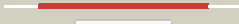



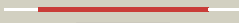


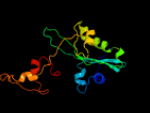







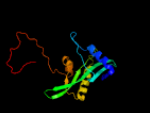

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0262c_(aac)_314309_314854
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	cf9ce85e783bbf99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1m4ia_</a>	 Alignment		100.0	99	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
2	<a href="#">c5us1K_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> aminoglycoside 2'-n-acetyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(2')-ia in2 complex with n2'-acetylgentamicin c1a and coenzyme a
3	<a href="#">d2hv2a2</a>	 Alignment		99.9	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
4	<a href="#">c3n7zD_</a>	 Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase from bacillus anthracis
5	<a href="#">c2hv2D_</a>	 Alignment		99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
6	<a href="#">c2ozqA_</a>	 Alignment		99.8	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_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
7	<a href="#">d2ozqa2</a>	 Alignment		99.8	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
8	<a href="#">c2i00D_</a>	 Alignment		99.8	13	<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
9	<a href="#">d2i00a2</a>	 Alignment		99.8	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> EF1021-like
10	<a href="#">c3r1kA_</a>	 Alignment		99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> enhanced intracellular survival protein; <b>PDBTitle:</b> crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
11	<a href="#">c4rs2B_</a>	 Alignment		99.8	16	<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

12	<a href="#">c4my3A_</a>	Alignment		99.8	17	<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
13	<a href="#">c6rftB_</a>	Alignment		99.8	15	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized n-acetyltransferase d2e36_21790; <b>PDBTitle:</b> crystal structure of eis2 from mycobacterium abscessus bound to2 acetyl-coa
14	<a href="#">c3sxnC_</a>	Alignment		99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> enhanced intracellular survival protein; <b>PDBTitle:</b> mycobacterium tuberculosis eis protein initiates modulation of host2 immune responses by acetylation of dusp16/mkp-7
15	<a href="#">c2cntD_</a>	Alignment		99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> modification of 30s ribosomal subunit protein s18; <b>PDBTitle:</b> rimi - ribosomal s18 n-alpha-protein acetyltransferase in complex with2 coenzymeA.
16	<a href="#">c5k18D_</a>	Alignment		99.7	13	<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
17	<a href="#">c1ib1E_</a>	Alignment		99.7	15	<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
18	<a href="#">c2pswA_</a>	Alignment		99.7	13	<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
19	<a href="#">d1xeba_</a>	Alignment		99.7	20	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
20	<a href="#">d1tiqa_</a>	Alignment		99.7	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
21	<a href="#">d2jdca1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
22	<a href="#">c5z6nA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein elaa; <b>PDBTitle:</b> crystal structure of escherichia coli elaa
23	<a href="#">c3dddA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (np_142035.1) from2 pyrococcus horikoshii at 2.25 a resolution
24	<a href="#">d1cjwa_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
25	<a href="#">c2q0yA_</a>	Alignment	not modelled	99.7	15	<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
26	<a href="#">c2x7bA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase sso0209; <b>PDBTitle:</b> crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
27	<a href="#">d1mk4a_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
28	<a href="#">c3blnA_</a>	Alignment	not modelled	99.7	10	<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 (np_981174.1) from2 bacillus cereus atcc 10987 at 1.31 a resolution
						<b>PDB header:</b> transferase

29	<a href="#">c4kvoF_</a>	Alignment	not modelled	99.7	12	<b>Chain:</b> F; <b>PDB Molecule:</b> n-terminal acetyltransferase a complex catalytic subunit <b>PDBTitle:</b> the nata (naa10p/naa15p) amino-terminal acetyltransferase complex bound to accoa
30	<a href="#">c4pv6E_</a>	Alignment	not modelled	99.7	12	<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="#">c4e2aA_</a>	Alignment	not modelled	99.7	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
32	<a href="#">c6c95B_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> n-alpha-acetyltransferase 10; <b>PDBTitle:</b> the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
33	<a href="#">c5hgza_</a>	Alignment	not modelled	99.7	17	<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
34	<a href="#">c3efaA_</a>	Alignment	not modelled	99.7	17	<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
35	<a href="#">c2r98A_</a>	Alignment	not modelled	99.7	15	<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
36	<a href="#">c2r7hA_</a>	Alignment	not modelled	99.7	17	<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
37	<a href="#">d1n71a_</a>	Alignment	not modelled	99.7	10	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
38	<a href="#">c3lodA_</a>	Alignment	not modelled	99.7	20	<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
39	<a href="#">d1q2ya_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
40	<a href="#">c5nnrB_</a>	Alignment	not modelled	99.7	15	<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
41	<a href="#">c4hnyB_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> n-terminal acetyltransferase a complex catalytic subunit <b>PDBTitle:</b> apo n-terminal acetyltransferase complex a
42	<a href="#">d1s3za_</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
43	<a href="#">d1i12a_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
44	<a href="#">c3d8pB_</a>	Alignment	not modelled	99.7	16	<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
45	<a href="#">c5icwB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> n-alpha-acetyltransferase 60; <b>PDBTitle:</b> crystal structure of human natf (hnaa60) homodimer bound to coenzyme a
46	<a href="#">d1wwza1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
47	<a href="#">d1ghea_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
48	<a href="#">c2ozhA_</a>	Alignment	not modelled	99.7	23	<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
49	<a href="#">c4ua3A_</a>	Alignment	not modelled	99.7	14	<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
50	<a href="#">d1qsra_</a>	Alignment	not modelled	99.7	13	<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="#">d1y9wa1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
52	<a href="#">c3fb3A_</a>	Alignment	not modelled	99.6	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
53	<a href="#">c2qecA_</a>	Alignment	not modelled	99.6	20	<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
54	<a href="#">c5wjda_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cg8481, isoform b; <b>PDBTitle:</b> crystal structure of naa80 bound to acetyl-coa
55	<a href="#">c3zj0a_</a>	Alignment	not modelled	99.6	15	<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
56	<a href="#">c3e0ka_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amino-acid acetyltransferase; <b>PDBTitle:</b> crystal structure of c-terminal domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
57	<a href="#">d1y7ra1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
58	<a href="#">c4e8ob_</a>	Alignment	not modelled	99.6	10	<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
59	<a href="#">c3t90a_</a>	Alignment	not modelled	99.6	15	<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
60	<a href="#">c4zbgA_</a>	Alignment	not modelled	99.6	17	<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
61	<a href="#">c3frmF_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown conserved protein from2 staphylococcus epidermidis atcc 12228.
62	<a href="#">c5k9nb_</a>	Alignment	not modelled	99.6	20	<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
63	<a href="#">c3mgdB_</a>	Alignment	not modelled	99.6	16	<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
64	<a href="#">c3ec4B_</a>	Alignment	not modelled	99.6	23	<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
65	<a href="#">c3ey5A_</a>	Alignment	not modelled	99.6	12	<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.
66	<a href="#">c4u9wA_</a>	Alignment	not modelled	99.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-alpha-acetyltransferase 40; <b>PDBTitle:</b> crystal structure of natd bound to h4/h2a peptide and coa
67	<a href="#">d1ygha_</a>	Alignment	not modelled	99.6	10	<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="#">d1z4ra1</a>	Alignment	not modelled	99.6	7	<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="#">d2fiwa1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
70	<a href="#">c3gy9A_</a>	Alignment	not modelled	99.6	16	<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 exiguibacterium sp. 255-15 at 1.52 a resolution
71	<a href="#">c2huzB_</a>	Alignment	not modelled	99.6	19	<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 gnpmat1
72	<a href="#">c2vxkA_</a>	Alignment	not modelled	99.6	17	<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
73	<a href="#">c3c26A_</a>	Alignment	not modelled	99.6	16	<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
74	<a href="#">c2pdoG_</a>	Alignment	not modelled	99.6	12	<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
75	<a href="#">d2ae6a1</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
76	<a href="#">c2q7bA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> crystal structure of acetyltransferase (np_689019.1) from2 streptococcus agalactiae 2603 at 2.00 a resolution
77	<a href="#">c3i9sA_</a>	Alignment	not modelled	99.6	14	<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 <b>PDB header:</b> transferase

78	<a href="#">c2dxqA</a>	Alignment	not modelled	99.6	12	<b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> putative acetyltransferase from agrobacterium tumefaciens str. c58
79	<a href="#">c4ubrA</a>	Alignment	not modelled	99.6	14	<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
80	<a href="#">c4zm6A</a>	Alignment	not modelled	99.6	16	<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
81	<a href="#">c5jtfB</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphinothricin n-acetyltransferase; <b>PDBTitle:</b> crystal structure of arsn n-acetyltransferase from pseudomonas putida2 kt2440
82	<a href="#">c4bmbA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of sshat
83	<a href="#">c2reeB</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
84	<a href="#">c4m85C</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyltransferase from staphylococcus aureus2 mu50
85	<a href="#">c3f8kA</a>	Alignment	not modelled	99.6	12	<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 sulfobolus2 solfataricus
86	<a href="#">c3te4A</a>	Alignment	not modelled	99.6	16	<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
87	<a href="#">d2fiaa1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
88	<a href="#">d2atra1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
89	<a href="#">d2beia1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
90	<a href="#">c4ag9B</a>	Alignment	not modelled	99.6	15	<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 glcnc
91	<a href="#">c3dsbB</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> the crystal structure of a possible acetyltransferase from clostridium2 difficile 630
92	<a href="#">c5hmnE</a>	Alignment	not modelled	99.6	13	<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
93	<a href="#">c2pc1A</a>	Alignment	not modelled	99.6	18	<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 (np_688560.1) from2 streptococcus agalactiae 2603 at 1.28 a resolution
94	<a href="#">c4e0aB</a>	Alignment	not modelled	99.6	13	<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
95	<a href="#">c6ao7A</a>	Alignment	not modelled	99.5	16	<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
96	<a href="#">c4fd4B</a>	Alignment	not modelled	99.5	17	<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
97	<a href="#">d1cm0a</a>	Alignment	not modelled	99.5	9	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
98	<a href="#">c5kf2A</a>	Alignment	not modelled	99.5	17	<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
99	<a href="#">c3fncA</a>	Alignment	not modelled	99.5	13	<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
100	<a href="#">d1u6ma</a>	Alignment	not modelled	99.5	27	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
101	<a href="#">c3dr8B</a>	Alignment	not modelled	99.5	20	<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
102	<a href="#">c5f46A</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside acetyltransferase meta-aac0020; <b>PDBTitle:</b> crystal structure of an aminoglycoside acetyltransferase



						meta-aac00202 from an uncultured soil metagenomic sample, apoenzyme form
103	<a href="#">c4fd5A_</a>	Alignment	not modelled	99.5	16	<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
104	<a href="#">d1y9ka1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
105	<a href="#">d1yvka1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
106	<a href="#">c2k5tA_</a>	Alignment	not modelled	99.5	13	<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
107	<a href="#">c3s6fA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (dr_1678) from2 deinococcus radiodurans r1 at 1.19 a resolution
108	<a href="#">c5ygeA_</a>	Alignment	not modelled	99.5	17	<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
109	<a href="#">d1yvoa1</a>	Alignment	not modelled	99.5	19	<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="#">c5t7eD_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphinothricin n-acetyltransferase; <b>PDBTitle:</b> crystal structure of streptomyces hygrosopicus bialaphos resistance2 (bar) protein in complex with coenzyme a and l-phosphinothricin
111	<a href="#">c2oh1A_</a>	Alignment	not modelled	99.5	14	<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
112	<a href="#">d2cy2a1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
113	<a href="#">c2r1iB_</a>	Alignment	not modelled	99.5	18	<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) from2 arthrobacter sp. fb24 at 1.65 a resolution
114	<a href="#">c3fixA_</a>	Alignment	not modelled	99.5	15	<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
115	<a href="#">c3d3sA_</a>	Alignment	not modelled	99.5	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
116	<a href="#">d1bo4a_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
117	<a href="#">c1bo4A_</a>	Alignment	not modelled	99.5	15	<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
118	<a href="#">c5fvjA_</a>	Alignment	not modelled	99.5	13	<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
119	<a href="#">c3fynA_</a>	Alignment	not modelled	99.5	14	<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
120	<a href="#">c4y49l_</a>	Alignment	not modelled	99.5	8	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> n-terminal acetyltransferase a complex subunit nat5; <b>PDBTitle:</b> crystal structure of yeast n-terminal acetyltransferase (ppgpp) nate2 in complex with a bisubstrate