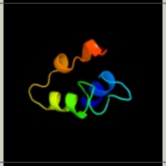
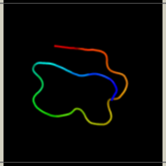
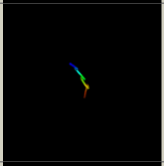
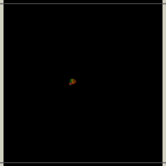
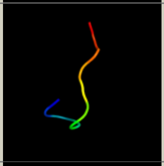
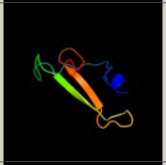
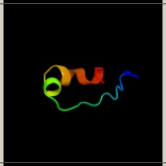
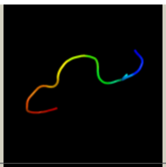
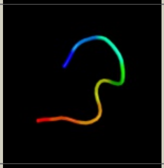
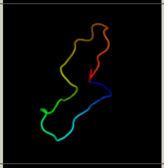
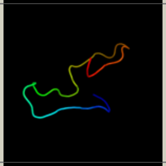
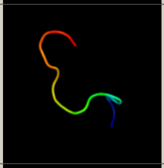
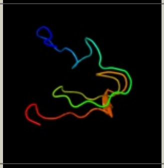
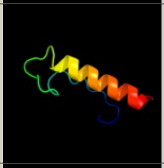
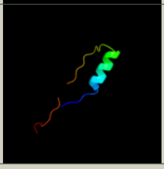
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P18471
Date	Thu Jan 5 11:36:58 GMT 2012
Unique Job ID	f855596d3a7b5ce3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qr3B_	Alignment		20.9	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase eg-ii; **PDBTitle:** crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
2	c3ifuA_	Alignment		19.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**non-structural protein; **PDBTitle:** the crystal structure of porcine reproductive and2 respiratory syndrome virus (prrsv) leader protease nsp1
3	c2pnmA_	Alignment		18.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of vp4 protease from infectious pancreatic necrosis2 virus (ipnv) in space group p6122
4	d2go8a1	Alignment		12.4	33	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
5	d1yvua1	Alignment		10.2	63	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
6	c3bmzA_	Alignment		9.0	39	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** violacein biosynthetic enzyme vioe
7	d1lg4a_	Alignment		8.7	21	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
8	d1rutx1	Alignment		8.7	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
9	c1w62B_	Alignment		8.2	17	**PDB header:**racemase **Chain:** B: **PDB Molecule:**b-cell mitogen; **PDBTitle:** proline racemase in complex with one molecule of pyrrole-2-2 carboxylic acid (hemi form)
10	d1i17a_	Alignment		7.4	21	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
11	d1skza1	Alignment		7.4	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like

12	d1v47a1	Alignment		7.4	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
13	d1j2oa1	Alignment		7.3	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
14	c2p0vA_	Alignment		7.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
15	d2p0va1	Alignment		7.1	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
16	d1x6va1	Alignment		7.0	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
17	d1l5ja3	Alignment		6.9	21	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
18	c2jb1B_	Alignment		6.9	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
19	d1g8fa1	Alignment		6.7	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
20	d1jl0a_	Alignment		6.7	33	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**S-adenosylmethionine decarboxylase
21	c2zkrg_	Alignment	not modelled	6.6	36	**PDB header:**ribosomal protein/rna **Chain:** G: **PDB Molecule:**rna expansion segment es9; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
22	d1zata2	Alignment	not modelled	6.2	0	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
23	d1m8pa1	Alignment	not modelled	6.1	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
24	c2hnhA_	Alignment	not modelled	6.1	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
25	c2ezvA_	Alignment	not modelled	6.0	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**type ii restriction enzyme sfii; **PDBTitle:** crystal structure of tetrameric restriction endonuclease2 sfii bound to cognate dna.
26	d1u7ka_	Alignment	not modelled	6.0	50	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
27	d1yy9a4	Alignment	not modelled	5.8	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
28	c2k2iB_	Alignment	not modelled	5.6	36	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**sfi1 peptide; **PDBTitle:** nmr solution structure of the c-terminal domain (t94-y172)2 of the human centrin 2 in complex with a repeat sequence of3 human sfi1 (r641-t660)

29	d1uzka3	Alignment	not modelled	5.3	42	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
30	d1jhda1	Alignment	not modelled	5.2	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
31	d1tm0a_	Alignment	not modelled	5.2	15	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Proline racemase
32	c3k4iC_	Alignment	not modelled	5.0	31	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000