




















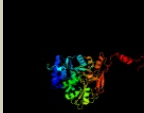











Phyre2

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Description	RVBD0648 (-) _742722_746369
Date	Fri Jul 26 01:50:21 BST 2019
Unique Job ID	42e4687887891a2c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5jm0A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; PDBTitle: structure of the s. cerevisiae alpha-mannosidase 1
2	c2wyhA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase; PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
3	c6b9pA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase from canavalia ensiformis (jack bean); PDBTitle: structure of gh 38 jack bean alpha-mannosidase in complex with a 36-2 valent iminosugar cluster inhibitor
4	c2ow7A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase 2; PDBTitle: golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thionibicyclo[4.3.0]nonan-7,8-diol chloride
5	c3lvtA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 38; PDBTitle: the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a
6	c1htyA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase ii; PDBTitle: golgi alpha-mannosidase ii
7	c2vsqA_	 Alignment		100.0	10	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
8	c5ja2A_	 Alignment		100.0	13	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	c5es8A_	 Alignment		100.0	11	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
10	d3bvua3	 Alignment		100.0	20	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: alpha-mannosidase
11	c5wmmA_	 Alignment		100.0	14	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

12	c4zxiA	Alignment		100.0	12	PDB header: biosynthetic protein Chain: A; PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide synthetase bound to amp and glycine
13	c5u89A	Alignment		100.0	11	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
14	d3bvua2	Alignment		100.0	25	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: alpha-mannosidase, C-terminal domain
15	c6p1jA	Alignment		100.0	14	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	c1o7dA	Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
17	c6eqoB	Alignment		100.0	15	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
18	c4zxiA	Alignment		100.0	14	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
19	c5ifiA	Alignment		100.0	11	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
20	d1pg4a	Alignment		100.0	11	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
21	c6ozvA	Alignment	not modelled	100.0	13	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
22	c4gr5B	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B; PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
23	c5gxdA	Alignment	not modelled	100.0	11	PDB header: lyase Chain: A; PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfi2 12
24	c4wd1A	Alignment	not modelled	100.0	13	PDB header: ligase Chain: A; PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
25	d1ry2a	Alignment	not modelled	100.0	12	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
26	c3tsyA	Alignment	not modelled	100.0	11	PDB header: ligase, transferase Chain: A; PDB Molecule: fuson protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
27	c5msdA	Alignment	not modelled	99.9	12	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
28	c5mssA	Alignment	not modelled	99.9	13	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
29	d1mdba_	Alignment	not modelled	99.9	10	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
30	c3etcb_	Alignment	not modelled	99.9	10	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
31	c5u2aA_	Alignment	not modelled	99.9	10	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
32	d3cw9a1	Alignment	not modelled	99.9	10	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
33	c4dg9A_	Alignment	not modelled	99.9	14	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
34	c1o7dC_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: C: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
35	c4dg8A_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
36	c3rg2H_	Alignment	not modelled	99.9	9	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
37	d3bvua1	Alignment	not modelled	99.9	20	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: alpha-mannosidase, domain 2
38	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
39	c3e7wA_	Alignment	not modelled	99.9	9	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
40	c5x8gA_	Alignment	not modelled	99.9	9	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
41	c5jjqB_	Alignment	not modelled	99.9	14	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
42	c6h1bA_	Alignment	not modelled	99.9	11	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
43	c5wm7A_	Alignment	not modelled	99.9	11	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
44	c3vngA_	Alignment	not modelled	99.9	11	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
45	c5keiA_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
46	c5mstA_	Alignment	not modelled	99.9	12	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
47	c4d56A_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
48	c3ni2A_	Alignment	not modelled	99.9	11	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
49	c5ie2A_	Alignment	not modelled	99.9	9	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
50	c4wv3A_	Alignment	not modelled	99.9	9	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
51	c3r44A_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
52	c3eynB_	Alignment	not modelled	99.9	12	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 Fold: Acetyl-CoA synthetase-like

53	d1v25a_	Alignment	not modelled	99.9	13	Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
54	c5buqA_	Alignment	not modelled	99.9	8	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
55	c5aplA_	Alignment	not modelled	99.9	11	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
56	c4fuqD_	Alignment	not modelled	99.9	9	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodospseudomonas palustris
57	c3nyrA_	Alignment	not modelled	99.9	14	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
58	d1amua_	Alignment	not modelled	99.9	9	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
59	c4oxiA_	Alignment	not modelled	99.9	10	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
60	c4ir7A_	Alignment	not modelled	99.9	10	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
61	c6ijbA_	Alignment	not modelled	99.9	10	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
62	c3iteB_	Alignment	not modelled	99.9	11	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
63	c1amuB_	Alignment	not modelled	99.9	8	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
64	c6ac3B_	Alignment	not modelled	99.9	9	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)
65	c4r0mA_	Alignment	not modelled	99.9	8	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
66	c2v7bB_	Alignment	not modelled	99.8	9	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
67	c3iplB_	Alignment	not modelled	99.8	10	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
68	c5ey8D_	Alignment	not modelled	99.8	11	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
69	c3g7sA_	Alignment	not modelled	99.8	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
70	c5e7qB_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
71	c3kxwA_	Alignment	not modelled	99.8	8	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
72	c5jipC_	Alignment	not modelled	99.8	14	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
73	d1k1xa3	Alignment	not modelled	99.8	10	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
74	c3dhvA_	Alignment	not modelled	99.8	12	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
75	c4r0mB_	Alignment	not modelled	99.8	9	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
76	c6akdA_	Alignment	not modelled	99.8	11	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
77	c2d1tA_	Alignment	not modelled	99.8	8	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
78	c5jipB_	Alignment	not modelled	99.8	12	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6

79	c5c5hA	Alignment	not modelled	99.8	11	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
80	c3o82B	Alignment	not modelled	99.7	9	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
81	c3l8cA	Alignment	not modelled	99.7	10	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
82	c3ivrA	Alignment	not modelled	99.7	11	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
83	c3gqwB	Alignment	not modelled	99.7	12	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
84	d1lclA	Alignment	not modelled	99.7	8	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
85	c4w8oA	Alignment	not modelled	99.7	5	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
86	c5burB	Alignment	not modelled	99.7	7	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
87	c3o82A	Alignment	not modelled	99.7	9	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
88	c5oe3C	Alignment	not modelled	99.7	14	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)
89	c5n81B	Alignment	not modelled	99.7	10	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
90	c3wv4B	Alignment	not modelled	99.6	12	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
91	c1k1yA	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
92	c3qyaA	Alignment	not modelled	99.6	8	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
93	c4lqcA	Alignment	not modelled	99.6	8	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
94	c3t5cA	Alignment	not modelled	99.5	9	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
95	c6abhG	Alignment	not modelled	99.5	10	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)
96	c2y27B	Alignment	not modelled	99.4	9	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
97	c3qovD	Alignment	not modelled	99.4	8	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
98	c4gs5A	Alignment	not modelled	99.4	10	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
99	c2y4oA	Alignment	not modelled	99.4	10	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
100	c3e53A	Alignment	not modelled	99.3	11	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
101	c3hguB	Alignment	not modelled	98.9	9	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
102	c1o7dB	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: B: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation PDB header: structural genomics, unknown function

103	c1ufaA_	Alignment	not modelled	98.8	17	Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
104	c5wu7A_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii
105	c2b5dX_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
106	c3n92A_	Alignment	not modelled	98.5	14	PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
107	d2b5dx2	Alignment	not modelled	98.4	11	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
108	c1o7dD_	Alignment	not modelled	98.3	15	PDB header: hydrolase Chain: D: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
109	c5cd6C_	Alignment	not modelled	98.0	12	PDB header: unknown function Chain: C: PDB Molecule: tpr-domain containing protein; PDBTitle: crystal structure of a tpr-domain containing protein (bdi_1685) from2 parabacteroides distazonis atcc 8503 at 2.26 a resolution
110	c5xqgC_	Alignment	not modelled	97.8	11	PDB header: lyase Chain: C: PDB Molecule: pargcx protein; PDBTitle: crystal structure of a pl 26 exo-rhamnogalacturonan lyase from2 penicillium chrysogenum complexed with unsaturated galacturonosyl3 rhamnose
111	d1ufaa2	Alignment	not modelled	97.7	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
112	c3laxA_	Alignment	not modelled	96.9	7	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
113	d1w8oa1	Alignment	not modelled	95.9	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
114	c3mwxA_	Alignment	not modelled	93.3	18	PDB header: isomerase Chain: A: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution
115	c3blcB_	Alignment	not modelled	93.0	13	PDB header: chaperone,protein transport Chain: B: PDB Molecule: inner membrane protein oxaa; PDBTitle: crystal structure of the periplasmic domain of the escherichia coli2 yidc
116	c3dcdA_	Alignment	not modelled	92.6	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: x-ray structure of the galactose mutarotase related enzyme q5fk7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.
117	c3q1nA_	Alignment	not modelled	92.0	16	PDB header: isomerase Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: crystal structure of a galactose mutarotase-like protein (lsej_2598)2 from lactobacillus casei atcc 334 at 1.61 a resolution
118	c3nreB_	Alignment	not modelled	91.9	16	PDB header: isomerase Chain: B: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative aldose 1-epimerase (b2544) from2 escherichia coli k12 at 1.59 a resolution
119	c4l1gB_	Alignment	not modelled	91.9	15	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
120	c6dq3B_	Alignment	not modelled	90.3	14	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate