



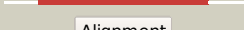

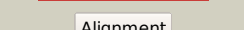

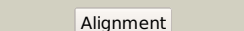





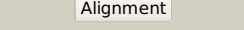

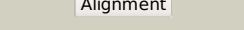

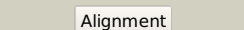














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0301 (-) _364044_364469
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	6a7cbc7dcbdd6b3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87B_	 Alignment		100.0	100	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	c5sv2A_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
3	d1v96a1	 Alignment		100.0	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
4	c4chgC_	 Alignment		99.9	22	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	23	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	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
7	c3tndC_	 Alignment		99.9	21	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
8	c6a7vG_	 Alignment		99.9	27	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
9	c6nklA_	 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
10	c3zvkc_	 Alignment		99.9	16	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
11	c5l6mC_	 Alignment		99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)

12	d2h1ca1	Alignment		99.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xgrG_	Alignment		99.8	20	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD_	Alignment		99.6	22	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	c5wzfB_	Alignment		99.6	18	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		99.5	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c2fe1A_	Alignment		99.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
18	c3ix7A_	Alignment		98.8	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
19	c3i8oA_	Alignment		98.6	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.
20	c5ywwA_	Alignment		98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
21	d1w8ia_	Alignment	not modelled	98.5	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
22	d1v8pa_	Alignment	not modelled	98.5	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	c5f4hF_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	c1v8pK_	Alignment	not modelled	98.4	24	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
25	d1o4wa_	Alignment	not modelled	98.2	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
26	c2lcqA_	Alignment	not modelled	98.2	17	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	97.4	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	95.9	17	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
29	c5jppd_	Alignment	not modelled	95.9	20	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c6g5iy_	Alignment	not modelled	81.7	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
31	c4mj7B_	Alignment	not modelled	81.5	14	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	c2hwyB_	Alignment	not modelled	81.5	16	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
33	c3v32B_	Alignment	not modelled	64.2	28	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
34	d1cmwa2	Alignment	not modelled	56.3	30	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
35	c3v33A_	Alignment	not modelled	50.6	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
36	c3zddA_	Alignment	not modelled	49.9	30	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	c1sy9B_	Alignment	not modelled	35.0	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
38	d1tfra2	Alignment	not modelled	26.0	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
39	d1xo1a2	Alignment	not modelled	20.8	31	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c1ut8B_	Alignment	not modelled	18.5	26	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
41	c4mitG_	Alignment	not modelled	16.6	33	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
42	c4csqA_	Alignment	not modelled	15.1	56	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of pa3793 from pseudomonas aeruginosa
43	d1aisb2	Alignment	not modelled	14.0	19	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
44	c1cmwA_	Alignment	not modelled	13.1	30	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
45	c2n22B_	Alignment	not modelled	8.6	43	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
46	c2ihnA_	Alignment	not modelled	8.0	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
47	d1vola2	Alignment	not modelled	7.6	18	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
48	c2m0jB_	Alignment	not modelled	7.4	29	PDB header: metal binding protein/metal transport Chain: B: PDB Molecule: peptide from cyclic nucleotide-gated olfactory channel; PDBTitle: 3d structure of calmodulin and calmodulin binding domain of olfactory2 cyclic nucleotide-gated ion channel complex
49	c2m0kB_	Alignment	not modelled	7.4	29	PDB header: metal binding protein/metal transport Chain: B: PDB Molecule: peptide from cyclic nucleotide-gated olfactory channel; PDBTitle: 3d structure of calmodulin and calmodulin binding domain of rat2 olfactory cyclic nucleotide-gated ion channel
50	c5jx6C_	Alignment	not modelled	7.1	27	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme
51	c2mvzA_	Alignment	not modelled	6.3	0	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure for cyclophilin a from geobacillus kaustophilus
52	c5urnB_	Alignment	not modelled	5.8	46	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
53	c3q8lA_	Alignment	not modelled	5.7	17	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+
54	c4mitE_	Alignment	not modelled	5.4	33	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

55	d1qjwa_	Alignment	not modelled	5.2	9	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
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