

Phyre2

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 Description RVBD0868c_(moaD2)_965986_966264
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6jzbD_	Alignment		100.0	100	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
2	c6jc0A_	Alignment		100.0	55	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
3	c5mpoA_	Alignment		99.9	28	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
4	c2m19A_	Alignment		99.9	32	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
5	c3po0A_	Alignment		99.9	28	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
6	c2qieB_	Alignment		99.9	23	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
7	d1vjka_	Alignment		99.9	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
8	d1fm0d_	Alignment		99.9	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
9	c2I52A_	Alignment		99.9	29	PDB header: protein binding Chain: A: PDB Molecule: methanosarcina acetivorans samp1 homolog; PDBTitle: solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
10	c2g1eA_	Alignment		99.8	29	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
11	c2qjlA_	Alignment		99.8	21	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1

12	c1v8cA_	Alignment		99.8	37	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
13	c3rpfC_	Alignment		99.8	27	PDB header: transferase Chain: C: PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
14	d1v8ca1	Alignment		99.8	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
15	c4n6eB_	Alignment		99.8	31	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
16	d1wgka_	Alignment		99.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
17	d1xo3a_	Alignment		99.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
18	c3dwmA_	Alignment		99.7	24	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
19	c2k9xA_	Alignment		99.7	22	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
20	d1zud21	Alignment		98.4	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
21	c2ki0A_	Alignment	not modelled	98.3	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
22	c3cwiA_	Alignment	not modelled	98.1	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
23	c4idiA_	Alignment	not modelled	97.7	14	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
24	d1wh3a_	Alignment	not modelled	97.5	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
25	d2cu3a1	Alignment	not modelled	97.4	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
26	d1tygb_	Alignment	not modelled	97.4	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
27	d1rwsa_	Alignment	not modelled	97.3	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
28	d1v5oa_	Alignment	not modelled	97.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

29	c1oqyA	Alignment	not modelled	97.1	15	PDB header: replication Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
30	d1c3ta	Alignment	not modelled	97.0	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
31	d1ud7a	Alignment	not modelled	97.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	c1yx5B	Alignment	not modelled	96.8	11	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
33	c2ekeC	Alignment	not modelled	96.7	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
34	d1uela	Alignment	not modelled	96.7	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
35	d1v5ta	Alignment	not modelled	96.6	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
36	d1oqya4	Alignment	not modelled	96.6	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
37	c2kmmA	Alignment	not modelled	96.5	25	PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
38	c2kd0A	Alignment	not modelled	96.5	18	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
39	c4wwmB	Alignment	not modelled	96.4	17	PDB header: signaling protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of sulfobolus solfataricus urm1
40	c1qzeA	Alignment	not modelled	96.4	15	PDB header: replication Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: hhr23a protein structure based on residual dipolar coupling2 data
41	c2hj1A	Alignment	not modelled	96.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
42	d2hj1a1	Alignment	not modelled	96.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: HI0395-like
43	d1euvb	Alignment	not modelled	96.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	d1p1aa	Alignment	not modelled	96.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
45	c2jxxA	Alignment	not modelled	96.2	19	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
46	c1tygG	Alignment	not modelled	96.1	17	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
47	d1ryja	Alignment	not modelled	96.0	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
48	c5xqmA	Alignment	not modelled	96.0	22	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
49	c2dziA	Alignment	not modelled	95.9	25	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)
50	d1j8ca	Alignment	not modelled	95.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
51	c2lrwA	Alignment	not modelled	95.8	19	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin, putative; PDBTitle: solution structure of a ubiquitin-like protein from trypanosoma brucei
52	c2k8hA	Alignment	not modelled	95.7	21	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin protein; PDBTitle: solution structure of sumo from trypanosoma brucei
53	d1v2ya	Alignment	not modelled	95.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
						Fold: beta-Grasp (ubiquitin-like)

54	d1wx8a1	Alignment	not modelled	95.6	21	Superfamily: Ubiquitin-like Family: Ubiquitin-related
55	d1yqba1	Alignment	not modelled	95.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
56	d1sifa_	Alignment	not modelled	95.5	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
57	c2kdiA_	Alignment	not modelled	95.5	11	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin, vacuolar protein sorting-associated PDBTitle: solution structure of a ubiquitin/uim fusion protein
58	d1ndda_	Alignment	not modelled	95.4	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
59	c5jp1B_	Alignment	not modelled	95.4	16	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
60	c3hvvzB_	Alignment	not modelled	95.3	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
61	c2l7rA_	Alignment	not modelled	95.2	23	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
62	c2k25A_	Alignment	not modelled	95.2	9	PDB header: unknown function Chain: A: PDB Molecule: ubb; PDBTitle: automated nmr structure of the ubb by fapsy
63	d1wx7a1	Alignment	not modelled	95.1	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
64	d2zeqa1	Alignment	not modelled	94.9	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
65	c3q3fA_	Alignment	not modelled	94.9	12	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	94.8	12	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-binding tag
67	c3ai5A_	Alignment	not modelled	94.7	9	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
68	d1wz0a1	Alignment	not modelled	94.7	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	c5gjlA_	Alignment	not modelled	94.7	23	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sumo from plasmodium falciparum
70	d1bt0a_	Alignment	not modelled	94.6	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
71	c5xmjl_	Alignment	not modelled	94.6	10	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
72	c2mqjA_	Alignment	not modelled	94.6	13	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
73	c6a42A_	Alignment	not modelled	94.6	9	PDB header: dna binding protein Chain: A: PDB Molecule: rna-directed dna polymerase homolog (r1),polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion
74	d1a5ra_	Alignment	not modelled	94.5	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
75	c3goeA_	Alignment	not modelled	94.5	16	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
76	d1wgga_	Alignment	not modelled	94.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
77	c4k95G_	Alignment	not modelled	94.3	15	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
78	d1wxqa2	Alignment	not modelled	94.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
79	d1iyfa_	Alignment	not modelled	94.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

80	c3tixA	Alignment	not modelled	94.0	19	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
81	d1nekb2	Alignment	not modelled	94.0	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
82	d1kf6b2	Alignment	not modelled	93.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
83	d1wiaa	Alignment	not modelled	93.8	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
84	c3pgeA	Alignment	not modelled	93.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
85	c2kicA	Alignment	not modelled	93.4	16	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
86	c4hwiB	Alignment	not modelled	93.3	15	PDB header: chaperone/apoptosis Chain: B: PDB Molecule: bag family molecular chaperone regulator 1; PDBTitle: crystal structure of atbag1 in complex with hsp70
87	c2bs2E	Alignment	not modelled	93.3	16	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
88	c4dbgA	Alignment	not modelled	93.2	15	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hoil-1-ubl complexed with a hoip-uba derivative
89	d2uyzb1	Alignment	not modelled	93.1	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
90	d2bwfa1	Alignment	not modelled	93.1	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	c2kanA	Alignment	not modelled	93.0	25	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
92	d2bs2b2	Alignment	not modelled	92.6	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
93	d1tkea1	Alignment	not modelled	92.6	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
94	c3v7oB	Alignment	not modelled	92.3	19	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)
95	d1wy8a1	Alignment	not modelled	92.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
96	d1ogwa	Alignment	not modelled	92.3	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
97	c4gocB	Alignment	not modelled	92.2	26	PDB header: protein binding Chain: B: PDB Molecule: golgi to er traffic protein 5; PDBTitle: crystal structure of the get5 ubiquitin-like domain
98	d2faza1	Alignment	not modelled	92.2	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
99	d2io3b1	Alignment	not modelled	92.0	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
100	c2n9pC	Alignment	not modelled	91.9	18	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
101	c2n7dA	Alignment	not modelled	91.8	12	PDB header: unknown function Chain: A: PDB Molecule: protein ddi1 homolog 2; PDBTitle: solution structure of the ubl domain of human ddi2
102	c2kk8A	Alignment	not modelled	91.8	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
103	c3a4rB	Alignment	not modelled	91.8	19	PDB header: transcription Chain: B: PDB Molecule: nfatc2-interacting protein; PDBTitle: the crystal structure of sumo-like domain 2 in nip45
104	c5ycaA	Alignment	not modelled	91.8	17	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
105	c6dixA	Alignment	not modelled	91.7	8	PDB header: transferase Chain: A: PDB Molecule: rbr-type e3 ubiquitin transferase,rbr-type

105	c0vj6A_	Alignment	not modelled	91.7	8	e3 ubiquitin PDBTitle: crystal structure of pparkin-pub-ubch7 complex
106	d1we7a_	Alignment	not modelled	91.4	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
107	c2ns5A_	Alignment	not modelled	91.2	25	PDB header: signaling protein Chain: A: PDB Molecule: partitioning-defective 3 homolog; PDBTitle: the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
108	d1wm3a_	Alignment	not modelled	91.0	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
109	c3m62B_	Alignment	not modelled	90.2	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
110	c2l76A_	Alignment	not modelled	89.6	27	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
111	d1wjua_	Alignment	not modelled	89.5	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
112	d1z2ma2	Alignment	not modelled	89.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
113	c2ekiA_	Alignment	not modelled	89.1	23	PDB header: signaling protein Chain: A: PDB Molecule: developmentally-regulated gtp-binding protein 1; PDBTitle: solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
114	c2istA_	Alignment	not modelled	88.9	12	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
115	c2mlbA_	Alignment	not modelled	88.8	20	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
116	c5y3tC_	Alignment	not modelled	88.7	13	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
117	c4x57D_	Alignment	not modelled	88.4	15	PDB header: ligase/protein binding Chain: D: PDB Molecule: membrane-anchored ubiquitin-fold protein 3; PDBTitle: structure of an arabidopsis e2 / membrane-anchored ubiquitin-fold2 protein complex
118	d1v86a_	Alignment	not modelled	88.2	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
119	c5y3tA_	Alignment	not modelled	88.1	17	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
120	d1ttna1	Alignment	not modelled	86.5	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related