

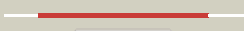






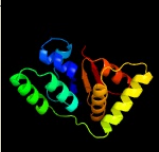

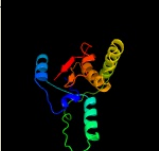





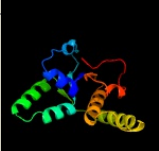

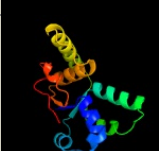







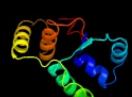





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0229c (-) _274306_274719
Date	Tue Jul 23 14:50:28 BST 2019
Unique Job ID	64a68bfd6b51349f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5sv2A_	 Alignment		100.0	44	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
2	c3h87B_	 Alignment		100.0	41	PDB header: toxin/antitoxin Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
3	c4chgC_	 Alignment		99.9	21	PDB header: toxin/antitoxin Chain: C; PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
4	d1v96a1	 Alignment		99.9	10	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c6a7vG_	 Alignment		99.9	29	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
6	c3dboB_	 Alignment		99.9	24	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		99.9	20	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	d1y82a1	 Alignment		99.9	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
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	c3tndC_	 Alignment		99.9	19	PDB header: translation, toxin Chain: C; PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
11	c5l6mC_	 Alignment		99.8	24	PDB header: hydrolase Chain: C; PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)

12	d2h1ca1	Alignment		99.8	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	c4xqrG	Alignment		99.8	17	PDB header: toxin/antitoxin Chain: G; PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addition module from mycobacterial species
14	c5x3tD	Alignment		99.5	16	PDB header: antitoxin/toxin Chain: D; PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
15	d2fe1a1	Alignment		99.4	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
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	c5wzfB	Alignment		99.4	17	PDB header: hydrolase Chain: B; PDB Molecule: 23s rna-specific endonuclease vapc20; PDBTitle: crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
18	c3ix7A	Alignment		99.0	17	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		98.8	15	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		98.8	15	PDB header: hydrolase Chain: A; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
21	c5f4hF	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: F; PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
22	d1o4wa	Alignment	not modelled	98.5	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
23	d1v8pa	Alignment	not modelled	98.3	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
24	d1w8ia	Alignment	not modelled	98.3	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c1v8pK	Alignment	not modelled	98.2	20	PDB header: structural genomics, unknown function Chain: K; PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
26	c2lcqA	Alignment	not modelled	98.1	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	21	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	97.3	14	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
29	c5jpd	Alignment	not modelled	97.2	16	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c4mj7B_	Alignment	not modelled	94.5	18	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
31	c2hwyB_	Alignment	not modelled	84.1	13	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
32	c3v32B_	Alignment	not modelled	70.1	25	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
33	c6g5iy_	Alignment	not modelled	64.5	13	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
34	c3v33A_	Alignment	not modelled	64.2	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
35	c3zddA_	Alignment	not modelled	41.5	22	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	41.4	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
37	c1sy9B_	Alignment	not modelled	26.5	36	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	c4mitG_	Alignment	not modelled	26.2	32	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
39	d1tfra2	Alignment	not modelled	23.2	31	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
40	c5gkeB_	Alignment	not modelled	17.6	22	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
41	c1ut8B_	Alignment	not modelled	16.2	17	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
42	c4mitE_	Alignment	not modelled	15.3	38	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
43	c2lvfA_	Alignment	not modelled	12.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
44	c2qipA_	Alignment	not modelled	11.8	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
45	c1cmwA_	Alignment	not modelled	10.1	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
46	c6f8ll_	Alignment	not modelled	9.0	15	PDB header: motor protein Chain: J: PDB Molecule: type iv pilus assembly protein pilf; PDBTitle: thermus thermophilus pilf atpase (amppnp-bound form)
47	c3d23A_	Alignment	not modelled	8.6	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: main protease of hcov-hku1
48	c2q6fB_	Alignment	not modelled	8.4	14	PDB header: hydrolase Chain: B: PDB Molecule: infectious bronchitis virus (ibv) main protease; PDBTitle: crystal structure of infectious bronchitis virus (ibv) main protease2 in complex with a michael acceptor inhibitor n3
49	c2n22B_	Alignment	not modelled	8.2	50	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
50	c5d0qG_	Alignment	not modelled	8.1	24	PDB header: protein transport Chain: G: PDB Molecule: outer membrane protein assembly factor bamc; PDBTitle: bamacde complex, outer membrane beta-barrel assembly machinery (bam)2 complex
51	c2cxaA_	Alignment	not modelled	7.8	9	PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
52	d2cxaa1	Alignment	not modelled	7.8	9	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTR-like
53	d1y5ia2	Alignment	not modelled	7.8	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
54	c3tloA_	Alignment	not modelled	7.6	17	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like proteinase;

						PDBTitle: crystal structure of hcov-nl63 3c-like protease
55	c4g25A_	Alignment	not modelled	7.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: pentatricopeptide repeat-containing protein at2g32230, PDBTitle: crystal structure of proteinaceous rna se p 1 (prop1) from a.2 thaliana, semet substituted form with sr
56	d1q0qa2	Alignment	not modelled	7.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	d1lc0a2	Alignment	not modelled	6.9	21	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Biliverdin reductase
58	c4mozC_	Alignment	not modelled	6.9	42	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
59	d2gp4a2	Alignment	not modelled	6.5	29	Fold: lIvD/EDD N-terminal domain-like Superfamily: lIvD/EDD N-terminal domain-like Family: lIvD/EDD N-terminal domain-like
60	c4xfqB_	Alignment	not modelled	6.5	24	PDB header: hydrolase Chain: B: PDB Molecule: pedv main protease; PDBTitle: crystal structure basis for pedv 3c like protease
61	d1dysa_	Alignment	not modelled	6.4	20	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
62	c1y5iA_	Alignment	not modelled	6.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
63	c2h7dB_	Alignment	not modelled	5.9	17	PDB header: structural protein Chain: B: PDB Molecule: chimera of 24-mer peptide from integrin beta-3 PDBTitle: solution structure of the talin f3 domain in complex with a2 chimeric beta3 integrin-pip kinase peptide
64	c5urnB_	Alignment	not modelled	5.7	50	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
65	c3ebnD_	Alignment	not modelled	5.6	17	PDB header: hydrolase Chain: D: PDB Molecule: replicase polyprotein 1ab; PDBTitle: a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
66	d1lvoa_	Alignment	not modelled	5.4	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
67	d2hi6a1	Alignment	not modelled	5.3	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/lIvD-like Family: AF0055-like
68	d1p9sa_	Alignment	not modelled	5.3	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold