



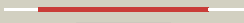




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1eu8a_	 Alignment		100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	c3osqA_	 Alignment		100.0	25	PDB header: fluorescent protein, 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
3	c3k02A_	 Alignment		100.0	16	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.
4	c3uorB_	 Alignment		100.0	17	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
5	c2uvqA_	 Alignment		100.0	16	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
6	c3h4zC_	 Alignment		100.0	17	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
7	c2zykA_	 Alignment		100.0	16	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
8	c3qufB_	 Alignment		100.0	16	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
9	c3c4mA_	 Alignment		100.0	17	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)
10	c3f5fA_	 Alignment		100.0	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.
11	c3ob4A_	 Alignment		100.0	17	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

12	c2vgqA_	Alignment		100.0	16	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
13	c3dm0A_	Alignment		100.0	18	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
14	c3py7A_	Alignment		100.0	18	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin 1d1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with 1d1 motif of paxillin at 2.3a resolution
15	c3d4cA_	Alignment		100.0	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)
16	c3o3uN_	Alignment		100.0	18	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)
17	c1y4cA_	Alignment		100.0	17	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
18	c1r6zA_	Alignment		100.0	16	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)
19	c2z8fB_	Alignment		100.0	14	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
20	c3csgA_	Alignment		100.0	18	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
21	c3mp6A_	Alignment	not modelled	100.0	17	PDB header: histone binding protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, linker, saga- PDBTitle: complex structure of sgf29 and dimethylated h3k4
22	c3oaiB_	Alignment	not modelled	100.0	17	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
23	c1hsjA_	Alignment	not modelled	100.0	17	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure
24	d1elja_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
25	c3oo6A_	Alignment	not modelled	100.0	14	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
26	c2w7yA_	Alignment	not modelled	100.0	16	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.
27	c3ehuA_	Alignment	not modelled	100.0	16	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

28	c2xd3A	Alignment	not modelled	100.0	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.
29	c2nvuB	Alignment	not modelled	100.0	18	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
30	c2b3fD	Alignment	not modelled	100.0	12	PDB header: sugar binding protein Chain: D: PDB Molecule: glucose-binding protein; PDBTitle: thermus thermophilus glucose/galactose binding protein2 bound with galactose
31	c1mg1A	Alignment	not modelled	100.0	17	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
32	c2fncA	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose abc transporter, periplasmic maltose-binding PDBTitle: thermotoga maritima maltotriose binding protein bound with2 maltotriose.
33	c2gh9A	Alignment	not modelled	100.0	16	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
34	dlursa	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	clursa	Alignment	not modelled	100.0	16	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
36	c1mh3A	Alignment	not modelled	100.0	18	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
37	c3iouB	Alignment	not modelled	100.0	18	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
38	dl1axa	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
39	c3i3vC	Alignment	not modelled	100.0	13	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
40	c2i58B	Alignment	not modelled	100.0	18	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
41	c3osrA	Alignment	not modelled	100.0	17	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
42	clsvxB	Alignment	not modelled	100.0	17	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
43	dlj1na	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
44	dly3na1	Alignment	not modelled	100.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
45	d3thia	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
46	c3ombA	Alignment	not modelled	100.0	12	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
47	d1a99a	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
48	c3c9hB	Alignment	not modelled	100.0	11	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
49	d1pota	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
50	c2v84A	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: spermidine/putrescine abc transporter, periplasmic PDBTitle: crystal structure of the tp0655 (tpptod) lipoprotein of2 treponema pallidum
						PDB header: transport protein

51	c3rpwA	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: abc transporter; PDBTitle: the crystal structure of an abc transporter from rhodopseudomonas2 palustris cga009
52	c3pu5A	Alignment	not modelled	100.0	13	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
53	c2pt1A	Alignment	not modelled	100.0	14	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
54	d1y4ta	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	d1xvxa	Alignment	not modelled	100.0	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
56	d1xc1a	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
57	d1nnfa	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
58	d1xvya	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
59	c2qryD	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
60	d2onsa1	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
61	d1q35a	Alignment	not modelled	100.0	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	c2vozA	Alignment	not modelled	100.0	13	PDB header: metal-binding protein Chain: A: PDB Molecule: periplasmic iron-binding protein; PDBTitle: apo futa2 from synechocystis pcc6803
63	d1y9ua	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
64	c3k6wA	Alignment	not modelled	99.9	13	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
65	c3cfxA	Alignment	not modelled	99.9	12	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
66	c3cfzA	Alignment	not modelled	99.9	12	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
67	c3cg1A	Alignment	not modelled	99.9	9	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein pf0080; PDBTitle: crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate
68	c3cg3A	Alignment	not modelled	99.9	8	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
69	d1sbpa	Alignment	not modelled	99.8	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
70	d1atga	Alignment	not modelled	99.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
71	c2h5yC	Alignment	not modelled	99.5	13	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
72	d1amfa	Alignment	not modelled	99.5	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	c3fj7A	Alignment	not modelled	99.4	11	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
74	c3lr1A	Alignment	not modelled	99.4	10	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
75	c3kn3C	Alignment	not modelled	99.3	11	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinetla succinogenes
76	c3muqB	Alignment	not modelled	99.2	12	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
77	d1twya	Alignment	not modelled	98.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
78	c1twyG_	Alignment	not modelled	98.8	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
79	d1pc3a_	Alignment	not modelled	96.8	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
80	d1al3a_	Alignment	not modelled	85.8	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
81	c1al3A_	Alignment	not modelled	85.8	10	PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
82	d2fyia1	Alignment	not modelled	85.5	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
83	c2f78A_	Alignment	not modelled	84.2	10	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
84	c3n6uA_	Alignment	not modelled	83.5	26	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
85	c2f7cA_	Alignment	not modelled	83.0	13	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
86	c2h9qC_	Alignment	not modelled	82.1	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)
87	c3cvgC_	Alignment	not modelled	81.7	11	PDB header: metal binding protein Chain: C: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
88	c2hxrA_	Alignment	not modelled	81.0	17	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
89	c2h9bB_	Alignment	not modelled	80.7	10	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)
90	c2ql3G_	Alignment	not modelled	80.2	12	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
91	c3ho7A_	Alignment	not modelled	78.4	6	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
92	c3jv9B_	Alignment	not modelled	78.3	8	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
93	d1i6aa_	Alignment	not modelled	77.6	4	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	d1ixca2	Alignment	not modelled	75.9	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
95	d2esna2	Alignment	not modelled	74.6	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
96	c3oxnD_	Alignment	not modelled	67.9	12	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
97	c2hpgB_	Alignment	not modelled	62.5	14	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
98	c3k2dA_	Alignment	not modelled	57.6	13	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
99	c2uyeA_	Alignment	not modelled	57.4	8	PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dntR from burkholderia sp. strain2 dnt in complex with thiocyanate
100	c3un6A_	Alignment	not modelled	54.5	9	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
101	d1lutha_	Alignment	not modelled	53.2	6	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
						Fold: Periplasmic binding protein-like II

102	d1us5a_	Alignment	not modelled	52.8	16	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
103	c3hhfB_	Alignment	not modelled	51.5	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
104	c3mz1D_	Alignment	not modelled	49.0	15	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021
105	c2x26A_	Alignment	not modelled	38.8	13	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
106	c2qsxB_	Alignment	not modelled	37.2	27	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
107	c3kosA_	Alignment	not modelled	34.4	19	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii
108	c3fd3A_	Alignment	not modelled	32.3	9	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.
109	c3tpaA_	Alignment	not modelled	31.0	16	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
110	c3lvuB_	Alignment	not modelled	29.8	17	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
111	d2pp4a1	Alignment	not modelled	29.4	9	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
112	c3o9pA_	Alignment	not modelled	29.2	15	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
113	d1vr5a1	Alignment	not modelled	28.2	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
114	c3e4rA_	Alignment	not modelled	27.1	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
115	c1ztyA_	Alignment	not modelled	26.7	12	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein
116	c3ir1F_	Alignment	not modelled	26.4	20	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
117	c3gxaA_	Alignment	not modelled	26.3	20	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
118	c3uifA_	Alignment	not modelled	24.6	16	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
119	d1zlqa1	Alignment	not modelled	24.1	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
120	c3ry3B_	Alignment	not modelled	22.5	16	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.