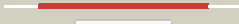



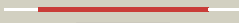



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3384c_(-)_3799423_3799815
Date	Fri Aug 9 18:20:05 BST 2019
Unique Job ID	6e6f3f988b722ad2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fe1A_	 Alignment		99.7	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
2	d2fe1a1	 Alignment		99.7	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	d1v8pa_	 Alignment		99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c1v8pK_	 Alignment		99.7	21	PDB header: structural genomics, unknown function Chain: K; PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
5	c4xgrG_	 Alignment		99.6	19	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
6	c5wzfB_	 Alignment		99.6	19	PDB header: hydrolase Chain: B; PDB Molecule: 23s rna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
7	d1y82a1	 Alignment		99.5	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	c6a7vG_	 Alignment		99.5	16	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	c3zvkc_	 Alignment		99.5	13	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
10	c3h87B_	 Alignment		99.4	17	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	d2h1ca1	 Alignment		99.4	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c3tndC_	Alignment		99.4	17	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
13	c5sv2A_	Alignment		99.4	17	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
14	c5l6mC_	Alignment		99.3	19	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
15	d1v96a1	Alignment		99.3	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c6nkIA_	Alignment		99.3	16	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
17	c4chgC_	Alignment		99.3	16	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
18	c5x3tD_	Alignment		99.3	18	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
19	c3dboB_	Alignment		99.1	20	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
20	c3i8oA_	Alignment		98.8	13	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.
21	d1w8ia_	Alignment	not modelled	98.6	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
22	c3ix7A_	Alignment	not modelled	98.6	22	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
23	c5ywwA_	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: A; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	c5f4hF_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	d1o4wa_	Alignment	not modelled	98.4	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c2lcqA_	Alignment	not modelled	98.2	18	PDB header: metal binding protein Chain: A; PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
27	c2hwwC_	Alignment	not modelled	97.7	17	PDB header: rna binding protein Chain: C; PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5jpd_	Alignment	not modelled	97.3	12	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
29	c5yz4A_	Alignment	not modelled	97.2	14	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1;

						PDBTitle: structure of the pin domain endonuclease utp24
30	c6g5iy_	Alignment	not modelled	96.2	21	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
31	c4mj7B_	Alignment	not modelled	94.7	12	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	c2mdtA_	Alignment	not modelled	93.7	27	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
33	c2hwyB_	Alignment	not modelled	75.3	11	PDB header: rna binding protein Chain: B; PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
34	d1tfra2	Alignment	not modelled	47.2	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c2zkr9_	Alignment	not modelled	45.9	24	PDB header: ribosomal protein/rna Chain: 9; PDB Molecule: 60s ribosomal protein l32; 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
36	d1vqoy1	Alignment	not modelled	39.7	29	Fold: Barstar-like Superfamily: Ribosomal protein L32e Family: Ribosomal protein L32e
37	c3cceY_	Alignment	not modelled	39.7	29	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l32e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
38	d1ulza2	Alignment	not modelled	34.6	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
39	d2j9ga2	Alignment	not modelled	34.1	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
40	c2ihnA_	Alignment	not modelled	31.9	14	PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
41	c3j21b_	Alignment	not modelled	30.6	29	PDB header: ribosome Chain: B; PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
42	c4a1cX_	Alignment	not modelled	29.4	17	PDB header: ribosome Chain: X; PDB Molecule: 60s ribosomal protein l32; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
43	c3j3be_	Alignment	not modelled	28.0	22	PDB header: ribosome Chain: E; PDB Molecule: 60s ribosomal protein l6; PDBTitle: structure of the human 60s ribosomal proteins
44	c3zf7i_	Alignment	not modelled	28.0	17	PDB header: ribosome Chain: I; PDB Molecule: 60s ribosomal protein l18; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
45	d1xo1a2	Alignment	not modelled	26.7	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
46	d1cmwa2	Alignment	not modelled	21.6	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
47	d1y81a1	Alignment	not modelled	21.3	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
48	c3v33A_	Alignment	not modelled	20.1	17	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
49	c2duwA_	Alignment	not modelled	20.0	15	PDB header: ligand binding protein Chain: A; PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
50	d1iuka_	Alignment	not modelled	19.3	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
51	c3v32B_	Alignment	not modelled	17.2	20	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
52	c1s1i0_	Alignment	not modelled	17.2	55	PDB header: ribosome Chain: 0; PDB Molecule: 60s ribosomal protein l32; 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.
53	c3iz5h_	Alignment	not modelled	17.0	18	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
54	c3ff4A_	Alignment	not modelled	16.7	10	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412

55	c4g94B_	Alignment	not modelled	16.6	24	PDB header: dna binding protein Chain: B: PDB Molecule: orf067; PDBTitle: g1 orf67 / staphylococcus aureus sigmaa domain 4 complex
56	c1jqsB_	Alignment	not modelled	13.7	27	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
57	d1w96a2	Alignment	not modelled	12.7	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
58	c5wt2A_	Alignment	not modelled	10.9	50	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
59	d1hi9a_	Alignment	not modelled	9.4	23	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
60	c5mq9A_	Alignment	not modelled	9.4	22	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
61	c5usrC_	Alignment	not modelled	8.4	30	PDB header: transferase Chain: C: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
62	c2eqyA_	Alignment	not modelled	7.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: jumonji, at rich interactive domain 1b; PDBTitle: solution structure of the arid domain of jarid1b protein
63	c6cluC_	Alignment	not modelled	7.5	23	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhp) f17l e208k2 double mutant structure
64	c4mwaA_	Alignment	not modelled	7.5	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
65	d2csua1	Alignment	not modelled	7.1	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
66	d1uc8a1	Alignment	not modelled	6.4	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
67	c3va7A_	Alignment	not modelled	6.4	14	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
68	d1kzyc2	Alignment	not modelled	6.2	15	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
69	c6g2dC_	Alignment	not modelled	6.1	18	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
70	c2jrza_	Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: histone demethylase jarid1c; PDBTitle: solution structure of the bright/arid domain from the human2 jarid1c protein.
71	c5k9nB_	Alignment	not modelled	5.5	18	PDB header: transferase Chain: B: PDB Molecule: polyamine n acetyltransferase; PDBTitle: structural and mechanistic analysis of drosophila melanogaster2 polyamine n acetyltransferase, an enzyme that catalyzes the formation3 of n acetylglmatine
72	c4hecB_	Alignment	not modelled	5.5	25	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
73	c4hnbV_	Alignment	not modelled	5.2	16	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase