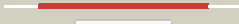



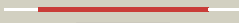




















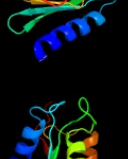



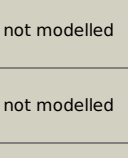


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2365c_(-)_2646757_2647098
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	fb97549603df3ca7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fr5a1	 Alignment		100.0	22	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
2	d2z3ga1	 Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
3	d1mq0a_	 Alignment		100.0	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
4	c3oj6C_	 Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: blastidicin-s deaminase; PDBTitle: crystal structure of blastidicin s deaminase from coccidioides immitis
5	d1uwza_	 Alignment		100.0	27	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
6	c3b8fB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative blastidicin s deaminase; PDBTitle: crystal structure of the cytidine deaminase from bacillus anthracis
7	d2d30a1	 Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
8	c3dmoD_	 Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: cytidine deaminase; PDBTitle: 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
9	c3r2nC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium leprae
10	d1r5ta_	 Alignment		100.0	13	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
11	c3ijfX_	 Alignment		100.0	29	PDB header: hydrolase Chain: X: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium2 tuberculosis

12	c4eg2G	Alignment		100.0	27	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
13	c1alnA	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase complexed with 3-deazacytidine
14	d1alna1	Alignment		99.9	26	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
15	d1alna2	Alignment		99.9	24	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
16	c4p9eA	Alignment		98.4	11	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
17	d1p6oa	Alignment		98.0	12	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
18	c5xkrA	Alignment		97.9	17	PDB header: hydrolase Chain: A: PDB Molecule: cmp/dcmp deaminase, zinc-binding protein; PDBTitle: crystal structure of msmeg3575 in complex with benzoguanamine
19	c2hvwC	Alignment		97.9	10	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from streptococcus mutans
20	c2w4IC	Alignment		97.8	14	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: human dcmp deaminase
21	c5jfyC	Alignment	not modelled	97.7	9	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine deaminase; PDBTitle: crystal structure of a plant cytidine deaminase
22	d2b3ja1	Alignment	not modelled	97.6	14	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
23	d2g84a1	Alignment	not modelled	97.4	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
24	c2hxA	Alignment	not modelled	97.4	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine 2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
25	d1z3aa1	Alignment	not modelled	97.3	13	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
26	d1wkqa	Alignment	not modelled	97.3	12	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
27	c3ocqA	Alignment	not modelled	97.1	12	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/adenosine deaminase; PDBTitle: crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
						Fold: Cytidine deaminase-like

28	d1wwra1	Alignment	not modelled	97.1	15	Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
29	c2o7pA	Alignment	not modelled	97.1	15	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
30	c2nx8A	Alignment	not modelled	97.1	10	PDB header: hydrolase Chain: A: PDB Molecule: trna-specific adenosine deaminase; PDBTitle: the crystal structure of a bifunctional deaminase and deaminase from2 streptococcus pyogenes
31	d1vq2a	Alignment	not modelled	97.0	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
32	d2a8na1	Alignment	not modelled	97.0	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
33	c2d5nB	Alignment	not modelled	95.8	24	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
34	d2b3za2	Alignment	not modelled	95.6	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
35	c3dh1D	Alignment	not modelled	95.2	14	PDB header: hydrolase Chain: D: PDB Molecule: trna-specific adenosine deaminase 2; PDBTitle: crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
36	c3zpgA	Alignment	not modelled	95.2	16	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
37	d2hxva2	Alignment	not modelled	94.9	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
38	d1l5ja3	Alignment	not modelled	39.6	9	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
39	c4uwqK	Alignment	not modelled	33.5	17	PDB header: hydrolase Chain: K: PDB Molecule: soxy protein; PDBTitle: crystal structure of the disulfide-linked complex of the2 thiosulfodyrolase soxb with the carrier-protein soxyz from3 thermus thermophilus
40	c3dmIA	Alignment	not modelled	32.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the periplasmic thioredoxin soxs from paracoccus2 pantotrophus (reduced form)
41	c2zkqn	Alignment	not modelled	30.8	17	PDB header: ribosomal protein/rna Chain: N: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
42	c1l5jB	Alignment	not modelled	30.8	9	PDB header: lyase Chain: B: PDB Molecule: aconitate hydratase 2; PDBTitle: crystal structure of e. coli aconitase b.
43	c5xyid	Alignment	not modelled	29.3	25	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
44	c3c4nB	Alignment	not modelled	21.1	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein dr_0571; PDBTitle: crystal structure of dr_0571 protein from deinococcus radiodurans in2 complex with adp. northeast structural genomics consortium target3 drr125
45	d1njra	Alignment	not modelled	20.1	11	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
46	c3g9bA	Alignment	not modelled	20.0	9	PDB header: transferase Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide-protein PDBTitle: crystal structure of reduced ost6l
47	d3d37a2	Alignment	not modelled	18.9	0	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
48	d1hyua4	Alignment	not modelled	18.5	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
49	c3zey8	Alignment	not modelled	18.1	25	PDB header: ribosome Chain: 8: PDB Molecule: ribosomal protein s29, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
50	c2xznN	Alignment	not modelled	17.8	33	PDB header: ribosome Chain: N: PDB Molecule: rps29e; 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
51	c3j20P	Alignment	not modelled	17.5	33	PDB header: ribosome Chain: P: PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
52	c2oxgD	Alignment	not modelled	17.5	22	PDB header: transport protein Chain: D: PDB Molecule: soxy protein; PDBTitle: the soxyz complex of paracoccus pantotrophus
53	d1b4ub	Alignment	not modelled	17.0	14	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like

						Family: LigB-like
54	c3jyvN_	Alignment	not modelled	16.7	25	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29(a); PDBTitle: structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
55	c5cb9A_	Alignment	not modelled	15.7	29	PDB header: lyase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of c-as lyase with mercaptoethonal
56	d1liua3	Alignment	not modelled	15.5	20	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
57	c3wrbB_	Alignment	not modelled	15.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
58	c5xxud_	Alignment	not modelled	15.1	25	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein us3; PDBTitle: small subunit of toxoplasma gondii ribosome
59	d1booa_	Alignment	not modelled	14.2	5	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
60	c1oatB_	Alignment	not modelled	14.2	17	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
61	c3bh1A_	Alignment	not modelled	13.3	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae
62	c6az1S_	Alignment	not modelled	12.9	25	PDB header: ribosome/antibiotic Chain: S: PDB Molecule: ribosomal protein s14; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
63	d1e0ta3	Alignment	not modelled	12.8	26	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
64	d2g50a3	Alignment	not modelled	12.6	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
65	d3bzka5	Alignment	not modelled	12.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
66	d1pkla3	Alignment	not modelled	12.3	17	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
67	c1s1hN_	Alignment	not modelled	11.8	27	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29-b; 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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
68	c6h9cD_	Alignment	not modelled	11.6	59	PDB header: virus Chain: D: PDB Molecule: vp7; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at3 3.74 angstroms resolution.
69	c4pv3D_	Alignment	not modelled	11.6	14	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations
70	d1siqa2	Alignment	not modelled	11.4	22	Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
71	c6ib5B_	Alignment	not modelled	11.4	24	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
72	c6bwsA_	Alignment	not modelled	11.3	22	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
73	d1gawa1	Alignment	not modelled	10.6	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
74	c5n1tA_	Alignment	not modelled	10.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-binding subunit of sulfide dehydrogenase; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
75	c3vowB_	Alignment	not modelled	10.4	15	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
76	d1fnda1	Alignment	not modelled	10.2	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
77	c2mzza_	Alignment	not modelled	10.2	6	PDB header: hydrolase, antiviral protein Chain: A: PDB Molecule: apolipoprotein b mrna-editing enzyme, catalytic PDBTitle: nmr structure of apobec3g ntd variant, sntd
78	c1senA_	Alignment	not modelled	9.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-like protein p19;

						PDBTitle: endoplasmic reticulum protein rp19 o95881
79	d1sena_	Alignment	not modelled	9.8	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
80	c4yodA_	Alignment	not modelled	9.1	6	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of a thioredoxin-like protein (baccac_02376) from2 bacteroides caccae atcc 43185 at 1.90 a resolution
81	c4ml1D_	Alignment	not modelled	9.1	5	PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
82	c2e7uA_	Alignment	not modelled	8.4	26	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
83	c4e6kl_	Alignment	not modelled	8.3	11	PDB header: metal binding protein/electron transport Chain: I: PDB Molecule: bacterioferritin-associated ferredoxin; PDBTitle: 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd)
84	c3g12A_	Alignment	not modelled	8.3	36	PDB header: lyase Chain: A: PDB Molecule: putative lactoylglutathione lyase; PDBTitle: crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
85	c2fgxA_	Alignment	not modelled	8.2	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
86	c4kp1A_	Alignment	not modelled	8.2	18	PDB header: isomerase Chain: A: PDB Molecule: isopropylmalate/citramalate isomerase large subunit; PDBTitle: crystal structure of ipm isomerase large subunit from methanococcus2 jannaschii (mj0499)
87	c4mubA_	Alignment	not modelled	8.1	14	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: schistosoma mansoni (blood fluke) sulfotransferase/oxamniquine complex
88	c1yspA_	Alignment	not modelled	7.9	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
89	c3ruyB_	Alignment	not modelled	7.8	15	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
90	d1a3xa3	Alignment	not modelled	7.8	22	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
91	c4z04A_	Alignment	not modelled	7.7	27	PDB header: lyase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance /dioxygenase superfamily PDBTitle: crystal structure of a probable lactoylglutathione lyase from brucella2 melitensis in complex with glutathione
92	c3fosA_	Alignment	not modelled	7.7	23	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
93	c4m90A_	Alignment	not modelled	7.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: tumor suppressor candidate 3; PDBTitle: crystal structure of oxidized hn33/tusc3
94	d2bmwa1	Alignment	not modelled	7.6	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
95	d1g5ca_	Alignment	not modelled	7.5	9	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
96	c2k8vA_	Alignment	not modelled	7.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin domain-containing protein 12; PDBTitle: solution structure of oxidised erp18
97	c5k83C_	Alignment	not modelled	7.3	9	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
98	c4e6kG_	Alignment	not modelled	7.3	11	PDB header: metal binding protein/electron transport Chain: G: PDB Molecule: bacterioferritin-associated ferredoxin; PDBTitle: 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd)
99	d2f9wa1	Alignment	not modelled	7.2	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like