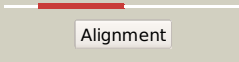

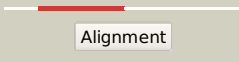

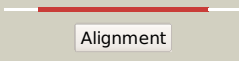
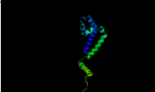


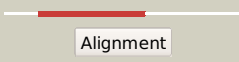

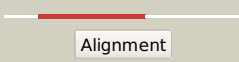

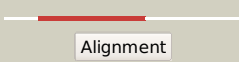

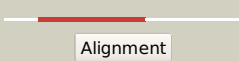

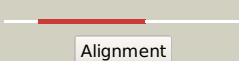

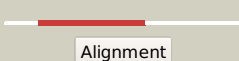

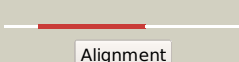

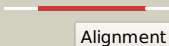

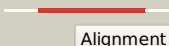







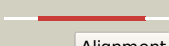







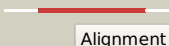



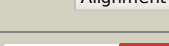
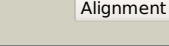
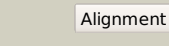
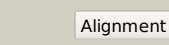
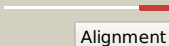


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0730 (-) _822869_823597
Date	Fri Jul 26 01:50:30 BST 2019
Unique Job ID	b9994dfdbf20084d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1x75a1</a>	 Alignment		100.0	26	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
2	<a href="#">c3ku8A</a>	 Alignment		100.0	26	<b>PDB header:</b> toxin/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> ccdbvfi:gyra14ec
3	<a href="#">c1zvua</a>	 Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit a; <b>PDBTitle:</b> structure of the full-length e. coli parc subunit
4	<a href="#">c6gauB</a>	 Alignment		99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b,dna gyrase subunit a; <b>PDBTitle:</b> extremely 'open' clamp structure of dna gyrase: role of the2 corynebacteriales gyrb specific insert
5	<a href="#">c3rafA</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase/dna/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> quinazolidinedione-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
6	<a href="#">c4i3hA</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit b, dna topoisomerase 4 subunit a <b>PDBTitle:</b> a three-gate structure of topoisomerase iv from streptococcus2 pneumoniae
7	<a href="#">c4z2cA</a>	 Alignment		99.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
8	<a href="#">c2xcqA</a>	 Alignment		99.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
9	<a href="#">c2xcsD</a>	 Alignment		99.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
10	<a href="#">c2inrA</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
11	<a href="#">c3ilwA</a>	 Alignment		99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> structure of dna gyrase subunit a n-terminal domain

12	<a href="#">d1ab4a_</a>	 Alignment		99.9	24	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
13	<a href="#">c3ifzA_</a>	 Alignment		99.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
14	<a href="#">c2wl2B_</a>	 Alignment		99.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
15	<a href="#">c2novD_</a>	 Alignment		99.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> breakage-reunion domain of s.pneumoniae topo iv: crystal structure of2 a gram-positive quinolone target
16	<a href="#">c5eixB_</a>	 Alignment		99.8	22	<b>PDB header:</b> isomerase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit <b>PDBTitle:</b> quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
17	<a href="#">c2xkjE_</a>	 Alignment		99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> topoisomerase iv; <b>PDBTitle:</b> crystal structure of catalytic core of a. baumannii topo iv (pare-2 parc fusion truncate)
18	<a href="#">c5eixG_</a>	 Alignment		99.8	23	<b>PDB header:</b> isomerase/dna <b>Chain:</b> G: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit <b>PDBTitle:</b> quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
19	<a href="#">c4fm9A_</a>	 Alignment		99.4	10	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2-alpha; <b>PDBTitle:</b> human topoisomerase ii alpha bound to dna
20	<a href="#">c3qx3B_</a>	 Alignment		99.2	13	<b>PDB header:</b> isomerase/dna/isomerase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 2-beta; <b>PDBTitle:</b> human topoisomerase iibeta in complex with dna and etoposide
21	<a href="#">c6ca8A_</a>	 Alignment	not modelled	99.2	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
22	<a href="#">c1bjtA_</a>	 Alignment	not modelled	99.1	13	<b>PDB header:</b> topoisomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase ii; <b>PDBTitle:</b> topoisomerase ii residues 409-1201
23	<a href="#">d1bjta_</a>	 Alignment	not modelled	99.1	13	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
24	<a href="#">c4gfhA_</a>	 Alignment	not modelled	99.0	11	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> topoisomerase ii-dna-ampnp complex
25	<a href="#">c3l6vA_</a>	 Alignment	not modelled	95.7	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of the xanthomonas campestris gyrase a c-2 terminal domain
26	<a href="#">c1zvtA_</a>	 Alignment	not modelled	94.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit a; <b>PDBTitle:</b> structure of the e. coli parc c-terminal domain
27	<a href="#">d1wp5a_</a>	 Alignment	not modelled	92.6	13	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> GyrA/ParC C-terminal domain-like <b>Family:</b> GyrA/ParC C-terminal domain-like
28	<a href="#">c3uc1A_</a>	 Alignment	not modelled	92.5	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> mycobacterium tuberculosis gyrase type iia topoisomerase c-terminal2 domain
29	<a href="#">c2zw7A_</a>	 Alignment	not modelled	92.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bleomycin acetyltransferase;

29	<a href="#">c2zw1A</a>	Alignment	not modelled	92.2	10	<b>PDBTitle:</b> crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a <b>PDB header:</b> transferase
30	<a href="#">c4h89A</a>	Alignment	not modelled	87.2	13	<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
31	<a href="#">c3frmF</a>	Alignment	not modelled	84.4	13	<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.
32	<a href="#">d1suua</a>	Alignment	not modelled	84.0	6	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> GyrA/ParC C-terminal domain-like <b>Family:</b> GyrA/ParC C-terminal domain-like
33	<a href="#">c1zi0A</a>	Alignment	not modelled	82.1	4	<b>PDB header:</b> isomerase, dna bindng protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> a superhelical spiral in escherichia coli dna gyrase a c-2 terminal domain imparts unidirectional supercoiling bias
34	<a href="#">c5t7eD</a>	Alignment	not modelled	79.6	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
35	<a href="#">c3no0B</a>	Alignment	not modelled	79.1	9	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> aquifex aeolicus type iia topoisomerase c-terminal domain
36	<a href="#">d1s7ka1</a>	Alignment	not modelled	79.0	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
37	<a href="#">c2wpaA</a>	Alignment	not modelled	78.7	18	<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)
38	<a href="#">c3juwC</a>	Alignment	not modelled	78.2	18	<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.
39	<a href="#">d1yvoa1</a>	Alignment	not modelled	77.5	18	<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="#">c4u5yA</a>	Alignment	not modelled	77.2	15	<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
41	<a href="#">c2jlmE</a>	Alignment	not modelled	73.8	12	<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
42	<a href="#">c2vzza</a>	Alignment	not modelled	71.6	22	<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
43	<a href="#">c3igrA</a>	Alignment	not modelled	69.8	10	<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
44	<a href="#">c5dwnC</a>	Alignment	not modelled	67.7	21	<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
45	<a href="#">c2vi7C</a>	Alignment	not modelled	66.2	17	<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 pseudomonas2 aeruginosa
46	<a href="#">c1nfoA</a>	Alignment	not modelled	65.4	13	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein e2; <b>PDBTitle:</b> apolipoprotein e2 (apoe2, d154a mutation)
47	<a href="#">c5frgA</a>	Alignment	not modelled	63.4	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
48	<a href="#">c5x2hA</a>	Alignment	not modelled	62.4	12	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of campylobacter jejuni cas9 in complex with sgrna2 and target dna (agaaca pam)
49	<a href="#">c2fsrA</a>	Alignment	not modelled	61.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase; <b>PDBTitle:</b> crystal structure of the acetyltransferase from agrobacterium2 tumefaciens str. c58
50	<a href="#">c5jtfB</a>	Alignment	not modelled	61.1	16	<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
51	<a href="#">d1yx0a1</a>	Alignment	not modelled	60.9	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
52	<a href="#">c3thhL</a>	Alignment	not modelled	60.2	17	<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
53	<a href="#">d1b4ua</a>	Alignment	not modelled	59.7	14	<b>Fold:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Superfamily:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Family:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB
						<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat)

54	<a href="#">d1y9wa1</a>	Alignment	not modelled	59.2	26	<b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
55	<a href="#">c3d8pB</a>	Alignment	not modelled	59.2	8	<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
56	<a href="#">d2ge3a1</a>	Alignment	not modelled	58.0	12	<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="#">c3dnsA</a>	Alignment	not modelled	57.3	15	<b>PDB header:</b> transferase <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
58	<a href="#">c4jxqA</a>	Alignment	not modelled	57.3	18	<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
59	<a href="#">c2nuxB</a>	Alignment	not modelled	56.5	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate <b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
60	<a href="#">c3wrbB</a>	Alignment	not modelled	55.9	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gallate dioxygenase; <b>PDBTitle:</b> crystal structure of the anaerobic h124f desb-gallate complex
61	<a href="#">c3lodA</a>	Alignment	not modelled	55.7	24	<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
62	<a href="#">c3r95A</a>	Alignment	not modelled	55.5	12	<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
63	<a href="#">c3dr8B</a>	Alignment	not modelled	55.1	18	<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
64	<a href="#">c1t3jA</a>	Alignment	not modelled	54.7	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin 1; <b>PDBTitle:</b> mitofusin domain hr2 v686m/i708m mutant
65	<a href="#">d2g3aa1</a>	Alignment	not modelled	54.4	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
66	<a href="#">d1vhsa</a>	Alignment	not modelled	53.1	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
67	<a href="#">d1s3za</a>	Alignment	not modelled	51.3	21	<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="#">c3f8kA</a>	Alignment	not modelled	50.8	22	<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
69	<a href="#">c3ibpA</a>	Alignment	not modelled	49.3	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein mukb; <b>PDBTitle:</b> the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
70	<a href="#">d2ae6a1</a>	Alignment	not modelled	49.2	20	<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="#">c6c37A</a>	Alignment	not modelled	48.4	15	<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
72	<a href="#">c3g3sA</a>	Alignment	not modelled	47.8	19	<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-like protein2 (zp_00874857) (zp_00874857.1) from streptococcus suis 89/1591 at 1.803 a resolution
73	<a href="#">c3owcA</a>	Alignment	not modelled	47.1	21	<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 pseudomonas2 aeruginosa
74	<a href="#">c5ktaA</a>	Alignment	not modelled	46.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fdhc; <b>PDBTitle:</b> apo fdhc- a nucleotide-linked sugar gnat
75	<a href="#">c4e8oB</a>	Alignment	not modelled	45.8	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
76	<a href="#">c3ec4B</a>	Alignment	not modelled	45.6	15	<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
77	<a href="#">c3tcbB</a>	Alignment	not modelled	45.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> crystal structure of a gcn5-related n-acetyltransferase from brucella2 melitensis
78	<a href="#">c4errB</a>	Alignment	not modelled	45.1	23	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> autotransporter adhesin; <b>PDBTitle:</b> 1.55 angstrom crystal structure of the four helical bundle

						membrane2 localization domain (4hbm) of the vibrio vulnificus marx effector3 domain duf5
79	<a href="#">d1yr0a1</a>	Alignment	not modelled	43.7	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
80	<a href="#">c3dsbB</a>	Alignment	not modelled	42.7	13	<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
81	<a href="#">c4r9mC</a>	Alignment	not modelled	41.6	22	<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
82	<a href="#">c6nukB</a>	Alignment	not modelled	41.6	26	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferredog-diesel; <b>PDBTitle:</b> de novo designed protein ferredog-diesel
83	<a href="#">c2cntD</a>	Alignment	not modelled	40.8	15	<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.
84	<a href="#">c3iwgB</a>	Alignment	not modelled	38.8	19	<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 psychrerythraea.
85	<a href="#">c3eg7F</a>	Alignment	not modelled	38.4	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> spermidine n1-acetyltransferase; <b>PDBTitle:</b> spermidine n1-acetyltransferase from vibrio cholerae
86	<a href="#">c2zxvD</a>	Alignment	not modelled	38.1	10	<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 t.2 thermophilus hb8
87	<a href="#">c4mbuB</a>	Alignment	not modelled	36.0	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
88	<a href="#">c3ld2B</a>	Alignment	not modelled	35.5	13	<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
89	<a href="#">c5bqtC</a>	Alignment	not modelled	34.6	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator trmb12; <b>PDBTitle:</b> structure of trmb12, an archaeal chromatin protein, shows a novel mode2 of dna binding.
90	<a href="#">c4n6jA</a>	Alignment	not modelled	33.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> striatin-3; <b>PDBTitle:</b> crystal structure of human striatin-3 coiled coil domain
91	<a href="#">c5ukhA</a>	Alignment	not modelled	33.2	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of telc from streptococcus intermedius b196
92	<a href="#">c4n6jB</a>	Alignment	not modelled	33.2	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> striatin-3; <b>PDBTitle:</b> crystal structure of human striatin-3 coiled coil domain
93	<a href="#">d1w3ia</a>	Alignment	not modelled	32.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
94	<a href="#">d2aj6a1</a>	Alignment	not modelled	32.6	16	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
95	<a href="#">c3i9sA</a>	Alignment	not modelled	31.4	12	<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
96	<a href="#">c5z6nA</a>	Alignment	not modelled	31.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein elaa; <b>PDBTitle:</b> crystal structure of escherichia coli elaa
97	<a href="#">c2zkrv</a>	Alignment	not modelled	31.2	25	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> V: <b>PDB Molecule:</b> rna expansion segment es9 part2; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
98	<a href="#">c2pdoG</a>	Alignment	not modelled	31.2	27	<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
99	<a href="#">c3mgdB</a>	Alignment	not modelled	31.1	11	<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
100	<a href="#">d1p0ha</a>	Alignment	not modelled	31.0	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
101	<a href="#">c4orfA</a>	Alignment	not modelled	30.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase pat; <b>PDBTitle:</b> camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
102	<a href="#">c5ix3A</a>	Alignment	not modelled	30.3	18	<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.
103	<a href="#">c4iusA</a>	Alignment	not modelled	30.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5-related n-acetyltransferase; <b>PDBTitle:</b> gcn5-related n-acetyltransferase from kribbella flavida.

104	<a href="#">c5b83C_</a>	Alignment	not modelled	29.8	41	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
105	<a href="#">c5tuuB_</a>	Alignment	not modelled	29.5	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f4; <b>PDBTitle:</b> crystal structure of the e2f4-dp1 coiled coil and marked-box domains
106	<a href="#">c4xplA_</a>	Alignment	not modelled	29.5	17	<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
107	<a href="#">d1yrea1</a>	Alignment	not modelled	28.9	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
108	<a href="#">c3h0mE_</a>	Alignment	not modelled	28.8	17	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> aspartyl/glutamyl-trna(asn/gln) amidotransferase <b>PDBTitle:</b> structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
109	<a href="#">d1ghea_</a>	Alignment	not modelled	28.8	9	<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="#">d1nsla_</a>	Alignment	not modelled	28.7	17	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
111	<a href="#">c3j3bh_</a>	Alignment	not modelled	28.3	25	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
112	<a href="#">d1io1a_</a>	Alignment	not modelled	28.1	10	<b>Fold:</b> Phase 1 flagellin <b>Superfamily:</b> Phase 1 flagellin <b>Family:</b> Phase 1 flagellin
113	<a href="#">c2yf2C_</a>	Alignment	not modelled	28.1	26	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> c4b binding protein; <b>PDBTitle:</b> crystal structure of the oligomerisation domain of c4b-binding2 protein from gallus gallus
114	<a href="#">c1zq1D_</a>	Alignment	not modelled	27.5	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit e; <b>PDBTitle:</b> structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
115	<a href="#">c4nx9A_</a>	Alignment	not modelled	27.2	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa flagellin flic
116	<a href="#">d2fl4a1</a>	Alignment	not modelled	27.1	16	<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="#">c4a1eU_</a>	Alignment	not modelled	27.1	21	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> rpl35; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
118	<a href="#">c5tuvB_</a>	Alignment	not modelled	27.0	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f5; <b>PDBTitle:</b> crystal structure of the e2f5-dp1-p107 ternary complex
119	<a href="#">c4j3gD_</a>	Alignment	not modelled	26.9	14	<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
120	<a href="#">c4mxeA_</a>	Alignment	not modelled	26.4	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase esco1; <b>PDBTitle:</b> human esco1 (eco1/ctf7 ortholog), acetyltransferase domain in complex2 with acetyl-coa