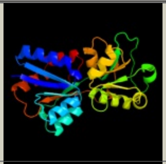
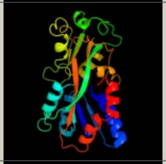
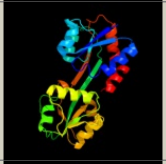
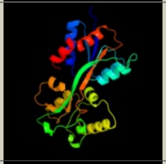
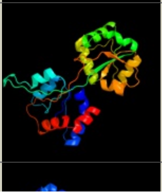
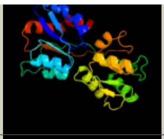
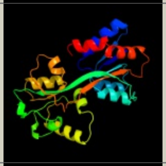
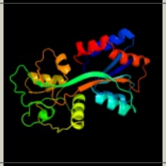
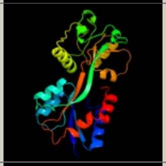
Email	l.a.kelley@imperial.ac.uk
Description	P37329
Date	Thu Jan 5 11:55:15 GMT 2012
Unique Job ID	3bedeef5e41dc2fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1amfa_	Alignment		100.0	100	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
2	c2h5yC_	Alignment		100.0	52	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**molybdate-binding periplasmic protein; **PDBTitle:** crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
3	d1atga_	Alignment		100.0	25	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
4	c3fj7A_	Alignment		100.0	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major antigenic peptide peb3; **PDBTitle:** crystal structure of l-phospholactate bound peb3
5	c2qryD_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**thiamine-binding periplasmic protein; **PDBTitle:** periplasmic thiamin binding protein
6	c3muqB_	Alignment		99.9	17	**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
7	c3c9hB_	Alignment		99.9	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
8	d1xvxa_	Alignment		99.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
9	d1sbpa_	Alignment		99.9	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	d1xc1a_	Alignment		99.9	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
11	c3kn3C_	Alignment		99.9	14	**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

12	c3lr1A_	Alignment		99.9	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
13	d1y9ua_	Alignment		99.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
14	d1xvya_	Alignment		99.9	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
15	c3rpwA_	Alignment		99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter; **PDBTitle:** the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
16	d1y4ta_	Alignment		99.9	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
17	d1nnfa_	Alignment		99.9	20	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
18	d1q35a_	Alignment		99.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
19	c2pt1A_	Alignment		99.9	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** futa1 synechocystis pcc 6803
20	c1twyG_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
21	d1twya_	Alignment	not modelled	99.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
22	c3cfxA_	Alignment	not modelled	99.9	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein ma_0280; **PDBTitle:** crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
23	c2v84A_	Alignment	not modelled	99.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**spermidine/putrescine abc transporter, periplasmic **PDBTitle:** crystal structure of the tp0655 (tppotd) lipoprotein of2 treponema pallidum
24	c3k6wA_	Alignment	not modelled	99.9	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute-binding protein ma_0280; **PDBTitle:** apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
25	d2onsa1	Alignment	not modelled	99.9	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
26	c3cg3A_	Alignment	not modelled	99.9	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein ph0151; **PDBTitle:** crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate
27	c3pu5A_	Alignment	not modelled	99.9	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular solute-binding protein; **PDBTitle:** the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
28	d1pota_	Alignment	not modelled	99.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
						PDB header:transport protein

29	c3cg1A_	Alignment	not modelled	99.9	20	**Chain:** A: **PDB Molecule:**upf0100 protein pf0080; **PDBTitle:** crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate
30	c2vozA_	Alignment	not modelled	99.8	17	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**periplasmic iron-binding protein; **PDBTitle:** apo futa2 from synechocystis pcc6803
31	d1a99a_	Alignment	not modelled	99.8	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
32	c3osrA_	Alignment	not modelled	99.8	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
33	c3cfzA_	Alignment	not modelled	99.8	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**upf0100 protein mj1186; **PDBTitle:** crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
34	c3ob4A_	Alignment	not modelled	99.7	15	**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
35	d1pc3a_	Alignment	not modelled	99.7	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
36	c3py7A_	Alignment	not modelled	99.7	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
37	c3o3uN_	Alignment	not modelled	99.7	15	**PDB header:**transport protein, signaling protein **Chain:** N: **PDB Molecule:**maltose-binding periplasmic protein, advanced glycosylation **PDBTitle:** crystal structure of human receptor for advanced glycation endproducts2 (rage)
38	c3h4zC_	Alignment	not modelled	99.7	18	**PDB header:**allergen **Chain:** C: **PDB Molecule:**maltose-binding periplasmic protein fused with allergen **PDBTitle:** crystal structure of an mbp-der p 7 fusion protein
39	d1ixha_	Alignment	not modelled	99.7	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
40	c3d4cA_	Alignment	not modelled	99.7	17	**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)
41	c1r6zA_	Alignment	not modelled	99.7	18	**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)
42	c3mp6A_	Alignment	not modelled	99.7	17	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, saga- **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
43	c3f5fA_	Alignment	not modelled	99.7	17	**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.
44	c2nvuB_	Alignment	not modelled	99.7	16	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
45	c3c4mA_	Alignment	not modelled	99.7	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)
46	c3dm0A_	Alignment	not modelled	99.7	15	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
47	c1y4cA_	Alignment	not modelled	99.7	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
48	c2vgqA_	Alignment	not modelled	99.7	17	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
49	c2gh9A_	Alignment	not modelled	99.7	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding protein; **PDBTitle:** thermus thermophilus maltotriose binding protein bound with2 maltotriose
50	c3oaiB_	Alignment	not modelled	99.7	15	**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
51	c3csgA_	Alignment	not modelled	99.7	17	**PDB header:**de novo protein, sugar binding protein **Chain:** A: **PDB Molecule:**maltose-binding protein monobody ys1 fusion; **PDBTitle:** crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex

52	c1hsjA_	Alignment	not modelled	99.7	16	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
53	c2xd3A_	Alignment	not modelled	99.7	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding protein; **PDBTitle:** the crystal structure of malx from streptococcus pneumoniae2 in complex with maltopentaose.
54	d1ursa_	Alignment	not modelled	99.6	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
55	c1ursA_	Alignment	not modelled	99.6	13	**PDB header:**maltose-binding protein **Chain:** A: **PDB Molecule:**maltose-binding protein; **PDBTitle:** x-ray structures of the maltose-maltodextrin binding2 protein of the thermoacidophilic bacterium alicyclobacillus3 acidocaldarius
56	c3oo6A_	Alignment	not modelled	99.6	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**abc transporter binding protein acbh; **PDBTitle:** crystal structures and biochemical characterization of the bacterial2 solute receptor acbh reveal an unprecedented exclusive substrate3 preference for b-d-galactopyranose
57	c3k02A_	Alignment	not modelled	99.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acarbose/maltose binding protein gach; **PDBTitle:** crystal structures of the gach receptor of streptomyces glaucescens2 gla.o in the unliganded form and in complex with acarbose and an3 acarbose homolog. comparison with acarbose-loaded maltose binding4 protein of salmonella typhimurium.
58	c1svxB_	Alignment	not modelled	99.6	14	**PDB header:**de novo protein/sugar binding protein **Chain:** B: **PDB Molecule:**maltose-binding periplasmic protein; **PDBTitle:** crystal structure of a designed selected ankyrin repeat2 protein in complex with the maltose binding protein
59	d1elja_	Alignment	not modelled	99.6	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
60	c2zykA_	Alignment	not modelled	99.6	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**solute-binding protein; **PDBTitle:** crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
61	c1mh3A_	Alignment	not modelled	99.6	16	**PDB header:**sugar binding, dna binding protein **Chain:** A: **PDB Molecule:**maltose binding-a1 homeodomain protein chimera; **PDBTitle:** maltose binding-a1 homeodomain protein chimera, crystal2 form i
62	c3uorB_	Alignment	not modelled	99.6	11	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**abc transporter sugar binding protein; **PDBTitle:** the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
63	c3osqA_	Alignment	not modelled	99.6	25	**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 175
64	c3ehuA_	Alignment	not modelled	99.6	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of crfr1 extracellular domain and mbp; **PDBTitle:** crystal structure of the extracellular domain of human corticotropin2 releasing factor receptor type 1 (crfr1) in complex with crf
65	d1laxa_	Alignment	not modelled	99.6	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
66	d1eu8a_	Alignment	not modelled	99.5	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
67	c3qufB_	Alignment	not modelled	99.5	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**extracellular solute-binding protein, family 1; **PDBTitle:** the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
68	c1mg1A_	Alignment	not modelled	99.5	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (htlv-1 gp21 ectodomain/maltose-binding protein **PDBTitle:** htlv-1 gp21 ectodomain/maltose-binding protein chimera
69	c3iouB_	Alignment	not modelled	99.5	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**maltose-binding protein, huntingtin fusion **PDBTitle:** huntingtin amino-terminal region with 17 gln residues -2 crystal c94
70	c2fncA_	Alignment	not modelled	99.5	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose abc transporter, periplasmic maltose-binding **PDBTitle:** thermotoga maritima maltotriose binding protein bound with2 maltotriose.
71	c2b3fD_	Alignment	not modelled	99.5	17	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**glucose-binding protein; **PDBTitle:** thermus thermophilus glucose/galactose binding protein2 bound with galactose
72	c2i58B_	Alignment	not modelled	99.4	12	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**sugar abc transporter, sugar-binding protein; **PDBTitle:** crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose
73	d3thia_	Alignment	not modelled	99.3	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
74	c2uvgA_	Alignment	not modelled	99.2	11	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2

						protein from yersinia enterocolitica
75	c3n5lA_	Alignment	not modelled	99.2	14	**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
76	c3cvgC_	Alignment	not modelled	99.2	10	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**putative metal binding protein; **PDBTitle:** crystal structure of a periplasmic putative metal binding protein
77	c2w7yA_	Alignment	not modelled	99.2	11	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**probable sugar abc transporter, sugar-binding **PDBTitle:** structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide.
78	c2z8fB_	Alignment	not modelled	99.1	13	**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
79	c3i3vC_	Alignment	not modelled	99.1	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**probable secreted solute-binding lipoprotein; **PDBTitle:** crystal structure of probable secreted solute-binding2 lipoprotein from streptomyces coelicolor
80	d1y3na1	Alignment	not modelled	98.9	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
81	d1j1na_	Alignment	not modelled	98.8	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
82	d1xs5a_	Alignment	not modelled	98.7	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
83	c3k2dA_	Alignment	not modelled	98.7	14	**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
84	c3tqwA_	Alignment	not modelled	98.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
85	c3e4rA_	Alignment	not modelled	98.7	9	**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
86	c3ombA_	Alignment	not modelled	98.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular solute-binding protein, family 1; **PDBTitle:** crystal structure of extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
87	d2fyia1	Alignment	not modelled	98.6	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
88	c3ir1F_	Alignment	not modelled	98.6	15	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
89	c3gxaA_	Alignment	not modelled	98.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane lipoprotein gna1946; **PDBTitle:** crystal structure of gna1946
90	c3l6gA_	Alignment	not modelled	98.5	13	**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
91	c2f5xC_	Alignment	not modelled	98.5	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
92	d1p99a_	Alignment	not modelled	98.4	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
93	c1p99A_	Alignment	not modelled	98.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg110; **PDBTitle:** 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
94	c2qpqC_	Alignment	not modelled	98.3	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
95	c2hxrA_	Alignment	not modelled	98.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator cynr; **PDBTitle:** structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
96	c3tmgA_	Alignment	not modelled	98.3	10	**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
97	c2dvzA_	Alignment	not modelled	98.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
						PDB header:transcription regulation

98	c1al3A_	Alignment	not modelled	98.2	9	**Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb; **PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes
99	d1al3a_	Alignment	not modelled	98.2	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
100	c2x26A_	Alignment	not modelled	98.1	8	**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
101	c3ho7A_	Alignment	not modelled	98.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**oxyr; **PDBTitle:** crystal structure of oxyr from porphyromonas gingivalis
102	c2ql3G_	Alignment	not modelled	98.0	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**probable transcriptional regulator, lysr family protein; **PDBTitle:** crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
103	d2v3qa1	Alignment	not modelled	97.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
104	c3oxnD_	Alignment	not modelled	97.8	7	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
105	d1ixca2	Alignment	not modelled	97.8	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
106	d1i6aa_	Alignment	not modelled	97.7	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
107	c3r6uA_	Alignment	not modelled	97.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
108	c3n6uA_	Alignment	not modelled	97.6	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
109	c3jv9B_	Alignment	not modelled	97.6	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** the structure of a reduced form of oxyr from n. meningitidis
110	c2rejA_	Alignment	not modelled	97.6	9	**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
111	c3qslA_	Alignment	not modelled	97.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50
112	c2f7cA_	Alignment	not modelled	97.6	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** catm effector binding domain with its effector cis,cis-muconate
113	c2h9bB_	Alignment	not modelled	97.5	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
114	c2f78A_	Alignment	not modelled	97.5	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** benm effector binding domain with its effector benzoate
115	c3uifA_	Alignment	not modelled	97.5	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
116	c3un6A_	Alignment	not modelled	97.4	11	**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
117	c3ix1B_	Alignment	not modelled	97.3	18	**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
118	c3ix1A_	Alignment	not modelled	97.3	18	**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
119	c2h9qC_	Alignment	not modelled	97.3	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator catm; **PDBTitle:** crystal structure of the effector binding domain of a catm2 variant (r156h)
120	c2q89A_	Alignment	not modelled	97.3	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