


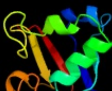












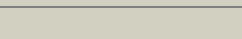







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1335_(-)_1503109_1503390
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	d84627e92508b4f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4n6eB_</a>	 Alignment		99.9	65	<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
2	<a href="#">c3dwmA_</a>	 Alignment		99.9	100	<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
3	<a href="#">c2l52A_</a>	 Alignment		99.9	28	<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
4	<a href="#">c2m19A_</a>	 Alignment		99.9	34	<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
5	<a href="#">d1wgka_</a>	 Alignment		99.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
6	<a href="#">d1xo3a_</a>	 Alignment		99.9	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
7	<a href="#">c1v8cA_</a>	 Alignment		99.9	31	<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
8	<a href="#">c2qjlA_</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
9	<a href="#">c2g1eA_</a>	 Alignment		99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
10	<a href="#">d1v8ca1</a>	 Alignment		99.9	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
11	<a href="#">c2k9xA_</a>	 Alignment		99.9	24	<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

12	<a href="#">c3po0A_</a>	Alignment		99.9	24	<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
13	<a href="#">d1vjka_</a>	Alignment		99.8	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
14	<a href="#">c6jbzD_</a>	Alignment		99.8	29	<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
15	<a href="#">c6jc0A_</a>	Alignment		99.8	24	<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
16	<a href="#">d1fm0d_</a>	Alignment		99.8	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
17	<a href="#">c5mpoA_</a>	Alignment		99.8	21	<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
18	<a href="#">c2qieB_</a>	Alignment		99.7	23	<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
19	<a href="#">c3rpfC_</a>	Alignment		99.7	24	<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
20	<a href="#">c4idiA_</a>	Alignment		99.2	14	<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
21	<a href="#">d1zud21</a>	Alignment	not modelled	98.3	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
22	<a href="#">c2ki0A_</a>	Alignment	not modelled	98.2	21	<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	27	<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="#">c4wwmB_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray crystal structure of sulfolobus solfataricus urm1
25	<a href="#">d2cu3a1</a>	Alignment	not modelled	97.6	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
26	<a href="#">d1tygb_</a>	Alignment	not modelled	97.3	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
27	<a href="#">d1ud7a_</a>	Alignment	not modelled	96.0	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
28	<a href="#">c1tygG_</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> yljbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex

29	<a href="#">d1rwsa_</a>	Alignment	not modelled	95.6	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
30	<a href="#">c1yx5B_</a>	Alignment	not modelled	95.5	19	<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
31	<a href="#">d1c3ta_</a>	Alignment	not modelled	95.4	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
32	<a href="#">d1v5oa_</a>	Alignment	not modelled	95.2	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
33	<a href="#">c2kmmA_</a>	Alignment	not modelled	95.0	30	<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)
34	<a href="#">d1wh3a_</a>	Alignment	not modelled	94.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
35	<a href="#">c2lrwA_</a>	Alignment	not modelled	94.4	15	<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
36	<a href="#">c1oqyA_</a>	Alignment	not modelled	92.9	13	<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
37	<a href="#">d2hj1a1</a>	Alignment	not modelled	92.6	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> HI0395-like
38	<a href="#">c2hj1A_</a>	Alignment	not modelled	92.6	17	<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
39	<a href="#">c1wwtA_</a>	Alignment	not modelled	92.4	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
40	<a href="#">c3hvbB_</a>	Alignment	not modelled	91.1	20	<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
41	<a href="#">c2ns5A_</a>	Alignment	not modelled	90.5	17	<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
42	<a href="#">d1tkeal</a>	Alignment	not modelled	89.8	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
43	<a href="#">c2l7rA_</a>	Alignment	not modelled	89.6	11	<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
44	<a href="#">d1ryja_</a>	Alignment	not modelled	89.4	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
45	<a href="#">c3q3fA_</a>	Alignment	not modelled	88.6	15	<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
46	<a href="#">d1bt0a_</a>	Alignment	not modelled	87.7	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
47	<a href="#">d1uela_</a>	Alignment	not modelled	87.2	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
48	<a href="#">c2kdiA_</a>	Alignment	not modelled	86.3	18	<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
49	<a href="#">d1oqya4</a>	Alignment	not modelled	85.3	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
50	<a href="#">d1kf6b2</a>	Alignment	not modelled	85.2	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
51	<a href="#">d1ndda_</a>	Alignment	not modelled	84.8	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
52	<a href="#">d1sifa_</a>	Alignment	not modelled	84.7	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
53	<a href="#">c2ekeC_</a>	Alignment	not modelled	83.9	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 <b>PDB header:</b> hydrolase

54	<a href="#">c5jp1B</a>	Alignment	not modelled	83.8	8	<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
55	<a href="#">c2ojrA</a>	Alignment	not modelled	82.4	18	<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
56	<a href="#">c2k25A</a>	Alignment	not modelled	82.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubb; <b>PDBTitle:</b> automated nmr structure of the ubb by fapsy
57	<a href="#">c2mqjA</a>	Alignment	not modelled	82.0	21	<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
58	<a href="#">d1ogwa</a>	Alignment	not modelled	81.6	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
59	<a href="#">c3goeA</a>	Alignment	not modelled	80.9	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
60	<a href="#">c2k8hA</a>	Alignment	not modelled	80.6	16	<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
61	<a href="#">c1qzeA</a>	Alignment	not modelled	80.2	10	<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
62	<a href="#">c2dziA</a>	Alignment	not modelled	80.1	13	<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)
63	<a href="#">d1nekb2</a>	Alignment	not modelled	80.1	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
64	<a href="#">c4k95G</a>	Alignment	not modelled	79.5	13	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase parkin; <b>PDBTitle:</b> crystal structure of parkin
65	<a href="#">d1we7a</a>	Alignment	not modelled	79.5	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
66	<a href="#">d1iyfa</a>	Alignment	not modelled	79.1	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
67	<a href="#">c6a42A</a>	Alignment	not modelled	78.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed dna polymerase homolog (r1),polyubiquitin-c; <b>PDBTitle:</b> r1en(5-223)-ubiquitin fusion
68	<a href="#">d1euvb</a>	Alignment	not modelled	78.5	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
69	<a href="#">d1wxqa2</a>	Alignment	not modelled	77.8	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
70	<a href="#">d1v2ya</a>	Alignment	not modelled	77.6	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
71	<a href="#">c4dbgA</a>	Alignment	not modelled	76.6	9	<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
72	<a href="#">d2faza1</a>	Alignment	not modelled	76.4	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
73	<a href="#">d1p1aa</a>	Alignment	not modelled	76.3	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
74	<a href="#">c2kd0A</a>	Alignment	not modelled	76.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> Irr 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
75	<a href="#">d1yqba1</a>	Alignment	not modelled	75.9	18	<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	75.4	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
77	<a href="#">d1c06a</a>	Alignment	not modelled	74.5	17	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
78	<a href="#">d1wx8a1</a>	Alignment	not modelled	74.0	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
79	<a href="#">d1wx7a1</a>	Alignment	not modelled	72.8	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
						<b>Fold:</b> beta-Grasp (ubiquitin-like)

80	<a href="#">d1wz0a1</a>	Alignment	not modelled	72.3	14	<b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
81	<a href="#">c2ekiA</a>	Alignment	not modelled	72.0	19	<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
82	<a href="#">d1v86a</a>	Alignment	not modelled	71.3	5	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
83	<a href="#">d1v5ta</a>	Alignment	not modelled	70.8	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
84	<a href="#">c5o5jD</a>	Alignment	not modelled	70.5	17	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> 30s ribosomal protein s4; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
85	<a href="#">c5xmjl</a>	Alignment	not modelled	69.8	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
86	<a href="#">d1wy8a1</a>	Alignment	not modelled	69.5	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
87	<a href="#">c4eqxA</a>	Alignment	not modelled	68.1	23	<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
88	<a href="#">d2g1la1</a>	Alignment	not modelled	67.6	23	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
89	<a href="#">c2n7dA</a>	Alignment	not modelled	67.5	21	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> protein ddi1 homolog 2; <b>PDBTitle:</b> solution structure of the ubl domain of human ddi2
90	<a href="#">c4ejqB</a>	Alignment	not modelled	67.5	18	<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="#">c3fm8A</a>	Alignment	not modelled	66.9	27	<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)
92	<a href="#">d2zeqa1</a>	Alignment	not modelled	66.2	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
93	<a href="#">c3ai5A</a>	Alignment	not modelled	65.9	15	<b>PDB header:</b> fluorescent protein, transcription <b>Chain:</b> A; <b>PDB Molecule:</b> yeast enhanced green fluorescent protein,ubiquitin; <b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
94	<a href="#">c2klcA</a>	Alignment	not modelled	64.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquilin-1; <b>PDBTitle:</b> nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
95	<a href="#">c2eh0A</a>	Alignment	not modelled	64.2	23	<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
96	<a href="#">c5djoB</a>	Alignment	not modelled	63.7	32	<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
97	<a href="#">c6gf2A</a>	Alignment	not modelled	63.4	14	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin d; <b>PDBTitle:</b> the structure of the ubiquitin-like modifier fat10 reveals a novel2 targeting mechanism for degradation by the 26s proteasome
98	<a href="#">d1wm3a</a>	Alignment	not modelled	63.4	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
99	<a href="#">d1j8ca</a>	Alignment	not modelled	62.4	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
100	<a href="#">c5xqmA</a>	Alignment	not modelled	62.2	11	<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
101	<a href="#">d1gxca</a>	Alignment	not modelled	62.1	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
102	<a href="#">c1gxca</a>	Alignment	not modelled	62.1	18	<b>PDB header:</b> phosphoprotein-binding domain <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
103	<a href="#">c2b76N</a>	Alignment	not modelled	61.8	10	<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
104	<a href="#">c4jonA</a>	Alignment	not modelled	61.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> centrosomal protein of 170 kda; <b>PDBTitle:</b> crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
105	<a href="#">d2uubd1</a>	Alignment	not modelled	60.9	26	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4

106	<a href="#">c5fwhA_</a>	Alignment	not modelled	60.5	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> essc; <b>PDBTitle:</b> n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
107	<a href="#">c4hwiB_</a>	Alignment	not modelled	60.2	15	<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
108	<a href="#">d1g3ga_</a>	Alignment	not modelled	60.0	21	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
109	<a href="#">d1a5ra_</a>	Alignment	not modelled	59.8	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
110	<a href="#">c5gjlA_</a>	Alignment	not modelled	58.7	17	<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
111	<a href="#">c2istA_</a>	Alignment	not modelled	57.7	13	<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
112	<a href="#">c1ttnA_</a>	Alignment	not modelled	57.3	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dendritic cell-derived ubiquitin-like protein; <b>PDBTitle:</b> solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
113	<a href="#">d1ttna1</a>	Alignment	not modelled	57.3	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
114	<a href="#">c2jxxA_</a>	Alignment	not modelled	57.1	16	<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
115	<a href="#">c3u7zA_</a>	Alignment	not modelled	56.4	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal binding protein rumgna_00854; <b>PDBTitle:</b> crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
116	<a href="#">d2piea1</a>	Alignment	not modelled	56.4	13	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
117	<a href="#">c1dm9A_</a>	Alignment	not modelled	56.3	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
118	<a href="#">d1dm9a_</a>	Alignment	not modelled	56.3	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
119	<a href="#">d1lgpa_</a>	Alignment	not modelled	56.3	15	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
120	<a href="#">c2kanA_</a>	Alignment	not modelled	55.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ar3433a; <b>PDBTitle:</b> solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a