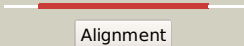

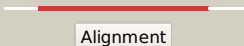

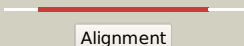







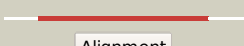








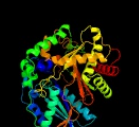





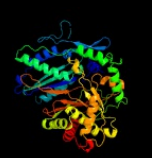





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0221 (-) _264067_265476
Date	Tue Jul 23 14:50:27 BST 2019
Unique Job ID	b85551665f9d3836

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6chjB_</a>			100.0	26	<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="#">c4zxiA_</a>			100.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
3	<a href="#">c2vsqA_</a>			100.0	12	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
4	<a href="#">c5u89A_</a>			100.0	13	<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
5	<a href="#">c5t81A_</a>			100.0	12	<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
6	<a href="#">c6p1jA_</a>			100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> txo2; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
7	<a href="#">c5m6pB_</a>			100.0	11	<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)
8	<a href="#">c6aefB_</a>			100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
9	<a href="#">c2xhgA_</a>			100.0	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
10	<a href="#">c5t3eA_</a>			100.0	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.
11	<a href="#">c4znmB_</a>			100.0	13	<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 globisporus (apo2 form)

12	<a href="#">c2jgpA_</a>	Alignment		100.0	14	<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
13	<a href="#">c4tx3B_</a>	Alignment		100.0	11	<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
14	<a href="#">c6m7lB_</a>	Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
15	<a href="#">c6cgoB_</a>	Alignment		100.0	15	<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 from2 the enacyloxin polyketide synthase
16	<a href="#">c6ad3A_</a>	Alignment		100.0	13	<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
17	<a href="#">c4jn3B_</a>	Alignment		100.0	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
18	<a href="#">c5ja2A_</a>	Alignment		100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
19	<a href="#">c4zxiA_</a>	Alignment		100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
20	<a href="#">c1l5aa_</a>	Alignment		100.0	11	<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="#">c6ozvA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
22	<a href="#">c5dijA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
23	<a href="#">c1q9jA_</a>	Alignment	not modelled	100.0	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
24	<a href="#">c4hvmC_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallysomycin biosynthesis protein tlmii
25	<a href="#">c3fotA_</a>	Alignment	not modelled	100.0	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
26	<a href="#">c6dd2A_</a>	Alignment	not modelled	99.9	11	<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
27	<a href="#">c4g0bA_</a>	Alignment	not modelled	99.9	11	<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
28	<a href="#">d1l5aa1</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)

29	<a href="#">d1q9ja1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
30	<a href="#">c2e1uA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
31	<a href="#">c2bghA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
32	<a href="#">d1l5aa2</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
33	<a href="#">c2xr7A</a>	Alignment	not modelled	99.7	12	<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
34	<a href="#">d1q9ja2</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
35	<a href="#">c4ke4A</a>	Alignment	not modelled	99.6	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
36	<a href="#">c3b2sA</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
37	<a href="#">c2zbaD</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. sporotrichoides tri101 complexed with2 coenzyme a and t-2
38	<a href="#">c6eqoB</a>	Alignment	not modelled	98.8	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nADP+ and phosphomethylphosphonic acid adenylate ester
39	<a href="#">c5es8A</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a; <b>PDBTitle:</b> crystal structure of the initiation module of lgra in the thiolation2 state
40	<a href="#">c1xl8B</a>	Alignment	not modelled	91.1	17	<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
41	<a href="#">d1xl7a2</a>	Alignment	not modelled	90.8	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
42	<a href="#">d1nm8a2</a>	Alignment	not modelled	90.3	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
43	<a href="#">d1q23a</a>	Alignment	not modelled	89.5	16	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
44	<a href="#">d3claa</a>	Alignment	not modelled	88.8	27	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
45	<a href="#">c3rqcB</a>	Alignment	not modelled	85.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable lipoamide acyltransferase; <b>PDBTitle:</b> crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
46	<a href="#">c2i9dC</a>	Alignment	not modelled	84.9	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
47	<a href="#">d1ndba2</a>	Alignment	not modelled	84.8	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
48	<a href="#">c6h60A</a>	Alignment	not modelled	83.7	13	<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
49	<a href="#">c3maeA</a>	Alignment	not modelled	83.7	11	<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
50	<a href="#">c1t7qA</a>	Alignment	not modelled	81.9	12	<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
51	<a href="#">c2fyoA</a>	Alignment	not modelled	79.4	12	<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
52	<a href="#">d1scza</a>	Alignment	not modelled	79.1	27	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
53	<a href="#">c2fy2A</a>	Alignment	not modelled	75.1	12	<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
54	<a href="#">c3l60A_</a>	Alignment	not modelled	74.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain alpha-keto acid dehydrogenase; <b>PDBTitle:</b> crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
55	<a href="#">c1q6xA_</a>	Alignment	not modelled	73.9	13	<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
56	<a href="#">c2h4tB_</a>	Alignment	not modelled	65.2	12	<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
57	<a href="#">d1t1ua2</a>	Alignment	not modelled	63.0	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
58	<a href="#">c4n72B_</a>	Alignment	not modelled	52.0	17	<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
59	<a href="#">c3b8kA_</a>	Alignment	not modelled	51.9	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase; <b>PDBTitle:</b> structure of the truncated human dihydrolipoyl acetyltransferase (e2)
60	<a href="#">d1dpba_</a>	Alignment	not modelled	51.7	23	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
61	<a href="#">d1b5sa_</a>	Alignment	not modelled	49.4	23	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
62	<a href="#">c2ii4C_</a>	Alignment	not modelled	49.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> lipamide acyltransferase component of branched-chain <b>PDBTitle:</b> crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
63	<a href="#">d1ywqa1</a>	Alignment	not modelled	16.9	11	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
64	<a href="#">c2h0uA_</a>	Alignment	not modelled	16.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
65	<a href="#">d1dk0a_</a>	Alignment	not modelled	12.2	32	<b>Fold:</b> Heme-binding protein A (HasA) <b>Superfamily:</b> Heme-binding protein A (HasA) <b>Family:</b> Heme-binding protein A (HasA)
66	<a href="#">d1p94a_</a>	Alignment	not modelled	11.4	14	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
67	<a href="#">c3ddrC_</a>	Alignment	not modelled	11.1	32	<b>PDB header:</b> membrane protein/heme binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> hemophore hasa; <b>PDBTitle:</b> structure of the serratia marcescens hemophore receptor hasr-ile671gly2 mutant in complex with its hemophore hasa and heme
68	<a href="#">c2k5jB_</a>	Alignment	not modelled	8.3	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
69	<a href="#">c2kw3A_</a>	Alignment	not modelled	8.1	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rfx5; <b>PDBTitle:</b> heterotrimeric interaction between rfx5 and rfxap
70	<a href="#">c5wmma_</a>	Alignment	not modelled	7.7	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> nrps; <b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
71	<a href="#">c6gtsC_</a>	Alignment	not modelled	6.7	4	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat-atar complex bound dna
72	<a href="#">d1mnta_</a>	Alignment	not modelled	6.0	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
73	<a href="#">d1ykia1</a>	Alignment	not modelled	6.0	5	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
74	<a href="#">c6ajnf_</a>	Alignment	not modelled	5.1	5	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atat bound with accoa
75	<a href="#">c3eo8A_</a>	Alignment	not modelled	5.0	6	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> blub-like flavoprotein; <b>PDBTitle:</b> crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution