

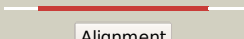

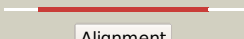

















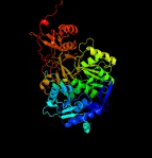


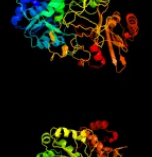


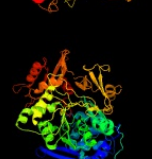

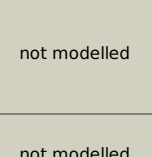


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2941_(fadD28)_3283345_3285087
Date	Thu Aug 8 16:20:10 BST 2019
Unique Job ID	1d2cd71d6070bb2c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	Alignment 		100.0	18	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
2	c5gxdA_	Alignment 		100.0	19	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae df12 12
3	c5es8A_	Alignment 		100.0	21	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
4	d1pg4a_	Alignment 		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
5	c6p1jA_	Alignment 		100.0	25	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
6	c5u89A_	Alignment 		100.0	24	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	c5ifiA_	Alignment 		100.0	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99
8	c5wmmA_	Alignment 		100.0	24	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
9	c5ja2A_	Alignment 		100.0	19	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
10	c3kxwA_	Alignment 		100.0	32	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
11	d1ry2a_	Alignment 		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like

12	c2vsqA_	Alignment		100.0	21	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
13	c5msdA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from2 nocardia iowensis in complex with amp and benzoic acid
14	c5ey8D_	Alignment		100.0	36	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
15	c4wd1A_	Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
16	c6n8eA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
17	c3gqwB_	Alignment		100.0	28	PDB header: ligase Chain: B: PDB Molecule: fatty acid amp ligase; PDBTitle: crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
18	c5mstA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid
19	c4r0mB_	Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
20	c5mssA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
21	c3e7wA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains
22	c4zxiA_	Alignment	not modelled	100.0	19	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	c4zxiA_	Alignment	not modelled	100.0	21	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
24	c5ie2A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
25	c4r0mA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
26	c4wv3A_	Alignment	not modelled	100.0	19	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: anthranilate-coa ligase; PDBTitle: crystal structure of the anthranilate coa ligase auaeii in complex2 with anthranoyl-amp
27	d3cw9a1	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
28	c3vnqA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with

					atp from2 streptomyces
29	d1mdba_	Alignment	not modelled	100.0	20 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
30	c3ni2A_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase; PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
31	c4eatB_	Alignment	not modelled	100.0	24 PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
32	c5x8gA_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: binary complex structure of a double mutant i454ra456k of o-2 succinylbenzoate coa synthetase (mene) from bacillus subtilis bound3 with its product analogue osb-ncoa at 1.90 angstrom
33	c3tsyA_	Alignment	not modelled	100.0	19 PDB header: ligase, transferase Chain: A: PDB Molecule: fusion protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
34	c5wm7A_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
35	c3etcB_	Alignment	not modelled	100.0	16 PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
36	c3eynB_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: B: PDB Molecule: acyl-coenzyme a synthetase acsm2a; PDBTitle: crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
37	c4oxiA_	Alignment	not modelled	100.0	17 PDB header: ligase Chain: A: PDB Molecule: enterobactin synthetase component f-related protein; PDBTitle: crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycyL-adenosine-5'-phosphate
38	c4dg9A_	Alignment	not modelled	100.0	19 PDB header: ligase/inhibitor Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
39	c4dg8A_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
40	c2d1tA_	Alignment	not modelled	100.0	21 PDB header: oxidoreductase Chain: A: PDB Molecule: luciferin 4-monooxygenase; PDBTitle: crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
41	c5u2aA_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
42	c3iteB_	Alignment	not modelled	100.0	16 PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
43	c6h1bA_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
44	c3r44A_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
45	c6ijbA_	Alignment	not modelled	100.0	15 PDB header: ligase Chain: A: PDB Molecule: amp-binding domain protein; PDBTitle: structure of 3-methylmercaptopropionate coa ligase mutant k523a in2 complex with amp and mmpa
46	c6ac3B_	Alignment	not modelled	100.0	19 PDB header: luminescent protein Chain: B: PDB Molecule: red-bioluminescence eliciting luciferase; PDBTitle: structure of a natural red emitting luciferase from phrixothrix hirtus2 (p3121 crystal form)
47	c5aplA_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: A: PDB Molecule: adenylation domain; PDBTitle: structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure
48	c3rg2H_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
49	c5keiA_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
50	c4ir7A_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A: PDB Molecule: long chain fatty acid coa ligase fadd10; PDBTitle: crystal structure of mtb fadd10 in complex with dodecanoyl-amp
51	d1amua_	Alignment	not modelled	100.0	16 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
52	c3dhvA_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate

78	c3wv4B_	Alignment	not modelled	100.0	23	Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
79	c3ivrA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodospseudomonas palustris cga009
80	c3t5cA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fad13; PDBTitle: crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2
81	c5oe3C_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: C: PDB Molecule: anthranilate--coa ligase; PDBTitle: crystal structure of the n-terminal domain of pqsa in complex with2 anthraniloyl-amp (crystal form 1)
82	c5burB_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
83	c5jipC_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
84	c6abhG_	Alignment	not modelled	100.0	18	PDB header: luminescent protein Chain: G: PDB Molecule: red-bioluminescence eliciting luciferase; PDBTitle: structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)
85	c2y4oA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
86	c2y27B_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
87	c4gs5A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like PDBTitle: the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053
88	c3qovD_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
89	c3hguB_	Alignment	not modelled	99.8	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c3laxA_	Alignment	not modelled	99.6	24	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
91	c5kodA_	Alignment	not modelled	98.7	11	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
92	c4b2gB_	Alignment	not modelled	98.2	12	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
93	c4ep1A_	Alignment	not modelled	98.0	12	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
94	c4ewvB_	Alignment	not modelled	97.1	10	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
95	c6avhA_	Alignment	not modelled	96.9	13	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
96	c5ghrA_	Alignment	not modelled	76.2	8	PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein
97	c6hnuA_	Alignment	not modelled	56.8	22	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
98	d1uzhc1	Alignment	not modelled	44.3	10	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
99	c4z1oB_	Alignment	not modelled	40.4	9	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
100	c4je5C_	Alignment	not modelled	39.6	21	PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoadipate aminotransferase 1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
101	d1lr1s_	Alignment	not modelled	35.6	22	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
						Fold: RuBisCO, small subunit

102	d1rbli_	Alignment	not modelled	35.4	11	Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
103	c6hbbA_	Alignment	not modelled	35.3	11	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein ccm; PDBTitle: crystal structure of the small subunit-like domain 1 of ccm from2 synechococcus elongatus (strain pcc 7942)
104	d1svdm1	Alignment	not modelled	33.2	11	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
105	c6mr1A_	Alignment	not modelled	33.1	11	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: rbcs-like subdomain of ccm
106	c5dlcC_	Alignment	not modelled	26.5	15	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
107	c4oxqB_	Alignment	not modelled	26.5	10	PDB header: metal binding protein Chain: B: PDB Molecule: manganese abc transporter, periplasmic-binding protein PDBTitle: structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc
108	c3hjtB_	Alignment	not modelled	26.4	7	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
109	c2ybvN_	Alignment	not modelled	26.2	11	PDB header: lyase Chain: N: PDB Molecule: ribulose bisphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus
110	c4trbA_	Alignment	not modelled	24.6	21	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase
111	c5vogA_	Alignment	not modelled	23.9	17	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppgpp
112	c4j5uB_	Alignment	not modelled	23.4	8	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
113	d2ayia1	Alignment	not modelled	23.3	24	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
114	d2at2a1	Alignment	not modelled	22.4	12	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
115	c2ps3A_	Alignment	not modelled	21.0	10	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
116	d1zjca1	Alignment	not modelled	20.7	16	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
117	d1nula_	Alignment	not modelled	20.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
118	c5uyvA_	Alignment	not modelled	20.5	11	PDB header: metal transport Chain: A: PDB Molecule: periplasmic chelated iron-binding protein yfea; PDBTitle: yfea ancillary sites that do not co-load with site 2