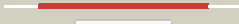



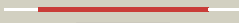



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2514c_(-)_2830887_2831348
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	ac1069c579a90532

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h1ca1	 Alignment		99.7	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	d1v96a1	 Alignment		99.7	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	d1y82a1	 Alignment		99.7	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c3zvkc	 Alignment		99.7	17	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
5	c6nkla	 Alignment		99.6	15	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
6	c3h87B	 Alignment		99.6	14	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
7	c4chgC	 Alignment		99.6	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
8	c3tndC	 Alignment		99.6	15	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
9	c5sv2A	 Alignment		99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
10	c5l6mC	 Alignment		99.5	24	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
11	c3dboB	 Alignment		99.5	19	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis

12	c3ix7A_	Alignment		99.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
13	c6a7vG_	Alignment		99.3	18	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
14	c4xgrG_	Alignment		99.1	11	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
15	c5ywwA_	Alignment		98.9	20	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
16	c5f4hF_	Alignment		98.8	18	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
17	c3i8oA_	Alignment		98.8	14	PDB header: rna binding protein Chain: A: PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
18	c2fe1A_	Alignment		98.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
19	d2fe1a1	Alignment		98.7	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c2lcqA_	Alignment		98.6	18	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
21	c5x3tD_	Alignment	not modelled	98.6	20	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
22	c2hwwC_	Alignment	not modelled	98.4	13	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
23	c5wzfb_	Alignment	not modelled	98.3	12	PDB header: hydrolase Chain: B: PDB Molecule: 23s rrna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
24	d1o4wa_	Alignment	not modelled	98.3	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c1v8pK_	Alignment	not modelled	97.6	15	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
26	d1v8pa_	Alignment	not modelled	97.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
27	c6g5iy_	Alignment	not modelled	96.7	18	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
28	c5jppd_	Alignment	not modelled	96.6	15	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
						PDB header: hydrolase

29	c5yz4A_	Alignment	not modelled	96.5	19	Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
30	c2hwyB_	Alignment	not modelled	93.3	13	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	89.2	9	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
32	d1w8ia_	Alignment	not modelled	81.5	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
33	c3v32B_	Alignment	not modelled	64.5	30	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
34	c6md3F_	Alignment	not modelled	64.3	15	PDB header: hydrolase/rna Chain: F: PDB Molecule: rrp44p homologue; PDBTitle: structure of t. brucei rrp44 pin domain
35	c3v33A_	Alignment	not modelled	62.7	27	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
36	c5mq9A_	Alignment	not modelled	54.7	20	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
37	c6d6rK_	Alignment	not modelled	50.9	19	PDB header: hydrolase Chain: K: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
38	d1rlga_	Alignment	not modelled	40.5	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
39	c3zddA_	Alignment	not modelled	39.5	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
40	c3izcH_	Alignment	not modelled	33.2	17	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein rpl8 (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
41	c5xyiM_	Alignment	not modelled	30.8	7	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
42	c2zkrf_	Alignment	not modelled	30.3	21	PDB header: ribosomal protein/rna Chain: F: PDB Molecule: rna expansion segment es7 part iii; 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
43	c1s1iG_	Alignment	not modelled	28.4	17	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8-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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
44	c3u5iG_	Alignment	not modelled	27.5	17	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
45	c2xznU_	Alignment	not modelled	27.0	7	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l7ae 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 2
46	c3v7eB_	Alignment	not modelled	27.0	10	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: ribosome-associated protein l7ae-like; PDBTitle: crystal structure of ybxf bound to the sam-i riboswitch aptamer
47	c3j39G_	Alignment	not modelled	25.8	21	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
48	d1g7sa3	Alignment	not modelled	25.6	7	Fold: Initiation factor IF2/eIF5b, domain 3 Superfamily: Initiation factor IF2/eIF5b, domain 3 Family: Initiation factor IF2/eIF5b, domain 3
49	d1w41a1	Alignment	not modelled	25.2	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
50	c4a1eF_	Alignment	not modelled	23.3	17	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
51	c1z9bA_	Alignment	not modelled	23.3	12	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
52	c3cpqB_	Alignment	not modelled	23.2	10	PDB header: ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
53	d1xbia1	Alignment	not modelled	23.0	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins

54	d2bo1a1	Alignment	not modelled	23.0	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
55	c2mdtA	Alignment	not modelled	22.0	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfobolus solfataricus p2
56	c3zf7x	Alignment	not modelled	21.4	14	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l23a; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
57	c5xxuM	Alignment	not modelled	20.8	17	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein es12; PDBTitle: small subunit of toxoplasma gondii ribosome
58	d1t0kb	Alignment	not modelled	20.6	9	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
59	c2zkr6	Alignment	not modelled	19.7	5	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; 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
60	c3v7qB	Alignment	not modelled	18.5	19	PDB header: rna binding protein Chain: B: PDB Molecule: probable ribosomal protein ylxq; PDBTitle: crystal structure of b. subtilis ylxq at 1.55 a resolution
61	c3j61G	Alignment	not modelled	18.3	17	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8e; PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
62	c3zf7g	Alignment	not modelled	16.9	12	PDB header: ribosome Chain: G: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
63	c3on1A	Alignment	not modelled	16.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
64	c2z5bB	Alignment	not modelled	16.3	32	PDB header: chaperone Chain: B: PDB Molecule: uncharacterized protein ylr021w; PDBTitle: crystal structure of a novel chaperone complex for yeast2 20s proteasome assembly
65	c2z5cB	Alignment	not modelled	16.2	32	PDB header: chaperone/hydrolase Chain: B: PDB Molecule: uncharacterized protein ylr021w; PDBTitle: crystal structure of a novel chaperone complex for yeast 20s2 proteasome assembly
66	c3j38M	Alignment	not modelled	14.6	13	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
67	c5udwB	Alignment	not modelled	14.4	18	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
68	c3iz5H	Alignment	not modelled	14.3	31	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
69	c2w69B	Alignment	not modelled	14.3	24	PDB header: transcription Chain: B: PDB Molecule: polymerase acidic protein; PDBTitle: influenza polymerase fragment
70	c4a1dG	Alignment	not modelled	13.8	8	PDB header: ribosome Chain: G: PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
71	d2gtad1	Alignment	not modelled	13.4	11	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
72	c3j21Z	Alignment	not modelled	13.3	7	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
73	c3kxeD	Alignment	not modelled	12.4	13	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
74	c3j3bG	Alignment	not modelled	12.2	38	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the human 60s ribosomal proteins
75	c4qamB	Alignment	not modelled	11.8	30	PDB header: signaling protein Chain: B: PDB Molecule: x-linked retinitis pigmentosa gtpase regulator-interacting PDBTitle: crystal structure of the rpgr rcc1-like domain in complex with the2 rpgr-interacting domain of rpgr1p1
76	c2x9qA	Alignment	not modelled	11.6	11	PDB header: ligase Chain: A: PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
77	d1knxa1	Alignment	not modelled	10.3	23	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
78	c3oqhB	Alignment	not modelled	9.5	7	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yymc; PDBTitle: crystal structure of b. licheniformis cdps yymc-blic
						PDB header: toxin

79	c5cegC_	Alignment	not modelled	9.2	25	Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
80	c4n3gA_	Alignment	not modelled	9.2	14	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5b-like protein, PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (870-1116) from chaetomium thermophilum, domains iii and iv
81	d2ipqx1	Alignment	not modelled	8.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like
82	c3j3aM_	Alignment	not modelled	8.9	7	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: structure of the human 40s ribosomal proteins
83	c5udtD_	Alignment	not modelled	8.6	13	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
84	c2zbtB_	Alignment	not modelled	8.4	13	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
85	c3femB_	Alignment	not modelled	8.2	22	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
86	c3nfiB_	Alignment	not modelled	7.9	21	PDB header: dna binding protein, transcription Chain: B: PDB Molecule: dna-directed rna polymerase i subunit rpa49; PDBTitle: crystal structure of tandem winged helix domain of rna polymerase i2 subunit a49
87	d3pnga3	Alignment	not modelled	7.9	11	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
88	c5d0nA_	Alignment	not modelled	7.8	26	PDB header: transferase Chain: A: PDB Molecule: pyruvate, phosphate dikinase regulatory protein, PDBTitle: crystal structure of maize pdrp bound with amp
89	c2nv2U_	Alignment	not modelled	7.5	22	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
90	c2lbwA_	Alignment	not modelled	7.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
91	c3dy0B_	Alignment	not modelled	7.0	11	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: cc-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
92	c4v19S_	Alignment	not modelled	6.8	7	PDB header: ribosome Chain: S: PDB Molecule: mitoribosomal protein u18m, mrpl18; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
93	c6j6qF_	Alignment	not modelled	6.7	9	PDB header: splicing Chain: F: PDB Molecule: splicing factor yju2; PDBTitle: cryo-em structure of the yeast b*-b2 complex at an average resolution2 of 3.7 angstrom
94	c1lq8H_	Alignment	not modelled	6.7	11	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
95	d1cmwa2	Alignment	not modelled	6.4	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
96	d2isya1	Alignment	not modelled	6.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
97	c5h1pB_	Alignment	not modelled	6.3	21	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crispr-associated protein
98	c2exxB_	Alignment	not modelled	6.2	24	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
99	c2e2zA_	Alignment	not modelled	6.2	14	PDB header: protein transport, chaperone regulator Chain: A: PDB Molecule: tim15; PDBTitle: solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70