


















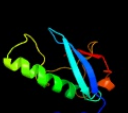




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3887c_(-)_4370333_4371862
Date	Sat Aug 10 22:05:07 BST 2019
Unique Job ID	52170fe7a09790b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kv3A_	 Alignment		99.7	27	PDB header: protein transport Chain: A: PDB Molecule: chimera fusion protein of esx-1 secretion system protein PDBTitle: ubiquitin-like domain of the mycobacterium tuberculosis type vii2 secretion system protein eccd1 as maltose-binding protein fusion
2	d1j8ca_	 Alignment		97.4	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
3	c2klcA_	 Alignment		97.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
4	d1yqba1	 Alignment		97.0	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
5	c4hwiB_	 Alignment		96.7	19	PDB header: chaperone/apoptosis Chain: B: PDB Molecule: bag family molecular chaperone regulator 1; PDBTitle: crystal structure of atbag1 in complex with hsp70
6	d2bwfa1	 Alignment		96.6	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
7	c2kd0A_	 Alignment		96.4	13	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
8	d1wx7a1	 Alignment		96.3	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
9	c2dzmA_	 Alignment		96.2	10	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)
10	d1wx8a1	 Alignment		96.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
11	c2kmaA_	 Alignment		95.8	17	PDB header: structural protein Chain: A: PDB Molecule: talin 1; PDBTitle: nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain

12	d1bt0a_	Alignment		95.8	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
13	d1v2ya_	Alignment		95.7	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
14	d1v86a_	Alignment		95.5	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
15	c2dziA_	Alignment		95.5	19	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)
16	d1v5oa_	Alignment		95.5	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
17	c2kzrA_	Alignment		95.4	11	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase otu1; PDBTitle: solution nmr structure of ubiquitin thioesterase otu1 (ec 3.1.2.-)2 from mus musculus, northeast structural genomics consortium target3 mmt2a
18	d1wy8a1	Alignment		95.4	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
19	c3m63B_	Alignment		95.3	18	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
20	c3goeA_	Alignment		95.3	13	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
21	d1a5ra_	Alignment	not modelled	95.1	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
22	c1yx5B_	Alignment	not modelled	94.9	18	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
23	d1euvb_	Alignment	not modelled	94.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
24	c1ttnA_	Alignment	not modelled	94.6	13	PDB header: signaling protein 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
25	d1ttna1	Alignment	not modelled	94.6	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
26	c2kanA_	Alignment	not modelled	94.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ar3433a; PDBTitle: solution nmr structure of ubiquitin-like domain of f2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
27	d1ud7a_	Alignment	not modelled	94.4	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
28	c2dajA_	Alignment	not modelled	94.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa0977 protein; PDBTitle: solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein

29	c2bpsA	Alignment	not modelled	94.3	13	PDB header: ubiquitin Chain: A: PDB Molecule: yukd protein; PDBTitle: ubiquitin-like protein yukd of bacillus subtilis
30	c5y3tA	Alignment	not modelled	94.2	9	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
31	d2zeqa1	Alignment	not modelled	94.2	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	d2uyzb1	Alignment	not modelled	94.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
33	c2mqjA	Alignment	not modelled	94.1	24	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
34	c2k8hA	Alignment	not modelled	94.1	16	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin protein; PDBTitle: solution structure of sumo from trypanosoma brucei
35	d1wh3a	Alignment	not modelled	94.0	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
36	c2ekeC	Alignment	not modelled	94.0	14	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
37	c5xqmA	Alignment	not modelled	94.0	14	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
38	c5jp1B	Alignment	not modelled	94.0	14	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
39	c2l76A	Alignment	not modelled	93.8	17	PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
40	d1wxva1	Alignment	not modelled	93.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
41	d1v5ta	Alignment	not modelled	93.7	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
42	c5ycaA	Alignment	not modelled	93.2	12	PDB header: membrane protein Chain: A: PDB Molecule: ubiquitin-like protein smt3,bouquet formation protein 4; PDBTitle: crystal structure of inner membrane protein bqt4 in complex with lem2
43	d1ndda	Alignment	not modelled	93.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	d1we6a	Alignment	not modelled	93.1	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
45	c6gf2A	Alignment	not modelled	92.9	19	PDB header: immune system Chain: A: PDB Molecule: ubiquitin d; PDBTitle: the structure of the ubiquitin-like modifier fat10 reveals a novel2 targeting mechanism for degradation by the 26s proteasome
46	c2n7dA	Alignment	not modelled	92.8	20	PDB header: unknown function Chain: A: PDB Molecule: protein ddi1 homolog 2; PDBTitle: solution structure of the ubl domain of human ddi2
47	d1v6ea	Alignment	not modelled	92.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
48	d1zkha1	Alignment	not modelled	92.8	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
49	d1c3ta	Alignment	not modelled	92.4	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
50	d1wz0a1	Alignment	not modelled	92.4	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
51	d1sifa	Alignment	not modelled	92.3	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
52	c1t0yA	Alignment	not modelled	92.3	22	PDB header: chaperone Chain: A: PDB Molecule: tubulin folding cofactor b; PDBTitle: solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b
53	d1t0ya	Alignment	not modelled	92.3	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
54	d1x1ma1	Alignment	not modelled	92.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

55	d1z2ma1	Alignment	not modelled	91.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
56	d1wm3a_	Alignment	not modelled	91.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
57	d2io3b1	Alignment	not modelled	91.5	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
58	c2inpE_	Alignment	not modelled	91.4	13	PDB header: oxidoreductase Chain: E: PDB Molecule: phenol hydroxylase component pho; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex
59	d1wgga_	Alignment	not modelled	91.2	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
60	c2k25A_	Alignment	not modelled	90.9	18	PDB header: unknown function Chain: A: PDB Molecule: ubb; PDBTitle: automated nmr structure of the ubb by fapsy
61	d1we7a_	Alignment	not modelled	90.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
62	c2kj6A_	Alignment	not modelled	90.9	18	PDB header: chaperone Chain: A: PDB Molecule: tubulin folding cofactor b; PDBTitle: nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
63	c2mlbA_	Alignment	not modelled	90.0	25	PDB header: de novo protein Chain: A: PDB Molecule: redesigned ubiquitin; PDBTitle: nmr solution structure of a computational designed protein based on2 template of human erythrocytic ubiquitin
64	c1oqyA_	Alignment	not modelled	89.6	13	PDB header: replication Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
65	c3q3fA_	Alignment	not modelled	89.6	18	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: ribonuclease/ubiquitin chimeric protein; PDBTitle: engineering domain-swapped binding interfaces by mutually exclusive2 folding: insertion of ubiquitin into position 103 of barnase
66	c2ojrA_	Alignment	not modelled	89.4	17	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-binding tag
67	c3m62B_	Alignment	not modelled	89.1	18	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
68	c2kxjA_	Alignment	not modelled	88.4	17	PDB header: protein binding Chain: A: PDB Molecule: ubx domain-containing protein 4; PDBTitle: solution structure of ubx domain of human ubxd2 protein
69	d2faza1	Alignment	not modelled	88.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
70	d1uela_	Alignment	not modelled	88.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
71	c2jxxA_	Alignment	not modelled	87.9	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
72	c3tixA_	Alignment	not modelled	87.6	13	PDB header: gene regulation/protein binding Chain: A: PDB Molecule: ubiquitin-like protein smt3,rna-induced transcriptional PDBTitle: crystal structure of the chp1-tas3 complex core
73	c2mbeA_	Alignment	not modelled	87.5	19	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin d; PDBTitle: backbone 1h and 15n chemical shift assignments for the first domain of2 fat10
74	d1p1aa_	Alignment	not modelled	87.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
75	c3pgeA_	Alignment	not modelled	86.8	14	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
76	c2kc2A_	Alignment	not modelled	86.5	41	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the f1 domain (residues 86-202) of the2 talin
77	d1iyfa_	Alignment	not modelled	85.6	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
78	c2pjhA_	Alignment	not modelled	85.4	17	PDB header: transport protein Chain: A: PDB Molecule: nuclear protein localization protein 4 homolog; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
79	c2l7rA_	Alignment	not modelled	85.0	16	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
80	c3a4rB_	Alignment	not modelled	84.7	16	PDB header: transcription Chain: B: PDB Molecule: nfatc2-interacting protein; PDBTitle: the crystal structure of sumo-like domain 2 in nip45

81	c2kk8A	Alignment	not modelled	84.4	7	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
82	c2kdiA	Alignment	not modelled	83.7	17	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin, vacuolar protein sorting-associated PDBTitle: solution structure of a ubiquitin/uim fusion protein
83	d1ogwa	Alignment	not modelled	83.7	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
84	c4dbgA	Alignment	not modelled	82.5	15	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
85	c2w9nA	Alignment	not modelled	82.3	17	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin; PDBTitle: crystal structure of linear di-ubiquitin
86	c2mrpA	Alignment	not modelled	80.2	15	PDB header: ubiquitin-binding protein Chain: A: PDB Molecule: dna damage-inducible protein 1; PDBTitle: nmr solution structure of the ubiquitin like domain (ubl) of dna-2 damage-inducible 1 protein (ddi1)
87	d1oqya4	Alignment	not modelled	78.7	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
88	c5y3tC	Alignment	not modelled	77.5	21	PDB header: ligase Chain: C: PDB Molecule: sharpin; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
89	c3v7oB	Alignment	not modelled	75.7	15	PDB header: transcription Chain: B: PDB Molecule: minor nucleoprotein vp30; PDBTitle: crystal structure of the c-terminal domain of ebola virus vp30 (strain2 reston-89)
90	d1z2ma2	Alignment	not modelled	75.6	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	c6a42A	Alignment	not modelled	75.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: rna-directed dna polymerase homolog (r1), polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion
92	c4k95G	Alignment	not modelled	75.2	12	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
93	c1qzeA	Alignment	not modelled	74.2	12	PDB header: replication Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: hhr23a protein structure based on residual dipolar coupling2 data
94	d1wjua	Alignment	not modelled	73.9	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
95	c5gjlA	Alignment	not modelled	72.7	14	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sumo from plasmodium falciparum
96	c2mx2A	Alignment	not modelled	72.5	11	PDB header: hydrolase Chain: A: PDB Molecule: deubiquitinating protein vcip135; PDBTitle: ubx-l domain of vcip135
97	c2lrwA	Alignment	not modelled	71.6	14	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin, putative; PDBTitle: solution structure of a ubiquitin-like protein from trypanosoma brucei
98	c2kdbA	Alignment	not modelled	69.7	17	PDB header: protein binding Chain: A: PDB Molecule: homocysteine-responsive endoplasmic reticulum-resident PDBTitle: solution structure of human ubiquitin-like domain of herpud2_9_85,2 northeast structural genomics consortium (nesg) target ht53a
99	d1wiaa	Alignment	not modelled	69.2	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
100	c5chfB	Alignment	not modelled	69.1	16	PDB header: antiviral protein Chain: B: PDB Molecule: ubiquitin-like protein isg15; PDBTitle: crystal structure of murine isg15 in space group p21212
101	d1wx9a1	Alignment	not modelled	68.7	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
102	d1h8ca	Alignment	not modelled	68.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
103	c6mdhA	Alignment	not modelled	64.8	15	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-like protein isg15; PDBTitle: x-ray crystal structure of isg15 from myotis davidii
104	c5xq0B	Alignment	not modelled	62.8	17	PDB header: signaling protein Chain: B: PDB Molecule: fermitin family homolog 2,integrin beta-1; PDBTitle: structural basis of kindlin-mediated integrin recognition and2 activation
105	d2al3a1	Alignment	not modelled	61.1	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
106	c2d7kA	Alignment	not modelled	60.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubx domain-containing protein 2;

106	c2uznA_	Alignment	not modelled	60.7	13	PDBTitle: structure of the ubx domain in mouse ubx domain-containing2 protein 2 PDB header: signaling protein Chain: A; PDB Molecule: interferon, alpha-inducible protein (clone ifi-
107	c1z2mA_	Alignment	not modelled	59.5	14	PDBTitle: crystal structure of isg15, the interferon-induced2 ubiquitin cross reactive protein
108	d1wjna_	Alignment	not modelled	56.9	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
109	d1i42a_	Alignment	not modelled	55.1	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
110	c3ivfA_	Alignment	not modelled	54.1	15	PDB header: structural protein Chain: A; PDB Molecule: tal1n-1; PDBTitle: crystal structure of the talin head ferm domain
111	c5b83A_	Alignment	not modelled	54.1	17	PDB header: signaling protein Chain: A; PDB Molecule: tetra ubiquitin; PDBTitle: crystal structure of optineurin uban in complex with linear ubiquitin
112	c4b6wA_	Alignment	not modelled	53.4	14	PDB header: chaperone Chain: A; PDB Molecule: tubulin-specific chaperone; PDBTitle: architecture of trypanosoma brucei tubulin-binding cofactor b
113	d1y8xb1	Alignment	not modelled	49.7	40	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
114	c2kjrA_	Alignment	not modelled	49.5	22	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)
115	c4pyzA_	Alignment	not modelled	47.3	19	PDB header: hydrolase Chain: A; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 7; PDBTitle: crystal structure of the first two ubl domains of deubiquitylase usp7
116	c5nsaA_	Alignment	not modelled	46.0	20	PDB header: transport protein Chain: A; PDB Molecule: transcobalamin-2; PDBTitle: beta domain of human transcobalamin bound to co-beta-[2-(2,4-2 difluorophenyl)ethynyl]cobalamin
117	d1vjka_	Alignment	not modelled	44.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
118	c2n9pC_	Alignment	not modelled	44.1	23	PDB header: ligase Chain: C; PDB Molecule: large proline-rich protein bag6; PDBTitle: solution structure of rnf126 n-terminal zinc finger domain in complex2 with bag6 ubiquitin-like domain
119	c2qjlA_	Alignment	not modelled	42.3	12	PDB header: signaling protein Chain: A; PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
120	c2jphA_	Alignment	not modelled	37.0	44	PDB header: signaling protein, protein binding Chain: A; PDB Molecule: plexin-b1; PDBTitle: nmr solution structure of the rho gtpase binding domain of2 human plexin-b1