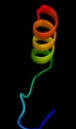
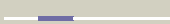
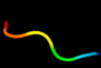
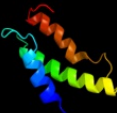


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76513
Date	Thu Jan 5 12:23:53 GMT 2012
Unique Job ID	30e70a993a851358

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1to0a_	 Alignment		30.0	30	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
2	d1ns5a_	 Alignment		30.0	26	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
3	d1vh0a_	 Alignment		25.5	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
4	d3cdda1	 Alignment		22.4	15	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
5	d1o6da_	 Alignment		20.9	25	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
6	c2gaaA_	 Alignment		16.1	29	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 39.9 kda protein; PDBTitle: crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
7	d1cmra_	 Alignment		15.4	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
8	c1ykuB_	 Alignment		13.5	13	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein pxo2-61; PDBTitle: crystal structure of a sensor domain homolog
9	c3pq1A_	 Alignment		12.0	19	PDB header: transferase Chain: A: PDB Molecule: poly(a) rna polymerase; PDBTitle: crystal structure of human mitochondrial poly(a) polymerase (papd1)
10	d2al6a3	 Alignment		10.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
11	d2gycf1	 Alignment		10.2	12	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain

12	d1lib_	Alignment		9.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
13	d1x57a1	Alignment		9.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
14	c3ktsA_	Alignment		8.7	18	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
15	c3q7cA_	Alignment		8.7	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleoprotein; PDBTitle: exonuclease domain of lassa virus nucleoprotein bound to manganese
16	d1p71a_	Alignment		8.6	13	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
17	c3bpjD_	Alignment		8.2	12	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunitj; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
18	c1tiic_	Alignment		8.0	33	PDB header: enterotoxin Chain: C: PDB Molecule: heat labile enterotoxin type iib; PDBTitle: escherichia coli heat labile enterotoxin type iib
19	c3omtA_	Alignment		7.6	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
20	c2opkC_	Alignment		7.6	18	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
21	c3dnvB_	Alignment	not modelled	7.4	18	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
22	c3bs3A_	Alignment	not modelled	7.3	9	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
23	c3f6wE_	Alignment	not modelled	7.2	14	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
24	c3nctC_	Alignment	not modelled	6.7	18	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
25	d1vkfa_	Alignment	not modelled	6.6	23	Fold: TIM beta/alpha-barrel Superfamily: GlpP-like Family: GlpP-like
26	c2np2B_	Alignment	not modelled	6.4	22	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hbb; PDBTitle: hbb-dna complex
27	c1r8jB_	Alignment	not modelled	6.4	11	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus
28	d1huua_	Alignment	not modelled	6.3	13	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
						PDB header: hydrolase

29	c1qhhA_	Alignment	not modelled	6.3	21	Chain: A: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
30	d2a5yb2	Alignment	not modelled	6.3	38	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
31	c3f52A_	Alignment	not modelled	6.1	14	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
32	c2jvIA_	Alignment	not modelled	6.1	10	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
33	c2ef8A_	Alignment	not modelled	5.8	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
34	d1owfa_	Alignment	not modelled	5.8	9	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
35	c3lisB_	Alignment	not modelled	5.7	18	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
36	d2auwa1	Alignment	not modelled	5.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
37	d2ppxa1	Alignment	not modelled	5.6	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
38	c2ppxA_	Alignment	not modelled	5.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
39	c3nybA_	Alignment	not modelled	5.5	9	PDB header: transferase/rna binding protein Chain: A: PDB Molecule: poly(a) rna polymerase protein 2; PDBTitle: structure and function of the polymerase core of tramp, a rna2 surveillance complex