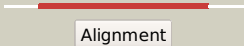

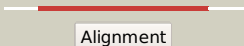

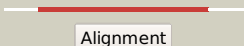







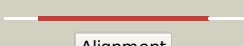




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3234c (- )_3610371_3611186
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	5f41599a12d7e2db

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6chjB_</a>	 Alignment		100.0	28	<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="#">c6n8eA_</a>	 Alignment		100.0	15	<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
3	<a href="#">c2vsqA_</a>	 Alignment		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="#">c4zxiA_</a>	 Alignment		100.0	11	<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
5	<a href="#">c4znmB_</a>	 Alignment		100.0	15	<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)
6	<a href="#">c6p1jA_</a>	 Alignment		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="#">c4zxiA_</a>	 Alignment		100.0	14	<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
8	<a href="#">c6cgoB_</a>	 Alignment		100.0	16	<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
9	<a href="#">c6ad3A_</a>	 Alignment		99.9	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="#">c5t81A_</a>	 Alignment		99.9	13	<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
11	<a href="#">c5m6pB_</a>	 Alignment		99.9	10	<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)

12	<a href="#">c5t3eA_</a>	Alignment		99.9	11	<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.
13	<a href="#">c2xhgA_</a>	Alignment		99.9	10	<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
14	<a href="#">c6aefB_</a>	Alignment		99.9	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
15	<a href="#">c6m7lB_</a>	Alignment		99.9	16	<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
16	<a href="#">c4jn3B_</a>	Alignment		99.9	12	<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
17	<a href="#">c1l5aA_</a>	Alignment		99.9	12	<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
18	<a href="#">c5ja2A_</a>	Alignment		99.9	14	<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="#">c6ozvA_</a>	Alignment		99.9	20	<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
20	<a href="#">c4tx3B_</a>	Alignment		99.9	12	<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
21	<a href="#">c5u89A_</a>	Alignment	not modelled	99.9	15	<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
22	<a href="#">c4hvmC_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallisomycin biosynthesis protein tlmii
23	<a href="#">c2jgpA_</a>	Alignment	not modelled	99.9	10	<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
24	<a href="#">c5dijA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tgaa; <b>PDBTitle:</b> the crystal structure of ct
25	<a href="#">c1q9jA_</a>	Alignment	not modelled	99.9	16	<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
26	<a href="#">d1l5aa1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
27	<a href="#">c3fotA_</a>	Alignment	not modelled	99.8	9	<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
28	<a href="#">d1q9ja1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
						<b>PDB header:</b> transferase

29	<a href="#">c6dd2A_</a>	Alignment	not modelled	99.5	10	<b>Chain:</b> A: <b>PDB Molecule:</b> probable hydroxycinnamoyl transferase; <b>PDBTitle:</b> crystal structure of selaginella moellendorffii hct
30	<a href="#">c4g0bA_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinate <b>PDBTitle:</b> structure of native hct from coffea canephora
31	<a href="#">c2bghA_</a>	Alignment	not modelled	99.1	8	<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="#">c2e1uA_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
33	<a href="#">c2xr7A_</a>	Alignment	not modelled	99.0	11	<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="#">c4ke4A_</a>	Alignment	not modelled	98.7	15	<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
35	<a href="#">c3b2sA_</a>	Alignment	not modelled	98.5	13	<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
36	<a href="#">c2zbaD_</a>	Alignment	not modelled	98.3	12	<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
37	<a href="#">c6eqoB_</a>	Alignment	not modelled	97.5	13	<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 erythro bacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
38	<a href="#">c3rqcB_</a>	Alignment	not modelled	88.9	20	<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
39	<a href="#">d3claa_</a>	Alignment	not modelled	78.7	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
40	<a href="#">d1q23a_</a>	Alignment	not modelled	75.0	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
41	<a href="#">c2i9dC_</a>	Alignment	not modelled	71.8	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
42	<a href="#">c3maeA_</a>	Alignment	not modelled	66.6	18	<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
43	<a href="#">c6h60A_</a>	Alignment	not modelled	63.9	9	<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
44	<a href="#">d1scza_</a>	Alignment	not modelled	39.9	17	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
45	<a href="#">d1bw6a_</a>	Alignment	not modelled	28.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
46	<a href="#">d1myla_</a>	Alignment	not modelled	14.1	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
47	<a href="#">d1l5aa2</a>	Alignment	not modelled	12.6	6	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
48	<a href="#">d1b28a_</a>	Alignment	not modelled	12.0	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
49	<a href="#">c3b8kA_</a>	Alignment	not modelled	9.4	7	<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)
50	<a href="#">c1y9qA_</a>	Alignment	not modelled	9.3	0	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
51	<a href="#">d1tlua1</a>	Alignment	not modelled	8.5	10	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acetyltransferase
52	<a href="#">d1e0ga_</a>	Alignment	not modelled	8.0	7	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
53	<a href="#">d1b5sa_</a>	Alignment	not modelled	7.8	22	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
						<b>Fold:</b> Histone-fold

54	<a href="#">d1h3oa_</a>	Alignment	not modelled	7.5	0	<b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
55	<a href="#">c1h3oA_</a>	Alignment	not modelled	7.5	0	<b>PDB header:</b> transcription/tbp-associated factors <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid 135 kda subunit; <b>PDBTitle:</b> crystal structure of the human taf4-taf12 (tafi135-tafii20) complex
56	<a href="#">d1y7ma2</a>	Alignment	not modelled	7.3	7	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
57	<a href="#">d1i2va_</a>	Alignment	not modelled	7.2	40	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
58	<a href="#">d1ozza_</a>	Alignment	not modelled	7.2	40	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
59	<a href="#">d1mylb_</a>	Alignment	not modelled	6.9	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
60	<a href="#">d1hlva1</a>	Alignment	not modelled	6.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
61	<a href="#">c3kk4B_</a>	Alignment	not modelled	6.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
62	<a href="#">c2elhA_</a>	Alignment	not modelled	6.4	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
63	<a href="#">c2ltuA_</a>	Alignment	not modelled	5.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-2; <b>PDBTitle:</b> solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
64	<a href="#">d1xl7a1</a>	Alignment	not modelled	5.5	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
65	<a href="#">c3cecA_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
66	<a href="#">c3hugA_</a>	Alignment	not modelled	5.5	7	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
67	<a href="#">d1b0na2</a>	Alignment	not modelled	5.4	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like