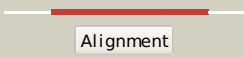
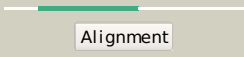
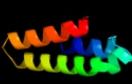
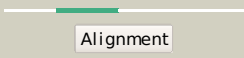
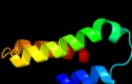
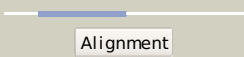
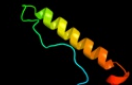
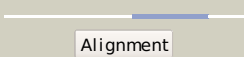
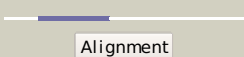
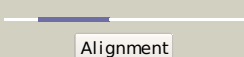
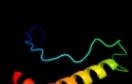
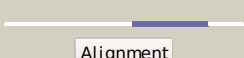
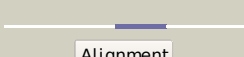
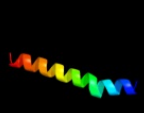


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4B8
Date	Sun Jul 8 11:45:07 BST 2012
Unique Job ID	ba076dc4639ed3ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ng6a_	 Alignment		100.0	27	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/YqeY domain
2	d1t6ua_	 Alignment		46.0	19	Fold: Four-helical up-and-down bundle Superfamily: Nickel-containing superoxide dismutase, NiSOD Family: Nickel-containing superoxide dismutase, NiSOD
3	c2d7dB_	 Alignment		45.7	15	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
4	d1q0ga_	 Alignment		42.6	14	Fold: Four-helical up-and-down bundle Superfamily: Nickel-containing superoxide dismutase, NiSOD Family: Nickel-containing superoxide dismutase, NiSOD
5	c3bnwA_	 Alignment		22.9	16	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase, putative; PDBTitle: crystal structure of riboflavin kinase from trypanosoma brucei
6	c2owvB_	 Alignment		20.7	16	PDB header: dna binding protein Chain: B: PDB Molecule: recombination-associated protein rdgc; PDBTitle: the recombination-associated protein rdgc adopts a novel toroidal architecture for dna binding
7	c2x0kB_	 Alignment		18.8	18	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from corynebacterium ammoniagenes
8	d1nb9a_	 Alignment		18.1	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
9	d1n08a_	 Alignment		17.8	16	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
10	c2ow1A_	 Alignment		17.6	25	PDB header: recombination Chain: A: PDB Molecule: recombination-associated protein rdgc; PDBTitle: crystal structure of e. coli rdgc
11	d2fnaa1	 Alignment		15.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain

12	c3tsiC_	Alignment		14.6	27	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin-neuraminidase; PDBTitle: structure of the parainfluenza virus 5 (piv5) hemagglutinin-2 neuraminidase (hn) stalk domain
13	d1q5qh_	Alignment		11.5	6	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
14	c1t6zB_	Alignment		9.0	18	PDB header: transferase Chain: B: PDB Molecule: riboflavin kinase/fmn adenylyltransferase; PDBTitle: crystal structure of riboflavin bound tm379
15	c2fhgC_	Alignment		7.6	7	PDB header: hydrolase Chain: C: PDB Molecule: proteasome, beta subunit; PDBTitle: crystal structure of mycobacterial tuberculosis proteasome
16	d1ykha1	Alignment		7.6	9	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: MED7 hinge region
17	c2o8kA_	Alignment		7.5	18	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
18	d1mrza1	Alignment		6.7	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
19	d1jmsa1	Alignment		6.6	11	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
20	c1xi4D_	Alignment		6.2	19	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
21	c1lt1G_	Alignment	not modelled	6.2	26	PDB header: de novo protein Chain: G: PDB Molecule: l13g-df1; PDBTitle: sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
22	c1m46B_	Alignment	not modelled	5.7	20	PDB header: cell cycle protein Chain: B: PDB Molecule: iq4 motif from myo2p, a class v myosin; PDBTitle: crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
23	c2f9jP_	Alignment	not modelled	5.5	5	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
24	d1smyf2	Alignment	not modelled	5.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
25	c2l82A_	Alignment	not modelled	5.3	33	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32