



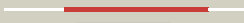



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2onkc1	 Alignment		99.9	12	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
2	c2onkC_	 Alignment		99.9	12	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
3	c3d31D_	 Alignment		99.9	16	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
4	d3d31c1	 Alignment		99.9	16	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
5	d3dhwa1	 Alignment		99.9	17	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
6	c2r6gF_	 Alignment		99.9	13	PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter
7	d2r6gf2	 Alignment		99.9	15	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
8	c3fh6F_	 Alignment		99.9	14	PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli
9	d2r6gg1	 Alignment		99.9	13	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
10	c1umqA_	 Alignment		72.0	16	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
11	d1umqa_	 Alignment		72.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

12	d1fipa_	Alignment		70.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	d1ntca_	Alignment		68.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
14	d1etob_	Alignment		64.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	c3e7lD_	Alignment		60.0	9	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
16	d1etxa_	Alignment		57.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	d1g2ha_	Alignment		49.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	c2cw1A_	Alignment		31.7	40	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
19	d1t98a1	Alignment		23.3	55	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MukF N-terminal domain-like
20	c2auwB_	Alignment		13.3	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
21	d1g72b_	Alignment	not modelled	11.7	33	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
22	c3no7A_	Alignment	not modelled	11.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: putative plasmid related protein; PDBTitle: crystal structure of the centromere-binding protein parb from plasmid2 pcxc100
23	d1w6sb_	Alignment	not modelled	11.3	42	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
24	d2ad6b1	Alignment	not modelled	11.2	33	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
25	d3orca_	Alignment	not modelled	11.0	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	d1lrwb_	Alignment	not modelled	10.0	33	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
27	c3ifuA_	Alignment	not modelled	9.2	40	PDB header: transcription Chain: A: PDB Molecule: non-structural protein; PDBTitle: the crystal structure of porcine reproductive and2 respiratory syndrome virus (prsv) leader protease nsp1
28	c2d7dB_	Alignment	not modelled	9.0	16	PDB header: hydrolase/dna Chain: B: PDB Molecule: 40-mer from uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
						Fold: lambda repressor-like DNA-binding domains

29	d2auwa1	Alignment	not modelled	8.7	16	Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
30	c1pnbA	Alignment	not modelled	8.1	33	PDB header: seed storage protein Chain: A: PDB Molecule: napin bnib; PDBTitle: structure of napin bnib, nmr, 10 structures
31	c2jwaA	Alignment	not modelled	7.2	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
32	c2zihC	Alignment	not modelled	6.4	27	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 74; PDBTitle: crystal structure of yeast vps74
33	c2ziiA	Alignment	not modelled	6.3	27	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 74; PDBTitle: crystal structure of yeast vps74-n-term truncation variant
34	c2vn2B	Alignment	not modelled	5.7	31	PDB header: replication Chain: B: PDB Molecule: chromosome replication initiation protein; PDBTitle: crystal structure of the n-terminal domain of dnaD protein2 from geobacillus kaustophilus hta426
35	d1ciia1	Alignment	not modelled	5.7	17	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
36	c3c4mC	Alignment	not modelled	5.5	50	PDB header: membrane protein Chain: C: PDB Molecule: parathyroid hormone; PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
37	c3c4mD	Alignment	not modelled	5.5	50	PDB header: membrane protein Chain: D: PDB Molecule: parathyroid hormone; PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
38	c2qksA	Alignment	not modelled	5.4	16	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
39	c2hx6A	Alignment	not modelled	5.2	8	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb