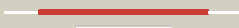
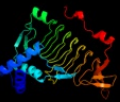








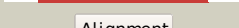
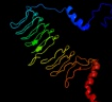
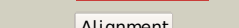

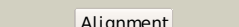

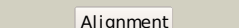
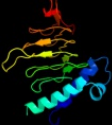
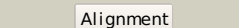

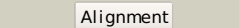
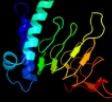
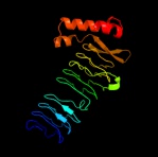
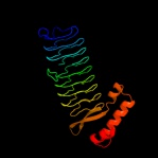






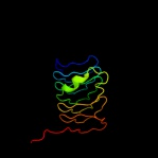


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tdta_	 Alignment		100.0	95	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
2	c3eg4A_	 Alignment		100.0	64	PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
3	c2iu9C_	 Alignment		100.0	13	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
4	c2rijA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- PDBTitle: 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
5	c3eh0C_	 Alignment		100.0	15	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
6	c3pmoA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; PDBTitle: the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
7	c3fsyC_	 Alignment		100.0	26	PDB header: transferase Chain: C: PDB Molecule: tetrahydrodipicolinate n-succinyltransferase; PDBTitle: structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
8	c3cj8B_	 Alignment		99.9	33	PDB header: transferase Chain: B: PDB Molecule: 2,3,4,5-tetrahydropyridine-2-carboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
9	d1t3da_	 Alignment		99.9	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
10	d1ssqa_	 Alignment		99.9	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
11	c1t3dB_	 Alignment		99.9	19	PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a

12	d2jf2a1	Alignment		99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
13	c3i3aC	Alignment		99.9	14	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n- PDBTitle: structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
14	d1j2za	Alignment		99.9	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
15	c3r0sA	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n- acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
16	c3q1xA	Alignment		99.9	13	PDB header: transferase Chain: A: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
17	c3f1xA	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: serine acetyltransferase; PDBTitle: three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
18	c3mc4A	Alignment		99.9	22	PDB header: transferase Chain: A: PDB Molecule: ww/rsp5/wwp domain:bacterial transferase PDBTitle: crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
19	c2v0hA	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
20	d3bswa1	Alignment		99.9	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: PglD-like
21	c3mqhD	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D: PDB Molecule: lipopolysaccharides biosynthesis acetyltransferase; PDBTitle: crystal structure of the 3-n-acetyl transferase wlibb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
22	c3c8vA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
23	c1hm8A	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
24	c3fsbB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: qdtc; PDBTitle: 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
25	c3jqyB	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystal strucutre of the polysia specific acetyltransferase neuo
26	c3srtB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: maltose o-acetyltransferase; PDBTitle: the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
27	c3fttA	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sacol2570;

27	c3ltwA	Alignment	not modelled	99.9	22	PDBTitle: crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
28	d1mr7a	Alignment	not modelled	99.9	20	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
29	d1krra	Alignment	not modelled	99.9	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
30	c2oi6A	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
31	c3ectA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: hexapeptide-repeat containing-acetyltransferase; PDBTitle: crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
32	c2ic7A	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: maltose transacetylase; PDBTitle: crystal structure of maltose transacetylase from2 geobacillus kaustophilus
33	d1g97a1	Alignment	not modelled	99.8	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
34	d2oi6a1	Alignment	not modelled	99.8	17	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
35	c3r3rA	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
36	c2wlgA	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
37	d1v3wa	Alignment	not modelled	99.8	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
38	d1ocxa	Alignment	not modelled	99.8	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
39	d1xhda	Alignment	not modelled	99.8	14	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
40	c3ixcA	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: hexapeptide transferase family protein; PDBTitle: crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
41	c2ggqA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii
42	c1qreA	Alignment	not modelled	99.8	17	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
43	d1qrea	Alignment	not modelled	99.8	17	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
44	d1xata	Alignment	not modelled	99.8	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
45	d2f9ca1	Alignment	not modelled	99.8	12	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: YdcK-like
46	c3r1wA	Alignment	not modelled	99.7	18	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
47	c2qkxA	Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
48	c3d98A	Alignment	not modelled	99.7	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
49	c3eevC	Alignment	not modelled	99.7	12	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
50	c3kwdA	Alignment	not modelled	99.7	16	PDB header: lyase, protein binding, photosynthesis Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
51	d1yp2a1	Alignment	not modelled	99.6	14	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
52	c1yp3C	Alignment	not modelled	99.5	15	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyllyltransferase small

						PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
53	c3brkX_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
54	d1fxja1	Alignment	not modelled	99.3	20	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmlU C-terminal domain-like
55	c1fwyA_	Alignment	not modelled	99.2	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnaC
56	c3cqxD_	Alignment	not modelled	6.1	32	PDB header: chaperone Chain: D: PDB Molecule: bag family molecular chaperone regulator 2; PDBTitle: chaperone complex
57	d1nu9c2	Alignment	not modelled	5.7	28	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Staphylocoagulase Family: Staphylocoagulase