


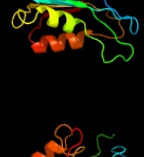
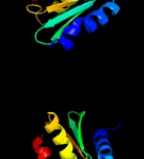
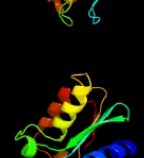
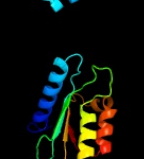

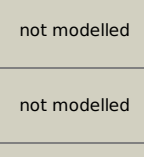


Phyre2

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 Description RVBD3315c_cdd_3703635_3704036
 Date Thu Aug 8 16:20:52 BST 2019
 Unique Job ID d83a172193558129

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uwza_	Alignment		100.0	36	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
2	c3jifX_	Alignment		100.0	100	PDB header: hydrolase Chain: X: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
3	d1r5ta_	Alignment		100.0	32	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
4	d2fr5a1	Alignment		100.0	39	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
5	d1mq0a_	Alignment		100.0	37	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
6	c3r2nC_	Alignment		100.0	58	PDB header: hydrolase Chain: C: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase from mycobacterium leprae
7	d2d30a1	Alignment		100.0	42	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
8	c3dmoD_	Alignment		100.0	44	PDB header: hydrolase Chain: D: PDB Molecule: cytidine deaminase; PDBTitle: 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
9	c3b8fB_	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: putative blasticidin s deaminase; PDBTitle: crystal structure of the cytidine deaminase from bacillus anthracis
10	c3oj6C_	Alignment		100.0	35	PDB header: hydrolase Chain: C: PDB Molecule: blasticidin-s deaminase; PDBTitle: crystal structure of blasticidin s deaminase from coccidioides immitis
11	c1alnA_	Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: cytidine deaminase; PDBTitle: crystal structure of cytidine deaminase complexed with 3-deazacytidine

12	c4eg2G	Alignment		100.0	30	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	d2z3ga1	Alignment		100.0	32	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
14	d1alna1	Alignment		100.0	31	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
15	d1alna2	Alignment		100.0	21	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
16	c4p9eA	Alignment		98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
17	c2hvwC	Alignment		98.3	26	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: crystal structure of dcmp deaminase from streptococcus mutans
18	c5jfyC	Alignment		98.2	17	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine deaminase; PDBTitle: crystal structure of a plant cytidine deaminase
19	c5xkrA	Alignment		98.2	14	PDB header: hydrolase Chain: A: PDB Molecule: cmp/dcmp deaminase, zinc-binding protein; PDBTitle: crystal structure of msmeg3575 in complex with benzoguanamine
20	d1wkqa	Alignment		98.1	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
21	d1p6oa	Alignment	not modelled	98.0	20	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
22	c2w4IC	Alignment	not modelled	98.0	24	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidylate deaminase; PDBTitle: human dcmp deaminase
23	c3ocqA	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/adenosine deaminase; PDBTitle: crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
24	d1z3aa1	Alignment	not modelled	97.8	15	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
25	d1wwra1	Alignment	not modelled	97.8	17	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
26	d2b3ja1	Alignment	not modelled	97.8	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
27	c2o7pA	Alignment	not modelled	97.6	17	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
28	d2g84a1	Alignment	not modelled	97.5	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
						Fold: Cytidine deaminase-like

29	d2a8na1	Alignment	not modelled	97.5	18	Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
30	c2nx8A	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: A: PDB Molecule: trna-specific adenosine deaminase; PDBTitle: the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
31	c2hxA	Alignment	not modelled	97.3	20	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
32	d1vq2a	Alignment	not modelled	97.2	22	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
33	d2hxa2	Alignment	not modelled	97.2	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
34	c3zpgA	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
35	c2d5nB	Alignment	not modelled	96.6	16	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
36	d2b3za2	Alignment	not modelled	96.3	18	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
37	c3dh1D	Alignment	not modelled	96.1	17	PDB header: hydrolase Chain: D: PDB Molecule: trna-specific adenosine deaminase 2; PDBTitle: crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
38	d3d37a2	Alignment	not modelled	44.6	23	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
39	c2gacD	Alignment	not modelled	35.0	14	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
40	c2eqjA	Alignment	not modelled	30.5	33	PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
41	d2eppa1	Alignment	not modelled	25.4	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c2eppA	Alignment	not modelled	23.0	36	PDB header: transcription Chain: A: PDB Molecule: poz-, at hook-, and zinc finger-containing PDBTitle: solution structure of the first c2h2 type zinc finger2 domain of zinc finger protein 278
43	c3trkA	Alignment	not modelled	21.4	24	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
44	c5if9A	Alignment	not modelled	20.9	21	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
45	c2f42A	Alignment	not modelled	20.7	28	PDB header: chaperone Chain: A: PDB Molecule: stip1 homology and u-box containing protein 1; PDBTitle: dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
46	c5cm2M	Alignment	not modelled	19.0	27	PDB header: transferase Chain: M: PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
47	c2kreA	Alignment	not modelled	18.2	33	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin conjugation factor e4 b; PDBTitle: solution structure of e4b/ufd2a u-box domain
48	c6g4wr	Alignment	not modelled	16.4	27	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
49	c1apzB	Alignment	not modelled	16.1	11	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product
50	d2pg3a1	Alignment	not modelled	15.4	29	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
51	c4m90A	Alignment	not modelled	15.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: tumor suppressor candidate 3; PDBTitle: crystal structure of oxidized hn33/tusc3
52	c6dnuB	Alignment	not modelled	15.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsbd; PDBTitle: crystal structure of neisseria meningitidis dsbd c-terminal domain in2 the oxidised form
53	c3dmIA	Alignment	not modelled	14.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the periplasmic thioredoxin soxs from paracoccus2 pantotrophus (reduced form)
						Fold: Ribokinase-like

54	d1ua4a_	Alignment	not modelled	14.2	36	Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
55	c2j6aA_	Alignment	not modelled	14.1	27	PDB header: transferase Chain: A: PDB Molecule: protein trm112; PDBTitle: crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
56	d1r2za1	Alignment	not modelled	14.0	10	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
57	d1no1a_	Alignment	not modelled	13.4	36	Fold: Replisome organizer (g39p helicase loader/inhibitor protein) Superfamily: Replisome organizer (g39p helicase loader/inhibitor protein) Family: Replisome organizer (g39p helicase loader/inhibitor protein)
58	d1sjya_	Alignment	not modelled	13.4	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
59	c3cwfA_	Alignment	not modelled	13.3	33	PDB header: transferase Chain: A: PDB Molecule: alkaline phosphatase synthesis sensor protein phor; PDBTitle: crystal structure of pas domain of two-component sensor histidine2 kinase
60	d2dja1	Alignment	not modelled	13.2	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
61	c4pv3D_	Alignment	not modelled	13.0	17	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
62	c3gwnA_	Alignment	not modelled	12.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-linked sulfhydryl oxidase r596; PDBTitle: crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
63	c1q5rD_	Alignment	not modelled	12.8	20	PDB header: hydrolase Chain: D: PDB Molecule: proteasome alpha-type subunit 1; PDBTitle: the rhodococcus 20s proteasome with unprocessed pro-peptides
64	d1q5qa_	Alignment	not modelled	12.8	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
65	c4wz1B_	Alignment	not modelled	12.7	17	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase lubx; PDBTitle: crystal structure of u-box 2 of lubx / legu2 / lpp2887 from legionella2 pneumophila str. paris, wild-type
66	d1r0ka3	Alignment	not modelled	12.5	7	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
67	c2knnA_	Alignment	not modelled	12.4	80	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin-o2; PDBTitle: solution structure of the cyclotide cycloviolacin o2 with2 glu6 methylated (cyo2me)
68	c3gw1B_	Alignment	not modelled	12.4	33	PDB header: oxidoreductase Chain: B: PDB Molecule: fad-linked sulfhydryl oxidase; PDBTitle: crystal structure of asfv pb1191, a viral sulfhydryl oxidase
69	c3p8dB_	Alignment	not modelled	12.3	26	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
70	c1no1C_	Alignment	not modelled	12.2	36	PDB header: replication Chain: C: PDB Molecule: replisome organizer; PDBTitle: structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
71	c2ldmA_	Alignment	not modelled	12.0	26	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
72	d1l5ja3	Alignment	not modelled	12.0	12	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
73	c3htkC_	Alignment	not modelled	12.0	10	PDB header: recombination/replication/ligase Chain: C: PDB Molecule: e3 sumo-protein ligase mms21; PDBTitle: crystal structure of mms21 and smc5 complex
74	c3jugA_	Alignment	not modelled	11.6	38	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
75	c3g9bA_	Alignment	not modelled	11.2	18	PDB header: transferase Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide-protein PDBTitle: crystal structure of reduced ost6l
76	d1jr8a_	Alignment	not modelled	11.0	33	Fold: Four-helical up-and-down bundle Superfamily: FAD-dependent thiol oxidase Family: FAD-dependent thiol oxidase
77	c2ppvA_	Alignment	not modelled	11.0	21	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
78	c5hkaA_	Alignment	not modelled	10.7	16	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: crystal structure of cdi complex from escherichia coli stec_o31
79	c4e6kl_	Alignment	not modelled	10.6	16	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)
80	c2r2jA_	Alignment	not modelled	10.2	9	PDB header: chaperone Chain: A: PDB Molecule: thioredoxin domain-containing protein 4; PDBTitle: crystal structure of human erp44
81	d1sena_	Alignment	not modelled	10.2	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
82	c1senA_	Alignment	not modelled	10.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-like protein p19; PDBTitle: endoplasmic reticulum protein rp19 o95881
83	c5ly0B_	Alignment	not modelled	9.9	50	PDB header: transcription Chain: B: PDB Molecule: lob family transfactor ramosa2.1; PDBTitle: crystal structure of lob domain of ramosa2 from wheat
84	c5fmga_	Alignment	not modelled	9.9	11	PDB header: hydrolase Chain: A: PDB Molecule: proteasome subunit alpha, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
85	c1p4vA_	Alignment	not modelled	9.8	14	PDB header: hydrolase Chain: A: PDB Molecule: n(4)-(beta-n-acetylglucosaminyll)-l-asparaginase PDBTitle: crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
86	c3hypB_	Alignment	not modelled	9.6	36	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
87	c2vocA_	Alignment	not modelled	9.6	18	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin a active site mutants form mixed disulfide dimers that2 resemble enzyme-substrate reaction intermediate
88	c2xb1A_	Alignment	not modelled	9.5	56	PDB header: transcription Chain: A: PDB Molecule: pygopus homolog 2, b-cell clil/lymphoma 9-like protein; PDBTitle: crystal structure of the human pygo2 phd finger in complex with the2 b9l hd1 domain
89	c3td7A_	Alignment	not modelled	9.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-linked sulfhydryl oxidase r596; PDBTitle: crysal structure of the mimivirus sulfhydryl oxidase r596
90	d1ryp1_	Alignment	not modelled	9.5	8	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
91	d2hzba1	Alignment	not modelled	9.5	30	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
92	d1j9ba_	Alignment	not modelled	9.4	40	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
93	d1t1ha_	Alignment	not modelled	9.4	17	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
94	c6qm7V_	Alignment	not modelled	9.1	22	PDB header: hydrolase Chain: V: PDB Molecule: proteasome beta1 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
95	c1wkyA_	Alignment	not modelled	9.1	20	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-mannanase; PDBTitle: crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
96	d1qqra_	Alignment	not modelled	9.0	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
97	c4a0tB_	Alignment	not modelled	9.0	35	PDB header: viral protein Chain: B: PDB Molecule: tail fiber protein; PDBTitle: structure of the carboxy-terminal domain of bacteriophage t7 fibre2 gp17 containing residues 371-553.
98	c1jlzA_	Alignment	not modelled	8.9	67	PDB header: toxin Chain: A: PDB Molecule: tityustoxin alpha-ktx; PDBTitle: solution structure of a k+-channel blocker from the2 scorpion toxin of tityus cambridgei
99	d1jlza_	Alignment	not modelled	8.9	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins