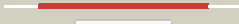



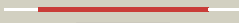



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2546 (-)_2868164_2868577
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	aff827aedbc77d2a

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5sv2A_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
2	c3h87B_	 Alignment		100.0	32	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
3	c4chgC_	 Alignment		99.9	20	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	d1v96a1	 Alignment		99.9	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c3zvkc_	 Alignment		99.9	15	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to a dna fragment from their promoter
6	c6a7vG_	 Alignment		99.9	30	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
7	c6nklA_	 Alignment		99.9	17	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
8	c3tndC_	 Alignment		99.9	18	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
9	c3dboB_	 Alignment		99.9	21	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
10	d1y82a1	 Alignment		99.8	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	d2h1ca1	 Alignment		99.8	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain

12	c5l6mC_	Alignment		99.8	17	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
13	c4xgrG_	Alignment		99.8	16	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD_	Alignment		99.5	21	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.5	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
16	d2fe1a1	Alignment		99.4	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	c5f4hF_	Alignment		99.3	15	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
19	c5ywwA_	Alignment		99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
20	c3ix7A_	Alignment		99.2	15	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
21	c3i8oA_	Alignment	not modelled	99.1	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.
22	d1o4wa_	Alignment	not modelled	98.7	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	d1v8pa_	Alignment	not modelled	98.5	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c1v8pK_	Alignment	not modelled	98.5	17	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
25	c2lcqA_	Alignment	not modelled	98.3	15	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
26	c2hwwC_	Alignment	not modelled	98.0	13	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
27	d1w8ja_	Alignment	not modelled	97.9	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
28	c5yz4A_	Alignment	not modelled	97.6	19	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	97.5	19	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c4mj7B_	Alignment	not modelled	92.2	18	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
31	c2hwyB_	Alignment	not modelled	89.9	15	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c6g5iy_	Alignment	not modelled	89.7	20	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
33	c3v33A_	Alignment	not modelled	86.4	24	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 conserved domain with zinc-finger motif
34	c3v32B_	Alignment	not modelled	84.7	24	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
35	d1cmwa2	Alignment	not modelled	62.3	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	c3zddA_	Alignment	not modelled	54.6	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
37	d1tfra2	Alignment	not modelled	34.0	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1xo1a2	Alignment	not modelled	26.1	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c1sy9B_	Alignment	not modelled	21.6	36	PDB header: calcium-binding protein Chain: B: PDB Molecule: cyclic-nucleotide-gated olfactory channel; PDBTitle: structure of calmodulin complexed with a fragment of the2 olfactory cng channel
40	c1ut8B_	Alignment	not modelled	18.0	26	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
41	c4mitG_	Alignment	not modelled	17.6	29	PDB header: signaling protein Chain: G: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpak4 pbd
42	d1a77a2	Alignment	not modelled	14.7	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
43	c1cmwA_	Alignment	not modelled	14.4	26	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
44	c2wqfA_	Alignment	not modelled	13.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: copper induced nitroreductase d; PDBTitle: crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
45	c2qipA_	Alignment	not modelled	13.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
46	c3eofB_	Alignment	not modelled	12.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
47	c2ihnA_	Alignment	not modelled	12.4	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
48	c3q8IA_	Alignment	not modelled	12.2	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
49	d1ul1x2	Alignment	not modelled	11.5	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
50	d1bkja_	Alignment	not modelled	11.0	19	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
51	c5hdjA_	Alignment	not modelled	10.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nfra1; PDBTitle: structure of b. megaterium nfra1
52	d1zcha1	Alignment	not modelled	9.1	17	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
53	c5heiE_	Alignment	not modelled	8.6	17	PDB header: oxidoreductase Chain: E: PDB Molecule: nfra2; PDBTitle: structure of b. megaterium nfra2
54	d2bodx1	Alignment	not modelled	8.5	38	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
55	c2n22B_	Alignment	not modelled	8.2	23	PDB header: transcription Chain: B: PDB Molecule: transcription factor p65; PDBTitle: nmr structure of the complex between the ph domain of

						the tfb1 subunit2 from tfiih and the transactivation domain of p65
56	c3bm2B_	Alignment	not modelled	7.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: protein ydja; PDBTitle: crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
57	d2cxaa1	Alignment	not modelled	7.0	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTTR-like
58	c2cxaA_	Alignment	not modelled	7.0	10	PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
59	c6faoA_	Alignment	not modelled	6.7	50	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 6; PDBTitle: discovery and characterization of a thermostable gh6 endoglucanase2 from a compost metagenome
60	d1ywqa1	Alignment	not modelled	6.6	25	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
61	d1qjwa_	Alignment	not modelled	6.5	25	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
62	c5jx6C_	Alignment	not modelled	6.5	75	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme
63	c1b43A_	Alignment	not modelled	6.3	9	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
64	c5urnB_	Alignment	not modelled	6.2	23	PDB header: transcription Chain: B: PDB Molecule: transcription factor p65; PDBTitle: nmr structure of the complex between the ph domain of the tfb1 subunit2 from tfiih and the transactivation domain 1 of p65
65	d1txka2	Alignment	not modelled	6.2	19	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: MdoG-like
66	d1mc8a2	Alignment	not modelled	6.0	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
67	c4urpB_	Alignment	not modelled	6.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid repression mutant protein 2; PDBTitle: the crystal structure of nitroreductase from saccharomyces2 cerevisiae
68	d1rxwa2	Alignment	not modelled	5.9	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
69	c5gkeB_	Alignment	not modelled	5.8	27	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
70	c3gr3B_	Alignment	not modelled	5.7	11	PDB header: flavoprotein Chain: B: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution
71	c5xczA_	Alignment	not modelled	5.7	38	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: structure of the cellobiohydrolase cel6a from phanerochaete2 chrysosporium in complex with cellobiose at 2.1 angstrom
72	c6c34A_	Alignment	not modelled	5.5	11	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
73	c5yaaD_	Alignment	not modelled	5.3	14	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
74	c4g25A_	Alignment	not modelled	5.3	14	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rna p 1 (prop1) from a.2 thaliana, semet substituted form with sr
75	c5xyhA_	Alignment	not modelled	5.2	38	PDB header: hydrolase Chain: A: PDB Molecule: cbsa; PDBTitle: crystal structure of catalytic domain of 1,4-beta-cellobiosidase2 (cbsa) from xanthomonas oryzae pv. oryzae
76	c2wzvB_	Alignment	not modelled	5.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis