

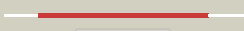























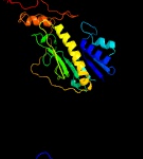

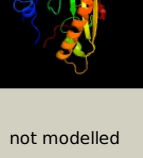


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3404c (-)_3824060_3824764
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	a83b907ee8348d22

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4pzuF_	 Alignment		100.0	100	PDB header: transferase Chain: F; PDB Molecule: uncharacterized protein rv3404c/mt3512; PDBTitle: crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
2	c4yfvA_	 Alignment		100.0	38	PDB header: transferase Chain: A; PDB Molecule: viof; PDBTitle: x-ray structure of the 4-n-formyltransferase viof from providencia2 alcalifaciens o30
3	c1z7eC_	 Alignment		100.0	21	PDB header: hydrolase Chain: C; PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
4	c4nv1D_	 Alignment		100.0	38	PDB header: transferase Chain: D; PDB Molecule: formyltransferase; PDBTitle: crystal structure of a 4-n formyltransferase from francisella2 tularensis
5	c6nbpA_	 Alignment		100.0	50	PDB header: transferase Chain: A; PDB Molecule: n-formyltransferase; PDBTitle: crystal structure of a sugar n-formyltransferase from the plant2 pathogen pantoea ananatis
6	c3tqqA_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: methionyl-trna formyltransferase; PDBTitle: structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
7	c1fmtA_	 Alignment		100.0	22	PDB header: formyltransferase Chain: A; PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
8	c1s3iA_	 Alignment		100.0	23	PDB header: hydrolase, oxidoreductase Chain: A; PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
9	c3q0iA_	 Alignment		100.0	23	PDB header: transferase Chain: A; PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from vibrio cholerae
10	c5uaiA_	 Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
11	c1yrwA_	 Alignment		100.0	23	PDB header: transferase Chain: A; PDB Molecule: protein arna; PDBTitle: crystal structure of e.coli arna transformylase domain

12	c3rfoA	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
13	c5vvtD	Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- PDBTitle: crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
14	c1zghA	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from clostridium thermocellum
15	c4lxuB	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: wlard, a sugar 3n-formyl transferase; PDBTitle: dtdp-fuc3n and 5-n-formyl-thf
16	c5uimB	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: formyltransferase; PDBTitle: x-ray structure of the fdtf n-formyltransferase from salmonella2 enteric o60 in complex with folinic acid and tdp-qui3n
17	d1s3ia2	Alignment		100.0	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
18	c6ci2A	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: formyltransferase psej; PDBTitle: crystal structure of the formyltransferase psej from anoxybacillus2 kamchatkensis
19	d2bw0a2	Alignment		100.0	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
20	d2blna2	Alignment		100.0	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
21	c3kcgA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
22	d1fmta2	Alignment	not modelled	100.0	24	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
23	d1jkxa	Alignment	not modelled	100.0	18	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
24	c3aufA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
25	c2ywrA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus
26	c3p9xB	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
27	c3tqrA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella

						burnetii
28	c3av3A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
29	c3louB	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
30	c3n0vD	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
31	c3dcjA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide formyltransferase PDBTitle: crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
32	c3w7bB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
33	d1meoa	Alignment	not modelled	100.0	15	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
34	c4ds3A	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
35	c3obiC	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
36	c3o1lB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
37	c3nrbd	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
38	c4s1nA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
39	c5cjjA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
40	d1zgah2	Alignment	not modelled	100.0	16	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
41	c4xd0A	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: tdp-3-aminoquinovose-n-formyltransferase; PDBTitle: x-ray structure of the n-formyltransferase qdtf from providencia2 alcalifaciens
42	d1s3ia1	Alignment	not modelled	98.7	15	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
43	d2bw0a1	Alignment	not modelled	98.6	13	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
44	d2blna1	Alignment	not modelled	98.5	20	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
45	d1fmta1	Alignment	not modelled	98.4	17	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
46	c6culG	Alignment	not modelled	97.6	22	PDB header: transferase Chain: G: PDB Molecule: pyoverdine synthetase f; PDBTitle: pdf of pyoverdin biosynthesis is a structurally unique n10-2 formyltetrahydrofolate-dependent formyltransferase
47	d1zgah1	Alignment	not modelled	95.0	12	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
48	d1vlva2	Alignment	not modelled	64.8	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
49	c2xd4A	Alignment	not modelled	62.9	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
50	c5ig9H	Alignment	not modelled	61.9	16	PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc

51	c6p2iA	Alignment	not modelled	61.6	10	PDB header: oxidoreductase, biosynthetic protein Chain: A: PDB Molecule: glycerate dehydrogenase; PDBTitle: acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
52	d1gsoa2	Alignment	not modelled	60.6	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
53	d1pvva2	Alignment	not modelled	60.6	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
54	c2yyaB	Alignment	not modelled	57.6	16	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
55	c3d8tB	Alignment	not modelled	57.5	17	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
56	d2at2a2	Alignment	not modelled	57.4	23	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
57	c1vkzA	Alignment	not modelled	53.5	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
58	c2l2qA	Alignment	not modelled	53.5	24	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
59	c4mgeB	Alignment	not modelled	52.2	18	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
60	c3gg9C	Alignment	not modelled	50.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
61	c3vpbC	Alignment	not modelled	50.3	17	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
62	c3nbmA	Alignment	not modelled	50.1	13	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
63	c2p2gD	Alignment	not modelled	48.7	14	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
64	d1wd7a	Alignment	not modelled	45.7	18	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
65	d1vkza2	Alignment	not modelled	45.2	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
66	c5es8A	Alignment	not modelled	42.0	28	PDB header: ligase Chain: A: PDB Molecule: linear gramicidin synthetase subunit a; PDBTitle: crystal structure of the initiation module of lgra in the thiolation2 state
67	d1dxya2	Alignment	not modelled	41.8	13	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
68	c1jr2A	Alignment	not modelled	40.7	11	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
69	d1jr2a	Alignment	not modelled	40.7	11	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
70	c1gsoA	Alignment	not modelled	38.2	16	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
71	c4njmA	Alignment	not modelled	37.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
72	c4s1vD	Alignment	not modelled	36.0	11	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
73	c6jnkA	Alignment	not modelled	35.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p)(+)); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
74	c1a1sA	Alignment	not modelled	34.4	14	PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus

75	c3lp8A_	Alignment	not modelled	33.9	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
76	c1v1vA_	Alignment	not modelled	31.2	13	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
77	c5vevB_	Alignment	not modelled	29.4	25	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
78	d1gsaa1	Alignment	not modelled	29.3	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
79	d1eqza_	Alignment	not modelled	28.9	14	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
80	c3e9mC_	Alignment	not modelled	27.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
81	d1ybha1	Alignment	not modelled	26.1	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	c1ks9A_	Alignment	not modelled	25.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
83	c1xdwA_	Alignment	not modelled	24.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
84	c2w37A_	Alignment	not modelled	24.0	9	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
85	c2f8nK_	Alignment	not modelled	23.9	22	PDB header: structural protein/dna Chain: K: PDB Molecule: histone h2a type 1; PDBTitle: 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
86	c1dxyA_	Alignment	not modelled	23.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
87	c4ew6A_	Alignment	not modelled	23.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
88	d1a0ic_	Alignment	not modelled	23.5	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
89	c1titB_	Alignment	not modelled	23.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
90	d1ydga_	Alignment	not modelled	22.9	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
91	d1kx3c_	Alignment	not modelled	22.6	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
92	c3l7nA_	Alignment	not modelled	22.4	15	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
93	d2gk3a1	Alignment	not modelled	21.7	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
94	c2wmkB_	Alignment	not modelled	20.9	16	PDB header: hydrolase Chain: B: PDB Molecule: fucosyltransferase-related protein; PDBTitle: crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae sp3-bs713 (sp3gh98) in complex with the a-lewisy pentasaccharide4 blood group antigen.
95	d1id3c_	Alignment	not modelled	20.9	33	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
96	d1tzya_	Alignment	not modelled	20.8	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
97	c2z04A_	Alignment	not modelled	20.5	17	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
98	c5b3uB_	Alignment	not modelled	20.3	6	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
99	d1xi3a_	Alignment	not modelled	20.0	13	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase