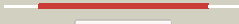



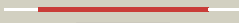







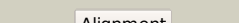











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3820c_(papA2)_4284597_4286003
 Date Fri Aug 9 18:20:53 BST 2019
 Unique Job ID 057b3af3ac4dd240

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6aefB_	 Alignment		100.0	100	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
2	c6n8eA_	 Alignment		100.0	10	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	c4zxiA_	 Alignment		100.0	11	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
4	c5u89A_	 Alignment		100.0	12	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
5	c2vsgA_	 Alignment		100.0	13	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
6	c6p1jA_	 Alignment		100.0	13	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
7	c2jgpA_	 Alignment		100.0	13	PDB header: ligase Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
8	c5t81A_	 Alignment		100.0	12	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
9	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
10	c4tx3B_	 Alignment		100.0	14	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	13	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	c5ja2A_	Alignment		100.0	14	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
13	c2xhgA_	Alignment		100.0	12	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
14	c5m6pB_	Alignment		100.0	10	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)
15	c4znmB_	Alignment		100.0	13	PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
16	c6ozvA_	Alignment		100.0	14	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
17	c6cgoB_	Alignment		100.0	17	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
18	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
19	c5t3eA_	Alignment		100.0	11	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
20	c4jn3B_	Alignment		100.0	12	PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
21	c5dijA_	Alignment	not modelled	100.0	12	PDB header: unknown function Chain: A; PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
22	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
23	c4hvmC_	Alignment	not modelled	100.0	12	PDB header: biosynthetic protein Chain: C; PDB Molecule: tlmii; PDBTitle: crystal structure of tallisomycin biosynthesis protein tlmii
24	c3fotA_	Alignment	not modelled	100.0	10	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	13	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	8	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	c4g0bA_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora
31	d1q9ja1	Alignment	not modelled	99.9	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	d1q9ja2	Alignment	not modelled	99.9	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	c2e1uA_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
34	c2bghA_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
35	c6eqoB_	Alignment	not modelled	99.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
36	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
37	c5es8A_	Alignment	not modelled	99.5	6	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
38	c3b2sA_	Alignment	not modelled	99.3	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	99.3	10	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	99.0	7	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	90.5	9	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
42	d1b5sa_	Alignment	not modelled	78.7	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
43	d1nija2	Alignment	not modelled	59.0	10	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	56.5	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
45	d1q23a_	Alignment	not modelled	49.5	8	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
46	d3claa_	Alignment	not modelled	39.5	8	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
47	c6h60A_	Alignment	not modelled	36.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component, mitochondrial; PDBTitle: pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
48	c5wmma_	Alignment	not modelled	33.5	12	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
49	c1vs3B_	Alignment	not modelled	24.0	25	PDB header: isomerase Chain: B: PDB Molecule: trna pseudouridine synthase a; PDBTitle: crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
50	c3kk4B_	Alignment	not modelled	20.9	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
51	d1dj0a_	Alignment	not modelled	14.8	17	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase I TrUA
52	c5msvB_	Alignment	not modelled	14.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
53	c5ifiA_	Alignment	not modelled	12.8	13	PDB header: ligase Chain: A: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99 PDB header: immune system

54	c5hypB	Alignment	not modelled	12.3	22	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
55	d1dpba	Alignment	not modelled	10.9	7	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
56	d2bm0a4	Alignment	not modelled	9.6	7	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
57	c3l60A	Alignment	not modelled	9.3	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
58	c1nijA	Alignment	not modelled	9.2	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
59	d2dy1a4	Alignment	not modelled	8.6	11	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
60	c6h6pA	Alignment	not modelled	8.5	12	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
61	d1u8sa2	Alignment	not modelled	8.5	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
62	c4q6rB	Alignment	not modelled	8.1	2	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: sphingosine-1-phosphate lyase 1; PDBTitle: 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
63	c1o7dC	Alignment	not modelled	7.7	33	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	d1qnaa2	Alignment	not modelled	7.6	8	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
65	d2h1ta1	Alignment	not modelled	7.5	44	Fold: Spiral beta-roll Superfamily: PA1994-like Family: PA1994-like
66	c5ti8A	Alignment	not modelled	7.5	10	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
67	d1k3ea	Alignment	not modelled	7.5	10	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
68	c6io1B	Alignment	not modelled	7.3	10	PDB header: transferase Chain: B: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a novel thermostable (s)-enantioselective omega-2 transaminase from thermomicrobium roseum
69	c2p0yA	Alignment	not modelled	7.3	5	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
70	c6noyB	Alignment	not modelled	7.0	7	PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb
71	c4fxeB	Alignment	not modelled	6.7	15	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
72	d1zh2a1	Alignment	not modelled	6.7	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	c2k5jB	Alignment	not modelled	6.4	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
74	c2k29A	Alignment	not modelled	6.3	15	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
75	c1u8sB	Alignment	not modelled	6.3	13	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
76	d1p94a	Alignment	not modelled	6.2	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
77	c3b8kA	Alignment	not modelled	6.1	11	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
78	c3n0vD	Alignment	not modelled	5.9	3	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution PDB header: dna binding protein

79	c2k9iB_	Alignment	not modelled	5.6	4	Chain: B; PDB Molecule: uncharacterized protein orf5b; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolobus2 islandicus
80	c3g98B_	Alignment	not modelled	5.5	14	PDB header: ligase Chain: B; PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
81	c2ii4C_	Alignment	not modelled	5.3	16	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
82	d2cpga_	Alignment	not modelled	5.3	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
83	c1ea4K_	Alignment	not modelled	5.3	15	PDB header: gene regulation/dna Chain: K; PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
84	d1m6sa_	Alignment	not modelled	5.2	0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like