

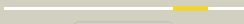










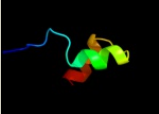

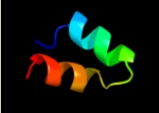







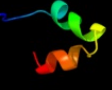
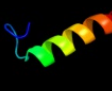









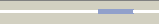


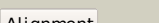
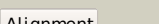
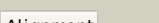

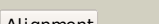
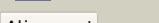
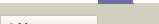

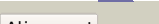
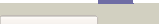



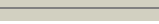
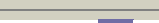


Phyre2

Email	l.a.kelley@imperial.ac.uk
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Date	Thu Jan 5 12:30:15 GMT 2012
Unique Job ID	bbefcf8d874204b8

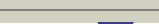
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vh4a_	 Alignment		100.0	20	Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD Family: Stabilizer of iron transporter SufD
2	c2dagA_	 Alignment		73.2	10	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)
3	d1whca_	 Alignment		64.7	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
4	c2daiA_	 Alignment		63.0	23	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)
5	d1dd9a_	 Alignment		57.1	22	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
6	c1dd9A_	 Alignment		57.1	22	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: structure of the dnaG catalytic core
7	c2crnA_	 Alignment		54.3	17	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
8	d1veka_	 Alignment		50.0	15	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
9	c2o2kA_	 Alignment		45.8	26	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
10	d1p32a_	 Alignment		45.2	18	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
11	d1nuia1	 Alignment		45.1	33	Fold: DNA primase core Superfamily: DNA primase core Family: Primase fragment of primase-helicase protein

12	dlwiva_	Alignment		43.2	22	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
13	dlmska_	Alignment		43.1	22	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Methionine synthase SAM-binding domain
14	c3ic3C_	Alignment		40.4	25	PDB header: oxidoreductase Chain: C: PDB Molecule: putative pyruvate dehydrogenase; PDBTitle: structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodopseudomonas palustris cga009
15	dlyqfa1	Alignment		39.3	18	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
16	dlkx5d_	Alignment		36.9	29	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
17	c3qv0A_	Alignment		35.8	29	PDB header: protein binding Chain: A: PDB Molecule: mitochondrial acidic protein mam33; PDBTitle: crystal structure of saccharomyces cerevisiae mam33
18	dleqzb_	Alignment		35.5	26	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
19	d2cpwa1	Alignment		34.4	15	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
20	d2crna1	Alignment		34.3	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
21	c1q57G_	Alignment	not modelled	32.8	33	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
22	c3jv1A_	Alignment	not modelled	32.8	15	PDB header: hydrolase Chain: A: PDB Molecule: p22 protein; PDBTitle: crystal structure of the trypanosoma brucei p22 protein
23	d1s32d_	Alignment	not modelled	31.5	29	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
24	d1n9pa_	Alignment	not modelled	31.0	5	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
25	c2cpwA_	Alignment	not modelled	30.4	17	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
26	d1tzyb_	Alignment	not modelled	29.9	26	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
27	c2dakA_	Alignment	not modelled	29.6	20	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)
28	c2e4fA_	Alignment	not modelled	29.2	7	PDB header: transport protein Chain: A: PDB Molecule: g protein-activated inward rectifier potassium channel 2; PDBTitle: crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2

29	c3sf5D_	 Alignment	not modelled	24.8	5	PDB header: chaperone Chain: D: PDB Molecule: urease accessory protein ureh; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
30	c2wknE_	 Alignment	not modelled	24.6	25	PDB header: hydrolase Chain: E: PDB Molecule: formamidase; PDBTitle: gamma lactamase from delftia acidovorans
31	d2csba4	 Alignment	not modelled	22.9	42	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
32	c1xdoB_	 Alignment	not modelled	22.7	10	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
33	d1vega_	 Alignment	not modelled	22.7	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
34	d1id3d_	 Alignment	not modelled	21.0	29	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
35	d2elza2	 Alignment	not modelled	20.1	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetkinase-like
36	d1g99a2	 Alignment	not modelled	19.8	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetkinase-like
37	c2au3A_	 Alignment	not modelled	18.6	25	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
38	c2o8rA_	 Alignment	not modelled	17.4	18	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
39	d1ifya_	 Alignment	not modelled	16.5	19	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
40	c2iw0A_	 Alignment	not modelled	16.5	29	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
41	c3jurA_	 Alignment	not modelled	14.3	21	PDB header: hydrolase Chain: A: PDB Molecule: exo-poly-alpha-d-galacturonosidase; PDBTitle: the crystal structure of a hyperthermoactive exopolysaccharuronase from2 thermotoga maritima
42	c1nuiA_	 Alignment	not modelled	13.5	33	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
43	c1tuuA_	 Alignment	not modelled	13.5	7	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
44	c2vyoA_	 Alignment	not modelled	13.5	14	PDB header: hydrolase Chain: A: PDB Molecule: chito oligosaccharide deacetylase; PDBTitle: chitin deacetylase family member from encephalitozoon2 cuniculi
45	d2g3qa1	 Alignment	not modelled	13.0	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
46	c1x3nA_	 Alignment	not modelled	13.0	12	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
47	c3khyA_	 Alignment	not modelled	13.0	14	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
48	c1sazA_	 Alignment	not modelled	12.8	19	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
49	c2zc1A_	 Alignment	not modelled	12.7	39	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
50	d1rfza_	 Alignment	not modelled	12.4	10	Fold: YutG-like Superfamily: YutG-like Family: YutG-like
51	d1oqya1	 Alignment	not modelled	12.1	15	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
52	c3iz6M_	 Alignment	not modelled	11.9	21	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
53	d1pgya_	 Alignment	not modelled	11.9	19	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
54	d1v3aa_	 Alignment	not modelled	11.6	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
55	c2gm2A_	 Alignment	not modelled	11.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein;

55	c2gm2A_	Alignment	not modelled	11.4	17	PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
56	d1hiob_	Alignment	not modelled	11.3	21	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
57	c2uveA_	Alignment	not modelled	11.1	17	PDB header: hydrolase Chain: A: PDB Molecule: exopolygalacturonase; PDBTitle: structure of yersinia enterocolitica family 282 exopolygalacturonase
58	c2gu3A_	Alignment	not modelled	11.1	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ypmb protein; PDBTitle: ypmb protein from bacillus subtilis
59	d1saza2	Alignment	not modelled	11.1	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinese-like
60	d1ivza_	Alignment	not modelled	11.1	8	Fold: Ferredoxin-like Superfamily: SEA domain Family: SEA domain
61	c2xu6B_	Alignment	not modelled	11.0	12	PDB header: protein binding Chain: B: PDB Molecule: mdv1 coiled coil; PDBTitle: mdv1 coiled coil domain
62	c2k2eA_	Alignment	not modelled	10.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bp2786; PDBTitle: solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
63	d1p3mh_	Alignment	not modelled	10.4	29	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
64	c3e3vA_	Alignment	not modelled	10.3	9	PDB header: recombination Chain: A: PDB Molecule: regulatory protein recx; PDBTitle: crystal structure of recx from lactobacillus salivarius
65	d2iw0a1	Alignment	not modelled	10.3	29	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
66	c2d9sA_	Alignment	not modelled	10.2	13	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
67	c3ff5B_	Alignment	not modelled	10.1	10	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
68	d1yqga1	Alignment	not modelled	9.9	11	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
69	d1k8ba_	Alignment	not modelled	9.3	29	Fold: Ribosome binding domain-like Superfamily: Translation initiation factor 2 beta, aIF2beta, N-terminal domain Family: Translation initiation factor 2 beta, aIF2beta, N-terminal domain
70	c1k98A_	Alignment	not modelled	9.1	22	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
71	c2iirJ_	Alignment	not modelled	9.0	14	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
72	c2xznm_	Alignment	not modelled	9.0	18	PDB header: ribosome Chain: M: PDB Molecule: rps18e; 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
73	c3flvA_	Alignment	not modelled	8.7	20	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 5; PDBTitle: the crystal structure of human acyl-coenzyme a binding domain2 containing 5
74	c2zkqm_	Alignment	not modelled	8.5	18	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
75	c2qh9B_	Alignment	not modelled	8.5	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0215 protein af_1433; PDBTitle: the crystal structure of a protein of unknown function from2 archaeoglobus fulgidus dsm 4304
76	c3rhgA_	Alignment	not modelled	8.4	25	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
77	c2e0tA_	Alignment	not modelled	8.2	28	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
78	c3d5lA_	Alignment	not modelled	8.2	12	PDB header: signaling protein Chain: A: PDB Molecule: regulatory protein recx; PDBTitle: crystal structure of regulatory protein recx
79	c2lm4A_	Alignment	not modelled	8.0	28	PDB header: protein binding Chain: A: PDB Molecule: succinate dehydrogenase assembly factor 2, mitochondrial; PDBTitle: solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a

80	c2w85A_	 Alignment	not modelled	7.9	8	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in comex with pex19
81	c3my3A_	 Alignment	not modelled	7.9	21	PDB header: transcription Chain: A: PDB Molecule: nterf domain-containing protein 1, mitochondrial; PDBTitle: crystal structure of human mitochondrial transcription termination2 factor 3
82	c3m66A_	 Alignment	not modelled	7.8	21	PDB header: transcription Chain: A: PDB Molecule: nterf domain-containing protein 1, mitochondrial; PDBTitle: crystal structure of human mitochondrial transcription termination2 factor 3
83	c2y96A_	 Alignment	not modelled	7.5	36	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
84	c3fp5A_	 Alignment	not modelled	7.5	16	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa binding protein; PDBTitle: crystal structure of acbp from moniliophthora perniciosa
85	c3dntB_	 Alignment	not modelled	7.5	12	PDB header: transferase Chain: B: PDB Molecule: protein hipa; PDBTitle: structures of mdt proteins
86	d2gcl1	 Alignment	not modelled	7.4	8	Fold: PH domain-like barrel Superfamily: PH domain-like Family: SSRP1-like
87	d1oqya2	 Alignment	not modelled	7.2	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
88	c3p04B_	 Alignment	not modelled	7.2	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
89	c2h9aB_	 Alignment	not modelled	7.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron- PDBTitle: corrinoid iron-sulfur protein
90	d1bhea_	 Alignment	not modelled	7.0	31	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Galacturonase
91	d1y02a1	 Alignment	not modelled	7.0	31	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
92	d2ahra1	 Alignment	not modelled	7.0	15	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
93	c2do6A_	 Alignment	not modelled	6.9	6	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
94	d1kv5a_	 Alignment	not modelled	6.9	19	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
95	d1oiza1	 Alignment	not modelled	6.9	15	Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain
96	c3p04A_	 Alignment	not modelled	6.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
97	d1uw4a_	 Alignment	not modelled	6.9	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Smg-4/UPF3
98	c2pyhB_	 Alignment	not modelled	6.8	45	PDB header: isomerase Chain: B: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
99	c3p4iA_	 Alignment	not modelled	6.6	19	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium