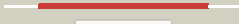



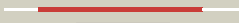







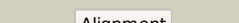




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3916c_(-)_4404610_4405344
Date	Sat Aug 10 22:05:10 BST 2019
Unique Job ID	afe969f7426c26f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zj0A_</a>	 Alignment		97.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> the human o-glcnacase c-terminal domain is a pseudo histone2 acetyltransferase
2	<a href="#">c2q0yA_</a>	 Alignment		97.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
3	<a href="#">d1tiqa_</a>	 Alignment		96.8	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
4	<a href="#">c3fynA_</a>	 Alignment		96.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> integron gene cassette protein hfx_cass3; <b>PDBTitle:</b> crystal structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass3
5	<a href="#">c4rs2B_</a>	 Alignment		96.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted acyltransferase with acyl-coa n-acyltransferase <b>PDBTitle:</b> 1.55 angstrom crystal structure of gnat family n-acetyltransferase2 (yhbs) from escherichia coli in complex with coa
6	<a href="#">d2fiwa1</a>	 Alignment		96.8	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
7	<a href="#">d2gana1</a>	 Alignment		96.7	10	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
8	<a href="#">c2r7hA_</a>	 Alignment		96.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative d-alanine n-acetyltransferase of gnat family; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution
9	<a href="#">c3fb3A_</a>	 Alignment		96.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase; <b>PDBTitle:</b> crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
10	<a href="#">c3i9sA_</a>	 Alignment		96.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> integron cassette protein; <b>PDBTitle:</b> structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
11	<a href="#">c2reeB_</a>	 Alignment		96.3	14	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> crystal structure of the loading gnatI domain of cura from lnygbya2 majuscula

12	<a href="#">d2cy2a1</a>	Alignment		96.3	11	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
13	<a href="#">d2beia1</a>	Alignment		96.3	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
14	<a href="#">c4bmhA</a>	Alignment		96.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of sshot
15	<a href="#">c2r1iB</a>	Alignment		96.1	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of putative acetyltransferase (yp_831484.1) from 2 arthrobacter sp. fb24 at 1.65 a resolution
16	<a href="#">d2jdca1</a>	Alignment		96.1	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
17	<a href="#">c3k9uA</a>	Alignment		96.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> paia acetyltransferase; <b>PDBTitle:</b> crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
18	<a href="#">c4e8oB</a>	Alignment		96.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aac(6')-ih protein; <b>PDBTitle:</b> crystal structure of aminoglycoside antibiotic 6'-n-acetyltransferase2 aac(6')-ih from acinetobacter baumannii
19	<a href="#">d2euia1</a>	Alignment		96.0	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
20	<a href="#">d1u6ma</a>	Alignment		96.0	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
21	<a href="#">c4ubrA</a>	Alignment	not modelled	95.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n-acetyltransferase pa4534
22	<a href="#">c3exnA</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable acetyltransferase; <b>PDBTitle:</b> crystal structure of acetyltransferase from thermus thermophilus hb8
23	<a href="#">c5k18D</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> n-terminal acetyltransferase b complex subunit nat3; <b>PDBTitle:</b> the natb acetyltransferase complex bound to bisubstrate inhibitor
24	<a href="#">d2i00a2</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
25	<a href="#">d1p0ha</a>	Alignment	not modelled	95.7	20	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
26	<a href="#">c5ygeA</a>	Alignment	not modelled	95.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amino-acid acetyltransferase; <b>PDBTitle:</b> arga complexed with acecoa and glutamate
27	<a href="#">c1ib1E</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> signaling protein/transferase <b>Chain:</b> E: <b>PDB Molecule:</b> serotonin n-acetyltransferase; <b>PDBTitle:</b> crystal structure of the 14-3-3 zeta:serotonin n-acetyltransferase2 complex
28	<a href="#">c2wpwA</a>	Alignment	not modelled	95.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orf14; <b>PDBTitle:</b> tandem gnat protein from the clavulanic acid biosynthesis pathway2 (without accoa)

