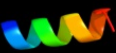
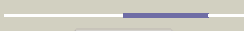
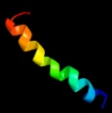
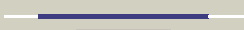
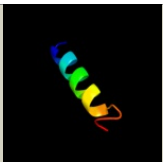


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4B6
Date	Sun Jul 8 11:45:07 BST 2012
Unique Job ID	c51d1787447e73e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1prtf_	 Alignment		14.4	29	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
2	c3kk4B_	 Alignment		14.3	16	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
3	c3d5bj_	 Alignment		10.4	42	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l10; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
4	c2kb1A_	 Alignment		10.1	17	PDB header: membrane protein Chain: A; PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsc
5	c3ctwB_	 Alignment		9.1	25	PDB header: protein binding Chain: B; PDB Molecule: rcda; PDBTitle: crystal structure of rcda from caulobacter crescentus cb15
6	c1l5jB_	 Alignment		8.6	13	PDB header: lyase Chain: B; PDB Molecule: aconitate hydratase 2; PDBTitle: crystal structure of e. coli aconitase b.
7	c3uinD_	 Alignment		7.8	7	PDB header: ligase/isomerase/protein binding Chain: D; PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
8	c2plxB_	 Alignment		6.9	29	PDB header: hydrolase Chain: B; PDB Molecule: peptide inhibitor; PDBTitle: trypsin complexed to a synthetic peptide from veronica hederifolia
9	d1wxma1	 Alignment		6.8	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
10	d2pmaa1	 Alignment		6.7	18	Fold: Acid proteases Superfamily: Acid proteases Family: LPG0085-like
11	d1qcsa1	 Alignment		6.2	29	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like

12 c2dyoB_ Alignment		6.2	17 PDB header:protein turnover/protein turnover Chain: B: PDB Molecule:autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
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13 d1pzqa_

Alignment



6.0

31

Fold:Dimerisation interlock

Superfamily:Docking domain A of the erythromycin polyketide synthase (DEBS)

Family:Docking domain A of the erythromycin polyketide synthase (DEBS)