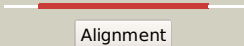

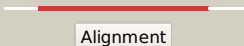

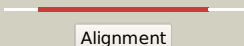







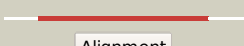











Phyre2

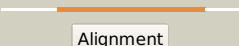

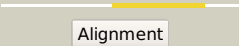
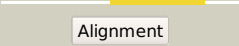

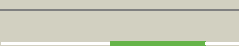
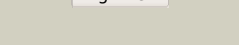
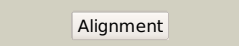


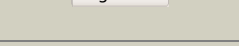
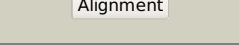
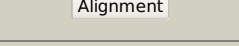
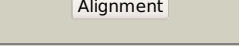
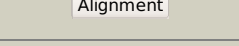
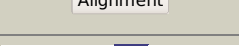
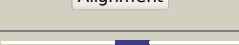
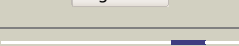
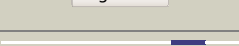
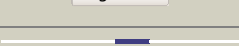
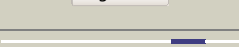
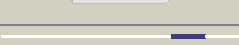



Email	mdejesus@rockefeller.edu
Description	RVBD1425_(-)_1599664_1601043
Date	Wed Jul 31 22:05:53 BST 2019
Unique Job ID	14ee6f3b5bd78886

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	35	PDB header: transferase Chain: B; PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	c6n8eA_	 Alignment		100.0	14	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	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
4	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
5	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.
6	c4zxiA_	 Alignment		100.0	12	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	c6aefB_	 Alignment		100.0	10	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
8	c4znmB_	 Alignment		100.0	10	PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
9	c2xhgA_	 Alignment		100.0	11	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
10	c5u89A_	 Alignment		100.0	14	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
11	c6p1jA_	 Alignment		100.0	15	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

12	c4jn3B_	Alignment		100.0	17	PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
13	c6ad3A_	Alignment		100.0	10	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
14	c5m6pB_	Alignment		100.0	12	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	c2jgpA_	Alignment		100.0	14	PDB header: ligase Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tyc5-6 pcp-c bidomain of the tyrocidine synthetase2 tyc5
16	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
17	c4zxjA_	Alignment		100.0	12	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
18	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
19	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
20	c4tx3B_	Alignment		100.0	11	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis
21	c1l5aA_	Alignment	not modelled	100.0	12	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	13	PDB header: unknown function Chain: A; PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
23	c6ozvA_	Alignment	not modelled	100.0	17	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
24	c4hvmC_	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: C; PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
25	c1q9jA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A; PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
26	c3fotA_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: A; PDB Molecule: 15-o-acetyltransferase; PDBTitle: structural and functional characterization of tri3 trichotheocene 15-o-2 acetyltransferase from fusarium sporotrichioides
27	c6dd2A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A; PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
28	c4g0bA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A; PDB Molecule: hydroxycinnamoyl-coa shikimate/quinatase PDBTitle: structure of native hct from coffea canephora

29	d1l5aa1	Alignment	not modelled	99.9	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
30	c2e1uA	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
31	d1q9ja1	Alignment	not modelled	99.8	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	c2bghA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
33	d1l5aa2	Alignment	not modelled	99.8	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
34	c2xr7A	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
35	d1q9ja2	Alignment	not modelled	99.8	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
36	c4ke4A	Alignment	not modelled	99.7	14	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
37	c3b2sA	Alignment	not modelled	99.5	11	PDB header: transferase Chain: A: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
38	c2zbaD	Alignment	not modelled	99.2	11	PDB header: transferase Chain: D: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. sporotrichoides tri101 complexed with2 coenzyme a and t-2
39	c6eqoB	Alignment	not modelled	98.9	10	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
40	d3claa	Alignment	not modelled	93.2	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
41	c2fyoA	Alignment	not modelled	93.2	12	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
42	c3rqcB	Alignment	not modelled	93.0	18	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	c2i9dC	Alignment	not modelled	93.0	18	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
44	d1nm8a2	Alignment	not modelled	91.8	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
45	d1ndba2	Alignment	not modelled	91.7	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
46	c2h4tB	Alignment	not modelled	91.1	11	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
47	d1q23a	Alignment	not modelled	91.1	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
48	c1q6xA	Alignment	not modelled	90.9	11	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
49	c1xl8B	Alignment	not modelled	90.8	11	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
50	c5es8A	Alignment	not modelled	90.8	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
51	c2fy2A	Alignment	not modelled	87.2	12	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
52	c3b8kA	Alignment	not modelled	86.3	14	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
53	d1dpba	Alignment	not modelled	84.2	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like

54	c1t7qA_	 Alignment	not modelled	84.2	13	PDB header: transferase Chain: A: PDB Molecule: carnitine acetyltransferase; PDBTitle: crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
55	d1xl7a2	 Alignment	not modelled	83.1	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
56	d1t1ua2	 Alignment	not modelled	77.7	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
57	d1b5sa_	 Alignment	not modelled	77.4	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
58	c3l60A_	 Alignment	not modelled	60.5	14	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
59	c2ii4C_	 Alignment	not modelled	58.0	10	PDB header: transferase Chain: C: PDB Molecule: lipoaamide 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
60	c4n72B_	 Alignment	not modelled	58.0	11	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoiltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
61	c6h60A_	 Alignment	not modelled	57.5	9	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
62	c3maeA_	 Alignment	not modelled	48.0	11	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
63	c1z2iA_	 Alignment	not modelled	31.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
64	d1scza_	 Alignment	not modelled	23.2	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
65	c1vbiA_	 Alignment	not modelled	19.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
66	d1mnta_	 Alignment	not modelled	18.4	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
67	c4isyB_	 Alignment	not modelled	16.0	31	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
68	d2ay0a1	 Alignment	not modelled	9.9	10	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
69	c6iyaD_	 Alignment	not modelled	9.0	8	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
70	c5zsqA_	 Alignment	not modelled	8.2	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
71	d1ry9a_	 Alignment	not modelled	7.9	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
72	c2rbfB_	 Alignment	not modelled	7.1	10	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
73	c4eb5B_	 Alignment	not modelled	6.2	15	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
74	c3mafB_	 Alignment	not modelled	6.2	9	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of tsspl (asymmetric form)
75	d2fm8a1	 Alignment	not modelled	6.2	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
76	c2huuA_	 Alignment	not modelled	6.2	17	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
77	c2k5jB_	 Alignment	not modelled	6.1	4	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
78	c3i0pA_	 Alignment	not modelled	6.1	10	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from

				entamoeba histolytica	
79	c6gtsC_	Alignment	not modelled	6.1	6 PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
80	c4q6rB_	Alignment	not modelled	5.8	7 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
81	c5wmmA_	Alignment	not modelled	5.7	6 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
82	d1p3wa_	Alignment	not modelled	5.3	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
83	c3kk4B_	Alignment	not modelled	5.2	7 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i