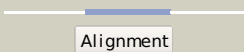
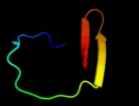
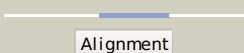
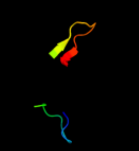
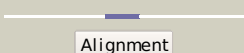

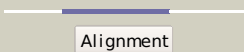
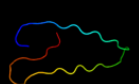
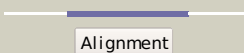

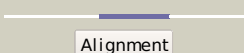
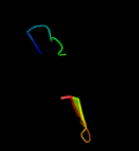


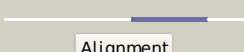
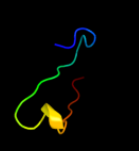
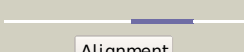
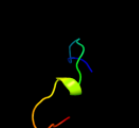
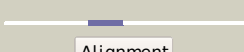
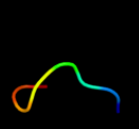
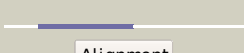
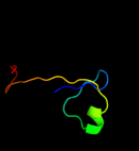


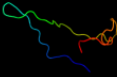








# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P64503
Date	Thu Jan 5 12:08:58 GMT 2012
Unique Job ID	7453dbccab807e00

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pcia_</a>	 Alignment		23.3	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
2	<a href="#">d1xaua_</a>	 Alignment		21.1	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
3	<a href="#">c2hacA_</a>	 Alignment		19.9	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd3 zeta chain; <b>PDBTitle:</b> structure of zeta-zeta transmembrane dimer
4	<a href="#">c3pnrB_</a>	 Alignment		16.4	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> pbicp-c; <b>PDBTitle:</b> structure of pbicp-c in complex with falcipain-2
5	<a href="#">d1fltx_</a>	 Alignment		15.4	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
6	<a href="#">d2aw2a1</a>	 Alignment		15.1	33	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
7	<a href="#">c2c0yA_</a>	 Alignment		14.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> procathepsin s; <b>PDBTitle:</b> the crystal structure of a cys25ala mutant of human2 procathepsin s
8	<a href="#">d1ysja1</a>	 Alignment		13.5	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
9	<a href="#">c3razA_</a>	 Alignment		12.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
10	<a href="#">c3fjuB_</a>	 Alignment		11.6	75	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> carboxypeptidase a inhibitor; <b>PDBTitle:</b> ascaris suum carboxypeptidase inhibitor in complex with human2 carboxypeptidase a1
11	<a href="#">d2nn6e2</a>	 Alignment		11.4	22	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like

12	<a href="#">c1xbsA_</a>	Alignment		11.0	13	<b>PDB header:</b> transcription, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dim1-like protein; <b>PDBTitle:</b> crystal structure of human dim2: a dim1-like protein
13	<a href="#">c2opkC_</a>	Alignment		10.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
14	<a href="#">c2g8gA_</a>	Alignment		9.9	20	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid; <b>PDBTitle:</b> structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4
15	<a href="#">d1ppoa_</a>	Alignment		8.7	16	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
16	<a href="#">c2vscD_</a>	Alignment		7.8	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> leukocyte surface antigen cd47; <b>PDBTitle:</b> structure of the immunoglobulin-superfamily ectodomain of2 human cd47
17	<a href="#">c1w4sA_</a>	Alignment		6.9	13	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> polybromo 1 protein; <b>PDBTitle:</b> crystal structure of the proximal bah domain of polybromo
18	<a href="#">d1b25a1</a>	Alignment		6.6	63	<b>Fold:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Superfamily:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Family:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains
19	<a href="#">c3iv6C_</a>	Alignment		6.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative zn-dependent alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative zn-dependent alcohol dehydrogenases from2 rhodobacter sphaeroides.
20	<a href="#">c2eq5D_</a>	Alignment		6.3	30	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 228aa long hypothetical hydantoin racemase; <b>PDBTitle:</b> crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
21	<a href="#">d2vzsa2</a>	Alignment	not modelled	6.3	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
22	<a href="#">c1ybiA_</a>	Alignment	not modelled	6.1	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> non-toxin haemagglutinin ha34; <b>PDBTitle:</b> crystal structure of ha33a, a neurotoxin-associated protein2 from clostridium botulinum type a
23	<a href="#">d1oaza_</a>	Alignment	not modelled	5.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
24	<a href="#">d1a79a2</a>	Alignment	not modelled	5.8	31	<b>Fold:</b> MutS N-terminal domain-like <b>Superfamily:</b> tRNA-intron endonuclease N-terminal domain-like <b>Family:</b> tRNA-intron endonuclease N-terminal domain-like
25	<a href="#">c2klIA_</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-33; <b>PDBTitle:</b> solution structure of human interleukin-33
26	<a href="#">d2tssa1</a>	Alignment	not modelled	5.4	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Superantigen toxins, N-terminal domain
27	<a href="#">d1xmba1</a>	Alignment	not modelled	5.4	25	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
28	<a href="#">c2wmpB_</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> pagp protein; <b>PDBTitle:</b> structure of the e. coli chaperone pagp in complex with the pilin2 domain of the paggii adhesin