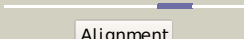

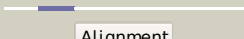

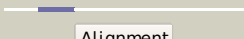



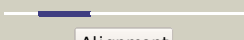


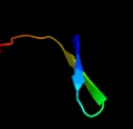

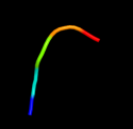



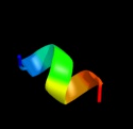




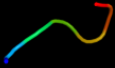

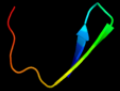

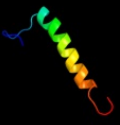
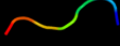



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P29010
Date	Wed Jan 25 15:20:47 GMT 2012
Unique Job ID	8ddc8f202c6cde4d

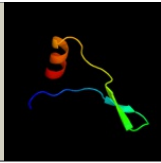
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1wqkA_</a>	 Alignment		15.9	100	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin apetx1; <b>PDBTitle:</b> solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
2	<a href="#">d2guya1</a>	 Alignment		11.3	27	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
3	<a href="#">d2aaaa1</a>	 Alignment		10.2	36	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
4	<a href="#">d2taaa1</a>	 Alignment		8.7	27	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
5	<a href="#">c2qtxL_</a>	 Alignment		8.5	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> L: <b>PDB Molecule:</b> uncharacterized protein mj1435; <b>PDBTitle:</b> crystal structure of an hfq-like protein from methanococcus2 jannaschii
6	<a href="#">c1kq1W_</a>	 Alignment		7.0	20	<b>PDB header:</b> translation <b>Chain:</b> W: <b>PDB Molecule:</b> host factor for q beta; <b>PDBTitle:</b> 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
7	<a href="#">c1wxnA_</a>	 Alignment		6.4	60	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin apetx2; <b>PDBTitle:</b> solution structure of apetx2, a specific peptide inhibitor2 of ASIC3 proton-gated channels
8	<a href="#">c2qsdB_</a>	 Alignment		6.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of a protein il1583 from idiomarina loihiensis
9	<a href="#">c2hwnF_</a>	 Alignment		6.0	50	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> a kinase binding peptide; <b>PDBTitle:</b> crystal structure of rii alpha dimerization/docking domain of pka2 bound to the d-akap2 peptide
10	<a href="#">c2hwnE_</a>	 Alignment		6.0	50	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> a kinase binding peptide; <b>PDBTitle:</b> crystal structure of rii alpha dimerization/docking domain of pka2 bound to the d-akap2 peptide
11	<a href="#">d2qamc1</a>	 Alignment		6.0	40	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> C-terminal domain of ribosomal protein L2

12	<a href="#">d1p9qc3</a>	Alignment		5.9	43	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
13	<a href="#">d1qf8a_</a>	Alignment		5.9	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Casein kinase II beta subunit <b>Family:</b> Casein kinase II beta subunit
14	<a href="#">d1u1sa1</a>	Alignment		5.6	15	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Pleiotropic translational regulator Hfq
15	<a href="#">d1t95a3</a>	Alignment		5.6	43	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
16	<a href="#">c1w7vD_</a>	Alignment		5.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> xaa-pro aminopeptidase; <b>PDBTitle:</b> znmg substituted aminopeptidase p from e. coli
17	<a href="#">c2aivA_</a>	Alignment		5.4	100	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> fragment of nucleoporin nup116/nsp116; <b>PDBTitle:</b> multiple conformations in the ligand-binding site of the2 yeast nuclear pore targeting domain of nup116p
18	<a href="#">d2guka1</a>	Alignment		5.2	13	<b>Fold:</b> PG1857-like <b>Superfamily:</b> PG1857-like <b>Family:</b> PG1857-like

19 [d2i9xa1](#)

Alignment



5.0

23

**Fold:**SpoVG-like  
**Superfamily:**SpoVG-like  
**Family:**SpoVG-like