
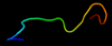
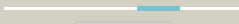
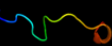
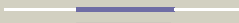







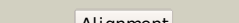
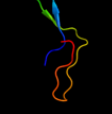

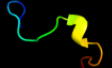

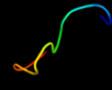


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A5A628
Date	Thu Jan 5 10:55:31 GMT 2012
Unique Job ID	460ca850ba7440ca

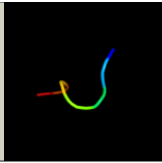
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zupa1	 Alignment		51.0	38	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: TM1739-like
2	c2jlnA_	 Alignment		38.1	28	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
3	c3mcuF_	 Alignment		14.6	26	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
4	c1zc1A_	 Alignment		11.9	30	PDB header: protein turnover Chain: A: PDB Molecule: ubiquitin fusion degradation protein 1; PDBTitle: ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
5	c2yujA_	 Alignment		10.9	36	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
6	c3pvcA_	 Alignment		8.9	26	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mmc from yersinia pestis
7	c3lqkA_	 Alignment		8.9	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
8	c2l14B_	 Alignment		6.7	41	PDB header: protein binding Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
9	d1q3ja_	 Alignment		6.5	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Gurmarin-like Family: Antifungal peptide

10 [dlc99a_](#)



Alignment



5.3

86

Fold: Transmembrane helix hairpin
Superfamily: F1F0 ATP synthase subunit C
Family: F1F0 ATP synthase subunit C