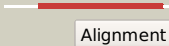

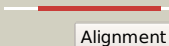

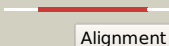




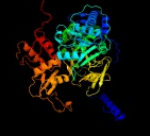


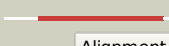
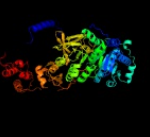










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2590_(fadD9)_2917881_2921387
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	2ff14b355ace1a0f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mssA_	 Alignment		100.0	51	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
2	c5es8A_	 Alignment		100.0	24	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
3	c5msdA_	 Alignment		100.0	57	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
4	c2vsgA_	 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
5	c5ja2A_	 Alignment		100.0	26	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
6	c5mstA_	 Alignment		100.0	52	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
7	c6n8eA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
8	c5u89A_	 Alignment		100.0	25	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
9	c4zxiA_	 Alignment		100.0	23	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
10	c4zxiA_	 Alignment		100.0	24	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
11	c6eqoB_	 Alignment		100.0	18	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 adenylylate ester

12	c5wmmA_	Alignment		100.0	24	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
13	c4dg9A_	Alignment		100.0	21	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
14	c6pljA_	Alignment		100.0	23	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
15	c3rg2H_	Alignment		100.0	20	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
16	c5gxdA_	Alignment		100.0	20	PDB header: lyase Chain: A; PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
17	c4r0mA_	Alignment		100.0	16	PDB header: ligase Chain: A; PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
18	c5msvB_	Alignment		100.0	61	PDB header: oxidoreductase Chain: B; PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
19	d1pg4a_	Alignment		100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
20	c5ifiA_	Alignment		100.0	16	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
21	c4wd1A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A; PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
22	d1ry2a_	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
23	c5msuC_	Alignment	not modelled	100.0	84	PDB header: oxidoreductase Chain: C; PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
24	c3tsyA_	Alignment	not modelled	100.0	17	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
25	c4dqvA_	Alignment	not modelled	100.0	68	PDB header: ligase Chain: A; PDB Molecule: probable peptide synthetase nrp (peptide synthase); PDBTitle: crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
26	d1mdba_	Alignment	not modelled	100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
27	c3e7wA_	Alignment	not modelled	100.0	22	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
						PDB header: ligase Chain: A; PDB Molecule: 2-succinylbenzoate--coa liqase;

28	c5x8gA_	Alignment	not modelled	100.0	24	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
29	c5ie2A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
30	c6ozvA_	Alignment	not modelled	100.0	22	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
31	c3etcB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
32	d3cw9a1	Alignment	not modelled	100.0	25	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
33	c3vngA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
34	c3ni2A_	Alignment	not modelled	100.0	20	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
35	c5wm7A_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
36	c4wv3A_	Alignment	not modelled	100.0	17	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
37	c6ac3B_	Alignment	not modelled	100.0	20	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)
38	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
39	c5ey8D_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
40	c3gqwB_	Alignment	not modelled	100.0	18	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
41	c3kxwA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
42	c5u2aA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
43	c4d56A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
44	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
45	c5ijqB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
46	c3r44A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
47	c4dg8A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
48	c6ijbA_	Alignment	not modelled	100.0	19	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
49	c3iteB_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
50	d1v25a_	Alignment	not modelled	100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
51	c3g7sA_	Alignment	not modelled	100.0	19	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
52	c4r0mB_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
53	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

54	c3eynB_	Alignment	not modelled	100.0	18	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
55	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 glycy-l-adenosine-5'-phosphate
56	c5aplA_	Alignment	not modelled	100.0	23	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
57	c6h1bA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
58	c4gr5B_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
59	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
60	c3iplB_	Alignment	not modelled	100.0	21	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
61	c2v7bB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
62	c6akdA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
63	c3nyrA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
64	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
65	c5buqA_	Alignment	not modelled	100.0	22	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
66	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
67	d1amua_	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
68	d1lcia_	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
69	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
70	c3l8cA_	Alignment	not modelled	100.0	19	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
71	c3dhvA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
72	c4w8oA_	Alignment	not modelled	100.0	24	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
73	c5c5hA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
74	c3qyaA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
75	c5ijpB_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
76	c3o82B_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
77	c4lgcA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: bile acid-coenzyme a ligase; PDBTitle: crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
78	c6abhG_	Alignment	not modelled	100.0	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)

79	c3wv4B	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
80	c3o82A	Alignment	not modelled	100.0	17	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	c3ivrA	Alignment	not modelled	100.0	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 rhodospseudomonas palustris cga009
82	c5burB	Alignment	not modelled	100.0	21	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	100.0	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	c5oe3C	Alignment	not modelled	100.0	19	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)
85	c3t5cA	Alignment	not modelled	100.0	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
86	c3e53A	Alignment	not modelled	100.0	20	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
87	c5jipC	Alignment	not modelled	100.0	23	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
88	c4w4tA	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: mxaa; PDBTitle: the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
89	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
90	c2y4oA	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
91	c4f6cA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
92	c2y27B	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
93	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
94	c5df1A	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
95	c2v6gA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
96	c1z7eC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
97	c6el3A	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxo-delta(4,5)-steroid 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp
98	c3pvzD	Alignment	not modelled	100.0	14	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
99	c1z45A	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
100	d1i24a	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
101	c3w1vA	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap8e; PDBTitle: crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor
102	c3oh8A	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cqr91

103	d1y1pa1	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	c2iodD	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
105	c6bwcA	Alignment	not modelled	100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis
106	c6nbrC	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
107	c4r1sB	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase
108	c5zedA	Alignment	not modelled	100.0	11	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein adh; PDBTitle: crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s)
109	c4qukA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroflavonol-4-reductase; PDBTitle: crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
110	c4j2oD	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase/5-epimerase; PDBTitle: crystal structure of nadp-bound wbjb from a. baumannii community2 strain d1279779
111	c4lisA	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-galactose-4-epimerase from aspergillus2 nidulans
112	c5b6kA	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein cgkr1; PDBTitle: crystal structure of ketoreductase 1 from candida glabrata
113	c4pvcB	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
114	c3wj7B	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
115	c6d2vA	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: terb oxidoreductase; PDBTitle: apo structure of terb, an nadp dependent oxidoreductase in the2 terfestatin biosynthesis pathway
116	c2zklA	Alignment	not modelled	99.9	24	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
117	c3nzoB	Alignment	not modelled	99.9	15	PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
118	c2gn9B	Alignment	not modelled	99.9	19	PDB header: lyase Chain: B: PDB Molecule: udp-glcnc6 dehydratase; PDBTitle: crystal structure of udp-glcnc6 inverting 4,6-dehydratase in complex2 with nadp and udp-glc
119	d1e6ua	Alignment	not modelled	99.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c3hguB	Alignment	not modelled	99.9	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein