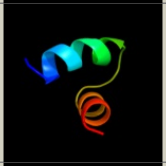
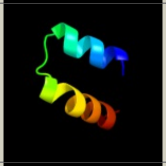
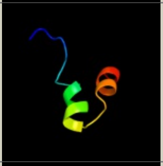
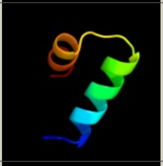
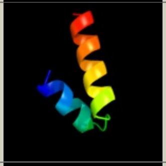
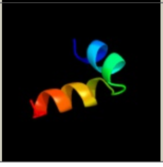
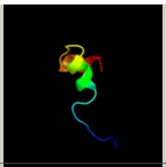
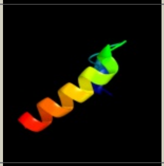
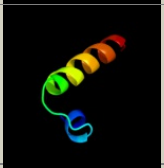
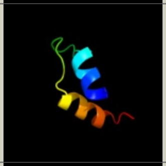
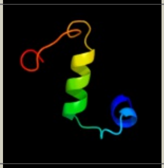
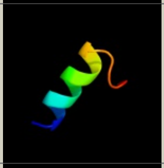
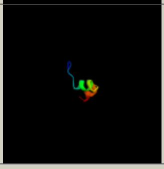
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A828
Date	Thu Jan 5 11:06:43 GMT 2012
Unique Job ID	521477ee6ce1da2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1stzB_	Alignment		66.9	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
2	d1oqya1	Alignment		54.4	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
3	c3d5lA_	Alignment		43.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of regulatory protein recx
4	d1ifya_	Alignment		40.1	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
5	c2dakA_	Alignment		39.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
6	d3e46a1	Alignment		38.7	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
7	c3dfgA_	Alignment		36.8	24	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
8	d2cosa1	Alignment		36.7	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
9	c2fu4B_	Alignment		32.1	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
10	c2cosA_	Alignment		31.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
11	c2l02B_	Alignment		28.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375

12	c2crnA_	Alignment		26.4	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
13	c1dpuA_	Alignment		26.1	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
14	d1dpua_	Alignment		26.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
15	d1t95a1	Alignment		25.4	12	**Fold:**RuvA C-terminal domain-like **Superfamily:**Hypothetical protein AF0491, middle domain **Family:**Hypothetical protein AF0491, middle domain
16	c2w57A_	Alignment		22.4	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
17	d2g3qa1	Alignment		20.6	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
18	d1whqa_	Alignment		19.2	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
19	d1whca_	Alignment		19.1	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
20	c2cpwA_	Alignment		18.6	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant; **PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna
21	c3l9kZ_	Alignment	not modelled	18.0	22	**PDB header:**motor protein **Chain:** Z: **PDB Molecule:**dynein intermediate chain, cytosolic; **PDBTitle:** insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
22	c3kevA_	Alignment	not modelled	17.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**galieria sulfuraria dcun1 domain-containing protein; **PDBTitle:** x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria
23	d1wiva_	Alignment	not modelled	17.0	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
24	c1fuiB_	Alignment	not modelled	16.5	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
25	d1vega_	Alignment	not modelled	16.3	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
26	c3qqmD_	Alignment	not modelled	16.2	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mlr3007 protein; **PDBTitle:** crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
27	c3a1yF_	Alignment	not modelled	15.5	21	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
28	c3e3vA_	Alignment	not modelled	15.0	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius

29	d1r4wa_	Alignment	not modelled	13.8	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
30	d1veka_	Alignment	not modelled	13.3	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
31	c3eyyA_	Alignment	not modelled	13.3	21	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
32	c2wbmA_	Alignment	not modelled	12.8	12	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**ribosome maturation protein sdo1 homolog; **PDBTitle:** crystal structure of mthsbds, the homologue of the2 shwachman-bodian-diamond syndrome protein in the3 euriarchaeon methanothermobacter thermautotrophicus
33	c1qzeA_	Alignment	not modelled	12.4	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**uv excision repair protein rad23 homolog a; **PDBTitle:** hhr23a protein structure based on residual dipolar coupling2 data
34	d2cpwa1	Alignment	not modelled	12.3	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
35	c2dagA_	Alignment	not modelled	12.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
36	c2do6A_	Alignment	not modelled	11.8	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
37	c3itcA_	Alignment	not modelled	11.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
38	d2fi0a1	Alignment	not modelled	11.7	31	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
39	d1dhsa_	Alignment	not modelled	11.3	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Deoxyhypusine synthase, DHS
40	c3fpnB_	Alignment	not modelled	11.2	23	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
41	c2fe3B_	Alignment	not modelled	11.0	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
42	c2jnhA_	Alignment	not modelled	10.4	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
43	d1ntha_	Alignment	not modelled	10.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Monomethylamine methyltransferase MtmB **Family:**Monomethylamine methyltransferase MtmB
44	c2k2pA_	Alignment	not modelled	9.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
45	c2is9A_	Alignment	not modelled	9.8	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
46	c2d9sA_	Alignment	not modelled	9.7	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
47	d1oqya2	Alignment	not modelled	9.6	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
48	c2v79B_	Alignment	not modelled	9.6	11	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
49	c3dp7B_	Alignment	not modelled	8.6	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
50	c2daiA_	Alignment	not modelled	8.6	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
51	c3ocjA_	Alignment	not modelled	8.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** the crystal structure of a possilbe exported protein from bordetella2 parapertussis
52	d1jjcb1	Alignment	not modelled	8.0	23	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
53	d1daaa_	Alignment	not modelled	7.9	19	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent

						enzymes
54	c3o10D_	Alignment	not modelled	7.7	18	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**sacsin; **PDBTitle:** crystal structure of the hepn domain from human sacsin
55	c3nznA_	Alignment	not modelled	7.5	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
56	d1okra_	Alignment	not modelled	7.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
57	c2l01A_	Alignment	not modelled	7.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
58	c2kdoA_	Alignment	not modelled	7.1	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ribosome maturation protein sbds; **PDBTitle:** structure of the human shwachman-bodian-diamond syndrome protein, sbds
59	c3gp4B_	Alignment	not modelled	7.0	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
60	d1t5la1	Alignment	not modelled	6.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
61	d1sb6a_	Alignment	not modelled	6.8	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
62	d1jb0f_	Alignment	not modelled	6.6	22	**Fold:**Single transmembrane helix **Superfamily:**Subunit III of photosystem I reaction centre, PsaF **Family:**Subunit III of photosystem I reaction centre, PsaF
63	d2eyqa4	Alignment	not modelled	6.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
64	c3hjhA_	Alignment	not modelled	6.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair-coupling factor; **PDBTitle:** a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
65	c2e75H_	Alignment	not modelled	6.2	57	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
66	c2e74H_	Alignment	not modelled	6.2	57	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
67	c2e76H_	Alignment	not modelled	6.2	57	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
68	c3lulA_	Alignment	not modelled	6.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-amino-4-deoxychorismate lyase; **PDBTitle:** crystal structure of putative 4-amino-4-deoxychorismate lyase.2 (yp_094631.1) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 1.78 a resolution
69	d1iyea_	Alignment	not modelled	5.9	19	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
70	d1efub3	Alignment	not modelled	5.7	29	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
71	c3c1dA_	Alignment	not modelled	5.6	19	**PDB header:**recombination, dna binding protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** x-ray crystal structure of recx
72	c2zc2A_	Alignment	not modelled	5.6	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnad-like replication protein; **PDBTitle:** crystal structure of dnad-like replication protein from2 streptococcus mutans ua159, gi 24377835, residues 127-199
73	d1w6ka1	Alignment	not modelled	5.5	22	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
74	c2abjG_	Alignment	not modelled	5.4	20	**PDB header:**transferase **Chain:** G: **PDB Molecule:**branched-chain-amino-acid aminotransferase, cytosolic; **PDBTitle:** crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
75	c1t95A_	Alignment	not modelled	5.4	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af0491; **PDBTitle:** crystal structure of the shwachman-bodian-diamond syndrome2 protein orthologue from archaeoglobus fulgidus
76	d2b2na1	Alignment	not modelled	5.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
77	d1m2ia_	Alignment	not modelled	5.3	33	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
78	c3itfA_	Alignment	not modelled	5.3	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp

adaptor2 protein