href="#">d1pota_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
95	<a href="#">c4kd5A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type transport system, molybdenum-specific <b>PDBTitle:</b> substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
96	<a href="#">c4ua8A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate abc transporter substrate-binding protein, <b>PDBTitle:</b> eur_01830 (maltotriose-binding protein) complexed with maltotriose
97	<a href="#">c4eloD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> metal transport <b>Chain:</b> D: <b>PDB Molecule:</b> iron abc transporter, periplasmic iron-binding protein; <b>PDBTitle:</b> ferric binding protein in apo form 1
98	<a href="#">c3qufB_</a>	Alignment	not modelled	100.0	16	<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
99	<a href="#">d1eu8a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
100	<a href="#">c5k94B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein,protein translocase <b>PDBTitle:</b> deletion-insertion chimera of mbp with the preprotein cross-linking2 domain of the seca atpase
101	<a href="#">c5f7vA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> cycloalternan 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 cycloalternan
102	<a href="#">c6g7qB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular solute-binding protein, family 1; <b>PDBTitle:</b> trichodesmium tery_3377 (idia) (futa) in complex with iron and citrate2 ligands.
103	<a href="#">c4rk2B_</a>	Alignment	not modelled	100.0	16	<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
104	<a href="#">c5tu0A_</a>	Alignment	not modelled	100.0	11	<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
105	<a href="#">c4hs7A_</a>	Alignment	not modelled	100.0	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.
106	<a href="#">c4r6kA_</a>	Alignment	not modelled	100.0	14	<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
107	<a href="#">c5ixpA_</a>	Alignment	not modelled	100.0	15	<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
108	<a href="#">c2zykA_</a>	Alignment	not modelled	100.0	15	<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
109	<a href="#">c2gh9A_</a>	Alignment	not modelled	100.0	17	<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
110	<a href="#">c4ifpC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> maltose-binding periplasmic protein,nacht, lrr and pyd <b>PDBTitle:</b> x-ray crystal structure of human nlrp1 card domain
111	<a href="#">d1q35a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
112	<a href="#">c5i9sA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein (mannopine); <b>PDBTitle:</b> structure of agrobacterium tumefaciens c58 strain pbp attc in open2 unliganded conformation
113	<a href="#">c2xd3A_</a>	Alignment	not modelled	100.0	17	<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.
114	<a href="#">c3ttlB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> polyamine transport protein; <b>PDBTitle:</b> crystal structure of apo-spue
115	<a href="#">c4aq4A_</a>	Alignment	not modelled	100.0	14	<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
116	<a href="#">c5az6A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein, peptide binding p <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,mitochondrial import

					<b>PDBTitle:</b> crystal structure of mbp-tom20 fusion protein with a 2-residue spacer2 in the connector helix
117	<a href="#">c4exkA</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, uncharacterized <b>PDBTitle:</b> a chimera protein containing mbp fused to the c-terminal domain of the2 uncharacterized protein stm14_2015 from salmonella enterica
118	<a href="#">d1xc1a</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
119	<a href="#">c4xzsA</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,tp53-regulated <b>PDBTitle:</b> crystal structure of triap1-mbp fusion
120	<a href="#">c4o2xA</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, atp-dependent clp <b>PDBTitle:</b> structure of a malarial protein