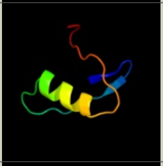
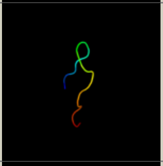
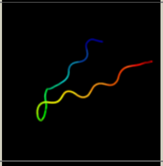
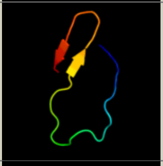
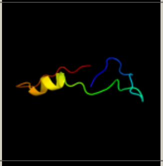
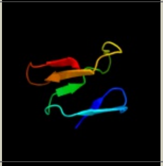
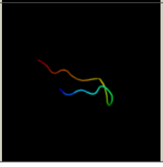
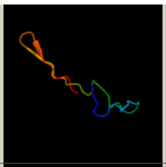
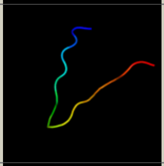
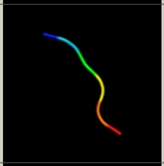
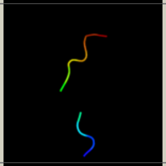
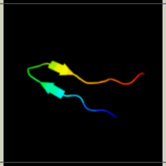
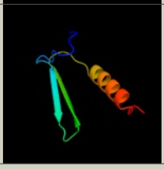
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEE1
Date	Thu Jan 5 11:23:06 GMT 2012
Unique Job ID	eaab27d17d8a7902

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tu1a_	Alignment		99.0	16	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**PA0094-like
2	c2xb3A_	Alignment		97.7	13	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**psbp protein; **PDBTitle:** the structure of cyanobacterial psbp
3	d1v2ba_	Alignment		89.6	10	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**PsbP-like
4	c2vu4A_	Alignment		89.3	10	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**oxygen-evolving enhancer protein 2; **PDBTitle:** structure of psbp protein from spinacia oleracea at 1.98 a2 resolution
5	c2jx5A_	Alignment		45.6	26	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**glub(s27a); **PDBTitle:** solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
6	d1qhoa3	Alignment		31.1	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
7	d1ji1a2	Alignment		30.2	17	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
8	c3orjA_	Alignment		24.0	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar-binding protein; **PDBTitle:** crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
9	d2c7fa1	Alignment		22.0	28	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
10	d1jhsa_	Alignment		21.9	23	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**Ran-binding protein mog1p
11	d1cgta3	Alignment		20.9	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

12	d1qw9a1	Alignment		16.9	29	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
13	d1wzla2	Alignment		16.5	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
14	c3lydA_	Alignment		13.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative uncharacterized protein from jonesia2 denitrificans
15	c3iz5W_	Alignment		12.3	30	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
16	d1xrsb2	Alignment		12.3	83	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
17	d3bmva3	Alignment		12.1	45	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
18	c1bagA_	Alignment		10.7	28	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
19	c2j98A_	Alignment		10.6	13	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** human coronavirus 229e non structural protein 9 cys69ala2 mutant (nsp9)
20	c4a1dM_	Alignment		9.7	27	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein l22; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
21	d1lmia_	Alignment	not modelled	8.2	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Antigen MPT63/MPB63 (immunoprotective extracellular protein) **Family:**Antigen MPT63/MPB63 (immunoprotective extracellular protein)
22	d1ni2a3	Alignment	not modelled	8.2	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
23	c3es1A_	Alignment	not modelled	7.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
24	c3mx7A_	Alignment	not modelled	6.8	18	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
25	d1szwa_	Alignment	not modelled	6.8	44	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
26	c1bplB_	Alignment	not modelled	6.6	18	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
27	c1z2zB_	Alignment	not modelled	6.5	44	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2 synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
						Fold:ADP-ribosylation

28	d1s21a_	Alignment	not modelled	6.4	42	**Superfamily:**ADP-ribosylation **Family:**AvrPphF ORF2, a type III effector
29	c1s21A_	Alignment	not modelled	6.4	42	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**orf2; **PDBTitle:** crystal structure of avrpphf orf2, a type iii effector from2 p. syringae
30	c2gs8A_	Alignment	not modelled	6.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate pyrophosphate decarboxylase; **PDBTitle:** structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
31	c1sb7A_	Alignment	not modelled	6.2	44	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
32	d2bsya1	Alignment	not modelled	5.6	17	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
33	d1zupa1	Alignment	not modelled	5.6	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**TM1739-like
34	c2zt9E_	Alignment	not modelled	5.5	42	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
35	d1ua7a1	Alignment	not modelled	5.4	26	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
36	d1x38a2	Alignment	not modelled	5.3	15	**Fold:**Flavodoxin-like **Superfamily:**Beta-D-glucan exohydrolase, C-terminal domain **Family:**Beta-D-glucan exohydrolase, C-terminal domain
37	d1cxla3	Alignment	not modelled	5.3	45	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain