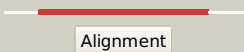

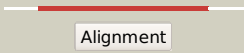



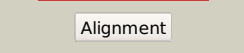



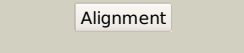

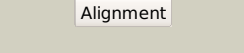



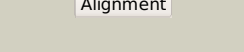

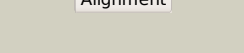

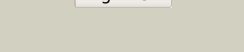

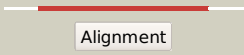



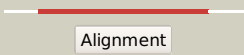

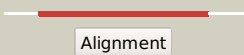

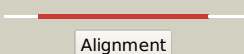
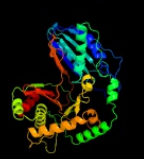
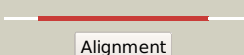

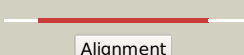





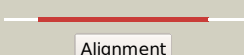

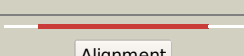

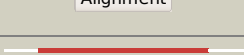
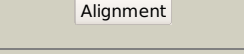

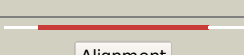


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2305 (-) _2575819_2577108
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	f86e136feb96bb65

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6n8eA_</a>	 Alignment		100.0	14	<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
2	<a href="#">c2vsqA_</a>	 Alignment		100.0	10	<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
3	<a href="#">c2xhgA_</a>	 Alignment		100.0	15	<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
4	<a href="#">c5m6pB_</a>	 Alignment		100.0	17	<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="#">c6aefB_</a>	 Alignment		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
6	<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
7	<a href="#">c5u89A_</a>	 Alignment		100.0	12	<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
8	<a href="#">c5t3eA_</a>	 Alignment		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.
9	<a href="#">c5t81A_</a>	 Alignment		100.0	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
10	<a href="#">c6m7iB_</a>	 Alignment		100.0	15	<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
11	<a href="#">c6cgoB_</a>	 Alignment		100.0	12	<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

12	<a href="#">c4znmB_</a>			100.0	14	<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)
13	<a href="#">c4jn3B_</a>			100.0	18	<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
14	<a href="#">c6p1jA_</a>			100.0	16	<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
15	<a href="#">c2jgpA_</a>			100.0	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
16	<a href="#">c5ja2A_</a>			100.0	12	<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
17	<a href="#">c4zxjA_</a>			100.0	13	<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
18	<a href="#">c6ad3A_</a>			100.0	12	<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
19	<a href="#">c4tx3B_</a>			100.0	15	<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
20	<a href="#">c1l5aa_</a>			100.0	15	<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>		not modelled	100.0	15	<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>		not modelled	100.0	14	<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="#">c4hvmC_</a>		not modelled	100.0	12	<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
24	<a href="#">c1q9jA_</a>		not modelled	100.0	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
25	<a href="#">c6chjB_</a>		not modelled	100.0	18	<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
26	<a href="#">c3fotA_</a>		not modelled	100.0	12	<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
27	<a href="#">c6dd2A_</a>		not modelled	100.0	13	<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
28	<a href="#">d1l5aa1</a>		not modelled	99.9	16	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)

29	<a href="#">d1l5aa2</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
30	<a href="#">c4g0bA</a>	Alignment	not modelled	99.9	12	<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="#">d1q9ja1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
32	<a href="#">c2bghA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
33	<a href="#">c2e1uA</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
34	<a href="#">d1q9ja2</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
35	<a href="#">c2xr7A</a>	Alignment	not modelled	99.8	13	<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
36	<a href="#">c4ke4A</a>	Alignment	not modelled	99.6	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
37	<a href="#">c3b2sA</a>	Alignment	not modelled	99.6	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
38	<a href="#">c2zbaD</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
39	<a href="#">c6eqoB</a>	Alignment	not modelled	99.1	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 erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
40	<a href="#">c5es8A</a>	Alignment	not modelled	98.3	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
41	<a href="#">c3b8kA</a>	Alignment	not modelled	97.3	14	<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)
42	<a href="#">d1dpba</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
43	<a href="#">d1b5sa</a>	Alignment	not modelled	96.5	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
44	<a href="#">c4n72B</a>	Alignment	not modelled	96.5	13	<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
45	<a href="#">c3i60A</a>	Alignment	not modelled	96.3	14	<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
46	<a href="#">d1q23a</a>	Alignment	not modelled	96.1	9	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
47	<a href="#">d3claa</a>	Alignment	not modelled	95.6	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
48	<a href="#">c6h60A</a>	Alignment	not modelled	94.5	14	<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	94.1	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="#">c2ii4C</a>	Alignment	not modelled	93.9	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> lipoamide 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
51	<a href="#">d1scza</a>	Alignment	not modelled	93.1	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
52	<a href="#">c3rqcB</a>	Alignment	not modelled	84.0	15	<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
53	<a href="#">c2i9dC</a>	Alignment	not modelled	79.4	13 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
54	<a href="#">d1nija2</a>	Alignment	not modelled	48.1	11 <b>Fold:</b> Hypothetical protein YjiA, C-terminal domain <b>Superfamily:</b> Hypothetical protein YjiA, C-terminal domain <b>Family:</b> Hypothetical protein YjiA, C-terminal domain
55	<a href="#">d2dy1a4</a>	Alignment	not modelled	17.7	22 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
56	<a href="#">c1nija</a>	Alignment	not modelled	16.3	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
57	<a href="#">c2fy2A</a>	Alignment	not modelled	15.8	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
58	<a href="#">d2bm0a4</a>	Alignment	not modelled	15.2	13 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
59	<a href="#">c1vs3B</a>	Alignment	not modelled	11.0	25 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
60	<a href="#">d1dj0a</a>	Alignment	not modelled	8.7	13 <b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase I TruA
61	<a href="#">c6cb6A</a>	Alignment	not modelled	7.8	30 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein a6; <b>PDBTitle:</b> crystal structure of vaccinia virus a6 n-terminus (space group c2)
62	<a href="#">c3n0vD</a>	Alignment	not modelled	7.7	19 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
63	<a href="#">c6f1sA</a>	Alignment	not modelled	6.7	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cgliir protein; <b>PDBTitle:</b> c-terminal domain of cglii restriction endonuclease h subunit
64	<a href="#">c5flmK</a>	Alignment	not modelled	5.7	10 <b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb11; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
65	<a href="#">d1n0ua4</a>	Alignment	not modelled	5.5	18 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
66	<a href="#">c5hypB</a>	Alignment	not modelled	5.5	33 <b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> m28 protein; <b>PDBTitle:</b> structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein