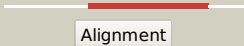

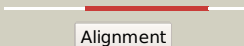

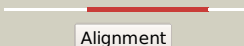







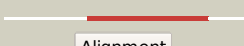











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3225c_(-)_3601013_3602437
Date	Thu Aug 8 16:20:42 BST 2019
Unique Job ID	5640e059bd5df1c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5uxbA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase mphh; <b>PDBTitle:</b> crystal structure of macrolide 2'-phosphotransferase mphh from <i>Brachybacterium faecium</i> , apoenzyme
2	<a href="#">c3lzhA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aph(2'')-id/aph(2'')-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(2'')-2 id/aph(2'')-iva
3	<a href="#">c3tdvB_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> gentamicin resistance protein; <b>PDBTitle:</b> structure of the gdp complex of wild-type aminoglycoside 2'-2 phosphotransferase-iiiA
4	<a href="#">c5igrA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type i - complex with gdp and 2 oleandomycin
5	<a href="#">c5igwA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase ii; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type ii - complex with gdp and 2 clarithromycin
6	<a href="#">c4orkB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional aac/aph; <b>PDBTitle:</b> crystal structure of the phosphotransferase domain of the bifunctional 2 aminoglycoside resistance enzyme aac(6')-ie-aph(2'')-ia
7	<a href="#">c3ovcA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> hygromycin-b 4-o-kinase; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(4)-ia
8	<a href="#">c3hamA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the gentamicin-aph(2'')-ia complex
9	<a href="#">c3dxaA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from <i>Ralstonia eutropha</i> jmp134 at 2.32 Å resolution
10	<a href="#">c6ef6A_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the microcompartment-associated aminopropanol kinase
11	<a href="#">c3jr1A_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_719053.1) from <i>Haemophilus somnus</i> 129pt at 2.32 Å resolution

12	<a href="#">c3attA_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rv3168 with atp
13	<a href="#">d1nd4a_</a>	Alignment		100.0	23	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
14	<a href="#">c2zw7A_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bleomycin acetyltransferase; <b>PDBTitle:</b> crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
15	<a href="#">c4h05B_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside-o-phosphotransferase viii; <b>PDBTitle:</b> crystal structure of aminoglycoside-3'-phosphotransferase of type viii
16	<a href="#">c6fucA_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of aminoglycoside phosphotransferase aph(3''-id from2 streptomyces rimosus atcc10970
17	<a href="#">c3r78B_</a>	Alignment		99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside 3'-phosphotransferase apha1-iab; <b>PDBTitle:</b> crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound
18	<a href="#">d1zyla1</a>	Alignment		99.9	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
19	<a href="#">c2vzza_</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0802c; <b>PDBTitle:</b> crystal structure of rv0802c from mycobacterium2 tuberculosis in complex with succinyl-coa
20	<a href="#">d2ppqa1</a>	Alignment		99.9	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
21	<a href="#">c3juwC_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> probable gnat-family acetyltransferase; <b>PDBTitle:</b> putative gnat-family acetyltransferase from bordetella pertussis.
22	<a href="#">c3c5iD_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of plasmodium knowlesi choline kinase, pkh_134520
23	<a href="#">c5ktaA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fdhc; <b>PDBTitle:</b> apo fdhc- a nucleotide-linked sugar gnat
24	<a href="#">c3mesB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
25	<a href="#">c3tcbB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of a gcn5-related n-acetyltransferase from brucella2 melitensis
26	<a href="#">c3dxqB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline/ethanolamine kinase family protein; <b>PDBTitle:</b> crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
27	<a href="#">d1j7la_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
28	<a href="#">c3igrA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal-protein-s5-alanine n-acetyltransferase; <b>PDBTitle:</b> the crystal structure of ribosomal-protein-s5-alanine2

					acetyltransferase from vibrio fischeri to 2.0a
29	<a href="#">c3f7wA_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_290396.1) from <i>Thermobifida fusca</i> yx-er1 at 1.85 Å resolution
30	<a href="#">c4r77A_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase lica from <i>Streptococcus pneumoniae</i>
31	<a href="#">c6c37A_</a>	Alignment	not modelled	99.9	21 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase, gnat family protein; <b>PDBTitle:</b> mycobacterium smegmatis rimj in complex with coa-disulfide
32	<a href="#">c6eddB_</a>	Alignment	not modelled	99.9	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase pa3944; <b>PDBTitle:</b> crystal structure of a gnat superfamily pa3944 acetyltransferase in2 complex with coa (p1 space group)
33	<a href="#">c2fsrA_</a>	Alignment	not modelled	99.9	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of the acetyltransferase from <i>Agrobacterium tumefaciens</i> str. c58
34	<a href="#">d1s7ka1</a>	Alignment	not modelled	99.9	19 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
35	<a href="#">d1yrea1</a>	Alignment	not modelled	99.9	16 <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="#">d2fcka1</a>	Alignment	not modelled	99.9	15 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
37	<a href="#">c3r95A_</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mcce protein; <b>PDBTitle:</b> crystal structure of microcin c7 self immunity acetyltransferase mcce2 in complex with acetyl-coa
38	<a href="#">c2zxvD_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein ttha1799; <b>PDBTitle:</b> crystal structure of putative acetyltransferase from <i>T. thermophilus</i> hb8
39	<a href="#">c4ockA_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylhexosamine 1-phosphate kinase; <b>PDBTitle:</b> n-acetylhexosamine 1-phosphate kinase in complex with glcnaC and2 ampnp
40	<a href="#">c3i0oA_</a>	Alignment	not modelled	99.9	9 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spectinomycin phosphotransferase; <b>PDBTitle:</b> crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomycin
41	<a href="#">d1yk3a1</a>	Alignment	not modelled	99.9	13 <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="#">c3fbuB_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> the crystal structure of the acetyltransferase (gnat family) from <i>Bacillus anthracis</i>
43	<a href="#">c1nw1A_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline kinase (49.2 kd); <b>PDBTitle:</b> crystal structure of choline kinase
44	<a href="#">d1nw1a_</a>	Alignment	not modelled	99.9	16 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Choline kinase
45	<a href="#">d2fsra1</a>	Alignment	not modelled	99.9	24 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
46	<a href="#">c4orfA_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase pat; <b>PDBTitle:</b> camp-binding acyltransferase from <i>Mycobacterium smegmatis</i> , mutant r95k
47	<a href="#">c1s7fA_</a>	Alignment	not modelled	99.9	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl transferase; <b>PDBTitle:</b> rimI- ribosomal I7/I12 alpha-n-protein acetyltransferase crystal form2 i (apo)
48	<a href="#">c3eg7F_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> spermidine n1-acetyltransferase; <b>PDBTitle:</b> spermidine n1-acetyltransferase from <i>Vibrio cholerae</i>
49	<a href="#">c3owcA_</a>	Alignment	not modelled	99.9	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable acetyltransferase; <b>PDBTitle:</b> crystal structure of gnat superfamily protein pa2578 from <i>Pseudomonas aeruginosa</i>
50	<a href="#">c2qmIA_</a>	Alignment	not modelled	99.9	12 <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 <i>Bacillus halodurans</i> at 1.55 Å resolution
51	<a href="#">c2vi7C_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyltransferase pa1377; <b>PDBTitle:</b> structure of a putative acetyltransferase (pa1377)from <i>Pseudomonas aeruginosa</i>
52	<a href="#">c5t7eD_</a>	Alignment	not modelled	99.9	10 <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
53	<a href="#">c2ig7A_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline/ethanolamine kinase; <b>PDBTitle:</b> crystal structure of human choline kinase b
54	<a href="#">c4r9mC_</a>	Alignment	not modelled	99.9	17 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> spermidine n(1)-acetyltransferase; <b>PDBTitle:</b> crystal structure of spermidine n-acetyltransferase from

					escherichia2 coli
55	<a href="#">c5ix3A_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diamine n-acetyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyltransferase from staphylococcus aureus.
56	<a href="#">c4qc6A_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional aac/aph; <b>PDBTitle:</b> crystal structure of aminoglycoside 6'-acetyltransferase-ie
57	<a href="#">d2pula1</a>	Alignment	not modelled	99.9	16 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
58	<a href="#">d1nsla_</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
59	<a href="#">c3dr8B_</a>	Alignment	not modelled	99.9	15 <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
60	<a href="#">c3tthL_</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> spermidine n1-acetyltransferase; <b>PDBTitle:</b> structure of the spermidine n1-acetyltransferase (speg) from coxiella2 burnetii
61	<a href="#">d1yvoa1</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
62	<a href="#">c2jlmE_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> putative phosphinothricin n-acetyltransferase; <b>PDBTitle:</b> structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
63	<a href="#">c5jtfB_</a>	Alignment	not modelled	99.9	14 <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
64	<a href="#">c3csvA_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
65	<a href="#">c6erdD_</a>	Alignment	not modelled	99.8	16 <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.
66	<a href="#">c4jxqA_</a>	Alignment	not modelled	99.8	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 melliotti 1021
67	<a href="#">c5jy7K_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> isomerase/transferase <b>Chain:</b> K: <b>PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> complex of mycobacterium smegmatis trehalose synthase with maltokinase
68	<a href="#">c2pywA_</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr
69	<a href="#">d2ge3a1</a>	Alignment	not modelled	99.8	18 <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="#">c6bffB_</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase; <b>PDBTitle:</b> structure of the aminoglycoside acetyltransferase aac(6')-im
71	<a href="#">d1vhsa_</a>	Alignment	not modelled	99.8	16 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
72	<a href="#">c4ri1A_</a>	Alignment	not modelled	99.8	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-4-amino-4,6-dideoxy-n-acetyl-beta-l-altrosamine n- <b>PDBTitle:</b> crystal structure of helicobacter pylori pseudaminic acid biosynthesis2 n -acetyltransferase pseh complex with acetyl-coa
73	<a href="#">c2ckpB_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
74	<a href="#">c3pzjB_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable acetyltransferases; <b>PDBTitle:</b> crystal structure of a probable acetyltransferases (gnat family) from2 chromobacterium violaceum atcc 12472
75	<a href="#">c2i79B_</a>	Alignment	not modelled	99.8	10 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> the crystal structure of the acetyltransferase of gnat family from2 streptococcus pneumoniae
76	<a href="#">c2ckpA_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
77	<a href="#">d2i6ca1</a>	Alignment	not modelled	99.8	16 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
78	<a href="#">c4j3gD_</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of ribosomal-protein-alanine n-acetyltransferase2 from brucella melitensis
79	<a href="#">c4u5yA_</a>	Alignment	not modelled	99.8	19 <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 <b>PDB header:</b> transferase
80	<a href="#">c4avcA_</a>	Alignment	not modelled	99.8	16 <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
81	<a href="#">c3f2rA_</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
82	<a href="#">d2ae6a1</a>	Alignment	not modelled	99.8	16 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
83	<a href="#">c4h89A_</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> the structure of a gcn5-related n-acetyltransferase from kribbella2 flavida
84	<a href="#">c3eo4A_</a>	Alignment	not modelled	99.8	11 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1062; <b>PDBTitle:</b> the crystal structure of a domain from methanocaldococcus jannaschii2 dsm 2661
85	<a href="#">c4mbuB_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> similar to n-acetyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyltransferase from staphylococcus aureus2 mu50
86	<a href="#">c2pr8B_</a>	Alignment	not modelled	99.8	18 <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
87	<a href="#">d1yr0a1</a>	Alignment	not modelled	99.8	18 <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="#">c3d3sA_</a>	Alignment	not modelled	99.8	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
89	<a href="#">c1ufhB_</a>	Alignment	not modelled	99.8	15 <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
90	<a href="#">c5dwnC_</a>	Alignment	not modelled	99.8	12 <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
91	<a href="#">d1ghea_</a>	Alignment	not modelled	99.8	18 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
92	<a href="#">c3ld2B_</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> the crystal structure of smu.2055 from streptococcus mutans ua159
93	<a href="#">d2fl4a1</a>	Alignment	not modelled	99.8	17 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
94	<a href="#">d1ufha_</a>	Alignment	not modelled	99.8	15 <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
95	<a href="#">c2q83A_</a>	Alignment	not modelled	99.7	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ytaa protein; <b>PDBTitle:</b> crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
96	<a href="#">c3w6sA_</a>	Alignment	not modelled	99.7	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mpr1 protein; <b>PDBTitle:</b> yeast n-acetyltransferase mpr1 involved in oxidative stress tolerance2 via proline metabolism
97	<a href="#">c3f5bA_</a>	Alignment	not modelled	99.7	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(6')acetyltransferase; <b>PDBTitle:</b> the crystal structure of aminoglycoside n(6')acetyltransferase from2 legionella pneumophila subsp. pneumophila str. philadelphia 1.
98	<a href="#">c3exnA_</a>	Alignment	not modelled	99.7	18 <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
99	<a href="#">d1tiqa_</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
100	<a href="#">d2cy2a1</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
101	<a href="#">c4xplA_</a>	Alignment	not modelled	99.7	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase, pseh; <b>PDBTitle:</b> the crystal structure of campylobacter jejuni n-acetyltransferase pseh2 in complex with acetyl coenzyme a
102	<a href="#">c2pswA_</a>	Alignment	not modelled	99.7	11 <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
103	<a href="#">c3c26A_</a>	Alignment	not modelled	99.7	20 <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
104	<a href="#">c3g8wB_</a>	Alignment	not modelled	99.7	10 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lactococcal prophage ps3 protein 05; <b>PDBTitle:</b> crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228
					<b>PDB header:</b> transferase

105	<a href="#">c3dnsA_</a>	Alignment	not modelled	99.7	11	<b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal-protein-alanine acetyltransferase; <b>PDBTitle:</b> the n-terminal domain of ribosomal-protein-alanine acetyltransferase2 from clostridium acetobutylicum atcc 824
106	<a href="#">d1qsmA_</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
107	<a href="#">c2r7hA_</a>	Alignment	not modelled	99.7	12	<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
108	<a href="#">c3lodA_</a>	Alignment	not modelled	99.7	15	<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
109	<a href="#">d2beia1</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
110	<a href="#">c3iwgB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyltransferase, gnat family; <b>PDBTitle:</b> acetyltransferase from gnat family from colwellia psychrethraea.
111	<a href="#">c4pv6E_</a>	Alignment	not modelled	99.7	17	<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
112	<a href="#">d1sqha_</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> Hypothetical protein cg14615-pa
113	<a href="#">c3f8kA_</a>	Alignment	not modelled	99.7	16	<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
114	<a href="#">c4e2aA_</a>	Alignment	not modelled	99.7	11	<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
115	<a href="#">d1s3za_</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
116	<a href="#">c4e8oB_</a>	Alignment	not modelled	99.7	20	<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
117	<a href="#">c2qg7A_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ethanolamine kinase pv091845; <b>PDBTitle:</b> plasmodium vivax ethanolamine kinase pv091845
118	<a href="#">c3i9sA_</a>	Alignment	not modelled	99.6	11	<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
119	<a href="#">c3pp9B_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative streptothricin acetyltransferase; <b>PDBTitle:</b> 1.6 angstrom resolution crystal structure of putative streptothricin2 acetyltransferase from bacillus anthracis str. ames in complex with3 acetyl coenzyme a
120	<a href="#">c4luaA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyltransferase from staphylococcus aureus2 mu50