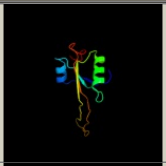
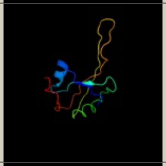
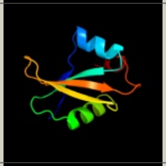
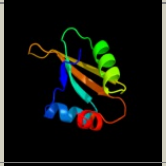
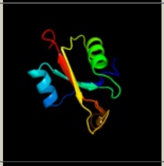
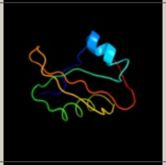
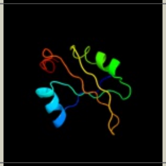
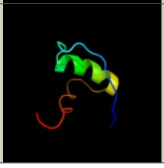
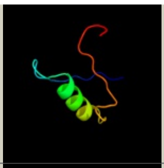
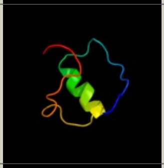
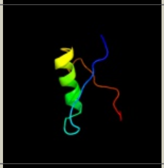
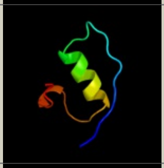
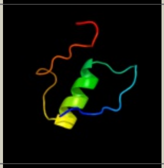
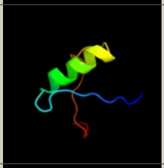
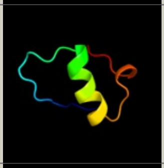
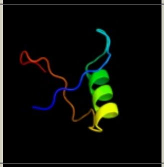
Email	l.a.kelley@imperial.ac.uk
Description	P0ADZ0
Date	Thu Jan 5 11:22:07 GMT 2012
Unique Job ID	8b138deb78ecc8fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2zjrq1	Alignment		100.0	47	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
2	d2qamt1	Alignment		100.0	100	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
3	d2j01x1	Alignment		100.0	43	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
4	c2ww9K_	Alignment		100.0	42	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l25; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
5	c2go54_	Alignment		99.9	39	**PDB header:**translation/rna **Chain:** 4: **PDB Molecule:**ribosomal protein l23; **PDBTitle:** structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex
6	d1vqos1	Alignment		99.9	40	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
7	c2zkrs_	Alignment		99.9	40	**PDB header:**ribosomal protein/rna **Chain:** S: **PDB Molecule:**rna expansion segment es39 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
8	c4a17R_	Alignment		99.9	42	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**rpl23a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
9	c1s1iT_	Alignment		99.9	47	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l25; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
10	c3bboV_	Alignment		99.9	30	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**ribosomal protein l23; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
11	d1wx7a1	Alignment		80.9	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related

12	d1yqba1	Alignment		65.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
13	d1v86a_	Alignment		62.4	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
14	c2dzmA_	Alignment		59.4	15	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfaf1)
15	c2kanA_	Alignment		54.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ar3433a; **PDBTitle:** solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
16	c2ojrA_	Alignment		53.8	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin; **PDBTitle:** structure of ubiquitin solved by sad using the lanthanide-2 binding tag
17	d1wx8a1	Alignment		53.7	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
18	c2klcA_	Alignment		51.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr solution structure of human ubiquitin-like domain of2 ubiquilin 1, northeast structural genomics consortium3 (nesg) target ht5a
19	c1yx5B_	Alignment		49.2	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
20	c1z2mA_	Alignment		48.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon, alpha-inducible protein (clone ifi- **PDBTitle:** crystal structure of isg15, the interferon-induced2 ubiquitin cross reactive protein
21	d1wm3a_	Alignment	not modelled	46.9	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
22	c2kd0A_	Alignment	not modelled	46.4	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lrr repeats and ubiquitin-like domain-containing **PDBTitle:** nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
23	d1z2ma2	Alignment	not modelled	44.2	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
24	d1bt0a_	Alignment	not modelled	43.1	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
25	d1sifa_	Alignment	not modelled	43.0	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
26	d2znvb1	Alignment	not modelled	42.3	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
27	c2dziA_	Alignment	not modelled	41.6	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin-like protein 4a; **PDBTitle:** 2dzi/solution structure of the n-terminal ubiquitin-like2 domain in human ubiquitin-like protein 4a (gdx)
28	c2kdiA_	Alignment	not modelled	39.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin, vacuolar protein sorting-associated **PDBTitle:** solution structure of a ubiquitin/uim fusion protein

29	d2v94a1	Alignment	not modelled	37.9	9	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
30	d1wjua_	Alignment	not modelled	36.5	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
31	c2w9nA_	Alignment	not modelled	36.4	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**ubiquitin; **PDBTitle:** crystal structure of linear di-ubiquitin
32	d1v5oa_	Alignment	not modelled	36.0	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
33	d1zkha1	Alignment	not modelled	35.2	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
34	d2bwfa1	Alignment	not modelled	34.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
35	d2g1da1	Alignment	not modelled	33.9	19	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
36	d1ndda_	Alignment	not modelled	32.1	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
37	d1wh3a_	Alignment	not modelled	31.7	3	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
38	d1wx9a1	Alignment	not modelled	30.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
39	c2kk8A_	Alignment	not modelled	29.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at4g05270; **PDBTitle:** nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3449a
40	c2jxxA_	Alignment	not modelled	29.4	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
41	d1v2ya_	Alignment	not modelled	28.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
42	d2zeqa1	Alignment	not modelled	28.7	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
43	c3m62B_	Alignment	not modelled	27.2	17	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
44	c2kjrA_	Alignment	not modelled	26.5	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cg11242; **PDBTitle:** solution nmr structure of the n-terminal ubiquitin-like2 domain from tubulin-binding cofactor b, cg11242, from3 drosophila melanogaster. northeast structural genomics4 consortium target fr629a (residues 8-92)
45	d1j8ca_	Alignment	not modelled	25.9	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
46	c3m63B_	Alignment	not modelled	25.0	24	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**ubiquitin domain-containing protein dsk2; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of dsk2
47	d1ywxa1	Alignment	not modelled	24.8	14	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
48	d1c3ta_	Alignment	not modelled	24.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
49	d1ogwa_	Alignment	not modelled	24.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
50	d2fnjb1	Alignment	not modelled	24.2	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
51	c2ekeC_	Alignment	not modelled	23.5	18	**PDB header:**ligase/protein binding **Chain:** C: **PDB Molecule:**ubiquitin-like protein smt3; **PDBTitle:** structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
52	c2l7rA_	Alignment	not modelled	22.6	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin-like protein fubi; **PDBTitle:** solution nmr structure of n-terminal ubiquitin-like domain of fubi, a2 ribosomal protein s30 precursor from homo sapiens. northeast3 structural genomics consortium (nesg) target hr6166
53	d1ttna1	Alignment	not modelled	21.6	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
						PDB header:signaling protein

54	c1ttnA_	Alignment	not modelled	21.6	17	**Chain:** A: **PDB Molecule:**dendritic cell-derived ubiquitin-like protein; **PDBTitle:** solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
55	d1ud7a_	Alignment	not modelled	21.0	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
56	d2faza1	Alignment	not modelled	20.5	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
57	c2k25A_	Alignment	not modelled	20.4	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ubb; **PDBTitle:** automated nmr structure of the ubb by fapsy
58	c3ai5A_	Alignment	not modelled	20.3	28	**PDB header:**fluorescent protein, transcription **Chain:** A: **PDB Molecule:**yeast enhanced green fluorescent protein, ubiquitin; **PDBTitle:** crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
59	c1s21A_	Alignment	not modelled	20.0	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**orf2; **PDBTitle:** crystal structure of avrpphf orf2, a type iii effector from2 p. syringae
60	d1s21a_	Alignment	not modelled	20.0	29	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**AvrPphF ORF2, a type III effector
61	d1v5ta_	Alignment	not modelled	18.9	34	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
62	d1xn9a_	Alignment	not modelled	18.8	7	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
63	d1wy8a1	Alignment	not modelled	18.1	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
64	c2o37A_	Alignment	not modelled	18.0	34	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
65	d1uawa_	Alignment	not modelled	17.4	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
66	d1wgga_	Alignment	not modelled	17.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
67	d1iyfa_	Alignment	not modelled	16.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
68	d1ckqa_	Alignment	not modelled	15.8	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRI
69	c3p6yD_	Alignment	not modelled	15.4	12	**PDB header:**rna binding protein/rna **Chain:** D: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 6; **PDBTitle:** cf im25-cf im68-uguaa complex
70	c2dgpA_	Alignment	not modelled	14.0	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**bruno-like 4, rna binding protein; **PDBTitle:** solution structure of the n-terminal rna binding domain in2 bruno-like 4 rna-binding protein
71	d1we7a_	Alignment	not modelled	13.5	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
72	d2c9wb1	Alignment	not modelled	13.2	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
73	d1v6ea_	Alignment	not modelled	12.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
74	d2io3b1	Alignment	not modelled	12.1	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
75	d1vqod1	Alignment	not modelled	11.5	24	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**Ribosomal protein L5
76	d1euvb_	Alignment	not modelled	11.0	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
77	d1l3ka1	Alignment	not modelled	11.0	10	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
78	d1twfc2	Alignment	not modelled	10.8	33	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
79	d1wjna_	Alignment	not modelled	10.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
80	d1z2ma1	Alignment	not modelled	10.1	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related

81	c3izbU_	Alignment	not modelled	9.3	17	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
82	c2xzmP_	Alignment	not modelled	9.1	23	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**rps24e; **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 1
83	c2divA_	Alignment	not modelled	8.9	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**trna selenocysteine associated protein; **PDBTitle:** solution structure of the rrm domain of trna selenocysteine2 associated protein
84	d1wi8a_	Alignment	not modelled	8.9	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
85	c2gj2A_	Alignment	not modelled	8.5	41	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**wsv230; **PDBTitle:** crystal structure of vp9 from white spot syndrome virus
86	c1qzeA_	Alignment	not modelled	8.4	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**uv excision repair protein rad23 homolog a; **PDBTitle:** hhr23a protein structure based on residual dipolar coupling2 data
87	d1fxla2	Alignment	not modelled	8.4	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
88	c2eqoA_	Alignment	not modelled	8.1	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3-interacting **PDBTitle:** solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
89	c2kqxA_	Alignment	not modelled	7.8	29	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
90	d2u2fa_	Alignment	not modelled	7.6	7	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
91	d1iura_	Alignment	not modelled	7.3	24	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
92	d1whxa_	Alignment	not modelled	7.3	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
93	d2j0111	Alignment	not modelled	7.2	30	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
94	d1fxla1	Alignment	not modelled	7.2	22	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
95	d1x5ua1	Alignment	not modelled	7.1	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
96	d1q1va_	Alignment	not modelled	7.0	17	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
97	d2cqda1	Alignment	not modelled	7.0	24	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
98	c2lgwA_	Alignment	not modelled	6.9	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
99	c2ctpA_	Alignment	not modelled	6.8	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 menber 12