Phyre2

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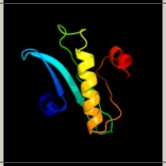
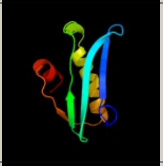
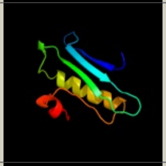
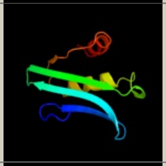
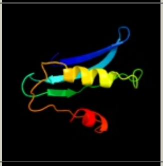
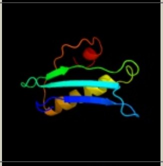
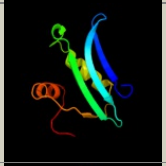
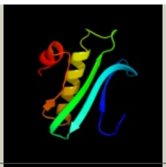
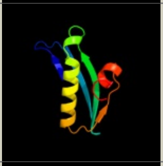
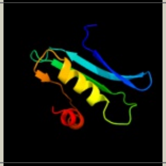
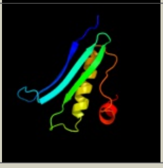
Description	P39274
Date	Thu Jan 5 11:58:44 GMT 2012
Unique Job ID	040dece43d893093

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r57a_	Alignment		99.9	43	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
2	d1xmta_	Alignment		99.8	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
3	c2r98A_	Alignment		99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
4	c2q7bA_	Alignment		99.5	15	**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
5	d1yvka1	Alignment		99.4	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
6	d1y9ka1	Alignment		99.4	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
7	d1z4ra1	Alignment		99.4	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
8	c2ozhA_	Alignment		99.4	16	**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
9	c3d8pB_	Alignment		99.4	18	**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
10	d1cm0a_	Alignment		99.4	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
11	c3lodA_	Alignment		99.4	19	**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	d1qsra_	Alignment		99.3	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
13	d1yx0a1	Alignment		99.3	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
14	c3e0kA_	Alignment		99.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amino-acid acetyltransferase; **PDBTitle:** crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
15	d1n71a_	Alignment		99.3	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
16	d1y9wa1	Alignment		99.3	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
17	c3blnA_	Alignment		99.3	8	**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
18	c3frmF_	Alignment		99.3	15	**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.
19	d1ghea_	Alignment		99.3	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
20	d2g3aa1	Alignment		99.3	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
21	d1ygha_	Alignment	not modelled	99.3	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
22	c3efaA_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
23	d2atra1	Alignment	not modelled	99.3	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
24	d2aj6a1	Alignment	not modelled	99.3	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
25	c3pp9B_	Alignment	not modelled	99.2	25	**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
26	d2jdca1	Alignment	not modelled	99.2	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
27	d2gana1	Alignment	not modelled	99.2	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
28	c3gy9A_	Alignment	not modelled	99.2	13	**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

29	c3dddA_	Alignment	not modelled	99.2	14	**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
30	c3s6fA_	Alignment	not modelled	99.2	12	**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
31	d2fiaa1	Alignment	not modelled	99.2	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
32	d1y7ra1	Alignment	not modelled	99.2	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
33	c2aj6A_	Alignment	not modelled	99.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mw0638; **PDBTitle:** crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
34	c2k5tA_	Alignment	not modelled	99.2	10	**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
35	d1q2ya_	Alignment	not modelled	99.2	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
36	c3c26A_	Alignment	not modelled	99.2	12	**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
37	c3ey5A_	Alignment	not modelled	99.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase-like, gnat family; **PDBTitle:** putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
38	d1tiqa_	Alignment	not modelled	99.2	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
39	c2q0yA_	Alignment	not modelled	99.1	16	**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
40	c2r7hA_	Alignment	not modelled	99.1	15	**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
41	d2ozga2	Alignment	not modelled	99.1	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
42	c2pdoG_	Alignment	not modelled	99.1	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
43	d2hv2a2	Alignment	not modelled	99.1	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
44	d2i00a2	Alignment	not modelled	99.1	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**EF1021-like
45	c3fynA_	Alignment	not modelled	99.1	10	**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
46	d1mk4a_	Alignment	not modelled	99.1	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
47	c3i9sA_	Alignment	not modelled	99.1	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
48	d1xeba_	Alignment	not modelled	99.1	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
49	c3dsbB_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of a possible acetyltransferase from clostridium2 difficile 630
50	c2i00D_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
51	d1m4ia_	Alignment	not modelled	99.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	d1vkca_	Alignment	not modelled	99.0	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
53	d1s3za_	Alignment	not modelled	99.0	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
						PDB header:transferase **Chain:** B: **PDB Molecule:**predicted acetyltransferase;

54	c3mgdB_	Alignment	not modelled	99.0	16	**PDBTitle:** crystal structure of predicted acetyltransferase with acetyl-coa from2 clostridium acetobutylicum at the resolution 1.9a, northeast3 structural genomics consortium target car165
55	c3t9yA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of gnat family acetyltransferase staphylococcus2 aureus subsp. aureus usa300_tch1516
56	d2fl4a1	Alignment	not modelled	99.0	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
57	c2ozgA_	Alignment	not modelled	99.0	18	**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
58	c2huzB_	Alignment	not modelled	99.0	17	**PDB header:**structural genomics, transferase **Chain:** B: **PDB Molecule:**glucosamine 6-phosphate n-acetyltransferase; **PDBTitle:** crystal structure of gnpnat1
59	c3fncA_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase from listeria2 innocua
60	c3ec4B_	Alignment	not modelled	99.0	16	**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
61	d2beia1	Alignment	not modelled	99.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
62	c3n7zD_	Alignment	not modelled	99.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase from bacillus anthracis
63	c2cntD_	Alignment	not modelled	98.9	11	**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.
64	c3f8kA_	Alignment	not modelled	98.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein acetyltransferase; **PDBTitle:** crystal structure of protein acetyltransferase (pat) from2 sulfolobus solfataricus
65	c2hv2D_	Alignment	not modelled	98.9	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
66	c2pswA_	Alignment	not modelled	98.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase 13; **PDBTitle:** human mak3 homolog in complex with coa
67	c3fb3A_	Alignment	not modelled	98.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase; **PDBTitle:** crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
68	d1wwza1	Alignment	not modelled	98.9	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
69	d1i12a_	Alignment	not modelled	98.9	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
70	c2wpwA_	Alignment	not modelled	98.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orf14; **PDBTitle:** tandem gnat protein from the clavulanic acid biosynthesis2 pathway (without accoa)
71	c3g8wB_	Alignment	not modelled	98.9	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lactococcal prophage ps3 protein 05; **PDBTitle:** crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228
72	c3g3sA_	Alignment	not modelled	98.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase-like protein2 (zp_00874857) (zp_00874857.1) from streptococcus suis 89/1591 at 1.803 a resolution
73	d2ae6a1	Alignment	not modelled	98.9	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
74	c2dxqA_	Alignment	not modelled	98.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** putative acetyltransferase from agrobacterium tumefaciens str. c58
75	c1bo4A_	Alignment	not modelled	98.9	13	**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
76	d1bo4a_	Alignment	not modelled	98.9	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
77	d1qsma_	Alignment	not modelled	98.9	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
78	c1ib1E_	Alignment	not modelled	98.9	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
79	c3fixA_	Alignment	not modelled	98.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase; **PDBTitle:** crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum
80	c3iwgB_	Alignment	not modelled	98.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** acetyltransferase from gnat family from colwellia psychrerythraea.
81	c2r1iB_	Alignment	not modelled	98.8	13	**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
82	c2vxkA_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate acetyltransferase; **PDBTitle:** structural comparison between aspergillus fumigatus and2 human gna1
83	d1u6ma_	Alignment	not modelled	98.8	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
84	d2euia1	Alignment	not modelled	98.8	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
85	d1p0ha_	Alignment	not modelled	98.8	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
86	d2i6ca1	Alignment	not modelled	98.8	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
87	d2b5ga1	Alignment	not modelled	98.8	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
88	c2jlmE_	Alignment	not modelled	98.8	9	**PDB header:**transferase **Chain:** E: **PDB Molecule:**putative phosphinothricin n-acetyltransferase; **PDBTitle:** structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
89	c2qecA_	Alignment	not modelled	98.8	13	**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
90	c3k9uA_	Alignment	not modelled	98.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**paia acetyltransferase; **PDBTitle:** crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
91	c3dr8B_	Alignment	not modelled	98.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ynca; **PDBTitle:** structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
92	c3jvnA_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** crystal structure of the acetyltransferase vf_1542 from vibrio2 fischeri, northeast structural genomics consortium target vfr136
93	c2q04C_	Alignment	not modelled	98.7	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetoin utilization protein; **PDBTitle:** crystal structure of acetoin utilization protein (zp_00540088.1) from2 exiguobacterium sibiricum 255-15 at 2.33 a resolution
94	d2fiwa1	Alignment	not modelled	98.7	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
95	c2oh1A_	Alignment	not modelled	98.7	11	**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
96	c3d3sA_	Alignment	not modelled	98.7	8	**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
97	c3exnA_	Alignment	not modelled	98.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of acetyltransferase from thermus thermophilus hb8
98	c3r1kA_	Alignment	not modelled	98.7	8	**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
99	c2pc1A_	Alignment	not modelled	98.7	8	**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
100	d2cy2a1	Alignment	not modelled	98.7	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
101	c2reeB_	Alignment	not modelled	98.7	18	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
102	d1yvoa1	Alignment	not modelled	98.7	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat)

						Family:N-acetyl transferase, NAT
103	d1vhsa_	Alignment	not modelled	98.6	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
104	d1cjwa_	Alignment	not modelled	98.6	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
105	d1ro5a_	Alignment	not modelled	98.6	9	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
106	c2kcwA_	Alignment	not modelled	98.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized acetyltransferase yjab; **PDBTitle:** solution structure of apo-form yjab from escherichia coli
107	c1ufhB_	Alignment	not modelled	98.5	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yycn protein; **PDBTitle:** structure of putative acetyltransferase, yycn protein of bacillus2 subtilis
108	c3ld2B_	Alignment	not modelled	98.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** the crystal structure of smu.2055 from streptococcus mutans ua159
109	d1sqha_	Alignment	not modelled	98.5	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Hypothetical protein cg14615-pa
110	c2x7bA_	Alignment	not modelled	98.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase sso0209; **PDBTitle:** crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
111	d1yr0a1	Alignment	not modelled	98.4	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
112	c2ft0B_	Alignment	not modelled	98.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tdp-fucosamine acetyltransferase; **PDBTitle:** crystal structure of tdp-fucosamine acetyltransferase (wecd)- complex2 with acetyl-coa
113	d2fe7a1	Alignment	not modelled	98.4	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
114	d1s7ka1	Alignment	not modelled	98.4	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
115	d1z4ea1	Alignment	not modelled	98.4	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
116	d1ufha_	Alignment	not modelled	98.3	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
117	c3h4qA_	Alignment	not modelled	98.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (np_371943.1) from2 staphylococcus aureus mu50 at 2.50 a resolution
118	d2ge3a1	Alignment	not modelled	98.1	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
119	c2g0bG_	Alignment	not modelled	98.1	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**feem; **PDBTitle:** the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
120	c2pr8B_	Alignment	not modelled	98.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside 6-n-acetyltransferase type ib11; **PDBTitle:** crystal structure of aminoglycoside n-acetyltransferase2 aac(6')-ib11