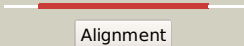

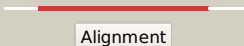

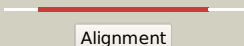







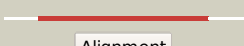




















Phyre2

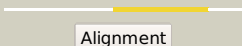
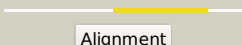

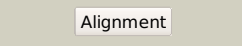
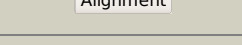
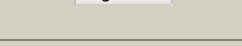
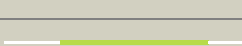
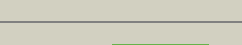


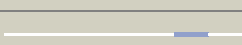

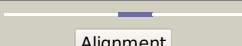
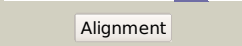
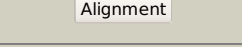

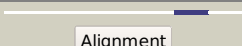

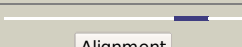


Email	mdejesus@rockefeller.edu
Description	RVBD2285 (-) _2557483_2558820
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	3cf57dff19eabe63

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_			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_			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
3	c5t81A_			100.0	14	PDB header: biosynthetic protein Chain: A; PDB Molecule: repob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
4	c2vsgA_			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
5	c4zxiA_			100.0	14	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
6	c5t3eA_			100.0	7	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
7	c5u89A_			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
8	c6p1jA_			100.0	14	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
9	c6ad3A_			100.0	11	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	c6aefB_			100.0	11	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
11	c2jgpA_			100.0	12	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	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 of2 tyrocidine synthetase b, tycb3(e)
13	c4znmB_	Alignment		100.0	11	PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
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	c6cgoB_	Alignment		100.0	12	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
16	c4jn3B_	Alignment		100.0	16	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	c4tx3B_	Alignment		100.0	12	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis
18	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
19	c4zxiA_	Alignment		100.0	11	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
20	c6m7IB_	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
21	c1l5aA_	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
22	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 in3 complex with amp
23	c5dijA_	Alignment	not modelled	100.0	9	PDB header: unknown function Chain: A; PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
24	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 from2 mycobacterium tuberculosis
25	c4hvmC_	Alignment	not modelled	100.0	11	PDB header: biosynthetic protein Chain: C; PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
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 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
27	c6dd2A_	Alignment	not modelled	99.9	9	PDB header: transferase Chain: A; PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
28	d1l5aa1	Alignment	not modelled	99.9	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)

29	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
30	c2e1uA	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
31	d1q9ja1	Alignment	not modelled	99.8	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	d1l5aa2	Alignment	not modelled	99.8	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	c2bghA	Alignment	not modelled	99.7	12	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
34	d1q9ja2	Alignment	not modelled	99.7	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
35	c2xr7A	Alignment	not modelled	99.6	13	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	99.5	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
37	c3b2sA	Alignment	not modelled	99.4	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
38	c6eqoB	Alignment	not modelled	98.7	8	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
39	c2zbaD	Alignment	not modelled	98.6	14	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
40	c2fy2A	Alignment	not modelled	97.2	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
41	c2fyoA	Alignment	not modelled	95.8	9	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	c1t7qA	Alignment	not modelled	95.6	16	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
43	c1q6xA	Alignment	not modelled	95.5	11	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
44	c2h4tB	Alignment	not modelled	95.2	10	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
45	d1t1ua2	Alignment	not modelled	94.6	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
46	d1nm8a2	Alignment	not modelled	94.0	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
47	d3claa	Alignment	not modelled	93.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
48	d1q23a	Alignment	not modelled	93.7	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
49	d1ndba2	Alignment	not modelled	92.9	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
50	c5es8A	Alignment	not modelled	86.8	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
51	c3b8kA	Alignment	not modelled	84.9	12	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
52	c3maeA	Alignment	not modelled	82.7	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
53	c2i9dC	Alignment	not modelled	74.6	19	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase

54	c2ii4C_	 Alignment	not modelled	73.3	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
55	d1dpba_	 Alignment	not modelled	72.8	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
56	c3rqcB_	 Alignment	not modelled	72.7	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
57	d1scza_	 Alignment	not modelled	71.3	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
58	d1b5sa_	 Alignment	not modelled	70.0	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
59	c6h60A_	 Alignment	not modelled	69.8	10	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
60	d1xl7a2	 Alignment	not modelled	68.1	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
61	c1xl8B_	 Alignment	not modelled	63.7	15	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
62	c4n72B_	 Alignment	not modelled	57.5	7	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
63	c4isyB_	 Alignment	not modelled	46.6	14	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
64	c3l60A_	 Alignment	not modelled	24.2	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
65	c4dweA_	 Alignment	not modelled	21.9	17	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
66	c2huuA_	 Alignment	not modelled	20.5	20	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
67	c2k9iB_	 Alignment	not modelled	11.7	15	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
68	c5zsqA_	 Alignment	not modelled	10.4	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
69	c4eb5B_	 Alignment	not modelled	10.0	18	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
70	c3mafB_	 Alignment	not modelled	7.5	7	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
71	d1ry9a_	 Alignment	not modelled	7.0	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
72	d2fm8a1	 Alignment	not modelled	6.4	18	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
73	c3ke3A_	 Alignment	not modelled	6.4	21	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
74	c2fyfB_	 Alignment	not modelled	6.2	10	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis