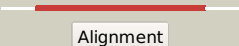
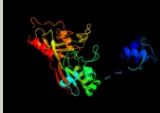


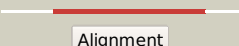





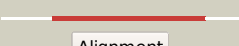














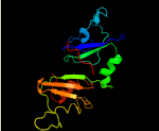




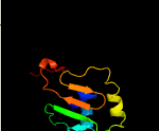


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1540_(-)_1742851_1743777
Date	Fri Aug 2 13:30:13 BST 2019
Unique Job ID	e99c84e4837ba2ef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2istA_	 Alignment		100.0	35	PDB header: isomerase Chain: A; PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
2	c1qyuA_	 Alignment		100.0	38	PDB header: lyase Chain: A; PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
3	d1v9fa_	 Alignment		100.0	38	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
4	c1v9fA_	 Alignment		100.0	38	PDB header: lyase Chain: A; PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
5	d1v9ka_	 Alignment		100.0	33	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
6	c2i82D_	 Alignment		100.0	32	PDB header: lyase/rna Chain: D; PDB Molecule: ribosomal large subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
7	c5ubaA_	 Alignment		100.0	28	PDB header: rna binding protein Chain: A; PDB Molecule: rna pseudouridylate synthase domain-containing protein 4; PDBTitle: human rna pseudouridylate synthase domain containing 4
8	c5vbbA_	 Alignment		100.0	37	PDB header: rna binding protein Chain: A; PDB Molecule: rna pseudouridylate synthase domain-containing protein 1; PDBTitle: human rna pseudouridylate synthase domain containing 1
9	c1kskA_	 Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
10	c1vioA_	 Alignment		100.0	20	PDB header: lyase Chain: A; PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylate synthase
11	c3dh3C_	 Alignment		100.0	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 nucleotide rna2 substrate

12	c4lgtA	Alignment		100.0	22	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
13	c2omIA	Alignment		100.0	16	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
14	c2olwB	Alignment		100.0	17	PDB header: isomerase Chain: B: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
15	d1vioa1	Alignment		100.0	19	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
16	d1kska4	Alignment		100.0	19	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
17	c2gmIA	Alignment		100.0	13	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of catalytic domain of e.coli rluf
18	c2k6pA	Alignment		99.5	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
19	c5z81A	Alignment		99.1	24	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
20	c3bbnD	Alignment		99.0	14	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.
21	c1dm9A	Alignment	not modelled	99.0	22	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
22	d1dm9a	Alignment	not modelled	99.0	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
23	d1vioa2	Alignment	not modelled	98.8	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
24	d1c06a	Alignment	not modelled	98.4	19	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
25	d2uubd1	Alignment	not modelled	98.4	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
26	d1p9ka	Alignment	not modelled	98.3	16	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
27	c5o5jD	Alignment	not modelled	98.3	27	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
28	d2gy9d1	Alignment	not modelled	98.0	24	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
29	c2cqiA	Alignment	not modelled	97.9	19	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
30	d1k8wa5	Alignment	not modelled	97.8	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
31	d2apoa2	Alignment	not modelled	97.7	24	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
32	d2ey4a2	Alignment	not modelled	97.7	25	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
33	d1r3ea2	Alignment	not modelled	97.5	20	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
34	c2ey4A	Alignment	not modelled	97.5	30	PDB header: isomerase/biosynthetic protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of a cbf5-nop10-gar1 complex
35	d1sgva2	Alignment	not modelled	97.5	32	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
36	c3uaiA	Alignment	not modelled	97.5	19	PDB header: isomerase/chaperone Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
37	c2apoA	Alignment	not modelled	97.5	23	PDB header: isomerase/rna binding protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of the methanococcus jannaschii cbf52 nop10 complex
38	c3hp7A	Alignment	not modelled	97.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
39	c3j20D	Alignment	not modelled	97.3	17	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)
40	c1k8wA	Alignment	not modelled	97.2	20	PDB header: lyase/rna Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
41	c6nd4Z	Alignment	not modelled	97.2	14	PDB header: ribosome Chain: Z: PDB Molecule: imp3; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
42	d1kska3	Alignment	not modelled	97.1	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
43	c1sgvA	Alignment	not modelled	97.0	30	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: structure of trna psi55 pseudouridine synthase (trub)
44	c5xyij	Alignment	not modelled	96.8	13	PDB header: ribosome Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
45	c5jpbq	Alignment	not modelled	96.6	18	PDB header: ribosome Chain: B: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
46	c1s1hD	Alignment	not modelled	96.3	13	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.
47	d1h3fa2	Alignment	not modelled	96.2	12	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
48	c2xzmD	Alignment	not modelled	96.1	14	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
49	c3zey6	Alignment	not modelled	96.0	13	PDB header: ribosome Chain: 6: PDB Molecule: 40s ribosomal protein s9, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
50	c1ze2B	Alignment	not modelled	95.9	21	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
51	c5wxmA	Alignment	not modelled	95.9	15	PDB header: ribosomal protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein imp3; PDBTitle: crystal structure of the imp3 and mpp10 complex
52	d1jh3a	Alignment	not modelled	95.0	19	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
53	c3j20E	Alignment	not modelled	94.9	14	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)
54	c3zey1	Alignment	not modelled	94.0	18	PDB header: ribosome Chain: 1: PDB Molecule: 40s ribosomal protein s4, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

55	c5xxuE_	Alignment	not modelled	93.8	7	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome
56	c5xyiE_	Alignment	not modelled	93.5	15	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
57	c1h3eA_	Alignment	not modelled	93.3	13	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
58	c2xzmW_	Alignment	not modelled	92.9	15	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
59	c4oudA_	Alignment	not modelled	92.4	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
60	c3iz6D_	Alignment	not modelled	91.6	13	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
61	c3u5cE_	Alignment	not modelled	91.3	14	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
62	c2janD_	Alignment	not modelled	91.2	23	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
63	c3kbgA_	Alignment	not modelled	90.8	17	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.
64	c6otjA_	Alignment	not modelled	90.4	26	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
65	c3izbD_	Alignment	not modelled	89.2	15	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
66	d1fm0d_	Alignment	not modelled	80.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
67	c6jc0A_	Alignment	not modelled	77.8	19	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
68	c6jzbD_	Alignment	not modelled	72.7	17	PDB header: transferase Chain: D: PDB Molecule: moad/thiS family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
69	c5fwhA_	Alignment	not modelled	72.6	27	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
70	c4egxA_	Alignment	not modelled	72.2	20	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem
71	c3po0A_	Alignment	not modelled	71.5	23	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
72	d2g1la1	Alignment	not modelled	71.2	23	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
73	c4ejqB_	Alignment	not modelled	70.4	23	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
74	c5djoB_	Alignment	not modelled	68.6	16	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a
75	c2g1eA_	Alignment	not modelled	66.3	13	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
76	d1wgka_	Alignment	not modelled	64.6	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
77	c3iz6C_	Alignment	not modelled	62.4	14	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
78	c3fm8A_	Alignment	not modelled	60.5	16	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)
79	c1v8cA_	Alignment	not modelled	59.9	31	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
						PDB header: transferase

80	c2qieB_	Alignment	not modelled	59.8	23	Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor 2 z
81	c3izbC_	Alignment	not modelled	58.9	15	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
82	c4n6eB_	Alignment	not modelled	58.1	21	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
83	c2eh0A_	Alignment	not modelled	57.6	20	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
84	d1vjka_	Alignment	not modelled	57.2	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
85	c2qjlA_	Alignment	not modelled	50.0	14	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
86	d1wlna1	Alignment	not modelled	47.9	24	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
87	c2kmmA_	Alignment	not modelled	47.9	20	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)
88	c4a0eB_	Alignment	not modelled	45.1	24	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
89	d1xo3a_	Alignment	not modelled	42.9	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
90	c3hvvB_	Alignment	not modelled	42.9	14	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
91	c3dwmA_	Alignment	not modelled	42.9	8	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
92	d1rwsa_	Alignment	not modelled	42.2	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
93	d1v8ca1	Alignment	not modelled	42.0	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
94	d2affa1	Alignment	not modelled	41.0	20	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
95	c5mpoA_	Alignment	not modelled	40.1	12	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
96	d2ff4a3	Alignment	not modelled	39.8	12	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
97	c3rpfC_	Alignment	not modelled	38.4	18	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
98	d1wxqa2	Alignment	not modelled	33.9	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
99	c4j2nB_	Alignment	not modelled	30.9	24	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
100	c1r21A_	Alignment	not modelled	29.5	20	PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
101	c3u0aA_	Alignment	not modelled	29.3	23	PDB header: transferase Chain: A: PDB Molecule: selenide, water dikinase; PDBTitle: the crystal structure of selenophosphate synthetase from e. coli
102	c2m19A_	Alignment	not modelled	28.3	27	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
103	c4j2nA_	Alignment	not modelled	28.2	24	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
104	c2zodB_	Alignment	not modelled	24.1	16	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of selenophosphate synthetase from aquifex aeolicus
						PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase zranb1;

105	c3zrhA_	Alignment	not modelled	24.0	40	PDBTitle: crystal structure of the lys29, lys33-linkage-specific trabd otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
106	d1tkea1	Alignment	not modelled	23.8	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
107	c2l52A_	Alignment	not modelled	23.1	15	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
108	c3gqsB_	Alignment	not modelled	21.9	12	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