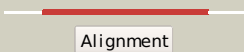

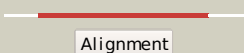

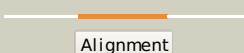

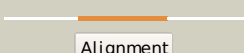
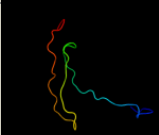
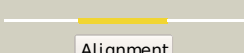

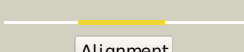

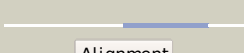
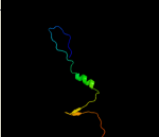
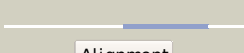
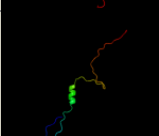







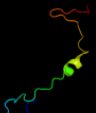



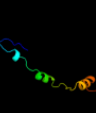
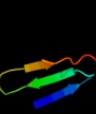
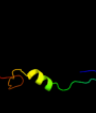



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P52644
Date	Thu Jan 5 12:05:57 GMT 2012
Unique Job ID	4e6b7933f021cb31

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ktsA_</a>	 Alignment		100.0	100	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hslj; <b>PDBTitle:</b> nmr structure of the protein np_415897.1
2	<a href="#">c2la7A_</a>	 Alignment		99.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein yp_557733.1 from burkholderia xenovorans
3	<a href="#">c2y6tE_</a>	 Alignment		83.4	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> ecotin; <b>PDBTitle:</b> molecular recognition of chymotrypsin by the serine2 protease inhibitor ecotin from yersinia pestis
4	<a href="#">d1e2sa_</a>	 Alignment		81.9	21	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
5	<a href="#">d1xxfc_</a>	 Alignment		78.5	21	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
6	<a href="#">d1slua_</a>	 Alignment		72.4	22	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
7	<a href="#">d1svba2</a>	 Alignment		25.4	13	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
8	<a href="#">c1urzC_</a>	 Alignment		21.1	13	<b>PDB header:</b> virus/viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
9	<a href="#">d1rl6a1</a>	 Alignment		20.7	25	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
10	<a href="#">c3ge2A_</a>	 Alignment		18.4	9	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein, putative; <b>PDBTitle:</b> crystal structure of putative lipoprotein sp_0198 from streptococcus2 pneumoniae
11	<a href="#">d2j01h1</a>	 Alignment		17.9	16	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6

12	<a href="#">d2hnxa1</a>	Alignment		15.3	38	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
13	<a href="#">c2of6C_</a>	Alignment		13.6	13	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein e; <b>PDBTitle:</b> structure of immature west nile virus
14	<a href="#">c2q9sA_</a>	Alignment		13.2	38	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> linoleic acid bound to fatty acid binding protein 4
15	<a href="#">d1jiwi_</a>	Alignment		11.6	22	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> beta-Barrel protease inhibitors <b>Family:</b> Metalloprotease inhibitor
16	<a href="#">d2ot9a1</a>	Alignment		9.6	12	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like
17	<a href="#">c1p58C_</a>	Alignment		9.1	18	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
18	<a href="#">c3c0uA_</a>	Alignment		8.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaeq; <b>PDBTitle:</b> crystal structure of e.coli yaeq protein
19	<a href="#">d1ok8a2</a>	Alignment		7.8	16	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
20	<a href="#">d2zjre2</a>	Alignment		7.2	16	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
21	<a href="#">d2qamg1</a>	Alignment	not modelled	7.1	22	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
22	<a href="#">d1vqoe1</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
23	<a href="#">d1g7na_</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
24	<a href="#">d2g3wa1</a>	Alignment	not modelled	5.6	9	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like
25	<a href="#">c3c6dB_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> the pseudo-atomic structure of dengue immature virus