







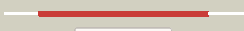















Phyre2

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Description	RVBD3114 (-) _3480756_3481286
Date	Thu Aug 8 16:20:29 BST 2019
Unique Job ID	86b3484f9dcf70a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nx8A_	 Alignment		100.0	21	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	d2g84a1	 Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
3	d2b3ja1	 Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
4	d1z3aa1	 Alignment		100.0	26	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
5	c3ocqA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/adenosine deaminase; PDBTitle: crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
6	d1wwra1	 Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
7	c3dh1D_	 Alignment		100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: trna-specific adenosine deaminase 2; PDBTitle: crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
8	c5xkrA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: cmp/dcmp deaminase, zinc-binding protein; PDBTitle: crystal structure of msmeg3575 in complex with benzoguanamine
9	d1p6oa_	 Alignment		100.0	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
10	d2b3za2	 Alignment		100.0	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
11	c2d5nB_	 Alignment		100.0	19	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

12	d1wkqa_	Alignment		100.0	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
13	d2a8na1	Alignment		100.0	30	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
14	c2o7pA_	Alignment		100.0	21	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	22	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	c3zpgA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
17	d2hxa2	Alignment		100.0	22	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
18	c5ifyC_	Alignment		100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine deaminase; PDBTitle: crystal structure of a plant cytidine deaminase
19	c4p9eA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
20	c2w4IC_	Alignment		100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: human dcmp deaminase
21	c2hvwC_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from streptococcus mutans
22	d1vq2a_	Alignment	not modelled	99.9	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
23	d1r5ta_	Alignment	not modelled	98.2	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
24	d1mq0a_	Alignment	not modelled	98.1	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
25	d2fr5a1	Alignment	not modelled	98.1	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
26	c3jifX_	Alignment	not modelled	98.0	23	PDB header: hydrolase Chain: X: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
27	d1uwza_	Alignment	not modelled	98.0	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
28	d2d30a1	Alignment	not modelled	97.9	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
29	d1alna2	Alignment	not modelled	97.8	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like

						Family: Cytidine deaminase
30	d1alna1	Alignment	not modelled	97.8	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
31	c3r2nC	Alignment	not modelled	97.8	16	PDB header: hydrolase Chain: C; PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium leprae
32	c3dmoD	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: D; PDB Molecule: cytidine deaminase; PDBTitle: 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
33	c4eg2G	Alignment	not modelled	97.6	14	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
34	c3b8fB	Alignment	not modelled	97.4	11	PDB header: hydrolase Chain: B; PDB Molecule: putative blasticidin s deaminase; PDBTitle: crystal structure of the cytidine deaminase from bacillus anthracis
35	c1alnA	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: A; PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase complexed with 3-deazacytidine
36	c3oj6C	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: C; PDB Molecule: blasticidin-s deaminase; PDBTitle: crystal structure of blasticidin s deaminase from coccidioides immitis
37	d2z3ga1	Alignment	not modelled	97.2	16	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
38	c3vowB	Alignment	not modelled	95.8	20	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	c5k83C	Alignment	not modelled	95.6	17	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
40	c3g8qA	Alignment	not modelled	95.0	22	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
41	c5tkmA	Alignment	not modelled	94.8	19	PDB header: hydrolase Chain: A; PDB Molecule: dna dc->du-editing enzyme apobec-3b; PDBTitle: crystal structure of human apobec3b n-terminal domain
42	c6b0bE	Alignment	not modelled	93.4	22	PDB header: hydrolase/rna Chain: E; PDB Molecule: apobec3h; PDBTitle: crystal structure of human apobec3h
43	c2nytB	Alignment	not modelled	92.8	24	PDB header: hydrolase Chain: B; PDB Molecule: probable c->u-editing enzyme apobec-2; PDBTitle: the apobec2 crystal structure and functional implications2 for aid
44	c2mzzA	Alignment	not modelled	90.8	19	PDB header: hydrolase, antiviral protein Chain: A; PDB Molecule: apolipoprotein b mrna-editing enzyme, catalytic PDBTitle: nmr structure of apobec3g ntd variant, sntd
45	c2kboA	Alignment	not modelled	90.6	21	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
46	c6bwyA	Alignment	not modelled	89.0	24	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	87.2	23	PDB header: hydrolase Chain: A; PDB Molecule: probable dna dc->du-editing enzyme apobec-3a; PDBTitle: nmr structure of human restriction factor apobec3a
48	c6bwsA	Alignment	not modelled	59.9	16	PDB header: unknown function Chain: A; PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
49	c6f5fC	Alignment	not modelled	52.2	18	PDB header: dna binding protein Chain: C; PDB Molecule: poly [adp-ribose] polymerase 2; PDBTitle: structure of artd2/parp2 wgr domain bound to double strand dna with 52 nucleotide overhang and 5'phosphate
50	c2eocA	Alignment	not modelled	51.0	10	PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 3; PDBTitle: solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3
51	d2cr9a1	Alignment	not modelled	50.4	9	Fold: WGR domain-like Superfamily: WGR domain-like Family: WGR domain
52	d2hi7b1	Alignment	not modelled	45.2	43	Fold: Bromodomain-like Superfamily: DsbB-like Family: DsbB-like
53	c3e9jC	Alignment	not modelled	45.2	43	PDB header: oxidoreductase Chain: C; PDB Molecule: thiol/disulfide oxidoreductase dsbb; PDBTitle: structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
54	c2k74A	Alignment	not modelled	42.3	29	PDB header: membrane protein, oxidoreductase Chain: A; PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
						PDB header: hydrolase

