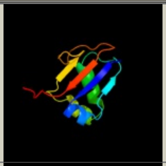
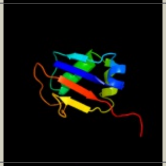
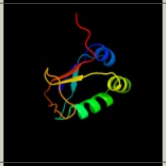
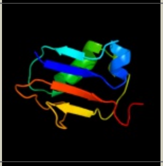
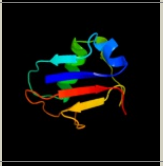
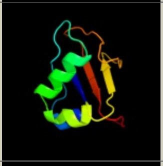
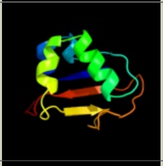
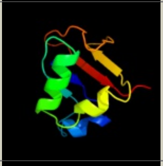
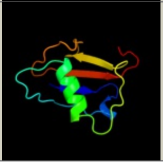
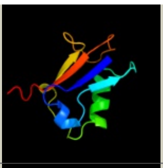
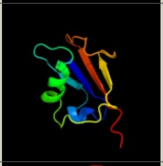
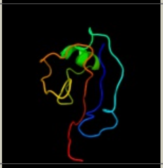
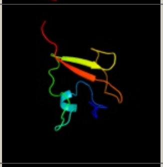
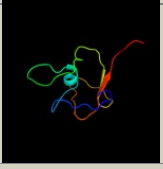
Email	l.a.kelley@imperial.ac.uk
Description	P30748
Date	Thu Jan 5 11:46:22 GMT 2012
Unique Job ID	80261a79cacc719f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fm0d_	Alignment		100.0	100	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
2	c3po0A_	Alignment		99.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
3	c2qieB_	Alignment		99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
4	c2g1eA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
5	c2l52A_	Alignment		99.9	27	**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
6	d1vjka_	Alignment		99.9	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
7	c1v8cA_	Alignment		99.9	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
8	d1v8ca1	Alignment		99.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
9	c3rpfC_	Alignment		99.8	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
10	c3dwmA_	Alignment		99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
11	c2qjlA_	Alignment		99.8	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1

12	d1xo3a_	Alignment		99.8	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
13	d1wgka_	Alignment		99.7	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
14	c2k9xA_	Alignment		99.7	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
15	d1zud21	Alignment		98.3	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
16	c2kl0A_	Alignment		98.2	30	**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
17	d1rwsa_	Alignment		98.2	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
18	c3cwiA_	Alignment		97.7	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
19	d2cu3a1	Alignment		97.3	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
20	d1tygb_	Alignment		96.9	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
21	d1tkea1	Alignment	not modelled	95.9	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
22	c3hvzB_	Alignment	not modelled	95.3	13	**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
23	d1ryja_	Alignment	not modelled	95.0	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
24	d1wxqa2	Alignment	not modelled	94.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
25	c2kmmA_	Alignment	not modelled	94.9	21	**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)
26	c1tygG_	Alignment	not modelled	94.9	20	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
27	d2hj1a1	Alignment	not modelled	93.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
28	c2hj1A_	Alignment	not modelled	93.4	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

29	d1ud7a_	Alignment	not modelled	91.9	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
30	d1c3ta_	Alignment	not modelled	91.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
31	c1wwtA_	Alignment	not modelled	89.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
32	c1yx5B_	Alignment	not modelled	89.6	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
33	c2ekiA_	Alignment	not modelled	89.0	19	**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
34	d1wh3a_	Alignment	not modelled	86.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
35	d1v5oa_	Alignment	not modelled	83.9	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
36	c1tkeA_	Alignment	not modelled	82.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
37	d1nyra2	Alignment	not modelled	80.6	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
38	c2k8hA_	Alignment	not modelled	78.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**small ubiquitin protein; **PDBTitle:** solution structure of sumo from trypanosoma brucei
39	d2g1la1	Alignment	not modelled	77.4	27	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
40	d1euvb_	Alignment	not modelled	77.2	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
41	c3fm8A_	Alignment	not modelled	75.4	32	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
42	c2k6pA_	Alignment	not modelled	74.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
43	c2eh0A_	Alignment	not modelled	74.1	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
44	c2jxxA_	Alignment	not modelled	70.1	21	**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
45	c2l7rA_	Alignment	not modelled	69.7	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
46	c1dm9A_	Alignment	not modelled	69.6	5	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
47	d1dm9a_	Alignment	not modelled	69.6	5	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
48	c3tixA_	Alignment	not modelled	69.2	18	**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
49	d2io3b1	Alignment	not modelled	67.0	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
50	d1wgga_	Alignment	not modelled	66.0	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
51	c3goeA_	Alignment	not modelled	63.7	16	**PDB header:**recombination, replication **Chain:** A: **PDB Molecule:**dna repair protein rad60; **PDBTitle:** molecular mimicry of sumo promotes dna repair
52	d1we7a_	Alignment	not modelled	63.1	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
53	d1v86a_	Alignment	not modelled	62.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
54	d1wlna1	Alignment	not modelled	60.6	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
						Fold:beta-Grasp (ubiquitin-like)

55	d1v5ta_	Alignment	not modelled	59.5	16	**Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
56	c1wxqA_	Alignment	not modelled	57.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
57	c3m62B_	Alignment	not modelled	56.9	16	**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
58	d1yqba1	Alignment	not modelled	55.5	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
59	d1vioa2	Alignment	not modelled	52.1	26	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
60	d2ff4a3	Alignment	not modelled	51.3	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
61	d1wm3a_	Alignment	not modelled	49.4	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
62	d1wjua_	Alignment	not modelled	49.4	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
63	d1gxca_	Alignment	not modelled	48.3	31	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
64	c1gxcA_	Alignment	not modelled	48.3	31	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
65	c2kdiA_	Alignment	not modelled	48.1	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin, vacuolar protein sorting-associated **PDBTitle:** solution structure of a ubiquitin/uim fusion protein
66	d2affa1	Alignment	not modelled	47.4	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
67	d1wz0a1	Alignment	not modelled	46.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
68	c2kd0A_	Alignment	not modelled	46.3	9	**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
69	d1c06a_	Alignment	not modelled	45.3	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
70	d1sifa_	Alignment	not modelled	44.1	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
71	d1p9ka_	Alignment	not modelled	43.7	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
72	d1oqya4	Alignment	not modelled	42.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
73	c2jqlA_	Alignment	not modelled	42.3	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
74	d2uubd1	Alignment	not modelled	41.7	32	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
75	d2uyzb1	Alignment	not modelled	40.6	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
76	c2k25A_	Alignment	not modelled	39.8	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ubb; **PDBTitle:** automated nmr structure of the ubb by fapsy
77	c3a4rB_	Alignment	not modelled	39.1	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** the crystal structure of sumo-like domain 2 in nip45
78	d2piea1	Alignment	not modelled	38.9	14	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
79	c2klcA_	Alignment	not modelled	38.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr solution structure of human ubiquitin-like domain of2 ubiquilin 1, northeast structural genomics consortium3 (nesg) target ht5a
80	d1lgpa_	Alignment	not modelled	38.1	22	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
						PDB header:ligase/protein binding

81	c2ekeC_	Alignment	not modelled	37.0	15	**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
82	c1r21A_	Alignment	not modelled	36.8	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
83	d1kf6b2	Alignment	not modelled	36.4	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
84	d1wiaa_	Alignment	not modelled	36.2	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
85	c3bbnD_	Alignment	not modelled	36.1	18	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
86	c2kklA_	Alignment	not modelled	35.8	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
87	c3m63B_	Alignment	not modelled	34.8	19	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**ubiquitin domain-containing protein dsk2; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of dsk2
88	c2ns5A_	Alignment	not modelled	34.8	15	**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
89	c1kskA_	Alignment	not modelled	34.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
90	c1nyqA_	Alignment	not modelled	34.4	22	**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
91	d2bwfa1	Alignment	not modelled	33.7	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
92	c3gqsB_	Alignment	not modelled	33.6	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
93	d1a5ra_	Alignment	not modelled	32.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
94	d1uela_	Alignment	not modelled	32.1	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
95	c3kt9A_	Alignment	not modelled	31.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
96	d1g3ga_	Alignment	not modelled	31.0	27	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
97	c3hx1B_	Alignment	not modelled	30.3	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
98	d1ndda_	Alignment	not modelled	29.0	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
99	c2ojrA_	Alignment	not modelled	28.8	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin; **PDBTitle:** structure of ubiquitin solved by sad using the lanthanide-2 binding tag
100	d1g6ga_	Alignment	not modelled	28.5	29	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
101	c3dh3C_	Alignment	not modelled	28.3	18	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
102	c3u7zA_	Alignment	not modelled	27.2	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative metal binding protein rumgna_00854; **PDBTitle:** crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
103	d2gy9d1	Alignment	not modelled	27.0	27	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
104	c2kdbA_	Alignment	not modelled	26.3	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**homocysteine-responsive endoplasmic reticulum- **PDBTitle:** solution structure of human ubiquitin-like domain of2 herpud2_9_85, northeast structural genomics consortium3 (nesg) target ht53a

105	d1wx8a1	Alignment	not modelled	26.3	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
106	c1qf6A_	Alignment	not modelled	26.3	12	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
107	d1j8ca_	Alignment	not modelled	26.1	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
108	d1bt0a_	Alignment	not modelled	26.0	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
109	d1yjma1	Alignment	not modelled	25.4	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
110	d1p1aa_	Alignment	not modelled	25.4	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
111	c3poaA_	Alignment	not modelled	25.1	33	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
112	d1wx7a1	Alignment	not modelled	24.0	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
113	d2bs2b2	Alignment	not modelled	23.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
114	d1wgda_	Alignment	not modelled	23.8	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
115	d1wxma1	Alignment	not modelled	23.6	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
116	c2dzmA_	Alignment	not modelled	22.7	17	**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	d1wf9a1	Alignment	not modelled	22.5	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
118	c1yj5C_	Alignment	not modelled	22.2	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
119	c1qzeA_	Alignment	not modelled	22.1	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
120	d2zeqa1	Alignment	not modelled	22.1	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related