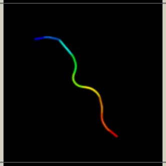
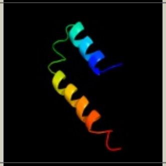
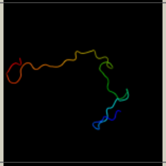
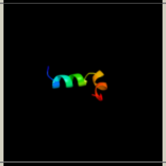
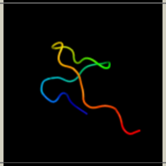
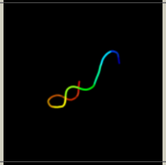
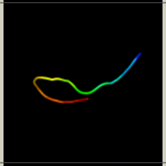
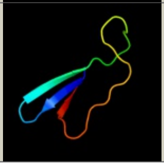
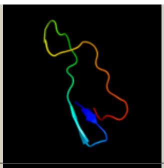
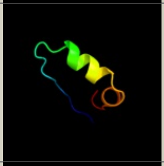
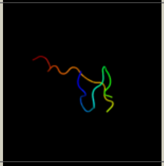
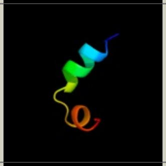
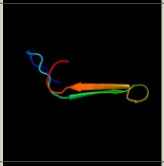
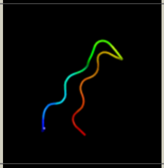
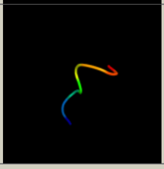
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q47319
Date	Thu Jan 5 12:36:46 GMT 2012
Unique Job ID	50aacaf3b68994f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rk8C_	Alignment		53.4	67	**PDB header:**translation **Chain:** C: **PDB Molecule:**within the bgcn gene intron protein; **PDBTitle:** structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
2	d1rk8c_	Alignment		53.4	67	**Fold:**WW domain-like **Superfamily:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain **Family:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
3	d1xrxa1	Alignment		40.6	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
4	c1xrxD_	Alignment		40.6	23	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
5	c3mopC_	Alignment		32.1	20	**PDB header:**signaling protein, immune system **Chain:** C: **PDB Molecule:**myeloid differentiation primary response protein myd88; **PDBTitle:** the ternary death domain complex of myd88, irak4, and irak2
6	c3c6fD_	Alignment		30.7	7	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yetf protein; **PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis
7	d2dofa1	Alignment		22.5	22	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
8	c3bvoA_	Alignment		22.3	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
9	d1ffya1	Alignment		22.2	27	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
10	d2dara2	Alignment		20.0	31	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
11	d1yuda1	Alignment		18.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YML079-like

12	c3lzzB_	Alignment		15.5	6	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
13	d1esza_	Alignment		15.2	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Periplasmic ferric siderophore binding protein FhuD
14	d2apob1	Alignment		14.8	28	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
15	c2kiqA_	Alignment		14.8	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of the ff domain 2 of human transcription2 elongation factor ca150
16	c2knqA_	Alignment		13.4	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**general secretion pathway protein h; **PDBTitle:** solution structure of e.coli gsph
17	d1ctla1	Alignment		13.3	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
18	d2vkva2	Alignment		13.3	12	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
19	d1imla1	Alignment		13.1	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
20	d1ibia1	Alignment		12.1	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
21	c2elpA_	Alignment	not modelled	11.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
22	c2a7yA_	Alignment	not modelled	11.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
23	d2a7ya1	Alignment	not modelled	11.6	25	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
24	d2etva1	Alignment	not modelled	11.2	6	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
25	d2ey4e1	Alignment	not modelled	10.4	31	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
26	c2yetB_	Alignment	not modelled	10.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gh61 isozyme a; **PDBTitle:** thermoascus gh61 isozyme a
27	c2nrrA_	Alignment	not modelled	10.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal rnaseh endonuclase2 domain of uvrc
28	c2kfdA_	Alignment	not modelled	10.0	32	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**pre-mrna-processing protein prp40; **PDBTitle:** prp40 ff4 domain
						Fold: Anticodon-binding domain-like

29	d1v95a_	Alignment	not modelled	9.7	8	**Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
30	d2afaa1	Alignment	not modelled	9.5	7	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
31	d1zbdb_	Alignment	not modelled	9.1	19	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
32	c2iy3A_	Alignment	not modelled	9.0	11	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
33	c2rr7A_	Alignment	not modelled	8.9	36	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**dynein heavy chain 9; **PDBTitle:** microtubule binding domain of dynein-c
34	d2ewoa1	Alignment	not modelled	8.8	12	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
35	c3n43B_	Alignment	not modelled	8.6	58	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.
36	c2hw4A_	Alignment	not modelled	8.5	21	**PDB header:**structural genomics, hydrolase **Chain:** A: **PDB Molecule:**14 kda phosphohistidine phosphatase; **PDBTitle:** crystal structure of human phosphohistidine phosphatase
37	d2cu8a1	Alignment	not modelled	8.4	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	c2xfbI_	Alignment	not modelled	8.4	58	**PDB header:**virus **Chain:** I: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
39	c3mhsE_	Alignment	not modelled	8.4	40	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
40	d1lf6a2	Alignment	not modelled	8.3	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
41	c2k85A_	Alignment	not modelled	8.2	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** p190-a rhogap ff1 domain
42	c2iv0A_	Alignment	not modelled	8.2	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
43	c2hfvA_	Alignment	not modelled	8.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
44	c1qu2A_	Alignment	not modelled	7.8	27	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
45	d1xo1a2	Alignment	not modelled	7.6	27	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
46	d1ulva4	Alignment	not modelled	7.6	25	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
47	c3errB_	Alignment	not modelled	7.4	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
48	d1kl7a_	Alignment	not modelled	7.4	12	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
49	c3muwU_	Alignment	not modelled	7.1	42	**PDB header:**virus **Chain:** U: **PDB Molecule:**structural polyprotein; **PDBTitle:** pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
50	d2doea1	Alignment	not modelled	6.9	10	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
51	c2ofqA_	Alignment	not modelled	6.9	14	**PDB header:**protein transport/protein transport **Chain:** A: **PDB Molecule:**trao; **PDBTitle:** nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
52	d1ryqa_	Alignment	not modelled	6.9	15	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
53	c3k7bA_	Alignment	not modelled	6.7	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a33; **PDBTitle:** the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
						PDB header:protein transport, rna binding protein **Chain:** A: **PDB Molecule:**nucleoporin nup145;

54	c3kepA_	Alignment	not modelled	6.7	15	**PDBTitle:** crystal structure of the autoproteolytic domain from the2 nuclear pore complex component nup145 from saccharomyces3 cerevisiae
55	d1pn0a2	Alignment	not modelled	6.6	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
56	c3chxG_	Alignment	not modelled	6.5	67	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
57	c3n40P_	Alignment	not modelled	6.5	58	**PDB header:**viral protein **Chain:** P: **PDB Molecule:**p62 envelope glycoprotein; **PDBTitle:** crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.
58	c2jyvA_	Alignment	not modelled	6.2	57	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin-2; **PDBTitle:** human granulin f
59	d1omza_	Alignment	not modelled	6.1	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
60	d2hfva1	Alignment	not modelled	6.0	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
61	d1bpoa1	Alignment	not modelled	6.0	20	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin heavy-chain linker domain
62	c1yewC_	Alignment	not modelled	5.9	57	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
63	c3g9yA_	Alignment	not modelled	5.9	29	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**zinc finger ran-binding domain-containing protein 2; **PDBTitle:** crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt ssrna sequence agguaa
64	d2gnra1	Alignment	not modelled	5.8	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
65	c2xzn5_	Alignment	not modelled	5.7	36	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
66	d2cqna1	Alignment	not modelled	5.7	29	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
67	c2nvuB_	Alignment	not modelled	5.6	29	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
68	d1j3kc_	Alignment	not modelled	5.5	7	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
69	d3blza1	Alignment	not modelled	5.3	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Sbal0622-like
70	c3eabD_	Alignment	not modelled	5.3	23	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**spastin; **PDBTitle:** crystal structure of spastin mit in complex with escrt iii
71	c1ko6A_	Alignment	not modelled	5.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of c-terminal autoproteolytic domain of2 nucleoporin nup98
72	d1aa7a_	Alignment	not modelled	5.1	26	**Fold:**Influenza virus matrix protein M1 **Superfamily:**Influenza virus matrix protein M1 **Family:**Influenza virus matrix protein M1
73	d1vkpa_	Alignment	not modelled	5.1	17	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase