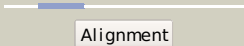
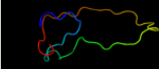



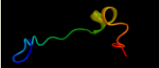


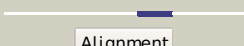

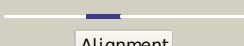



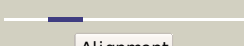
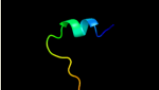






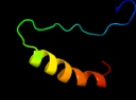

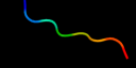



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0JLT2
Date	Tue Apr 3 15:10:21 BST 2012
Unique Job ID	d2d26d79caee891d

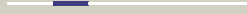
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2gqba1</a>	 Alignment		23.3	47	<b>Fold:</b> RPA2825-like <b>Superfamily:</b> RPA2825-like <b>Family:</b> RPA2825-like
2	<a href="#">d2grga1</a>	 Alignment		15.8	24	<b>Fold:</b> Profilin-like <b>Superfamily:</b> YNR034W-A-like <b>Family:</b> YNR034W-A-like
3	<a href="#">c3kysC_</a>	 Alignment		9.4	32	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional enhancer factor tef-1; <b>PDBTitle:</b> crystal structure of human yap and tead complex
4	<a href="#">c3dboA_</a>	 Alignment		9.3	62	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
5	<a href="#">d1dxsa_</a>	 Alignment		9.1	57	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
6	<a href="#">c3q87A_</a>	 Alignment		7.8	26	<b>PDB header:</b> transferase activator/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ecu08_1170; <b>PDBTitle:</b> structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
7	<a href="#">d1kcfa1</a>	 Alignment		7.5	25	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
8	<a href="#">c3gn6B_</a>	 Alignment		7.2	45	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ct0912, orfan protein with a ferredoxin-like domain repeat; <b>PDBTitle:</b> crystal structure of ct0912, orfan protein from chlorobium tepidum2 with a ferredoxin-like domain repeat (np_661805.1) from chlorobium3 tepidum t1s at 1.80 a resolution
9	<a href="#">d1k4za_</a>	 Alignment		7.2	50	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> C-terminal domain of adenyllyl cyclase associated protein <b>Family:</b> C-terminal domain of adenyllyl cyclase associated protein
10	<a href="#">c2eqoA_</a>	 Alignment		7.1	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 3-interacting <b>PDBTitle:</b> solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
11	<a href="#">d2h4oa1</a>	 Alignment		6.2	31	<b>Fold:</b> YonK-like <b>Superfamily:</b> YonK-like <b>Family:</b> YonK-like

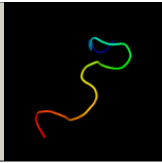
12	<a href="#">d2pw6a1</a>	Alignment		5.8	8	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> LigB-like <b>Family:</b> LigB-like
13	<a href="#">d1k8fa_</a>	Alignment		5.8	50	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> C-terminal domain of adenylcyclase associated protein <b>Family:</b> C-terminal domain of adenylcyclase associated protein
14	<a href="#">c2b0rB_</a>	Alignment		5.7	38	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> possible adenyl cyclase-associated protein; <b>PDBTitle:</b> crystal structure of cyclase-associated protein from <i>2</i> cryptosporidium parvum
15	<a href="#">c2j9wB_</a>	Alignment		5.4	33	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vps28-prov protein; <b>PDBTitle:</b> structural insight into the escrt-i-ii link and its role in <i>2</i> mvb trafficking

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[dlgzb\\_](#)



Alignment



5.2

50

**Fold:**SopE-like GEF domain  
**Superfamily:**SopE-like GEF domain  
**Family:**SopE-like GEF domain