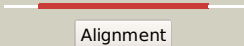

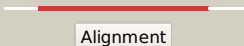
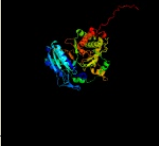
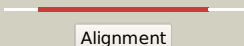




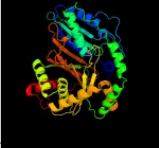


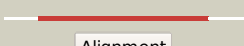


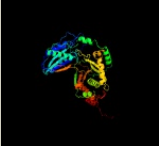








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3371 (-) _3785112_3786452
Date	Fri Aug 9 18:20:03 BST 2019
Unique Job ID	ee8728eabf583147

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	22	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	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	c5t81A_	 Alignment		100.0	11	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	12	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	12	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	11	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	c6m71B_	 Alignment		100.0	12	PDB header: biosynthetic protein Chain: B; PDB Molecule: putative non-ribosomal peptide synthetase; PDBTitle: complex of oxa with the x-domain from gpa biosynthesis
8	c5ja2A_	 Alignment		100.0	11	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
9	c6ad3A_	 Alignment		100.0	7	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	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
11	c4jn3B_	 Alignment		100.0	15	PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase

12	c1l5aA_	Alignment		100.0	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
13	c6aefB_	Alignment		100.0	8	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
14	c5m6pB_	Alignment		100.0	11	PDB header: isomerase Chain: B: PDB Molecule: tyrocidine synthase 2; PDBTitle: crystal structure of the epimerization domain from module 3 of 2 tyrocidine synthetase b, tycb3(e)
15	c2jgpA_	Alignment		100.0	11	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	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: condensation domain protein; PDBTitle: molecular basis for condensation domain-mediated chain release from 2 the enacyloxin polyketide synthase
17	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)
18	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
19	c2xhgA_	Alignment		100.0	12	PDB header: isomerase Chain: A: PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation 2 module of tyrocidine biosynthesis
20	c4zxiA_	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 in 2 the thioester-forming conformation
21	c4tx3B_	Alignment	not modelled	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
22	c5dijA_	Alignment	not modelled	100.0	10	PDB header: unknown function Chain: A: PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
23	c6ozvA_	Alignment	not modelled	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 in 3 complex with amp
24	c4hvmC_	Alignment	not modelled	100.0	10	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
25	c1q9jA_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from 2 mycobacterium tuberculosis
26	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
27	d1l5aa1	Alignment	not modelled	99.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
28	c6dd2A_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct

29	c4g0bA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora
30	d1l5aa2	Alignment	not modelled	99.8	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
31	d1q9ja1	Alignment	not modelled	99.8	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	c2e1uA	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
33	d1q9ja2	Alignment	not modelled	99.6	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
34	c2bghA	Alignment	not modelled	99.6	13	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
35	c2xr7A	Alignment	not modelled	99.5	10	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
36	c4ke4A	Alignment	not modelled	99.2	15	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	98.9	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	c5es8A	Alignment	not modelled	98.4	13	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
39	c2zbaD	Alignment	not modelled	98.4	12	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
40	c6eqoB	Alignment	not modelled	97.7	14	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
41	c2i9dC	Alignment	not modelled	95.1	13	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
42	d3claa	Alignment	not modelled	82.0	5	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
43	c3rqcB	Alignment	not modelled	81.1	17	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
44	d1q23a	Alignment	not modelled	74.9	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
45	d1nm8a2	Alignment	not modelled	74.8	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
46	d1ndba2	Alignment	not modelled	69.8	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
47	c3maeA	Alignment	not modelled	61.2	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
48	d1xl7a2	Alignment	not modelled	58.2	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
49	d1scza	Alignment	not modelled	48.5	7	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
50	c2fyoA	Alignment	not modelled	47.5	8	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
51	c4dweA	Alignment	not modelled	41.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative polysaccharide deacetylase2 (bacova_03992) from bacteroides ovatus atcc 8483 at 2.01 a resolution
52	c1t7qA	Alignment	not modelled	39.4	10	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
53	d1t1ua2	Alignment	not modelled	33.7	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase

54	d1dpba_	Alignment	not modelled	27.6	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
55	c3b8kA_	Alignment	not modelled	22.2	13	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
56	c1xl8B_	Alignment	not modelled	13.4	8	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
57	c6h60A_	Alignment	not modelled	11.7	12	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
58	c5wmmA_	Alignment	not modelled	11.7	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
59	c3ke3A_	Alignment	not modelled	10.2	15	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
60	c4q6rB_	Alignment	not modelled	9.0	14	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
61	c3mafB_	Alignment	not modelled	8.1	11	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stsp1 (asymmetric form)
62	c1q6xA_	Alignment	not modelled	7.6	9	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
63	c4n72B_	Alignment	not modelled	7.3	14	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
64	c3lvmB_	Alignment	not modelled	6.5	10	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
65	c2fy2A_	Alignment	not modelled	6.5	11	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
66	d1nija2	Alignment	not modelled	5.8	10	Fold: Hypothetical protein YjiA, C-terminal domain Superfamily: Hypothetical protein YjiA, C-terminal domain Family: Hypothetical protein YjiA, C-terminal domain
67	c4lw2C_	Alignment	not modelled	5.7	21	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
68	c2ii4C_	Alignment	not modelled	5.5	10	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