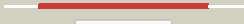
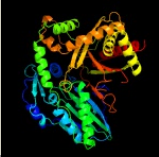

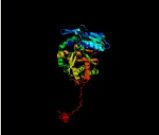
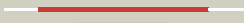


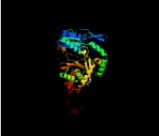







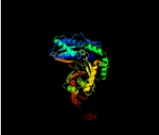



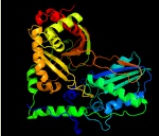




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3824c_papA1_4291817_4293352
 Date Fri Aug 9 18:20:53 BST 2019
 Unique Job ID 55b9a14d53aec4f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6aefB_	 Alignment		100.0	51	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
2	c6n8eA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
3	c2vsqA_	 Alignment		100.0	15	PDB header: ligase Chain: A; PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
4	c6p1jA_	 Alignment		100.0	17	PDB header: biosynthetic protein Chain: A; PDB Molecule: txo2; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
5	c5u89A_	 Alignment		100.0	15	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: amino acid adenylation domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
6	c4zxiA_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
7	c5ja2A_	 Alignment		100.0	13	PDB header: ligase Chain: A; PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
8	c4zxiA_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: enterobactin synthase component f; PDBTitle: crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
9	c6ozvA_	 Alignment		100.0	15	PDB header: biosynthetic protein Chain: A; PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
10	c4tx3B_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis
11	c6m7IB_	 Alignment		100.0	14	PDB header: biosynthetic protein Chain: B; PDB Molecule: putative non-ribosomal peptide synthetase; PDBTitle: complex of oxa with the x-domain from gpa biosynthesis

12	c5t81A_	Alignment		100.0	14	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
13	c2jgpA_	Alignment		100.0	16	PDB header: ligase Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
14	c6cgoB_	Alignment		100.0	14	PDB header: biosynthetic protein Chain: B; PDB Molecule: condensation domain protein; PDBTitle: molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
15	c4jn3B_	Alignment		100.0	14	PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
16	c2xhgA_	Alignment		100.0	13	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
17	c4znmB_	Alignment		100.0	16	PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
18	c5t3eA_	Alignment		100.0	10	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
19	c6ad3A_	Alignment		100.0	14	PDB header: biosynthetic protein Chain: A; PDB Molecule: lovastatin nonaketide synthase moka; PDBTitle: structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
20	c5m6pB_	Alignment		100.0	13	PDB header: isomerase Chain: B; PDB Molecule: tyrocidine synthase 2; PDBTitle: crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
21	c1l5aA_	Alignment	not modelled	100.0	9	PDB header: biosynthetic protein Chain: A; PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
22	c5dijA_	Alignment	not modelled	100.0	11	PDB header: unknown function Chain: A; PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
23	c4hvmC_	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: C; PDB Molecule: tlmii; PDBTitle: crystal structure of tallsomycin biosynthesis protein tlmii
24	c3fotA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: 15-o-acetyltransferase; PDBTitle: structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
25	c1q9jA_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A; PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
26	c6chjB_	Alignment	not modelled	100.0	9	PDB header: transferase Chain: B; PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
27	d1l5aa2	Alignment	not modelled	100.0	7	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
28	d1l5aa1	Alignment	not modelled	100.0	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)

29	c6dd2A	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
30	d1q9ja1	Alignment	not modelled	99.9	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
31	d1q9ja2	Alignment	not modelled	99.9	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	c4g0bA	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinat PDBTitle: structure of native hct from coffea canephora
33	c2e1uA	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
34	c6eqoB	Alignment	not modelled	99.8	8	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadt+ and phosphomethylphosphonic acid adenylate ester
35	c5es8A	Alignment	not modelled	99.8	9	PDB header: ligase Chain: A: PDB Molecule: linear gramicidin synthetase subunit a; PDBTitle: crystal structure of the initiation module of lgra in the thiolation2 state
36	c2bghA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
37	c2xr7A	Alignment	not modelled	99.6	8	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
38	c3b2sA	Alignment	not modelled	99.1	9	PDB header: transferase Chain: A: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
39	c4ke4A	Alignment	not modelled	98.8	12	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl PDBTitle: elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
40	c2zbaD	Alignment	not modelled	98.3	8	PDB header: transferase Chain: D: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
41	c2i9dC	Alignment	not modelled	84.7	13	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
42	c3rqcB	Alignment	not modelled	57.8	20	PDB header: transferase Chain: B: PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
43	d1nija2	Alignment	not modelled	49.3	19	Fold: Hypothetical protein YjiA, C-terminal domain Superfamily: Hypothetical protein YjiA, C-terminal domain Family: Hypothetical protein YjiA, C-terminal domain
44	d1scza	Alignment	not modelled	43.9	22	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
45	c3l60A	Alignment	not modelled	36.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: branched-chain alpha-keto acid dehydrogenase; PDBTitle: crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
46	c3b8kA	Alignment	not modelled	28.3	11	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
47	c1vs3B	Alignment	not modelled	25.7	33	PDB header: isomerase Chain: B: PDB Molecule: trna pseudouridine synthase a; PDBTitle: crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
48	c4n72B	Alignment	not modelled	24.4	12	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
49	d1dpba	Alignment	not modelled	22.2	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
50	d1q23a	Alignment	not modelled	21.9	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
51	d1b5sa	Alignment	not modelled	20.6	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
52	d1dj0a	Alignment	not modelled	14.1	17	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase I TruA
53	c5hypB	Alignment	not modelled	13.6	22	PDB header: immune system Chain: B: PDB Molecule: m28 protein; PDBTitle: 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 PDB header: biosynthetic protein Chain: A: PDB Molecule: nrps; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
54	c5wmmA_	Alignment	not modelled	13.0	9	
55	c2ii4C_	Alignment	not modelled	11.4	25	PDB header: transferase Chain: C: PDB Molecule: lipoamide acyltransferase component of branched-chain PDBTitle: 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
56	c4gr5B_	Alignment	not modelled	9.4	22	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
57	c1njiA_	Alignment	not modelled	8.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
58	d1g4ma1	Alignment	not modelled	8.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
59	d2h1ta1	Alignment	not modelled	8.0	33	Fold: Spiral beta-roll Superfamily: PA1994-like Family: PA1994-like
60	c3maeA_	Alignment	not modelled	7.8	14	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
61	c2k5jB_	Alignment	not modelled	7.2	3	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
62	c2p0yA_	Alignment	not modelled	7.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
63	c1o7dC_	Alignment	not modelled	6.8	28	PDB header: hydrolase Chain: C: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
64	d1zh2a1	Alignment	not modelled	6.1	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	d3claa_	Alignment	not modelled	5.7	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
66	d1p94a_	Alignment	not modelled	5.6	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
67	c6bk9A_	Alignment	not modelled	5.5	8	PDB header: signaling protein Chain: A: PDB Molecule: visual arrestin; PDBTitle: crystal structure of squid arrestin
68	d1u8sa2	Alignment	not modelled	5.4	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor