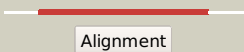

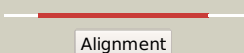

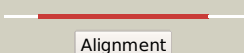

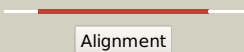

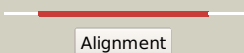

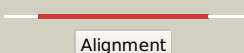

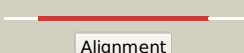





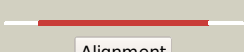

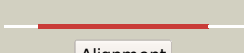



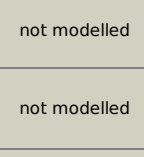


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1125_(-)_1248087_1249331
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	354ebf297d857d98

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	17	PDB header: transferase Chain: B; PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	c1q9jA_	 Alignment		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
3	c2jgpA_	 Alignment		100.0	15	PDB header: ligase Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
4	c5m6pB_	 Alignment		100.0	9	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)
5	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.
6	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
7	c6aefB_	 Alignment		100.0	12	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
8	c5t81A_	 Alignment		100.0	15	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
9	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
10	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
11	c6m7iB_	 Alignment		100.0	15	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	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)
13	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
14	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
15	c2vsqA_	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
16	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
17	c1l5aA_	Alignment		100.0	9	PDB header: biosynthetic protein Chain: A: PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
18	c6p1jA_	Alignment		100.0	18	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
19	c5ja2A_	Alignment		100.0	15	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	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
21	c5dijA_	Alignment	not modelled	100.0	11	PDB header: unknown function Chain: A: PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
22	c4zxiA_	Alignment	not modelled	100.0	14	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
23	c6ozvA_	Alignment	not modelled	100.0	19	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	c3fotA_	Alignment	not modelled	99.9	9	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	c4hvmC_	Alignment	not modelled	99.9	13	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
26	c6dd2A_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
27	c4g0bA_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinat PDBTitle: structure of native hct from coffea canephora
28	d1q9ja2	Alignment	not modelled	99.7	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)

29	d1l5aa1	Alignment	not modelled	99.6	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
30	c2e1uA	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
31	c2xr7A	Alignment	not modelled	99.5	11	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
32	c2bqhA	Alignment	not modelled	99.4	11	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
33	d1q9ja1	Alignment	not modelled	99.4	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
34	c4ke4A	Alignment	not modelled	99.3	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
35	d1l5aa2	Alignment	not modelled	99.0	8	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
36	c3b2sA	Alignment	not modelled	98.8	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	c2zbaD	Alignment	not modelled	98.4	10	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
38	c6eqoB	Alignment	not modelled	92.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nasp+ and phosphomethylphosphonic acid adenylate ester
39	c5es8A	Alignment	not modelled	89.4	8	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
40	d1nm8a2	Alignment	not modelled	77.6	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
41	c3l60A	Alignment	not modelled	68.2	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
42	c4n72B	Alignment	not modelled	56.0	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
43	d1b5sa	Alignment	not modelled	54.9	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
44	d1dpba	Alignment	not modelled	42.7	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
45	c3maeA	Alignment	not modelled	40.1	12	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
46	d3claa	Alignment	not modelled	38.1	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
47	c3b8kA	Alignment	not modelled	34.3	11	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
48	d1q23a	Alignment	not modelled	32.5	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
49	d1scza	Alignment	not modelled	32.4	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
50	c2i9dC	Alignment	not modelled	30.8	11	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
51	c3rqcB	Alignment	not modelled	21.8	16	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	c6h60A	Alignment	not modelled	14.9	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 Fold: PLP-dependent transferase-like

53	d1m32a_	Alignment	not modelled	12.4	20	Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
54	d1xl7a2	Alignment	not modelled	11.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
55	c3f42A_	Alignment	not modelled	11.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
56	d1puqb_	Alignment	not modelled	10.4	23	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
57	c2fy2A_	Alignment	not modelled	9.0	14	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
58	d1t1ua2	Alignment	not modelled	7.6	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
59	c2ii4C_	Alignment	not modelled	6.8	14	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
60	d2q3la1	Alignment	not modelled	6.3	23	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
61	c4yepA_	Alignment	not modelled	6.0	8	PDB header: sugar binding protein Chain: A: PDB Molecule: laminin subunit alpha-2; PDBTitle: l4b domain of human laminin alpha-2
62	c5zhbB_	Alignment	not modelled	5.4	23	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
63	c2czhB_	Alignment	not modelled	5.3	14	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
64	c3qmfA_	Alignment	not modelled	5.1	11	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of an inositol monophosphatase family protein2 (sas2203) from staphylococcus aureus mssa476