55	c3u3gA_	Alignment	not modelled	35.4	20	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
56	d1zbfA_1	Alignment	not modelled	35.1	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
57	c4nkpD_	Alignment	not modelled	33.0	14	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
58	d1rila_	Alignment	not modelled	32.8	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
59	c3wvxA_	Alignment	not modelled	29.4	25	PDB header: hydrolase Chain: A: PDB Molecule: s12 family peptidase; PDBTitle: crystal structure of d-stereospecific amidohydrolase from streptomyces2 sp. 82f2
60	d1vdda_	Alignment	not modelled	28.1	30	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
61	c6hihB_	Alignment	not modelled	26.4	37	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: cytochrome c prime beta from methylococcus capsulatus (bath)
62	c1vddC_	Alignment	not modelled	26.2	30	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
63	d2a2la1	Alignment	not modelled	24.7	10	Fold: Profilin-like Superfamily: GlcG-like Family: GlcG-like
64	c5b0rA_	Alignment	not modelled	24.6	21	PDB header: transferase Chain: A: PDB Molecule: lin0857 protein; PDBTitle: beta-1,2-mannobiose phosphorylase from listeria innocua - beta-1,2-2 mannobiose complex
65	c3ic4A_	Alignment	not modelled	23.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin (grx-1); PDBTitle: the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
66	c5z2vB_	Alignment	not modelled	23.0	33	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
67	d1j1la_	Alignment	not modelled	22.5	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
68	c3fpvC_	Alignment	not modelled	19.8	14	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
69	c1zy7A_	Alignment	not modelled	18.1	24	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)
70	c4tr1A_	Alignment	not modelled	18.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
71	c3l48B_	Alignment	not modelled	15.7	25	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
72	c3ve5D_	Alignment	not modelled	15.7	20	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
73	c3ef5A_	Alignment	not modelled	15.4	18	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
74	c3h08B_	Alignment	not modelled	13.7	21	PDB header: hydrolase Chain: B: PDB Molecule: rnh (ribonuclease h); PDBTitle: crystal structure of the ribonuclease h1 from chlorobium2 tepidum
75	c2kq2A_	Alignment	not modelled	13.3	7	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h-related protein; PDBTitle: solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfitobacterium3 hafniense, northeast structural genomics target dhr1a
76	c2muqA_	Alignment	not modelled	13.3	50	PDB header: ubiquitin binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 20 kda; PDBTitle: solution structure of the human faap20 ubz
77	d1h75a_	Alignment	not modelled	13.0	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
78	c2murA_	Alignment	not modelled	13.0	50	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
79	d1tza_	Alignment	not modelled	12.7	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

80	c2rsoA_	Alignment	not modelled	12.6	19	PDB header: transcription Chain: A: PDB Molecule: chromatin-associated protein swi6; PDBTitle: solution structure of the chromodomain of swi6
81	c2m1cA_	Alignment	not modelled	11.8	31	PDB header: hydrolase Chain: A: PDB Molecule: dhh subfamily 1 protein; PDBTitle: haddock structure of gtyybt pas homodimer
82	c4jfcA_	Alignment	not modelled	11.8	13	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from polaromonas sp. js666
83	c3hstD_	Alignment	not modelled	11.6	14	PDB header: hydrolase Chain: D: PDB Molecule: protein rv2228c/mt2287; PDBTitle: n-terminal rnase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein
84	d1xfna1	Alignment	not modelled	11.3	33	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
85	c3watA_	Alignment	not modelled	11.2	16	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
86	c2pbyB_	Alignment	not modelled	10.8	26	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase; PDBTitle: probable glutaminase from geobacillus kaustophilus hta426
87	c3ld0Q_	Alignment	not modelled	10.5	63	PDB header: gene regulation Chain: Q: PDB Molecule: inhibitor of trap, regulated by t-box (trp) sequence rtpa; PDBTitle: crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
88	c3nznA_	Alignment	not modelled	10.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
89	c6hiuA_	Alignment	not modelled	10.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from methylococcus capsulatus (bath)
90	c4or1A_	Alignment	not modelled	9.6	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4783 family protein (bacova_04304) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
91	c1avoA_	Alignment	not modelled	9.4	25	PDB header: proteasome activator Chain: A: PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
92	c2kncA_	Alignment	not modelled	9.1	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
93	d1nuia2	Alignment	not modelled	8.6	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
94	c4ouqA_	Alignment	not modelled	8.4	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4783 family protein (bf1468) from2 bacteroides fragilis ych46 at 1.55 a resolution
95	c5oi9A_	Alignment	not modelled	8.2	25	PDB header: protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: trichoplax adhaerens stil n-terminal domain
96	c5yt6B_	Alignment	not modelled	8.1	80	PDB header: protein binding Chain: B: PDB Molecule: tax1-binding protein 1; PDBTitle: crystal structure of tax1bp1 ubz2 in complex with mono-ubiquitin
97	c4wyhA_	Alignment	not modelled	8.0	17	PDB header: replication Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pxi from the hyperthermophilic archaeon2 sulfolobus solfataricus
98	c3tawA_	Alignment	not modelled	7.5	13	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bdi_3141) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
99	c3qmxA_	Alignment	not modelled	7.5	13	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a