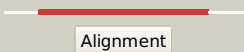
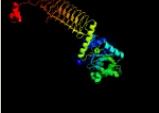
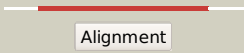

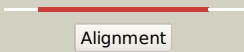

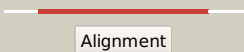

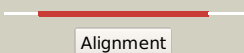

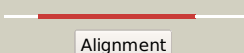

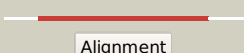





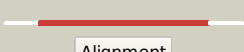

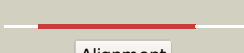








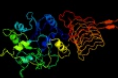



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1018c_glmU_1136577_1138064
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	deed5b3f221e37e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d8vA_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
2	c1hm8A_	 Alignment		100.0	42	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
3	c3foqA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
4	c2v0hA_	 Alignment		100.0	40	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)
5	c2oi6A_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
6	c3d98A_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
7	c5vmkB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
8	c2qkxA_	 Alignment		100.0	100	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
9	c5b04I_	 Alignment		100.0	15	PDB header: translation Chain: I: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
10	c1yp3C_	 Alignment		100.0	17	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
11	c1fwyA_	 Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcnac

12	c6jlwJ_	Alignment		100.0	13	PDB header: translation Chain: J; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
13	c6i3mG_	Alignment		100.0	14	PDB header: translation Chain: G; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
14	c5l6sF_	Alignment		100.0	16	PDB header: transferase Chain: F; PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
15	c2gggA_	Alignment		100.0	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
16	c3brkX_	Alignment		100.0	15	PDB header: transferase Chain: X; PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
17	c5b04F_	Alignment		100.0	13	PDB header: translation Chain: F; PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
18	c6qq2F_	Alignment		100.0	16	PDB header: translation Chain: F; PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
19	c6ezoJ_	Alignment		100.0	14	PDB header: membrane protein Chain: J; PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
20	c6ezoF_	Alignment		100.0	20	PDB header: membrane protein Chain: F; PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
21	d1lwva_	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
22	d1g97a2	Alignment	not modelled	100.0	43	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
23	d1h5ra_	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
24	d1fxoa_	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
25	d1iina_	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
26	c2pa4B_	Alignment	not modelled	100.0	26	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
27	d2oi6a2	Alignment	not modelled	100.0	40	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
28	d1mc3a_	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase

29	c5i1fA_	 Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
30	c2ux8G_	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
31	c2e3dB_	 Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
32	d1yp2a2	 Alignment	not modelled	100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
33	c3pnnA_	 Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
34	c6b5kA_	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
35	c2cu2A_	 Alignment	not modelled	100.0	22	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
36	c2x5sB_	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
37	c4aa7A_	 Alignment	not modelled	100.0	38	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e.coli glmu in complex with an antibacterial inhibitor
38	c2iu9C_	 Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
39	c3jukA_	 Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
40	c4e75A_	 Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-acylglucosamine n-acyltransferase; PDBTitle: structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
41	c3t57A_	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
42	c4e6tA_	 Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
43	c3i3aC_	 Alignment	not modelled	100.0	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
44	d1j2za_	 Alignment	not modelled	100.0	13	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
45	c3pmoA_	 Alignment	not modelled	100.0	14	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
46	c3eh0C_	 Alignment	not modelled	100.0	14	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
47	c4r36A_	 Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]-udp-n- PDBTitle: crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
48	c3hl3A_	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
49	c4evwB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: nucleoside-diphosphate-sugar pyrophosphorylase; PDBTitle: crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesg) target vcr193.
50	d2oi6a1	Alignment	not modelled	100.0	39	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
		Alignment				Fold: Single-stranded left-handed beta-helix

51	d2jf2a1	Alignment	not modelled	100.0	18	Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
52	c5jxC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
53	c5f42B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
54	c4eqyC_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of acyl-[acyl-carrier-protein]-udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
55	d1tzfa_	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
56	d2cu2a2	Alignment	not modelled	100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
57	d1g97a1	Alignment	not modelled	100.0	39	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
58	c5xhwA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
59	c3r0sA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
60	c4jd0A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
61	c3fsbB_	Alignment	not modelled	100.0	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
62	d1vica_	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
63	c5dg3D_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glnac
64	c4mndA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
65	c4y7uA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structural analysis of muru
66	c3oamD_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
67	c5e3pA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of dapd from corynebacterium glutamicum
68	d1jyka_	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
69	c1jvIC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
70	c4xwiA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
71	c2qh5B_	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
72	c2xwIB_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
73	c3r5dA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: tetrahydrodipicolinate n-succinyletransferase; PDBTitle: pseudomonas aeruginosa dapd (pa3666) apoprotein
						PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate

74	c5ddtA	Alignment	not modelled	99.9	19	cytidyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
75	d1i52a	Alignment	not modelled	99.9	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
76	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 wlb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
77	d1vpaa	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
78	c3vbnA	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: galactoside o-acetyltransferase; PDBTitle: crystal structure of the d94a mutant of antd, an n-acyltransferase2 from bacillus cereus in complex with dtdp and coenzyme a
79	c4mzuG	Alignment	not modelled	99.9	20	PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
80	c3polA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
81	d1vh1a	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
82	c2xmhB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
83	d1h7ea	Alignment	not modelled	99.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
84	c3tqdA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
85	c3jqyB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystal structure of the polysia specific acetyltransferase neuo
86	c3c8vA	Alignment	not modelled	99.9	17	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
87	c6mfkA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis
88	d1vh3a	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
89	c6i7tl	Alignment	not modelled	99.9	12	PDB header: translation Chain: I: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eif2b:eif2 complex
90	d1mr7a	Alignment	not modelled	99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
91	d1qrea	Alignment	not modelled	99.9	19	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
92	c1qreA	Alignment	not modelled	99.9	19	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
93	c4ea8A	Alignment	not modelled	99.9	30	PDB header: transferase Chain: A: PDB Molecule: perosamine n-acetyltransferase; PDBTitle: x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-acetylperosamine at 1 angstrom resolution
94	c2y6pC	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the kdo-2 cytidyltransferase kdsb
95	d1w55a1	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
96	c3cj8B	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
97	c2wlnA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: polysialic acid o-acetyltransferase;

97	c2w1gA_	Alignment	not modelled	99.9	10	PDBTitle: crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy PDB header: transferase
98	c4e8lC_	Alignment	not modelled	99.9	16	Chain: C: PDB Molecule: virginiamycin a acetyltransferase; PDBTitle: crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
99	c3f1cB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
100	c4kt7A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
101	c4mybA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd)
102	d1krra_	Alignment	not modelled	99.9	25	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
103	d1eyra_	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
104	c4m98A_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: pilin glycosylation protein; PDBTitle: acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090
105	c2ic7A_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: A: PDB Molecule: maltose transacetylase; PDBTitle: crystal structure of maltose transacetylase from geobacillus2 kaustophilus
106	d1xata_	Alignment	not modelled	99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
107	c3kwcD_	Alignment	not modelled	99.9	27	PDB header: lyase, protein binding, photosynthesis Chain: D: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: oxidized, active structure of the beta-carboxysomal gamma-carbonic2 anhydrase, ccmm
108	c3eg4A_	Alignment	not modelled	99.9	14	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
109	c3srtB_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: B: PDB Molecule: maltose o-acetyltransferase; PDBTitle: the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
110	c3r3rA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
111	c3okrA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
112	d1qwja_	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
113	c3ectA_	Alignment	not modelled	99.8	23	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
114	c3fttA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sac02570; PDBTitle: crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus
115	d1t3da_	Alignment	not modelled	99.8	23	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
116	c1t3dB_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a
117	c5ux9D_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: D: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114
118	c3r8yD_	Alignment	not modelled	99.8	25	PDB header: transferase Chain: D: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase
119	d1ocxa_	Alignment	not modelled	99.8	20	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
120	c2vshB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae