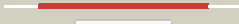



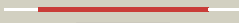

















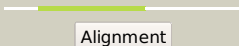
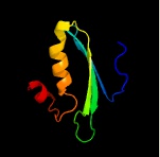
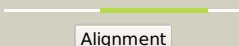
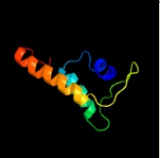
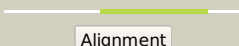

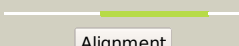
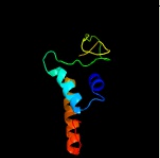
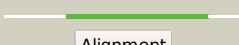

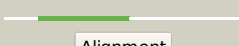
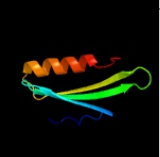



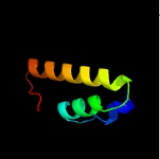

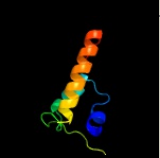
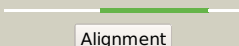

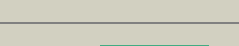
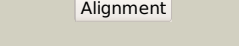
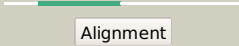
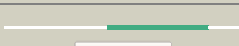
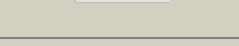
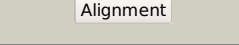


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1465_(-)_1652774_1653262
Date	Fri Aug 2 13:30:04 BST 2019
Unique Job ID	1fe4e1ed9065cc64

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uftA_	 Alignment		100.0	28	PDB header: metal binding protein Chain: A: PDB Molecule: nitrogen-fixing nifu-like, n-terminal; PDBTitle: crystal structure of a nitrogen-fixing nifu-like protein (n-terminal)2 from brucella abortus
2	d1xjsa_	 Alignment		100.0	37	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
3	d1su0b_	 Alignment		100.0	40	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
4	c2qq4A_	 Alignment		100.0	42	PDB header: metal binding protein Chain: A: PDB Molecule: iron-sulfur cluster biosynthesis protein iscu; PDBTitle: crystal structure of iron-sulfur cluster biosynthesis protein iscu2 (ttha1736) from thermus thermophilus hb8
5	c2z7eB_	 Alignment		100.0	25	PDB header: biosynthetic protein Chain: B: PDB Molecule: nifu-like protein; PDBTitle: crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
6	c4eb5C_	 Alignment		100.0	23	PDB header: transferase/metal binding protein Chain: C: PDB Molecule: nifu protein (nifu-1); PDBTitle: a. fulgidus iscs-iscu complex structure
7	d1r9pa_	 Alignment		100.0	26	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
8	d1wfza_	 Alignment		100.0	27	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
9	c2e5aA_	 Alignment		85.6	11	PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase 1; PDBTitle: crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
10	c3r07C_	 Alignment		83.0	17	PDB header: transferase Chain: C: PDB Molecule: putative lipoate-protein ligase a subunit 2; PDBTitle: structural analysis of an archaeal lipoylation system. a bi-partite2 lipoate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
11	d1v97a4	 Alignment		78.3	9	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like

12	c5t8uA_	 Alignment		68.3	9	PDB header: lipase Chain: A: PDB Molecule: lipoate-protein ligase 1; PDBTitle: crystal structure of p. falciparum lip1 in complex lipoate
13	c3j21S_	 Alignment		65.7	20	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein I22p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
14	c4a17Q_	 Alignment		63.0	13	PDB header: ribosome Chain: Q: PDB Molecule: rpl17; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 2.
15	d1vqor1	 Alignment		60.6	13	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
16	d1ffvc1	 Alignment		53.1	13	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
17	c1x2gB_	 Alignment		52.9	16	PDB header: lipase Chain: B: PDB Molecule: lipoate-protein ligase a; PDBTitle: crystal structure of lipate-protein ligase a from2 escherichia coli
18	c3jywN_	 Alignment		52.8	15	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein I17(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
19	c1vw4Q_	 Alignment		51.7	18	PDB header: ribosome Chain: O: PDB Molecule: 54s ribosomal protein I22, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
20	c2zkr_	 Alignment		51.1	25	PDB header: ribosomal protein/rna Chain: R: PDB Molecule: rna expansion segment es39 part i; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
21	c3zf7R_	 Alignment	not modelled	50.6	21	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein I17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
22	c5ibyA_	 Alignment	not modelled	50.3	11	PDB header: lipase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-2) in complex with lipoic acid
23	c3u5eP_	 Alignment	not modelled	49.9	21	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein I17-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
24	c5ij6A_	 Alignment	not modelled	46.4	15	PDB header: lipase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid
25	c5mlcU_	 Alignment	not modelled	46.3	19	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein I22, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
26	c3j39P_	 Alignment	not modelled	44.2	20	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein I17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
27	c1vqzA_	 Alignment	not modelled	43.2	13	PDB header: lipase Chain: A: PDB Molecule: lipoate-protein ligase, putative; PDBTitle: crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
						PDB header: hydrolase

28	c3kioA_	Alignment	not modelled	42.6	12	Chain: A: PDB Molecule: ribonuclease h2 subunit a; PDBTitle: mouse rnase h2 complex
29	d2zjrp1	Alignment	not modelled	42.3	18	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
30	c4v19W_	Alignment	not modelled	41.9	24	PDB header: ribosome Chain: W: PDB Molecule: mitoribosomal protein ul22m, mrp122; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
31	d1fs1b1	Alignment	not modelled	41.8	4	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
32	c3ibqA_	Alignment	not modelled	41.1	17	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp
33	c5o60T_	Alignment	not modelled	40.8	24	PDB header: ribosome Chain: T: PDB Molecule: 50s ribosomal protein l22; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
34	d1ekea_	Alignment	not modelled	40.6	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
35	d1i4ja_	Alignment	not modelled	39.8	21	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
36	d1u0la1	Alignment	not modelled	39.6	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
37	c3iz5V_	Alignment	not modelled	39.4	22	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein l17 (l22p); PDBTitle: localization of the 50s large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	d1fs2b1	Alignment	not modelled	37.1	4	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
39	d1n62c1	Alignment	not modelled	36.1	12	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
40	c4ce4W_	Alignment	not modelled	35.3	22	PDB header: ribosome Chain: W: PDB Molecule: mrp122; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
41	d1t3qc1	Alignment	not modelled	33.5	12	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
42	d1mzga_	Alignment	not modelled	33.5	15	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
43	c2ftcM_	Alignment	not modelled	33.0	24	PDB header: ribosome Chain: M: PDB Molecule: mitochondrial ribosomal protein l22 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
44	d1nexa1	Alignment	not modelled	32.9	15	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
45	d1vqza1	Alignment	not modelled	32.4	14	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
46	d2ovra1	Alignment	not modelled	31.9	4	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
47	c3j3wS_	Alignment	not modelled	31.6	18	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
48	d1vi9a_	Alignment	not modelled	30.5	25	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
49	c1i3aA_	Alignment	not modelled	30.4	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: rnase hii from archaeoglobus fulgidus with cobalt hexammine2 chloride
50	d1t9ha1	Alignment	not modelled	30.0	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
51	d1ni7a_	Alignment	not modelled	29.7	20	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
52	d1x2ga1	Alignment	not modelled	28.0	14	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
53	d1i39a_	Alignment	not modelled	27.1	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
54	c3zs7A_	Alignment	not modelled	26.3	14	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from trypanosoma brucei

55	c3rm5B_	Alignment	not modelled	24.2	26	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylpyrimidine/phosphomethylpyrimidine kinase PDBTitle: structure of trifunctional thi20 from yeast
56	d2axoa1	Alignment	not modelled	23.1	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Atu2684-like
57	d1io2a_	Alignment	not modelled	21.7	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
58	d1uaxa_	Alignment	not modelled	20.4	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
59	d1jxha_	Alignment	not modelled	19.3	25	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
60	d1jroa3	Alignment	not modelled	19.0	11	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
61	c2axoA_	Alignment	not modelled	17.5	24	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein atu2684; PDBTitle: x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
62	d1r8ja1	Alignment	not modelled	17.1	11	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
63	d1v2za_	Alignment	not modelled	17.0	22	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
64	d1sv1a_	Alignment	not modelled	16.7	22	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
65	c5y1aA_	Alignment	not modelled	16.6	5	PDB header: electron transport Chain: A: PDB Molecule: 35 kda hemin binding protein; PDBTitle: hbp35 of porphyromonas gingivalis
66	d1r5ga_	Alignment	not modelled	14.8	17	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
67	c3bboU_	Alignment	not modelled	14.6	21	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l22; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
68	c2p1nD_	Alignment	not modelled	14.2	4	PDB header: signaling protein Chain: D: PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
69	c4xgrF_	Alignment	not modelled	14.1	50	PDB header: toxin/antitoxin Chain: F: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
70	c4xgrH_	Alignment	not modelled	13.9	50	PDB header: toxin/antitoxin Chain: H: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
71	c2w3rG_	Alignment	not modelled	13.9	15	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
72	c1nexC_	Alignment	not modelled	13.7	15	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccd4-cpd peptide complex
73	d1y5ia2	Alignment	not modelled	13.3	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
74	d1lhpa_	Alignment	not modelled	13.1	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
75	c4xgqB_	Alignment	not modelled	13.1	50	PDB header: toxin/antitoxin Chain: B: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
76	c4xgqD_	Alignment	not modelled	12.4	50	PDB header: toxin/antitoxin Chain: D: PDB Molecule: antitoxin vapp30; PDBTitle: crystal structure of addiction module from mycobacterial species
77	c3nyeA_	Alignment	not modelled	12.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
78	c5y9pA_	Alignment	not modelled	11.5	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: staphylococcus aureus rnase hii
79	c3etrM_	Alignment	not modelled	11.2	10	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with lumazine
80	c3b9jl_	Alignment	not modelled	11.2	10	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine

81	d1v65a_	Alignment	not modelled	10.8	15	Fold: KRAB domain (Kruppel-associated box) Superfamily: KRAB domain (Kruppel-associated box) Family: KRAB domain (Kruppel-associated box)
82	c5yepC_	Alignment	not modelled	10.7	12	PDB header: antitoxin/toxin Chain: C: PDB Molecule: toxin-antitoxin system toxin hepn family; PDBTitle: crystal structure of so_3166-so_3165 from shewanella oneidensis
83	c5jwrE_	Alignment	not modelled	10.5	22	PDB header: transcription regulator Chain: E: PDB Molecule: circadian clock protein kaia; PDBTitle: crystal structure of foldswitch-stabilized kaib in complex with the n-2 terminal ci domain of kaic and a dimer of kaia c-terminal domains3 from thermosynechococcus elongatus
84	c1zeqX_	Alignment	not modelled	9.9	19	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
85	c4qe0B_	Alignment	not modelled	9.7	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf5043 family protein (bacuni_01052) from2 bacteroides uniformis atcc 8492 at 1.85 a resolution
86	c5i1tA_	Alignment	not modelled	9.6	21	PDB header: hydrolase Chain: A: PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoid) from clostridium difficile in complex with3 triacetylchitotriose
87	c4yl5A_	Alignment	not modelled	8.6	18	PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: structure of a putative phosphomethylpyrimidine kinase from2 acinetobacter baumannii
88	c6d7kD_	Alignment	not modelled	8.6	23	PDB header: oxidoreductase/inhibitor Chain: D: PDB Molecule: methane monooxygenase hydroxylase, mmod; PDBTitle: complex structure of methane monooxygenase hydroxylase in complex with2 inhibitory subunit
89	c3iz5w_	Alignment	not modelled	8.5	27	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
90	d1o5ha_	Alignment	not modelled	8.5	17	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
91	d1iloa_	Alignment	not modelled	8.4	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
92	c2ovqA_	Alignment	not modelled	8.2	4	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
93	c5vodD_	Alignment	not modelled	7.9	24	PDB header: viral protein/immune system Chain: D: PDB Molecule: envelope glycoprotein ul130; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 9i6
94	c2fqxA_	Alignment	not modelled	7.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
95	c2l55A_	Alignment	not modelled	7.6	29	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
96	c3w4sB_	Alignment	not modelled	7.5	15	PDB header: transferase Chain: B: PDB Molecule: carbohydrate/pyrimidine kinase, pfbk family; PDBTitle: myo-inositol kinase from thermococcus kodakarensis
97	c1r8jB_	Alignment	not modelled	7.3	11	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus
98	c2lqoA_	Alignment	not modelled	7.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative glutaredoxin rv3198.1/mt3292; PDBTitle: mrx1 reduced
99	c3axbA_	Alignment	not modelled	6.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix