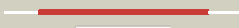


















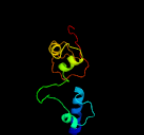




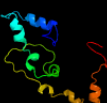








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3458c_(rpsD)_3878838_3879443
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	d7e8a4625847b1ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jD_	 Alignment		100.0	89	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	d2uubd1	 Alignment		100.0	47	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
3	d2gy9d1	 Alignment		100.0	48	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
4	c3bbnD_	 Alignment		100.0	36	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.
5	d1c06a_	 Alignment		100.0	53	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
6	c3j20D_	 Alignment		99.9	37	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
7	c5wxmA_	 Alignment		99.8	23	PDB header: ribosomal protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein imp3; PDBTitle: crystal structure of the imp3 and mpp10 complex
8	c2xzmD_	 Alignment		99.8	32	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
9	c1s1hD_	 Alignment		99.7	25	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s9-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
10	c5jpbq_	 Alignment		99.7	19	PDB header: ribosome Chain: B: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
11	c5xyij_	 Alignment		99.7	21	PDB header: ribosome Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome

12	c6nd4Z_	Alignment		99.7	31	PDB header: ribosome Chain: Z: PDB Molecule: imp3; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
13	c3zey6_	Alignment		99.7	26	PDB header: ribosome Chain: 6: PDB Molecule: 40s ribosomal protein s9, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
14	c3izbC_	Alignment		99.6	28	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein rps9 (s4p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	c3iz6C_	Alignment		99.5	32	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s9 (s4p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
16	c2cqjA_	Alignment		99.5	29	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
17	c5z81A_	Alignment		99.3	33	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
18	c1dm9A_	Alignment		99.3	31	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
19	d1dm9a_	Alignment		99.3	31	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
20	d1p9ka_	Alignment		99.3	15	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
21	d1vioa2	Alignment	not modelled	99.2	29	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
22	c2k6pA_	Alignment	not modelled	98.9	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
23	c3hp7A_	Alignment	not modelled	98.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
24	c1kskA_	Alignment	not modelled	98.8	19	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
25	c3dh3C_	Alignment	not modelled	98.7	27	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
26	c1vioA_	Alignment	not modelled	98.7	29	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylylate synthase
27	c2istA_	Alignment	not modelled	98.5	20	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
28	c4lgtA_	Alignment	not modelled	98.4	21	PDB header: isomerase/rna Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase b; PDBTitle: crystal structure of the catalytic domain of rlub in

						complex with a2 21-nucleotide rna substrate
29	d1h3fa2	Alignment	not modelled	97.8	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
30	d1jh3a_	Alignment	not modelled	97.7	20	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
31	c1h3eA_	Alignment	not modelled	97.7	18	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
32	c4oudA_	Alignment	not modelled	97.6	22	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
33	c2janD_	Alignment	not modelled	97.5	19	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
34	c6otjA_	Alignment	not modelled	97.3	13	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
35	c3j20E_	Alignment	not modelled	96.8	31	PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
36	c5xyiE_	Alignment	not modelled	96.7	21	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
37	c3kbgA_	Alignment	not modelled	96.5	21	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: crystal structure of the 30s ribosomal protein s4e from thermoplasma2 acidophilum. northeast structural genomics consortium target tar28.
38	c5xxuE_	Alignment	not modelled	96.5	19	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome
39	c3u5cE_	Alignment	not modelled	96.5	19	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
40	c3zey1_	Alignment	not modelled	96.3	21	PDB header: ribosome Chain: 1: PDB Molecule: 40s ribosomal protein s4, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
41	c3iz6D_	Alignment	not modelled	96.3	21	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	c2xzmW_	Alignment	not modelled	96.0	18	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
43	c3izbD_	Alignment	not modelled	95.7	19	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein rps4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
44	d1kska3	Alignment	not modelled	95.3	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
45	c6jzbD_	Alignment	not modelled	91.3	28	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
46	c6jc0A_	Alignment	not modelled	87.9	24	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
47	c4eqxA_	Alignment	not modelled	86.7	19	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem
48	c4eqjB_	Alignment	not modelled	82.9	19	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
49	d2g1la1	Alignment	not modelled	82.5	19	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
50	c5fwhA_	Alignment	not modelled	82.4	15	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
51	c5djoB_	Alignment	not modelled	81.1	19	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a
52	c2eh0A_	Alignment	not modelled	80.9	21	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
53	c4n6eB_	Alignment	not modelled	79.9	22	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso

						complex
54	c3rpfC	Alignment	not modelled	75.5	13	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
55	c2jqlA	Alignment	not modelled	74.5	17	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
56	c5mpoA	Alignment	not modelled	73.7	18	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
57	d1fm0d	Alignment	not modelled	73.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
58	d1xo3a	Alignment	not modelled	72.4	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
59	c3dwmA	Alignment	not modelled	72.3	22	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
60	c3fm8A	Alignment	not modelled	70.7	23	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)
61	d1zud21	Alignment	not modelled	69.7	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
62	d1vjka	Alignment	not modelled	67.3	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
63	c3po0A	Alignment	not modelled	67.0	14	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
64	c3hvvB	Alignment	not modelled	66.7	36	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
65	d2hzab1	Alignment	not modelled	66.3	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
66	c6a8wA	Alignment	not modelled	65.2	30	PDB header: protein binding Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 64; PDBTitle: crystal structure of the fha domain of far9
67	c2qjlA	Alignment	not modelled	65.2	17	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
68	c1v8cA	Alignment	not modelled	64.7	19	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
69	d1v8ca1	Alignment	not modelled	64.1	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
70	c2kmmA	Alignment	not modelled	63.4	38	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)
71	d2hzaa1	Alignment	not modelled	61.4	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
72	c3poaA	Alignment	not modelled	61.4	19	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
73	c4a0eB	Alignment	not modelled	60.4	14	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
74	d2bj7a1	Alignment	not modelled	59.5	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
75	c2g1eA	Alignment	not modelled	57.4	22	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
76	d1gxca	Alignment	not modelled	55.4	15	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
77	c1gxCA	Alignment	not modelled	55.4	15	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
78	c6cahA	Alignment	not modelled	54.7	33	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
79	d1g3ga_	Alignment	not modelled	54.5	35	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
80	c2kt1A_	Alignment	not modelled	54.1	18	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mttyrrs of a. nidulans
81	c3hx1B_	Alignment	not modelled	54.0	19	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
82	c2l52A_	Alignment	not modelled	54.0	13	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
83	c4jonA_	Alignment	not modelled	54.0	17	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)
84	d1wgka_	Alignment	not modelled	53.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
85	c1r21A_	Alignment	not modelled	53.4	27	PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
86	c2zxeA_	Alignment	not modelled	53.1	19	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
87	c3ixzA_	Alignment	not modelled	53.0	12	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
88	d2piea1	Alignment	not modelled	52.8	19	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
89	d1g6ga_	Alignment	not modelled	52.5	30	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
90	c3gqsB_	Alignment	not modelled	52.4	19	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
91	c2k9xA_	Alignment	not modelled	52.2	30	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
92	d2ff4a3	Alignment	not modelled	52.0	12	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
93	c3j08A_	Alignment	not modelled	51.7	31	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
94	c2m19A_	Alignment	not modelled	51.5	26	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
95	c3ounA_	Alignment	not modelled	50.5	20	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
96	c2qieB_	Alignment	not modelled	50.4	27	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
97	d2affa1	Alignment	not modelled	50.1	23	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
98	c6ccdA_	Alignment	not modelled	49.5	19	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
99	d1yjma1	Alignment	not modelled	49.5	18	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
100	d2cu3a1	Alignment	not modelled	49.4	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
101	c3cwiA_	Alignment	not modelled	48.7	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
102	c3kt9A_	Alignment	not modelled	48.6	4	PDB header: hydrolase Chain: A: PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
103	c2n84A_	Alignment	not modelled	48.5	11	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the fha domain of tbpar42
						Fold: beta-Grasp (ubiquitin-like)

104	d1wxqa2	Alignment	not modelled	47.8	23	Superfamily: TGS-like Family: G domain-linked domain
105	c2hc8A	Alignment	not modelled	47.3	35	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
106	c2kkIA	Alignment	not modelled	47.1	28	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).
107	d1wlna1	Alignment	not modelled	46.9	8	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
108	d1tkea1	Alignment	not modelled	46.7	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
109	c6ar2B	Alignment	not modelled	46.6	22	PDB header: membrane protein Chain: B: PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: structure of human slmap fha domain in complex with pmst2
110	c3elsA	Alignment	not modelled	46.5	15	PDB header: splicing Chain: A: PDB Molecule: pre-mrna leakage protein 1; PDBTitle: crystal structure of yeast pml1p, residues 51-204
111	c5yyxA	Alignment	not modelled	46.4	17	PDB header: transferase Chain: A: PDB Molecule: meiosis-specific serine/threonine-protein kinase mek1; PDBTitle: crystal structure of the mek1 fha domain
112	c1vj5C	Alignment	not modelled	45.6	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
113	c4umwA	Alignment	not modelled	45.4	17	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
114	c3j09A	Alignment	not modelled	44.9	17	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
115	c1mhsA	Alignment	not modelled	44.4	19	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
116	c1q5vB	Alignment	not modelled	44.1	35	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
117	d1i6za	Alignment	not modelled	43.3	25	Fold: Spectrin repeat-like Superfamily: BAG domain Family: BAG domain
118	d1lgpa	Alignment	not modelled	42.2	15	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
119	c4h87A	Alignment	not modelled	41.8	16	PDB header: peptide binding protein Chain: A: PDB Molecule: kanadapтин; PDBTitle: crystal structure of a fha domain of kanadapтин (slc4a1ap) from homo2 sapiens at 1.55 a resolution
120	d1xnea	Alignment	not modelled	41.7	12	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain