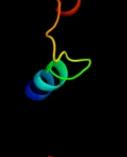
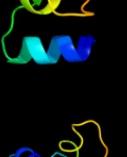
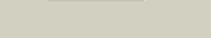


Phyre²

Email	i.a.kelley@imperial.ac.uk
Description	Q2EEQ8
Date	Thu Jan 5 12:33:44 GMT 2012
Unique Job ID	55ef19fa48cb5610

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kvca_	 Alignment		48.5	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
2	c3ol4B_	 Alignment		48.4	25	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
3	d1pdnc_	 Alignment		34.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	d3bpva1	 Alignment		30.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
5	c21kyA_	 Alignment		23.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mymsa.17112.b
6	c1e17A_	 Alignment		21.4	12	PDB header: dna binding domain Chain: A: PDB Molecule: afx; PDBTitle: solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
7	c3hefB_	 Alignment		19.5	25	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
8	d2fnna1	 Alignment		18.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
9	c3co7C_	 Alignment		17.7	14	PDB header: transcription/dna Chain: C: PDB Molecule: forkhead box protein o1; PDBTitle: crystal structure of foxo1 dbd bound to dbe2 dna
10	d1pm6a_	 Alignment		13.1	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
11	d2ezia_	 Alignment		13.1	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain

12	d2i7pa1			11.7	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
13	d1m5wa			11.1	28	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
14	c3gk0H			10.3	24	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
15	d1rh6a			9.6	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
16	c2k27A			9.3	19	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
17	c2i7pA			8.5	23	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 3; PDBTitle: crystal structure of human pank3 in complex with accoa
18	c6paxA			8.3	17	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
19	d2i7na2			8.1	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
20	c3smpA			7.8	23	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 1; PDBTitle: monoclinic crystal structure of human pantothenate kinase 1 alpha
21	d2v9va2		not modelled	7.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
22	c3iacA		not modelled	7.4	14	PDB header: isomerase Chain: A: PDB Molecule: glucuronate isomerase; PDBTitle: 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
23	d6paxa2		not modelled	7.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
24	d1k78a2		not modelled	6.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
25	c3u5gK		not modelled	6.7	20	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s10-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 \AA resolution
26	c2l1xA		not modelled	6.6	11	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone; PDBTitle: the solution structure of human parathyroid hormone-related protein
27	c3g73A		not modelled	6.5	16	PDB header: transcription/dna Chain: A: PDB Molecule: forkhead box protein m1; PDBTitle: structure of the foxm1 dna binding
28	d2ezha		not modelled	6.4	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
						PDB header: actin binding peptide

29	c1hj0A	Alignment	not modelled	6.3	22	Chain: A; PDB Molecule: thymosin beta9; PDBTitle: thymosin beta9
30	d1d5va	Alignment	not modelled	6.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
31	d2ezla	Alignment	not modelled	5.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
32	d2hfha	Alignment	not modelled	5.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
33	c2k8oA	Alignment	not modelled	5.5	25	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-I; PDBTitle: solution structure of integrin alpha I
34	c1qcrD	Alignment	not modelled	5.3	8	PDB header: PDB COMPND:
35	d1ni7a	Alignment	not modelled	5.3	5	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
36	d1evsa	Alignment	not modelled	5.3	22	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines