Phyre^2

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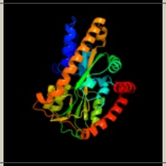
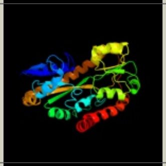
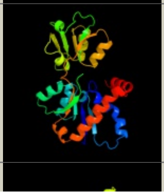
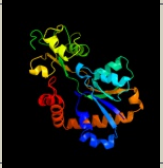
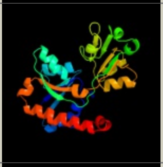
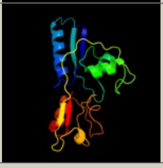
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pfyA_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
2	c3b50A_	Alignment		100.0	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sialic acid-binding periplasmic protein siap; **PDBTitle:** structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
3	c2pfzA_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
4	c3fxbB_	Alignment		100.0	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
5	c2vpnB_	Alignment		100.0	24	**PDB header:**transport **Chain:** B: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
6	c2hzkB_	Alignment		100.0	19	**PDB header:**ligand binding, transport protein **Chain:** B: **PDB Molecule:**trap-t family sorbitol/mannitol transporter, periplasmic **PDBTitle:** crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
7	c2hpgB_	Alignment		100.0	25	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding **PDBTitle:** the crystal structure of a thermophilic trap periplasmic2 binding protein
8	c2zzxD_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
9	c3gyyC_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
10	c3uifA_	Alignment		99.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfonate abc transporter, periplasmic sulfonate-binding **PDBTitle:** crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
11	c2x26A_	Alignment		99.5	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic aliphatic sulphonates-binding protein; **PDBTitle:** crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli

12	c3e4rA_	Alignment		99.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
13	c2x7pA_	Alignment		99.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme; **PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
14	c3qslA_	Alignment		99.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
15	c3ix1B_	Alignment		99.2	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
16	c3ix1A_	Alignment		99.2	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
17	c2de4B_	Alignment		99.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dibenzothiophene desulfurization enzyme b; **PDBTitle:** crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
18	c3un6A_	Alignment		99.1	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein saouhsc_00137; **PDBTitle:** 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
19	c3hn0A_	Alignment		99.0	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein; **PDBTitle:** crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
20	d1us5a_	Alignment		99.0	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
21	d1p99a_	Alignment	not modelled	98.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
22	c1p99A_	Alignment	not modelled	98.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
23	c3n5lA_	Alignment	not modelled	98.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter; **PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
24	c3gxaA_	Alignment	not modelled	98.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
25	c2g29A_	Alignment	not modelled	98.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein nrta; **PDBTitle:** crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
26	c3k2dA_	Alignment	not modelled	98.8	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**abc-type metal ion transport system, periplasmic component; **PDBTitle:** crystal structure of immunogenic lipoprotein a from vibrio vulnificus
27	c3tmgA_	Alignment	not modelled	98.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
						Fold: Periplasmic binding protein-like II

28	d1xs5a_	Alignment	not modelled	98.8	15	**Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
29	d2czla1	Alignment	not modelled	98.7	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
30	c2i4cA_	Alignment	not modelled	98.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bicarbonate transporter; **PDBTitle:** crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
31	d1zbma1	Alignment	not modelled	98.6	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
32	c2qpqC_	Alignment	not modelled	98.6	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
33	c3tqwA_	Alignment	not modelled	98.5	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** crystal structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
34	c3l6gA_	Alignment	not modelled	98.5	14	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
35	d2nxoa1	Alignment	not modelled	98.4	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
36	c3ir1F_	Alignment	not modelled	98.3	17	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
37	c2dvzA_	Alignment	not modelled	98.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
38	c2f5xC_	Alignment	not modelled	98.2	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
39	c1q1kA_	Alignment	not modelled	97.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
40	c3r6uA_	Alignment	not modelled	97.1	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
41	d2a5sa1	Alignment	not modelled	97.1	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
42	c2rejA_	Alignment	not modelled	96.9	14	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
43	d1h3da1	Alignment	not modelled	96.9	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	c3kzgB_	Alignment	not modelled	96.8	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**arginine 3rd transport system periplasmic binding **PDBTitle:** crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
45	c3pppA_	Alignment	not modelled	96.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
46	c2rc9A_	Alignment	not modelled	96.5	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit 3a; **PDBTitle:** crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
47	c2vd3B_	Alignment	not modelled	96.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
48	c2o1mB_	Alignment	not modelled	96.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable amino-acid abc transporter **PDBTitle:** crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
49	c3o66A_	Alignment	not modelled	96.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
50	c2ylnA_	Alignment	not modelled	96.3	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter, periplasmic binding protein, **PDBTitle:** crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
51	c1nh7A_	Alignment	not modelled	96.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
52	d1pb7a_	Alignment	not modelled	96.1	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
53	d1sw5a_	Alignment	not modelled	95.2	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
54	c2q2aD_	Alignment	not modelled	95.1	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**artj; **PDBTitle:** crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
55	d1z7me1	Alignment	not modelled	94.1	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
56	d1nh8a1	Alignment	not modelled	93.7	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
57	c2pyyB_	Alignment	not modelled	92.8	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ionotropic glutamate receptor bacterial homologue; **PDBTitle:** crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
58	c3k4uA_	Alignment	not modelled	91.9	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding component of abc transporter; **PDBTitle:** crystal structure of putative binding component of abc transporter2 from wolinella succinogenes dsm 1740 complexed with lysine
59	d1vmda_	Alignment	not modelled	90.6	21	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
60	c2ypnA_	Alignment	not modelled	89.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
61	c3mplA_	Alignment	not modelled	89.5	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**virulence sensor protein bvgs; **PDBTitle:** crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
62	d1lsta_	Alignment	not modelled	89.2	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
63	d1ii5a_	Alignment	not modelled	88.7	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
64	c2y7iB_	Alignment	not modelled	88.6	16	**PDB header:**arginine-binding protein **Chain:** B: **PDB Molecule:**stm4351; **PDBTitle:** structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
65	d2ozza1	Alignment	not modelled	87.2	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
66	d1pdaa1	Alignment	not modelled	86.5	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
67	c3r39A_	Alignment	not modelled	85.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative periplasmic binding protein; **PDBTitle:** crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
68	d1ve4a1	Alignment	not modelled	85.1	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
69	d1r9la_	Alignment	not modelled	84.5	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
70	c2vd2A_	Alignment	not modelled	83.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the crystal structure of hisg from b. subtilis
71	c3eq1A_	Alignment	not modelled	82.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
72	d1b1xa1	Alignment	not modelled	82.3	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
73	c3lr1A_	Alignment	not modelled	81.9	17	**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
74	c3g41A_	Alignment	not modelled	80.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid abc transporter, periplasmic amino acid-binding **PDBTitle:** the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
75	c3kn3C_	Alignment	not modelled	80.7	19	**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
76	c1y4cA_	Alignment	not modelled	79.9	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
77	d1b93a_	Alignment	not modelled	78.8	15	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
						Fold: Periplasmic binding protein-like II

78	d1eh3a_	Alignment	not modelled	78.1	18	**Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
79	d1o63a_	Alignment	not modelled	78.0	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
80	d1hsla_	Alignment	not modelled	77.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
81	c2v25B_	Alignment	not modelled	76.6	15	**PDB header:**receptor **Chain:** B: **PDB Molecule:**major cell-binding factor; **PDBTitle:** structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
82	d1ryoa_	Alignment	not modelled	76.2	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
83	c3luyA_	Alignment	not modelled	73.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
84	d1dtza1	Alignment	not modelled	72.8	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
85	d1sbpa_	Alignment	not modelled	71.8	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c3delC_	Alignment	not modelled	70.7	13	**PDB header:**protein binding, transport protein **Chain:** C: **PDB Molecule:**arginine binding protein; **PDBTitle:** the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
87	d2i6ea1	Alignment	not modelled	69.0	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
88	d1wo8a1	Alignment	not modelled	68.5	16	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
89	c3hv1A_	Alignment	not modelled	65.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polar amino acid abc uptake transporter substrate **PDBTitle:** crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
90	c2z8fB_	Alignment	not modelled	63.2	9	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**galacto-n-biose/lacto-n-biose i transporter substrate- **PDBTitle:** the galacto-n-biose-/lacto-n-biose i-binding protein (gl-bp) of the2 abc transporter from bifidobacterium longum in complex with lacto-n-3 tetraose
91	c2i6eG_	Alignment	not modelled	58.3	12	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein dr0370 from deinococcus radiodurans, pfam2 duf178
92	d2qmwa1	Alignment	not modelled	56.8	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
93	c3h7mA_	Alignment	not modelled	56.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
94	c3c4mA_	Alignment	not modelled	55.6	16	**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)
95	c3kbrA_	Alignment	not modelled	55.0	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclohexadienyl dehydratase; **PDBTitle:** the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
96	c3ob4A_	Alignment	not modelled	54.8	14	**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
97	d1tfda_	Alignment	not modelled	54.0	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
98	c1hsjA_	Alignment	not modelled	53.8	13	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
99	d1y9ba1	Alignment	not modelled	53.8	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
100	d2hava1	Alignment	not modelled	53.3	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
101	c3oaiB_	Alignment	not modelled	51.0	14	**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
102	c1r6zA_	Alignment	not modelled	48.9	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**chimera of maltose-binding periplasmic protein and **PDBTitle:** the crystal structure of the argonaute2 paz domain (as a mbp fusion)
						PDB header:transcription

103	c2h9bB_	Alignment	not modelled	48.5	15	**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
104	c3osrA_	Alignment	not modelled	48.3	15	**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
105	c3muqB_	Alignment	not modelled	47.8	15	**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
106	c3d4cA_	Alignment	not modelled	46.6	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, zona pellucida **PDBTitle:** zp-n domain of mammalian sperm receptor zp3 (crystal form i)
107	d1ieja_	Alignment	not modelled	45.8	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
108	c3f5fA_	Alignment	not modelled	45.2	13	**PDB header:**transport, transferase **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, heparan **PDBTitle:** crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion.
109	d1jnfa1	Alignment	not modelled	44.8	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
110	d1wdna_	Alignment	not modelled	44.0	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
111	d1h76a1	Alignment	not modelled	42.3	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
112	c2qmwA_	Alignment	not modelled	42.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
113	c2ieeB_	Alignment	not modelled	42.1	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable abc transporter extracellular-binding **PDBTitle:** crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
114	c3i6vA_	Alignment	not modelled	41.7	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic his/glu/gln/arg/opine family-binding protein; **PDBTitle:** crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
115	c2q89A_	Alignment	not modelled	40.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter amino acid-binding protein; **PDBTitle:** crystal structure of ehub in complex with hydroxyectoine
116	d2iiza1	Alignment	not modelled	39.5	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
117	c3fj7A_	Alignment	not modelled	39.4	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
118	c3fd3A_	Alignment	not modelled	38.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**chromosome replication initiation inhibitor protein; **PDBTitle:** structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
119	c2vgqA_	Alignment	not modelled	37.8	14	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
120	d1pc3a_	Alignment	not modelled	36.9	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like