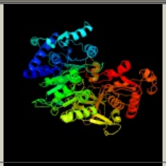
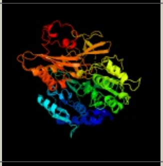
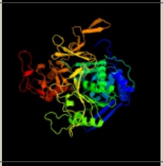
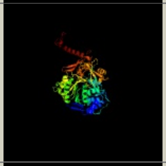
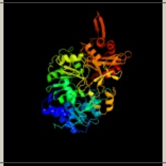
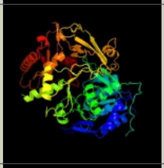
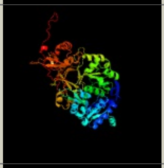
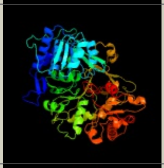
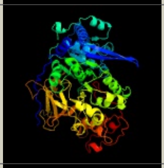
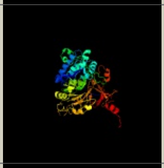
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3801c_(fadD32)_4261331_4263244
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	0cbd8e4b14f0fd83

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ey8D_	Alignment		100.0	74	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acyl-coa synthase; **PDBTitle:** structure of fadd32 from mycobacterium smegmatis complexed to ampc20
2	c6eqoB_	Alignment		100.0	21	**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
3	c6p1jA_	Alignment		100.0	19	**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
4	c5gxdA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
5	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
6	c5u89A_	Alignment		100.0	19	**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	c5wmmA_	Alignment		100.0	19	**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
8	c5ja2A_	Alignment		100.0	20	**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	d1pg4a_	Alignment		100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
10	c5ifiA_	Alignment		100.0	18	**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
11	d1ry2a_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like

12	c3kxwA_	Alignment		100.0	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
13	c5msdA_	Alignment		100.0	20	**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	c2vsqA_	Alignment		100.0	19	**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
15	c4wd1A_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetoacetate-coa ligase; **PDBTitle:** acetoacetyl-coa synthetase from streptomyces lividans
16	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
17	c6n8eA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holo-obif1; **PDBTitle:** crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
18	c3tsyA_	Alignment		100.0	23	**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
19	c5mssA_	Alignment		100.0	18	**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
20	c3gqwB_	Alignment		100.0	29	**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
21	c4r0mB_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mcyg protein; **PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate
22	c4zxjA_	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	19	**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	c3e7wA_	Alignment	not modelled	100.0	19	**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
25	c4r0mA_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**mcyg protein; **PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate
26	c5ie2A_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**oxalate--coa ligase; **PDBTitle:** crystal structure of a plant enzyme
27	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
28	d1mdba_	Alignment	not modelled	100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like

						Family: Acetyl-CoA synthetase-like
29	d3cw9a1	Alignment	not modelled	100.0	17	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
30	c3ni2A_	Alignment	not modelled	100.0	23	**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	c4wv3A_	Alignment	not modelled	100.0	22	**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
32	c6ozvA_	Alignment	not modelled	100.0	20	**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
33	c4eatB_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structure of a benzoate coenzyme a ligase
34	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
35	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
36	c3etcB_	Alignment	not modelled	100.0	17	**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
37	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
38	c5wm7A_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**salicylate-amp ligase; **PDBTitle:** crystal structure of cahj in complex with amp
39	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)
40	c3iteB_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
41	c3rg2H_	Alignment	not modelled	100.0	17	**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
42	c5aplA_	Alignment	not modelled	100.0	20	**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
43	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
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	c3eynB_	Alignment	not modelled	100.0	17	**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
46	c2d1tA_	Alignment	not modelled	100.0	22	**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
47	c6ijbA_	Alignment	not modelled	100.0	17	**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
48	d1amua_	Alignment	not modelled	100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
49	c4d56A_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**apnaa1; **PDBTitle:** understanding bi-specificity of a-domains
50	d1v25a_	Alignment	not modelled	100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
51	c4ir7A_	Alignment	not modelled	100.0	18	**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
52	c5u2aA_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of brucella canis acyl-coa synthetase

53	c5keiA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**2,3-dihydroxybenzoate-amp ligase; **PDBTitle:** mycobacterium smegmatis mbta apo structure
54	c1amuB_	Alignment	not modelled	100.0	19	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
55	c3g7sA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
56	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
57	c6akdA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of idnl7
58	c4fuqD_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**malonyl coa synthetase; **PDBTitle:** crystal structure of apo matb from rhodopseudomonas palustris
59	c4gr5B_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase; **PDBTitle:** crystal structure of slgn1deltaasub in complex with ampcpp
60	c5jjqB_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of idnl1
61	d1lcia_	Alignment	not modelled	100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
62	c2v7bB_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
63	c5e7qB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acyl-coa synthetase; **PDBTitle:** acyl-coa synthetase ptma2 from streptomyces platensis
64	c3dhvA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
65	c3nyrA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
66	c5buqA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
67	c4w8oA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferase-like enzymeamp-coa-ligase; **PDBTitle:** structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
68	c3iplB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
69	c3l8cA_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes
70	c3e53A_	Alignment	not modelled	100.0	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
71	c5jjpB_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nonribosomal peptide synthase; **PDBTitle:** crystal structure of cmis6
72	c5c5hA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** r195k e. coli mene with bound osb-ams
73	c3qyaA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferase; **PDBTitle:** crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
74	c5n81B_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrocidine synthase 1; **PDBTitle:** crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
75	c3o82B_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
76	c3wv4B_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase; **PDBTitle:** crystal structure of vinn
77	c4lgcA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bile acid-coenzyme a ligase; **PDBTitle:** crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
78	c3o82A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter

						baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
79	c3ivrA_	Alignment	not modelled	100.0	22	**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 rhodopseudomonas palustris cga009
80	c5oe3C_	Alignment	not modelled	100.0	16	**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)
81	c6abhG_	Alignment	not modelled	100.0	17	**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)
82	c3t5cA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable chain-fatty-acid-coa ligase fadd13; **PDBTitle:** crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2
83	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
84	c5jjpC_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** C: **PDB Molecule:**nonribosomal peptide synthase; **PDBTitle:** crystal structure of cmis6
85	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
86	c2y27B_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
87	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
88	c3qovD_	Alignment	not modelled	100.0	19	**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	100.0	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
90	c3laxA_	Alignment	not modelled	99.5	21	**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	99.1	15	**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	c4eplA_	Alignment	not modelled	98.8	15	**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
93	c4b2gB_	Alignment	not modelled	98.6	16	**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
94	c4ewvB_	Alignment	not modelled	97.5	18	**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	97.3	20	**PDB header:**ligase, plant protein **Chain:** A: **PDB Molecule:**gh3.15 acyl acid amido synthetase; **PDBTitle:** gh3.15 acyl acid amido synthetase
96	d1xvla1	Alignment	not modelled	72.2	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
97	c4oxqB_	Alignment	not modelled	71.4	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
98	c5uyvA_	Alignment	not modelled	70.4	13	**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
99	c3hjtB_	Alignment	not modelled	70.0	12	**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
100	c2ps3A_	Alignment	not modelled	69.9	9	**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
101	d1psza_	Alignment	not modelled	67.0	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
102	c4xrvB	Alignment	not modelled	65.0	12	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**periplasmic solute binding protein;

102	c4xrvB_	Alignment	not modelled	65.0	12	**PDBTitle:** structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
103	d1mwwa_	Alignment	not modelled	64.7	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
104	c4j5uB_	Alignment	not modelled	64.0	13	**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
105	c3cx3A_	Alignment	not modelled	62.5	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
106	c3h7fB_	Alignment	not modelled	59.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
107	c2ogwB_	Alignment	not modelled	56.5	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
108	c3mfqB_	Alignment	not modelled	54.2	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
109	c5hx7A_	Alignment	not modelled	52.2	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**manganese-binding lipoprotein mnta; **PDBTitle:** metal abc transporter from listeria monocytogenes
110	c4je5C_	Alignment	not modelled	50.6	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
111	c4cl2A_	Alignment	not modelled	48.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic solute binding protein; **PDBTitle:** structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
112	d1toaa_	Alignment	not modelled	46.8	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
113	c1toaA_	Alignment	not modelled	46.8	13	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
114	c2dkjB_	Alignment	not modelled	45.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
115	d1kl1a_	Alignment	not modelled	41.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
116	c4lkbA_	Alignment	not modelled	39.7	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein alr4568/putative 4-oxalocrotonate **PDBTitle:** crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
117	c5f1yA_	Alignment	not modelled	39.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mccc family protein; **PDBTitle:** crystal structure of ba3275, the member of s66 family of serine2 peptidases
118	c6r6kB_	Alignment	not modelled	38.6	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**abc transporter substrate-binding protein; **PDBTitle:** structure of a fpvc mutant from pseudomonas aeruginosa
119	d2ayia1	Alignment	not modelled	36.5	14	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
120	c2o1eB_	Alignment	not modelled	35.9	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583