












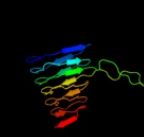

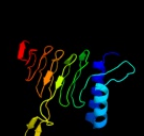

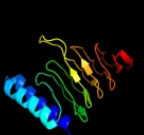













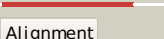
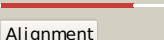



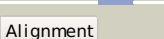
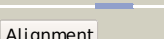
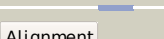


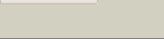
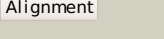
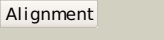
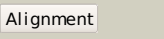
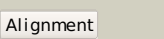
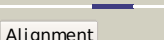



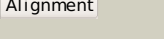
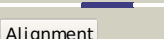


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ocxa_	 Alignment		100.0	100	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
2	c2ic7A_	 Alignment		100.0	67	PDB header: transferase Chain: A: PDB Molecule: maltose transacetylase; PDBTitle: crystal structure of maltose transacetylase from2 geobacillus kaustophilus
3	c3fttA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sacol2570; PDBTitle: crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
4	d1krra_	 Alignment		100.0	43	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
5	c3srtB_	 Alignment		100.0	56	PDB header: transferase Chain: B: PDB Molecule: maltose o-acetyltransferase; PDBTitle: the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
6	c3ectA_	 Alignment		100.0	40	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		99.9	30	PDB header: transferase Chain: B: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystal strucutre of the polysia specific acetyltransferase neuo
8	d1t3da_	 Alignment		99.9	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
9	c1t3dB_	 Alignment		99.9	21	PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a
10	c3cj8B_	 Alignment		99.9	32	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
11	d1xata_	 Alignment		99.9	33	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like

12	d1mr7a_	Alignment		99.9	30	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
13	c3eevC_	Alignment		99.9	38	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
14	d1ssqa_	Alignment		99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
15	c2wlgA_	Alignment		99.9	32	PDB header: transferase Chain: A: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
16	c3mc4A_	Alignment		99.9	27	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
17	d2jf2a1	Alignment		99.9	30	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
18	d3bswa1	Alignment		99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: PglD-like
19	c3r0sA_	Alignment		99.9	26	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
20	d1j2za_	Alignment		99.9	30	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
21	c3i3aC_	Alignment	not modelled	99.9	24	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
22	c3mqhD_	Alignment	not modelled	99.9	28	PDB header: transferase Chain: D: PDB Molecule: lipopolysaccharides biosynthesis acetyltransferase; PDBTitle: crystal structure of the 3-n-acetyl transferase wlbfb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
23	c2iu9C_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
24	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
25	c3ixcA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: hexapeptide transferase family protein; PDBTitle: crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
26	c3q1xA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
27	c3eh0C_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
						PDB header: transferase Chain: B: PDB Molecule: qdtc;

28	c3fsbB	Alignment	not modelled	99.9	36	PDBTitle: crystal structure of qdct, 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
29	c3pmoA	Alignment	not modelled	99.9	16	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
30	d1v3wa	Alignment	not modelled	99.8	27	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
31	c3f1xA	Alignment	not modelled	99.8	18	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.
32	d2oi6a1	Alignment	not modelled	99.8	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Glmu C-terminal domain-like
33	c1hm8A	Alignment	not modelled	99.8	26	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
34	c3r3rA	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
35	c3r1wA	Alignment	not modelled	99.8	24	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
36	c3eg4A	Alignment	not modelled	99.8	16	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
37	c2v0hA	Alignment	not modelled	99.8	22	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 uridylyltransferase (glmu)
38	d1xhda	Alignment	not modelled	99.8	25	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
39	c2oi6A	Alignment	not modelled	99.8	24	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcna, coa and glcn-1-po4
40	d3tdta	Alignment	not modelled	99.7	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
41	c3c8vA	Alignment	not modelled	99.7	16	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	d1qrea	Alignment	not modelled	99.6	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
43	c1qreA	Alignment	not modelled	99.6	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
44	c3fsyC	Alignment	not modelled	99.6	25	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
45	c2ggqA	Alignment	not modelled	99.6	20	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
46	c3kwdA	Alignment	not modelled	99.5	21	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
47	d2f9ca1	Alignment	not modelled	99.3	13	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: YdcK-like
48	d1fxja1	Alignment	not modelled	99.1	16	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Glmu C-terminal domain-like
49	d1yp2a1	Alignment	not modelled	99.0	20	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Glmu C-terminal domain-like
50	c2qkxA	Alignment	not modelled	99.0	13	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate

51	c3d98A	 Alignment	not modelled	99.0	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
52	c2rijA	 Alignment	not modelled	99.0	17	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
53	c1fwyA	 Alignment	not modelled	98.8	14	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcna
54	c3brkX	 Alignment	not modelled	98.7	15	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyllyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
55	c1yp3C	 Alignment	not modelled	98.6	11	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
56	d1ihwa	 Alignment	not modelled	22.6	42	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
57	d2icya1	 Alignment	not modelled	21.0	31	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
58	d1ex4a1	 Alignment	not modelled	21.0	42	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
59	c2z9fC	 Alignment	not modelled	17.1	53	PDB header: biosynthetic protein Chain: C: PDB Molecule: cellulose synthase operon protein d; PDBTitle: crystal structure of axcesd protein from acetobacter xylinum
60	c1c6vX	 Alignment	not modelled	13.1	42	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)
61	d1c6vx	 Alignment	not modelled	13.1	42	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
62	c3gt2A	 Alignment	not modelled	12.5	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
63	d2g46a1	 Alignment	not modelled	10.9	13	Fold: beta-clip Superfamily: SET domain Family: Viral histone H3 Lysine 27 Methyltransferase
64	c3ebkA	 Alignment	not modelled	9.5	33	PDB header: allergen Chain: A: PDB Molecule: allergen bla g 4; PDBTitle: crystal structure of major allergens, bla g 4 from2 cockroaches
65	c1h3lB	 Alignment	not modelled	7.0	17	PDB header: transferase Chain: B: PDB Molecule: histone h3 lysine 4 specific methyltransferase; PDBTitle: crystal structure of the histone methyltransferase set7/9
66	c1l4aE	 Alignment	not modelled	6.4	50	PDB header: endocytosis/exocytosis Chain: E: PDB Molecule: synaphin a; PDBTitle: x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
67	d2veaa2	 Alignment	not modelled	5.8	27	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain
68	c1xqhE	 Alignment	not modelled	5.7	18	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
69	c3smtA	 Alignment	not modelled	5.6	14	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd3; PDBTitle: crystal structure of human set domain-containing protein3
70	d1v97a4	 Alignment	not modelled	5.3	6	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
71	d3c2wa2	 Alignment	not modelled	5.3	30	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain