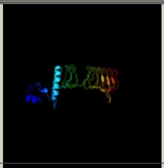
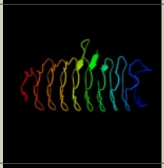
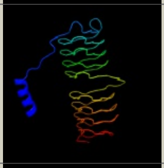
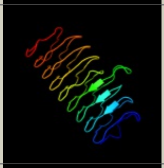
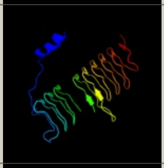
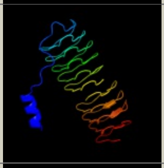
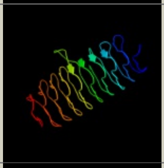
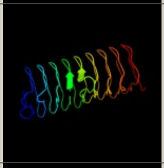
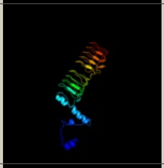
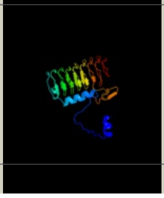
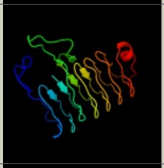
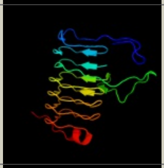
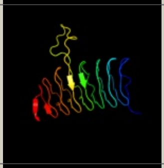
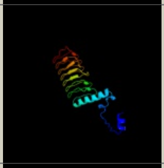
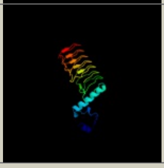
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75697
Date	Thu Jan 5 12:13:16 GMT 2012
Unique Job ID	337f6db310112e43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hm8A_	Alignment		100.0	17	**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
2	c3i3aC_	Alignment		100.0	12	**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
3	c2iu9C_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
4	c2v0hA_	Alignment		100.0	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)
5	d1j2za_	Alignment		100.0	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
6	c3pmoA_	Alignment		100.0	20	**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	c3eh0C_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
8	d2jf2a1	Alignment		100.0	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
9	c3r0sA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
10	c2oi6A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
11	c2ggqA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii

12	c1yp3C_	Alignment		99.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
13	c3fsbB_	Alignment		99.9	19	**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
14	d1qrea_	Alignment		99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
15	c1qreA_	Alignment		99.9	15	**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
16	d2oi6a1	Alignment		99.9	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
17	c3mqhD_	Alignment		99.9	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase; **PDBTitle:** crystal structure of the 3-n-acetyl transferase wlbb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
18	c3d98A_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
19	d1g97a1	Alignment		99.9	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
20	c2qkxA_	Alignment		99.9	16	**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
21	c3cj8B_	Alignment	not modelled	99.8	22	**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
22	c3ectA_	Alignment	not modelled	99.8	17	**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
23	c3eg4A_	Alignment	not modelled	99.8	17	**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
24	d1mr7a_	Alignment	not modelled	99.8	12	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
25	c3c8vA_	Alignment	not modelled	99.8	11	**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
26	c2ic7A_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from2 geobacillus kaustophilus
27	c3jqyB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo

28	c3fttA_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570; **PDBTitle:** crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
29	d1krra_	Alignment	not modelled	99.8	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
30	c3srtB_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maltose o-acetyltransferase; **PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
31	c2wlgA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
32	d3tdta_	Alignment	not modelled	99.8	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD
33	d2f9ca1	Alignment	not modelled	99.8	22	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
34	c3q1xA_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
35	c3brkX_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
36	d1ocxa_	Alignment	not modelled	99.7	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
37	d1v3wa_	Alignment	not modelled	99.7	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
38	d3bswa1	Alignment	not modelled	99.7	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
39	c3kwdA_	Alignment	not modelled	99.7	15	**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
40	c1fwyA_	Alignment	not modelled	99.7	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
41	c3r3rA_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
42	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
43	c3ixcA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
44	d1t3da_	Alignment	not modelled	99.7	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
45	c1t3dB_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
46	d1ssqa_	Alignment	not modelled	99.7	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
47	c3f1xA_	Alignment	not modelled	99.7	25	**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.
48	d1xhda_	Alignment	not modelled	99.6	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
49	d1xata_	Alignment	not modelled	99.6	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
50	d1yp2a1	Alignment	not modelled	99.6	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
51	c3fsyC_	Alignment	not modelled	99.6	12	**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
52	c3mc4A_	Alignment	not modelled	99.6	14	**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
53	c3eevC_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
54	d1fxja1	Alignment	not modelled	99.0	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
55	c2rijA_	Alignment	not modelled	99.0	18	**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
56	d1yp2a2	Alignment	not modelled	98.8	4	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
57	c2pa4B_	Alignment	not modelled	98.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
58	d1iina_	Alignment	not modelled	97.9	5	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
59	d1h5ra_	Alignment	not modelled	97.8	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
60	c2cu2A_	Alignment	not modelled	97.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative mannose-1-phosphate guanylyl transferase; **PDBTitle:** crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
61	d1mc3a_	Alignment	not modelled	97.8	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
62	d1lvwa_	Alignment	not modelled	97.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
63	d1fxoa_	Alignment	not modelled	97.4	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
64	c2x5sB_	Alignment	not modelled	96.5	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
65	c2i5kB_	Alignment	not modelled	16.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
66	d2icya1	Alignment	not modelled	13.8	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like