




















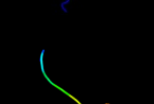
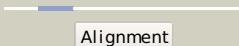

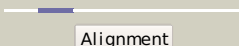
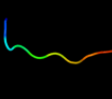


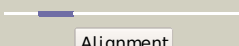

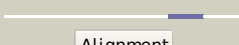

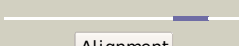

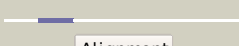




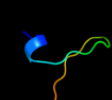

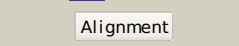

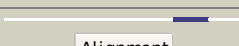

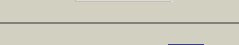
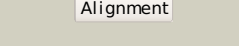



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q8NBR0
Date	Wed Jun 6 09:32:45 BST 2012
Unique Job ID	cf4e8fe59ea7199b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k3ra2	 Alignment		82.0	42	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
2	c1k3rA	 Alignment		69.6	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
3	c1x93B	 Alignment		56.3	25	PDB header: transcription Chain: B: PDB Molecule: hypothetical protein hp0222; PDBTitle: nmr structure of helicobacter pylori hp0222
4	d2ok5a4	 Alignment		51.7	42	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
5	d1x93a1	 Alignment		40.8	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c2nrzB	 Alignment		28.1	28	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrbc bound to2 its catalytic divalent cation
7	c2fwtA	 Alignment		27.6	14	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
8	c2nrnA	 Alignment		23.7	37	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease2 domain of uvrbc
9	c3ml6D	 Alignment		22.0	16	PDB header: protein transport Chain: D: PDB Molecule: chimeric complex between protein dishevelled2 homolog dvl-2 PDBTitle: a complex between dishevelled2 and clathrin adaptor ap-2
10	c3eopB	 Alignment		20.7	30	PDB header: unknown function Chain: B: PDB Molecule: thymocyte nuclear protein 1; PDBTitle: crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
11	d2gbsa1	 Alignment		20.5	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like

12	dlzcea1	 Alignment		20.4	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
13	d2g2xa1	 Alignment		19.7	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
14	d2ar1a1	 Alignment		18.2	30	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
15	d2evea1	 Alignment		18.0	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
16	d1q90n_	 Alignment		16.8	38	Fold: Single transmembrane helix Superfamily: PetN subunit of the cytochrome b6f complex Family: PetN subunit of the cytochrome b6f complex
17	c3c65A_	 Alignment		15.5	19	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearotherophilus uvrC 5'2 endonuclease domain
18	d1y5ia1	 Alignment		15.4	33	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
19	c2jy0A_	 Alignment		14.6	55	PDB header: membrane protein, viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
20	c4a8xB_	 Alignment		11.9	29	PDB header: transcription Chain: B: PDB Molecule: hook-like, isoform a; PDBTitle: structure of the core asap complex
21	c1kcnA_	 Alignment	not modelled	8.4	36	PDB header: protein binding Chain: A: PDB Molecule: e109 zeta peptide; PDBTitle: structure of e109 zeta peptide, an antagonist of the high-2 affinity ige receptor
22	d2dkya1	 Alignment	not modelled	8.2	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
23	c2dmqA_	 Alignment	not modelled	7.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: lim/homeobox protein lhx9; PDBTitle: solution structure of the homeobox domain of lim/homeobox2 protein lhx9
24	d1nfja_	 Alignment	not modelled	7.5	25	Fold: IF3-like Superfamily: AlbA-like Family: DNA-binding protein AlbA
25	c3toeB_	 Alignment	not modelled	7.0	25	PDB header: unknown function Chain: B: PDB Molecule: dna/rna-binding protein alba; PDBTitle: structure of nth10b
26	d1xmeb2	 Alignment	not modelled	6.9	39	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
27	d1t0ia_	 Alignment	not modelled	6.8	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
28	c3a0bL_	 Alignment	not modelled	6.7	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of br-substituted photosystem ii complex

29	d1j9ba_	Alignment	not modelled	6.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
30	d1rkla_	Alignment	not modelled	6.4	40	Fold: Single transmembrane helix Superfamily: Oligosaccharyltransferase subunit ost4p Family: Oligosaccharyltransferase subunit ost4p
31	c3zx1A_	Alignment	not modelled	6.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, putative; PDBTitle: multicopper oxidase from campylobacter jejuni: a metallo-oxidase
32	c3a0bl_	Alignment	not modelled	6.1	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
33	c3a0hl_	Alignment	not modelled	6.1	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
34	c3a0hL_	Alignment	not modelled	6.1	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex