Phyre2

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Description	P07464
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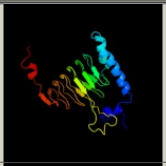
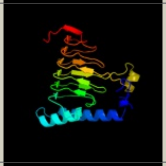
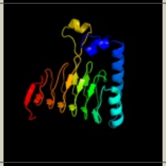
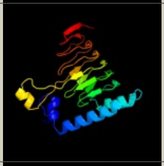
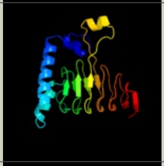
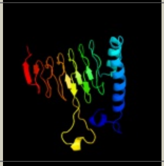
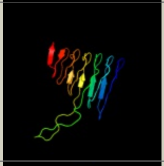
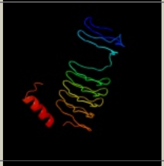
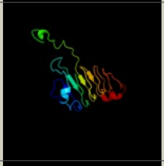
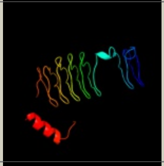
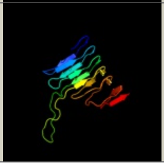
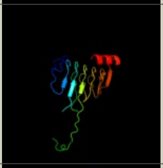
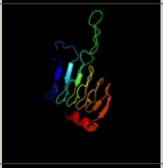
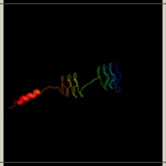
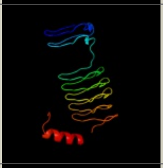
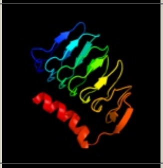
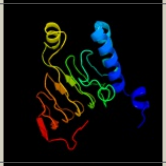
Unique Job ID	7ca74f9045f34c5c

Detailed template information

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

12	c3cj8B_	Alignment		100.0	28	**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
13	d1xata_	Alignment		99.9	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
14	c3eevC_	Alignment		99.9	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
15	c2iu9C_	Alignment		99.9	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
16	d1j2za_	Alignment		99.9	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
17	d2jf2a1	Alignment		99.9	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
18	c3ixcA_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
19	d1t3da_	Alignment		99.9	25	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
20	c1t3dB_	Alignment		99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
21	d3bswa1	Alignment	not modelled	99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
22	d1ssqa_	Alignment	not modelled	99.9	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
23	c3mqhD_	Alignment	not modelled	99.9	24	**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
24	d1v3wa_	Alignment	not modelled	99.9	22	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
25	c3eh0C_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
26	c3mc4A_	Alignment	not modelled	99.9	24	**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
27	c3pmoA_	Alignment	not modelled	99.9	25	**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

28	c3r3rA_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
29	d1g97a1	Alignment	not modelled	99.9	27	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
30	d1xhda_	Alignment	not modelled	99.9	28	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
31	c3fsbB_	Alignment	not modelled	99.9	32	**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
32	c3r1wA_	Alignment	not modelled	99.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
33	c1hm8A_	Alignment	not modelled	99.9	28	**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
34	c3q1xA_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
35	d2oi6a1	Alignment	not modelled	99.9	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
36	c3f1xA_	Alignment	not modelled	99.8	24	**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.
37	c2v0hA_	Alignment	not modelled	99.8	23	**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)
38	c3eg4A_	Alignment	not modelled	99.8	18	**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
39	d3tdta_	Alignment	not modelled	99.8	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD
40	c2oi6A_	Alignment	not modelled	99.8	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
41	c3c8vA_	Alignment	not modelled	99.8	20	**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
42	c3kwdA_	Alignment	not modelled	99.8	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
43	c3fsyC_	Alignment	not modelled	99.7	22	**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
44	d1qrea_	Alignment	not modelled	99.7	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
45	c1qreA_	Alignment	not modelled	99.7	21	**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
46	c2ggqA_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
47	c2rijA_	Alignment	not modelled	99.4	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
48	d2f9ca1	Alignment	not modelled	99.3	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
49	d1yp2a1	Alignment	not modelled	99.2	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
						Fold: Single-stranded left-handed beta-helix

50	d1fxja1	Alignment	not modelled	99.2	22	**Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
51	c2qkxA_	Alignment	not modelled	99.1	17	**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
52	c3d98A_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
53	c1fwyA_	Alignment	not modelled	98.9	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
54	c1yp3C_	Alignment	not modelled	98.8	15	**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
55	c3brkX_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	d2icya1	Alignment	not modelled	33.8	28	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
57	c1xqhE_	Alignment	not modelled	12.9	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
58	c1h3iB_	Alignment	not modelled	11.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone h3 lysine 4 specific methyltransferase; **PDBTitle:** crystal structure of the histone methyltransferase set7/9
59	d1ihwa_	Alignment	not modelled	9.8	27	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
60	d1ex4a1	Alignment	not modelled	9.8	27	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
61	d1bg3a2	Alignment	not modelled	8.2	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
62	d2g46a1	Alignment	not modelled	7.9	15	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Viral histone H3 Lysine 27 Methyltransferase
63	d1v4sa2	Alignment	not modelled	7.4	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
64	d1c6vx_	Alignment	not modelled	6.9	19	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
65	c1c6vX_	Alignment	not modelled	6.9	19	**PDB header:**dna binding protein **Chain:** X: **PDB Molecule:**protein (siu89134); **PDBTitle:** siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
66	d1ig8a2	Alignment	not modelled	6.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
67	c3gt2A_	Alignment	not modelled	6.5	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
68	c2z9fC_	Alignment	not modelled	6.5	36	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**cellulose synthase operon protein d; **PDBTitle:** crystal structure of axcesd protein from acetobacter xylinum
69	d1bg3a4	Alignment	not modelled	6.3	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase