







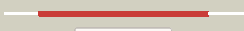
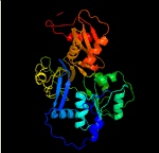























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0542c_(menE)_634419_635507
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	de84013d919a53ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	Alignment 		100.0	17	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 dfl2 12
3	c6p1jA_	Alignment 		100.0	21	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	c5es8A_	Alignment 		100.0	19	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
5	d1pg4a_	Alignment 		100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
6	c5u89A_	Alignment 		100.0	22	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	c5ja2A_	Alignment 		100.0	21	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
8	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
9	c2vsqA_	Alignment 		100.0	18	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
10	c5wmmA_	Alignment 		100.0	21	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
11	d1ry2a_	Alignment 		100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like

12	c4zxiA	Alignment		100.0	20	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
13	c4wd1A	Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
14	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
15	c5ifiA	Alignment		100.0	21	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
16	c4zxiA	Alignment		100.0	17	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
17	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
18	d1mdba	Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
19	c3e7wA	Alignment		100.0	17	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
20	c3vngA	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
21	c5x8gA	Alignment	not modelled	100.0	30	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
22	c5ie2A	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
23	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
24	c4wv3A	Alignment	not modelled	100.0	20	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
25	c5wm7A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
26	d3cw9a1	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
27	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)
28	c3ni2A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase;

28	c3i1zA	Alignment	not modelled	100.0	22	PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
29	c5u2aA	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
30	c3gqwB	Alignment	not modelled	100.0	20	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
31	c3kxwA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
32	c3iteB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
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	c4oxiA	Alignment	not modelled	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 glycy1-adenosine-5'-phosphate
35	c6ijbA	Alignment	not modelled	100.0	18	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
36	c4r0mB	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
37	c4eatB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
38	c3rg2H	Alignment	not modelled	100.0	21	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
39	c3nyrA	Alignment	not modelled	100.0	29	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
40	c6h1bA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
41	c5aplA	Alignment	not modelled	100.0	24	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
42	c3r44A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
43	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
44	c4ir7A	Alignment	not modelled	100.0	20	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
45	c4fuqD	Alignment	not modelled	100.0	21	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
46	c3eynB	Alignment	not modelled	100.0	21	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
47	c3etcB	Alignment	not modelled	100.0	22	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
48	c5ey8D	Alignment	not modelled	100.0	22	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
49	c4dg9A	Alignment	not modelled	100.0	24	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
50	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
51	c2y4oA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
52	c4dg8A	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains

53	c4r0mA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
54	c3dhvA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
55	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
56	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
57	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
58	c5e7qB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
59	c3iplB	Alignment	not modelled	100.0	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
60	d1amua	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
61	c1amuB	Alignment	not modelled	100.0	18	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
62	c6ozvA	Alignment	not modelled	100.0	18	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
63	c6akdA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
64	c4d56A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
65	d1lcia	Alignment	not modelled	100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
66	c5c5hA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
67	c3qovD	Alignment	not modelled	100.0	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
68	c5jjqB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
69	d1v25a	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
70	c3g7sA	Alignment	not modelled	100.0	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
71	c5buqA	Alignment	not modelled	100.0	27	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
72	c4gr5B	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
73	c4w8oA	Alignment	not modelled	99.9	18	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
74	c4lqcA	Alignment	not modelled	99.9	14	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
75	c3qyaA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
76	c5jipB	Alignment	not modelled	99.9	15	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
77	c6abhG	Alignment	not modelled	99.9	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)
78	c3o82B	Alignment	not modelled	99.9	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	c3hguB_	Alignment	not modelled	99.8	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
80	c3o82A_	Alignment	not modelled	99.8	16	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
81	c3wv4B_	Alignment	not modelled	99.8	20	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
82	c5burB_	Alignment	not modelled	99.8	20	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	c5n81B_	Alignment	not modelled	99.8	17	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	c3e53A_	Alignment	not modelled	99.8	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
85	c5oe3C_	Alignment	not modelled	99.7	16	PDB header: ligase Chain: C: PDB Molecule: anthranilate--coa ligase; PDBTitle: crystal structure of the n-terminal domain of pqsa in complex with 2 anthraniloyl-amp (crystal form 1)
86	c3ivrA_	Alignment	not modelled	99.7	19	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
87	c5jipC_	Alignment	not modelled	99.7	15	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
88	c3t5cA_	Alignment	not modelled	99.6	22	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
89	c3laxA_	Alignment	not modelled	98.5	17	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
90	c5kodA_	Alignment	not modelled	97.3	12	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
91	c4eplA_	Alignment	not modelled	96.6	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
92	c4b2gB_	Alignment	not modelled	94.4	13	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	c4ewvB_	Alignment	not modelled	68.5	14	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
94	d1whua_	Alignment	not modelled	40.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
95	c3g8qA_	Alignment	not modelled	33.8	20	PDB header: rna binding protein Chain: A: PDB Molecule: predicted rna-binding protein, contains thump PDBTitle: a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
96	c3zrrB_	Alignment	not modelled	31.7	7	PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfobolus3 solfataricus
97	c2wh7A_	Alignment	not modelled	27.8	55	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-phage associated; PDBTitle: the partial structure of a group a streptococcal phage-2 encoded tail fibre hyaluronate lyase hylp2
98	c2z9wA_	Alignment	not modelled	27.5	12	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
99	d2trcp_	Alignment	not modelled	26.3	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin
100	c3zia_	Alignment	not modelled	22.7	50	PDB header: hydrolase Chain: J: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae inhibited by2 its regulatory protein if1
101	c3ziaT_	Alignment	not modelled	22.7	50	PDB header: hydrolase Chain: T: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae inhibited by2 its regulatory protein if1