# Phyre$^2$

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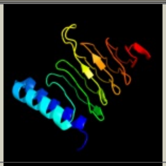
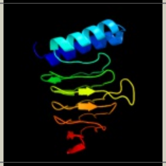
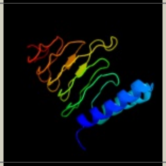
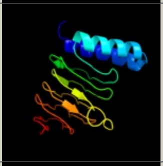
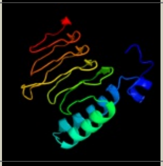
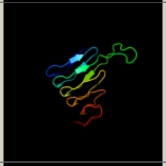
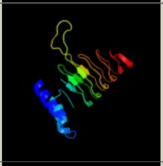
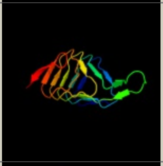
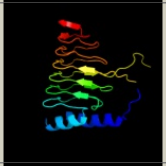
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ACC9 |
| Date | Thu Jan 5 11:17:55 GMT 2012 |
| Unique Job ID | 0532c7c9f1810aa3 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1t3da_ | Alignment |  | 100.0 | 32 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Serine acetyltransferase |
| 2 | c1t3dB_ | Alignment |  | 100.0 | 32 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine acetyltransferase;<br>**PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a |
| 3 | d1ssqa_ | Alignment |  | 100.0 | 31 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Serine acetyltransferase |
| 4 | c3mc4A_ | Alignment |  | 100.0 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase<br>**PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis |
| 5 | c3f1xA_ | Alignment |  | 100.0 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine acetyltransferase;<br>**PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62. |
| 6 | c3q1xA_ | Alignment |  | 100.0 | 27 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine acetyltransferase;<br>**PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine |
| 7 | c2ic7A_ | Alignment |  | 100.0 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**maltose transacetylase;<br>**PDBTitle:** crystal structure of maltose transacetylase from2 geobacillus kaustophilus |
| 8 | d1ocxa_ | Alignment |  | 100.0 | 21 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Galactoside acetyltransferase-like |
| 9 | c3fttA_ | Alignment |  | 100.0 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570;<br>**PDBTitle:** crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus |
| 10 | c3ectA_ | Alignment |  | 100.0 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase;<br>**PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae |
| 11 | c3srtB_ | Alignment |  | 99.9 | 30 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**maltose o-acetyltransferase;<br>**PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630 |

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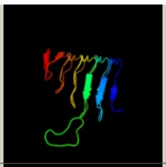
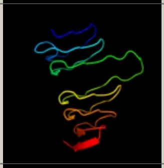
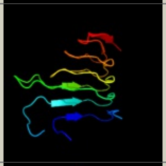
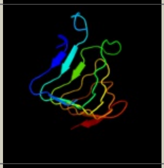
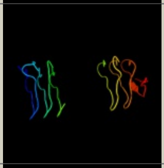
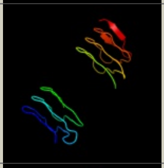
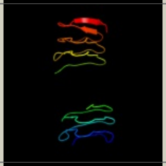
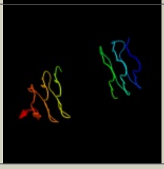
| 12 | d1krra_ | Alignment |  | 99.9 | 30 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Galactoside acetyltransferase-like |
| 13 | d1mr7a_ | Alignment |  | 99.9 | 25 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Galactoside acetyltransferase-like |
| 14 | c3cj8B_ | Alignment |  | 99.9 | 38 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2-carboxylate n-<br>**PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583 |
| 15 | c3eevC_ | Alignment |  | 99.9 | 19 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase;<br>**PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor |
| 16 | d1xata_ | Alignment |  | 99.9 | 26 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Galactoside acetyltransferase-like |
| 17 | c3r0sA_ | Alignment |  | 99.9 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o-<br>**PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni |
| 18 | d1j2za_ | Alignment |  | 99.9 | 22 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**UDP N-acetylglucosamine acyltransferase |
| 19 | c3i3aC_ | Alignment |  | 99.9 | 21 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-<br>**PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa |
| 20 | d2jf2a1 | Alignment |  | 99.9 | 22 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**UDP N-acetylglucosamine acyltransferase |
| 21 | c3jqyB_ | Alignment | not modelled | 99.9 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase;<br>**PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo |
| 22 | c2wlgA_ | Alignment | not modelled | 99.9 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase;<br>**PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy |
| 23 | c2iu9C_ | Alignment | not modelled | 99.9 | 27 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine<br>**PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii) |
| 24 | c3mqhD_ | Alignment | not modelled | 99.9 | 35 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase;<br>**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 |
| 25 | d3bswa1 | Alignment | not modelled | 99.9 | 20 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**PglD-like |
| 26 | d1g97a1 | Alignment | not modelled | 99.9 | 25 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**GlmU C-terminal domain-like |
| 27 | c3fsbB_ | Alignment | not modelled | 99.9 | 43 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**qdtc;<br>**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 |

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| 28 | c1hm8A_ | Alignment | not modelled | 99.8 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase;<br>**PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a |
| 29 | c3pmoA_ | Alignment | not modelled | 99.8 | 27 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase;<br>**PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution |
| 30 | c2v0hA_ | Alignment | not modelled | 99.8 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bifunctional protein glmu;<br>**PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu) |
| 31 | d2oi6a1 | Alignment | not modelled | 99.8 | 28 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**GlmU C-terminal domain-like |
| 32 | c3eh0C_ | Alignment | not modelled | 99.8 | 30 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-<br>**PDBTitle:** crystal structure of lpxd from escherichia coli |
| 33 | c2oi6A_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bifunctional protein glmu;<br>**PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4 |
| 34 | c3eg4A_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-<br>**PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308 |
| 35 | c3ixcA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hexapeptide transferase family protein;<br>**PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum |
| 36 | d3tdta_ | Alignment | not modelled | 99.8 | 16 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD |
| 37 | d1v3wa_ | Alignment | not modelled | 99.7 | 24 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**gamma-carbonic anhydrase-like |
| 38 | d1xhda_ | Alignment | not modelled | 99.7 | 26 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**gamma-carbonic anhydrase-like |
| 39 | c3r1wA_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library |
| 40 | c3fsyC_ | Alignment | not modelled | 99.7 | 26 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase;<br>**PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis |
| 41 | c3r3rA_ | Alignment | not modelled | 99.7 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ferripyochelin binding protein;<br>**PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica |
| 42 | c2ggqA_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate<br>**PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii |
| 43 | c3c8vA_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative acetyltransferase;<br>**PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution |
| 44 | c1qreA_ | Alignment | not modelled | 99.4 | 24 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila |
| 45 | d1qrea_ | Alignment | not modelled | 99.4 | 24 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**gamma-carbonic anhydrase-like |
| 46 | d2f9ca1 | Alignment | not modelled | 99.2 | 14 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**YdcK-like |
| 47 | c2rijA_ | Alignment | not modelled | 99.2 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative 2,3,4,5-tetrahydropyridine-2-carboxylate n-<br>**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 |
| 48 | c2qkxA_ | Alignment | not modelled | 99.1 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bifunctional protein glmu;<br>**PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate |
| 49 | c3d98A_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bifunctional protein glmu;<br>**PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form |
| 50 | d1yp2a1 | Alignment | not modelled | 99.0 | 16 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**GlmU C-terminal domain-like |

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| 51 | c3kwdA_ | Alignment | not modelled | 99.0 | 20 | **PDB header:**lyase, protein binding, photosynthesis<br>**Chain:** A: **PDB Molecule:**carbon dioxide concentrating mechanism protein;<br>**PDBTitle:** inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1 |
| 52 | d1fxja1 | Alignment | not modelled | 99.0 | 27 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**GlmU C-terminal domain-like |
| 53 | c1yp3C_ | Alignment | not modelled | 98.8 | 14 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small<br>**PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp |
| 54 | c1fwyA_ | Alignment | not modelled | 98.7 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase;<br>**PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac |
| 55 | c3brkX_ | Alignment | not modelled | 98.5 | 14 | **PDB header:**transferase<br>**Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase;<br>**PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens |
| 56 | d2icya1 | Alignment | not modelled | 30.7 | 34 | **Fold:**Single-stranded left-handed beta-helix<br>**Superfamily:**Trimeric LpxA-like enzymes<br>**Family:**GlmU C-terminal domain-like |
| 57 | d2z1ca1 | Alignment | not modelled | 6.4 | 21 | **Fold:**OB-fold<br>**Superfamily:**HupF/HypC-like<br>**Family:**HupF/HypC-like |
| 58 | c1dvaY_ | Alignment | not modelled | 5.8 | 30 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** Y: **PDB Molecule:**peptide e-76;<br>**PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia |
| 59 | c1dvaX_ | Alignment | not modelled | 5.8 | 30 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** X: **PDB Molecule:**peptide e-76;<br>**PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia |