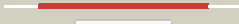

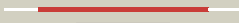














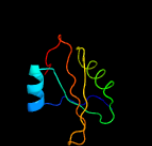
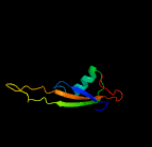



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0703_(rplW)_802136_802438
Date	Fri Jul 26 01:50:27 BST 2019
Unique Job ID	86e244886ba517a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o60U_</a>	 Alignment		100.0	87	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> 50s ribosomal protein l23; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">c3j3vT_</a>	 Alignment		100.0	44	<b>PDB header:</b> ribosome <b>Chain:</b> T; <b>PDB Molecule:</b> 50s ribosomal protein l23; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
3	<a href="#">d2zjrq1</a>	 Alignment		100.0	43	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> L23p
4	<a href="#">c4wfbQ_</a>	 Alignment		100.0	52	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> 50s ribosomal protein l23; <b>PDBTitle:</b> the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
5	<a href="#">d2j01x1</a>	 Alignment		100.0	48	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> L23p
6	<a href="#">d2qamt1</a>	 Alignment		100.0	36	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> L23p
7	<a href="#">c2ww9K_</a>	 Alignment		100.0	35	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> 60s ribosomal protein l25; <b>PDBTitle:</b> cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
8	<a href="#">c3zf7X_</a>	 Alignment		100.0	34	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> 60s ribosomal protein l23a; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
9	<a href="#">c4b6aX_</a>	 Alignment		100.0	36	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> 60s ribosomal protein l25; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
10	<a href="#">c3j39X_</a>	 Alignment		100.0	34	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> 60s ribosomal protein l23a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
11	<a href="#">c4a17R_</a>	 Alignment		100.0	42	<b>PDB header:</b> ribosome <b>Chain:</b> R; <b>PDB Molecule:</b> rpl23a; <b>PDBTitle:</b> 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.

12	<a href="#">c3izrX</a>	Alignment		100.0	31	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 60s ribosomal protein I23a (I23p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
13	<a href="#">c2go54</a>	Alignment		100.0	29	<b>PDB header:</b> translation/rna <b>Chain:</b> 4: <b>PDB Molecule:</b> ribosomal protein I23; <b>PDBTitle:</b> structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex
14	<a href="#">c3bboV</a>	Alignment		99.9	32	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> ribosomal protein I23; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
15	<a href="#">d1vqos1</a>	Alignment		99.9	30	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> L23p
16	<a href="#">c3j21T</a>	Alignment		99.9	35	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 50s ribosomal protein I23p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
17	<a href="#">c2zkrS</a>	Alignment		99.9	40	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> S: <b>PDB Molecule:</b> rna expansion segment es39 part ii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
18	<a href="#">c1s1tT</a>	Alignment		99.9	39	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein I25; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
19	<a href="#">c4v19X</a>	Alignment		99.9	26	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> mitoribosomal protein uI23m, mrpI23; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
20	<a href="#">c4ce4X</a>	Alignment		99.9	29	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> mrpI23; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
21	<a href="#">c1vw4P</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 54s ribosomal protein I41, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
22	<a href="#">d1wx7a1</a>	Alignment	not modelled	78.0	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
23	<a href="#">d2v94a1</a>	Alignment	not modelled	66.4	13	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> Ribosomal protein S24e
24	<a href="#">c2mqjA</a>	Alignment	not modelled	63.9	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein; <b>PDBTitle:</b> solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
25	<a href="#">d1v86a</a>	Alignment	not modelled	61.1	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
26	<a href="#">d1yqba1</a>	Alignment	not modelled	59.8	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
27	<a href="#">d2g1da1</a>	Alignment	not modelled	57.5	14	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> Ribosomal protein S24e
28	<a href="#">d1wjna</a>	Alignment	not modelled	56.3	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
29	<a href="#">c2dzmA</a>	Alignment	not modelled	55.4	13	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fas-associated factor 1;

29	<a href="#">c2zmlA</a>	Alignment	not modelled	53.4	13	<b>PDBTitle:</b> solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfa1) <b>PDB header:</b> immune system
30	<a href="#">c6gf2A</a>	Alignment	not modelled	53.8	23	<b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin d; <b>PDBTitle:</b> the structure of the ubiquitin-like modifier fat10 reveals a novel2 targeting mechanism for degradation by the 26s proteasome
31	<a href="#">d1zkha1</a>	Alignment	not modelled	53.4	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
32	<a href="#">d1t0ya</a>	Alignment	not modelled	48.5	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
33	<a href="#">c1t0yA</a>	Alignment	not modelled	48.5	13	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> tubulin folding cofactor b; <b>PDBTitle:</b> solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b
34	<a href="#">d1wx8a1</a>	Alignment	not modelled	48.4	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
35	<a href="#">c2kanA</a>	Alignment	not modelled	46.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ar3433a; <b>PDBTitle:</b> solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
36	<a href="#">c2klcA</a>	Alignment	not modelled	45.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquilin-1; <b>PDBTitle:</b> nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
37	<a href="#">c2ojrA</a>	Alignment	not modelled	45.3	12	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin; <b>PDBTitle:</b> structure of ubiquitin solved by sad using the lanthanide-binding tag
38	<a href="#">c2kd0A</a>	Alignment	not modelled	45.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> lrr repeats and ubiquitin-like domain-containing <b>PDBTitle:</b> nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
39	<a href="#">d1ywx1</a>	Alignment	not modelled	44.7	13	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> Ribosomal protein S24e
40	<a href="#">c2mlbA</a>	Alignment	not modelled	44.2	9	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> redesigned ubiquitin; <b>PDBTitle:</b> nmr solution structure of a computational designed protein based on2 template of human erythrocytic ubiquitin
41	<a href="#">c2xzmP</a>	Alignment	not modelled	43.4	21	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> rps24e; <b>PDBTitle:</b> 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
42	<a href="#">d1xn9a</a>	Alignment	not modelled	41.6	14	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> Ribosomal protein S24e
43	<a href="#">c1yx5B</a>	Alignment	not modelled	41.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquitin; <b>PDBTitle:</b> solution structure of s5a uim-1/ubiquitin complex
44	<a href="#">c1z2mA</a>	Alignment	not modelled	39.0	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> interferon, alpha-inducible protein (clone ifi- <b>PDBTitle:</b> crystal structure of isg15, the interferon-induced2 ubiquitin cross reactive protein
45	<a href="#">d1bt0a</a>	Alignment	not modelled	38.1	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
46	<a href="#">c3j3aY</a>	Alignment	not modelled	38.1	18	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
47	<a href="#">d1z2ma2</a>	Alignment	not modelled	37.2	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
48	<a href="#">d1v5oa</a>	Alignment	not modelled	36.3	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
49	<a href="#">c2dziA</a>	Alignment	not modelled	35.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> 2dzi/solution structure of the n-terminal ubiquitin-like2 domain in human ubiquitin-like protein 4a (gdx)
50	<a href="#">c2kdiA</a>	Alignment	not modelled	35.1	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin, vacuolar protein sorting-associated <b>PDBTitle:</b> solution structure of a ubiquitin/uim fusion protein
51	<a href="#">d1sifa</a>	Alignment	not modelled	34.9	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
52	<a href="#">d2znb1</a>	Alignment	not modelled	33.1	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
53	<a href="#">d1wh3a</a>	Alignment	not modelled	32.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
54	<a href="#">d2bwfa1</a>	Alignment	not modelled	32.3	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related

55	<a href="#">c4dbgA</a>	Alignment	not modelled	31.3	17	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> ranbp-type and c3hc4-type zinc finger-containing protein 1; <b>PDBTitle:</b> crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
56	<a href="#">c5xyiY</a>	Alignment	not modelled	31.1	16	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> ribosomal protein s24e, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
57	<a href="#">c4b6wA</a>	Alignment	not modelled	30.9	12	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> tubulin-specific chaperone; <b>PDBTitle:</b> architecture of trypanosoma brucei tubulin-binding cofactor b
58	<a href="#">c2kjrA</a>	Alignment	not modelled	30.7	15	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> cg11242; <b>PDBTitle:</b> 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)
59	<a href="#">c2dmxA</a>	Alignment	not modelled	30.1	32	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> dnaj homolog subfamily b member 8; <b>PDBTitle:</b> solution structure of the j domain of dnaj homolog2 subfamily b member 8
60	<a href="#">d1v2ya</a>	Alignment	not modelled	29.8	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
61	<a href="#">c3q3fA</a>	Alignment	not modelled	29.2	14	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> ribonuclease/ubiquitin chimeric protein; <b>PDBTitle:</b> engineering domain-swapped binding interfaces by mutually exclusive2 folding: insertion of ubiquitin into position 103 of barnase
62	<a href="#">c5wc3S</a>	Alignment	not modelled	28.7	30	<b>PDB header:</b> protein transport <b>Chain:</b> S; <b>PDB Molecule:</b> spoiiaag, stage iii sporulation engulfment assemblyprotein; <b>PDBTitle:</b> spoiiaag
63	<a href="#">c5y3tA</a>	Alignment	not modelled	28.7	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> ranbp-type and c3hc4-type zinc finger-containing protein 1; <b>PDBTitle:</b> crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
64	<a href="#">d1ndda</a>	Alignment	not modelled	28.4	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
65	<a href="#">c2w9nA</a>	Alignment	not modelled	28.0	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin; <b>PDBTitle:</b> crystal structure of linear di-ubiquitin
66	<a href="#">c5y3tC</a>	Alignment	not modelled	28.0	10	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> sharpin; <b>PDBTitle:</b> crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
67	<a href="#">c5chfB</a>	Alignment	not modelled	27.6	13	<b>PDB header:</b> antiviral protein <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquitin-like protein isg15; <b>PDBTitle:</b> crystal structure of murine isg15 in space group p21212
68	<a href="#">c2n7dA</a>	Alignment	not modelled	27.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> protein ddi1 homolog 2; <b>PDBTitle:</b> solution structure of the ubl domain of human ddi2
69	<a href="#">c3m62B</a>	Alignment	not modelled	26.5	5	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> uv excision repair protein rad23; <b>PDBTitle:</b> crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
70	<a href="#">c3u5cY</a>	Alignment	not modelled	26.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 40s ribosomal protein s24-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
71	<a href="#">d1wx9a1</a>	Alignment	not modelled	25.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
72	<a href="#">d1j8ca</a>	Alignment	not modelled	25.3	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
73	<a href="#">c2kk8A</a>	Alignment	not modelled	25.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein at4g05270; <b>PDBTitle:</b> nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3449a
74	<a href="#">d1v6ea</a>	Alignment	not modelled	24.3	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
75	<a href="#">c2n9pC</a>	Alignment	not modelled	24.1	19	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> large proline-rich protein bag6; <b>PDBTitle:</b> solution structure of rnf126 n-terminal zinc finger domain in complex2 with bag6 ubiquitin-like domain
76	<a href="#">d1wjua</a>	Alignment	not modelled	22.7	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
77	<a href="#">c2lkzA</a>	Alignment	not modelled	22.6	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna-binding protein 5; <b>PDBTitle:</b> solution structure of the second rrm domain of rbm5
78	<a href="#">d1c3ta</a>	Alignment	not modelled	21.4	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
79	<a href="#">c6mdhA</a>	Alignment	not modelled	21.2	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin-like protein isg15; <b>PDBTitle:</b> x-ray crystal structure of isg15 from myotis davidii

80	<a href="#">d2fnjb1</a>	Alignment	not modelled	21.2	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
81	<a href="#">d1fxla2</a>	Alignment	not modelled	20.8	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
82	<a href="#">c3m63B_</a>	Alignment	not modelled	20.6	28	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin domain-containing protein dsk2; <b>PDBTitle:</b> crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of dsk2
83	<a href="#">c2mrpA_</a>	Alignment	not modelled	19.9	12	<b>PDB header:</b> ubiquitin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage-inducible protein 1; <b>PDBTitle:</b> nmr solution structure of the ubiquitin like domain (ubl) of dna-2 damage-inducible 1 protein (ddi1)
84	<a href="#">c2l7rA_</a>	Alignment	not modelled	19.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein fubi; <b>PDBTitle:</b> 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
85	<a href="#">d1ogwa_</a>	Alignment	not modelled	19.5	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
86	<a href="#">d2faza1</a>	Alignment	not modelled	19.2	6	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
87	<a href="#">c3izbU_</a>	Alignment	not modelled	19.2	18	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
88	<a href="#">c2hgmA_</a>	Alignment	not modelled	19.0	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein f; <b>PDBTitle:</b> nmr structure of the second qrrm domain of human hnrnp f
89	<a href="#">d2zeqa1</a>	Alignment	not modelled	18.9	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
90	<a href="#">d1wgga_</a>	Alignment	not modelled	18.3	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
91	<a href="#">c2mx2A_</a>	Alignment	not modelled	17.9	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deubiquitinating protein vcip135; <b>PDBTitle:</b> ubx-l domain of vcip135
92	<a href="#">c2dgpA_</a>	Alignment	not modelled	17.9	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bruno-like 4, rna binding protein; <b>PDBTitle:</b> solution structure of the n-terminal rna binding domain in2 bruno-like 4 rna-binding protein
93	<a href="#">d1ud7a_</a>	Alignment	not modelled	17.1	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
94	<a href="#">c3zeyT_</a>	Alignment	not modelled	17.0	16	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s24; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
95	<a href="#">c1ttnA_</a>	Alignment	not modelled	16.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dendritic cell-derived ubiquitin-like protein; <b>PDBTitle:</b> solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
96	<a href="#">d1ttna1</a>	Alignment	not modelled	16.9	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
97	<a href="#">d2io3b1</a>	Alignment	not modelled	16.7	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
98	<a href="#">c2mdaB_</a>	Alignment	not modelled	16.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine 3-monooxygenase; <b>PDBTitle:</b> the solution structure of the regulatory domain of tyrosine2 hydroxylase
99	<a href="#">c2k25A_</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubb; <b>PDBTitle:</b> automated nmr structure of the ubb by fapsy