Phyre2

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Description	P0ADQ2
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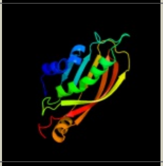
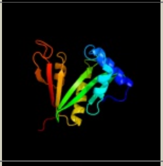
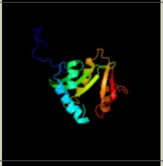
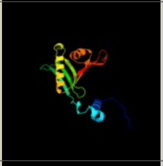
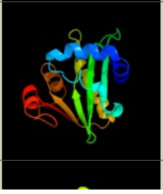
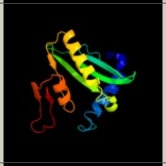
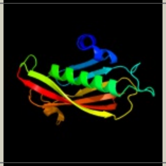
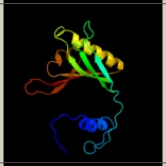
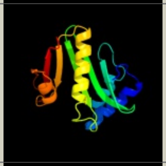
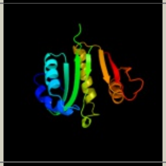
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lmbA_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum tls
2	d1t82a_	Alignment		100.0	38	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
3	c3efaA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
4	d1sh8a_	Alignment		100.0	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
5	d1q2ya_	Alignment		99.9	24	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
6	d2jdca1	Alignment		99.9	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
7	d1n71a_	Alignment		99.9	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
8	d1xeba_	Alignment		99.9	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
9	c1ib1E_	Alignment		99.9	17	**PDB header:**signaling protein/transferase **Chain:** E: **PDB Molecule:**serotonin n-acetyltransferase; **PDBTitle:** crystal structure of the 14-3-3 zeta:serotonin n-2 acetyltransferase complex
10	d1y9wa1	Alignment		99.9	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
11	c3lodA_	Alignment		99.8	16	**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

12	c2cntD_	Alignment		99.8	19	**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.
13	d1qsra_	Alignment		99.8	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
14	d1tiqa_	Alignment		99.8	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
15	c3d8pB_	Alignment		99.8	8	**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
16	d1yoca1	Alignment		99.8	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
17	d2g3aa1	Alignment		99.8	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
18	c2r7hA_	Alignment		99.8	14	**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
19	d1ghea_	Alignment		99.8	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
20	c2q7bA_	Alignment		99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase (np_689019.1) from2 streptococcus agalactiae 2603 at 2.00 a resolution
21	c2r98A_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
22	c2pswA_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase 13; **PDBTitle:** human mak3 homolog in complex with coa
23	d2fiwa1	Alignment	not modelled	99.8	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
24	c2q0yA_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
25	c3blnA_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase gnat family; **PDBTitle:** crystal structure of acetyltransferase gnat family (np_981174.1) from2 bacillus cereus atcc 10987 at 1.31 a resolution
26	d1u6ma_	Alignment	not modelled	99.8	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
27	d1mk4a_	Alignment	not modelled	99.8	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
28	d1yx0a1	Alignment	not modelled	99.8	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
29	d2i6ca1	Alignment	not modelled	99.8	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat)

						Family:N-acetyl transferase, NAT
30	d1y9ka1	Alignment	not modelled	99.8	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
31	d1z4ra1	Alignment	not modelled	99.8	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
32	c2x7bA_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase sso0209; **PDBTitle:** crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
33	d2cy2a1	Alignment	not modelled	99.8	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
34	c3fncA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase from listeria2 innocua
35	d2fiaa1	Alignment	not modelled	99.8	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
36	d1yvka1	Alignment	not modelled	99.8	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
37	d1cm0a_	Alignment	not modelled	99.7	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
38	c3ey5A_	Alignment	not modelled	99.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase-like, gnat family; **PDBTitle:** putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
39	c3mgdB_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted acetyltransferase; **PDBTitle:** crystal structure of predicted acetyltransferase with acetyl-coa from2 clostridium acetobutylicum at the resolution 1.9a, northeast3 structural genomics consortium target car165
40	c3s4kA_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase rv1847/mt1895; **PDBTitle:** structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
41	d1cjwa_	Alignment	not modelled	99.7	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
42	c2oh1A_	Alignment	not modelled	99.7	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
43	c2jlmE_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** E: **PDB Molecule:**putative phosphinothricin n-acetyltransferase; **PDBTitle:** structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
44	c2g0bG_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**feem; **PDBTitle:** the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
45	d1yvoa1	Alignment	not modelled	99.7	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
46	c2pdoG_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
47	d1s3za_	Alignment	not modelled	99.7	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
48	c3e8pA_	Alignment	not modelled	99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
49	d1ro5a_	Alignment	not modelled	99.7	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
50	c3dkzA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thioesterase superfamily protein; **PDBTitle:** crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
51	c2huzB_	Alignment	not modelled	99.7	20	**PDB header:**structural genomics, transferase **Chain:** B: **PDB Molecule:**glucosamine 6-phosphate n-acetyltransferase; **PDBTitle:** crystal structure of gnpnat1
52	d1ygha_	Alignment	not modelled	99.7	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
53	d1vhsa_	Alignment	not modelled	99.7	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
54	c2ozhA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein xcc2953; **PDBTitle:** crystal structure of a putative acetyltransferase belonging to the2 gnat family (xcc2953) from xanthomonas

						campestris pv. campestris at3 1.40 a resolution
55	d2beia1	Alignment	not modelled	99.7	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
56	c3g8wB_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lactococcal prophage ps3 protein 05; **PDBTitle:** crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228
57	c2reeB_	Alignment	not modelled	99.7	16	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
58	c3c26A_	Alignment	not modelled	99.7	15	**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
59	d1zkia1	Alignment	not modelled	99.7	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
60	d1y7ra1	Alignment	not modelled	99.7	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
61	d2atra1	Alignment	not modelled	99.7	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
62	c2qecA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase hpa2 and related **PDBTitle:** crystal structure of histone acetyltransferase hpa2 and related2 acetyltransferase (np_600742.1) from corynebacterium glutamicum atcc3 13032 at 1.90 a resolution
63	c3i9sA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
64	c3frmF_	Alignment	not modelled	99.7	14	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a functionally unknown conserved protein from2 staphylococcus epidermidis atcc 12228.
65	c3hduB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative thioesterase; **PDBTitle:** crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
66	d1wwza1	Alignment	not modelled	99.7	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
67	d2fl4a1	Alignment	not modelled	99.7	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
68	c3f8kA_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein acetyltransferase; **PDBTitle:** crystal structure of protein acetyltransferase (pat) from2 sulfolobus solfataricus
69	c3fb3A_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase; **PDBTitle:** crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
70	d2ae6a1	Alignment	not modelled	99.7	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
71	c3dddA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase (np_142035.1) from2 pyrococcus horikoshii at 2.25 a resolution
72	c3dr8B_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ynca; **PDBTitle:** structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
73	c3dsbB_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of a possible acetyltransferase from clostridium2 difficile 630
74	d1i12a_	Alignment	not modelled	99.7	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
75	c3k9uA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**paia acetyltransferase; **PDBTitle:** crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
76	c3e29C_	Alignment	not modelled	99.7	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein q7we92_borbr; **PDBTitle:** x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
77	c2vxkA_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate acetyltransferase; **PDBTitle:** structural comparison between aspergillus fumigatus and2 human gna1
78	c3e0kA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amino-acid acetyltransferase; **PDBTitle:** crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
79	c3e1eE_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**thioesterase family protein; **PDBTitle:** crystal structure of a thioesterase family protein from2

						silicibacter pomeroyi. northeast structural genomics3 target sir180a
80	c3fixA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase; **PDBTitle:** crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum
81	d1m4ia_	Alignment	not modelled	99.7	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
82	c3pp9B_	Alignment	not modelled	99.7	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
83	c1ufhB_	Alignment	not modelled	99.7	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yycn protein; **PDBTitle:** structure of putative acetyltransferase, yycn protein of bacillus2 subtilis
84	c2dxqA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** putative acetyltransferase from agrobacterium tumefaciens str. c58
85	d1wlua1	Alignment	not modelled	99.6	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
86	c2r1iB_	Alignment	not modelled	99.6	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
87	c3fynA_	Alignment	not modelled	99.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron gene cassette protein hfx_cass3; **PDBTitle:** crystal structure from the mobile metagenome of cole2 harbour salt marsh: integron cassette protein hfx_cass3
88	d1qsma_	Alignment	not modelled	99.6	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
89	c3ld2B_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of smu.2055 from streptococcus mutans ua159
90	c3d3sA_	Alignment	not modelled	99.6	12	**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
91	c2pc1A_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase gnat family (np_688560.1) from2 streptococcus agalactiae 2603 at 1.28 a resolution
92	d2euia1	Alignment	not modelled	99.6	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
93	c3s6fA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical acetyltransferase; **PDBTitle:** crystal structure of a hypotetical acetyltransferase (dr_1678) from2 deinococcus radiodurans at 1.19 a resolution
94	c2k5tA_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein yhhk; **PDBTitle:** solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
95	c2kcwA_	Alignment	not modelled	99.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized acetyltransferase yjab; **PDBTitle:** solution structure of apo-form yjab from escherichia coli
96	d1yr0a1	Alignment	not modelled	99.6	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
97	d1ufha_	Alignment	not modelled	99.6	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
98	c3exnA_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of acetyltransferase from thermus thermophilus hb8
99	d2b5ga1	Alignment	not modelled	99.6	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
100	d1q4ua_	Alignment	not modelled	99.6	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
101	d1vkca_	Alignment	not modelled	99.6	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
102	d2ozga2	Alignment	not modelled	99.6	9	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
103	c2ozgA_	Alignment	not modelled	99.6	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
104	d1p0ha_	Alignment	not modelled	99.6	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT

105	d1bo4a_	Alignment	not modelled	99.6	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
106	c1bo4A_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (serratia marcescens aminoglycoside-3-n- **PDBTitle:** crystal structure of a gcn5-related n-acetyltransferase: serratia2 marescens aminoglycoside 3-n-acetyltransferase
107	d2gana1	Alignment	not modelled	99.6	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
108	c2qwzB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phenylacetic acid degradation-related protein; **PDBTitle:** crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
109	d1vh5a_	Alignment	not modelled	99.6	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
110	d2i00a2	Alignment	not modelled	99.6	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
111	c3gy9A_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_001815201.1) from2 exiguobacterium sp. 255-15 at 1.52 a resolution
112	c3lbeA_	Alignment	not modelled	99.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.793; **PDBTitle:** the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
113	d1sc0a_	Alignment	not modelled	99.6	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
114	d2hv2a2	Alignment	not modelled	99.6	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
115	d1vh9a_	Alignment	not modelled	99.6	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
116	c2i00D_	Alignment	not modelled	99.6	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
117	c3r1kA_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enhanced intracellular survival protein; **PDBTitle:** crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
118	c3f1tB_	Alignment	not modelled	99.5	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein q9i3c8_pseae; **PDBTitle:** crystal structure of the q9i3c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
119	c3ec4B_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase from the gnat family; **PDBTitle:** crystal structure of putative acetyltransferase from the gnat family2 (yp_497011.1) from novosphingobium aromaticivorans dsm 12444 at 1.803 a resolution
120	d2fs2a1	Alignment	not modelled	99.5	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like