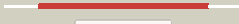



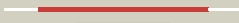



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0598c (-)_697157_697570
Date	Fri Jul 26 01:50:15 BST 2019
Unique Job ID	50f623b69465ceca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wzfB_	 Alignment		99.3	19	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	c5x3tD_	 Alignment		99.3	18	PDB header: antitoxin/toxin Chain: D: PDB Molecule: ribonuclease vapc26; PDBTitle: vapbc from mycobacterium tuberculosis
3	c5l6mC_	 Alignment		99.1	22	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
4	d2fe1a1	 Alignment		99.0	24	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
5	c2fe1A_	 Alignment		99.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein pae0151; PDBTitle: crystal structure of pae0151 from pyrobaculum aerophilum
6	d2h1ca1	 Alignment		99.0	22	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
7	c4xqrG_	 Alignment		99.0	11	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
8	c3tndC_	 Alignment		98.8	12	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
9	c6a7vG_	 Alignment		98.8	21	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c6nklA_	 Alignment		98.7	13	PDB header: antitoxin Chain: A: PDB Molecule: ribonuclease vapc; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
11	c3zvkc_	 Alignment		98.6	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

12	d1v8pa_	Alignment		98.5	26	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
13	d1v96a1	Alignment		98.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
14	c1v8pK_	Alignment		98.5	26	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum
15	c5sv2A_	Alignment		98.4	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease vapc21; PDBTitle: toxin vapc21 from mycobacterium tuberculosis
16	c3h87B_	Alignment		98.3	15	PDB header: toxin/antitoxin Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
17	c4chgC_	Alignment		98.3	24	PDB header: toxin/antitoxin Chain: C: PDB Molecule: probable ribonuclease vapc15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
18	d1y82a1	Alignment		98.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
19	c3dboB_	Alignment		97.6	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
20	d1w8ia_	Alignment		97.3	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
21	d1vqod1	Alignment	not modelled	57.3	29	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
22	c5f4hF_	Alignment	not modelled	48.8	13	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
23	c4a1cD_	Alignment	not modelled	47.5	10	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l11; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
24	d1o4wa_	Alignment	not modelled	45.1	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
25	c3zf7L_	Alignment	not modelled	43.9	12	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
26	c5ywwA_	Alignment	not modelled	43.3	17	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
27	c3i8oA_	Alignment	not modelled	39.8	22	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.
28	d1cjwa_	Alignment	not modelled	34.2	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT

29	d2p10a1	Alignment	not modelled	27.3	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Mil9387-like
30	c2moiA	Alignment	not modelled	26.9	21	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
31	c3j21E	Alignment	not modelled	26.7	19	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
32	c3ix7A	Alignment	not modelled	24.5	24	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
33	c2p10D	Alignment	not modelled	23.4	20	PDB header: hydrolase Chain: D: PDB Molecule: mil9387 protein; PDBTitle: crystal structure of a putative phosphoenolpyruvate hydrolase (mil9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
34	c1s1j	Alignment	not modelled	19.9	5	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l11; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
35	d1gmxA	Alignment	not modelled	19.7	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
36	c2hhgA	Alignment	not modelled	19.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa3614; PDBTitle: structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodospseudomonas palustris cga009
37	c6mxvA	Alignment	not modelled	16.7	15	PDB header: unknown function Chain: A: PDB Molecule: rhodanese-like family protein; PDBTitle: the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
38	c5aj3d	Alignment	not modelled	16.5	17	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: structure of the small subunit of the mammalian mitoribosome
39	c3ltiA	Alignment	not modelled	15.6	28	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
40	c6bevB	Alignment	not modelled	15.4	19	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain- PDBTitle: human single domain sulfurtransferase tstd1
41	c4jgiB	Alignment	not modelled	14.7	14	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
42	d16vpa	Alignment	not modelled	14.5	30	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
43	c3niwA	Alignment	not modelled	14.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
44	c3nhvE	Alignment	not modelled	13.7	8	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
45	c4ag9B	Alignment	not modelled	13.5	18	PDB header: transferase Chain: B: PDB Molecule: glucosamine-6-phosphate n-acetyltransferase; PDBTitle: c. elegans glucosamine-6-phosphate n-acetyltransferase (gna1):2 ternary complex with coenzyme a and glcnac
46	c2axqA	Alignment	not modelled	12.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
47	d1m4ia	Alignment	not modelled	11.3	23	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
48	d1yt8a4	Alignment	not modelled	11.3	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
49	d2apob1	Alignment	not modelled	11.0	23	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
50	c5craB	Alignment	not modelled	10.6	16	PDB header: hydrolase Chain: B: PDB Molecule: sdea; PDBTitle: structure of the sdea dub domain
51	d2ga9d1	Alignment	not modelled	10.4	36	Fold: Poly(A) polymerase catalytic subunit-like Superfamily: Poly(A) polymerase catalytic subunit-like Family: Poxvirus poly(A) polymerase catalytic subunit-like
52	d1tq1a	Alignment	not modelled	10.1	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
53	d1vh4a	Alignment	not modelled	9.7	23	Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD

						Family: Stabilizer of iron transporter SufD
54	c3d1pA	Alignment	not modelled	9.6	20	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
55	c1e8zA	Alignment	not modelled	9.3	25	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase catalytic subunit; PDBTitle: structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
56	d1zcza2	Alignment	not modelled	9.3	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
57	c2hwyB	Alignment	not modelled	9.0	36	PDB header: rna binding protein Chain: B: PDB Molecule: protein smg5; PDBTitle: structure of pin domain of human smg5.
58	d1xrsb1	Alignment	not modelled	9.0	24	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
59	c3s6fA	Alignment	not modelled	8.9	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical acetyltransferase; PDBTitle: crystal structure of a putative acetyltransferase (dr_1678) from2 deinococcus radiodurans r1 at 1.19 a resolution
60	d2hqya1	Alignment	not modelled	8.9	15	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
61	d2aq0a1	Alignment	not modelled	8.8	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
62	d1e7ua1	Alignment	not modelled	8.7	22	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Phosphoinositide 3-kinase (PI3K) helical domain
63	c2lmaA	Alignment	not modelled	8.7	33	PDB header: immune system Chain: A: PDB Molecule: thp5 peptide; PDBTitle: solution structure of cd4+ t cell derived peptide thp5
64	d1yt8a1	Alignment	not modelled	8.7	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
65	c2fsxA	Alignment	not modelled	8.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from m. tuberculosis
66	d1g8ma2	Alignment	not modelled	7.8	26	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
67	d2ey4e1	Alignment	not modelled	7.6	31	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
68	d1nvma1	Alignment	not modelled	7.5	24	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
69	c2ze3A	Alignment	not modelled	7.4	10	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
70	d1wu7a2	Alignment	not modelled	7.4	50	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
71	d1pkxa2	Alignment	not modelled	7.2	30	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
72	c1wv9B	Alignment	not modelled	7.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermophilus hb8
73	c3e5bB	Alignment	not modelled	6.8	11	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
74	c5tv6A	Alignment	not modelled	6.7	12	PDB header: ligase Chain: A: PDB Molecule: 6-carboxyhexanoate--coa ligase; PDBTitle: a. aeolicus biow with pimelate
75	d2f6mb1	Alignment	not modelled	6.5	22	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
76	c2qecA	Alignment	not modelled	6.4	29	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase hpa2 and related PDBTitle: crystal structure of histone acetyltransferase hpa2 and related2 acetyltransferase (np_600742.1) from corynebacterium glutamicum atcc3 13032 at 1.90 a resolution
77	c3i2vA	Alignment	not modelled	6.2	27	PDB header: transferase Chain: A: PDB Molecule: adenyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
78	c2jy0A	Alignment	not modelled	6.1	58	PDB header: membrane protein, viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution nmr structure of hcv ns2 protein, membrane

				segment2 (1-27)	
79	c5b42A_	Alignment	not modelled	6.1	10 PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
80	d2g3aa1	Alignment	not modelled	6.0	20 Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
81	c2pbxB_	Alignment	not modelled	5.6	16 PDB header: transcription Chain: B: PDB Molecule: hemagglutinin/protease regulatory protein; PDBTitle: vibrio cholerae hagr
82	c2hwwC_	Alignment	not modelled	5.4	33 PDB header: rna binding protein Chain: C: PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
83	d2aqaal	Alignment	not modelled	5.3	31 Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
84	c4uhpA_	Alignment	not modelled	5.3	67 PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
85	c2qyhD_	Alignment	not modelled	5.2	23 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical conserved protein, gk1056; PDBTitle: crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
86	c6ahrL_	Alignment	not modelled	5.2	60 PDB header: hydrolase/rna Chain: L: PDB Molecule: ribonuclease p protein subunit p40; PDBTitle: cryo-em structure of human ribonuclease p
87	c2cazB_	Alignment	not modelled	5.2	22 PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein vps28; PDBTitle: escrt-i core
88	d2cazb1	Alignment	not modelled	5.2	22 Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
89	c3s9vD_	Alignment	not modelled	5.2	14 PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
90	c5z6nA_	Alignment	not modelled	5.1	11 PDB header: transferase Chain: A: PDB Molecule: protein elaa; PDBTitle: crystal structure of escherichia coli elaa
91	c1thzA_	Alignment	not modelled	5.0	26 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