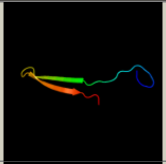
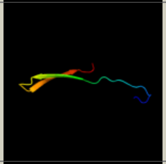
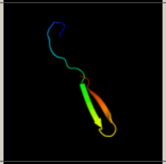
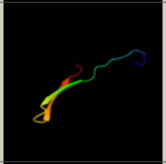
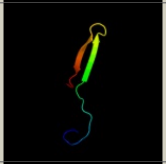
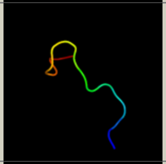
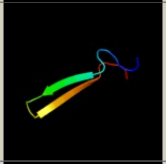
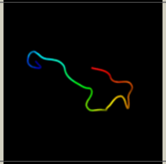
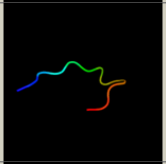
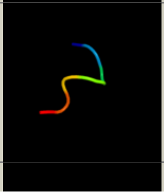
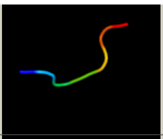
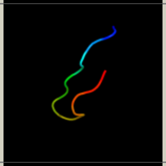
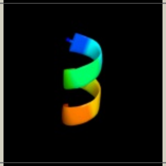
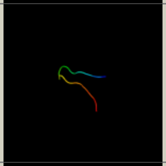
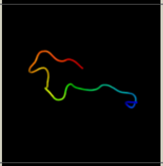
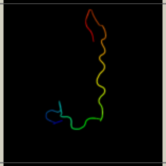
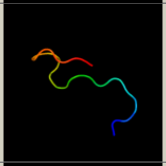
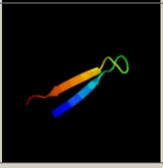
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	A0ZWU1
Date	Sun Jul 8 11:45:01 BST 2012
Unique Job ID	efd1bfbb2979b31f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e66B_	Alignment		49.4	26	**PDB header:**splicing **Chain:** B: **PDB Molecule:**prp8; **PDBTitle:** crystal structure of the beta-finger domain of yeast prp8
2	d3e9oa1	Alignment		47.6	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Prp8 beta-finger domain-like
3	d3e9la1	Alignment		40.8	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Prp8 beta-finger domain-like
4	d3enba1	Alignment		39.9	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Prp8 beta-finger domain-like
5	c3sbgA_	Alignment		33.7	26	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** crystal structure of a prp8 c-terminal fragment
6	d1hx0a1	Alignment		18.9	35	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
7	d1ujxa_	Alignment		18.7	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
8	d2brfa1	Alignment		17.5	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
9	d3bmva3	Alignment		13.2	32	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
10	c3natB_	Alignment		10.8	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved protein of unknown function ef_19772 from enterococcus faecalis
11	c2zkr3_	Alignment		10.8	43	**PDB header:**ribosomal protein/rna **Chain:** 3: **PDB Molecule:**60s ribosomal protein l39e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map

12	c4a1bB_	Alignment		10.6	43	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rpl39; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
13	d1o12a1	Alignment		10.4	36	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
14	c3btpB_	Alignment		10.2	50	**PDB header:**dna binding protein, chaperone **Chain:** B: **PDB Molecule:**protein vire1; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
15	c3q91D_	Alignment		9.3	31	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
16	d1cxla3	Alignment		9.0	37	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
17	d1bwvs_	Alignment		8.6	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
18	c3nfgG_	Alignment		8.1	13	**PDB header:**transcription **Chain:** G: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49; **PDBTitle:** crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5
19	d1pama3	Alignment		7.3	37	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
20	d1px5a2	Alignment		6.9	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**2'-5'-oligoadenylate synthetase 1, OAS1, N-terminal domain
21	d1in0a1	Alignment	not modelled	6.8	40	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
22	c3h6sE_	Alignment	not modelled	6.0	45	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**clitocypin analog; **PDBTitle:** strucure of clitocypin - cathepsin v complex
23	d1ytla1	Alignment	not modelled	5.9	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**ACDE2-like
24	c2qnkA_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
25	d1cgta3	Alignment	not modelled	5.7	37	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
26	d1z8ma1	Alignment	not modelled	5.7	18	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
27	c3a5pD_	Alignment	not modelled	5.5	14	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**haemagglutinin i; **PDBTitle:** crystal structure of hemagglutinin
28	d1qhoa3	Alignment	not modelled	5.4	26	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
29	c2ov2O_	Alignment	not modelled	5.4	33	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)

30	c2w7vB_	Alignment	not modelled	5.2	0	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus