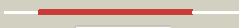




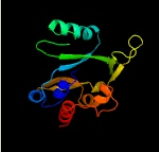
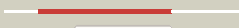














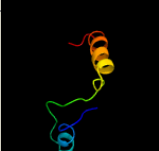


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0836c (-)_932282_932935
Date	Fri Jul 26 01:50:42 BST 2019
Unique Job ID	fe9cdcacfa80305

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uvdA	 Alignment		99.4	18	PDB header: transferase Chain: A; PDB Molecule: nucleotidyltransferase-like protein; PDBTitle: crystal structure of an antigenic nucleotidyltransferase-like protein2 from paracoccidioides brasiliensis
2	c4wqkA	 Alignment		99.0	21	PDB header: transferase Chain: A; PDB Molecule: 2"-aminoglycoside nucleotidyltransferase; PDBTitle: crystal structure of aminoglycoside nucleotidyltransferase ant(2")-2 ia, apo form
3	c4e8iA	 Alignment		98.2	14	PDB header: transferase Chain: A; PDB Molecule: lincosamide resistance protein; PDBTitle: crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
4	c4ok0B	 Alignment		97.4	17	PDB header: transferase Chain: B; PDB Molecule: putative; PDBTitle: crystal structure of putative nucleotidyltransferase from h. pylori
5	c1vfgB	 Alignment		96.9	15	PDB header: transferase/rna Chain: B; PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
6	c4x4wB	 Alignment		96.1	19	PDB header: rna binding protein Chain: B; PDB Molecule: cca trna nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of the full-length human mitochondrial cca-adding2 enzyme
7	d1vfga2	 Alignment		95.7	17	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
8	c3h37B	 Alignment		95.1	27	PDB header: transferase Chain: B; PDB Molecule: trna nucleotidyl transferase-related protein; PDBTitle: the structure of cca-adding enzyme apo form i
9	c6q52A	 Alignment		95.1	23	PDB header: rna binding protein Chain: A; PDB Molecule: cca-adding enzyme; PDBTitle: structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
10	d1r89a2	 Alignment		94.7	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Archaeal tRNA CCA-adding enzyme catalytic domain
11	d1ou5a2	 Alignment		94.5	28	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like

12	c1miyB_	Alignment		94.3	29	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
13	c3wfsD_	Alignment		94.1	21	PDB header: transferase/rna Chain: D: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
14	c3wfpA_	Alignment		94.0	21	PDB header: transferase Chain: A: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
15	c3wfrG_	Alignment		93.9	21	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
16	c3aqnA_	Alignment		93.6	17	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
17	c3wfrH_	Alignment		92.9	21	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
18	c3wfoB_	Alignment		92.7	18	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 1)
19	c3wfrE_	Alignment		92.5	18	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
20	d1miwa2	Alignment		92.5	39	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
21	c3wfrF_	Alignment	not modelled	92.2	19	PDB header: transferase/rna Chain: F: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
22	c3wfgG_	Alignment	not modelled	91.6	19	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
23	c1ou5A_	Alignment	not modelled	91.4	30	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
24	c3wfsC_	Alignment	not modelled	91.1	18	PDB header: transferase/rna Chain: C: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
25	c3wfgE_	Alignment	not modelled	90.7	18	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
26	c3wfgH_	Alignment	not modelled	90.6	18	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
27	c1sz1A_	Alignment	not modelled	89.9	16	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
28	c3wfpB_	Alignment	not modelled	86.0	18	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
						PDB header: transferase Chain: A: PDB Molecule: cgas/dncv-like nucleotidyltransferase in e.

29	c6e0kA	Alignment	not modelled	86.0	20	coli homolog; PDBTitle: structure of rhodothermus marinus cdne c-ump-amp synthase
30	c4xq7A	Alignment	not modelled	74.6	29	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase-like protein; PDBTitle: the crystal structure of the oas-like domain (old) of human oasl
31	d1no5a	Alignment	not modelled	64.1	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
32	c3somO	Alignment	not modelled	44.8	28	PDB header: oxidoreductase Chain: O: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of human mmachc
33	c1iv8A	Alignment	not modelled	43.5	24	PDB header: isomerase Chain: A: PDB Molecule: maltoooligosyl trehalose synthase; PDBTitle: crystal structure of maltoooligosyl trehalose synthase
34	c6e0oA	Alignment	not modelled	42.8	20	PDB header: transferase/rna Chain: A: PDB Molecule: cgas/dncv-like nucleotidyltransferase in e. coli homolog; PDBTitle: structure of elizabethkingia meningoseptica cdne cyclic dinucleotide2 synthase with pppa[3'-5']pa
35	d2q66a2	Alignment	not modelled	41.6	12	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly(A) polymerase, PAP, N-terminal domain
36	c3fpnB	Alignment	not modelled	36.9	8	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrB interaction domain; PDBTitle: crystal structure of uvra-uvrB interaction domains
37	d1iv8a2	Alignment	not modelled	35.9	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
38	c4s3nA	Alignment	not modelled	35.8	12	PDB header: transferase/rna Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase 3; PDBTitle: crystal structure of human oas3 domain i in complex with dsrna
39	d2nrka1	Alignment	not modelled	30.1	12	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GrpB-like
40	c3sc0A	Alignment	not modelled	27.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
41	c4dfcC	Alignment	not modelled	26.2	18	PDB header: hydrolase/dna binding protein Chain: C: PDB Molecule: transcription-repair-coupling factor; PDBTitle: core uvra/trcf complex
42	c5zcrB	Alignment	not modelled	25.7	20	PDB header: hydrolase Chain: B: PDB Molecule: maltoooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
43	c3hjeA	Alignment	not modelled	20.2	20	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfolobus tokodaii hypothetical maltoooligosyl2 trehalose synthase
44	c3c66B	Alignment	not modelled	15.2	14	PDB header: transferase Chain: B: PDB Molecule: poly(a) polymerase; PDBTitle: yeast poly(a) polymerase in complex with fip1 residues 80-105
45	c5n7sA	Alignment	not modelled	13.4	15	PDB header: transport protein Chain: A: PDB Molecule: type ii secretion system protein I; PDBTitle: crystal structure of the periplasmic domain of xcpy, op crystal form.
46	d2vana2	Alignment	not modelled	12.5	14	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
47	d1t5la1	Alignment	not modelled	11.7	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
48	c4nj7P	Alignment	not modelled	11.6	10	PDB header: protein binding Chain: P: PDB Molecule: auxin response factor 7; PDBTitle: pb1 domain of atarf7 - semet derivative
49	c1q78A	Alignment	not modelled	11.2	14	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase alpha; PDBTitle: crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride
50	d1ylqa1	Alignment	not modelled	11.0	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
51	c4ui9M	Alignment	not modelled	9.7	20	PDB header: cell cycle Chain: M: PDB Molecule: anaphase-promoting complex subunit 13; PDBTitle: atomic structure of the human anaphase-promoting complex
52	d2fmpa3	Alignment	not modelled	8.3	11	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
53	c3hjhA	Alignment	not modelled	8.2	17	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair-coupling factor; PDBTitle: a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
54	d2eyqa4	Alignment	not modelled	7.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
						Fold: Nucleotidyltransferase

55	d1q79a2	Alignment	not modelled	7.6	14	Superfamily: Nucleotidyltransferase Family: Poly(A) polymerase, PAP, N-terminal domain
56	c2la3A_	Alignment	not modelled	7.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
57	d2b2na1	Alignment	not modelled	6.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
58	d1wota_	Alignment	not modelled	6.6	11	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
59	d1j5ya2	Alignment	not modelled	6.2	14	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
60	c1px5A_	Alignment	not modelled	6.2	27	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthetase 1; PDBTitle: crystal structure of the 2'-specific and double-stranded2 rna-activated interferon-induced antiviral protein 2'-5'-3 oligoadenylate synthetase
61	c3dnlB_	Alignment	not modelled	6.1	29	PDB header: viral protein Chain: B: PDB Molecule: hiv-1 envelope glycoprotein gp120; PDBTitle: molecular structure for the hiv-1 gp120 trimer in the b12-bound state
62	d1wmhb_	Alignment	not modelled	5.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
63	c4p4oA_	Alignment	not modelled	5.6	11	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
64	c2qmhK_	Alignment	not modelled	5.5	11	PDB header: transferase Chain: K: PDB Molecule: hpr kinase/phosphorylase; PDBTitle: structure of v267f mutant hprk/p
65	d2bcqa3	Alignment	not modelled	5.4	25	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
66	c2bcuA_	Alignment	not modelled	5.4	25	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
67	d1fiua_	Alignment	not modelled	5.4	12	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease NgoIV
68	c5nv8A_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A: PDB Molecule: ef-p arginine 32 rhamnosyl-transferase; PDBTitle: structural basis for earp-mediated arginine glycosylation of2 translation elongation factor ef-p