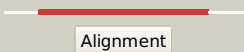

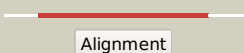

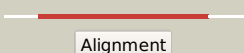
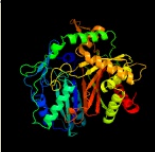
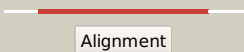

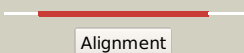

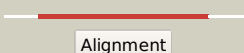
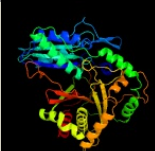
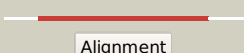


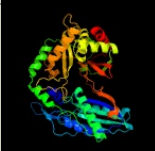

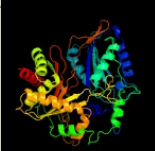
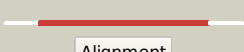
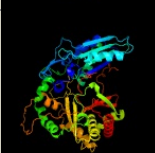
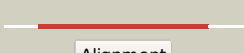



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3740c_(-)_4191011_4192357
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	22ef720b9873b34f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	44	PDB header: transferase Chain: B; PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	c5t81A_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
3	c5t3eA_	 Alignment		100.0	8	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
4	c6n8eA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
5	c6aefB_	 Alignment		100.0	12	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
6	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)
7	c5u89A_	 Alignment		100.0	16	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
8	c2vsaA_	 Alignment		100.0	10	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
9	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
10	c2xhgA_	 Alignment		100.0	14	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
11	c2jgpA_	 Alignment		100.0	14	PDB header: ligase Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc

12	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
13	c6cgoB_	Alignment		100.0	13	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
14	c4znmB_	Alignment		100.0	12	PDB header: ligase Chain: B: PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
15	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
16	c6m7lB_	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
17	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
18	c4jn3B_	Alignment		100.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
19	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
20	c1l5aA_	Alignment		100.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
21	c4zxiA_	Alignment	not modelled	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
22	c6ozvA_	Alignment	not modelled	100.0	16	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
23	c5dijA_	Alignment	not modelled	100.0	11	PDB header: unknown function Chain: A: PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
24	c1q9jA_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
25	c4hvmC_	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallisomycin biosynthesis protein tlmii
26	c3fotA_	Alignment	not modelled	100.0	12	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
27	c6dd2A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
28	c4g0bA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora
						PDB header: transferase

29	c2e1uA_	Alignment	not modelled	99.9	12	Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
30	d1l5aa1	Alignment	not modelled	99.8	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
31	d1q9ja2	Alignment	not modelled	99.8	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	d1l5aa2	Alignment	not modelled	99.8	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	c2bghA_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
34	d1q9ja1	Alignment	not modelled	99.7	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
35	c2xr7A_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
36	c3b2sA_	Alignment	not modelled	99.5	10	PDB header: transferase Chain: A: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
37	c4ke4A_	Alignment	not modelled	99.5	13	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
38	c2zbaD_	Alignment	not modelled	99.2	9	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	98.1	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	c5es8A_	Alignment	not modelled	92.9	11	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
41	d1ndba2	Alignment	not modelled	92.6	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
42	c2fy2A_	Alignment	not modelled	91.9	13	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
43	c2h4tB_	Alignment	not modelled	90.9	13	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
44	d1nm8a2	Alignment	not modelled	90.8	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
45	c1t7qA_	Alignment	not modelled	89.8	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
46	c1q6xA_	Alignment	not modelled	89.1	10	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
47	d1xl7a2	Alignment	not modelled	88.9	7	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
48	d1t1ua2	Alignment	not modelled	87.1	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
49	c3b8kA_	Alignment	not modelled	85.1	15	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
50	d1q23a_	Alignment	not modelled	83.8	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
51	c3rqcB_	Alignment	not modelled	77.2	13	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
52	c1xl8B_	Alignment	not modelled	77.0	7	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
53	c2fyoA_	Alignment	not modelled	71.2	11	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212

54	d3claa_	Alignment	not modelled	67.1	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
55	d1dpba_	Alignment	not modelled	64.3	19	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
56	c2i9dC_	Alignment	not modelled	52.5	9	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
57	c2ii4C_	Alignment	not modelled	38.6	13	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
58	c6h60A_	Alignment	not modelled	35.5	14	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
59	c4n72B_	Alignment	not modelled	34.2	12	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyl)transacetylase PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
60	c3maeA_	Alignment	not modelled	34.0	10	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	d1b5sa_	Alignment	not modelled	32.8	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
62	c3i60A_	Alignment	not modelled	22.6	16	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
63	d1scza_	Alignment	not modelled	20.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
64	c2k9iB_	Alignment	not modelled	12.5	13	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
65	c2dr1A_	Alignment	not modelled	11.0	22	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
66	c2rriA_	Alignment	not modelled	9.9	26	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
67	c3mafB_	Alignment	not modelled	9.8	9	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
68	c5zsqA_	Alignment	not modelled	8.6	3	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
69	c2huuA_	Alignment	not modelled	8.4	20	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
70	d1ry9a_	Alignment	not modelled	7.4	18	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
71	c3i5tB_	Alignment	not modelled	7.3	11	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
72	c4eb5B_	Alignment	not modelled	6.3	17	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
73	d2ay0a1	Alignment	not modelled	5.9	7	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
74	c4q6rB_	Alignment	not modelled	5.4	12	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
75	d2fm8a1	Alignment	not modelled	5.2	13	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone