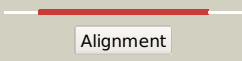



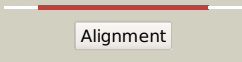




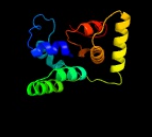
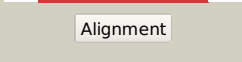

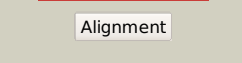

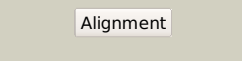

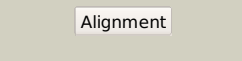

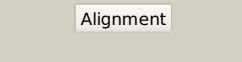

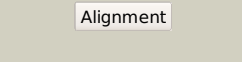



Phyre2

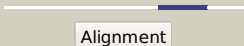
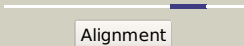


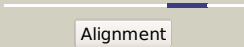
Email	mdejesus@rockefeller.edu
Description	RVBD0661c_(-)_755338_755775
Date	Fri Jul 26 01:50:22 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wzfB_	 Alignment		99.9	20	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
2	c3zvkc_	 Alignment		99.8	13	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
3	c5x3tD_	 Alignment		99.8	17	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
4	c6nkIA_	 Alignment		99.8	13	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
5	c6a7vG_	 Alignment		99.8	14	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
6	c5l6mC_	 Alignment		99.8	17	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
7	d2h1ca1	 Alignment		99.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
8	c4xqrG_	 Alignment		99.8	17	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
9	c3tndC_	 Alignment		99.7	14	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
10	c4chgC_	 Alignment		99.7	12	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3h87B_	 Alignment		99.7	17	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c3dboB_	Alignment		99.7	22	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
13	c5sv2A_	Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
14	d1w8ia_	Alignment		99.6	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
15	d1v96a1	Alignment		99.6	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
16	c2fe1A_	Alignment		99.6	17	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		99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.5	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c3i8oA_	Alignment		98.8	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	d1v8pa_	Alignment		98.5	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c1v8pK_	Alignment	not modelled	98.5	18	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
22	c3ix7A_	Alignment	not modelled	98.3	32	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
23	d1o4wa_	Alignment	not modelled	98.1	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	c2hwwC_	Alignment	not modelled	97.6	15	PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
25	c5jpdq_	Alignment	not modelled	97.3	21	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
26	c5ywwA_	Alignment	not modelled	97.2	12	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c5f4hf_	Alignment	not modelled	97.2	10	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
28	c5yz4A_	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
29	c2lgaA_	Alignment	not modelled	97.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6;

29	c2tqa	Alignment	not modelled	97.0	19	PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
30	c2hwyB	Alignment	not modelled	90.5	28	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B	Alignment	not modelled	89.8	11	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	c3v32B	Alignment	not modelled	89.5	15	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
33	c3v33A	Alignment	not modelled	82.2	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
34	c6g5iy	Alignment	not modelled	69.7	19	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
35	d1cmwa2	Alignment	not modelled	48.2	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	d1tfra2	Alignment	not modelled	48.1	32	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1xo1a2	Alignment	not modelled	39.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c3zddA	Alignment	not modelled	38.9	26	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
39	d1ul1x2	Alignment	not modelled	29.8	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c2ihnA	Alignment	not modelled	24.5	32	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
41	c2izoA	Alignment	not modelled	21.9	18	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
42	c3q8lA	Alignment	not modelled	21.8	18	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+
43	d1mc8a2	Alignment	not modelled	21.2	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
44	d1rxwa2	Alignment	not modelled	19.4	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
45	d1a77a2	Alignment	not modelled	18.8	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
46	c1ut8B	Alignment	not modelled	17.8	21	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
47	c3alzB	Alignment	not modelled	14.8	39	PDB header: viral protein/membrane protein Chain: B: PDB Molecule: cdw150; PDBTitle: crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (form i)
48	c1b43A	Alignment	not modelled	11.2	24	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
49	c1a77A	Alignment	not modelled	11.0	21	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
50	c1rxvA	Alignment	not modelled	10.1	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
51	d1zcza2	Alignment	not modelled	9.0	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
52	c1cmwA	Alignment	not modelled	8.7	33	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
53	d1pkxa2	Alignment	not modelled	8.4	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
54	d1g8ma2	Alignment	not modelled	8.4	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
55	c4g25A	Alignment	not modelled	7.8	31	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rnase p 1 (prorp1) from a.2 thaliana, semet substituted form with sr

56	c1thzA_	 Alignment	not modelled	7.1	23	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
57	d1b43a2	 Alignment	not modelled	6.2	29	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
58	c1ul1Y_	 Alignment	not modelled	6.0	12	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
59	c3qeaZ_	 Alignment	not modelled	5.9	18	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
60	c6c34A_	 Alignment	not modelled	5.2	26	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n