



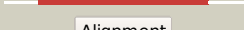

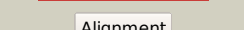

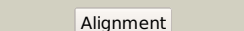





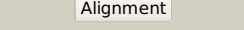

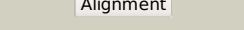

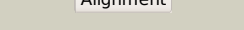

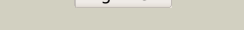



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2757c_(-)_3070180_3070596
Date	Wed Aug 7 12:50:41 BST 2019
Unique Job ID	0045a7e72bf31606

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5sv2A_	 Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
2	c3h87B_	 Alignment		100.0	39	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
3	d1v96a1	 Alignment		100.0	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c4chgC_	 Alignment		99.9	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
5	c3dboB_	 Alignment		99.9	25	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
6	d1y82a1	 Alignment		99.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
7	c6a7vG_	 Alignment		99.9	26	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
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	c3zvkc_	 Alignment		99.9	19	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	d2h1ca1	 Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
11	c6nkIA_	 Alignment		99.9	19	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae

12	c5l6mC_	Alignment		99.9	19	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		99.6	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.6	15	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	c2fe1A_	Alignment		99.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
17	d2fe1a1	Alignment		99.4	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	c5ywwA_	Alignment		99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
19	c3ix7A_	Alignment		99.0	19	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
20	c5f4hF_	Alignment		99.0	13	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
21	c3i8oA_	Alignment	not modelled	98.8	9	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	c2lcqA_	Alignment	not modelled	98.5	13	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
23	d1w8ia_	Alignment	not modelled	98.4	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	d1v8pa_	Alignment	not modelled	98.3	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	d1o4wa_	Alignment	not modelled	98.3	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c1v8pK_	Alignment	not modelled	98.3	22	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
27	c2hwwC_	Alignment	not modelled	97.5	17	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	96.4	18	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	96.2	18	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy_	Alignment	not modelled	93.6	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
31	c2hwyB_	Alignment	not modelled	89.6	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	84.9	13	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	71.6	25	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mczip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	66.5	25	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	56.2	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	c3zddA_	Alignment	not modelled	38.9	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	38.8	35	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	d1xo1a2	Alignment	not modelled	26.1	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	c4mitG_	Alignment	not modelled	18.8	38	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
40	c2qipA_	Alignment	not modelled	17.0	27	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
41	c2cxaA_	Alignment	not modelled	12.5	6	PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
42	d2cxaa1	Alignment	not modelled	12.5	6	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTR-like
43	c5gkeB_	Alignment	not modelled	12.1	32	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
44	c1ut8B_	Alignment	not modelled	11.2	19	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
45	c1cmwA_	Alignment	not modelled	10.9	20	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
46	c4mitE_	Alignment	not modelled	10.2	43	PDB header: signaling protein Chain: E: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpak4 pbd
47	c2n22B_	Alignment	not modelled	9.8	36	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
48	c1sy9B_	Alignment	not modelled	7.3	43	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
49	c2ihnA_	Alignment	not modelled	6.9	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
50	c5urnB_	Alignment	not modelled	6.7	36	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
51	c6f8lj_	Alignment	not modelled	6.4	21	PDB header: motor protein Chain: J: PDB Molecule: type iv pilus assembly protein pilf; PDBTitle: thermus thermophilus pilf atpase (ampnp-bound form)
52	d1a77a2	Alignment	not modelled	6.2	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
53	d1vola2	Alignment	not modelled	6.0	12	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
54	c5yaaD_	Alignment	not modelled	5.9	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

55

[c2vldA_](#)

Alignment

not modelled

5.9

27

PDB header:hydrolase
Chain: A: **PDB Molecule:**endonuclease nucs;
PDBTitle: crystal structure of a repair endonuclease from
pyrococcus abyssi