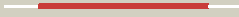
























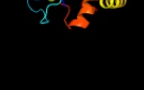




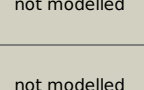


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0624 (-)_716667_717062
Date	Fri Jul 26 01:50:18 BST 2019
Unique Job ID	3303b776fce2ad9d

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgrG_	 Alignment		100.0	97	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	c5wzfB_	 Alignment		99.9	16	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
3	c3h87B_	 Alignment		99.9	21	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	d2h1ca1	 Alignment		99.9	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c5sv2A_	 Alignment		99.8	13	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
6	c3dboB_	 Alignment		99.8	18	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
7	c3zvkc_	 Alignment		99.8	8	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
8	c5l6mC_	 Alignment		99.8	15	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
9	c6nklA_	 Alignment		99.8	15	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
10	d1v96a1	 Alignment		99.8	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	c4chgC_	 Alignment		99.8	18	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis

12	d1y82a1	Alignment		99.8	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c3tndC	Alignment		99.8	13	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
14	c6a7vG	Alignment		99.8	19	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
15	c5x3tD	Alignment		99.8	20	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
16	d2fe1a1	Alignment		99.7	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A	Alignment		99.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	d1w8ia	Alignment		99.5	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	d1v8pa	Alignment		99.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
20	c1v8pK	Alignment		99.2	19	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
21	c3ix7A	Alignment	not modelled	98.3	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
22	c2lcqA	Alignment	not modelled	97.9	15	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
23	c3i8oA	Alignment	not modelled	97.8	17	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.
24	c5f4hF	Alignment	not modelled	97.2	15	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
25	d1o4wa	Alignment	not modelled	97.2	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c5ywwA	Alignment	not modelled	97.2	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2hwwC	Alignment	not modelled	95.8	13	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
28	c5yz4A	Alignment	not modelled	94.7	15	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
						PDB header: ribosome

29	c5jppd_	Alignment	not modelled	93.9	16	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy_	Alignment	not modelled	91.4	11	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	c2hwyB_	Alignment	not modelled	85.9	13	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c4mj7B_	Alignment	not modelled	80.7	7	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
33	c3v32B_	Alignment	not modelled	61.6	22	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	58.8	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 conserved domain with zinc-finger motif
35	d1cmwa2	Alignment	not modelled	46.1	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	c3zddA_	Alignment	not modelled	30.1	12	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
37	d1xo1a2	Alignment	not modelled	29.8	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1tfra2	Alignment	not modelled	26.7	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c4o9uB_	Alignment	not modelled	14.9	31	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
40	d1d4oa_	Alignment	not modelled	14.6	38	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
41	c1pt9B_	Alignment	not modelled	14.5	38	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
42	d1pnoa_	Alignment	not modelled	14.1	38	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
43	c4rodA_	Alignment	not modelled	10.7	14	PDB header: transcription Chain: A: PDB Molecule: transcription factor iib 50 kda subunit; PDBTitle: human tfiib-related factor 2 (brf2) and tpb bound to trnau1 promoter
44	c4mitG_	Alignment	not modelled	10.3	26	PDB header: signaling protein Chain: G: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd
45	c2ihnA_	Alignment	not modelled	10.0	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
46	c1ut8B_	Alignment	not modelled	9.9	19	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
47	c1cmwA_	Alignment	not modelled	8.8	23	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
48	c2bruC_	Alignment	not modelled	8.4	38	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
49	d1qf6a1	Alignment	not modelled	7.6	8	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
50	d1qd1a1	Alignment	not modelled	6.9	24	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
51	c4pn7A_	Alignment	not modelled	6.8	19	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of the tfih p34 n-terminal domain
52	c6f42V_	Alignment	not modelled	6.8	10	PDB header: transcription Chain: V: PDB Molecule: transcription factor iib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
53	c5a79A_	Alignment	not modelled	6.6	13	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: novel inter-subunit contacts in barley stripe mosaic virus revealed by2 cryo-em
54	c4mitE_	Alignment	not modelled	6.0	27	PDB header: signaling protein Chain: E: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpk4 pbd Fold: Cytidine deaminase-like

55	d1pkxa2	Alignment	not modelled	5.8	19	Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
56	c6cnbR_	Alignment	not modelled	5.7	12	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
57	d1g8ma2	Alignment	not modelled	5.4	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
58	c3if4C_	Alignment	not modelled	5.4	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm sewage outfall:2 integron cassette protein hfx_cass5
59	d1zcza2	Alignment	not modelled	5.3	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
60	d3eeqa1	Alignment	not modelled	5.3	11	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
61	c1jqsB_	Alignment	not modelled	5.2	33	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of I11 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