







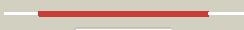
























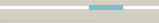
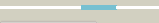
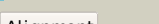
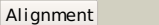



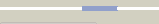
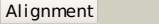
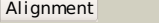
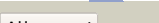

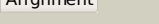



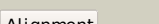


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o7jA_	 Alignment		100.0	19	PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
2	c1ztyA_	 Alignment		100.0	18	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein
3	d1xoca1	 Alignment		100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
4	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
5	d1vr5a1	 Alignment		100.0	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
6	d1zlqa1	 Alignment		100.0	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	d1dpea_	 Alignment		100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
8	c3tpaA_	 Alignment		100.0	18	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
9	c3m8uA_	 Alignment		100.0	18	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)
10	d1jeta_	 Alignment		100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
11	c3t66A_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: nickel abc transporter (nickel-binding protein); PDBTitle: crystal structure of nickel abc transporter from bacillus halodurans

12	c3o9pA_	Alignment		100.0	14	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
13	d1uqwa_	Alignment		100.0	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
14	c2grvC_	Alignment		100.0	16	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
15	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
16	c3ry3B_	Alignment		100.0	20	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
17	c2d5wA_	Alignment		100.0	17	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	c3rqtA_	Alignment		100.0	17	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
19	c3lvuB_	Alignment		100.0	35	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	35	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	19	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	96.3	15	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	95.8	12	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	95.6	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	d1r9la_	Alignment	not modelled	93.7	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	c2rejA_	Alignment	not modelled	93.2	12	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	d2p0la1	Alignment	not modelled	92.6	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
						PDB header: peptide binding protein

28	c3nohA	Alignment	not modelled	92.6	17	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
29	c3r6uA	Alignment	not modelled	87.8	9	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
30	d2fz5a1	Alignment	not modelled	82.1	3	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
31	c3k2dA	Alignment	not modelled	82.0	7	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
32	d1sw5a	Alignment	not modelled	81.5	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
33	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
34	d1f4pa	Alignment	not modelled	79.6	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
35	d2hfqa1	Alignment	not modelled	77.9	15	Fold: NE1680-like Superfamily: NE1680-like Family: NE1680-like
36	c2hfqa	Alignment	not modelled	77.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
37	c3gxaA	Alignment	not modelled	77.7	11	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
38	d1ykga1	Alignment	not modelled	77.3	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
39	c2uzhB	Alignment	not modelled	77.0	16	PDB header: lyase Chain: B: PDB Molecule: 2c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
40	d1b1ca	Alignment	not modelled	75.9	5	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
41	d5nula	Alignment	not modelled	74.0	6	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
42	d1xs5a	Alignment	not modelled	73.1	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
43	c3hlyA	Alignment	not modelled	71.3	4	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.
44	c3kzgB	Alignment	not modelled	70.1	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
45	d1ja1a2	Alignment	not modelled	69.5	5	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
46	c3f6sl	Alignment	not modelled	69.4	7	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
47	c3ombA	Alignment	not modelled	69.2	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
48	c2bpoA	Alignment	not modelled	68.8	8	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
49	d1ycga1	Alignment	not modelled	64.8	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
50	c3fniA	Alignment	not modelled	63.9	5	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
51	c3n5IA	Alignment	not modelled	62.5	17	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
52	d1bvvyf	Alignment	not modelled	61.7	9	Fold: Flavodoxin-like Superfamily: Flavoproteins

						Family: Flavodoxin-related
53	c1bvyF_	Alignment	not modelled	61.7	9	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fnm-binding domains of the2 cytochrome p450(bm-3)
54	c2rc9A_	Alignment	not modelled	61.6	11	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
55	c3pppA_	Alignment	not modelled	61.3	11	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
56	c2p3nB_	Alignment	not modelled	60.5	17	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
57	d1iv3a_	Alignment	not modelled	60.0	27	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
58	c3kn3C_	Alignment	not modelled	58.3	9	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
59	c2pmpA_	Alignment	not modelled	56.6	25	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
60	c1j9zB_	Alignment	not modelled	56.4	7	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
61	c3f0gA_	Alignment	not modelled	56.3	12	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
62	d1e5da1	Alignment	not modelled	56.2	7	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
63	d1vh8a_	Alignment	not modelled	55.9	14	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
64	d1w55a2	Alignment	not modelled	55.4	16	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
65	d1t0aa_	Alignment	not modelled	54.5	17	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
66	c3hr4C_	Alignment	not modelled	53.6	10	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
67	c3lr1A_	Alignment	not modelled	50.3	11	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
68	d1p99a_	Alignment	not modelled	50.1	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	c1p99A_	Alignment	not modelled	50.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
70	d1gx1a_	Alignment	not modelled	49.8	16	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
71	d1vmea1	Alignment	not modelled	49.6	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
72	c3re3B_	Alignment	not modelled	49.0	18	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
73	d1xvya_	Alignment	not modelled	48.1	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c3nbmA_	Alignment	not modelled	47.8	13	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.
75	c3s83A_	Alignment	not modelled	47.7	13	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: crystal structure of eal domain from caulobacter crescentus cb15
76	d2a5sa1	Alignment	not modelled	47.5	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like

77	d1twya_	Alignment	not modelled	47.2	6	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
78	c1twyG_	Alignment	not modelled	47.2	6	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	d1tlla2	Alignment	not modelled	46.0	3	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
80	c2y7iB_	Alignment	not modelled	43.1	5	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
81	c3r39A_	Alignment	not modelled	43.1	11	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
82	d1nnfa_	Alignment	not modelled	42.8	8	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
83	c3muqB_	Alignment	not modelled	42.0	11	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
84	c2hnbA_	Alignment	not modelled	41.8	5	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
85	d1xc1a_	Alignment	not modelled	41.6	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
86	c2axoA_	Alignment	not modelled	41.0	18	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein atu2684; PDBTitle: x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
87	c2ylnA_	Alignment	not modelled	39.7	9	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
88	c2f5xC_	Alignment	not modelled	39.5	10	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
89	d1wdna_	Alignment	not modelled	39.4	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
90	c2wc1A_	Alignment	not modelled	39.0	5	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
91	c3g41A_	Alignment	not modelled	37.7	9	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
92	c3hn0A_	Alignment	not modelled	36.5	7	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
93	c2q2aD_	Alignment	not modelled	36.2	11	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
94	c3k4uA_	Alignment	not modelled	36.2	7	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolfinella succinogenes dsm 1740 complexed with lysine
95	d2f06a2	Alignment	not modelled	36.0	27	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
96	c3b6nA_	Alignment	not modelled	35.2	17	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
97	c2q9uB_	Alignment	not modelled	34.6	11	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiiron protein from giardia2 intestinalis
98	d1hsla_	Alignment	not modelled	33.5	5	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
99	c1vmeB_	Alignment	not modelled	33.5	10	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
100	c2x5dD_	Alignment	not modelled	33.0	18	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
101	c3tgwA_	Alignment	not modelled	32.5	13	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-

						binding protein2 from coxiella burnetii 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.
102	c2xx7B_	 Alignment	not modelled	32.5	17	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
103	c1w57A_	 Alignment	not modelled	32.2	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
104	c3luuA_	 Alignment	not modelled	31.4	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
105	d1xvxa_	 Alignment	not modelled	31.1	13	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
106	c3delC_	 Alignment	not modelled	31.1	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Atu2684-like
107	d2axoa1	 Alignment	not modelled	30.8	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
108	d1pb7a_	 Alignment	not modelled	30.4	11	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
109	c2l2qA_	 Alignment	not modelled	29.4	16	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
110	c2ek8A_	 Alignment	not modelled	29.1	6	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
111	d1us5a_	 Alignment	not modelled	27.9	9	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
112	c2gguA_	 Alignment	not modelled	27.1	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
113	c3i6vA_	 Alignment	not modelled	26.8	18	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
114	c2qpqC_	 Alignment	not modelled	26.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
115	d1lsta_	 Alignment	not modelled	25.7	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
116	d1h3da1	 Alignment	not modelled	25.6	13	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.
117	c2ieeB_	 Alignment	not modelled	24.2	14	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
118	c1q1kA_	 Alignment	not modelled	23.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
119	d1z7me1	 Alignment	not modelled	23.4	18	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
120	c3uifA_	 Alignment	not modelled	23.4	19	