Phyre^{2}

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Description	P11454
Date	Thu Jan 5 11:32:39 GMT 2012
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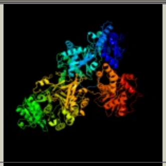
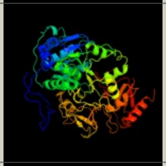
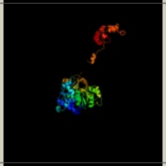
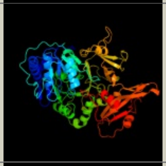
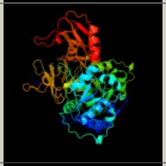
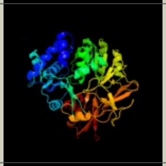
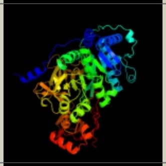
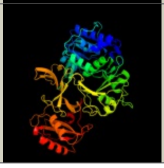
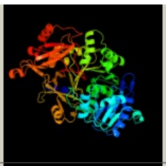
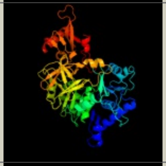
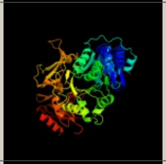
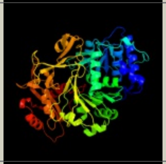
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vsqA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
2	d1pg4a_	Alignment		100.0	21	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	d1ry2a_	Alignment		100.0	22	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
4	c3tsyA_	Alignment		100.0	16	**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
5	c3e7wA_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
6	d3cw9a1	Alignment		100.0	26	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
7	d1mdba_	Alignment		100.0	22	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
8	c3ni2A_	Alignment		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
9	c3etcB_	Alignment		100.0	19	**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
10	d1amua_	Alignment		100.0	31	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
11	c3iteB_	Alignment		100.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase

12	c1amuB_	Alignment		100.0	30	**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
13	c3gqwB_	Alignment		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
14	c3kxwA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
15	c3eynB_	Alignment		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
16	c2v7bB_	Alignment		100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
17	c2d1tA_	Alignment		100.0	18	**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
18	c3nyrA_	Alignment		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
19	c3dhvA_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
20	d1v25a_	Alignment		100.0	23	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
21	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
22	c3iplB_	Alignment	not modelled	100.0	20	**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
23	c3l8cA_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
24	d1lcia_	Alignment	not modelled	100.0	14	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
25	c1l5aA_	Alignment	not modelled	100.0	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
26	c2jgpA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc
27	c3o82B_	Alignment	not modelled	100.0	20	**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
						PDB header:ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme;

28	c3o82A_	Alignment	not modelled	100.0	21	**PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
29	c2xhgA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
30	c3ivrA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
31	c2roqA_	Alignment	not modelled	100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enterobactin synthetase component f; **PDBTitle:** solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
32	c3e53A_	Alignment	not modelled	100.0	21	**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
33	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
34	c2y27B_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
35	c3qovD_	Alignment	not modelled	100.0	16	**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
36	c3fotA_	Alignment	not modelled	100.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
37	d1jmkc_	Alignment	not modelled	100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
38	c1q9jA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
39	c2cbgA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fengycin synthetase; **PDBTitle:** crystal structure of the pmsf-inhibited thioesterase domain2 of the fengycin biosynthesis cluster
40	c1mo2A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6; **PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
41	d1mo2a_	Alignment	not modelled	100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
42	c3lcrA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
43	d2h7xa1	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
44	c2h7xA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
45	d1l5aa1	Alignment	not modelled	100.0	25	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
46	d1l5aa2	Alignment	not modelled	100.0	24	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
47	c3hguB_	Alignment	not modelled	100.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
48	d1xkta_	Alignment	not modelled	100.0	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
49	c2px6A_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thioesterase domain; **PDBTitle:** crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
50	c3ilsA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** the thioesterase domain from pksa
51	c3qmwD_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** redj with peg molecule bound in the active site
52	d1q9ja1	Alignment	not modelled	99.9	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
53	c3flaB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1

54	c2ronA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
55	c2cq8A_	Alignment	not modelled	99.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
56	d1q9ja2	Alignment	not modelled	99.7	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
57	c1cr6A_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
58	c2bghA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vinorine synthase; **PDBTitle:** crystal structure of vinorine synthase
59	c2e1uA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl transferase; **PDBTitle:** crystal structure of dendranthema morifolium dmat
60	d2gdwa1	Alignment	not modelled	99.6	29	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
61	c3v48B_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd; **PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
62	c1y37A_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
63	c3l80A_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
64	c3qvmA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
65	c3om8A_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable hydrolase; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
66	d2vata1	Alignment	not modelled	99.5	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
67	c2qmqA_	Alignment	not modelled	99.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ndrg2; **PDBTitle:** crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
68	c2y6vB_	Alignment	not modelled	99.5	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
69	c2vavL_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
70	c3oosA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase family protein; **PDBTitle:** the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. sterne
71	c2xuaH_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
72	c2r11D_	Alignment	not modelled	99.5	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carboxylesterase np; **PDBTitle:** crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
73	c3kdaB_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif); **PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
74	c3ibtA_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; **PDBTitle:** structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
75	c3e0xB_	Alignment	not modelled	99.4	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lipase-esterase related protein; **PDBTitle:** the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
76	c2wj4B_	Alignment	not modelled	99.4	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; **PDBTitle:** crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine
77	c2fq1A_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains

78	c3i1iA_	Alignment	not modelled	99.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
79	c3fsgC_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta superfamily hydrolase; **PDBTitle:** crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
80	d1mj5a_	Alignment	not modelled	99.4	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
81	d2b61a1	Alignment	not modelled	99.4	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
82	c3bf7B_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase ybff; **PDBTitle:** 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
83	d1m33a_	Alignment	not modelled	99.4	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Biotin biosynthesis protein BioH
84	c2cjpA_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
85	c2ju2A_	Alignment	not modelled	99.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase; **PDBTitle:** minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
86	d1ehya_	Alignment	not modelled	99.4	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
87	c2liuA_	Alignment	not modelled	99.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cura; **PDBTitle:** nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
88	d1a8qa_	Alignment	not modelled	99.3	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
89	d1e89a_	Alignment	not modelled	99.3	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
90	d1hlga_	Alignment	not modelled	99.3	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
91	d1hkha_	Alignment	not modelled	99.3	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
92	d2pl5a1	Alignment	not modelled	99.3	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
93	d1cr6a2	Alignment	not modelled	99.3	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
94	d1mtza_	Alignment	not modelled	99.3	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
95	d1zd3a2	Alignment	not modelled	99.3	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
96	c2pseA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renilla-luciferin 2-monooxygenase; **PDBTitle:** crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
97	c3kxpD_	Alignment	not modelled	99.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid **PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase
98	d1k8qa_	Alignment	not modelled	99.2	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
99	c3bwxA_	Alignment	not modelled	99.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
100	c2xr7A_	Alignment	not modelled	99.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyltransferase; **PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
101	c2xmzA_	Alignment	not modelled	99.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
102	d1brta_	Alignment	not modelled	99.2	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
103	c2afdA_	Alignment	not modelled	99.2	20	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**protein asl1650; **PDBTitle:** solution structure of asl1650, an acyl carrier protein

						from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
104	c3r3xA_	Alignment	not modelled	99.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
105	c3laxA_	Alignment	not modelled	99.2	16	**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
106	c1u2eA_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid **PDBTitle:** crystal structure of the c-c bond hydrolase mhpc
107	d3c70a1	Alignment	not modelled	99.2	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
108	c3r0vA_	Alignment	not modelled	99.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
109	d1a8sa_	Alignment	not modelled	99.2	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
110	d1xkla_	Alignment	not modelled	99.2	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
111	d2rhwa1	Alignment	not modelled	99.2	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
112	c3fobA_	Alignment	not modelled	99.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
113	d1c4xa_	Alignment	not modelled	99.1	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
114	d1va4a_	Alignment	not modelled	99.1	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
115	c3e3aA_	Alignment	not modelled	99.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible peroxidase bpoc; **PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis
116	c3u1tA_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
117	c3qyjB_	Alignment	not modelled	99.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alr0039 protein; **PDBTitle:** crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
118	d1qo7a_	Alignment	not modelled	99.1	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
119	d1ispa_	Alignment	not modelled	99.1	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
120	c2qvbA_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase 3; **PDBTitle:** crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis