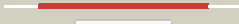
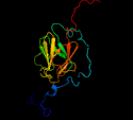


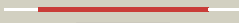
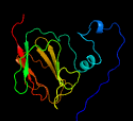





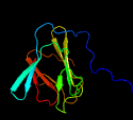










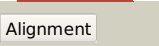





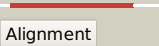
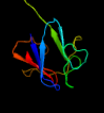
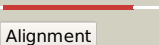

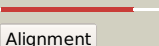
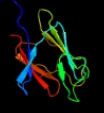
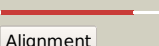

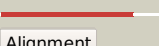

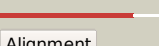

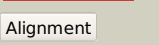
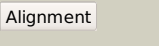

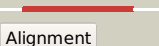

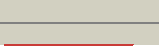
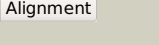
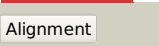


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1827_(cfp17)_2072603_2073091
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	68ddfca26d20ab6e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kfuA_	 Alignment		100.0	100	PDB header: protein binding Chain: A: PDB Molecule: rv1827 pthr 22; PDBTitle: pknb-phosphorylated rv1827
2	c2kkIA_	 Alignment		100.0	97	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).
3	c2n84A_	 Alignment		99.9	17	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the fha domain of tbpar42
4	c3poaA_	 Alignment		99.9	31	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
5	c3vpyA_	 Alignment		99.9	23	PDB header: protein binding Chain: A: PDB Molecule: fha domain-containing protein ddl; PDBTitle: crystal structure of arabidopsis ddl fha domain
6	c4h87A_	 Alignment		99.9	21	PDB header: peptide binding protein Chain: A: PDB Molecule: kanadaplin; PDBTitle: crystal structure of a fha domain of kanadaplin (slc4a1ap) from homo2 sapiens at 1.55 a resolution
7	d1mzka_	 Alignment		99.9	34	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
8	c4jonA_	 Alignment		99.9	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
9	c4a0eB_	 Alignment		99.9	20	PDB header: transport protein Chain: B: PDB Molecule: type iii secretion protein; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd
10	c3ounA_	 Alignment		99.9	31	PDB header: protein binding/transferase Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: crystal structure of the fhaa fha domain complexed with the2 intracellular domain of rv3910
11	d1luhta_	 Alignment		99.9	26	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain

12	c6cahA	 Alignment		99.9	34	PDB header: protein binding Chain: A: PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747
13	c3uotB	 Alignment		99.9	26	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
14	c3gqsB	 Alignment		99.9	31	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
15	c3hx1B	 Alignment		99.9	23	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
16	c6ccdA	 Alignment		99.8	28	PDB header: protein binding Chain: A: PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: the crystal structure of mycobacterium tuberculosis rv1747 fha-1
17	d2ff4a3	 Alignment		99.8	29	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
18	d2affa1	 Alignment		99.8	26	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
19	c1r21A	 Alignment		99.8	26	PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
20	c2jpeA	 Alignment		99.8	19	PDB header: transcription Chain: A: PDB Molecule: nuclear inhibitor of protein phosphatase 1; PDBTitle: fha domain of nipp1
21	c2jqIA	 Alignment	not modelled	99.8	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
22	c5a8iA	 Alignment	not modelled	99.8	27	PDB header: transcription Chain: A: PDB Molecule: arna; PDBTitle: crystal structure of the fha domain of arna from sulfolobus2 acidocaldarius
23	c3elsA	 Alignment	not modelled	99.8	22	PDB header: splicing Chain: A: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: crystal structure of yeast pm1p, residues 51-204
24	c2jkdB	 Alignment	not modelled	99.8	27	PDB header: gene regulation Chain: B: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: structure of the yeast pm1 splicing factor and its2 integration into the res complex
25	c5yyxA	 Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: meiosis-specific serine/threonine-protein kinase mek1; PDBTitle: crystal structure of the mek1 fha domain
26	c6ar2B	 Alignment	not modelled	99.8	26	PDB header: membrane protein Chain: B: PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: structure of human slmap fha domain in complex with pmst2
27	d2piea1	 Alignment	not modelled	99.8	24	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
28	c3fm8A	 Alignment	not modelled	99.8	19	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)
29	c2ff4B_	Alignment	not modelled	99.8	29 PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
30	d1g6ga_	Alignment	not modelled	99.8	25 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
31	d1g3ga_	Alignment	not modelled	99.7	27 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
32	d1dmza_	Alignment	not modelled	99.7	19 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
33	c1gxca_	Alignment	not modelled	99.7	22 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
34	d1gxca_	Alignment	not modelled	99.7	22 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
35	c5t2sa_	Alignment	not modelled	99.7	27 PDB header: cell cycle Chain: A: PDB Molecule: ddk kinase regulatory subunit dbf4,serine/threonine-protein PDBTitle: structure of the fha1 domain of rad53 bound simultaneously to the brct2 domain of dbf4 and a phosphopeptide.
36	d1wina1	Alignment	not modelled	99.7	19 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
37	c5e50A_	Alignment	not modelled	99.7	23 PDB header: lyase Chain: A: PDB Molecule: aprataxin and pnk-like factor; PDBTitle: aplf/xrcc4 complex
38	c6a8wA_	Alignment	not modelled	99.7	25 PDB header: protein binding Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 64; PDBTitle: crystal structure of the fha domain of far9
39	d1lgpa_	Alignment	not modelled	99.7	22 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
40	c3kt9A_	Alignment	not modelled	99.7	18 PDB header: hydrolase Chain: A: PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
41	c5djoB_	Alignment	not modelled	99.7	18 PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a
42	d1yjma1	Alignment	not modelled	99.7	18 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
43	c2eh0A_	Alignment	not modelled	99.7	24 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	c4eqxA_	Alignment	not modelled	99.7	26 PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem
45	c1vj5C_	Alignment	not modelled	99.7	19 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
46	d1qu5a_	Alignment	not modelled	99.7	17 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
47	d2g1la1	Alignment	not modelled	99.7	25 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
48	c5z58X_	Alignment	not modelled	99.6	28 PDB header: splicing Chain: X: PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
49	d1ujxa_	Alignment	not modelled	99.6	19 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
50	d2brfa1	Alignment	not modelled	99.6	20 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
51	c4ejqB_	Alignment	not modelled	99.6	26 PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
52	c3i0mA_	Alignment	not modelled	99.4	27 PDB header: cell cycle Chain: A: PDB Molecule: dna repair and telomere maintenance protein nbs1; PDBTitle: structure of the s. pombe nbs1 fha/brct-repeat domain
53	c5xzvB_	Alignment	not modelled	99.2	27 PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase rad53; PDBTitle: crystal structure of rad53 1-466 in complex with amp-pnp
54	c3i6uA_	Alignment	not modelled	99.0	20 PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: structure and activation mechanism of the chk2 dna-damage checkpoint2 kinase PDB header: transferase

55	c3i6wB_	Alignment	not modelled	98.7	24	Chain: B: PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: structure and activation mechanism of the chk2 dna-damage checkpoint2 kinase
56	c4zgiA_	Alignment	not modelled	97.8	15	PDB header: signaling protein Chain: A: PDB Molecule: traf-interacting protein with fha domain-containing protein PDBTitle: structure of truncated human tifa
57	c5fwhA_	Alignment	not modelled	97.7	16	PDB header: structural protein Chain: A: PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
58	c3uv0B_	Alignment	not modelled	95.5	25	PDB header: protein binding Chain: B: PDB Molecule: mutator 2, isoform b; PDBTitle: crystal structure of the drosophila mu2 fha domain
59	d1dm9a_	Alignment	not modelled	81.0	9	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
60	c1dm9A_	Alignment	not modelled	81.0	9	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
61	c3hvvB_	Alignment	not modelled	73.3	18	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
62	c5z81A_	Alignment	not modelled	72.9	14	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
63	d1xo3a_	Alignment	not modelled	72.2	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
64	c2qjIA_	Alignment	not modelled	70.0	24	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
65	d1wxqa2	Alignment	not modelled	69.2	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
66	c3j1wU_	Alignment	not modelled	67.9	13	PDB header: cell invasion Chain: U: PDB Molecule: protein prgh; PDBTitle: a refined model of the prototypical salmonella typhimurium t3ss basal2 body reveals the molecular basis for its assembly
67	d1wgka_	Alignment	not modelled	66.3	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
68	d1c06a_	Alignment	not modelled	66.2	19	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
69	c2kmmA_	Alignment	not modelled	66.1	45	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)
70	d2uubd1	Alignment	not modelled	65.9	38	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
71	c2k9xA_	Alignment	not modelled	64.5	43	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
72	c3dwmA_	Alignment	not modelled	63.8	37	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
73	c2g1eA_	Alignment	not modelled	62.0	11	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
74	d1vioa2	Alignment	not modelled	61.3	25	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
75	c4n6eB_	Alignment	not modelled	61.3	43	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
76	c5mpoA_	Alignment	not modelled	61.1	43	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
77	c5o5jD_	Alignment	not modelled	60.5	29	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
78	d1v8ca1	Alignment	not modelled	60.0	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
79	d1vjka_	Alignment	not modelled	58.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
80	d1fm0d_	Alignment	not modelled	58.1	38	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD

81	c3bbnD	Alignment	not modelled	57.7	29	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
82	c2m19A	Alignment	not modelled	57.5	29	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
83	d1p9ka	Alignment	not modelled	57.2	10	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
84	d1tkea1	Alignment	not modelled	56.3	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
85	d2gy9d1	Alignment	not modelled	55.8	33	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
86	c3po0A	Alignment	not modelled	55.7	21	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
87	d1udxa3	Alignment	not modelled	55.5	31	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
88	c1v8cA	Alignment	not modelled	55.5	15	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
89	d1h3fa2	Alignment	not modelled	55.4	24	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
90	c4xmmE	Alignment	not modelled	55.0	20	PDB header: transport protein/immune system Chain: E: PDB Molecule: nucleoporin nup120; PDBTitle: structure of the yeast coat nucleoporin complex, space group c2
91	c3egbA	Alignment	not modelled	53.0	17	PDB header: protein binding Chain: A: PDB Molecule: protein pellino homolog 2; PDBTitle: structure of pellino2 fha domain at 3.3 angstroms resolution.
92	c2qieB	Alignment	not modelled	51.0	33	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
93	c6jzbD	Alignment	not modelled	50.6	29	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
94	c2k6pA	Alignment	not modelled	50.6	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
95	c3u7zA	Alignment	not modelled	50.3	25	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
96	c2l52A	Alignment	not modelled	47.5	24	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
97	c6jc0A	Alignment	not modelled	46.7	14	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
98	c3hxrA	Alignment	not modelled	43.3	20	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin nup120; PDBTitle: nucleoporin nup120 from s.cerevisiae (aa 1-757)
99	d1jh3a	Alignment	not modelled	42.6	27	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
100	d2cu3a1	Alignment	not modelled	42.4	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
101	c3rpfC	Alignment	not modelled	41.8	24	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
102	d1ryja	Alignment	not modelled	40.5	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
103	c2kc1A	Alignment	not modelled	37.2	21	PDB header: structural protein Chain: A: PDB Molecule: mkiaa1027 protein; PDBTitle: nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
104	d1zud21	Alignment	not modelled	36.4	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
105	c2ki0A	Alignment	not modelled	35.6	29	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
						PDB header: lyase

106	c1kskA	Alignment	not modelled	35.4	25	Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
107	c2ekiA	Alignment	not modelled	34.8	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
108	c4oudA	Alignment	not modelled	34.6	21	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
109	d1tygb	Alignment	not modelled	33.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/This Family: This
110	c5lo7B	Alignment	not modelled	33.0	34	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein myfa,fimbrial protein myfa; PDBTitle: crystal structure of self-complemented myfa, the major subunit of myf2 fimbriae from yersinia enterocolitica
111	c3cwiA	Alignment	not modelled	32.1	24	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
112	c3h7nD	Alignment	not modelled	31.7	20	PDB header: structural protein Chain: D: PDB Molecule: nucleoporin nup120; PDBTitle: structure of nup120
113	c3dh3C	Alignment	not modelled	31.5	19	PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide rna2 substrate
114	d1nyra2	Alignment	not modelled	29.8	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
115	c1y96D	Alignment	not modelled	25.9	21	PDB header: rna binding protein Chain: D: PDB Molecule: gem-associated protein 7; PDBTitle: crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
116	c4mtnA	Alignment	not modelled	25.8	7	PDB header: transcription regulator Chain: A: PDB Molecule: transcription termination factor nusa; PDBTitle: crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776
117	c2dgaA	Alignment	not modelled	25.0	12	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna-binding protein 19; PDBTitle: solution structure of the second rna recognition motif in2 rna-binding protein 19
118	c3mmIE	Alignment	not modelled	24.8	17	PDB header: hydrolase Chain: E: PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
119	c1tygG	Alignment	not modelled	24.5	24	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
120	d1a62a2	Alignment	not modelled	23.7	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like