





















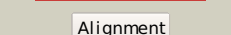



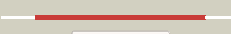
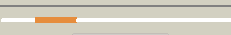


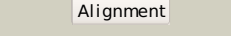
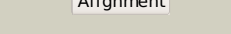
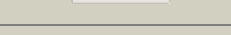

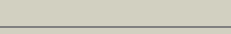
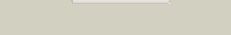
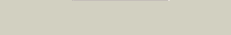
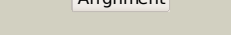
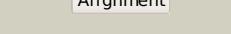
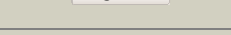

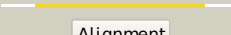
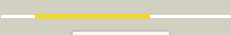



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1sw5a_</a>	 Alignment		100.0	28	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
2	<a href="#">c3r6uA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
3	<a href="#">c3o66A_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline abc transporter; <b>PDBTitle:</b> crystal structure of glycine betaine/carnitine/choline abc transporter
4	<a href="#">c3pppA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline-binding protein; <b>PDBTitle:</b> structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
5	<a href="#">d1r9la_</a>	 Alignment		100.0	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
6	<a href="#">c2rejA_</a>	 Alignment		100.0	18	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein; <b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation
7	<a href="#">c3tmgA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine, l-proline abc transporter, <b>PDBTitle:</b> crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
8	<a href="#">c3l6gA_</a>	 Alignment		100.0	15	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
9	<a href="#">c3chgB_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein; <b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
10	<a href="#">c3e4rA_</a>	 Alignment		99.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
11	<a href="#">c3uifA_</a>	 Alignment		99.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt

12	<a href="#">c3ix1A_</a>	Alignment		99.4	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
13	<a href="#">c2de4B_</a>	Alignment		99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> di-benzothiophene desulfurization enzyme b; <b>PDBTitle:</b> crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
14	<a href="#">c3ix1B_</a>	Alignment		99.4	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding <b>PDBTitle:</b> periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
15	<a href="#">c2x26A_</a>	Alignment		99.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic aliphatic sulphonates-binding protein; <b>PDBTitle:</b> crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
16	<a href="#">c3un6A_</a>	Alignment		99.3	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein saouhsc_00137; <b>PDBTitle:</b> 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
17	<a href="#">c3qslA_</a>	Alignment		99.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of cae31940 from bordetella bronchiseptica rb50
18	<a href="#">c2x7pA_</a>	Alignment		99.2	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme; <b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
19	<a href="#">c2g29A_</a>	Alignment		99.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein nrta; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
20	<a href="#">c3gxaA_</a>	Alignment		99.1	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of gna1946
21	<a href="#">c3hn0A_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
22	<a href="#">c1p99A_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg110; <b>PDBTitle:</b> 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
23	<a href="#">d1p99a_</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
24	<a href="#">c3tqwA_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-binding protein; <b>PDBTitle:</b> structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
25	<a href="#">c2i4cA_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bicarbonate transporter; <b>PDBTitle:</b> crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
26	<a href="#">c3k2dA_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type metal ion transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of immunogenic lipoprotein a from vibrio vulnificus
27	<a href="#">c3ir1F_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> outer membrane lipoprotein gna1946; <b>PDBTitle:</b> crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
28	<a href="#">d1us5a_</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like

29	<a href="#">dlxs5a_</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
30	<a href="#">d2nxoa1</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
31	<a href="#">c2h5yC_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> molybdate-binding periplasmic protein; <b>PDBTitle:</b> crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
32	<a href="#">c3n5lA_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter; <b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
33	<a href="#">c3muqB_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
34	<a href="#">c3lr1A_</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tungstate abc transporter, periplasmic tungstate- <b>PDBTitle:</b> the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
35	<a href="#">c3gyyC_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
36	<a href="#">d1sbpa_</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
37	<a href="#">d1zba1</a>	Alignment	not modelled	96.7	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
38	<a href="#">c2hpgB_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding <b>PDBTitle:</b> the crystal structure of a thermophilic trap periplasmic2 binding protein
39	<a href="#">d2czla1</a>	Alignment	not modelled	96.6	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
40	<a href="#">c2vpnB_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> transport <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic substrate binding protein; <b>PDBTitle:</b> high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
41	<a href="#">c2pfzA_</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
42	<a href="#">c2f5xC_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> bugd; <b>PDBTitle:</b> structure of periplasmic binding protein bugd
43	<a href="#">d1amfa_</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
44	<a href="#">c2pfyA_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
45	<a href="#">c3fj7A_</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> major antigenic peptide peb3; <b>PDBTitle:</b> crystal structure of l-phospholactate bound peb3
46	<a href="#">c2dvzA_</a>	Alignment	not modelled	94.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> structure of a periplasmic transporter
47	<a href="#">c3rpwA_</a>	Alignment	not modelled	94.6	12	<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 rhodopseudomonas2 palustris cga009
48	<a href="#">c2zzxD_</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc transporter, solute-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic substrate binding protein in2 complex with lactate
49	<a href="#">c3fxbB_</a>	Alignment	not modelled	93.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of the ectoine-binding protein ueha
50	<a href="#">c3b50A_</a>	Alignment	not modelled	93.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sialic acid-binding periplasmic protein siap; <b>PDBTitle:</b> structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
51	<a href="#">c3kn3C_</a>	Alignment	not modelled	93.2	9	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
52	<a href="#">d2fyia1</a>	Alignment	not modelled	93.1	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
53	<a href="#">c2qpqC_</a>	Alignment	not modelled	93.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein bug27; <b>PDBTitle:</b> structure of bug27 from bordetella pertussis

54	<a href="#">c3c9hB_</a>	 Alignment	not modelled	92.3	8	<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
55	<a href="#">c3kzgB_</a>	 Alignment	not modelled	92.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> arginine 3rd transport system periplasmic binding <b>PDBTitle:</b> crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
56	<a href="#">c1a13A_</a>	 Alignment	not modelled	90.8	17	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cys regulon transcriptional activator cysb; <b>PDBTitle:</b> cofactor binding fragment of cysb from klebsiella aerogenes
57	<a href="#">d1a13a_</a>	 Alignment	not modelled	90.8	17	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
58	<a href="#">c3k4uA_</a>	 Alignment	not modelled	90.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding component of abc transporter; <b>PDBTitle:</b> crystal structure of putative binding component of abc transporter2 from wolfinella succinogenes dsm 1740 complexed with lysine
59	<a href="#">c2f7cA_</a>	 Alignment	not modelled	89.9	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> catm effector binding domain with its effector cis,cis-muconate
60	<a href="#">d1i6aa_</a>	 Alignment	not modelled	88.8	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
61	<a href="#">d2esna2</a>	 Alignment	not modelled	88.7	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
62	<a href="#">c2h9bB_</a>	 Alignment	not modelled	88.1	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
63	<a href="#">c2h9qC_</a>	 Alignment	not modelled	87.4	16	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a catm2 variant (r156h)
64	<a href="#">c2f78A_</a>	 Alignment	not modelled	86.9	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> benm effector binding domain with its effector benzoate
65	<a href="#">c3jv9B_</a>	 Alignment	not modelled	86.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> the structure of a reduced form of oxyr from n. meningitidis
66	<a href="#">c2hzkB_</a>	 Alignment	not modelled	86.1	13	<b>PDB header:</b> ligand binding, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trap-t family sorbitol/mannitol transporter, periplasmic <b>PDBTitle:</b> crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
67	<a href="#">c3oxnD_</a>	 Alignment	not modelled	86.1	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
68	<a href="#">c3ho7A_</a>	 Alignment	not modelled	86.1	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> crystal structure of oxyr from porphyromonas gingivalis
69	<a href="#">c2ql3G_</a>	 Alignment	not modelled	83.9	20	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
70	<a href="#">c2q2aD_</a>	 Alignment	not modelled	83.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> artj; <b>PDBTitle:</b> crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
71	<a href="#">c3n6uA_</a>	 Alignment	not modelled	83.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lysyr type regulator of tsambcd; <b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
72	<a href="#">c3mplA_</a>	 Alignment	not modelled	80.7	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
73	<a href="#">c2hxrA_</a>	 Alignment	not modelled	80.1	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator cynr; <b>PDBTitle:</b> structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
74	<a href="#">dlixca2</a>	 Alignment	not modelled	78.9	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
75	<a href="#">d1lutha_</a>	 Alignment	not modelled	78.4	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
76	<a href="#">c2uyeA_</a>	 Alignment	not modelled	77.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> double mutant y110s,f111v dnt from burkholderia sp. strain2 dnt in complex with thiocyanate
77	<a href="#">c3osqA_</a>	 Alignment	not modelled	77.2	9	<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 <b>PDB header:</b> sugar binding protein,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with <b>PDBTitle:</b> maltose binding protein fusion with rack1 from a. thaliana
78	<a href="#">c3dm0A_</a>	Alignment	not modelled	76.3	9	
79	<a href="#">d1vr5a1</a>	Alignment	not modelled	73.0	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
80	<a href="#">c3tpaA_</a>	Alignment		72.2	13	<b>PDB header:</b> heme binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> structure of hbpa2 from haemophilus parasuis
81	<a href="#">d1dpea_</a>	Alignment		71.4	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
82	<a href="#">c3pamB_</a>	Alignment		70.7	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein; <b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
83	<a href="#">c2pyyB_</a>	Alignment	not modelled	69.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ionotropic glutamate receptor bacterial homologue; <b>PDBTitle:</b> crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
84	<a href="#">d3bula2</a>	Alignment	not modelled	69.0	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
85	<a href="#">c2yxbA_</a>	Alignment	not modelled	68.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
86	<a href="#">c2xx7B_</a>	Alignment	not modelled	68.6	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor 2; <b>PDBTitle:</b> crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
87	<a href="#">c1f7uA_</a>	Alignment	not modelled	68.4	19	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
88	<a href="#">d1ii5a_</a>	Alignment	not modelled	67.0	22	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
89	<a href="#">c3ombA_</a>	Alignment	not modelled	66.3	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 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
90	<a href="#">c3lvuB_</a>	Alignment	not modelled	66.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
91	<a href="#">c1y4cA_</a>	Alignment	not modelled	66.0	9	<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
92	<a href="#">c3fd3A_</a>	Alignment	not modelled	65.5	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome replication initiation inhibitor protein; <b>PDBTitle:</b> structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
93	<a href="#">c2zufA_</a>	Alignment	not modelled	65.2	15	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
94	<a href="#">c3onmB_</a>	Alignment	not modelled	64.6	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator lrrha; <b>PDBTitle:</b> effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
95	<a href="#">c3ob4A_</a>	Alignment	not modelled	64.5	10	<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
96	<a href="#">c1ztyA_</a>	Alignment	not modelled	63.5	16	<b>PDB header:</b> sugar binding protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein; <b>PDBTitle:</b> crystal structure of the chitin oligosaccharide binding2 protein
97	<a href="#">c2o1mB_</a>	Alignment	not modelled	63.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable amino-acid abc transporter <b>PDBTitle:</b> crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
98	<a href="#">d1a9xa2</a>	Alignment	not modelled	63.3	19	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
99	<a href="#">c3eq1A_</a>	Alignment	not modelled	62.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
						<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter,



100	<a href="#">c2o7JA</a>	Alignment	not modelled	62.2	17	periplasmic <b>PDBTitle:</b> the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
101	<a href="#">d1pdaa1</a>	Alignment	not modelled	62.0	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
102	<a href="#">c3m8uA</a>	Alignment	not modelled	61.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
103	<a href="#">c1twyG</a>	Alignment	not modelled	58.9	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
104	<a href="#">d1twya</a>	Alignment	not modelled	58.9	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
105	<a href="#">c2yvqA</a>	Alignment	not modelled	56.9	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
106	<a href="#">c2pt1A</a>	Alignment	not modelled	55.1	7	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> iron transport protein; <b>PDBTitle:</b> futa1 synechocystis pcc 6803
107	<a href="#">c2k89A</a>	Alignment	not modelled	54.4	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a-2-activating protein; <b>PDBTitle:</b> solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
108	<a href="#">c1svxB</a>	Alignment	not modelled	54.3	9	<b>PDB header:</b> de novo protein/sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein
109	<a href="#">d1xoca1</a>	Alignment	not modelled	54.3	9	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
110	<a href="#">c3ol4B</a>	Alignment	not modelled	53.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
111	<a href="#">c3o3uN</a>	Alignment	not modelled	53.7	8	<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)
112	<a href="#">d1f7ua2</a>	Alignment	not modelled	52.6	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
113	<a href="#">c2vgqA</a>	Alignment	not modelled	50.5	8	<b>PDB header:</b> immune system/transport <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, <b>PDBTitle:</b> crystal structure of human ips-1 card
114	<a href="#">c2nvuB</a>	Alignment	not modelled	50.2	9	<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
115	<a href="#">d1dtza1</a>	Alignment	not modelled	49.9	15	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Transferrin
116	<a href="#">c1r6zA</a>	Alignment	not modelled	49.6	9	<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)
117	<a href="#">c3osrA</a>	Alignment	not modelled	48.4	9	<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
118	<a href="#">d1s50a1</a>	Alignment	not modelled	48.3	7	<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="#">d1zlqa1</a>	Alignment	not modelled	47.9	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
120	<a href="#">c1iq0A</a>	Alignment	not modelled	47.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus arginyl-trna synthetase