29	<a href="#">d1s3za_</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
30	<a href="#">c4pv6E_</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> n-terminal acetyltransferase complex subunit [ard1]; <b>PDBTitle:</b> crystal structure analysis of ard1 from thermoplasma volcanium
31	<a href="#">c3lodA_</a>	Alignment	not modelled	95.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-coa n-acyltransferase; <b>PDBTitle:</b> the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
32	<a href="#">d2fl4a1</a>	Alignment	not modelled	95.3	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
33	<a href="#">c3te4A_</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dopamine n acetyltransferase, isoform a; <b>PDBTitle:</b> crystal structure of dopamine n acetyltransferase in complex with2 acetyl-coa from drosophila melanogaster
34	<a href="#">c4e2aA_</a>	Alignment	not modelled	95.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of the putative acetyltransferase from streptococcus2 mutans
35	<a href="#">d1n71a_</a>	Alignment	not modelled	95.1	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
36	<a href="#">d1cjwa_</a>	Alignment	not modelled	95.0	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
37	<a href="#">d1ghea_</a>	Alignment	not modelled	95.0	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
38	<a href="#">c3c26A_</a>	Alignment	not modelled	95.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase ta0821; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
39	<a href="#">c4zbgA_</a>	Alignment	not modelled	95.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of a gnat family acetyltransferase from brucella2 melitensis in complex with acetyl-coa
40	<a href="#">d2aj6a1</a>	Alignment	not modelled	94.9	6	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
41	<a href="#">d1y9ka1</a>	Alignment	not modelled	94.9	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
42	<a href="#">c4zm6A_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-beta-d glucosaminidase; <b>PDBTitle:</b> a unique gcn5-related glucosamine n-acetyltransferase region exist in2 the fungal multi-domain gh3 beta-n-acetylglucosaminidase
43	<a href="#">c5kf2A_</a>	Alignment	not modelled	94.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted acetyltransferase; <b>PDBTitle:</b> x-ray structure of a glucosamine n-acetyltransferase from clostridium2 acetobutylicum, apo form, ph 8
44	<a href="#">c4jxqA_</a>	Alignment	not modelled	94.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of a gnat superfamily phosphinothricin2 acetyltransferase (pat) from sinorhizobium meliloti 1021
45	<a href="#">c2aj6A_</a>	Alignment	not modelled	94.5	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mw0638; <b>PDBTitle:</b> crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
46	<a href="#">c5hmnE_</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> aac3-i; <b>PDBTitle:</b> crystal structure of an aminoglycoside acetyltransferase hmb0005 from2 an uncultured soil metagenomic sample, unknown active site density3 modeled as polyethylene glycol
47	<a href="#">c3dr8B_</a>	Alignment	not modelled	94.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ynca; <b>PDBTitle:</b> structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
48	<a href="#">c3efaA_</a>	Alignment	not modelled	94.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
49	<a href="#">d1y7ra1</a>	Alignment	not modelled	94.2	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
50	<a href="#">d1yvoo1</a>	Alignment	not modelled	94.2	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
51	<a href="#">c2qecA_</a>	Alignment	not modelled	94.1	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase hpa2 and related <b>PDBTitle:</b> crystal structure of histone acetyltransferase hpa2 and related2 acetyltransferase (np_600742.1) from corynebacterium glutamicum atcc3 13032 at 1.90 a resolution
52	<a href="#">d1q2ya_</a>	Alignment	not modelled	94.0	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
53	<a href="#">c5f46A_</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside acetyltransferase meta-aac0020;

53	<a href="#">c1r4wA</a>	Alignment	not modelled	93.9	14	<b>PDBTitle:</b> crystal structure of an aminoglycoside acetyltransferase meta-aac00202 from an uncultured soil metagenomic sample, apoenzyme form
54	<a href="#">c4fd4B</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arylalkylamine n-acetyltransferase like 5b; <b>PDBTitle:</b> crystal structure of mosquito arylalkylamine n-acetyltransferase like2 5b
55	<a href="#">c2kcwA</a>	Alignment	not modelled	93.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized acetyltransferase yjab; <b>PDBTitle:</b> solution structure of apo-form yjab from escherichia coli
56	<a href="#">d1yr0a1</a>	Alignment	not modelled	93.7	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
57	<a href="#">c2dxqA</a>	Alignment	not modelled	93.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> putative acetyltransferase from agrobacterium tumefaciens str. c58
58	<a href="#">c3e0kA</a>	Alignment	not modelled	93.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amino-acid acetyltransferase; <b>PDBTitle:</b> crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
59	<a href="#">d1yvka1</a>	Alignment	not modelled	93.4	18	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
60	<a href="#">c4fd5A</a>	Alignment	not modelled	93.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylalkylamine n-acetyltransferase 2; <b>PDBTitle:</b> crystal structure of arylalkylamine n-acetyltransferase 2 from aedes2 aegypti
61	<a href="#">c3f8kA</a>	Alignment	not modelled	93.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein acetyltransferase; <b>PDBTitle:</b> crystal structure of protein acetyltransferase (pat) from sulfolobus2 solfataricus
62	<a href="#">d1mk4a</a>	Alignment	not modelled	93.3	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
63	<a href="#">d1r57a</a>	Alignment	not modelled	93.2	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
64	<a href="#">c3t90A</a>	Alignment	not modelled	93.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate acetyltransferase 1; <b>PDBTitle:</b> crystal structure of glucosamine-6-phosphate n-acetyltransferase from2 arabidopsis thaliana
65	<a href="#">c5hgza</a>	Alignment	not modelled	93.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-alpha-acetyltransferase 60; <b>PDBTitle:</b> crystal structure of human naa60 in complex with acetyl-coa
66	<a href="#">c5fvjA</a>	Alignment	not modelled	93.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of tact (trna acetylating toxin) from salmonella
67	<a href="#">d2b5ga1</a>	Alignment	not modelled	93.0	7	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
68	<a href="#">d2fiaa1</a>	Alignment	not modelled	92.9	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
69	<a href="#">c2pdoG</a>	Alignment	not modelled	92.8	20	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyltransferase ypea; <b>PDBTitle:</b> crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
70	<a href="#">d1y9wa1</a>	Alignment	not modelled	92.8	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
71	<a href="#">d1i12a</a>	Alignment	not modelled	92.8	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
72	<a href="#">c2oh1A</a>	Alignment	not modelled	92.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase gnat family (yp_013287.1) from2 listeria monocytogenes 4b f2365 at 1.46 a resolution
73	<a href="#">d1qsmA</a>	Alignment	not modelled	92.6	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
74	<a href="#">c3fncA</a>	Alignment	not modelled	92.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase from listeria2 innocua
75	<a href="#">c2qmlA</a>	Alignment	not modelled	92.6	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2621 protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein (bh2621) from bacillus2 halodurans at 1.55 a resolution
76	<a href="#">c1ufhB</a>	Alignment	not modelled	92.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yycn protein; <b>PDBTitle:</b> structure of putative acetyltransferase, yycn protein of bacillus2 subtilis
77	<a href="#">c3d8pB</a>	Alignment	not modelled	92.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase of gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
78	<a href="#">d1yx0a1</a>	Alignment	not modelled	92.5	21	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
						<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat)

79	<a href="#">d1vhsa_</a>	Alignment	not modelled	92.5	13	<b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
80	<a href="#">c3t9yA_</a>	Alignment	not modelled	92.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of gnat family acetyltransferase staphylococcus2 aureus subsp. aureus usa300_tch1516
81	<a href="#">c2ozgA_</a>	Alignment	not modelled	92.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
82	<a href="#">c3ec4B_</a>	Alignment	not modelled	92.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acetyltransferase from the gnat family; <b>PDBTitle:</b> crystal structure of putative acetyltransferase from the gnat family2 (yp_497011.1) from novosphingobium aromaticivorans dsm 12444 at 1.803 a resolution
83	<a href="#">c3mgdB_</a>	Alignment	not modelled	92.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted acetyltransferase; <b>PDBTitle:</b> crystal structure of predicted acetyltransferase with acetyl-coa from2 clostridium acetobutylicum at the resolution 1.9a, northeast3 structural genomics consortium target car165
84	<a href="#">c2r98A_</a>	Alignment	not modelled	92.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetylglutamate synthase; <b>PDBTitle:</b> crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
85	<a href="#">d1sqha_</a>	Alignment	not modelled	92.0	21	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Hypothetical protein cg14615-pa
86	<a href="#">d1wwza1</a>	Alignment	not modelled	91.9	11	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
87	<a href="#">c5k9nB_</a>	Alignment	not modelled	91.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyamine n acetyltransferase; <b>PDBTitle:</b> structural and mechanistic analysis of drosophila melanogaster2 polyamine n acetyltransferase, an enzyme that catalyzes the formation3 of n acetylglutamine
88	<a href="#">c3fixA_</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum
89	<a href="#">c2ozhA_</a>	Alignment	not modelled	91.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein xcc2953; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase belonging to the2 gnat family (xcc2953) from xanthomonas campestris pv. campestris at3 1.40 a resolution
90	<a href="#">c6erdD_</a>	Alignment	not modelled	91.9	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aminoglycoside n6'-acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase from bacillus cereus2 species.
91	<a href="#">c5i0cA_</a>	Alignment	not modelled	91.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yj dj; <b>PDBTitle:</b> crystal structure of predicted acyltransferase yj dj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
92	<a href="#">c2vxkA_</a>	Alignment	not modelled	91.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate acetyltransferase; <b>PDBTitle:</b> structural comparison between aspergillus fumigatus and2 human gna1
93	<a href="#">c5dwnC_</a>	Alignment	not modelled	91.7	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphinothricin n-acetyltransferase; <b>PDBTitle:</b> crystal structure of phosphinothricin n-acetyltransferase from2 brucella ovis in complex with acetylcoa
94	<a href="#">d2ozga2</a>	Alignment	not modelled	91.7	22	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
95	<a href="#">c5nnrB_</a>	Alignment	not modelled	91.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> naa10; <b>PDBTitle:</b> structure of naa15/naa10 bound to hypk-thb
96	<a href="#">d1yk3a1</a>	Alignment	not modelled	91.6	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
97	<a href="#">c2i00D_</a>	Alignment	not modelled	91.5	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
98	<a href="#">c2k5tA_</a>	Alignment	not modelled	91.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yhhk; <b>PDBTitle:</b> solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
99	<a href="#">c3gy9A_</a>	Alignment	not modelled	91.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of putative acetyltransferase (yp_001815201.1) from2 exigubacterium sp. 255-15 at 1.52 a resolution
100	<a href="#">c4e0aB_</a>	Alignment	not modelled	91.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bh1408 protein; <b>PDBTitle:</b> crystal structure of the mutant f44r bh1408 protein from bacillus2 halodurans, northeast structural genomics consortium (nesg) target3 bhr182
101	<a href="#">c4my3A_</a>	Alignment	not modelled	91.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gcn5-related n-acetyltransferase from kribbella2 flavida
102	<a href="#">c4ag9B_</a>	Alignment	not modelled	90.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate n-acetyltransferase; <b>PDBTitle:</b> c. elegans glucosamine-6-phosphate n-acetyltransferase

					(gna1):2 ternary complex with coenzyme a and glcnae
103	<a href="#">c6ao7A_</a>	Alignment	not modelled	90.9	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of a gnat family acetyltransferase from2 elizabethkingia anophelis with acetyl-coa bound
104	<a href="#">d2atra1</a>	Alignment	not modelled	90.8	11 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
105	<a href="#">c3jvnA_</a>	Alignment	not modelled	90.8	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of the acetyltransferase vf_1542 from vibrio2 fischeri, northeast structural genomics consortium target vfr136
106	<a href="#">c3ey5A_</a>	Alignment	not modelled	90.7	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase-like, gnat family; <b>PDBTitle:</b> putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
107	<a href="#">c2pr8B_</a>	Alignment	not modelled	90.4	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside 6-n-acetyltransferase type ib11; <b>PDBTitle:</b> crystal structure of aminoglycoside n-acetyltransferase2 aac(6')-ib11
108	<a href="#">c2huzB_</a>	Alignment	not modelled	90.3	11 <b>PDB header:</b> structural genomics, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine 6-phosphate n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gnpnat1
109	<a href="#">d2g3aa1</a>	Alignment	not modelled	89.9	17 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
110	<a href="#">d2hv2a2</a>	Alignment	not modelled	89.7	17 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
111	<a href="#">c3d3sA_</a>	Alignment	not modelled	89.7	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2,4-diaminobutyric acid acetyltransferase; <b>PDBTitle:</b> crystal structure of l-2,4-diaminobutyric acid acetyltransferase from2 bordetella parapertussis
112	<a href="#">c4ua3A_</a>	Alignment	not modelled	89.5	9 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized n-acetyltransferase c825.04c; <b>PDBTitle:</b> crystal structure of selenomethionine labeled spnatd
113	<a href="#">d1m4ja_</a>	Alignment	not modelled	89.5	15 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
114	<a href="#">c1bo4A_</a>	Alignment	not modelled	89.3	11 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (serratia marcescens aminoglycoside-3-n- <b>PDBTitle:</b> crystal structure of a gcn5-related n-acetyltransferase: serratia2 marescens aminoglycoside 3-n-acetyltransferase
115	<a href="#">d1bo4a_</a>	Alignment	not modelled	89.3	11 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
116	<a href="#">c2pswA_</a>	Alignment	not modelled	89.1	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase 13; <b>PDBTitle:</b> human mak3 homolog in complex with coa
117	<a href="#">d1qsrA_</a>	Alignment	not modelled	88.9	14 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
118	<a href="#">c4u5yA_</a>	Alignment	not modelled	88.6	22 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa synthetase; <b>PDBTitle:</b> crystal structure of the complex between the gnat domain of s.2 lividans pat and the acetyl-coa synthetase c-terminal domain of s.3 enterica
119	<a href="#">c4avcA_</a>	Alignment	not modelled	87.9	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine acetyltransferase; <b>PDBTitle:</b> crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
120	<a href="#">d2ae6a1</a>	Alignment	not modelled	87.7	24 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT