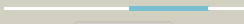
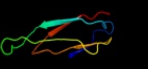
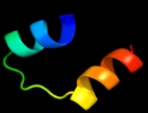
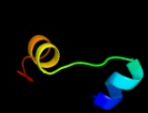
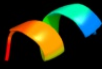


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76508
Date	Thu Jan 5 12:23:47 GMT 2012
Unique Job ID	3c4fdc27aeb808c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ccva1	 Alignment		82.1	10	Fold: HPA-like Superfamily: Agglutinin HPA-like Family: Agglutinin HPA-like
2	c2vmeC_	 Alignment		37.0	11	PDB header: cell adhesion Chain: C: PDB Molecule: discoidin-2; PDBTitle: structure of the wild-type discoidin ii from dictyostelium2 discoideum
3	c2w95B_	 Alignment		26.8	16	PDB header: cell adhesion Chain: B: PDB Molecule: discoidin-1 subunit a; PDBTitle: structure of the discoidin i from dictyostelium discoideum2 in complex with galnac at 1.75 angstrom resolution
4	c3a1yF_	 Alignment		25.3	38	PDB header: ribosomal protein Chain: F: PDB Molecule: 50s ribosomal protein p1 (l12p); PDBTitle: the structure of protein complex
5	c3hrzA_	 Alignment		13.7	15	PDB header: immune system Chain: A: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
6	c2w1oA_	 Alignment		12.1	9	PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
7	c3p45F_	 Alignment		12.1	22	PDB header: hydrolase Chain: F: PDB Molecule: caspase-6; PDBTitle: crystal structure of apo-caspase-6 at physiological ph
8	c3trkA_	 Alignment		11.6	24	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
9	d1jqpa2	 Alignment		10.4	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Papain-like
10	d1ev0a_	 Alignment		9.3	17	Fold: Cell division protein MinE topological specificity domain Superfamily: Cell division protein MinE topological specificity domain Family: Cell division protein MinE topological specificity domain
11	c2jsnA_	 Alignment		9.2	7	PDB header: protein transport Chain: A: PDB Molecule: trafficking protein particle complex subunit 4; PDBTitle: solution structure of the atypical pdz-like domain of2 synbindin

12	c1bqfA_	Alignment		9.0	50	PDB header: hormone/growth factor Chain: A: PDB Molecule: protein (growth-blocking peptide); PDBTitle: growth-blocking peptide (gbp) from pseudotelia separata
13	d1aoya_	Alignment		8.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
14	c2ct8A_	Alignment		7.8	19	PDB header: ligase/rna Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue
15	d2p5ka1	Alignment		7.8	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
16	d1f9na1	Alignment		7.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
17	d1fd9a_	Alignment		7.2	15	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
18	c2kxwB_	Alignment		7.1	50	PDB header: calcium-binding protein/metal transport Chain: B: PDB Molecule: sodium channel protein type 2 subunit alpha; PDBTitle: structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
19	d1b4aa1	Alignment		6.3	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
20	c1b4aA_	Alignment		6.0	29	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
21	c1dfwA_	Alignment	not modelled	6.0	67	PDB header: immune system Chain: A: PDB Molecule: lung surfactant protein b; PDBTitle: conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
22	d2sici_	Alignment	not modelled	5.7	19	Fold: Subtilisin inhibitor Superfamily: Subtilisin inhibitor Family: Subtilisin inhibitor
23	d2hgsa4	Alignment	not modelled	5.5	40	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Eukaryotic glutathione synthetase ATP-binding domain
24	c2xvcA_	Alignment	not modelled	5.4	10	PDB header: cell cycle Chain: A: PDB Molecule: escrt-iii; PDBTitle: molecular and structural basis of escrt-iii recruitment to2 membranes during archaeal cell division
25	d1m0wa2	Alignment	not modelled	5.4	30	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Eukaryotic glutathione synthetase ATP-binding domain