





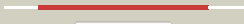















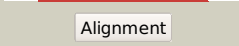







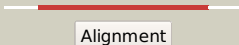

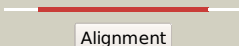

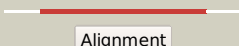

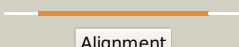



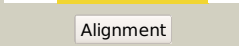
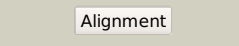
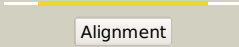
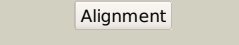

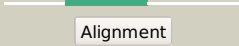
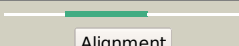




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0656c_(-)_752987_753370
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	417f629531888a48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87B_	 Alignment		99.9	22	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	c5sv2A_	 Alignment		99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
3	c4chgC_	 Alignment		99.8	20	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	d1y82a1	 Alignment		99.8	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	d1v96a1	 Alignment		99.7	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c3dboB_	 Alignment		99.7	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
7	c3zvkc_	 Alignment		99.6	14	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	c3tndC_	 Alignment		99.6	16	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
9	c6nklA_	 Alignment		99.6	11	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
10	c6a7vG_	 Alignment		99.6	21	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
11	c5l6mC_	 Alignment		99.5	13	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)

12	d2h1ca1	 Alignment		99.4	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xgrG	 Alignment		99.2	15	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5wzfB	 Alignment		98.5	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
15	c5x3tD	 Alignment		98.5	11	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
16	c2fe1A	 Alignment		97.8	15	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		97.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1w8ia	 Alignment		96.4	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c3ix7A	 Alignment		86.6	13	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	c3i8oA	 Alignment		85.5	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.
21	c2lcqA	 Alignment	not modelled	75.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
22	c1v8pK	 Alignment	not modelled	73.2	14	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
23	d1v8pa	 Alignment	not modelled	72.6	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	d1o4wa	 Alignment	not modelled	56.8	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c5ywwA	 Alignment	not modelled	54.6	11	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
26	d2eyqa6	 Alignment	not modelled	48.8	18	Fold: TRCF domain-like Superfamily: TRCF domain-like Family: TRCF domain
27	c2qsrA	 Alignment	not modelled	47.8	13	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
28	c3v32B	 Alignment	not modelled	41.1	27	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
29	c3v32A	 Alignment	not modelled	39.3	25	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a;

29	c3v33A	Alignment	not modelled	29.3	29	PDBTitle: crystal structure of mcpip1 conserved domain with zinc-finger motif
30	d1cmwa2	Alignment	not modelled	22.7	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
31	c5jppd	Alignment	not modelled	18.6	17	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
32	c5yz4A	Alignment	not modelled	16.2	14	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
33	c2eyqA	Alignment	not modelled	12.5	18	PDB header: hydrolase Chain: A; PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
34	c2qipA	Alignment	not modelled	10.6	18	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
35	c4gaoA	Alignment	not modelled	9.8	13	PDB header: ligase/peptide Chain: A; PDB Molecule: dcn1-like protein 2; PDBTitle: dcn1 complex with n-terminally acetylated nedd8 e2 peptide
36	c2is9A	Alignment	not modelled	8.4	10	PDB header: transcription Chain: A; PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
37	c3zddA	Alignment	not modelled	7.6	18	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
38	c2ejsA	Alignment	not modelled	7.4	22	PDB header: ligase Chain: A; PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: solution structure of ruh-076, a human cue domain
39	d1xo1a2	Alignment	not modelled	7.2	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c2lhuA	Alignment	not modelled	7.2	26	PDB header: structural protein Chain: A; PDB Molecule: mybpc3 protein; PDBTitle: structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
41	c5ifgB	Alignment	not modelled	7.2	14	PDB header: hydrolase/antitoxin Chain: B; PDB Molecule: antitoxin higa; PDBTitle: crystal structure of higa-high complex from e. coli
42	d1tfra2	Alignment	not modelled	7.2	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
43	c5f4hF	Alignment	not modelled	6.7	20	PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
44	c2n5mA	Alignment	not modelled	6.0	20	PDB header: unknown function Chain: A; PDB Molecule: protein khnyn; PDBTitle: unveiling the structural determinants of kiaa0323 binding preference2 for nedd8
45	d1efnb	Alignment	not modelled	5.8	24	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef