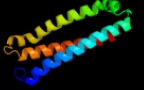
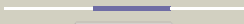
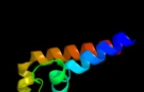
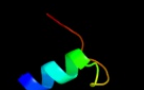
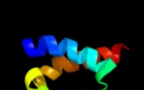


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76296
Date	Thu Jan 5 12:21:38 GMT 2012
Unique Job ID	076a6853b0cd4b21

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gi7A_	 Alignment		99.9	15	PDB header: unknown function Chain: A: PDB Molecule: secreted protein of unknown function duf1311; PDBTitle: crystal structure of a duf1311 family protein (pp0307) from2 pseudomonas putida kt2440 at 1.85 a resolution
2	d1n4ca_	 Alignment		12.2	13	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
3	c1zxaB_	 Alignment		10.9	14	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
4	d1pm6a_	 Alignment		9.2	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
5	c2rkhA_	 Alignment		9.2	19	PDB header: transcription Chain: A: PDB Molecule: putative apha-like transcription factor; PDBTitle: crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
6	d2noca1	 Alignment		6.6	21	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
7	d1rh6a_	 Alignment		6.5	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
8	c2jrmA_	 Alignment		5.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribosome modulation factor; PDBTitle: solution nmr structure of ribosome modulation factor vp1593 from2 vibrio parahaemolyticus. northeast structural genomics target vpr55

9

[c2dn9A_](#)

Alignment



5.2

14

PDB header:apoptosis, chaperone
Chain: A: **PDB Molecule:**dnaj homolog subfamily a member 3;
PDBTitle: solution structure of j-domain from the dnaj homolog, human2 tid1 protein