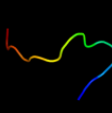
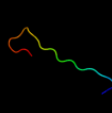
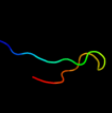
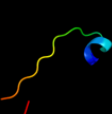
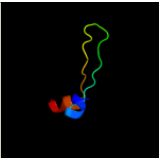
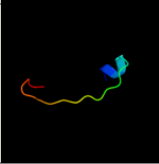


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4B9
Date	Sun Jul 8 11:45:08 BST 2012
Unique Job ID	358cbdc858c09f31

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2nvpal	 Alignment		27.9	43	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
2	c4emoB	 Alignment		26.8	73	PDB header: protein binding Chain: B: PDB Molecule: sharpin; PDBTitle: crystal structure of the ph domain of sharpin
3	d2p0val	 Alignment		25.1	42	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
4	c2p0vA	 Alignment		25.1	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bt3781; PDBTitle: crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
5	d2j3wb1	 Alignment		20.6	19	Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: TRAPP components
6	c3qspB	 Alignment		16.9	29	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
7	d1j0ga	 Alignment		15.0	47	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
8	c2logA	 Alignment		8.9	56	PDB header: membrane protein Chain: A: PDB Molecule: interferon alpha-inducible protein 27-like protein 1; PDBTitle: backbone structure of human membrane protein fam14b (interferon alpha-2 inducible protein 27-like protein 1)
9	c2zyzA	 Alignment		7.0	59	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1012; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
10	c2j3tB	 Alignment		6.2	19	PDB header: transport Chain: B: PDB Molecule: trafficking protein particle complex subunit 6a; PDBTitle: the crystal structure of the bet3-trs33-bet5-trs23 complex.
11	c3i6pF	 Alignment		6.1	45	PDB header: structural protein Chain: F: PDB Molecule: ethanolamine utilization protein eutm; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutm

12	c3cueH_	Alignment		5.6	20	PDB header: protein transport Chain: H: PDB Molecule: transport protein particle 31 kda subunit; PDBTitle: crystal structure of a trapp subassembly activating the rab ypt1p
13	c2cfhD_	Alignment		5.6	19	PDB header: transport Chain: D: PDB Molecule: trafficking protein particle complex subunit 6b; PDBTitle: structure of the bet3-tpc6b core of trapp

14 [c3mjhD_](#)

Alignment



5.4

83

PDB header:protein transport
Chain: D: **PDB Molecule:**early endosome antigen 1;
PDBTitle: crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1