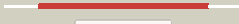



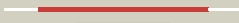








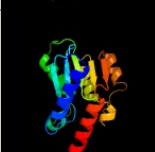



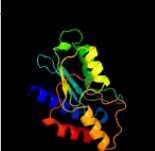






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3752c_(-)_4199425_4199883
Date	Fri Aug 9 18:20:45 BST 2019
Unique Job ID	622e20fae08c122c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nx8A_	Alignment 		100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: trna-specific adenosine deaminase; PDBTitle: the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
2	d2b3ja1	Alignment 		100.0	46	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
3	d1z3aa1	Alignment 		100.0	48	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
4	c3ocqA_	Alignment 		100.0	50	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/adenosine deaminase; PDBTitle: crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
5	d1wwra1	Alignment 		100.0	40	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
6	c3dh1D_	Alignment 		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: trna-specific adenosine deaminase 2; PDBTitle: crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
7	d2g84a1	Alignment 		100.0	26	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
8	d1p6oa_	Alignment 		100.0	29	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
9	c5xkrA_	Alignment 		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: cmp/dcmp deaminase, zinc-binding protein; PDBTitle: crystal structure of msmeg3575 in complex with benzoguanamine
10	d2a8na1	Alignment 		100.0	44	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
11	d2b3za2	Alignment 		100.0	31	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like

12	c2d5nB_	Alignment		100.0	32	PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
13	c3zpgA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
14	c2o7pA_	Alignment		100.0	33	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
15	c2hxA_	Alignment		100.0	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
16	d2hxva2	Alignment		100.0	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
17	d1wkqa_	Alignment		100.0	30	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
18	c2w4IC_	Alignment		100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: human dcmp deaminase
19	c5jfyC_	Alignment		100.0	35	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine deaminase; PDBTitle: crystal structure of a plant cytidine deaminase
20	c2hvwC_	Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from streptococcus mutans
21	c4p9eA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
22	d1vq2a_	Alignment	not modelled	100.0	29	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
23	d1uwza_	Alignment	not modelled	98.5	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
24	c3b8fB_	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: B: PDB Molecule: putative blasticidin s deaminase; PDBTitle: crystal structure of the cytidine deaminase from bacillus anthracis
25	d1mq0a_	Alignment	not modelled	98.5	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
26	d1r5ta_	Alignment	not modelled	98.4	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
27	d2fr5a1	Alignment	not modelled	98.4	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
28	d2d30a1	Alignment	not modelled	98.4	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
29	c3dmoD	Alignment	not modelled	98.4	22	PDB header: hydrolase Chain: D: PDB Molecule: cytidine deaminase;

29	c3umvD	Alignment	not modelled	98.4	44	PDBTitle: 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei PDB header: hydrolase
30	c3jifX	Alignment	not modelled	98.2	24	Chain: X: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
31	c4eg2G	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: G: PDB Molecule: cytidine deaminase; PDBTitle: 2.2 angstrom crystal structure of cytidine deaminase from vibrio2 cholerae in complex with zinc and uridine
32	d1alna1	Alignment	not modelled	98.2	27	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
33	c3r2nC	Alignment	not modelled	98.2	25	PDB header: hydrolase Chain: C: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium leprae
34	d1alna2	Alignment	not modelled	98.1	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
35	c1alnA	Alignment	not modelled	98.0	20	PDB header: hydrolase Chain: A: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase complexed with 3-deazacytidine
36	d2z3ga1	Alignment	not modelled	97.8	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
37	c3oj6C	Alignment	not modelled	97.7	20	PDB header: hydrolase Chain: C: PDB Molecule: blasticidin-s deaminase; PDBTitle: crystal structure of blasticidin s deaminase from coccidioides immitis
38	c3vowB	Alignment	not modelled	95.5	19	PDB header: hydrolase Chain: B: PDB Molecule: probable dna dc->du-editing enzyme apobec-3c; PDBTitle: crystal structure of the human apobec3c having hiv-1 vif-binding2 interface
39	c3g8qA	Alignment	not modelled	95.1	34	PDB header: rna binding protein Chain: A: PDB Molecule: predicted rna-binding protein, contains thump PDBTitle: a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
40	c5tkmA	Alignment	not modelled	94.9	21	PDB header: hydrolase Chain: A: PDB Molecule: dna dc->du-editing enzyme apobec-3b; PDBTitle: crystal structure of human apobec3b n-terminal domain
41	c5k83C	Alignment	not modelled	94.8	19	PDB header: hydrolase Chain: C: PDB Molecule: apolipoprotein b mrna editing enzyme, catalytic peptide- PDBTitle: crystal structure of a primate apobec3g n-domain, in complex with2 ssdna
42	c6b0bE	Alignment	not modelled	92.3	21	PDB header: hydrolase/rna Chain: E: PDB Molecule: apobec3h; PDBTitle: crystal structure of human apobec3h
43	c2mzZA	Alignment	not modelled	91.9	21	PDB header: hydrolase, antiviral protein Chain: A: PDB Molecule: apolipoprotein b mrna-editing enzyme, catalytic PDBTitle: nmr structure of apobec3g ntd variant, sntd
44	c2kboA	Alignment	not modelled	90.8	19	PDB header: hydrolase Chain: A: PDB Molecule: dna dc->du-editing enzyme apobec-3g; PDBTitle: structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
45	c2nytB	Alignment	not modelled	88.1	26	PDB header: hydrolase Chain: B: PDB Molecule: probable c->u-editing enzyme apobec-2; PDBTitle: the apobec2 crystal structure and functional implications2 for aid
46	c6bwyA	Alignment	not modelled	85.9	22	PDB header: hydrolase Chain: A: PDB Molecule: protection of telomeres protein 1, dna dc->du-editing PDBTitle: dna substrate selection by apobec3g
47	c2m65A	Alignment	not modelled	82.9	26	PDB header: hydrolase Chain: A: PDB Molecule: probable dna dc->du-editing enzyme apobec-3a; PDBTitle: nmr structure of human restriction factor apobec3a
48	d2hi7b1	Alignment	not modelled	28.5	43	Fold: Bromodomain-like Superfamily: DsbB-like Family: DsbB-like
49	c3e9jC	Alignment	not modelled	28.4	43	PDB header: oxidoreductase Chain: C: PDB Molecule: thio/disulfide oxidoreductase dsbb; PDBTitle: structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
50	c5mp0D	Alignment	not modelled	26.9	31	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppn-mrna hydrolase; PDBTitle: human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
51	c2k74A	Alignment	not modelled	25.9	29	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
52	d2a6ta2	Alignment	not modelled	23.7	25	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
53	c4zbpC	Alignment	not modelled	22.9	13	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccr-bound atnudt7
54	c2m1cA	Alignment	not modelled	20.4	13	PDB header: hydrolase Chain: A: PDB Molecule: dhh subfamily 1 protein; PDBTitle: haddock structure of gtyybt pas homodimer
						Fold: Phospholipase D/nuclease

55	d1xdpa4	Alignment	not modelled	19.9	16	Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
56	d2o8ra4	Alignment	not modelled	19.5	20	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
57	c3l48B_	Alignment	not modelled	19.1	36	PDB header: transport protein Chain: B: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the c-terminal domain of the papc usher
58	c3u3gA_	Alignment	not modelled	18.2	23	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: structure of lc11-rnase h1 isolated from compost by metagenomic2 approach: insight into the structural bases for unusual enzymatic3 properties of sto-rnase h1
59	d1xfna1	Alignment	not modelled	14.6	33	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
60	c2xzn5_	Alignment	not modelled	13.8	45	PDB header: ribosome Chain: 5: PDB Molecule: ribosomal protein s26e containing protein; 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
61	c6bwsA_	Alignment	not modelled	12.3	21	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
62	c3gqxgA_	Alignment	not modelled	12.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase (duf442); PDBTitle: crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
63	c3j38a_	Alignment	not modelled	12.0	33	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
64	c3ef5A_	Alignment	not modelled	11.6	21	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
65	d1zcca2	Alignment	not modelled	11.5	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
66	d1jfua_	Alignment	not modelled	11.4	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
67	c6hiuA_	Alignment	not modelled	10.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from methylococcus capsulatus (bath)
68	c2o8rA_	Alignment	not modelled	10.7	20	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
69	c4nkpD_	Alignment	not modelled	10.6	21	PDB header: chaperone Chain: D: PDB Molecule: putative extracellular heme-binding protein; PDBTitle: crystal structure of a putative extracellular heme-binding protein2 (despig_02683) from desulfovibrio piger atcc 29098 at 1.24 a3 resolution
70	c5xxua_	Alignment	not modelled	10.4	40	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein us2; PDBTitle: small subunit of toxoplasma gondii ribosome
71	d1ttza_	Alignment	not modelled	10.4	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
72	c2xetB_	Alignment	not modelled	9.9	17	PDB header: transport protein Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
73	c3u5ga_	Alignment	not modelled	9.7	35	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
74	c4a1oB_	Alignment	not modelled	9.5	22	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
75	d1j9ba_	Alignment	not modelled	9.1	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
76	c5xyia_	Alignment	not modelled	9.1	35	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: small subunit of trichomonas vaginalis ribosome
77	c1zy7A_	Alignment	not modelled	8.9	33	PDB header: hydrolase Chain: A: PDB Molecule: rna-specific adenosine deaminase b1, isoform PDBTitle: crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
78	d1psqa_	Alignment	not modelled	8.9	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like

79	d2a2la1	Alignment	not modelled	8.9	23	Fold: Profilin-like Superfamily: GlcG-like Family: GlcG-like
80	d1vcda1	Alignment	not modelled	8.5	38	Fold: Nudix Superfamily: Nudix Family: MutT-like
81	c6ggyB	Alignment	not modelled	8.4	27	PDB header: transferase Chain: B: PDB Molecule: diadenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
82	c3zeyV	Alignment	not modelled	8.3	35	PDB header: ribosome Chain: V: PDB Molecule: ribosomal protein s26, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
83	c4pdeA	Alignment	not modelled	8.3	14	PDB header: hydrolase Chain: A: PDB Molecule: protein fdhd; PDBTitle: crystal structure of fdhd in complex with gdp
84	c2k1aA	Alignment	not modelled	8.1	57	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
85	c2kncA	Alignment	not modelled	8.1	50	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
86	d1nuia2	Alignment	not modelled	7.9	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
87	c4gpuA	Alignment	not modelled	7.7	13	PDB header: hydrolase Chain: A: PDB Molecule: klla0e02245p; PDBTitle: crystal structure of k. lactis dxo1 (ydr370c) in complex with2 manganese
88	c5y4uA	Alignment	not modelled	7.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-3; PDBTitle: crystal structure of grx domain of grx3 from saccharomyces cerevisiae
89	c3watA	Alignment	not modelled	7.3	12	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc
90	c4ehiB	Alignment	not modelled	7.3	23	PDB header: hydrolase,transferase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purH; PDBTitle: an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
91	c2muqA	Alignment	not modelled	7.1	38	PDB header: ubiquitin binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 20 kda; PDBTitle: solution structure of the human faap20 ubz
92	d1q98a	Alignment	not modelled	7.0	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
93	c2murA	Alignment	not modelled	6.8	38	PDB header: protein binding Chain: A: PDB Molecule: fanconi anemia-associated protein of 20 kda; PDBTitle: solution structure of the human faap20 ubz-ubiquitin complex
94	c3a03A	Alignment	not modelled	6.7	22	PDB header: gene regulation Chain: A: PDB Molecule: t-cell leukemia homeobox protein 2; PDBTitle: crystal structure of hox1111 homeodomain
95	c2zvku	Alignment	not modelled	6.5	38	PDB header: transferase Chain: U: PDB Molecule: dna polymerase eta; PDBTitle: crystal structure of pcna in complex with dna polymerase eta fragment
96	c6dknA	Alignment	not modelled	6.4	27	PDB header: hydrolase Chain: A: PDB Molecule: decapping nuclease dxo homolog, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana decapping nuclease dxo1
97	c5zvqA	Alignment	not modelled	6.4	18	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
98	c2yzhD	Alignment	not modelled	6.4	8	PDB header: oxidoreductase Chain: D: PDB Molecule: probable thiol peroxidase; PDBTitle: crystal structure of peroxiredoxin-like protein from aquifex aeolicus
99	c3ipzA	Alignment	not modelled	6.2	15	PDB header: electron transport, oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-s14, chloroplastic; PDBTitle: crystal structure of arabidopsis monothiol glutaredoxin atgrxcp