



























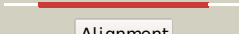
















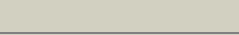


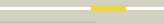




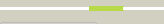











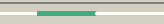
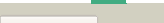
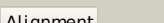
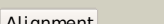
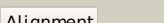
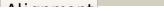


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dljeta_	 Alignment		100.0	46	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	c3o9pA_	 Alignment		100.0	42	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: periplasmic murein tripeptide-binding protein; PDBTitle: the structure of the escherichia coli murein tripeptide binding2 protein mppa
3	dlxoca1	 Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
4	dlppea_	 Alignment		100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
5	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
6	c2wokA_	 Alignment		100.0	20	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
7	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)
8	dlzlqa1	 Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	dluqwa_	 Alignment		100.0	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	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
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	17	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	19	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	d1vr5a1		Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
16	c2grvC_		Alignment		100.0	17	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
17	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
18	c3ry3B_		Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
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	17	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	25	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	96.6	21	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	95.5	15	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	95.1	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
25	c2rejA_		Alignment	not modelled	93.7	10	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
26	d1r9la_		Alignment	not modelled	93.4	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c3kn3C_		Alignment	not modelled	87.7	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 wolinnella succinogenes

28	c3lr1A		Alignment	not modelled	80.4	14	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
29	c3r6uA		Alignment	not modelled	78.3	11	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
30	c3ombA		Alignment	not modelled	75.6	6	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
31	c3lr1F		Alignment	not modelled	75.1	11	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
32	c3kzgB		Alignment	not modelled	71.0	22	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
33	c3gxaA		Alignment	not modelled	67.8	11	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
34	c1tvmA		Alignment	not modelled	66.7	9	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
35	c3muqB		Alignment	not modelled	66.0	18	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
36	c3k2dA		Alignment	not modelled	62.0	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
37	d1sw5a		Alignment	not modelled	61.8	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
38	c2rc9A		Alignment	not modelled	61.2	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
39	c3nohA		Alignment	not modelled	60.9	21	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
40	d2a5sa1		Alignment	not modelled	56.2	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
41	c3pppA		Alignment	not modelled	54.5	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
42	c2xx7B		Alignment	not modelled	54.4	19	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.
43	d1xs5a		Alignment	not modelled	50.5	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
44	c2v25B		Alignment	not modelled	48.4	14	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
45	c3tqwA		Alignment	not modelled	47.3	11	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
46	c2qpqC		Alignment	not modelled	47.3	15	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
47	c3r39A		Alignment	not modelled	46.9	15	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
48	c2zykA		Alignment	not modelled	44.6	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
49	c2ylnA		Alignment	not modelled	42.9	17	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
50	d1pb7a		Alignment	not modelled	42.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	c3m5A		Alignment	not modelled	42.8	13	PDB header: transport protein Chain: A: PDB Molecule: extracellular solute-binding protein;

51	c3p03A_	Alignment	not modelled	42.8	15	PDBTitle: the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
52	d1wdna_	Alignment	not modelled	41.7	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
53	c2y7iB_	Alignment	not modelled	39.8	15	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
54	c3ix1B_	Alignment	not modelled	38.2	12	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
55	c3ix1A_	Alignment	not modelled	38.2	12	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
56	c2gh9A_	Alignment	not modelled	35.1	4	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
57	c3k4uA_	Alignment	not modelled	35.1	15	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
58	c3nbmA_	Alignment	not modelled	34.9	11	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.
59	c2q2aD_	Alignment	not modelled	34.7	13	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
60	c3g41A_	Alignment	not modelled	34.2	15	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
61	c2uv9A_	Alignment	not modelled	32.5	12	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
62	c2l2qA_	Alignment	not modelled	32.5	7	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
63	c3delC_	Alignment	not modelled	31.2	15	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
64	d1hsla_	Alignment	not modelled	30.8	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
65	d1xvya_	Alignment	not modelled	30.6	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
66	c1twyG_	Alignment	not modelled	28.6	9	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
67	d1twya_	Alignment	not modelled	28.6	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
68	d1amfa_	Alignment	not modelled	28.3	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	c3cfzA_	Alignment	not modelled	27.4	5	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
70	c2h5yC_	Alignment	not modelled	27.3	7	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
71	d1lsta_	Alignment	not modelled	27.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
72	d2p0la1	Alignment	not modelled	26.7	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
73	c2ieeB_	Alignment	not modelled	26.2	22	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. PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-

74	c3i6vA	Alignment	not modelled	26.1	15	binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
75	c2f5xC	Alignment	not modelled	24.8	14	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
76	c2x7pA	Alignment	not modelled	23.7	7	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
77	d1g7da	Alignment	not modelled	23.6	25	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
78	c2dvzA	Alignment	not modelled	23.1	14	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
79	d1elja	Alignment	not modelled	22.7	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
80	d1iiba	Alignment	not modelled	22.6	7	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellulose specific IIB subunit
81	d1y4ta	Alignment	not modelled	22.5	6	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
82	c3qslA	Alignment	not modelled	22.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
83	c3kbrA	Alignment	not modelled	21.4	11	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
84	c3hv1A	Alignment	not modelled	20.1	20	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
85	d1nnfa	Alignment	not modelled	19.6	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
86	c3h7mA	Alignment	not modelled	19.6	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
87	c3hn0A	Alignment	not modelled	19.3	13	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
88	c3oo6A	Alignment	not modelled	19.1	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
89	d2f34a1	Alignment	not modelled	18.1	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
90	d1xc1a	Alignment	not modelled	18.1	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
91	c2pfyA	Alignment	not modelled	17.4	13	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
92	c3k02A	Alignment	not modelled	17.2	12	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.
93	d1mqia	Alignment	not modelled	17.2	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	c1xofA	Alignment	not modelled	16.9	40	PDB header: de novo protein Chain: A: PDB Molecule: bbahett1; PDBTitle: heterooligomeric beta beta alpha mini-protein
95	d2onsa1	Alignment	not modelled	14.9	5	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
96	c3un6A	Alignment	not modelled	14.4	8	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
97	d1e5da1	Alignment	not modelled	14.4	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
98	c2z8fB	Alignment	not modelled	14.0	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	
99	dlxvxa_	Alignment	not modelled	13.9	16
				Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like	