







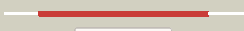




















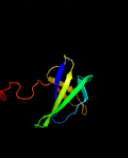
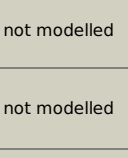


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0811c_(- )_905237_906343
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	b54626cf4e8ad016

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1pj6A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase; <b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
2	<a href="#">c4p9sA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylglycine dehydrogenase; <b>PDBTitle:</b> crystal structure of the mature form of rat dmgdh
3	<a href="#">c3girA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
4	<a href="#">c1worA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of t-protein of the glycine cleavage2 system
5	<a href="#">c1x31A_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
6	<a href="#">c1vloA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution
7	<a href="#">c1v5vA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
8	<a href="#">c1wsrA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of human t-protein of glycine cleavage2 system
9	<a href="#">c1yx2B_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of the probable aminomethyltransferase2 from bacillus subtilis
10	<a href="#">c3tfhB_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gcvt-like aminomethyltransferase protein; <b>PDBTitle:</b> dmsp-dependent demethylase from p. ubique - apo
11	<a href="#">c5tl4C_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> vanillate/3-o-methylgallate o-demethylase; <b>PDBTitle:</b> crystal structure of sphingomonas paucimobilis aryl o-demethylase ligm

12	<a href="#">c1vlyA</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> unknown protein from 2d-page; <b>PDBTitle:</b> crystal structure of a putative aminomethyltransferase (ygfz) from <i>Escherichia coli</i> at 1.30 Å resolution
13	<a href="#">c5oliA</a>	Alignment		100.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative transferase caf17, mitochondrial; <b>PDBTitle:</b> crystal structure of human iba57
14	<a href="#">d1vloa2</a>	Alignment		100.0	20	<b>Fold:</b> Folate-binding domain <b>Superfamily:</b> Folate-binding domain <b>Family:</b> Aminomethyltransferase folate-binding domain
15	<a href="#">d1wosa2</a>	Alignment		100.0	19	<b>Fold:</b> Folate-binding domain <b>Superfamily:</b> Folate-binding domain <b>Family:</b> Aminomethyltransferase folate-binding domain
16	<a href="#">d1pj5a4</a>	Alignment		100.0	20	<b>Fold:</b> Folate-binding domain <b>Superfamily:</b> Folate-binding domain <b>Family:</b> Aminomethyltransferase folate-binding domain
17	<a href="#">d1v5va2</a>	Alignment		100.0	18	<b>Fold:</b> Folate-binding domain <b>Superfamily:</b> Folate-binding domain <b>Family:</b> Aminomethyltransferase folate-binding domain
18	<a href="#">d1vlya2</a>	Alignment		100.0	18	<b>Fold:</b> Folate-binding domain <b>Superfamily:</b> Folate-binding domain <b>Family:</b> Aminomethyltransferase folate-binding domain
19	<a href="#">c2gagC</a>	Alignment		99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> heterotetrameric sarcosine oxidase gamma-subunit; <b>PDBTitle:</b> heterotetrameric sarcosine: structure of a diflavin metalloenzyme at 2.1.85 Å resolution
20	<a href="#">d1pj5a1</a>	Alignment		99.4	17	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
21	<a href="#">d1wosa1</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
22	<a href="#">c6ah3B</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop1; <b>PDBTitle:</b> cryo-em structure of yeast ribonuclease p with pre-trna substrate
23	<a href="#">d1v5va1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
24	<a href="#">c6ahrB</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleases p/mrp protein subunit pop1; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p
25	<a href="#">d1vloa1</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
26	<a href="#">d1vly1</a>	Alignment	not modelled	97.2	20	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
27	<a href="#">c1xzqA</a>	Alignment	not modelled	93.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna modification gtpase trme; <b>PDBTitle:</b> structure of the gtp-binding protein trme from <i>Thermotoga2 maritima</i> complexed with 5-formyl-thf
28	<a href="#">c3gehA</a>	Alignment	not modelled	92.8	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from <i>Nostoc</i> in complex with gdp, folinic2 acid and zn
						<b>Fold:</b> Folate-binding domain

29	<a href="#">d1xzpa3</a>	Alignment	not modelled	92.6	15	<b>Superfamily:</b> Folate-binding domain <b>Family:</b> TrmE formyl-THF-binding domain
30	<a href="#">c1xzqB</a>	Alignment	not modelled	92.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable trna modification gtpase trme; <b>PDBTitle:</b> structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
31	<a href="#">c3geiB</a>	Alignment	not modelled	91.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from chlorobium tepidum in complex2 with gcp
32	<a href="#">c2i5nH</a>	Alignment	not modelled	35.5	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
33	<a href="#">d1eysh1</a>	Alignment	not modelled	32.2	13	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
34	<a href="#">c1eysH</a>	Alignment	not modelled	28.7	13	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
35	<a href="#">c5uw8C</a>	Alignment	not modelled	28.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> probable phospholipid abc transporter-binding protein mlad; <b>PDBTitle:</b> structure of e. coli mce protein mlad, core mce domain
36	<a href="#">c3l48B</a>	Alignment	not modelled	26.5	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane usher protein papc; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the papc usher
37	<a href="#">c5uvnE</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
38	<a href="#">c5uvnB</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
39	<a href="#">c5uvnA</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
40	<a href="#">c5uvnC</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
41	<a href="#">c5uvnF</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
42	<a href="#">c5uvnD</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
43	<a href="#">d1w4ma</a>	Alignment	not modelled	19.9	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
44	<a href="#">d2i5nh1</a>	Alignment	not modelled	19.0	18	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
45	<a href="#">d3bzka5</a>	Alignment	not modelled	16.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
46	<a href="#">d1rzhh1</a>	Alignment	not modelled	15.7	9	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
47	<a href="#">c2ysrA</a>	Alignment	not modelled	15.4	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dep domain-containing protein 1; <b>PDBTitle:</b> solution structure of the dep domain from human dep domain-2 containing protein 1
48	<a href="#">c6ic4C</a>	Alignment	not modelled	11.7	16	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> toluene tolerance efflux transporter (abc superfamily, <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
49	<a href="#">d1uhwa</a>	Alignment	not modelled	10.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
50	<a href="#">c5d5pC</a>	Alignment	not modelled	9.5	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hcgb; <b>PDBTitle:</b> hcgb from methanococcus maripaludis
51	<a href="#">d1fsha</a>	Alignment	not modelled	9.2	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
52	<a href="#">d2hjsa1</a>	Alignment	not modelled	7.8	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	<a href="#">c3brcA</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein of unknown function; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
54	<a href="#">c3zbgA</a>	Alignment	not modelled	7.1	8	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phikz039; <b>PDBTitle:</b> protofilament of tubz from bacteriophage phikz
55	<a href="#">d1rmva</a>	Alignment	not modelled	6.9	14	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> TMV-like viral coat proteins <b>Family:</b> TMV-like viral coat proteins

56	<a href="#">c3kmlB_</a>	Alignment	not modelled	6.7	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> circular permutant of the tobacco mosaic virus
57	<a href="#">d2csoa1</a>	Alignment	not modelled	6.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
58	<a href="#">c5oqmh_</a>	Alignment	not modelled	6.5	28	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc3; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
59	<a href="#">d1ukfa_</a>	Alignment	not modelled	6.4	7	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Avirulence protein Avrpph3
60	<a href="#">c3jc6E_</a>	Alignment	not modelled	6.4	11	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> cell division control protein 45; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
61	<a href="#">d1vqod1</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> RL5-like <b>Superfamily:</b> RL5-like <b>Family:</b> Ribosomal protein L5
62	<a href="#">c2l37A_</a>	Alignment	not modelled	5.9	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome-inactivating protein luffin p1; <b>PDBTitle:</b> 3d solution structure of arginine/glutamate-rich polypeptide luffin p12 from the seeds of sponge gourd (luffa cylindrical)
63	<a href="#">c3r66A_</a>	Alignment	not modelled	5.7	23	<b>PDB header:</b> viral protein/antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
64	<a href="#">d2hxja1</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> FinO-like <b>Superfamily:</b> FinO-like <b>Family:</b> FinO-like
65	<a href="#">c6fxdB_</a>	Alignment	not modelled	5.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> mupz; <b>PDBTitle:</b> crystal structure of mupz from pseudomonas fluorescens
66	<a href="#">d1iq4a_</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> RL5-like <b>Superfamily:</b> RL5-like <b>Family:</b> Ribosomal protein L5
67	<a href="#">d2zjrd1</a>	Alignment	not modelled	5.5	18	<b>Fold:</b> RL5-like <b>Superfamily:</b> RL5-like <b>Family:</b> Ribosomal protein L5
68	<a href="#">c6o3sA_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> plant protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome-inactivating protein luffin p1; <b>PDBTitle:</b> nmr solution structure of vicilin-buried peptide-8 (vbp-8)
69	<a href="#">d1ei7a_</a>	Alignment	not modelled	5.3	10	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> TMV-like viral coat proteins <b>Family:</b> TMV-like viral coat proteins
70	<a href="#">d1v3fa_</a>	Alignment	not modelled	5.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
71	<a href="#">c2hxjF_</a>	Alignment	not modelled	5.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein of unknown function nmb1681 from2 neisseria meningitidis mc58, possible nucleic acid binding protein
72	<a href="#">d1a7ia1</a>	Alignment	not modelled	5.2	10	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
73	<a href="#">c3htrB_</a>	Alignment	not modelled	5.1	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized prc-barrel domain protein; <b>PDBTitle:</b> crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris