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 Description RVBD3323c_(moaX)_3709220_3709885
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qieA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
2	c6jzbC_	 Alignment		100.0	35	PDB header: transferase Chain: C: PDB Molecule: molybdenum cofactor biosynthesis protein e; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
3	c2omdB_	 Alignment		100.0	35	PDB header: lyase Chain: B: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
4	c6jc0D_	 Alignment		100.0	38	PDB header: transferase Chain: D: PDB Molecule: putative molybdenum cofactor biosynthesis protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
5	d1fm0e_	 Alignment		100.0	35	Fold: alpha/beta-Hammerhead Superfamily: Molybdopterin synthase subunit MoaE Family: Molybdopterin synthase subunit MoaE
6	c4ap8A_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase catalytic subunit; PDBTitle: crystal structure of human molybdopterin synthase catalytic subunit2 (mocs2b)
7	c3rpfB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase catalytic subunit; PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
8	c2wp4A_	 Alignment		100.0	80	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2 1; PDBTitle: crystal structure of rv3119 from mycobacterium tuberculosis
9	d1nvja_	 Alignment		100.0	38	Fold: alpha/beta-Hammerhead Superfamily: Molybdopterin synthase subunit MoaE Family: Molybdopterin synthase subunit MoaE
10	c1v8cA_	 Alignment		100.0	22	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
11	c6jzbD_	 Alignment		99.9	36	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens

12	c6jc0A_	Alignment		99.9	32	PDB header: transferase Chain: A; PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
13	c5mpoA_	Alignment		99.8	32	PDB header: transferase Chain: A; PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
14	c3po0A_	Alignment		99.8	21	PDB header: protein binding Chain: A; PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
15	c2m19A_	Alignment		99.8	28	PDB header: protein binding Chain: A; PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
16	c2qieB_	Alignment		99.8	39	PDB header: transferase Chain: B; PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
17	d1fm0d_	Alignment		99.8	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
18	d1vjka_	Alignment		99.8	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
19	c2l52A_	Alignment		99.8	32	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
20	c2qjlA_	Alignment		99.7	24	PDB header: signaling protein Chain: A; PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
21	c2g1eA_	Alignment	not modelled	99.7	27	PDB header: transferase Chain: A; PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
22	c4n6eB_	Alignment	not modelled	99.7	23	PDB header: lyase/biosynthetic protein Chain: B; PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
23	c3rpfC_	Alignment	not modelled	99.7	30	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
24	d1v8ca1	Alignment	not modelled	99.7	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
25	d1xo3a_	Alignment	not modelled	99.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
26	d1wgka_	Alignment	not modelled	99.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
27	c3dwmA_	Alignment	not modelled	99.6	27	PDB header: transferase Chain: A; PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
28	c2k9xA_	Alignment	not modelled	99.5	31	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
29	d1zud21	Alignment	not modelled	98.2	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS

						Family: ThiS
30	c2ki0A_	Alignment	not modelled	97.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamine biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
31	c3cwiA_	Alignment	not modelled	97.8	22	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
32	d1rwsa_	Alignment	not modelled	97.5	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
33	c4idiA_	Alignment	not modelled	97.2	13	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
34	d1tygb_	Alignment	not modelled	97.0	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
35	d2cu3a1	Alignment	not modelled	96.9	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
36	c2kmmA_	Alignment	not modelled	96.9	26	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)
37	c3hvvB_	Alignment	not modelled	96.4	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
38	c2hj1A_	Alignment	not modelled	96.2	15	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
39	d2hj1a1	Alignment	not modelled	96.2	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: HI0395-like
40	d1tkea1	Alignment	not modelled	96.1	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
41	d1ud7a_	Alignment	not modelled	96.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
42	d1c3ta_	Alignment	not modelled	96.0	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
43	d1wh3a_	Alignment	not modelled	95.7	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	d1ryja_	Alignment	not modelled	95.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
45	c1yx5B_	Alignment	not modelled	95.7	11	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
46	d1wxqa2	Alignment	not modelled	95.5	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
47	d1uela_	Alignment	not modelled	95.2	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
48	c1tygG_	Alignment	not modelled	95.1	23	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
49	c4hwiB_	Alignment	not modelled	95.0	12	PDB header: chaperone/apoptosis Chain: B: PDB Molecule: bag family molecular chaperone regulator 1; PDBTitle: crystal structure of atbag1 in complex with hsp70
50	d1v5oa_	Alignment	not modelled	94.7	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
51	c2lrwA_	Alignment	not modelled	93.9	14	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin, putative; PDBTitle: solution structure of a ubiquitin-like protein from trypanosoma brucei
52	d1kf6b2	Alignment	not modelled	93.3	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
53	c2ekiA_	Alignment	not modelled	93.2	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
54	d1yqba1	Alignment	not modelled	93.1	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
						PDB header: replication

55	c1oqyA	Alignment	not modelled	93.0	19	Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
56	d1oqya4	Alignment	not modelled	92.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
57	d1v5ta	Alignment	not modelled	92.8	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
58	d1p1aa	Alignment	not modelled	92.5	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
59	d2bs2b2	Alignment	not modelled	92.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
60	d1wx7a1	Alignment	not modelled	92.4	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
61	c4wwmB	Alignment	not modelled	92.3	11	PDB header: signaling protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of sulfolobus solfataricus urm1
62	c2kdiA	Alignment	not modelled	92.1	15	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin, vacuolar protein sorting-associated PDBTitle: solution structure of a ubiquitin/uim fusion protein
63	c2bs2E	Alignment	not modelled	92.0	21	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
64	c5xmjl	Alignment	not modelled	92.0	13	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
65	c3goeA	Alignment	not modelled	91.6	19	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
66	d1sifa	Alignment	not modelled	91.5	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
67	c2klcA	Alignment	not modelled	91.3	14	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
68	d1ogwa	Alignment	not modelled	90.8	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	d1nyra2	Alignment	not modelled	90.8	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
70	c1qzeA	Alignment	not modelled	90.8	17	PDB header: replication Chain: A: PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: hhr23a protein structure based on residual dipolar coupling2 data
71	d1ndda	Alignment	not modelled	90.7	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
72	c2kd0A	Alignment	not modelled	90.7	17	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
73	d1j8ca	Alignment	not modelled	90.6	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
74	c2l7rA	Alignment	not modelled	90.6	10	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
75	c3q3fA	Alignment	not modelled	90.1	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
76	c2k8hA	Alignment	not modelled	89.7	21	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin protein; PDBTitle: solution structure of sumo from trypanosoma brucei
77	d1wx8a1	Alignment	not modelled	89.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
78	d1v86a	Alignment	not modelled	89.1	7	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
79	c2mqjA	Alignment	not modelled	89.1	14	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
						Fold: beta-Grasp (ubiquitin-like)

80	d1wggg_	Alignment	not modelled	89.0	21	Superfamily: Ubiquitin-like Family: Ubiquitin-related
81	d1bt0a_	Alignment	not modelled	88.3	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
82	d1v2ya_	Alignment	not modelled	88.3	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
83	c1lwwtA_	Alignment	not modelled	88.3	18	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
84	c5jp1B_	Alignment	not modelled	88.0	11	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
85	c2ojrA_	Alignment	not modelled	87.1	10	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-binding tag
86	c2ns5A_	Alignment	not modelled	87.1	20	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
87	c4dbgA_	Alignment	not modelled	85.9	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
88	c1tkeA_	Alignment	not modelled	85.4	10	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
89	c2k25A_	Alignment	not modelled	85.2	11	PDB header: unknown function Chain: A: PDB Molecule: ubb; PDBTitle: automated nmr structure of the ubb by fapsy
90	c4k95G_	Alignment	not modelled	85.1	13	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
91	d1euvb_	Alignment	not modelled	85.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
92	d1wz0a1	Alignment	not modelled	84.9	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
93	c2mlbA_	Alignment	not modelled	84.1	18	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
94	c2dziA_	Alignment	not modelled	83.9	11	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)
95	d2zeqa1	Alignment	not modelled	83.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
96	d1lyfa_	Alignment	not modelled	83.1	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
97	c2jxxA_	Alignment	not modelled	82.9	11	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
98	c5y3tA_	Alignment	not modelled	82.1	15	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
99	d1vlba2	Alignment	not modelled	82.0	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
100	c2ekeC_	Alignment	not modelled	81.9	11	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
101	c2n9pC_	Alignment	not modelled	81.4	10	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
102	d1wy8a1	Alignment	not modelled	80.9	7	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
103	d1we7a_	Alignment	not modelled	79.7	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
104	d2io3b1	Alignment	not modelled	79.4	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
105	c3upsA_	Alignment	not modelled	79.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas

						mobilis
106	c1wxqA_	Alignment	not modelled	78.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
107	d1t3qa2	Alignment	not modelled	78.3	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
108	c2kanA_	Alignment	not modelled	78.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ar3433a; PDBTitle: solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
109	c3tixA_	Alignment	not modelled	78.2	11	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
110	c4gocB_	Alignment	not modelled	78.0	10	PDB header: protein binding Chain: B: PDB Molecule: golgi to er traffic protein 5; PDBTitle: crystal structure of the get5 ubiquitin-like domain
111	d2faza1	Alignment	not modelled	78.0	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
112	c2istA_	Alignment	not modelled	77.8	14	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
113	d1nekb2	Alignment	not modelled	77.0	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
114	c2kdbA_	Alignment	not modelled	76.2	24	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
115	c3m62B_	Alignment	not modelled	75.0	20	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
116	c2dzmA_	Alignment	not modelled	74.7	18	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)
117	d1wjua_	Alignment	not modelled	74.2	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
118	c1nyqA_	Alignment	not modelled	74.1	16	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase 1; PDBTitle: structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
119	c6odmA_	Alignment	not modelled	73.1	33	PDB header: viral protein Chain: A: PDB Molecule: triplex capsid protein 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
120	c6a42A_	Alignment	not modelled	73.0	11	PDB header: dna binding protein Chain: A: PDB Molecule: rna-directed dna polymerase homolog (r1),polyubiquitin-c; PDBTitle: r1en(5-223)-ubiquitin fusion