


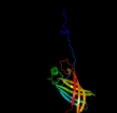
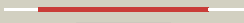












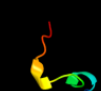




Phyre2

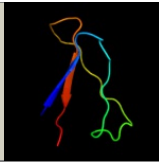
Email	I.a.kelley@imperial.ac.uk
Description	P0A8X2
Date	Thu Jan 5 11:08:55 GMT 2012
Unique Job ID	2ded0a1c582e2835

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y0ga_	 Alignment		100.0	100	Fold: Streptavidin-like Superfamily: Ycel-like Family: Ycel-like
2	c2fgsA_	 Alignment		100.0	37	PDB header: lipid binding protein Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of campylobacter jejuni ycei protein,2 structural genomics
3	d1wuba_	 Alignment		100.0	35	Fold: Streptavidin-like Superfamily: Ycel-like Family: Ycel-like
4	c3hpeB_	 Alignment		100.0	36	PDB header: transport protein Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: crystal structure of ycei (hp1286) from helicobacter pylori
5	c3q34A_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ycei-like family protein; PDBTitle: the crystal structure of ycei-like family protein from pseudomonas2 syringae
6	c2x34A_	 Alignment		100.0	21	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: cellulose-binding protein, x158; PDBTitle: structure of a polyisoprenoid binding domain from2 saccharophagus degradans implicated in plant cell wall3 breakdown
7	c3uc0B_	 Alignment		29.3	20	PDB header: viral protein/immune system Chain: B: PDB Molecule: envelope protein; PDBTitle: crystal structure of domain I of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
8	d2icha1	 Alignment		9.6	35	Fold: AttH-like Superfamily: AttH-like Family: AttH-like
9	c2cg9A_	 Alignment		8.7	17	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
10	d2o39a1	 Alignment		7.8	11	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain

11 [d2qlvb1](#)

Alignment



5.6

16

Fold:Immunoglobulin-like beta-sandwich
Superfamily:E set domains
Family:AMPK-beta glycogen binding domain-like