

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tpaA_	 Alignment		100.0	28	PDB header: heme binding protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: structure of hbpa2 from haemophilus parasuis
2	d1dpea_	 Alignment		100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c3m8uA_	 Alignment		100.0	26	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)
4	d1zlqa1	 Alignment		100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
5	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
6	d1jeta_	 Alignment		100.0	26	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
7	c3o9pA_	 Alignment		100.0	28	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
8	d1xoca1	 Alignment		100.0	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	d1uqwa_	 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	23	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	c1ztyA_	 Alignment		100.0	21	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligasaccharide binding2 protein

12	c2grvC_	Alignment		100.0	15	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
13	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
14	c2o7jA_	Alignment		100.0	22	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	c3ftoA_	Alignment		100.0	22	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
17	c3ry3B_	Alignment		100.0	23	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	19	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	17	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
20	c3pamB_	Alignment		100.0	18	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	33	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	96.2	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	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	95.5	17	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	94.5	17	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	94.4	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c3nohA_	Alignment	not modelled	93.6	20	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
28	c3r6uA_	Alignment	not modelled	90.9	20 PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
29	c3f6sl_	Alignment	not modelled	88.6	18 PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
30	d1sw5a_	Alignment	not modelled	87.6	11 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
31	c3pppA_	Alignment	not modelled	82.3	16 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
32	d1e5da1	Alignment	not modelled	80.9	14 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
33	d1ycga1	Alignment	not modelled	80.1	19 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
34	c3hlyA_	Alignment	not modelled	79.9	14 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.
35	d1f4pa_	Alignment	not modelled	77.1	16 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
36	d2fz5a1	Alignment	not modelled	72.3	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
37	d1ykga1	Alignment	not modelled	63.3	12 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
38	d1tlla2	Alignment	not modelled	63.1	8 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
39	d5nula_	Alignment	not modelled	62.7	10 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
40	d1ja1a2	Alignment	not modelled	61.8	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
41	c3ir1F_	Alignment	not modelled	59.8	19 PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
42	c3un6A_	Alignment	not modelled	56.9	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
43	c1bvyF_	Alignment	not modelled	54.6	22 PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fmN-binding domains of the2 cytochrome p450(bm-3)
44	d1bvyf_	Alignment	not modelled	54.6	22 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
45	c2ek8A_	Alignment	not modelled	54.0	10 PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
46	c3kzgB_	Alignment	not modelled	53.3	11 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
47	c3kn3C_	Alignment	not modelled	52.8	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 wolinetlla succinogenes
48	c3lr1A_	Alignment	not modelled	51.3	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
49	c2o1mB_	Alignment	not modelled	50.1	18 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 ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
50	c2hnbA_	Alignment	not modelled	49.6	14 PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
51	c3gxaA_	Alignment	not modelled	47.2	19 PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
52	c3fniA_	Alignment	not modelled	45.0	17 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
53	c3tqwA_	Alignment	not modelled	44.2	15	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
54	c3hr4C_	Alignment	not modelled	44.1	9	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
55	d1ydgA_	Alignment	not modelled	41.7	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
56	d2arka1	Alignment	not modelled	39.2	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
57	d1vmea1	Alignment	not modelled	38.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
58	d1s8na_	Alignment	not modelled	37.5	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c2rc9A_	Alignment	not modelled	35.6	12	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
60	c2ra9A_	Alignment	not modelled	35.6	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein duf1285; PDBTitle: crystal structure of a duf1285 family protein (sbal_2486) from2 shewanella baltica os155 at 1.40 a resolution
61	d1xs5a_	Alignment	not modelled	34.9	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	c3ix1B_	Alignment	not modelled	33.7	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
63	c3ix1A_	Alignment	not modelled	33.7	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
64	c3hn0A_	Alignment	not modelled	33.6	23	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
65	c2x26A_	Alignment	not modelled	32.4	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
66	c3k2dA_	Alignment	not modelled	31.7	14	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
67	c1vmeB_	Alignment	not modelled	31.5	18	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
68	c2q9uB_	Alignment	not modelled	31.0	9	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
69	d1b1ca_	Alignment	not modelled	30.5	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
70	c1xt8B_	Alignment	not modelled	28.1	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
71	d1twya_	Alignment	not modelled	27.8	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
72	c1twyG_	Alignment	not modelled	27.8	15	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
73	c3o66A_	Alignment	not modelled	27.1	9	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter; PDBTitle: crystal structure of glycine betaine/carnitine/choline abc transporter
74	c2wc1A_	Alignment	not modelled	26.0	8	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
75	d2a5la1	Alignment	not modelled	25.9	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
76	c3iibA_	Alignment	not modelled	25.8	17	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

77	c2y7iB_	Alignment	not modelled	25.2	4	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
78	c3e4rA_	Alignment	not modelled	25.0	14	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
79	c2zykA_	Alignment	not modelled	24.5	20	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
80	c2ylnA_	Alignment	not modelled	24.1	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
81	d1mb3a_	Alignment	not modelled	23.8	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	c3r39A_	Alignment	not modelled	23.3	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
83	c3kbrA_	Alignment	not modelled	22.4	7	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
84	c3c97A_	Alignment	not modelled	22.3	10	PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
85	c2bpoA_	Alignment	not modelled	21.9	18	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
86	d1wdna_	Alignment	not modelled	21.7	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
87	c1ychD_	Alignment	not modelled	21.5	17	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
88	d1xfha1	Alignment	not modelled	21.5	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	c2q2aD_	Alignment	not modelled	21.3	9	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
90	c1p99A_	Alignment	not modelled	21.2	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
91	d1p99a_	Alignment	not modelled	21.2	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
92	d1us5a_	Alignment	not modelled	21.0	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
93	d2a9pa1	Alignment	not modelled	20.9	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
94	c2j48A_	Alignment	not modelled	20.8	14	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
95	d1zgza1	Alignment	not modelled	20.5	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3muqB_	Alignment	not modelled	20.4	9	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
97	c3d7nA_	Alignment	not modelled	20.2	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
98	d2a5sa1	Alignment	not modelled	20.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
99	c3f6cB_	Alignment	not modelled	19.9	22	PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli