






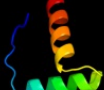






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		100.0	41	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c1q5vB_	 Alignment		97.9	20	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
3	c2bj3D_	 Alignment		97.9	12	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
4	d2bj7a1	 Alignment		97.9	9	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	c2ca9B_	 Alignment		97.7	17	PDB header: transcriptional regulation Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
6	d2hzaa1	 Alignment		97.1	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	d2hzab1	 Alignment		96.9	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	c2rbfB_	 Alignment		94.9	18	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
9	d2cpga_	 Alignment		93.9	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	c2an7A_	 Alignment		91.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
11	c2k9iB_	 Alignment		89.0	18	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid prn1, complete sequence; PDBTitle: nmr structure of plasmid copy control protein orf56 from2 sulfobolus islandicus

12	c3h87D_	Alignment		88.8	19	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
13	d2ay0a1	Alignment		79.1	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
14	d2bsqe1	Alignment		52.1	17	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
15	c2k29A_	Alignment		49.6	22	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
16	d1p94a_	Alignment		43.2	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
17	c2q2kA_	Alignment		25.3	26	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
18	d1fcdc1	Alignment		22.4	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
19	c1yxeA_	Alignment		21.2	23	PDB header: immune system Chain: A: PDB Molecule: apical membrane antigen 1; PDBTitle: structure and inter-domain interactions of domain ii from the blood2 stage malarial protein, apical membrane antigen 1
20	c2kelB_	Alignment		20.4	17	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
21	c3kxeD_	Alignment	not modelled	20.3	13	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
22	d1mnta_	Alignment	not modelled	18.6	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
23	c2dbiA_	Alignment	not modelled	18.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ybiu; PDBTitle: crystal structure of a hypothetical protein jw0805 from2 escherichia coli
24	c3mayE_	Alignment	not modelled	16.1	7	PDB header: heme-binding protein Chain: E: PDB Molecule: possible exported protein; PDBTitle: crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
25	c2qhoF_	Alignment	not modelled	15.2	30	PDB header: protein binding/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase edd1; PDBTitle: crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
26	c3o39A_	Alignment	not modelled	13.7	16	PDB header: chaperone Chain: A: PDB Molecule: periplasmic protein related to spheroblast formation; PDBTitle: crystal structure of spy
27	d1i27a_	Alignment	not modelled	13.0	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of the rap74 subunit of TFIIIF
28	c1ny9A_	Alignment	not modelled	11.0	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator tipa-s; PDBTitle: antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator Fold: Antibiotic binding domain of TipA-like multidrug resistance

29	dlny9a_	Alignment	not modelled	11.0	22	regulators Superfamily: Antibiotic binding domain of TipA-like multidrug resistance regulators Family: Antibiotic binding domain of TipA-like multidrug resistance regulators
30	d1l5aa2	Alignment	not modelled	10.2	20	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
31	c3qzcA_	Alignment	not modelled	9.8	12	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic protein cpxp; PDBTitle: structure of the periplasmic stress response protein cpxp
32	c2rqpA_	Alignment	not modelled	9.7	15	PDB header: gene regulation Chain: A: PDB Molecule: heterochromatin protein 1-binding protein 3; PDBTitle: the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
33	d1b3ta_	Alignment	not modelled	9.3	14	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
34	d1vh1b_	Alignment	not modelled	9.2	14	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
35	c3oeoD_	Alignment	not modelled	8.7	13	PDB header: signaling protein Chain: D: PDB Molecule: spheroplast protein y; PDBTitle: the crystal structure e. coli spy
36	d1fcdc2	Alignment	not modelled	8.6	4	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
37	c2hwyB_	Alignment	not modelled	8.3	14	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
38	c1kcfB_	Alignment	not modelled	8.3	22	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
39	c2fu2A_	Alignment	not modelled	8.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein spy2152; PDBTitle: crystal structure of protein spy2152 from streptococcus pyogenes
40	c1sfeA_	Alignment	not modelled	7.9	12	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
41	c1x93B_	Alignment	not modelled	7.7	21	PDB header: transcription Chain: B: PDB Molecule: hypothetical protein hp0222; PDBTitle: nmr structure of helicobacter pylori hp0222
42	d1x93a1	Alignment	not modelled	7.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
43	d2phcb1	Alignment	not modelled	7.0	6	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
44	d2outa2	Alignment	not modelled	7.0	21	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: YqbF N-terminal domain-like
45	c3g5oC_	Alignment	not modelled	6.8	23	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
46	c3epvB_	Alignment	not modelled	6.7	9	PDB header: metal binding protein Chain: B: PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
47	d1uxca_	Alignment	not modelled	6.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
48	c2e4jA_	Alignment	not modelled	6.2	12	PDB header: isomerase Chain: A: PDB Molecule: prostaglandin-h2 d-isomerase; PDBTitle: solution structure of mouse lipocalin-type prostaglandin d2 synthase
49	d1yqaa1	Alignment	not modelled	6.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
50	c3by0B_	Alignment	not modelled	6.0	12	PDB header: ligand binding protein Chain: B: PDB Molecule: neutrophil gelatinase-associated lipocalin; PDBTitle: crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
51	d1znda1	Alignment	not modelled	6.0	24	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
52	c2o3fC_	Alignment	not modelled	6.0	24	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
53	d2o3fa1	Alignment	not modelled	6.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like

54	d2csga1	Alignment	not modelled	5.8	13	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: YbiU-like
55	c3itfA_	Alignment	not modelled	5.8	19	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic adaptor protein cpxp; PDBTitle: structural basis for the inhibitory function of the cpxp adaptor2 protein
56	c2jobA_	Alignment	not modelled	5.6	11	PDB header: lipid binding protein Chain: A: PDB Molecule: antilipopolysaccharide factor; PDBTitle: solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
57	c2zqeA_	Alignment	not modelled	5.6	33	PDB header: dna binding protein Chain: A: PDB Molecule: mutS2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus mutS2
58	d1uhma_	Alignment	not modelled	5.5	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
59	c2zp2B_	Alignment	not modelled	5.4	12	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
60	d2je6b2	Alignment	not modelled	5.3	13	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
61	c2lcvA_	Alignment	not modelled	5.3	24	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation