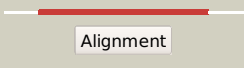

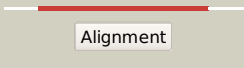

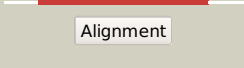

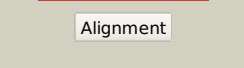

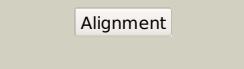

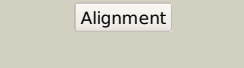

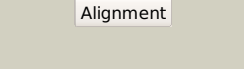

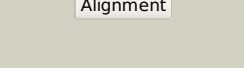

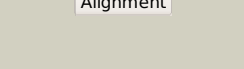

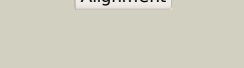

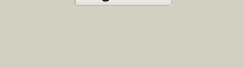



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1242_(-)_1384541_1384972
Date	Wed Jul 31 22:05:33 BST 2019
Unique Job ID	2634071ff1852596

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkc_			99.9	12	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
2	c5wzfb_			99.9	14	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
3	c6nkla_			99.9	14	PDB header: antitoxin Chain: A; PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
4	c5l6mc_			99.9	14	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
5	d2h1ca1			99.9	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c3tndc_			99.8	13	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
7	c4xqrg_			99.8	14	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	c5x3td_			99.8	16	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
9	c6a7vg_			99.8	16	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c4chgC_			99.8	17	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3h87B_			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	17	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin systems, vapbc-5, from mycobacterium tuberculosis
13	d2fe1a1	Alignment		99.7	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c2fe1A_	Alignment		99.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
15	c5sv2A_	Alignment		99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
16	d1v96a1	Alignment		99.6	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	d1w8ia_	Alignment		99.6	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
18	d1y82a1	Alignment		99.5	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c1v8pK_	Alignment		99.1	12	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
20	d1v8pa_	Alignment		99.1	12	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	c3i8oA_	Alignment	not modelled	98.8	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	c3ix7A_	Alignment	not modelled	98.6	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
23	c5ywwA_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
24	d1o4wa_	Alignment	not modelled	97.9	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c2lcqA_	Alignment	not modelled	97.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
26	c5f4hF_	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c2hwwC_	Alignment	not modelled	97.1	14	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	97.1	7	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	97.0	18	Chain: D: PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	93.9	19	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
31	c4mj7B_	Alignment	not modelled	91.4	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
32	c6g5iy_	Alignment	not modelled	90.5	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
33	c3v33A_	Alignment	not modelled	83.2	30	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
34	c3v32B_	Alignment	not modelled	82.9	30	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
35	c3zdA_	Alignment	not modelled	82.4	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
36	d1cmwa2	Alignment	not modelled	74.9	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	d1tfra2	Alignment	not modelled	67.4	28	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
38	c2mdtA_	Alignment	not modelled	40.0	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
39	c5dizB_	Alignment	not modelled	34.5	13	PDB header: hydrolase Chain: B: PDB Molecule: proteinaceous rnase p 2; PDBTitle: crystal structure of nuclear proteinaceous rnase p 2 (prorp2) from a.2 thaliana
40	c2ihnA_	Alignment	not modelled	32.3	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
41	d1xo1a2	Alignment	not modelled	32.1	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
42	c1ul1Y_	Alignment	not modelled	29.7	15	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
43	c1ut8B_	Alignment	not modelled	19.7	16	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
44	c3iefA_	Alignment	not modelled	16.8	20	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpcs.
45	d1k1sa1	Alignment	not modelled	16.6	13	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
46	c4g25A_	Alignment	not modelled	10.1	9	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
47	d2j01s1	Alignment	not modelled	8.6	12	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
48	c1cmwA_	Alignment	not modelled	8.1	24	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
49	d2zjr1	Alignment	not modelled	7.2	20	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
50	c3q8A_	Alignment	not modelled	7.1	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+
51	c2izoA_	Alignment	not modelled	6.8	16	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
52	c3dy0B_	Alignment	not modelled	6.7	44	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: c-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
53	c1lq8H_	Alignment	not modelled	6.4	44	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
54	c1k97A_	Alignment	not modelled	6.3	29	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
						PDB header: transferase

55	c1b43A_	Alignment	not modelled	6.2	20	Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
56	c6chgF_	Alignment	not modelled	6.0	56	PDB header: transferase Chain: F: PDB Molecule: kla0e03521p; PDBTitle: crystal structure of the yeast compass catalytic module
57	c5o60P_	Alignment	not modelled	5.6	12	PDB header: ribosome Chain: P: PDB Molecule: 50s ribosomal protein l18; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
58	d1ul1x2	Alignment	not modelled	5.5	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
59	c2j8S_	Alignment	not modelled	5.1	12	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l18; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
60	d1mc8a2	Alignment	not modelled	5.1	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain