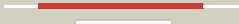



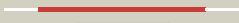



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2902c_(rnhB)_3212172_3212966
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	6c5868ba7afe41dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5y9pA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease hii; PDBTitle: staphylococcus aureus rnae hii
2	d2etja1	 Alignment		100.0	39	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
3	c2etjA_	 Alignment		100.0	39	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease hii; PDBTitle: crystal structure of ribonuclease hii (ec 3.1.26.4) (rnae hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
4	c3kioA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease h2 subunit a; PDBTitle: mouse rnae h2 complex
5	d1io2a_	 Alignment		100.0	28	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
6	d1uaxa_	 Alignment		100.0	29	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
7	d1i39a_	 Alignment		100.0	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
8	c1i3aA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease hii; PDBTitle: rnae hii from archaeoglobus fulgidus with cobalt hexammine2 chloride
9	d1ekea_	 Alignment		100.0	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
10	c2d0bA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease hiii; PDBTitle: crystal structure of bst-rnae hiii in complex with mg2+
11	c3vn5A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease hiii; PDBTitle: crystal structure of aquifex aeolicus rnae h3

12	c4py5A_	Alignment		100.0	24	PDB header: hydrolase/dna/rna Chain: A: PDB Molecule: ribonuclease; PDBTitle: thermovibrio ammonificans rnase h3 in complex with 19-mer rna/dna
13	c3gocB_	Alignment		92.0	27	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
14	c2w36B_	Alignment		55.7	26	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
15	c3ga2A_	Alignment		52.9	26	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624
16	c4xpuA_	Alignment		52.9	26	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: the crystal structure of endov from e.coli
17	c5us5B_	Alignment		40.6	24	PDB header: structural genomics Chain: B: PDB Molecule: supf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
18	d1c8ba_	Alignment		24.8	20	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Germination protease
19	c1zecA_	Alignment		23.3	75	PDB header: viral peptide Chain: A: PDB Molecule: nef1-25; PDBTitle: nmr solution structure of nef1-25, 20 structures
20	c2nrzB_	Alignment		23.0	17	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrbc bound to its2 catalytic divalent cation
21	c4nspA_	Alignment	not modelled	18.9	30	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of human endov
22	c2d7cD_	Alignment	not modelled	17.3	38	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of human rab11 in complex with fip3 rab-2 binding domain
23	d1tlha_	Alignment	not modelled	14.0	39	Fold: Anti-sigma factor AsiA Superfamily: Anti-sigma factor AsiA Family: Anti-sigma factor AsiA
24	c6mpnB_	Alignment	not modelled	13.8	40	PDB header: membrane protein Chain: B: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i42e crystallized from racemic detergent
25	c6mpnA_	Alignment	not modelled	13.8	40	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i42e crystallized from racemic detergent
26	c5klvl_	Alignment	not modelled	13.3	57	PDB header: oxidoreductase Chain: I: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: structure of bos taurus cytochrome bc1 with fenamidone inhibited
27	c3lwbB_	Alignment	not modelled	13.2	40	PDB header: transport protein Chain: B: PDB Molecule: m2 protein; PDBTitle: high resolution crystal structure of transmembrane domain of m2
28	c4rwcA_	Alignment	not modelled	13.2	40	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm crystallized from racemic detergent
						PDB header: transport protein

29	c3lbwD_	Alignment	not modelled	13.2	40	Chain: D: PDB Molecule: m2 protein; PDBTitle: high resolution crystal structure of transmembrane domain of m2
30	c3lbwC_	Alignment	not modelled	13.2	40	PDB header: transport protein Chain: C: PDB Molecule: m2 protein; PDBTitle: high resolution crystal structure of transmembrane domain of m2
31	c3lbwA_	Alignment	not modelled	13.2	40	PDB header: transport protein Chain: A: PDB Molecule: m2 protein; PDBTitle: high resolution crystal structure of transmembrane domain of m2
32	c4rwbA_	Alignment	not modelled	13.2	40	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic influenza m2-tm crystallized from monoolein lipidic cubic2 phase
33	c4rwbB_	Alignment	not modelled	13.2	40	PDB header: membrane protein Chain: B: PDB Molecule: matrix protein 2; PDBTitle: racemic influenza m2-tm crystallized from monoolein lipidic cubic2 phase
34	c6mpmA_	Alignment	not modelled	13.1	40	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i42a crystallized from racemic detergent
35	c6mplA_	Alignment	not modelled	13.1	40	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i39a crystallized from racemic detergent
36	c5viaA_	Alignment	not modelled	12.5	5	PDB header: oxidoreductase Chain: A: PDB Molecule: pseudoperoxidase; PDBTitle: crystal structural of leishmania major pseudoperoxidase
37	d2j9ga2	Alignment	not modelled	12.2	75	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
38	c2yhgA_	Alignment	not modelled	12.2	26	PDB header: hydrolase Chain: A: PDB Molecule: cellulose-binding protein; PDBTitle: ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
39	d1ulza2	Alignment	not modelled	12.2	75	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
40	c1b4nD_	Alignment	not modelled	11.3	16	PDB header: oxidoreductase Chain: D: PDB Molecule: formaldehyde ferredoxin oxidoreductase; PDBTitle: formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
41	d2pkqo1	Alignment	not modelled	10.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c4z42A_	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit gamma; PDBTitle: crystal structure of urease from yersinia enterocolitica
43	d1w96a2	Alignment	not modelled	10.3	38	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
44	d4ubpa_	Alignment	not modelled	9.3	24	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
45	c1qa4A_	Alignment	not modelled	9.0	75	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 nef anchor domain (2-57)); PDBTitle: hiv-1 nef anchor domain, nmr, 2 structures
46	c4furD_	Alignment	not modelled	8.9	21	PDB header: hydrolase Chain: D: PDB Molecule: urease subunit gamma 2; PDBTitle: crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
47	d1u2ca2	Alignment	not modelled	8.9	23	Fold: Dystroglycan, domain 2 Superfamily: Dystroglycan, domain 2 Family: Dystroglycan, domain 2
48	c3u5cG_	Alignment	not modelled	8.8	41	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
49	d1ejxa_	Alignment	not modelled	8.7	24	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
50	d1e9ya2	Alignment	not modelled	8.7	21	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
51	c4y9iA_	Alignment	not modelled	8.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
52	c5vobE_	Alignment	not modelled	8.5	20	PDB header: viral protein/immune system Chain: E: PDB Molecule: envelope glycoprotein ul131a; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 8i21
53	c2fvhB_	Alignment	not modelled	8.4	24	PDB header: hydrolase Chain: B: PDB Molecule: urease gamma subunit; PDBTitle: crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
54	c4hkuA_	Alignment	not modelled	8.4	13	PDB header: transcription Chain: A: PDB Molecule: tetr transcriptional regulator; PDBTitle: the crystal structure of tetr transcriptional regulator (lmo2814) from2 listeria monocytogenes egd-e PDB header: membrane protein

55	c3c9jC	Alignment	not modelled	8.1	31	Chain: C: PDB Molecule: proton channel protein m2, transmembrane segment; PDBTitle: the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
56	c3c9jA	Alignment	not modelled	7.8	31	PDB header: membrane protein Chain: A: PDB Molecule: proton channel protein m2, transmembrane segment; PDBTitle: the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
57	c3c9jB	Alignment	not modelled	7.8	31	PDB header: membrane protein Chain: B: PDB Molecule: proton channel protein m2, transmembrane segment; PDBTitle: the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
58	c3c9jD	Alignment	not modelled	7.5	31	PDB header: membrane protein Chain: D: PDB Molecule: proton channel protein m2, transmembrane segment; PDBTitle: the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
59	c2dzaA	Alignment	not modelled	7.4	24	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
60	c3j38G	Alignment	not modelled	6.8	24	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
61	c3h96B	Alignment	not modelled	6.7	31	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
62	d1qqga2	Alignment	not modelled	6.6	70	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
63	d1dx8a	Alignment	not modelled	6.4	56	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
64	c3r5yC	Alignment	not modelled	6.4	19	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
65	c5fp2A	Alignment	not modelled	6.4	23	PDB header: metal transport Chain: A: PDB Molecule: ferric enterobactin receptor pira; PDBTitle: crystal structure of the siderophore receptor pira from pseudomonas2 aeruginosa
66	d1b25a1	Alignment	not modelled	6.3	16	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
67	c2xznY	Alignment	not modelled	6.3	28	PDB header: ribosome Chain: Y: PDB Molecule: rps6e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
68	c5i8iD	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
69	d1p5ta	Alignment	not modelled	6.2	50	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
70	c1aorB	Alignment	not modelled	6.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde ferredoxin oxidoreductase; PDBTitle: structure of a hyperthermophilic tungstopterin enzyme,2 aldehyde ferredoxin oxidoreductase
71	c2n5jA	Alignment	not modelled	6.0	30	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 n-terminal domain
72	d2pjfa1	Alignment	not modelled	5.7	25	Fold: PSTPO5379-like Superfamily: PSTPO5379-like Family: PSTPO5379-like
73	c6cluC	Alignment	not modelled	5.5	30	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
74	d1xjsa	Alignment	not modelled	5.3	16	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
75	c3zey3	Alignment	not modelled	5.1	17	PDB header: ribosome Chain: 3: PDB Molecule: 40s ribosomal protein s6; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
76	c2nrrA	Alignment	not modelled	5.1	20	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease domain of uvrC
77	c6qk7C	Alignment	not modelled	5.1	40	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
78	c6bocA	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
79	c2kqtA	Alignment	not modelled	5.0	25	PDB header: transport protein Chain: A: PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
						PDB header: membrane protein

80	c6bocC_	Alignment	not modelled	5.0	25	Chain: C; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
81	c4qkIA_	Alignment	not modelled	5.0	25	PDB header: viral protein Chain: A; PDB Molecule: influenza m2 monomer, tm domain (22-46); PDBTitle: influenza a m2 wild type tm domain at high ph in the lipidic cubic2 phase under room temperature diffraction conditions
82	c6bocB_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: B; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
83	c6bkkE_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: E; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine
84	c2kqtD_	Alignment	not modelled	5.0	25	PDB header: transport protein Chain: D; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
85	c2kqtC_	Alignment	not modelled	5.0	25	PDB header: transport protein Chain: C; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
86	c4qk7A_	Alignment	not modelled	5.0	25	PDB header: viral protein Chain: A; PDB Molecule: influenza m2 monomer; PDBTitle: influenza a m2 wild type tm domain at high ph in the lipidic cubic2 phase under cryo diffraction conditions
87	c4qkCA_	Alignment	not modelled	5.0	25	PDB header: viral protein Chain: A; PDB Molecule: influenza m2 monomer; PDBTitle: influenza a m2 wild type tm domain at low ph in the lipidic cubic2 phase under cryo diffraction conditions
88	c5um1A_	Alignment	not modelled	5.0	25	PDB header: proton transport Chain: A; PDB Molecule: matrix protein 2; PDBTitle: xfel structure of influenza a m2 wild type tm domain at intermediate2 ph in the lipidic cubic phase at room temperature
89	c4qkmA_	Alignment	not modelled	5.0	25	PDB header: viral protein Chain: A; PDB Molecule: influenza m2 monomer; PDBTitle: influenza a m2 wild type tm domain at low ph in the lipidic cubic2 phase under room temperature diffraction conditions
90	c6bkkC_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: C; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine
91	c6bkkB_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: B; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine
92	c5jooA_	Alignment	not modelled	5.0	25	PDB header: viral protein Chain: A; PDB Molecule: matrix protein 2; PDBTitle: xfel structure of influenza a m2 wild type tm domain at low ph in the2 lipidic cubic phase at room temperature
93	c6bmzG_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: G; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
94	c6bkkD_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: D; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine
95	c6bmzN_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: N; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
96	c5ttcA_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: A; PDB Molecule: matrix protein 2; PDBTitle: xfel structure of influenza a m2 wild type tm domain at high ph in the2 lipidic cubic phase at room temperature
97	c6bocD_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: D; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
98	c6bkkG_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: G; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine
99	c6bkkF_	Alignment	not modelled	5.0	25	PDB header: membrane protein Chain: F; PDB Molecule: matrix protein 2; PDBTitle: influenza a m2 transmembrane domain bound to amantadine