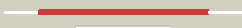







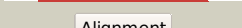

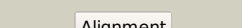
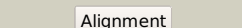

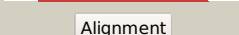




















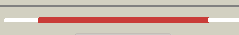

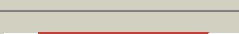
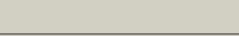


Phyre2

Email	mdejesus@rockefeller.edu
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Date	Thu Aug 8 16:20:47 BST 2019
Unique Job ID	1f311948e45e7d9d

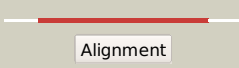
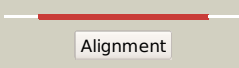
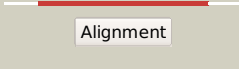
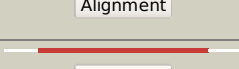
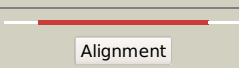
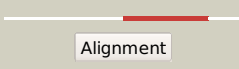
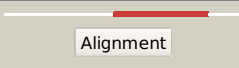
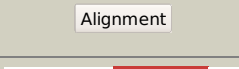

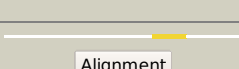
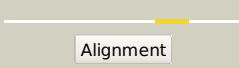
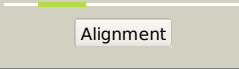
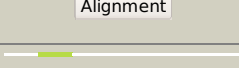
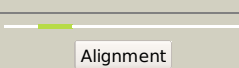
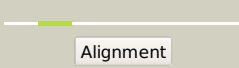
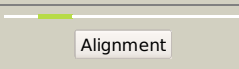
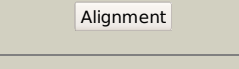
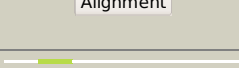
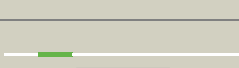


Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadt+ and phosphomethylphosphonic acid adenylate ester
2	c5gxdA_	 Alignment		100.0	13	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
3	c3tsyA_	 Alignment		100.0	14	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
4	c5u89A_	 Alignment		100.0	17	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
5	c5es8A_	 Alignment		100.0	17	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	c4wd1A_	 Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
7	d1pg4a_	 Alignment		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
8	d1ry2a_	 Alignment		100.0	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
9	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
10	c5mssA_	 Alignment		100.0	17	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
11	c6ozvA_	 Alignment		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

12	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
13	c5ja2A	 Alignment		100.0	16	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
14	c5msdA	 Alignment		100.0	15	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
15	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
16	c4gr5B	 Alignment		100.0	15	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
17	c2vsqA	 Alignment		100.0	17	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
18	c5mstA	 Alignment		100.0	13	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	c6n8eA	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
20	c4zxiA	 Alignment		100.0	17	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
21	c4lgcA	 Alignment	not modelled	100.0	13	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
22	c3etcB	 Alignment	not modelled	100.0	12	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
23	c3gqwB	 Alignment	not modelled	100.0	14	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
24	c4r0mB	 Alignment	not modelled	100.0	10	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
25	c3g7sA	 Alignment	not modelled	100.0	10	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
26	c3kxwA	 Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
27	c5x8gA	 Alignment	not modelled	100.0	13	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
28	c4r0mA	 Alignment	not modelled	100.0	10	PDB header: ligase Chain: A: PDB Molecule: mcyg protein;

28	c4v11A	Alignment	not modelled	100.0	10	PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate PDB header: ligase/inhibitor
29	c4dg9A	Alignment	not modelled	100.0	13	Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor PDB header: biosynthetic protein
30	c4zxiA	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
31	d1v25a	Alignment	not modelled	100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
32	c3vngA	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
33	d3cw9a1	Alignment	not modelled	100.0	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
34	c3iteB	Alignment	not modelled	100.0	12	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
35	c4wv3A	Alignment	not modelled	100.0	15	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
36	c4w8oA	Alignment	not modelled	100.0	10	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
37	c3e7wA	Alignment	not modelled	100.0	12	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
38	d1mdba	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
39	c5ey8D	Alignment	not modelled	100.0	16	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
40	c4dg8A	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
41	c3eynB	Alignment	not modelled	100.0	15	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
42	c3ni2A	Alignment	not modelled	100.0	12	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
43	c2v7bB	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
44	c2d1tA	Alignment	not modelled	100.0	12	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
45	c5ie2A	Alignment	not modelled	100.0	13	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
46	c3qyaA	Alignment	not modelled	100.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
47	c6ac3B	Alignment	not modelled	100.0	12	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)
48	c6abhG	Alignment	not modelled	100.0	11	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)
49	c5jipB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
50	c4ir7A	Alignment	not modelled	100.0	15	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	c6ijbA	Alignment	not modelled	100.0	13	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
52	c5c5hA	Alignment	not modelled	100.0	10	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
53	c3e53A	Alignment	not modelled	100.0	15	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

54	c1amuB_	Alignment	not modelled	100.0	13	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	c3nyrA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
56	c5wm7A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
57	c5n81B_	Alignment	not modelled	100.0	15	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
58	c5aplA_	Alignment	not modelled	100.0	19	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
59	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
60	c5e7qB_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
61	c3o82B_	Alignment	not modelled	99.9	19	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
62	c6h1bA_	Alignment	not modelled	99.9	17	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospira thermotolerans
63	c4fuqD_	Alignment	not modelled	99.9	13	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
64	c5buqA_	Alignment	not modelled	99.9	12	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
65	c3ip1B_	Alignment	not modelled	99.9	12	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
66	c5burB_	Alignment	not modelled	99.9	13	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
67	c3r44A_	Alignment	not modelled	99.9	16	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
68	c3o82A_	Alignment	not modelled	99.9	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
69	c3wv4B_	Alignment	not modelled	99.9	15	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
70	d1amuA_	Alignment	not modelled	99.9	13	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
71	c6akdA_	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
72	c3ivrA_	Alignment	not modelled	99.9	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 rhodopseudomonas palustris cga009
73	c3l8cA_	Alignment	not modelled	99.9	11	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
74	c4d56A_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
75	c5keiA_	Alignment	not modelled	99.9	20	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
76	c5jipC_	Alignment	not modelled	99.9	20	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
77	c4eatB_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
78	c5u2aA_	Alignment	not modelled	99.9	15	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase

79	c3t5cA	 Alignment	not modelled	99.9	16	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
80	c4oxiA	 Alignment	not modelled	99.9	14	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 glycylic-adenosine-5'-phosphate
81	c5oe3C	 Alignment	not modelled	99.9	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)
82	c5jqbB	 Alignment	not modelled	99.9	20	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
83	d1lcia	 Alignment	not modelled	99.9	10	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
84	c3dhvA	 Alignment	not modelled	99.9	9	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
85	c4gs5A	 Alignment	not modelled	99.6	12	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	c2y4oA	 Alignment	not modelled	99.5	9	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
87	c2y27B	 Alignment	not modelled	99.5	11	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
88	c3hguB	 Alignment	not modelled	99.2	7	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
89	c3qovD	 Alignment	not modelled	99.2	13	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
90	c4eplA	 Alignment	not modelled	77.2	10	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
91	c5kodA	 Alignment	not modelled	71.2	9	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	d2ayia1	 Alignment	not modelled	67.2	16	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
93	c4b2gB	 Alignment	not modelled	66.8	10	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	c6mb6A	 Alignment	not modelled	64.4	9	PDB header: transferase Chain: A: PDB Molecule: aac(3)-iiib protein; PDBTitle: aac-iiib binary with coash
95	c3e4fB	 Alignment	not modelled	64.3	23	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
96	c5ht0B	 Alignment	not modelled	62.7	14	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside acetyltransferase hmb0005; PDBTitle: crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
97	c6bc3A	 Alignment	not modelled	62.3	23	PDB header: transferase/antibiotic Chain: A: PDB Molecule: aac 3-vi protein; PDBTitle: cryo x-ray structure of isomicin bound aac-via
98	c3smaD	 Alignment	not modelled	61.8	14	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
99	c6mn5A	 Alignment	not modelled	61.2	18	PDB header: transferase/antibiotic Chain: A: PDB Molecule: aminoglycoside n(3)-acetyltransferase, aac(3)-iva; PDBTitle: crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
100	d2nyga1	Alignment	not modelled	60.7	14	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
101	c4z1oB	Alignment	not modelled	58.5	20	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxprt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
102	d1e3ia2	Alignment	not modelled	57.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Alcohol dehydrogenase-like, C-terminal domain
103	d1p0fa2	Alignment	not modelled	56.9	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
104	d1d1ta2	Alignment	not modelled	53.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
105	d1u3wa2	Alignment	not modelled	51.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
106	d1piwa2	Alignment	not modelled	48.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
107	d2jhfa2	Alignment	not modelled	47.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
108	d1pl8a2	Alignment	not modelled	46.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
109	d2fzwa2	Alignment	not modelled	45.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
110	d1kola2	Alignment	not modelled	43.1	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
111	c4icqB_	Alignment	not modelled	40.8	14	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase peps; PDBTitle: structural basis for substrate recognition and reaction mechanism of 2 bacterial aminopeptidase peps
112	c2glwA_	Alignment	not modelled	40.8	35	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
113	d1cdoa2	Alignment	not modelled	39.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
114	c5vogA_	Alignment	not modelled	38.6	11	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppppp
115	c4k2bA_	Alignment	not modelled	37.2	20	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the 2 internal aldimine
116	d1zjca1	Alignment	not modelled	36.9	16	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
117	d1ykfa2	Alignment	not modelled	36.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
118	d1e3ja2	Alignment	not modelled	36.6	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
119	d1f8fa2	Alignment	not modelled	32.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
120	d1lua2	Alignment	not modelled	32.7	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain