Email	l.a.kelley@imperial.ac.uk
Description	P76594
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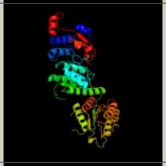
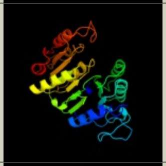
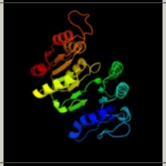
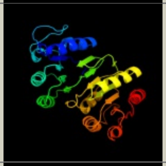
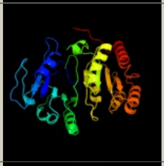
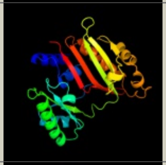
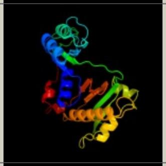
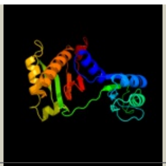
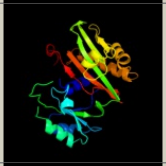
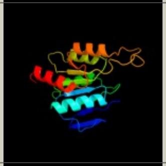
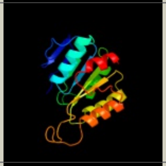
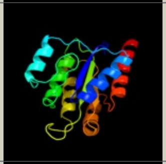
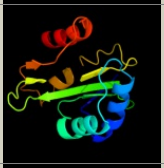
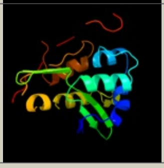
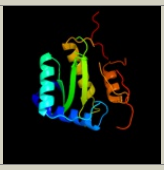
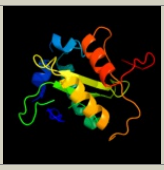
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2csuB_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
2	c3dmyA_	Alignment		100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
3	c2fpgA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
4	c2nu8D_	Alignment		100.0	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
5	c2yv2A_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
6	c1oi7A_	Alignment		100.0	20	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
7	c2yv1A_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
8	c3mwdB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
9	c1wr2A_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1789; **PDBTitle:** crystal structure of ph1788 from pyrococcus horikoshii ot3
10	d1eucb2	Alignment		100.0	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
11	d2nu7b2	Alignment		100.0	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain

12	c1eucB_	Alignment		100.0	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
13	c2nu9E_	Alignment		100.0	16	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
14	d1euca2	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
15	d2nu7a2	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
16	c3mwdA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
17	d2csua2	Alignment		100.0	33	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
18	d1oi7a2	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
19	d2csua3	Alignment		100.0	30	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
20	d2csua1	Alignment		100.0	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
21	c2duwA_	Alignment	not modelled	100.0	27	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
22	d2d59a1	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
23	d1y81a1	Alignment	not modelled	99.9	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
24	d1iuka_	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
25	c3ff4A_	Alignment	not modelled	99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
26	d2nu7b1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
27	d1eucb1	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
28	d1euca1	Alignment	not modelled	99.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
						

29	c3f8kA_	Alignment		99.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein acetyltransferase; **PDBTitle:** crystal structure of protein acetyltransferase (pat) from2 sulfolobus solfataricus
30	c3d3sA_	Alignment		99.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-2,4-diaminobutyric acid acetyltransferase; **PDBTitle:** crystal structure of l-2,4-diaminobutyric acid acetyltransferase from2 bordetella parapertussis
31	d2i6ca1	Alignment		99.5	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
32	d2nu7a1	Alignment	not modelled	99.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
33	c3g8wB_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lactococcal prophage ps3 protein 05; **PDBTitle:** crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228
34	c2r7hA_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative d-alanine n-acetyltransferase of gnat family; **PDBTitle:** crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution
35	c3eo4A_	Alignment	not modelled	99.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1062; **PDBTitle:** the crystal structure of a domain from methanocaldococcus jannaschii2 dsm 2661
36	d1oi7a1	Alignment	not modelled	99.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
37	d1s7ka1	Alignment	not modelled	99.4	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
38	d2beia1	Alignment	not modelled	99.4	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
39	c3dr8B_	Alignment		99.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ynca; **PDBTitle:** structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
40	c3exnA_	Alignment	not modelled	99.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of acetyltransferase from thermus thermophilus hb8
41	d1qsma_	Alignment	not modelled	99.3	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
42	c2fsrA_	Alignment		99.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** crystal structure of the acetyltransferase from agrobacterium2 tumefaciens str. c58
43	c3igrA_	Alignment	not modelled	99.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal-protein-s5-alanine n-acetyltransferase; **PDBTitle:** the crystal structure of ribosomal-protein-s5-alanine2 acetyltransferase from vibrio fischeri to 2.0a
44	d1yk3a1	Alignment	not modelled	99.3	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	c3tcvB_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of a gcn5-related n-acetyltransferase from brucella2 melitensis
46	d1yvoa1	Alignment		99.3	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
47	c2qmlA_	Alignment	not modelled	99.3	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bh2621 protein; **PDBTitle:** crystal structure of an uncharacterized protein (bh2621) from bacillus2 halodurans at 1.55 a resolution
48	c2i79B_	Alignment	not modelled	99.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** the crystal structure of the acetyltransferase of gnat family from2 streptococcus pneumoniae

49	d2ae6a1	Alignment	not modelled	99.3	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
50	c3fixA_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase; **PDBTitle:** crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum
51	d1vhsa_	Alignment	not modelled	99.3	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	c2pswA_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase 13; **PDBTitle:** human mak3 homolog in complex with coa
53	d2ge3a1	Alignment	not modelled	99.3	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
54	c3eg7F_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**spermidine n1-acetyltransferase; **PDBTitle:** spermidine n1-acetyltransferase from vibrio cholerae
55	d1nsla_	Alignment	not modelled	99.2	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
56	d1yr0a1	Alignment	not modelled	99.2	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
57	c2jlmE_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** E: **PDB Molecule:**putative phosphinothricin n-acetyltransferase; **PDBTitle:** structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
58	c3lodA_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa n-acyltransferase; **PDBTitle:** the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
59	d2b5ga1	Alignment	not modelled	99.2	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
60	c3i9sA_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
61	c2vzzA_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rv0802c; **PDBTitle:** crystal structure of rv0802c from mycobacterium2 tuberculosis in complex with succinyl-coa
62	c2r1iB_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_831484.1) from2 arthrobacter sp. fb24 at 1.65 a resolution
63	d2fsra1	Alignment	not modelled	99.2	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
64	c2oh1A_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase gnat family (yp_013287.1) from2 listeria monocytogenes 4b f2365 at 1.46 a resolution
65	c3pp9B_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative streptothricin acetyltransferase; **PDBTitle:** 1.6 angstrom resolution crystal structure of putative streptothricin2 acetyltransferase from bacillus anthracis str. ames in complex with3 acetyl coenzyme a
66	c2huzB_	Alignment	not modelled	99.2	18	**PDB header:**structural genomics, transferase **Chain:** B: **PDB Molecule:**glucosamine 6-phosphate n-acetyltransferase; **PDBTitle:** crystal structure of gnpnat1
67	c2zw7A_	Alignment	not modelled	99.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bleomycin acetyltransferase; **PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
68	c2vi7C_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyltransferase pa1377; **PDBTitle:** structure of a putative acetyltransferase (pa1377)from2 pseudomonas aeruginosa
69	c3r95A_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mcce protein; **PDBTitle:** crystal structure of microcin c7 self immunity acetyltransferase mcce2 in complex with acetyl-coa
70	c3k9uA_	Alignment	not modelled	99.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**paia acetyltransferase; **PDBTitle:** crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
71	c1s7fA_	Alignment	not modelled	99.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl transferase; **PDBTitle:** riml- ribosomal l7/l12 alpha-n-protein acetyltransferase crystal form2 i (apo)
72	c3c26A_	Alignment	not modelled	99.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase ta0821; **PDBTitle:** crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
73	c1ufhB_	Alignment	not modelled	99.1	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yycn protein; **PDBTitle:** structure of putative acetyltransferase, yycn protein of bacillus2 subtilis
						PDB header:transferase

74	c3juwC_	Alignment	not modelled	99.1	17	**Chain:** C: **PDB Molecule:**probable gnat-family acetyltransferase; **PDBTitle:** putative gnat-family acetyltransferase from bordetella pertussis.
75	d1ufha_	Alignment	not modelled	99.1	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
76	c2cntD_	Alignment	not modelled	99.1	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**modification of 30s ribosomal subunit protein s18; **PDBTitle:** rimi - ribosomal s18 n-alpha-protein acetyltransferase in2 complex with coenzymea.
77	d1tiqa_	Alignment	not modelled	99.1	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
78	c3owcA_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of gnat superfamily protein pa2578 from pseudomonas2 aeruginosa
79	c3fbuB_	Alignment	not modelled	99.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** the crystal structure of the acetyltransferase (gnat family) from2 bacillus anthracis
80	c2pdoG_	Alignment	not modelled	99.1	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
81	c3bg5C_	Alignment	not modelled	99.1	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
82	d1u6ma_	Alignment	not modelled	99.1	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
83	c3ld2B_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of smu.2055 from streptococcus mutans ua159
84	d2fiaa1	Alignment	not modelled	99.1	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
85	d2cy2a1	Alignment	not modelled	99.1	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
86	d1mk4a_	Alignment	not modelled	99.1	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
87	c3lp8A_	Alignment	not modelled	99.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
88	d2fcka1	Alignment	not modelled	99.1	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
89	c3d8pB_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase of gnat family; **PDBTitle:** crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
90	c1kjjA_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
91	c1ulzA_	Alignment	not modelled	99.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
92	d2fe7a1	Alignment	not modelled	99.1	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
93	d1yvka1	Alignment	not modelled	99.0	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
94	c3pzjB_	Alignment	not modelled	99.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable acetyltransferases; **PDBTitle:** crystal structure of a probable acetyltransferases (gnat family) from2 chromobacterium violaceum atcc 12472
95	d1yrea1	Alignment	not modelled	99.0	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
96	c3ouzA_	Alignment	not modelled	99.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
97	d1s3za_	Alignment	not modelled	99.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
98	d1y9ka1	Alignment	not modelled	99.0	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
99	c3dsbB_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of a possible acetyltransferase from clostridium2 difficile 630
						PDB header:ligase

100	c3g8cB_	Alignment	not modelled	99.0	15	**Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
101	d1z4ra1	Alignment	not modelled	99.0	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
102	d2fl4a1	Alignment	not modelled	99.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
103	d1sqha_	Alignment	not modelled	99.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Hypothetical protein cg14615-pa
104	c2dxqA_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** putative acetyltransferase from agrobacterium tumefaciens str. c58
105	d2euia1	Alignment	not modelled	99.0	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
106	c2zxvD_	Alignment	not modelled	99.0	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative uncharacterized protein ttha1799; **PDBTitle:** crystal structure of putative acetyltransferase from t.2 thermophilus hb8
107	c2hjwA_	Alignment	not modelled	99.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
108	c1m6vE_	Alignment	not modelled	99.0	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
109	d1p0ha_	Alignment	not modelled	99.0	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
110	c2dzdB_	Alignment	not modelled	98.9	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
111	c2reeB_	Alignment	not modelled	98.9	18	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
112	c2xd4A_	Alignment	not modelled	98.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
113	d1i12a_	Alignment	not modelled	98.9	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
114	c1w96B_	Alignment	not modelled	98.9	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
115	c2r98A_	Alignment	not modelled	98.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
116	c2vpqA_	Alignment	not modelled	98.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
117	d1n71a_	Alignment	not modelled	98.9	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
118	c2x7bA_	Alignment	not modelled	98.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase sso0209; **PDBTitle:** crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
119	d1ghea_	Alignment	not modelled	98.9	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
120	c3fncA_	Alignment	not modelled	98.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase from listeria2 innocua