
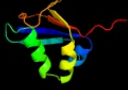



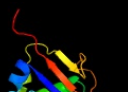

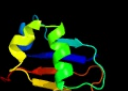
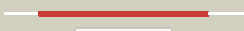
























# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3112\_(moaD1)\_3479697\_3479948  
 Date Thu Aug 8 16:20:29 BST 2019  
 Unique Job ID 631af81fd3168910

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6jzbD_</a>	 Alignment		99.9	31	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> moad/this family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
2	<a href="#">c6jc0A_</a>	 Alignment		99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein d2 <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
3	<a href="#">c3po0A_</a>	 Alignment		99.9	26	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> small archaeal modifier protein 1; <b>PDBTitle:</b> crystal structure of samp1 from haloferax volcanii
4	<a href="#">c5mpoA_</a>	 Alignment		99.9	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin synthase sulfur carrier subunit; <b>PDBTitle:</b> crystal structure of human molybdopterin synthase complex
5	<a href="#">c2m19A_</a>	 Alignment		99.9	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin converting factor subunit 1; <b>PDBTitle:</b> solution structure of the haloferax volcanii hvo 2177 protein
6	<a href="#">c2qieB_</a>	 Alignment		99.9	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
7	<a href="#">d1fm0d_</a>	 Alignment		99.9	36	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
8	<a href="#">c2I52A_</a>	 Alignment		99.9	34	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> methanosarcina acetivorans samp1 homolog; <b>PDBTitle:</b> solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
9	<a href="#">d1vjka_</a>	 Alignment		99.9	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
10	<a href="#">c2qjIA_</a>	 Alignment		99.9	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-related modifier 1; <b>PDBTitle:</b> crystal structure of urm1
11	<a href="#">c4n6eB_</a>	 Alignment		99.8	23	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> this/moaD family protein; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex

12	<a href="#">c2g1eA</a>	Alignment		99.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
13	<a href="#">c1v8cA</a>	Alignment		99.8	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> moad related protein; <b>PDBTitle:</b> crystal structure of moad related protein from thermus2 thermophilus hb8
14	<a href="#">d1v8ca1</a>	Alignment		99.8	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
15	<a href="#">c3rpfC</a>	Alignment		99.8	35	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> molybdopterin converting factor, subunit 1 (moad); <b>PDBTitle:</b> protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
16	<a href="#">d1xo3a</a>	Alignment		99.8	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
17	<a href="#">d1wgka</a>	Alignment		99.8	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
18	<a href="#">c3dwmA</a>	Alignment		99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 9.5 kda culture filtrate antigen cfp10a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyso, an antigen
19	<a href="#">c2k9xA</a>	Alignment		99.7	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of urm1 from trypanosoma brucei
20	<a href="#">d1zud21</a>	Alignment		98.4	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
21	<a href="#">d1rwsa</a>	Alignment	not modelled	98.2	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
22	<a href="#">c2ki0A</a>	Alignment	not modelled	98.1	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamin biosynthesis this; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
23	<a href="#">c3cwiA</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein this; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
24	<a href="#">c4idiA</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> oryza sativa rum1-related; <b>PDBTitle:</b> crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
25	<a href="#">d2cu3a1</a>	Alignment	not modelled	97.2	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
26	<a href="#">d1tygb</a>	Alignment	not modelled	97.2	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
27	<a href="#">d2hj1a1</a>	Alignment	not modelled	96.9	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> HI0395-like
28	<a href="#">c2hj1A</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae

29	<a href="#">c3hvvB</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
30	<a href="#">c2kmmA</a>	Alignment	not modelled	96.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'- <b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
31	<a href="#">d1wxqa2</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
32	<a href="#">d1ud7a</a>	Alignment	not modelled	96.1	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
33	<a href="#">d1c3ta</a>	Alignment	not modelled	95.8	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
34	<a href="#">d1tkea1</a>	Alignment	not modelled	95.6	6	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
35	<a href="#">c1tygG</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> cyjbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex
36	<a href="#">c2ekiA</a>	Alignment	not modelled	95.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> developmentally-regulated gtp-binding protein 1; <b>PDBTitle:</b> solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
37	<a href="#">c1yx5B</a>	Alignment	not modelled	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
38	<a href="#">c1oqyA</a>	Alignment	not modelled	95.0	7	<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
39	<a href="#">d1ryja</a>	Alignment	not modelled	94.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
40	<a href="#">c2lrwA</a>	Alignment	not modelled	94.7	7	<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
41	<a href="#">d1wh3a</a>	Alignment	not modelled	94.6	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
42	<a href="#">d1v5oa</a>	Alignment	not modelled	94.5	15	<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	93.6	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
44	<a href="#">d1uela</a>	Alignment	not modelled	93.3	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
45	<a href="#">c4wwmB</a>	Alignment	not modelled	93.2	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray crystal structure of sulfobolus solfataricus urm1
46	<a href="#">d1oqya4</a>	Alignment	not modelled	93.0	7	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
47	<a href="#">c4hwiB</a>	Alignment	not modelled	92.5	18	<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
48	<a href="#">c3goeA</a>	Alignment	not modelled	92.3	13	<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
49	<a href="#">d1kf6b2</a>	Alignment	not modelled	92.2	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
50	<a href="#">c1qzeA</a>	Alignment	not modelled	92.2	7	<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
51	<a href="#">c5jp1B</a>	Alignment	not modelled	92.1	13	<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
52	<a href="#">c2k8hA</a>	Alignment	not modelled	92.0	17	<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
53	<a href="#">d1euvb</a>	Alignment	not modelled	91.7	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
54	<a href="#">d1p1aa</a>	Alignment	not modelled	91.6	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related

55	<a href="#">c5xmjl_</a>	Alignment	not modelled	91.2	12	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
56	<a href="#">c2ekeC_</a>	Alignment	not modelled	91.0	9	<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
57	<a href="#">d1nyra2</a>	Alignment	not modelled	90.8	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
58	<a href="#">c2bs2E_</a>	Alignment	not modelled	90.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b; <b>PDBTitle:</b> quinol:fumarate reductase from wolinnella succinogenes
59	<a href="#">c2jxxA_</a>	Alignment	not modelled	90.4	9	<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
60	<a href="#">c1wwtA_</a>	Alignment	not modelled	90.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
61	<a href="#">d1yqba1</a>	Alignment	not modelled	90.3	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
62	<a href="#">d2bs2b2</a>	Alignment	not modelled	90.2	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
63	<a href="#">d1sifa_</a>	Alignment	not modelled	90.1	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
64	<a href="#">c1wxqA_</a>	Alignment	not modelled	89.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
65	<a href="#">c3tixA_</a>	Alignment	not modelled	89.2	10	<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
66	<a href="#">d2faza1</a>	Alignment	not modelled	89.2	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
67	<a href="#">c2kdiA_</a>	Alignment	not modelled	88.9	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
68	<a href="#">c2mqjA_</a>	Alignment	not modelled	88.8	18	<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
69	<a href="#">d1wgga_</a>	Alignment	not modelled	88.7	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
70	<a href="#">d1wy8a1</a>	Alignment	not modelled	88.3	7	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
71	<a href="#">d1wx7a1</a>	Alignment	not modelled	88.0	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
72	<a href="#">d1wx8a1</a>	Alignment	not modelled	87.6	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
73	<a href="#">c3q3fA_</a>	Alignment	not modelled	87.5	10	<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
74	<a href="#">d1wz0a1</a>	Alignment	not modelled	87.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
75	<a href="#">d1ndda_</a>	Alignment	not modelled	86.3	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
76	<a href="#">d2io3b1</a>	Alignment	not modelled	86.2	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
77	<a href="#">c3v7oB_</a>	Alignment	not modelled	85.8	10	<b>PDB header:</b> transcription <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)
78	<a href="#">c4k95G_</a>	Alignment	not modelled	85.7	19	<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
79	<a href="#">d1v2ya_</a>	Alignment	not modelled	85.5	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
80	<a href="#">c1tkeA_</a>	Alignment	not modelled	85.5	6	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2

						synthetase complexed with serine <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> partitioning-defective 3 homolog; <b>PDBTitle:</b> the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
81	<a href="#">c2ns5A_</a>	Alignment	not modelled	85.3	25	
82	<a href="#">d1bt0a_</a>	Alignment	not modelled	83.9	6	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
83	<a href="#">c5xqmA_</a>	Alignment	not modelled	83.5	18	<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
84	<a href="#">c3a4rB_</a>	Alignment	not modelled	83.3	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> infatc2-interacting protein; <b>PDBTitle:</b> the crystal structure of sumo-like domain 2 in nip45
85	<a href="#">c2istA_</a>	Alignment	not modelled	83.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d; <b>PDBTitle:</b> crystal structure of rlud from e. coli
86	<a href="#">c2klcA_</a>	Alignment	not modelled	82.9	18	<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
87	<a href="#">d1j8ca_</a>	Alignment	not modelled	81.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
88	<a href="#">d2g1la1</a>	Alignment	not modelled	81.1	23	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
89	<a href="#">c2b76N_</a>	Alignment	not modelled	81.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> fumarate reductase iron-sulfur protein; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda e49q mutation
90	<a href="#">c4ejqB_</a>	Alignment	not modelled	80.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a c-cc1-fha
91	<a href="#">c2kdbA_</a>	Alignment	not modelled	80.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> homocysteine-responsive endoplasmic reticulum-resident <b>PDBTitle:</b> solution structure of human ubiquitin-like domain of herpud2_9_85,2 northeast structural genomics consortium (nesg) target ht53a
92	<a href="#">c2ojrA_</a>	Alignment	not modelled	80.3	8	<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
93	<a href="#">c2k6pA_</a>	Alignment	not modelled	80.1	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423; <b>PDBTitle:</b> solution structure of hypothetical protein, hp1423
94	<a href="#">d1wiaa_</a>	Alignment	not modelled	78.5	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
95	<a href="#">c2kd0A_</a>	Alignment	not modelled	78.5	19	<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
96	<a href="#">d1wjua_</a>	Alignment	not modelled	78.4	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
97	<a href="#">d1v86a_</a>	Alignment	not modelled	77.8	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
98	<a href="#">c4eqxA_</a>	Alignment	not modelled	77.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a cc1-fha tandem
99	<a href="#">c3fm8A_</a>	Alignment	not modelled	77.0	23	<b>PDB header:</b> transport protein/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif13b; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
100	<a href="#">d1we7a_</a>	Alignment	not modelled	76.9	7	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
101	<a href="#">c5gjlA_</a>	Alignment	not modelled	76.8	15	<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
102	<a href="#">d1ogwa_</a>	Alignment	not modelled	76.6	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
103	<a href="#">c2eh0A_</a>	Alignment	not modelled	76.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1b; <b>PDBTitle:</b> solution structure of the fha domain from human kinesin-2 like protein kif1b
104	<a href="#">c4dbgA_</a>	Alignment	not modelled	76.4	14	<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
105	<a href="#">c2l7rA_</a>	Alignment	not modelled	75.9	8	<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
106	<a href="#">d1a5ra_</a>	Alignment	not modelled	75.5	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
107	<a href="#">c5z81A_</a>	Alignment	not modelled	75.4	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15; <b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
108	<a href="#">c2mlbA_</a>	Alignment	not modelled	75.3	14	<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
109	<a href="#">c5djoB_</a>	Alignment	not modelled	75.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein; <b>PDBTitle:</b> crystal structure of the cc1-fha tandem of kinesin-3 kif13a
110	<a href="#">c2dziA_</a>	Alignment	not modelled	74.6	9	<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)
111	<a href="#">d1dm9a_</a>	Alignment	not modelled	74.5	9	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
112	<a href="#">c1dm9A_</a>	Alignment	not modelled	74.5	9	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd
113	<a href="#">d1c06a_</a>	Alignment	not modelled	73.7	16	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
114	<a href="#">d1iyfa_</a>	Alignment	not modelled	73.3	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
115	<a href="#">d2uubd1</a>	Alignment	not modelled	72.3	20	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
116	<a href="#">c2n9pC_</a>	Alignment	not modelled	72.2	10	<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
117	<a href="#">d1wm3a_</a>	Alignment	not modelled	71.8	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
118	<a href="#">c1nekB_</a>	Alignment	not modelled	71.5	16	<b>PDB header:</b> oxidoreductase/electron transport protein; <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur protein; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
119	<a href="#">d1p9ka_</a>	Alignment	not modelled	70.5	11	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> YbcJ-like
120	<a href="#">d2zeqa1</a>	Alignment	not modelled	69.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related