

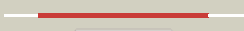





















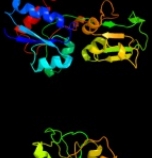
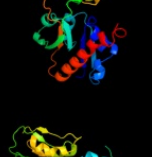
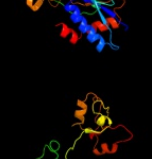
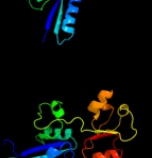


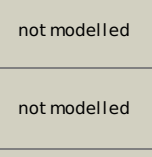


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ypnA	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
2	c3eq1A	 Alignment		100.0	46	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at 2.8a resolution
3	d1pdaa1	 Alignment		100.0	100	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
4	d1gtka2	 Alignment		99.9	100	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
5	d1pdaa2	 Alignment		99.9	98	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
6	c3gxaA	 Alignment		97.7	17	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
7	c2x26A	 Alignment		97.7	16	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
8	d1p99a	 Alignment		97.7	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
9	c1p99A	 Alignment		97.7	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
10	c3tqwA	 Alignment		97.3	21	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
11	c3uifA	 Alignment		97.2	17	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

12	c3ir1F_	Alignment		97.1	18	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
13	c3un6A_	Alignment		97.1	15	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
14	d1xs5a_	Alignment		97.1	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
15	c3e4rA_	Alignment		96.3	17	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
16	c3k2dA_	Alignment		95.7	15	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
17	c3l6gA_	Alignment		95.6	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
18	c3qslA_	Alignment		95.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
19	c3hn0A_	Alignment		95.2	15	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
20	c3tmgA_	Alignment		93.0	12	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
21	d1zbma1	Alignment	not modelled	92.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
22	c2h9bB_	Alignment	not modelled	92.3	32	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
23	c3kzgB_	Alignment	not modelled	91.9	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
24	d2czla1	Alignment	not modelled	91.8	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
25	d2ozza1	Alignment	not modelled	90.9	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	c2f7cA_	Alignment	not modelled	90.1	23	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
27	c3ix1A_	Alignment	not modelled	87.3	17	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
28	c3ix1B_	Alignment	not modelled	87.3	17	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
29	c3ho7A_	Alignment	not modelled	84.5	22 PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
30	c2x7pA_	Alignment	not modelled	84.0	17 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
31	c2f78A_	Alignment	not modelled	82.3	34 PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
32	c3g41A_	Alignment	not modelled	77.5	14 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
33	c3delC_	Alignment	not modelled	75.1	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
34	c3n6uA_	Alignment	not modelled	74.5	15 PDB header: transcription regulator Chain: A: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
35	d2nxoa1	Alignment	not modelled	73.9	16 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
36	c3fd3A_	Alignment	not modelled	72.6	22 PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
37	d1i6aa_	Alignment	not modelled	70.7	19 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
38	c2q2aD_	Alignment	not modelled	70.5	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
39	c2ylnA_	Alignment	not modelled	67.8	10 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
40	d1ixca2	Alignment	not modelled	66.9	17 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
41	d1ex2a_	Alignment	not modelled	63.8	21 Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
42	c2p5xB_	Alignment	not modelled	60.5	21 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
43	c1al3A_	Alignment	not modelled	59.4	16 PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
44	d1al3a_	Alignment	not modelled	59.4	16 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
45	c2o1mB_	Alignment	not modelled	56.7	15 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
46	c3r39A_	Alignment	not modelled	54.0	8 PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
47	d2amha1	Alignment	not modelled	52.4	30 Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
48	c2pfzA_	Alignment	not modelled	49.3	18 PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
49	c2y7iB_	Alignment	not modelled	49.2	13 PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
50	c2hpgB_	Alignment	not modelled	44.4	13 PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic2 binding protein
51	d1r9la_	Alignment	not modelled	44.0	13 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
52	c2de4B_	Alignment	not modelled	41.3	13 PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b;

						PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfonic acid
53	c1twyG_	Alignment	not modelled	39.7	27	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
54	d1twya_	Alignment	not modelled	39.7	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	c3r6uA_	Alignment	not modelled	39.2	16	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
56	d1tjna_	Alignment	not modelled	37.0	13	Fold: Chelataase-like Superfamily: Chelataase Family: CbiX-like
57	c1tjnA_	Alignment	not modelled	37.0	13	PDB header: lyase Chain: A: PDB Molecule: sirohdrochlorin cobaltochelataase; PDBTitle: crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
58	c2i4cA_	Alignment	not modelled	36.8	15	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
59	c2rejA_	Alignment	not modelled	36.4	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
60	c3hv1A_	Alignment	not modelled	35.7	12	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
61	c3n5lA_	Alignment	not modelled	33.7	18	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
62	c3pppA_	Alignment	not modelled	32.4	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
63	c3m1pA_	Alignment	not modelled	32.2	12	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
64	c3k7pA_	Alignment	not modelled	32.2	12	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
65	c2uyeA_	Alignment	not modelled	32.1	16	PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dnt from burkholderia sp. strain2 dnt in complex with thiocyanate
66	c3onmB_	Alignment	not modelled	31.2	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator lrrha; PDBTitle: effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
67	d2esna2	Alignment	not modelled	30.4	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
68	d1hsla_	Alignment	not modelled	29.6	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
69	c2vd3B_	Alignment	not modelled	29.2	16	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
70	c2dlnA_	Alignment	not modelled	29.0	22	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
71	d1mo0a_	Alignment	not modelled	27.3	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
72	c2ieeB_	Alignment	not modelled	26.5	11	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.
73	d2a5sa1	Alignment	not modelled	24.4	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	c2h9qC_	Alignment	not modelled	22.6	13	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
75	d1vhca_	Alignment	not modelled	22.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: transcription

76	c2ql3G_	Alignment	not modelled	22.0	15	Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
77	c3i6vA_	Alignment	not modelled	21.8	16	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
78	c1wloA_	Alignment	not modelled	20.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: safe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8
79	c2jl8S_	Alignment	not modelled	20.2	22	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l18; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
80	c2hxrA_	Alignment	not modelled	19.9	15	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
81	d1sw5a_	Alignment	not modelled	19.5	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
82	c3k6gA_	Alignment	not modelled	19.5	15	PDB header: protein binding Chain: A: PDB Molecule: telomeric repeat-binding factor 2-interacting protein 1; PDBTitle: crystal structure of rap1 and trf2 complex
83	c3k4uA_	Alignment	not modelled	19.2	11	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinetella succinogenes dsm 1740 complexed with lysine
84	d1t5ba_	Alignment	not modelled	19.0	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
85	d1us5a_	Alignment	not modelled	17.6	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
86	c3cz6A_	Alignment	not modelled	17.6	20	PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rap1; PDBTitle: crystal structure of the rap1 c-terminus
87	d1mzga_	Alignment	not modelled	17.5	20	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
88	d1lsta_	Alignment	not modelled	17.2	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
89	d1ni7a_	Alignment	not modelled	17.0	18	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
90	c3oxnD_	Alignment	not modelled	16.8	14	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
91	c3sc6F_	Alignment	not modelled	16.7	13	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of ddtp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
92	c2wfoA_	Alignment	not modelled	16.1	25	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein 1; PDBTitle: crystal structure of machupo virus envelope glycoprotein2 gp1
93	c3kosA_	Alignment	not modelled	16.0	14	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii
94	d2auna1	Alignment	not modelled	15.6	22	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like
95	c3hhfB_	Alignment	not modelled	14.9	24	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
96	d1khia2	Alignment	not modelled	13.9	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
97	c3jv9B_	Alignment	not modelled	13.5	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
98	c2f5zK_	Alignment	not modelled	13.4	40	PDB header: oxidoreductase/protein binding Chain: K: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
99	c1zy8M_	Alignment	not modelled	13.1	40	PDB header: oxidoreductase Chain: M: PDB Molecule: pyruvate dehydrogenase protein x component, PDBTitle: the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.