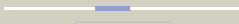
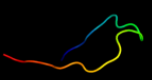
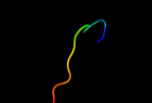
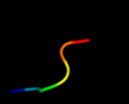


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P75972
Date	Thu Jan 5 12:16:40 GMT 2012
Unique Job ID	d1368aadd7045347

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gff2_	 Alignment		26.1	30	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
2	d1dx5i2	 Alignment		23.2	58	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
3	d1i8lc_	 Alignment		17.0	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
4	d1j8ia_	 Alignment		15.7	33	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
5	d2rh2a1	 Alignment		15.1	54	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: R67 dihydrofolate reductase
6	d1gpma3	 Alignment		11.6	56	Fold: Alpha-lytic protease prodomain-like Superfamily: GMP synthetase C-terminal dimerisation domain Family: GMP synthetase C-terminal dimerisation domain
7	c2wfuA_	 Alignment		10.3	100	PDB header: signaling protein Chain: A: PDB Molecule: probable insulin-like peptide 5 a chain; PDBTitle: crystal structure of dilp5 variant db
8	c2wfvA_	 Alignment		10.0	100	PDB header: signaling protein Chain: A: PDB Molecule: probable insulin-like peptide 5 a chain; PDBTitle: crystal structure of dilp5 variant c4
9	d1v5sa_	 Alignment		9.6	23	Fold: TBP-like Superfamily: KA1-like Family: Kinase associated domain 1, KA1
10	d4htci_	 Alignment		9.4	53	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Hirudin-like
11	c1wvoA_	 Alignment		9.3	54	PDB header: transferase Chain: A: PDB Molecule: sialic acid synthase; PDBTitle: solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene.

12	d1tyka_	Alignment		8.6	83	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
13	c1m3wD_	Alignment		8.5	70	PDB header: de novo protein Chain: D: PDB Molecule: h10h24; PDBTitle: crystal structure of a molecular maquette scaffold
14	c1m3wC_	Alignment		8.5	70	PDB header: de novo protein Chain: C: PDB Molecule: h10h24; PDBTitle: crystal structure of a molecular maquette scaffold
15	c1m3wB_	Alignment		8.5	70	PDB header: de novo protein Chain: B: PDB Molecule: h10h24; PDBTitle: crystal structure of a molecular maquette scaffold
16	c1m3wA_	Alignment		8.5	70	PDB header: de novo protein Chain: A: PDB Molecule: h10h24; PDBTitle: crystal structure of a molecular maquette scaffold
17	d1g3pa2	Alignment		8.4	35	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
18	d1ev7a_	Alignment		7.5	36	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease NaeI
19	d2op5a1	Alignment		7.2	55	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Marine metagenome family DABB1
20	c2ywcC_	Alignment		7.1	78	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
21	d2dexx2	Alignment	not modelled	7.1	47	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Peptidylarginine deiminase Pad4, N-terminal domain
22	d1p8ba_	Alignment	not modelled	6.4	46	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
23	c1h8lA_	Alignment	not modelled	6.4	19	PDB header: carboxypeptidase Chain: A: PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gemsA
24	d1kqha_	Alignment	not modelled	6.2	71	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
25	d1c8aa2	Alignment	not modelled	6.1	38	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
26	d1opsa_	Alignment	not modelled	5.8	38	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
27	d1bmlc1	Alignment	not modelled	5.6	54	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
28	c1y96D_	Alignment	not modelled	5.5	24	PDB header: rna binding protein Chain: D: PDB Molecule: gem-associated protein 7; PDBTitle: crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
						Fold: II 8-like

29	d1bo0a_	Alignment	not modelled	5.3	28	Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
30	d1xn8a_	Alignment	not modelled	5.2	35	Fold: Hypothetical protein YqbG Superfamily: Hypothetical protein YqbG Family: Hypothetical protein YqbG