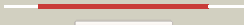
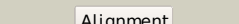
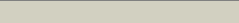
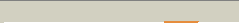
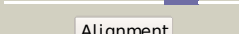
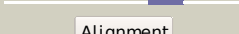
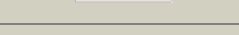
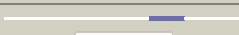
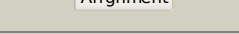
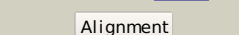
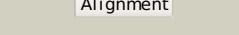
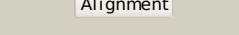


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dluqwa_	 Alignment		100.0	98	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
2	dldepa_	 Alignment		100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c3tpaA_	 Alignment		100.0	26	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
4	c3m8uA_	 Alignment		100.0	28	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)
5	c3o9pA_	 Alignment		100.0	20	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
6	c2wokA_	 Alignment		100.0	22	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	dljeta_	 Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
8	dlzlqa1	 Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	dlxoca1	 Alignment		100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	c3t66A_	 Alignment		100.0	25	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	21	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	20	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	c2o7jA	 Alignment		100.0	21	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
14	c2grvC	 Alignment		100.0	18	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
15	c3ftoA	 Alignment		100.0	20	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	22	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
17	d1vr5a1	 Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
18	c2d5wA	 Alignment		100.0	16	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	22	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	20	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	92.5	14	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	c3tmgA	 Alignment	not modelled	91.5	7	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
24	c3l6gA	 Alignment	not modelled	91.0	13	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
25	c2rejA	 Alignment	not modelled	88.3	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
26	c3r6uA	 Alignment	not modelled	72.9	8	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
27	d1e5da1	 Alignment	not modelled	70.5	7	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related

28	dlycga1	Alignment	not modelled	69.2	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
29	dlja1a2	Alignment	not modelled	60.3	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
30	dlr9la_	Alignment	not modelled	60.3	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
31	dlb1ca_	Alignment	not modelled	58.9	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
32	dlxs5a_	Alignment	not modelled	58.5	7	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
33	c3f6sl_	Alignment	not modelled	55.8	8	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
34	c3fniA_	Alignment	not modelled	54.1	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
35	c3hlyA_	Alignment	not modelled	51.9	15	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.
36	c2ek8A_	Alignment	not modelled	47.9	16	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
37	c3un6A_	Alignment	not modelled	47.1	13	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
38	c3gxaA_	Alignment	not modelled	46.2	10	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
39	dlf4pa_	Alignment	not modelled	44.2	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
40	c3k2dA_	Alignment	not modelled	43.7	12	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
41	c3hn0A_	Alignment	not modelled	43.5	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
42	dlbvyf_	Alignment	not modelled	43.4	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
43	clbvyF_	Alignment	not modelled	43.4	18	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fnn-binding domains of the2 cytochrome p450(bm-3)
44	c3ir1F_	Alignment	not modelled	42.8	10	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
45	dlsw5a_	Alignment	not modelled	42.5	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
46	c2zykA_	Alignment	not modelled	42.4	9	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
47	c3pppA_	Alignment	not modelled	39.9	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
48	c3tqwA_	Alignment	not modelled	39.0	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
49	d5nula_	Alignment	not modelled	38.1	6	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
50	c3nohA_	Alignment	not modelled	37.8	16	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
51	c2o1mB_	Alignment	not modelled	36.3	11	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
52	c2hnbA_	Alignment	not modelled	34.3	19	PDB header: electron transport Chain: A: PDB Molecule: protein mioc;

						PDBTitle: solution structure of a bacterial holo-flavodoxin
53	c3d7nA	Alignment	not modelled	33.0	7	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
54	c3guxA	Alignment	not modelled	32.1	16	PDB header: hydrolase Chain: A: PDB Molecule: putative zn-dependent exopeptidase; PDBTitle: crystal structure of a putative zn-dependent exopeptidase (bv_u_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
55	c1j9zB	Alignment	not modelled	31.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
56	d1vmea1	Alignment	not modelled	30.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
57	d1ydga	Alignment	not modelled	28.8	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
58	c3ix1B	Alignment	not modelled	28.5	13	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	28.5	13	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	d2fz5a1	Alignment	not modelled	28.4	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
61	d1g7da	Alignment	not modelled	26.3	16	Fold: ERP29 C domain-like Superfamily: ERP29 C domain-like Family: ERP29 C domain-like
62	d2arka1	Alignment	not modelled	25.6	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
63	d2vv5a2	Alignment	not modelled	24.0	15	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
64	c2x26A	Alignment	not modelled	23.7	10	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	c3oo6A	Alignment	not modelled	23.2	11	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
66	c3ombA	Alignment	not modelled	23.1	10	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
67	c2f06B	Alignment	not modelled	22.3	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
68	d2a5la1	Alignment	not modelled	22.2	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
69	c3iibA	Alignment	not modelled	21.3	6	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m28; PDBTitle: crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
70	c1xt8B	Alignment	not modelled	20.9	14	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
71	d1uwda	Alignment	not modelled	20.5	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
72	c3t6mA	Alignment	not modelled	20.3	6	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
73	c3nbmA	Alignment	not modelled	20.2	5	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.
74	c1ychD	Alignment	not modelled	20.1	7	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
75	c3kbrA	Alignment	not modelled	19.6	8	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01

76	c3e4rA	 Alignment	not modelled	19.2	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
77	c2l2qA	 Alignment	not modelled	18.9	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
78	c2x7vA	 Alignment	not modelled	18.3	6	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
79	c2q9uB	 Alignment	not modelled	18.2	6	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
80	d1iiba	 Alignment	not modelled	17.6	10	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
81	c2wteB	 Alignment	not modelled	16.7	9	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
82	c3a9lB	 Alignment	not modelled	16.6	20	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
83	d1vgya1	 Alignment	not modelled	16.0	9	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
84	d2p0la1	 Alignment	not modelled	15.7	13	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
85	c1p99A	 Alignment	not modelled	15.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
86	d1p99a	 Alignment	not modelled	15.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
87	d1ykga1	 Alignment	not modelled	15.2	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
88	c2ylnA	 Alignment	not modelled	15.1	18	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
89	c2uvga	 Alignment	not modelled	14.9	6	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
90	c2zkiH	 Alignment	not modelled	14.9	3	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
91	c3tc8A	 Alignment	not modelled	14.7	10	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
92	c2gh9A	 Alignment	not modelled	14.6	10	PDB header: sugar binding protein Chain: A: PDB Molecule: maltose/maltodextrin-binding protein; PDBTitle: thermus thermophilus maltotriose binding protein bound with2 maltotriose
93	c3i6vA	 Alignment	not modelled	14.3	15	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
94	c3r39A	 Alignment	not modelled	13.9	18	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
95	c2v25B	 Alignment	not modelled	13.7	8	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
96	d2q02a1	 Alignment	not modelled	13.6	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
97	c3n5fB	 Alignment	not modelled	13.6	4	PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
98	c3kzgB	Alignment	not modelled	13.3	7	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
99	c3hr4C	Alignment	not modelled	13.3	10	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex

