

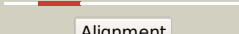

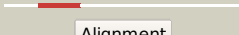



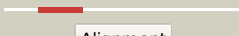
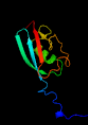







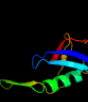












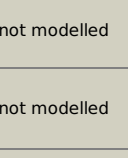


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1795 (-) _2032247_2033758
Date	Fri Aug 2 13:30:40 BST 2019
Unique Job ID	e2223b27eda7dbc1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4kv3A_</a>	 Alignment		99.4	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chimera fusion protein of esx-1 secretion system protein <b>PDBTitle:</b> ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
2	<a href="#">d1j8ca_</a>	 Alignment		96.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
3	<a href="#">d1yqba1</a>	 Alignment		96.3	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
4	<a href="#">c2klca_</a>	 Alignment		96.2	16	<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
5	<a href="#">d1a5ra_</a>	 Alignment		95.6	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
6	<a href="#">c2kmaA_</a>	 Alignment		95.6	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tal1n 1; <b>PDBTitle:</b> nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain
7	<a href="#">d1wx7a1</a>	 Alignment		95.6	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
8	<a href="#">d1bt0a_</a>	 Alignment		95.5	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
9	<a href="#">c3goeA_</a>	 Alignment		95.4	8	<b>PDB header:</b> recombination, replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad60; <b>PDBTitle:</b> molecular mimicry of sumo promotes dna repair
10	<a href="#">d1wz0a1</a>	 Alignment		95.3	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
11	<a href="#">c4hwiB_</a>	 Alignment		95.3	13	<b>PDB header:</b> chaperone/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bag family molecular chaperone regulator 1; <b>PDBTitle:</b> crystal structure of atbag1 in complex with hsp70

12	<a href="#">c2dzmA</a>	Alignment		95.2	13	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fas-associated factor 1; <b>PDBTitle:</b> solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfaf1)
13	<a href="#">c1yx5B</a>	Alignment		95.1	11	<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
14	<a href="#">d1wh3a</a>	Alignment		95.1	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
15	<a href="#">c2bpsA</a>	Alignment		95.0	20	<b>PDB header:</b> ubiquitin <b>Chain:</b> A: <b>PDB Molecule:</b> yukd protein; <b>PDBTitle:</b> ubiquitin-like protein yukd of bacillus subtilis
16	<a href="#">c2kzrA</a>	Alignment		94.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin thioesterase otu1; <b>PDBTitle:</b> solution nmr structure of ubiquitin thioesterase otu1 (ec 3.1.2.-)2 from mus musculus, northeast structural genomics consortium target3 mmt2a
17	<a href="#">d1v2ya</a>	Alignment		94.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
18	<a href="#">d1wggA</a>	Alignment		94.9	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
19	<a href="#">d2bwfa1</a>	Alignment		94.8	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
20	<a href="#">d1wy8a1</a>	Alignment		94.8	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
21	<a href="#">d1z2ma1</a>	Alignment	not modelled	94.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
22	<a href="#">c5xqmA</a>	Alignment	not modelled	94.6	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> small ubiquitin-related modifier; <b>PDBTitle:</b> nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
23	<a href="#">c2mqjA</a>	Alignment	not modelled	94.6	19	<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
24	<a href="#">c5ycaA</a>	Alignment	not modelled	94.6	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein smt3,bouquet formation protein 4; <b>PDBTitle:</b> crystal structure of inner membrane protein bqt4 in complex with lem2
25	<a href="#">c5jp1B</a>	Alignment	not modelled	94.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> small ubiquitin-related modifier; <b>PDBTitle:</b> structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
26	<a href="#">d1ud7a</a>	Alignment	not modelled	94.5	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
27	<a href="#">d2uyzb1</a>	Alignment	not modelled	94.5	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
28	<a href="#">d1v5oa</a>	Alignment	not modelled	94.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related

29	<a href="#">c2dziA</a>	Alignment	not modelled	94.3	15	<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)
30	<a href="#">d1wx8a1</a>	Alignment	not modelled	94.2	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
31	<a href="#">c2kd0A</a>	Alignment	not modelled	94.1	27	<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
32	<a href="#">d1ndda</a>	Alignment	not modelled	93.9	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
33	<a href="#">c2dajA</a>	Alignment	not modelled	93.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0977 protein; <b>PDBTitle:</b> solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein
34	<a href="#">c2k8hA</a>	Alignment	not modelled	93.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> small ubiquitin protein; <b>PDBTitle:</b> solution structure of sumo from trypanosoma brucei
35	<a href="#">d1wm3a</a>	Alignment	not modelled	93.8	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
36	<a href="#">d2zeqa1</a>	Alignment	not modelled	93.7	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
37	<a href="#">d2io3b1</a>	Alignment	not modelled	93.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
38	<a href="#">c2ekeC</a>	Alignment	not modelled	93.4	16	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin-like protein smt3; <b>PDBTitle:</b> 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
39	<a href="#">c3m63B</a>	Alignment	not modelled	93.3	13	<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
40	<a href="#">d1c3ta</a>	Alignment	not modelled	93.0	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
41	<a href="#">d1uela</a>	Alignment	not modelled	92.8	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
42	<a href="#">d1euvb</a>	Alignment	not modelled	92.7	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
43	<a href="#">d1v5ta</a>	Alignment	not modelled	92.6	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
44	<a href="#">c2kxjA</a>	Alignment	not modelled	92.6	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubx domain-containing protein 4; <b>PDBTitle:</b> solution structure of ubx domain of human ubxd2 protein
45	<a href="#">c2k25A</a>	Alignment	not modelled	92.5	11	<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
46	<a href="#">d1sifa</a>	Alignment	not modelled	92.5	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
47	<a href="#">c5y3tA</a>	Alignment	not modelled	92.3	16	<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
48	<a href="#">c2mlbA</a>	Alignment	not modelled	92.3	10	<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
49	<a href="#">d1zkha1</a>	Alignment	not modelled	92.2	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
50	<a href="#">c2n7dA</a>	Alignment	not modelled	92.2	15	<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
51	<a href="#">c1ttnA</a>	Alignment	not modelled	92.1	12	<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
52	<a href="#">d1ttna1</a>	Alignment	not modelled	92.1	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
53	<a href="#">c1oqyA</a>	Alignment	not modelled	92.1	10	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> uv excision repair protein rad23 homolog a; <b>PDBTitle:</b> structure of the dna repair protein hhr23a
54	<a href="#">d2faza1</a>	Alignment	not modelled	92.0	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related

55	<a href="#">d1x1ma1</a>	Alignment	not modelled	92.0	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
56	<a href="#">c2kj6A</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin folding cofactor b; <b>PDBTitle:</b> nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
57	<a href="#">c2inpE</a>	Alignment	not modelled	91.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> phenol hydroxylase component pho; <b>PDBTitle:</b> structure of the phenol hydroxylase-regulatory protein2 complex
58	<a href="#">d1we7a</a>	Alignment	not modelled	91.4	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
59	<a href="#">d1iyfa</a>	Alignment	not modelled	91.3	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
60	<a href="#">c2kdiA</a>	Alignment	not modelled	91.2	8	<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
61	<a href="#">d1v86a</a>	Alignment	not modelled	91.1	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
62	<a href="#">c3q3fA</a>	Alignment	not modelled	90.9	13	<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
63	<a href="#">c3m62B</a>	Alignment	not modelled	90.8	13	<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
64	<a href="#">d1v6ea</a>	Alignment	not modelled	90.7	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
65	<a href="#">c6gf2A</a>	Alignment	not modelled	90.6	11	<b>PDB header:</b> immune system <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
66	<a href="#">c2jxxA</a>	Alignment	not modelled	90.0	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> nfatc2-interacting protein; <b>PDBTitle:</b> nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
67	<a href="#">d1p1aa</a>	Alignment	not modelled	89.9	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
68	<a href="#">c2kk8A</a>	Alignment	not modelled	89.9	10	<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
69	<a href="#">c2ojrA</a>	Alignment	not modelled	89.5	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
70	<a href="#">c2w9nA</a>	Alignment	not modelled	88.7	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin; <b>PDBTitle:</b> crystal structure of linear di-ubiquitin
71	<a href="#">c2kanA</a>	Alignment	not modelled	88.5	20	<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
72	<a href="#">c5qjlA</a>	Alignment	not modelled	88.5	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of sumo from plasmodium falciparum
73	<a href="#">d1wxva1</a>	Alignment	not modelled	88.5	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
74	<a href="#">c2dzkA</a>	Alignment	not modelled	88.4	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubx domain-containing protein 2; <b>PDBTitle:</b> structure of the ubx domain in mouse ubx domain-containing2 protein 2
75	<a href="#">d1oqya4</a>	Alignment	not modelled	88.0	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
76	<a href="#">c2l76A</a>	Alignment	not modelled	87.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nfatc2-interacting protein; <b>PDBTitle:</b> solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
77	<a href="#">d1t0ya</a>	Alignment	not modelled	87.8	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
78	<a href="#">c1t0yA</a>	Alignment	not modelled	87.8	20	<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
79	<a href="#">d1z2ma2</a>	Alignment	not modelled	87.7	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
						<b>PDB header:</b> protein binding

80	<a href="#">c2mbeA_</a>	Alignment	not modelled	87.2	13	<b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin d; <b>PDBTitle:</b> backbone 1h and 15n chemical shift assignments for the first domain of2 fat10
81	<a href="#">c6a42A_</a>	Alignment	not modelled	86.6	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed dna polymerase homolog (r1),polyubiquitin-c; <b>PDBTitle:</b> r1en(5-223)-ubiquitin fusion
82	<a href="#">d1we6a_</a>	Alignment	not modelled	86.4	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
83	<a href="#">d1wjua_</a>	Alignment	not modelled	85.6	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
84	<a href="#">c1qzeA_</a>	Alignment	not modelled	85.6	11	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> uv excision repair protein rad23 homolog a; <b>PDBTitle:</b> hhr23a protein structure based on residual dipolar coupling2 data
85	<a href="#">c2kc2A_</a>	Alignment	not modelled	84.7	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> nmr structure of the f1 domain (residues 86-202) of the2 taln
86	<a href="#">d2al3a1</a>	Alignment	not modelled	84.6	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
87	<a href="#">c2lrwA_</a>	Alignment	not modelled	84.4	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin, putative; <b>PDBTitle:</b> solution structure of a ubiquitin-like protein from trypanosoma brucei
88	<a href="#">c3tixA_</a>	Alignment	not modelled	84.4	16	<b>PDB header:</b> gene regulation/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein smt3,rna-induced transcriptional <b>PDBTitle:</b> crystal structure of the chp1-tas3 complex core
89	<a href="#">c4dbgA_</a>	Alignment	not modelled	84.1	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 hoil-1l-ubl complexed with a hoip-uba derivative
90	<a href="#">d1ogwa_</a>	Alignment	not modelled	83.9	7	<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	83.6	16	<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="#">c3ivfA_</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> taln-1; <b>PDBTitle:</b> crystal structure of the talin head ferm domain
93	<a href="#">c4k95G_</a>	Alignment	not modelled	82.8	13	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase parkin; <b>PDBTitle:</b> crystal structure of parkin
94	<a href="#">c2l7rA_</a>	Alignment	not modelled	82.6	14	<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
95	<a href="#">d1h8ca_</a>	Alignment	not modelled	82.2	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
96	<a href="#">c3a4rB_</a>	Alignment	not modelled	80.1	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nfatc2-interacting protein; <b>PDBTitle:</b> the crystal structure of sumo-like domain 2 in nip45
97	<a href="#">c6mdhA_</a>	Alignment	not modelled	80.0	16	<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
98	<a href="#">c2pjhA_</a>	Alignment	not modelled	77.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear protein localization protein 4 homolog; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
99	<a href="#">d1wjna_</a>	Alignment	not modelled	77.1	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
100	<a href="#">c5y3tC_</a>	Alignment	not modelled	77.1	14	<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
101	<a href="#">c4b6wA_</a>	Alignment	not modelled	76.5	7	<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
102	<a href="#">c5b83A_</a>	Alignment	not modelled	75.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetra ubiquitin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
103	<a href="#">c3pgeA_</a>	Alignment	not modelled	75.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sumo-modified proliferating cell nuclear antigen; <b>PDBTitle:</b> structure of sumoylated pcna
104	<a href="#">d1i42a_</a>	Alignment	not modelled	75.1	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
105	<a href="#">c2mrpA_</a>	Alignment	not modelled	73.6	17	<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) <b>PDB header:</b> transcription

106	<a href="#">c3v7oB_</a>	Alignment	not modelled	73.4	18	<b>Chain:</b> B: <b>PDB Molecule:</b> minor nucleoprotein vp30; <b>PDBTitle:</b> crystal structure of the c-terminal domain of ebola virus vp30 (strain2 reston-89)
107	<a href="#">d1wiaa_</a>	Alignment	not modelled	71.9	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
108	<a href="#">c5chfB_</a>	Alignment	not modelled	71.5	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
109	<a href="#">c1z2mA_</a>	Alignment	not modelled	69.7	16	<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
110	<a href="#">c2n9pC_</a>	Alignment	not modelled	68.9	14	<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
111	<a href="#">d1wx9a1</a>	Alignment	not modelled	68.6	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
112	<a href="#">d1y8xb1</a>	Alignment	not modelled	66.7	28	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
113	<a href="#">c5xq0B_</a>	Alignment	not modelled	66.4	26	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> fermitin family homolog 2,integrin beta-1; <b>PDBTitle:</b> structural basis of kindlin-mediated integrin recognition and2 activation
114	<a href="#">c3ai5A_</a>	Alignment	not modelled	63.1	13	<b>PDB header:</b> fluorescent protein, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yeast enhanced green fluorescent protein,ubiquitin; <b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
115	<a href="#">c2kjrA_</a>	Alignment	not modelled	62.3	19	<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)
116	<a href="#">c5n9vA_</a>	Alignment	not modelled	57.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(p)(+)--arginine adp-ribosyltransferase; <b>PDBTitle:</b> nmr solution structure of ubl5 domain from polyubiquitin locus of2 t.thermophila.
117	<a href="#">d2cr5a1</a>	Alignment	not modelled	56.8	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
118	<a href="#">c5ifsA_</a>	Alignment	not modelled	56.2	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tether containing ubx domain for glut4; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
119	<a href="#">c3t9IA_</a>	Alignment	not modelled	55.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 15; <b>PDBTitle:</b> structure of n-terminal dusp-ubl domains of human usp15
120	<a href="#">c5nsaA_</a>	Alignment	not modelled	53.2	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcobalamin-2; <b>PDBTitle:</b> beta domain of human transcobalamin bound to co-beta-[2-(2,4-2 difluorophenyl)ethylanyl]cobalamin