
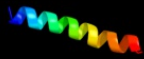
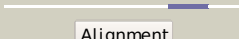

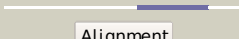
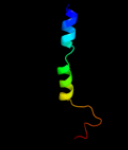
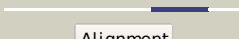

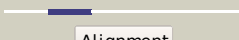




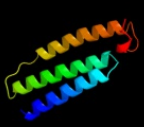



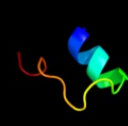





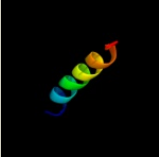

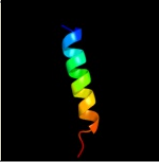


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	POC948
Date	Tue Jul 17 17:05:09 BST 2012
Unique Job ID	ffe9a7f68ff86912

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oqwa_	 Alignment		19.3	16	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
2	c2lf2A_	 Alignment		15.6	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
3	d1kqfb2	 Alignment		15.2	18	Fold: Single transmembrane helix Superfamily: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor Family: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
4	c3sokB_	 Alignment		9.9	16	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
5	d1jvra_	 Alignment		8.7	26	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: HTLV-II matrix protein
6	c2wocA_	 Alignment		7.7	40	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribosyl-[dinitrogen reductase] glycohydrolase; PDBTitle: crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
7	c3rkoK_	 Alignment		7.3	12	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
8	c3zqpB_	 Alignment		7.2	14	PDB header: dna-binding protein Chain: B: PDB Molecule: terminase small subunit; PDBTitle: crystal structure of the small terminase oligomerization2 domain from a spp1-like bacteriophage
9	d1a0pa1	 Alignment		6.8	5	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
10	d2pila_	 Alignment		6.7	16	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
11	d1jb3a_	 Alignment		6.6	24	Fold: OB-fold Superfamily: TIMP-like Family: The laminin-binding domain of agrin

<p>12 c1w5cL_</p>	<p>Alignment</p> 		<p>5.9</p>	<p>19 PDB header: photosynthesis Chain: L: PDB Molecule: cytochrome b559 beta subunit; PDBTitle: photosystem ii from thermosynechococcus elongatus</p>
<p>13 d2axtf1</p>	<p>Alignment</p> 		<p>5.8</p>	<p>19 Fold: Single transmembrane helix Superfamily: Cytochrome b559 subunits Family: Cytochrome b559 subunits</p>

14 [c2kxaA](#)

Alignment



5.0

56

PDB header: viral protein, immune system
Chain: A: **PDB Molecule:** haemagglutinin ha2 chain peptide;
PDBTitle: the hemagglutinin fusion peptide (h1 subtype) at ph 7.4