

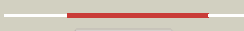
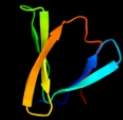









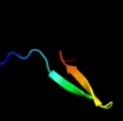

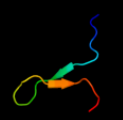

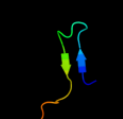
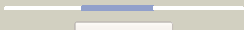
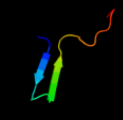

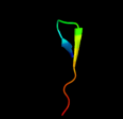

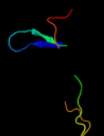

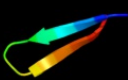
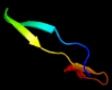

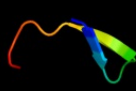
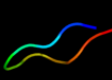



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P65292
Date	Thu Jan 5 12:10:10 GMT 2012
Unique Job ID	483b2d96e52ae7c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2rd1a1	 Alignment		99.9	48	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
2	d2k57a1	 Alignment		99.9	31	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
3	d2ra2a1	 Alignment		99.9	85	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
4	d2rb6a1	 Alignment		99.9	39	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
5	d3bdua1	 Alignment		99.9	63	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
6	d2jn0a1	 Alignment		99.8	57	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
7	d2npta1	 Alignment		39.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
8	d1wi0a_	 Alignment		31.0	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
9	c2h2wA_	 Alignment		29.8	33	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
10	d2ghra1	 Alignment		27.6	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
11	c3dsoA_	 Alignment		24.5	50	PDB header: metal binding protein Chain: A: PDB Molecule: putative uncharacterized protein copk; PDBTitle: crystal structure of cu(i) bound copper resistance protein copk

12	c2ktrA_	Alignment		16.7	12	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
13	c2kdkA_	Alignment		16.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: aryl hydrocarbon receptor nuclear translocator-like protein PDBTitle: structure of human circadian clock protein bmal2 c-terminal pas domain
14	d1br2a1	Alignment		14.1	31	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
15	d1gjwa1	Alignment		9.5	54	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
16	d2k5wa1	Alignment		8.6	28	Fold: OB-fold Superfamily: BC4932-like Family: BC4932-like
17	c2b38A_	Alignment		8.1	33	PDB header: plant protein Chain: A: PDB Molecule: kalata b8; PDBTitle: solution structure of kalata b8
18	d1wj6a_	Alignment		7.4	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
19	c3uc0B_	Alignment		6.4	45	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
20	d2bkfa1	Alignment		6.1	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
21	d1ip9a_	Alignment	not modelled	5.7	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
22	d1wmha_	Alignment	not modelled	5.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
23	d1epwa2	Alignment	not modelled	5.2	20	Fold: beta-Trefoil Superfamily: STI-like Family: Clostridium neurotoxins, C-terminal domain
24	d1f53a_	Alignment	not modelled	5.1	33	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Killer toxin-like protein SKLP
25	d1p97a_	Alignment	not modelled	5.0	14	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Hypoxia-inducible factor Hif2a, C-terminal domain