





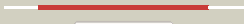
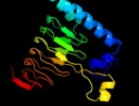









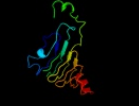






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1krra_</a>	 Alignment		100.0	100	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
2	<a href="#">c3fttA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase sacol2570; <b>PDBTitle:</b> crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
3	<a href="#">c3srtB_</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose o-acetyltransferase; <b>PDBTitle:</b> the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
4	<a href="#">c2ic7A_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose transacetylase; <b>PDBTitle:</b> crystal structure of maltose transacetylase from2 geobacillus kaustophilus
5	<a href="#">d1ocxa_</a>	 Alignment		100.0	43	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
6	<a href="#">c3ectA_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexapeptide-repeat containing-acetyltransferase; <b>PDBTitle:</b> crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
7	<a href="#">c3jqyB_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polysialic acid o-acetyltransferase; <b>PDBTitle:</b> crystal strucutre of the polysia specific acetyltransferase neuo
8	<a href="#">c3i3aC_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
9	<a href="#">d1mr7a_</a>	 Alignment		100.0	29	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
10	<a href="#">c3r0sA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> acetylglucosamine o- <b>PDBTitle:</b> udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
11	<a href="#">c2wlgA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid o-acetyltransferase; <b>PDBTitle:</b> crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy

12	<a href="#">c3cj8B_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2-carboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
13	<a href="#">d1xata_</a>	Alignment		99.9	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
14	<a href="#">c3eevC_</a>	Alignment		99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
15	<a href="#">c2iu9C_</a>	Alignment		99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine <b>PDBTitle:</b> chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
16	<a href="#">d1j2za_</a>	Alignment		99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
17	<a href="#">d2jf2a1</a>	Alignment		99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
18	<a href="#">c3ixcA_</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexapeptide transferase family protein; <b>PDBTitle:</b> crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
19	<a href="#">d1t3da_</a>	Alignment		99.9	25	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
20	<a href="#">c1t3dB_</a>	Alignment		99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> crystal structure of serine acetyltransferase from e.coli at 2.2a
21	<a href="#">d3bswa1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> PglD-like
22	<a href="#">d1ssqa_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
23	<a href="#">c3mqhD_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lipopolysaccharides biosynthesis acetyltransferase; <b>PDBTitle:</b> crystal structure of the 3-n-acetyl transferase w1bb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
24	<a href="#">d1v3wa_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
25	<a href="#">c3eh0C_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n- <b>PDBTitle:</b> crystal structure of lpxd from escherichia coli
26	<a href="#">c3mc4A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ww/rsp5/wwp domain:bacterial transferase <b>PDBTitle:</b> crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
27	<a href="#">c3pmoA_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; <b>PDBTitle:</b> the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution

28	<a href="#">c3r3rA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyochelin binding protein; <b>PDBTitle:</b> structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
29	<a href="#">dlg97a1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
30	<a href="#">dlxhda</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
31	<a href="#">c3fsbB</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtc; <b>PDBTitle:</b> crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
32	<a href="#">c3rlwA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
33	<a href="#">c1hm8A</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
34	<a href="#">c3q1xA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
35	<a href="#">d2oi6a1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
36	<a href="#">c3f1xA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
37	<a href="#">c2v0hA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
38	<a href="#">c3eg4A</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
39	<a href="#">d3tdta</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
40	<a href="#">c2oi6A</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> e. coli glmu- complex with udp-glcna, coa and glcn-1-po4
41	<a href="#">c3c8vA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
42	<a href="#">c3kwdA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> lyase, protein binding, photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein; <b>PDBTitle:</b> inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
43	<a href="#">c3fsyC</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tetrahydrodipicolinate n-succinyltransferase; <b>PDBTitle:</b> structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
44	<a href="#">dlqrea</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
45	<a href="#">c1qreA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
46	<a href="#">c2gggA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 401aa long hypothetical glucose-1-phosphate <b>PDBTitle:</b> complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
47	<a href="#">c2rijA</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- <b>PDBTitle:</b> crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution
48	<a href="#">d2f9ca1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> YdcK-like
49	<a href="#">d1yp2a1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
						<b>Fold:</b> Single-stranded left-handed beta-helix

50	<a href="#">d1fxja1</a>	Alignment	not modelled	99.2	22	<b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Glmu C-terminal domain-like
51	<a href="#">c2qkxA</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
52	<a href="#">c3d98A</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
53	<a href="#">c1fwyA</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
54	<a href="#">c1yp3C</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
55	<a href="#">c3brkX</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	<a href="#">d2icya1</a>	Alignment	not modelled	33.8	28	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Glmu C-terminal domain-like
57	<a href="#">c1xqhE</a>	Alignment	not modelled	12.9	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-4 <b>PDBTitle:</b> crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
58	<a href="#">c1h3iB</a>	Alignment	not modelled	11.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone h3 lysine 4 specific methyltransferase; <b>PDBTitle:</b> crystal structure of the histone methyltransferase set7/9
59	<a href="#">d1ihwa</a>	Alignment	not modelled	9.8	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
60	<a href="#">d1ex4a1</a>	Alignment	not modelled	9.8	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
61	<a href="#">d1bg3a2</a>	Alignment	not modelled	8.2	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
62	<a href="#">d2g46a1</a>	Alignment	not modelled	7.9	15	<b>Fold:</b> beta-clip <b>Superfamily:</b> SET domain <b>Family:</b> Viral histone H3 Lysine 27 Methyltransferase
63	<a href="#">d1v4sa2</a>	Alignment	not modelled	7.4	30	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
64	<a href="#">c1c6vX</a>	Alignment	not modelled	6.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> protein (siu89134); <b>PDBTitle:</b> siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
65	<a href="#">d1c6vx</a>	Alignment	not modelled	6.9	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
66	<a href="#">d1ig8a2</a>	Alignment	not modelled	6.5	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
67	<a href="#">c3gt2A</a>	Alignment	not modelled	6.5	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
68	<a href="#">c2z9fC</a>	Alignment	not modelled	6.5	36	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> cellulose synthase operon protein d; <b>PDBTitle:</b> crystal structure of xcesd protein from acetobacter xylinum
69	<a href="#">d1bg3a4</a>	Alignment	not modelled	6.3	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase