




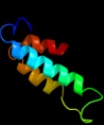








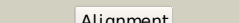










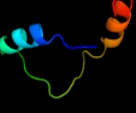

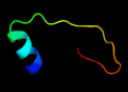


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P11291
Date	Thu Jan 5 11:32:34 GMT 2012
Unique Job ID	5de68c91f2084926

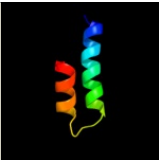
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2gu0A_</a>	 Alignment		41.6	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nonstructural protein 2; <b>PDBTitle:</b> crystal structure of human rotavirus nsp2 (group c /2 bristol strain)
2	<a href="#">dls5qb_</a>	 Alignment		29.9	21	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
3	<a href="#">d2f05a1</a>	 Alignment		21.1	19	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
4	<a href="#">d1vp8a_</a>	 Alignment		18.7	63	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
5	<a href="#">d1t57a_</a>	 Alignment		17.8	75	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
6	<a href="#">d3bl2a1</a>	 Alignment		16.0	78	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
7	<a href="#">c2rmrA_</a>	 Alignment		13.4	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> paired amphipathic helix protein sin3a; <b>PDBTitle:</b> solution structure of msin3a pah1 domain
8	<a href="#">d1utra_</a>	 Alignment		12.5	28	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
9	<a href="#">d1ccda_</a>	 Alignment		12.3	28	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
10	<a href="#">d1utga_</a>	 Alignment		9.5	22	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
11	<a href="#">d1n93x_</a>	 Alignment		9.0	29	<b>Fold:</b> P40 nucleoprotein <b>Superfamily:</b> P40 nucleoprotein <b>Family:</b> P40 nucleoprotein

12	<a href="#">c1n93X_</a>	Alignment		9.0	29	<b>PDB header:</b> viral protein <b>Chain:</b> X: <b>PDB Molecule:</b> p40 nucleoprotein; <b>PDBTitle:</b> crystal structure of the borna disease virus nucleoprotein
13	<a href="#">c3qk9B_</a>	Alignment		7.4	14	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> yeast tim44 c-terminal domain complexed with cymal-3
14	<a href="#">c2fhdA_</a>	Alignment		6.8	71	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rhp9/crb2; <b>PDBTitle:</b> crystal structure of crb2 tandem tudor domains
15	<a href="#">c3bd0D_</a>	Alignment		6.6	20	<b>PDB header:</b> peptide binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein memo1; <b>PDBTitle:</b> crystal structure of memo, form ii
16	<a href="#">d1mb4a1</a>	Alignment		6.2	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	<a href="#">d1s28a_</a>	Alignment		6.1	26	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone

18 [dlnlxa\\_](#)

Alignment



5.3

21 **Fold:**Four-helical up-and-down bundle  
**Superfamily:**Group V grass pollen allergen  
**Family:**Group V grass pollen allergen