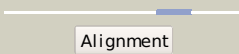

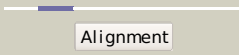
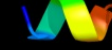
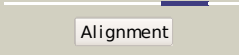

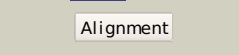

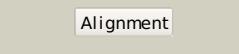

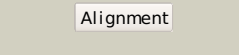

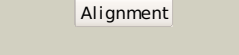



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C1P601
Date	Thu Jan 5 10:55:53 GMT 2012
Unique Job ID	adce3219c5c88ace

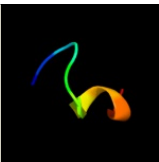
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sxma_	 Alignment		22.9	55	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
2	c1zllE_	 Alignment		11.6	75	PDB header: membrane protein/signaling protein Chain: E: PDB Molecule: cardiac phospholamban; PDBTitle: nmr structure of unphosphorylated human phospholamban2 pentamer
3	d1jlja_	 Alignment		9.5	47	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
4	d2cs3a1	 Alignment		9.5	38	Fold: RING/U-box Superfamily: RING/U-box Family: Variant RING domain
5	c3h0dB_	 Alignment		8.4	50	PDB header: transcription/dna Chain: B: PDB Molecule: ctsr; PDBTitle: crystal structure of ctrs in complex with a 26bp dna duplex
6	d2b0ja2	 Alignment		7.0	86	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
7	c3f46A_	 Alignment		6.0	86	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methenyltetrahydromethanopterin hydrogenase; PDBTitle: the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii

8

[d2cv4a1](#)

Alignment



5.9

27

Fold:Thioredoxin fold
Superfamily:Thioredoxin-like
Family:Glutathione peroxidase-like