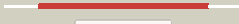



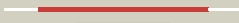























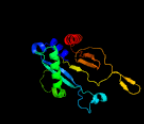




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3233c_(-)_3609778_3610368
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	bf587d3b142516dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6chjB_</a>	 Alignment		99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> diacylglycerol o-acyltransferase; <b>PDBTitle:</b> wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	<a href="#">d1q9ja2</a>	 Alignment		98.5	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
3	<a href="#">c1q9jA_</a>	 Alignment		98.4	13	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> polyketide synthase associated protein 5; <b>PDBTitle:</b> structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
4	<a href="#">c5m6pB_</a>	 Alignment		97.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> tyrocidine synthase 2; <b>PDBTitle:</b> crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
5	<a href="#">c2jgpA_</a>	 Alignment		97.6	11	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
6	<a href="#">c5dijA_</a>	 Alignment		97.4	9	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
7	<a href="#">c5t81A_</a>	 Alignment		97.3	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
8	<a href="#">c2xhgA_</a>	 Alignment		97.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase a; <b>PDBTitle:</b> crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
9	<a href="#">c6ad3A_</a>	 Alignment		97.1	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> lovastatin nonaketide synthase moka; <b>PDBTitle:</b> structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
10	<a href="#">c6aefB_</a>	 Alignment		97.1	9	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
11	<a href="#">c5t3eA_</a>	 Alignment		97.0	10	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.

12	<a href="#">c2e1uA</a>	Alignment		94.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
13	<a href="#">c5u89A</a>	Alignment		94.5	16	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
14	<a href="#">c4tx3B</a>	Alignment		93.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide synthetase, module 7; <b>PDBTitle:</b> complex of the x-domain and oxyb from teicoplanin biosynthesis
15	<a href="#">c6m7lB</a>	Alignment		92.9	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxya with the x-domain from gpa biosynthesis
16	<a href="#">c6cgoB</a>	Alignment		92.6	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from 2 the enacyloxin polyketide synthase
17	<a href="#">d1nda2</a>	Alignment		91.9	16	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
18	<a href="#">c4znmB</a>	Alignment		91.6	8	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> c-domain type ii peptide synthetase; <b>PDBTitle:</b> crystal structure of sgcc5 protein from streptomyces globosporus (apo2 form)
19	<a href="#">c4g0bA</a>	Alignment		91.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinat <b>PDBTitle:</b> structure of native hct from coffea canephora
20	<a href="#">c1l5aA</a>	Alignment		90.4	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> amide synthase; <b>PDBTitle:</b> crystal structure of vibh, an nrps condensation enzyme
21	<a href="#">c4jn3B</a>	Alignment	not modelled	89.8	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cda peptide synthetase i; <b>PDBTitle:</b> crystal structures of the first condensation domain of the cda2 synthetase
22	<a href="#">c6dd2A</a>	Alignment	not modelled	88.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydroxycinnamoyl transferase; <b>PDBTitle:</b> crystal structure of selaginella moellendorffii hct
23	<a href="#">c2xr7A</a>	Alignment	not modelled	86.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyltransferase; <b>PDBTitle:</b> crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
24	<a href="#">c1t7qA</a>	Alignment	not modelled	85.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine acetyltransferase; <b>PDBTitle:</b> crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
25	<a href="#">d1l5aa2</a>	Alignment	not modelled	84.4	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
26	<a href="#">d1nm8a2</a>	Alignment	not modelled	81.8	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
27	<a href="#">c2fyoA</a>	Alignment	not modelled	80.1	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
28	<a href="#">d1t1ua2</a>	Alignment	not modelled	78.1	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase

29	<a href="#">d1xl7a2</a>	Alignment	not modelled	74.2	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
30	<a href="#">c4ke4A</a>	Alignment	not modelled	72.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl <b>PDBTitle:</b> elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
31	<a href="#">c3maeA</a>	Alignment	not modelled	72.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase e2 component, <b>PDBTitle:</b> crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
32	<a href="#">c2fy2A</a>	Alignment	not modelled	70.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
33	<a href="#">c2bghA</a>	Alignment	not modelled	57.5	4	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
34	<a href="#">c1xl8B</a>	Alignment	not modelled	56.4	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal carnitine o-octanoyltransferase; <b>PDBTitle:</b> crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
35	<a href="#">c2h4tB</a>	Alignment	not modelled	43.4	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase ii
36	<a href="#">c1q6xA</a>	Alignment	not modelled	42.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> crystal structure of rat choline acetyltransferase
37	<a href="#">d1tu1a</a>	Alignment	not modelled	39.1	13	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> PA0094-like
38	<a href="#">d1scza</a>	Alignment	not modelled	28.0	25	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
39	<a href="#">d1b5sa</a>	Alignment	not modelled	25.7	18	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
40	<a href="#">c3fotA</a>	Alignment	not modelled	22.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 15-o-acetyltransferase; <b>PDBTitle:</b> structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
41	<a href="#">c3mafB</a>	Alignment	not modelled	22.1	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (asymmetric form)
42	<a href="#">c4q6rB</a>	Alignment	not modelled	20.8	5	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase 1; <b>PDBTitle:</b> crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
43	<a href="#">d1q23a</a>	Alignment	not modelled	20.6	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
44	<a href="#">c3ke3A</a>	Alignment	not modelled	20.4	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
45	<a href="#">c6n8eA</a>	Alignment	not modelled	18.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
46	<a href="#">c4n72B</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoyltransacetylase <b>PDBTitle:</b> catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
47	<a href="#">c2rr1A</a>	Alignment	not modelled	14.6	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-length control protein; <b>PDBTitle:</b> solution structure of the c-terminal domain of the flik
48	<a href="#">d1dpba</a>	Alignment	not modelled	14.4	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
49	<a href="#">c2huuA</a>	Alignment	not modelled	13.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine glyoxylate aminotransferase; <b>PDBTitle:</b> crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
50	<a href="#">c6h60A</a>	Alignment	not modelled	10.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, mitochondrial; <b>PDBTitle:</b> pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
51	<a href="#">c5k1rB</a>	Alignment	not modelled	10.5	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> burkholderia pseudomallei sphingosine-1-phosphate lyase <b>PDBTitle:</b> structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
52	<a href="#">c4n4A</a>	Alignment	not modelled	9.7	12	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen;

52	<a href="#">c4u4A_</a>	Alignment	not modelled	9.7	12	<b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis <b>PDB header:</b> hydrolase
53	<a href="#">c5mk0B_</a>	Alignment	not modelled	9.4	33	<b>Chain:</b> B: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 16; <b>PDBTitle:</b> crystal structure of the his domain protein tyrosine phosphatase (hd-2 ptp/ptpn23) bro1 domain (endofin peptide complex)
54	<a href="#">d1pugb_</a>	Alignment	not modelled	8.8	19	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
55	<a href="#">c3f42A_</a>	Alignment	not modelled	8.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hp0035; <b>PDBTitle:</b> crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
56	<a href="#">d1h0ca_</a>	Alignment	not modelled	8.7	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
57	<a href="#">c2owyB_</a>	Alignment	not modelled	8.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination-associated protein rdgc; <b>PDBTitle:</b> the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
58	<a href="#">c4uzzA_</a>	Alignment	not modelled	7.9	26	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport complex b protein 46 <b>PDBTitle:</b> crystal structure of the ttift52-46 complex
59	<a href="#">c4dweA_</a>	Alignment	not modelled	7.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative polysaccharide deacetylase2 (bacova_03992) from bacteroides ovatus atcc 8483 at 2.01 a resolution
60	<a href="#">c3mc6C_</a>	Alignment	not modelled	7.0	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
61	<a href="#">c3e56A_</a>	Alignment	not modelled	7.0	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme
62	<a href="#">d1pu1a_</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> Hypothetical protein MTH677 <b>Superfamily:</b> Hypothetical protein MTH677 <b>Family:</b> Hypothetical protein MTH677
63	<a href="#">c4ce42_</a>	Alignment	not modelled	6.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> 2: <b>PDB Molecule:</b> mrpl47; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
64	<a href="#">d2ch1a1</a>	Alignment	not modelled	5.9	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
65	<a href="#">d1p3wa_</a>	Alignment	not modelled	5.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
66	<a href="#">c2yxhB_</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mazg-related protein; <b>PDBTitle:</b> crystal structure of mazg-related protein from thermotoga maritima
67	<a href="#">d2cdqa3</a>	Alignment	not modelled	5.6	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Aspartokinase allosteric domain-like
68	<a href="#">d3claa_</a>	Alignment	not modelled	5.5	7	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
69	<a href="#">d1i7aa_</a>	Alignment	not modelled	5.5	25	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
70	<a href="#">c4yepA_</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> laminin subunit alpha-2; <b>PDBTitle:</b> l4b domain of human laminin alpha-2