


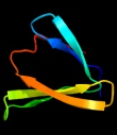
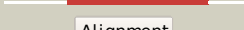
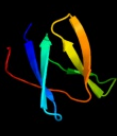
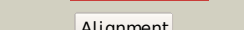






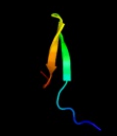
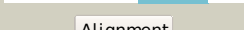
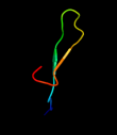
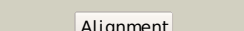
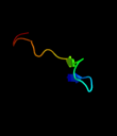
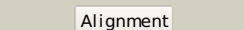
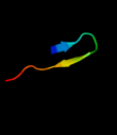

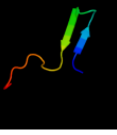
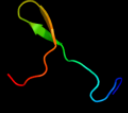
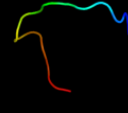
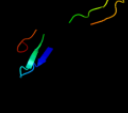




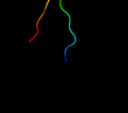



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P65294
Date	Thu Jan 5 12:10:11 GMT 2012
Unique Job ID	ca51ccaca33865ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2rb6a1	 Alignment		99.9	48	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
2	d2k57a1	 Alignment		99.9	27	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
3	d3bdua1	 Alignment		99.9	51	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
4	d2jn0a1	 Alignment		99.9	100	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
5	d2rd1a1	 Alignment		99.9	50	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
6	d2ra2a1	 Alignment		99.9	54	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
7	d2npta1	 Alignment		45.3	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
8	d1wi0a_	 Alignment		35.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
9	c2h2wA_	 Alignment		24.6	48	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	c3dsoA_	 Alignment		23.8	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
11	d2ghra1	 Alignment		22.6	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like

12	c2ktrA_	Alignment		20.1	15	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
13	d1br2a1	Alignment		16.6	19	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
14	c2kdkA_	Alignment		15.6	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
15	d1gvia2	Alignment		15.2	39	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
16	d1h6la_	Alignment		11.5	24	Fold: 6-bladed beta-propeller Superfamily: Thermostable phytase (3-phytase) Family: Thermostable phytase (3-phytase)
17	d2k5wa1	Alignment		9.4	34	Fold: OB-fold Superfamily: BC4932-like Family: BC4932-like
18	c2pxgA_	Alignment		9.3	20	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein; PDBTitle: nmr solution structure of omla
19	d1w0na_	Alignment		9.1	38	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 36 carbohydrate binding module, CBM36
20	c2b38A_	Alignment		9.0	47	PDB header: plant protein Chain: A: PDB Molecule: kalata b8; PDBTitle: solution structure of kalata b8
21	d1wmha_	Alignment	not modelled	8.1	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
22	d1wzaa1	Alignment	not modelled	7.0	23	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
23	d2bkfa1	Alignment	not modelled	6.9	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
24	d1u5sa1	Alignment	not modelled	6.6	11	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
25	d1wj6a_	Alignment	not modelled	6.6	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
26	d1sg5a1	Alignment	not modelled	5.9	11	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: Rof-like
27	c1tr8A_	Alignment	not modelled	5.5	21	PDB header: chaperone Chain: A: PDB Molecule: conserved protein (mth177); PDBTitle: crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
28	c3uc0B_	Alignment	not modelled	5.3	36	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