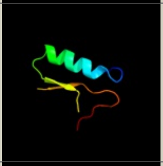
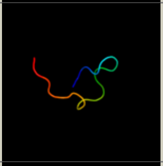
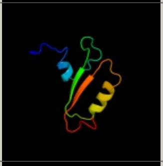
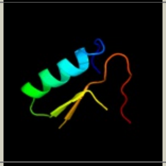
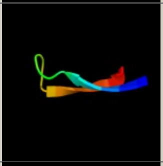
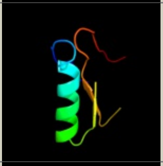
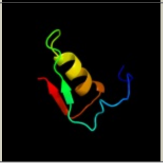
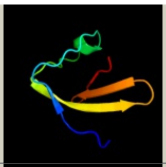
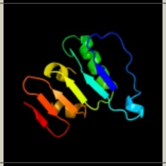
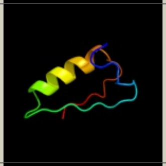
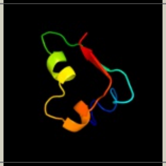
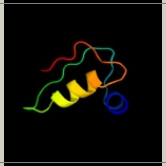
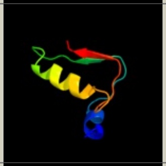
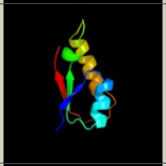
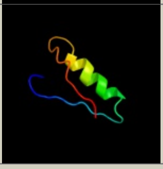
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P0AA97
Date	Wed Jan 25 15:20:21 GMT 2012
Unique Job ID	c15ce2dbe04537d3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g3wa1	Alignment		100.0	38	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**YaeQ-like
2	c3c0uA_	Alignment		100.0	98	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yaeq; **PDBTitle:** crystal structure of e.coli yaeq protein
3	d2ot9a1	Alignment		100.0	31	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**YaeQ-like
4	c3sftA_	Alignment		33.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
5	d2sh1a_	Alignment		32.1	25	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
6	d2csua2	Alignment		27.8	14	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
7	d1chda_	Alignment		24.0	7	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
8	c3be3A_	Alignment		23.5	47	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
9	c3pu5A_	Alignment		21.0	4	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular solute-binding protein; **PDBTitle:** the crystal structure of a putative extracellular solute-binding2 protein from bordetella parapertussis
10	c1a2oB_	Alignment		19.2	4	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
11	c1uarA_	Alignment		16.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8

12	d1qvpa_	Alignment		13.8	16	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
13	d1ekqa_	Alignment		13.6	12	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
14	c3hzuA_	Alignment		11.6	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
15	c1e0cA_	Alignment		11.3	12	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
16	d1urha2	Alignment		11.0	5	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
17	c3aaxB_	Alignment		10.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
18	c1urhA_	Alignment		10.7	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
19	c2p10D_	Alignment		10.0	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
20	c3olhA_	Alignment		9.9	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
21	d1mjsa_	Alignment	not modelled	9.8	37	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
22	c2kvoA_	Alignment	not modelled	8.7	33	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
23	d1khua_	Alignment	not modelled	8.4	42	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
24	d2hy5b1	Alignment	not modelled	8.1	21	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
25	d1wija_	Alignment	not modelled	6.9	36	**Fold:**LEM/SAP HeH motif **Superfamily:**DNA-binding domain of EIN3-like **Family:**DNA-binding domain of EIN3-like
26	c3pg6D_	Alignment	not modelled	6.7	27	**PDB header:**ligase **Chain:** D: **PDB Molecule:**e3 ubiquitin-protein ligase dtx3l; **PDBTitle:** the carboxyl terminal domain of human deltex 3-like
27	c3eytA_	Alignment	not modelled	6.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
28	d1oi0a_	Alignment	not modelled	6.4	14	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain

29	d1uara2	Alignment	not modelled	6.3	9	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
30	c2oq2B_	Alignment	not modelled	6.2	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
31	d2ok5a4	Alignment	not modelled	5.7	21	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
32	c3ddrC_	Alignment	not modelled	5.6	23	**PDB header:**membrane protein/heme binding protein **Chain:** C: **PDB Molecule:**hemophore hasa; **PDBTitle:** structure of the serratia marcescens hemophore receptor hasr-ile671gly2 mutant in complex with its hemophore hasa and heme
33	c2z5bB_	Alignment	not modelled	5.6	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**uncharacterized protein ylr021w; **PDBTitle:** crystal structure of a novel chaperone complex for yeast2 20s proteasome assembly
34	d1hpla2	Alignment	not modelled	5.5	5	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
35	c3gztF_	Alignment	not modelled	5.5	18	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
36	d2cu2a2	Alignment	not modelled	5.3	25	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
37	c1boiA_	Alignment	not modelled	5.3	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
38	d1gpla2	Alignment	not modelled	5.1	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
39	d1lpbb2	Alignment	not modelled	5.0	5	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain