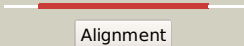

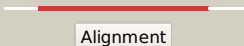
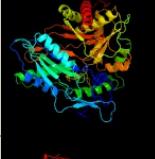
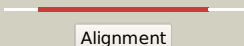
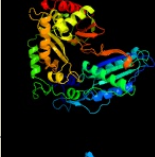



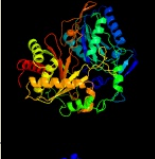


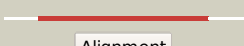











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1760_(-)_1993160_1994668
Date	Fri Aug 2 13:30:36 BST 2019
Unique Job ID	453a48b63272c0ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	30	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	11	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	c2vsqA_	 Alignment		100.0	11	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
4	c5t81A_	 Alignment		100.0	12	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
5	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
6	c6aefB_	 Alignment		100.0	11	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
7	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
8	c5m6pB_	 Alignment		100.0	14	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)
9	c6p1jA_	 Alignment		100.0	17	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
10	c2xhgA_	 Alignment		100.0	13	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	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.

12	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
13	c6m7lB_			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
14	c4zxlA_			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
15	c2jgpA_			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
16	c4jn3B_			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	c4znmB_			100.0	13	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	c5ja2A_			100.0	12	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	c4tx3B_			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
20	c6cgoB_			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
21	c6ozvA_		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
22	c1l5aA_		not modelled	100.0	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
23	c5dljA_		not modelled	100.0	12	PDB header: unknown function Chain: A: PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
24	c4hvmC_		not modelled	100.0	15	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
25	c1q9jA_		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
26	c3fotA_		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	c6dd2A_		not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
28	c4g0bA_		not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora

29	d1l5aa1	Alignment	not modelled	99.9	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
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	18	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	d1l5aa2	Alignment	not modelled	99.8	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	c2bghA	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
34	c2xr7A	Alignment	not modelled	99.7	11	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	99.6	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
36	c4ke4A	Alignment	not modelled	99.6	16	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	12	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	99.0	11	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
39	c6eqoB	Alignment	not modelled	98.7	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	96.9	10	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	96.5	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
42	c1t7qA	Alignment	not modelled	96.5	11	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	c2fyoA	Alignment	not modelled	96.2	13	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
44	c2fy2A	Alignment	not modelled	96.0	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
45	c2h4tB	Alignment	not modelled	95.9	12	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
46	d1nm8a2	Alignment	not modelled	95.4	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
47	d1t1ua2	Alignment	not modelled	93.3	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
48	c1q6xA	Alignment	not modelled	92.3	10	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
49	d1xl7a2	Alignment	not modelled	86.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
50	c3maeA	Alignment	not modelled	86.8	13	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolopoamide acetyltransferase from2 listeria monocytogenes 4b f2365
51	d3claa	Alignment	not modelled	86.3	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
52	d1q23a	Alignment	not modelled	85.9	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
53	c1xl8B	Alignment	not modelled	85.7	11	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine

54	d1b5sa_	Alignment	not modelled	81.3	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
55	c3i60A_	Alignment	not modelled	77.7	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
56	c2i9dC_	Alignment	not modelled	77.4	15	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
57	c4n72B_	Alignment	not modelled	71.6	12	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
58	c3rqcB_	Alignment	not modelled	70.4	14	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
59	d1dpba_	Alignment	not modelled	68.3	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
60	c3b8kA_	Alignment	not modelled	62.7	14	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
61	c6h60A_	Alignment	not modelled	61.4	13	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	d1scza_	Alignment	not modelled	56.3	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
63	c2ii4C_	Alignment	not modelled	36.9	12	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
64	c2h0uA_	Alignment	not modelled	10.4	7	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
65	d1ywqa1	Alignment	not modelled	10.2	16	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
66	d1ppji_	Alignment	not modelled	8.1	24	Fold: Non-globular alpha+beta subunits of globular proteins Superfamily: Non-globular alpha+beta subunits of globular proteins Family: Ubiquinol-cytochrome c reductase 8 kDa protein
67	c5wmmA_	Alignment	not modelled	7.8	7	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
68	c3kk4B_	Alignment	not modelled	7.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
69	d1nija2	Alignment	not modelled	7.4	8	Fold: Hypothetical protein YjiA, C-terminal domain Superfamily: Hypothetical protein YjiA, C-terminal domain Family: Hypothetical protein YjiA, C-terminal domain
70	d1b7go2	Alignment	not modelled	7.0	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
71	d1myla_	Alignment	not modelled	6.8	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
72	c6dy1A_	Alignment	not modelled	6.5	8	PDB header: hydrolase Chain: A: PDB Molecule: n-acylethanolamine acid amidase alpha-subunit; PDBTitle: rabbit n-acylethanolamine-hydrolyzing acid amidase (naaa) with fatty2 acid (myristate), in presence of triton x-100
73	d2phcb2	Alignment	not modelled	6.5	11	Fold: DCoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
74	d2o3la1	Alignment	not modelled	6.3	15	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
75	d1b28a_	Alignment	not modelled	6.3	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
76	d1mnta_	Alignment	not modelled	6.1	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
77	c6dy2C_	Alignment	not modelled	6.0	12	PDB header: hydrolase Chain: C: PDB Molecule: n-acylethanolamine acid amidase alpha-subunit; PDBTitle: guinea pig n-acylethanolamine-hydrolyzing acid amidase (naaa)2 covalently bound to beta-lactam inhibitor arn726 Fold: Ribbon-helix-helix

78	d1mylb_	Alignment	not modelled	6.0	17	Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
79	c3f42A_	Alignment	not modelled	5.8	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
80	c2kw3A_	Alignment	not modelled	5.7	32	PDB header: dna binding protein Chain: A; PDB Molecule: dna-binding protein rfx5; PDBTitle: heterotrimeric interaction between rfx5 and rfxap
81	c6dy3G_	Alignment	not modelled	5.7	20	PDB header: hydrolase Chain: G; PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
82	c2rr1A_	Alignment	not modelled	5.7	17	PDB header: protein transport Chain: A; PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
83	c5u7zA_	Alignment	not modelled	5.7	4	PDB header: hydrolase Chain: A; PDB Molecule: acid ceramidase; PDBTitle: human acid ceramidase (asah1, acdase) self-activated
84	c3ke3A_	Alignment	not modelled	5.6	30	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
85	d2czca1	Alignment	not modelled	5.5	15	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
86	c4ol4A_	Alignment	not modelled	5.5	12	PDB header: lipid binding protein Chain: A; PDB Molecule: proline-rich 28 kda antigen; PDBTitle: crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
87	d1vg0a2	Alignment	not modelled	5.4	15	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
88	d2o34a1	Alignment	not modelled	5.4	28	Fold: T-fold Superfamily: AppE-like Family: DVU1097-like
89	c2a06V_	Alignment	not modelled	5.3	17	PDB header: oxidoreductase Chain: V; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: bovine cytochrome bc1 complex with stigmatellin bound
90	d1ykia1	Alignment	not modelled	5.2	14	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
91	c3of4A_	Alignment	not modelled	5.0	11	PDB header: oxidoreductase Chain: A; PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution