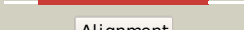
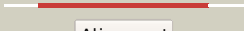
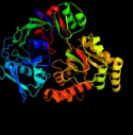
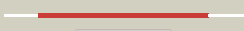
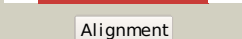
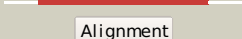
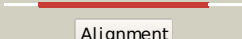
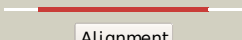
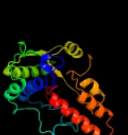
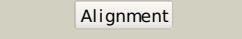
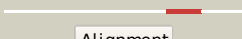
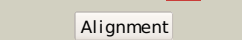
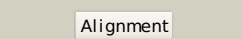


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o9pA_	 Alignment		100.0	100	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein peptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
2	d1jeta_	 Alignment		100.0	49	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	d1dpea_	 Alignment		100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
4	c3tpaA_	 Alignment		100.0	25	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
5	c3m8uA_	 Alignment		100.0	23	PDB header: transport protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
6	d1zlqa1	 Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	d1xoca1	 Alignment		100.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
8	c2wokA_	 Alignment		100.0	17	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: clavulanic acid biosynthesis oligopeptide PDBTitle: clavulanic acid biosynthesis oligopeptide2 binding protein 2 complexed with bradykinin
9	c3t66A_	 Alignment		100.0	20	PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans
10	d1uqwa_	 Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
11	c3rqtA_	 Alignment		100.0	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines

12	c1ztyA_		Alignment		100.0	19	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein
13	c3ftoA_		Alignment		100.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
14	c2o7jA_		Alignment		100.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentase
15	c2grvC_		Alignment		100.0	16	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
16	d1vr5a1		Alignment		100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
17	c3ry3B_		Alignment		100.0	21	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
18	c2d5wA_		Alignment		100.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
19	c3lvuB_		Alignment		100.0	19	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
20	c3pamB_		Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
21	c3o6pA_		Alignment	not modelled	100.0	27	PDB header: protein binding Chain: A: PDB Molecule: peptide abc transporter, peptide-binding protein; PDBTitle: crystal structure of peptide abc transporter, peptide-binding protein
22	c3chgB_		Alignment	not modelled	96.8	20	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
23	c3l6gA_		Alignment	not modelled	96.0	22	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
24	c3tmgA_		Alignment	not modelled	95.7	15	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
25	d1r9la_		Alignment	not modelled	94.8	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	c2rejA_		Alignment	not modelled	94.5	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
27	c3r6uA_		Alignment	not modelled	88.0	8	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis

28	c3kn3C	Alignment	not modelled	85.2	21	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 wolinnella succinogenes
29	c3ir1F	Alignment	not modelled	80.7	11	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
30	d1sw5a	Alignment	not modelled	80.5	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
31	c3ombA	Alignment	not modelled	79.9	13	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
32	c3pppA	Alignment	not modelled	77.2	12	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
33	c3nohA	Alignment	not modelled	77.2	17	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
34	c3lr1A	Alignment	not modelled	76.2	16	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
35	c3gxaA	Alignment	not modelled	72.4	11	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
36	c3muqB	Alignment	not modelled	68.3	16	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
37	c3kzgB	Alignment	not modelled	60.7	11	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
38	c3un6A	Alignment	not modelled	59.1	10	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
39	c3k2dA	Alignment	not modelled	57.1	19	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
40	c2rc9A	Alignment	not modelled	56.7	14	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
41	c3tqwA	Alignment	not modelled	54.5	9	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
42	d1xs5a	Alignment	not modelled	50.8	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
43	d2a5sa1	Alignment	not modelled	49.6	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
44	c3hlyA	Alignment	not modelled	48.5	11	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
45	d1e5da1	Alignment	not modelled	48.4	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
46	c1tvma	Alignment	not modelled	46.8	10	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
47	c2xx7B	Alignment	not modelled	40.7	15	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: 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.
48	c2zykA	Alignment	not modelled	40.6	16	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/malto-dextrin-binding protein2 complexed with gamma-cyclodextrin
49	d1ycga1	Alignment	not modelled	39.4	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
50	c3hn0A	Alignment	not modelled	38.1	21	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 PDB header: electron transport

51	c3f6sl_	Alignment	not modelled	37.6	14	Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
52	c2o1mB_	Alignment	not modelled	36.3	14	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 ytnk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
53	d1pb7a_	Alignment	not modelled	36.1	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	c2ylnA_	Alignment	not modelled	34.5	22	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
55	c1twyG_	Alignment	not modelled	33.3	17	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
56	d1twya_	Alignment	not modelled	33.3	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
57	c3r39A_	Alignment	not modelled	32.9	13	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
58	c3ix1B_	Alignment	not modelled	32.8	10	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
59	c3ix1A_	Alignment	not modelled	32.8	10	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
60	d1g7da_	Alignment	not modelled	32.8	28	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
61	d1wdna_	Alignment	not modelled	31.5	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	c2y7iB_	Alignment	not modelled	31.4	24	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
63	d1xvya_	Alignment	not modelled	30.4	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
64	c2x26A_	Alignment	not modelled	27.1	9	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
65	d1amfa_	Alignment	not modelled	26.2	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
66	c2q2aD_	Alignment	not modelled	25.9	17	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
67	c3nbmA_	Alignment	not modelled	25.1	23	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
68	d1hsla_	Alignment	not modelled	25.1	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	c3e4rA_	Alignment	not modelled	24.9	11	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
70	d1xc1a_	Alignment	not modelled	24.9	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
71	c2v25B_	Alignment	not modelled	24.6	12	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
72	c3g41A_	Alignment	not modelled	24.0	17	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
73	d1elja_	Alignment	not modelled	23.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c3k4uA_	Alignment	not modelled	23.6	26	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinetella succinogenes dsm 1740 complexed

					with lysine
75	c2uvga_	Alignment	not modelled	23.5	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
76	d1nnfa_	Alignment	not modelled	22.9	21 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
77	c2gh9A_	Alignment	not modelled	22.4	11 PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
78	c3o66A_	Alignment	not modelled	22.2	8 PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter; PDBTitle: crystal structure of glycine betaine/carnitine/choline abc transporter
79	c3cfza_	Alignment	not modelled	21.2	14 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
80	d2fz5a1	Alignment	not modelled	21.2	13 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
81	c3mplA_	Alignment	not modelled	21.0	11 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)
82	c2pt1A_	Alignment	not modelled	21.0	11 PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
83	d2p0la1	Alignment	not modelled	20.9	14 Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
84	d1f4pa_	Alignment	not modelled	20.2	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
85	c2h5yC_	Alignment	not modelled	20.1	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
86	c2l2qa_	Alignment	not modelled	19.5	9 PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
87	c3d7nA_	Alignment	not modelled	19.5	9 PDB header: electron transport Chain: A: PDB Molecule: flavodoxin, wrba-like protein; PDBTitle: the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
88	c3pu5A_	Alignment	not modelled	18.8	16 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
89	c2ieeB_	Alignment	not modelled	18.7	17 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.
90	c2x7pA_	Alignment	not modelled	18.5	14 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
91	d1y4ta_	Alignment	not modelled	18.3	9 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
92	d1ykga1	Alignment	not modelled	18.3	10 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
93	c3n5lA_	Alignment	not modelled	17.9	12 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
94	d1tlla2	Alignment	not modelled	17.9	17 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
95	d1lsta_	Alignment	not modelled	17.8	18 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
96	c3oo6A_	Alignment	not modelled	16.9	13 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
97	d2onsa1	Alignment	not modelled	16.8	15 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
98	c1xt8B_	Alignment	not modelled	15.2	10 PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding

				PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution	
				PDB header: oxidoreductase	
99	c2q9uB_	Alignment	not modelled	15.1	9
				Chain: B: PDB Molecule: a-type flavoprotein;	
				PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis	