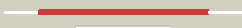



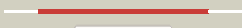



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3513c_(fadD18)_3945271_3945927
 Date Fri Aug 9 18:20:19 BST 2019
 Unique Job ID 3174759a7e45b7e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	Alignment 		100.0	20	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	c6p1jA_	Alignment 		100.0	20	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
3	c5es8A_	Alignment 		100.0	18	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	c6n8eA_	Alignment 		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
5	c4zxiA_	Alignment 		100.0	20	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	c4eatB_	Alignment 		100.0	27	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
7	c5ifiA_	Alignment 		100.0	24	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	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
9	c4oxiA_	Alignment 		100.0	16	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 glycy-l-adenosine-5'-phosphate
10	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 dfi2 12
11	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

12	c5ie2A_	Alignment		100.0	24	PDB header: ligase Chain: A; PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
13	c3e7wA_	Alignment		100.0	15	PDB header: ligase Chain: A; PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction mechanism of 2 non-ribosomal peptide synthetase (nrps) adenylation domains
14	c4zxiA_	Alignment		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 in 2 the thioester-forming conformation
15	c6h1bA_	Alignment		100.0	29	PDB header: ligase Chain: A; PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from 2 marinatingospora thermotolerans
16	c5u2aA_	Alignment		100.0	27	PDB header: ligase Chain: A; PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
17	c3r44A_	Alignment		100.0	24	PDB header: ligase Chain: A; PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa) PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
18	c5aplA_	Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: adenylation domain; PDBTitle: structure of the adenylation domain thr1 involved in the biosynthesis 2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure
19	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) from 2 nocardia iowensis in complex with amp and benzoic acid
20	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
21	d1mdba_	Alignment	not modelled	100.0	30	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
22	c4wv3A_	Alignment	not modelled	100.0	23	PDB header: ligase/ligase inhibitor Chain: A; PDB Molecule: anthranilate-coa ligase; PDBTitle: crystal structure of the anthranilate coa ligase auaeii in complex 2 with anthranoyl-amp
23	c3vngA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A; PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from 2 streptomyces
24	c4wd1A_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A; PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
25	d1pg4a_	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
26	d1ry2a_	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
27	c5ey8D_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: D; PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
28	c3eynB_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: B; PDB Molecule: acyl-coenzyme a synthetase acsm2a; PDBTitle: crystal structure of human acyl-coa synthetase medium-chain 2 family member 2a (l64p mutation) in a complex with coa
						PDB header: ligase

29	c5wm7A_	Alignment	not modelled	100.0	29	Chain: A; PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
30	d3cw9a1	Alignment	not modelled	100.0	26	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
31	c5x8gA_	Alignment	not modelled	100.0	23	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
32	c5mstA_	Alignment	not modelled	100.0	20	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
33	c3ni2A_	Alignment	not modelled	100.0	22	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
34	c5wmmA_	Alignment	not modelled	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
35	c4fuqD_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: D; PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodospseudomonas palustris
36	d1amua_	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
37	c5keiA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A; PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
38	c5mssA_	Alignment	not modelled	100.0	22	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
39	c3rg2H_	Alignment	not modelled	100.0	22	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
40	c3kxwA_	Alignment	not modelled	100.0	11	PDB header: ligase Chain: A; PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
41	c6ijbA_	Alignment	not modelled	100.0	22	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
42	c3iteB_	Alignment	not modelled	100.0	10	PDB header: ligase Chain: B; PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
43	c2v7bB_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: B; PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
44	c6ac3B_	Alignment	not modelled	100.0	21	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)
45	c3dhvA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A; PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
46	c5e7qB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B; PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
47	c4ir7A_	Alignment	not modelled	100.0	22	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
48	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
49	d1lcia_	Alignment	not modelled	100.0	25	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
50	c2d1tA_	Alignment	not modelled	100.0	25	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
51	c3gqwB_	Alignment	not modelled	100.0	15	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
52	c4dg9A_	Alignment	not modelled	100.0	17	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
53	c6akdA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A; PDB Molecule: amp-dependent synthetase and ligase;

						PDBTitle: crystal structure of idn17
54	c4dg8A_	Alignment	not modelled	99.9	16	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
55	c3l8cA_	Alignment	not modelled	99.9	21	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
56	c3nyrA_	Alignment	not modelled	99.9	23	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
57	c4r0mB_	Alignment	not modelled	99.9	14	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
58	c3tsyA_	Alignment	not modelled	99.9	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
59	c4r0mA_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
60	c3etcB_	Alignment	not modelled	99.9	33	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
61	c5jqbB_	Alignment	not modelled	99.9	22	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
62	c5buqA_	Alignment	not modelled	99.9	24	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
63	c4d56A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
64	c3iplB_	Alignment	not modelled	99.9	24	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
65	c4gs5A_	Alignment	not modelled	99.9	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
66	c3g7sA_	Alignment	not modelled	99.8	23	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
67	c5c5hA_	Alignment	not modelled	99.8	19	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
68	d1v25a_	Alignment	not modelled	99.8	26	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
69	c6ozvA_	Alignment	not modelled	99.8	17	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
70	c3ivrA_	Alignment	not modelled	99.8	15	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
71	c4gr5B_	Alignment	not modelled	99.8	24	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
72	c5jipB_	Alignment	not modelled	99.8	15	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
73	c5burB_	Alignment	not modelled	99.8	11	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
74	c3qyaA_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
75	c5oe3C_	Alignment	not modelled	99.8	18	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)
76	c3wv4B_	Alignment	not modelled	99.8	14	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
77	c5jipC_	Alignment	not modelled	99.7	14	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
78	c3o82B_	Alignment	not modelled	99.7	16	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
79	c3o82A_	Alignment	not modelled	99.7	19	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
80	c3t5cA_	Alignment	not modelled	99.7	14	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2
81	c2y4oA_	Alignment	not modelled	99.7	10	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
82	c4w8oA_	Alignment	not modelled	99.7	17	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
83	c5n81B_	Alignment	not modelled	99.7	20	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
84	c2y27B_	Alignment	not modelled	99.6	10	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
85	c3qovD_	Alignment	not modelled	99.6	10	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
86	c6abhG_	Alignment	not modelled	99.6	13	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)
87	c4lqcA_	Alignment	not modelled	99.5	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
88	c3e53A_	Alignment	not modelled	99.4	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
89	c3hguB_	Alignment	not modelled	97.9	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c3laxA_	Alignment	not modelled	97.7	14	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	c3mhxB_	Alignment	not modelled	18.2	19	PDB header: metal transport Chain: B: PDB Molecule: putative ferrous iron transport protein a; PDBTitle: crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
92	c2xetB_	Alignment	not modelled	16.0	17	PDB header: transport protein Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
93	d2nn6g3	Alignment	not modelled	14.2	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
94	c4chdA_	Alignment	not modelled	10.4	21	PDB header: viral protein Chain: A: PDB Molecule: polymerase acidic protein; PDBTitle: crystal structure of the '627' domain of the pb2 subunit of2 thogoto virus polymerase
95	d1ogmx1	Alignment	not modelled	7.3	18	Fold: Dextranase, N-terminal domain Superfamily: Dextranase, N-terminal domain Family: Dextranase, N-terminal domain
96	d2je6i3	Alignment	not modelled	6.6	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
97	c4wfb3_	Alignment	not modelled	5.9	20	PDB header: ribosome Chain: 3: PDB Molecule: 50s ribosomal protein l35; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
98	d2ja9a2	Alignment	not modelled	5.4	5	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
99	d1g9pa_	Alignment	not modelled	5.4	19	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins