Supporting Information for:

Detecting glucose fluctuations in the *Campylobacter jejuni* N-glycan structure

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Experimental Methods

Oligonucleotides used in this study are listed in Table S1. Bacterial strains and plasmids are listed in Table S2. *Campylobacter* was routinely grown in Brain-Heart Infusion (BHI) medium (BD Biosciences) under microaerobic conditions (10% CO_2, 5% O_2, 85% N_2) at 37 °C. *E. coli* was grown on Luria-Bertani (LB) or 2x Yeast-Tryptone (YT) agar at 37 °C. Growth media were supplemented with antibiotics, as required, at the following final concentrations: spectinomycin (100 μg/ml), chloramphenicol (30 μg/ml) and kanamycin (25 μg/ml).

Whole cell lysates, SDS-PAGE and western blots. Bacterial whole cell lysates were prepared as described previously[1]. Protein concentrations were determined with the PierceTM BCA protein Assay kit (Thermo Scientific) or the DC Bradford assay kit (Biorad) and bovine serum albumin at various standard concentrations. Protein samples were analyzed immediately or stored at -20ºC until further use. For western blot analyses, proteins were separated on standard 10-12.5% Tris-Glycine SDS-PAGE gels and transferred to polyvinylidene fluoride (PVDF) membranes (BioRad) as described[2]. If appropriate, duplicate SDS-PAGE gels were stained with Coomassie Blue as a loading control. Rabbit-anti-His (1:2000) (Rockland), anti-*Cj*-N-glycan (R1, 1:7500)[2] or rabbit-anti-CmeA (1:5000)[3] served as the primary antibody, and alkaline phosphatase-labelled goat-anti-rabbit IgG (1:2000) (Santa Cruz Biotechnology) or HRP-labelled goat-anti-rabbit IgG (1:3000) (Thermo Fisher) served as the secondary antibody. Bands were either visualized directly on the membrane with nitro-blue tetrazolium chloride and 5-bromo-4-chloro-3'-indolyphosphate p-toluidine salt alkaline phosphatase substrate solution (NBT/BCIP, Roche), or used the ClarityTM Western ECL substrate (BioRad) followed by image capturing on a ChemiDoc XRS+ system (BioRad).

Mass spectrometry. Liquid chromatography-mass spectrometric (LC-MS)-based analyses of CmeA glycopeptides were carried out as follows: Whole cell lysates were separated by 10% SDS-PAGE and stained by Coomassie Blue. A gel slice containing CmeA (45 kDa region) was cut out, the gel pieces with proteins were cut into small pieces of about 1 mm^2, and the gel pieces were de-stained by 1:1 digestion buffer (50 mM aq. ammonium bicarbonate) - acetonitrile followed by 100 % acetonitrile. The proteins were reduced by adding 100 µl of DTT solution (25 mM) to the gels, carbamidomethylated by adding 100 µl of iodoacetamide solution (25 mM) and finally washed with acetonitrile. 100 µl of digestion buffer was added to the gel pieces and proteins were digested by adding 5 µL sequencing-grade trypsin (Promega, 0.4 µg/µl) and incubated at 37 ºC for 12 h. The digested peptides were extracted by 1:2 5 % formic acid in water-acetonitrile. The digests were dried under speed-vac. The peptides and glycopeptides were subsequently re-dissolved in solvent A (0.1% formic acid in water) and stored at -30 ºC until analysis by nano-LC-MS/MS.

Data acquisition of protein digest samples using nano-LC-MS/MS. The peptides were analyzed on an Orbitrap Fusion Tribrid mass spectrometer (Thermo Scientific) equipped with a nanospray ion source with CID, HCD and ETD fragmentation options and connected to a Dionex binary solvent system. Pre-packed nano-LC columns of 15 cm length with 75 µm internal diameter (id) and filled with 3 µm C18 material (reverse phase) were used for chromatographic separation of samples. After the precursor ion scan at 120,000 resolution in the Orbitrap analyzer, precursors at a time frame of 3 sec were selected for subsequent fragmentation using HCD at a normalized collision energy of 30. An HCD product triggered the CID program, where CID fragmentation occurs based on the presence of glycan oxonium ions in the HCD fragmentation of the same peptide. The threshold for triggering an MS/MS event on the Orbitrap was set to 500 counts.

Charge state screening was enabled, and precursors with an unknown charge state or a charge state of +1 were excluded (positive ion mode). Dynamic exclusion was enabled (exclusion duration of 30 s). The fragment ions were analyzed on the Orbitrap for HCD and CID at 30,000 resolution.

Analysis of glycopeptides. The LC-MS/MS spectra of trypsin-digested proteins were analyzed manually for the glycopeptides with the support of Xcalibur software. Since the exact amino acid sequence of the protein was not available, only the attached glycans were sequenced. The HCD and CID MS2 spectra of the glycopeptides were evaluated for the glycan neutral loss pattern, oxonium ions and the glycopeptide fragmentations to assign the presence of glycans in the glycopeptides and to determine the glycan sequence.

Sequence analyses and homology modelling. Survey and analysis of available *pglI* sequences: 1069 *C. jejuni* and *C. coli pglI* gene sequences were downloaded from PubMLST (https://pubmlst.org/organisms/campylobacter-jejunicoli). The allele sequences were initially aligned using MegAlign (ver. 15.3; DNASTAR) to identify alleles yielding identical protein sequences. The *pglI* allele list was subsequently culled to 701 alleles that encode unique PglI proteins. The culled list was translated and aligned using MUSCLE in Geneious (ver. 2020.0.5; https://www.geneious.com/). Aligned residues were color-coded according to a 90% consensus threshold filter. Individual PglI sequences were aligned using the NCBI-Blast server (https://blast.ncbi.nlm.nih.gov). Multiple sequence alignments of individual *Cj* and GEMS PglI sequences were generated with ClustalW and BOXshade (http://www.ch.embnet.org/). Homology models were generated by I-TASSER[4] using the crystal structures of several GT-2 family members (6HLJ, 5HEA and 2Z86) as templates that produced structures with reasonable C-scores and a

central cleft suitable for accommodating the hexasaccharide acceptor. The structure of the acceptor hexasaccharide was derived from the NMR structures calculated from the *Cj*-AcrA(CmeA)-heptasaccharide conjugate[5] by deleting the structure of the protein and the Glc residue at the branch point. The *Cj*-hexasaccharide structure was manually docked to position the 3-OH of the fourth residue within 4 Å of the anomeric carbon of the expected location of the UDP-Glc residue.

Introduction of point mutations in PglI. cDNA (for GEMS strain *pglI*) or pACYC184$_{pgl}$ plasmid DNA (for *Cj*81116 *pglI*) served as a template; the *pglI* forward oligonucleotide was used in combination with a reverse primer to introduce nucleotide exchanges at the desired nt positions within the *pglI* genes (1st PCR product). The reverse *pglI* oligonucleotide was used in combination with a universal phosphorylated forward oligonucleotide. The 1st product was digested with *Bam*HI, the second PCR product was digested with *Xho*I and the ligation reaction contained both digested PCR products and plasmid pCE111/28 cut with *Bam*HI and *Xho*I. After ligation and transformation of *E. coli* DH5α*,* candidates carrying the full length *pglI* genes were identified by restriction analyses and the introduction of each point mutation was confirmed by DNA sequencing of 3 candidates for each mutation.

Construction and verification of an *E. coli* -based live vaccine strain for the use in mammals. For stable expression of the *pgl* operon in the chromosome of the attenuated enterotoxigenic *E. coli* ACAM2025[6], we created an operon that contains the minimal set of genes required for N-glycan expression. First, the *pglB* gene was removed from plasmid pACYC184$_{pgl}$ (p*pgl*), Using p*pgl* as a template, one PCR product (*gne-pglH*) was amplified with oligonucleotides gne-SalI-F and pglH-SbfI-R, using the plasmid-borne *Sal*I site upstream of *gne* and introducing a unique *Sbf*I

site after the stop codon of *pglH*. A second PCR product was generated with oligonucleotides pglA-SbfI-F and pglG-BamHI-R to amplify *pglA* to *pglG*, taking advantage of the *Bam*HI site on the plasmid downstream of *pglG* and introducing a *Sbf*I sequence upstream of *pglA*. Digested PCR products were inserted into plasmid pACYC184 cut with *Bam*HI and *Sal*I in a 3-fragment ligation reaction, resulting in the plasmid p*pgl*Δ*pglB*. For the insertion of the removable selection marker (a kanamycin (*kan*) cassette flanked by FRT sites), a unique *Xho*I restriction site was generated between *pglK* and *pglH.* PCR products with oligonucleotide combinations pglK-XhoI-R, gne-SalI-F, pglH-XhoI-F, and pglH-SbfI-R were used to amplify *gne-pglK* and *pglH* from the template plasmid p*pgl* Δ*pglB*. *Sal*I-*Xho*I-digested *gne-pglK* and *Xho*I-*Sbf*I-digested *pglH* PCR products were inserted (3-fragment ligation reaction) into *Sal*I-*Sbf*I digested p*pgl*Δ*pglB*, resulting in the plasmid p*pgl*Δ*pglB-Xho*I. Next, the *kan* cassette flanked by FRT sites was PCR-amplified from plasmid pKD4 using the oligonucleotides P1-pKD4-XhoI and P2_star-pKD4-XhoI, that introduced *Xho*I sites in the 3' and 5' ends. The amplicon was then digested with *Xho*I and inserted into the *Xho*I-linearized p*pgl*Δ*pglB-Xho*I plasmid. One positive candidate plasmid, where the kan cassette is transcribed in the same orientation as the *pgl* genes, was named p*pgl*-kan. To remove the upstream region of *gne* and genes *pglC* to *pglG*, a PCR product encompassing *gne-pglK-kan-pglHIJA* was generated with oligonucleotides gne-BamHI-F1 and pglA-BamHI-R and inserted into *Bam*HI-digested plasmid pACYC184.

The targeted insertion locus, the *wzy* (*rfc*) gene of ACAM2025, was amplified from chromosomal DNA with oligonucleotides ACAM2025-BamHI-F and ACAM2025-EcoRI-R and ligated into *Bam*HI-*Eco*RI digested pBlueskriptSK(+). For the insertion of the minimal, *kan* cassette containing *pgl* operon, the unique *Bam*HI compatible *Bgl*II site in $wzy^{ACAM2025}$ was used to insert PCR amplified *gne-pglK-kan-pglHIJA*. After ligation and selection for Kan and Amp resistant

colonies, one candidate in which the *pgl* genes are transcribed in the same orientation as the *wzy*^{ACAM2025} gene was (after linearization with *Eco*RV) used for integration into the chromosome of ACAM2025 following the method of Datsenko and Wanner[7]. After the selection procedure, the correct insertion of the construct was verified by PCR with *pgl*-gene-specific oligonucleotides and primers that hybridize outside of the recombination event. Expression of the Lipid-A-*Cj*-N-glycan compound was further verified by western blotting with *Cj*-N-glycan-specific (R1) antiserum as described[8].

Table S1 Oligonucleotides used in this study

Oligo	Sequence 5' to 3'	use
pglI-81116-BamHI-F	ATA**GGATCC**TAAGAAGGAGATATACATATGCCTAA ACTTTCTGTTATAGTGC, *Bam*HI	PCR, cloning of *pglI* (81116 and GEMS) in pCE111/28
81116-pglI-XhoI-R_short	ATAT**CTCGAG**CTAATTTTTGCATAAAGCCACCCG, *Xho*I	PCR, cloning of *pglI* (81116 and GEMS) in pCE111/28
M13 forward (-20)	GTAAAACGACGGCCAGT	sequencing
M13 reverse (-27)	CAGGAAACAGCTATGAC	sequencing
pglI mut F-universal-P	/5Phos/GCTTTTATCTGGGGCTTTAAGTACCTTGATGC	PCR, generation of *pglI* point mutants
1D7 insert D-R	TCATCATCATCATCTAAAAAAGTTACAAACTCGC	PCR, insert D94 in 1D7; insert D94 and I88T in 1J2 *pglI*
1J2 I to T no D-R	TCATCATCATCTAAAAAAGTTACAAACTCGC	PCR, I88T in 1J2 *pglI*
1J2 insert D-R	TCATCATCATCATCTAAAAAAATTACAAACTCGC	PCR, insert D94 in 1J2 *pglI*
pglI wt T to I delete D-R	TCATCATCATCTAAAAAAATTACAAACTCGC	PCR, delete D94, T88I in 81116 *pglI*
pglI wt D to A-R	TCAGCATCATCATCTAAAAAAGTTACAAACTCGC	PCR, D94A in 81116 *pglI*
pglI wt D to E-R	TCTTCATCATCATCTAAAAAAGTTACAAACTCGC	PCR, D94E in 81116 *pglI*
pglI wt T to I-R	TCATCATCATCATCTAAAAAAATTACAAACTCGC	PCR, T88I in 81116 *pglI*
pglI wt no D-R	TCATCATCATCTAAAAAAGTTACAAACTCGC	PCR, delete D94 in 81116 *pglI*
ACAM 2025-BamHI-F	ATGGATCCTGCTCTGCACGCTGTTTATTGCCACGCT GACC, *Bam*HI	PCR, amplify *wzy* of ACAM2025
ACAM 2025-EcoRI-R	TT**GAATTC**TTTATGAATGAGTCCGGCGCTTTCAAA AAGC, *Eco*R1	PCR, amplify *wzy* of ACAM2025
2025-outside-F	TTCTTTAGCCCTAACTATCTACAAGG	PCR, confirm integration
2025-outside-R	TTTTCAGCATTAATGGCAACCAGCGTTC	PCR, confirm integration
pglA-F	AAATGCTGCCCAAGATGCTTTACAATACG	PCR, confirm integration
gne-R	TTAAAGTATGAGAACCTATATAACCTGC	PCR, confirm integration

Restriction sites (if present) are in bold and corresponding restriction enzymes are indicated; 5' phosphorylation is indicated by /5Phos

Table S2 Strains and plasmids used in this study

Strain	Genotype or relevant markers	Reference
Campylobacter		
C. jejuni (GEMS study)	*C. jejuni* wild-type isolates from symptomatic or asymptomatic children < 1 year of age from various locations (a complete list of GEMS strains is provided in the supplement, Table S3)	[9]
Cj-81-176	*C. jejuni* wild-type, clinical isolate	[10]
Cj-81-176 *pglB*::*kan*	*C. jejuni* 81-176 *pglB* mutant	[11]
Cj-11168	*C. jejuni* wild-type, clinical isolate	[12]
Cj-11168 *pglB*::*kan*	*C. jejuni* 11168 *pglB* mutant; Kan^R	[13]
Cj-11168 *pglI*::*kan*	*C. jejuni* 11168 *pglI* mutant; Kan^R	[14]
Cj-11168 *cmeA*::*cat*	*C. jejuni*-11168 *cmeA* mutant, Cm^R	[15]
E. coli		
DH5α	F-*endA1 hsdR17 supE44 thi-1 recA1* Δ(*argF-lacZYA*) *U169*(80d *lacZ* Δ *M15*) *gyrA96 λ*-	Invitrogen
CLM24	W3110, *ΔwaaL*	[16]
ACAM2025	O71:H_CFA/I _*astA* _*estA* _*aroC* _*ompC* _*ompF*::pLLTB	[6]
ACAM2025/*wzy*::*pgl*::*kan*	ACAM2025 with *pgl (gne-pglK*-FRT-*kan*-FRT-*pglHIJA)* inserted into *wzy* locus, Kan^R	This study
Plasmid		
pCE111/28	*C. jejuni-E. coli* expression vector with σ^{28} promoter from *flaA,* Cm^R	[17]
pIH18b	Constitutive expression of CmeA-His_6 of *C. jejuni* in *E. coli,* $Spec^R$	[18]
pBluescript II KS(+)	Cloning vector, pUC ori, Amp^R	Agilent
pACYC184	Cloning vector, P15A ori, Cm^R, Tet^R	[19]
pACYC184$_{pgl}$ (p*pgl)*	Plasmid pACYC184 containing the 16 kb *C. jejuni pgl* locus from *Cj*-81116, Cm^R	[3]
pACYC184$_{pgl}$ *pglI*::*kan, cat*-	p*pgl* with a kanamycin cassette inserted within *pglI* and *cat* cassette removed, Km^R	[20]
pCE111/28 *pglI*^{Cj81116}	*pglI* of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1J2}	*pglI* of *C. jejuni* GEMS 1J2 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1J5}	*pglI* of *C. jejuni* GEMS 1J5 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1D7}	*pglI* of *C. jejuni* GEMS 1D7 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1H2}	*pglI* of *C. jejuni* GEMS 1H2 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{Cj81116}ΔD94	*pglI* ΔD94 of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{Cj81116}T88I	*pglI* T88I of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{Cj81116}ΔD94/T88I	*pglI* ΔD94/T88I of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{Cj81116}D94A	*pglI* D94A of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{Cj81116}D94E	*pglI* D94E of *C. jejuni* 81116 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1D7}D94	*pglI* of *C. jejuni* GEMS 1D7 with D94 insertion cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1J2}D94	*pglI* of *C. jejuni* GEMS 1J2 with D94 insertion cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1J2}I88T	*pglI* I88T of *C. jejuni* GEMS 1J2 cloned into pCE111/28, Cm^R	This study
pCE111/28 *pglI*^{GEMS1J2}D94/I88T	*pglI* I88T of *C. jejuni* GEMS 1J2 with D94 insertion cloned into pCE111/28, Cm^R	This study

p*pgl* Δ*pglB*	p*pgl* with a deletion of *pglB,* Cm^R	This study
p*pgl* Δ*pglB-Xho*I	p*pgl* Δ*pglB* with *Xho*I site between *pglK* and *pglH,* Cm^R	This study
p*pgl*-Kan	p*pgl* Δ*pglB, Xho*I with Kan cassette (flanked by FRT sites) inserted between *pglK* and *pglH* (via *Xho*I), Cm^R	This study
p*pgl*gneK-kan-HIJA	PCR product containing *gne-pglK*-FRT-*kan*-FRT-*pglHIJA* inserted into pACYC184, Cm^R	This study
pBKS-*wzy*^{ACAM2025}	*wzy* (*rfc*) of ACAM2025 inserted into pBluescript II KS(+), Amp^R	This study
pBKS-*wzy*^{ACAM2025}-*pgl*-kanFRT	pBKS-*wzy* ^{ACAM2025} with PCR product *gne-pglK*-FRT-*kan*-FRT-*pglHIJA* inserted into *Bgl*II site of *wzy*^{ACAM2025}, Amp^R	This study
pKD4	FRT flanked kan cassette, template plasmid for PCR, Kan^R, Amp^R	[7]
pKD46	λ Red recombinase (γ , β, and exo from λ phage), *ara*C-*Para*B, Amp^R	[7]

Table S3 GEMS isolates

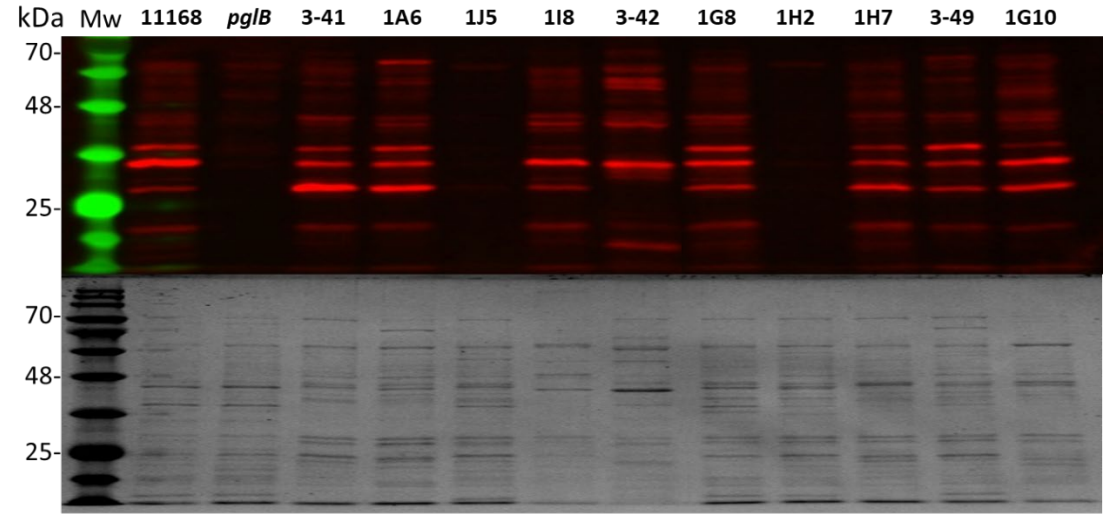
Designation[1]	Specimen ID	Site	Type	Campylobacter strain isolated
3 41	100801	The Gambia	Control	*C. coli*
1 A5	102878	The Gambia	Case	*C. jejuni*
1 A6	103067	The Gambia	Case	*C. jejuni*
1 J5	**103169**	**The Gambia**	**Control**	***C. jejuni***
1 I8	110498	The Gambia	Case	*C. jejuni*
1 J2	**120617**	**The Gambia**	**Control**	***C. jejuni***
3 42	121307	The Gambia	Case	*C. coli*
3 43	202388	Mali	Case	*C. jejuni*
1 A3	203886	Mali	Case	*C. jejuni*
3 44	204304	Mali	Case	*C. jejuni*
1 B2	204462	Mali	Case	*C. jejuni*
*1 A4	204464	Mali	Case	*E. coli*
1 H6	320256	Mozambique	Control	*C. jejuni*
1 F1	320435	Mozambique	Control	*C. jejuni*
1 G9	400526	Kenya	Case	*C. jejuni*
3 45	400679	Kenya	Case	*C. coli*
1 G8	400738	Kenya	Case	*C. jejuni*
3 46	400879	Kenya	Case	*C. coli*
1 A1	400956	Kenya	Case	*C. jejuni*
1 H2	**401022**	**Kenya**	**Control**	***C. jejuni***
1 H4	401051	Kenya	Control	*C. jejuni*
1 H3	402870	Kenya	Case	*C. jejuni*
1 H1	403205	Kenya	Case	*C. jejuni*
1 H7	403257	Kenya	Control	*C. jejuni*
3 49	403362	Kenya	Case	*C. coli*
1 H5	403385	Kenya	Case	*C. jejuni*

1 G10	403459	Kenya	Case	*C. jejuni*
3 47	403965	Kenya	Case	*C. coli*
1 A8	500287	India	Case	*C. jejuni*
1 B1	500429	India	Case	*C. jejuni*
3 48	500573	India	Control	*C. coli*
1 A9	503175	India	Control	*C. jejuni*
1 A10	503190	India	Control	*C. jejuni*
2 A7	503610	India	Case	*C. jejuni*
1 J6	503818	India	Case	*C. jejuni*
2 A6	504196	India	Control	*C. jejuni*
2 A3	504611	India	Case	*C. jejuni*
2 A9	504730	India	Control	*C. jejuni*
2 A2	504764	India	Control	*C. jejuni*
3 53	510333	India	Control	*C. coli*
2 A10	510831	India	Case	*C. jejuni*
2 B2	511171	India	Control	*C. jejuni*
1 J9	520016	India	Case	*C. jejuni*
1 J10	520188	India	Control	*C. jejuni*
2 B6	521162	India	Control	*C. jejuni*
1 F7	600021	Bangladesh	Case	*C. jejuni*
1 F6	600099	Bangladesh	Case	*C. jejuni*
1 G5	600883	Bangladesh	Case	*C. jejuni*
1 G4	600978	Bangladesh	Case	*C. jejuni*
3 54	601035	Bangladesh	Control	*C. coli*
1 G6	601037	Bangladesh	Case	*C. jejuni*
3 56	602330	Bangladesh	Control	*C. coli*
3 57	602497	Bangladesh	Case	*C. coli*
3 58	602723	Bangladesh	Control	*C. coli*
1 F10	603060	Bangladesh	Control	*C. jejuni*
1 F9	603180	Bangladesh	Case	*C. jejuni*
3 59	603567	Bangladesh	Control	*C. coli*
1 F5	603771	Bangladesh	Control	*C. jejuni*
1 F8	604419	Bangladesh	Case	*C. jejuni*
3 60	610001	Bangladesh	Case	*C. coli*
1 E7	610396	Bangladesh	Case	*C. jejuni*
3 61	610647	Bangladesh	Case	*C. coli*
1 E8	620425	Bangladesh	Control	*C. jejuni*
1 I5	621131	Bangladesh	Control	*C. jejuni*
1 C9	700006	Pakistan	Case	*C. jejuni*
1 C8	700541	Pakistan	Case	*C. jejuni*
1 C10	700544	Pakistan	Case	*C. jejuni*

1 D1	700690	Pakistan	Case	*C. jejuni*
1 D2	702296	Pakistan	Case	*C. jejuni*
1 D3	702519	Pakistan	Case	*C. jejuni*
1 C2	702567	Pakistan	Control	*C. jejuni*
1 C3	703207	Pakistan	Case	*C. jejuni*
2 B8	703438	Pakistan	Case	*C. jejuni*
2 B7	703493	Pakistan	Control	*C. jejuni*
1 J3	703533	Pakistan	Case	*C. jejuni*
1 H9	703637	Pakistan	Case	*C. jejuni*
1 H10	703664	Pakistan	Case	*C. jejuni*
1 H8	703672	Pakistan	Control	*C. jejuni*
1 I2	703779	Pakistan	Case	*C. jejuni*
1 I3	703871	Pakistan	Control	*C. jejuni*
1 I1	703882	Pakistan	Control	*C. jejuni*
1 B6	703934	Pakistan	Case	*C. jejuni*
1 B5	704012	Pakistan	Control	*C. jejuni*
1 B7	704017	Pakistan	Control	*C. jejuni*
1 B10	704058	Pakistan	Control	*C. jejuni*
1 B3	704064	Pakistan	Control	*C. jejuni*
1 B9	704137	Pakistan	Control	*C. jejuni*
1 B8	704138	Pakistan	Control	*C. jejuni*
1 G7	704231	Pakistan	Case	*C. jejuni*
1 G1	710087	Pakistan	Control	*C. jejuni*
1 E4	710121	Pakistan	Case	*C. jejuni*
*1 D9	710136	Pakistan	Control	*E. coli*
1 D10	710352	Pakistan	Control	*C. jejuni*
1 F4	720005	Pakistan	Case	*C. jejuni*
1 G2	720255	Pakistan	Case	*C. jejuni*
1 E2	720296	Pakistan	Case	*C. jejuni*
1 D7	**720390**	**Pakistan**	**Control**	***C. jejuni***
1 E9	720607	Pakistan	Control	*C. jejuni*
1 I7	720839	Pakistan	Case	*C. jejuni*
2 C5	721319	Pakistan	Control	*C. jejuni*

[1]Designation of strains as they appear in the manuscript; isolates that do not react with the *Cj*-N-glycan specific antiserum (R1) are in bold. *No Campylobacter isolate based on colony morphology, identified as *E. coli* by 16S sequencing.

Figure S1


kDa
Mw
11168
pglB
3-41
1A6
1J5
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1G8
1H2
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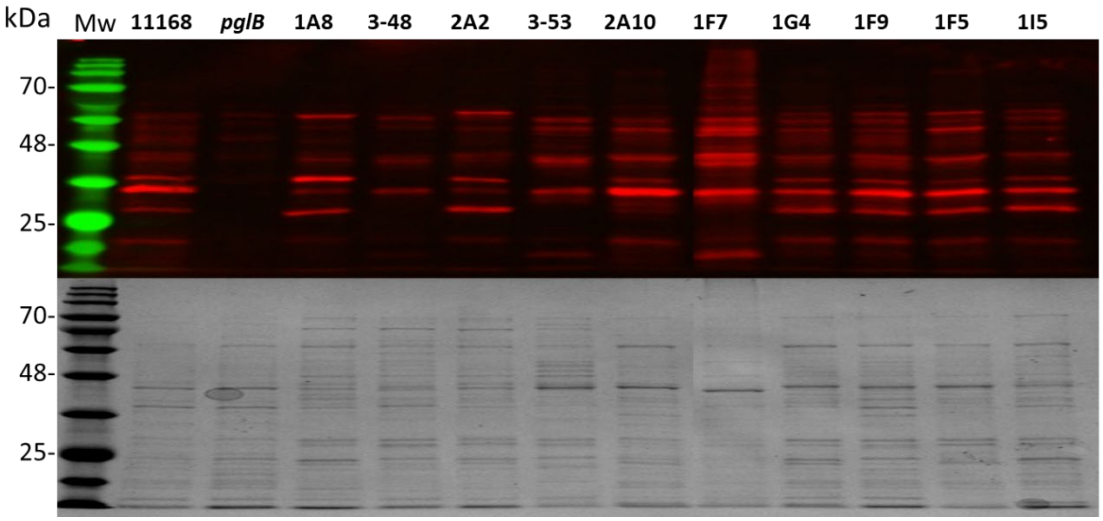
3-49
1G10
70-
48-
25-
70-
48-
25-


kDa
Mw
11168
pglB
1A8
3-48
2A2
3-53
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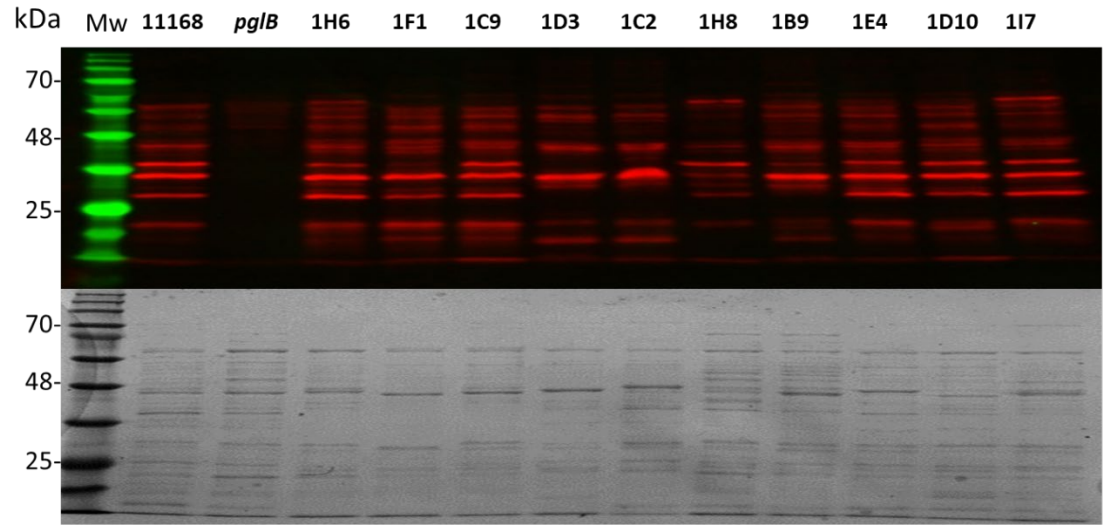
70-
48-
25-
70-
48-
25-

Figure S1 cont.



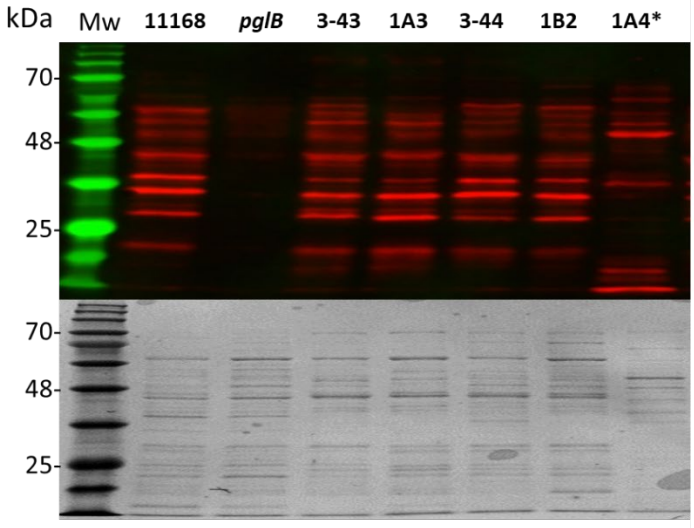


Figure S1 cont.

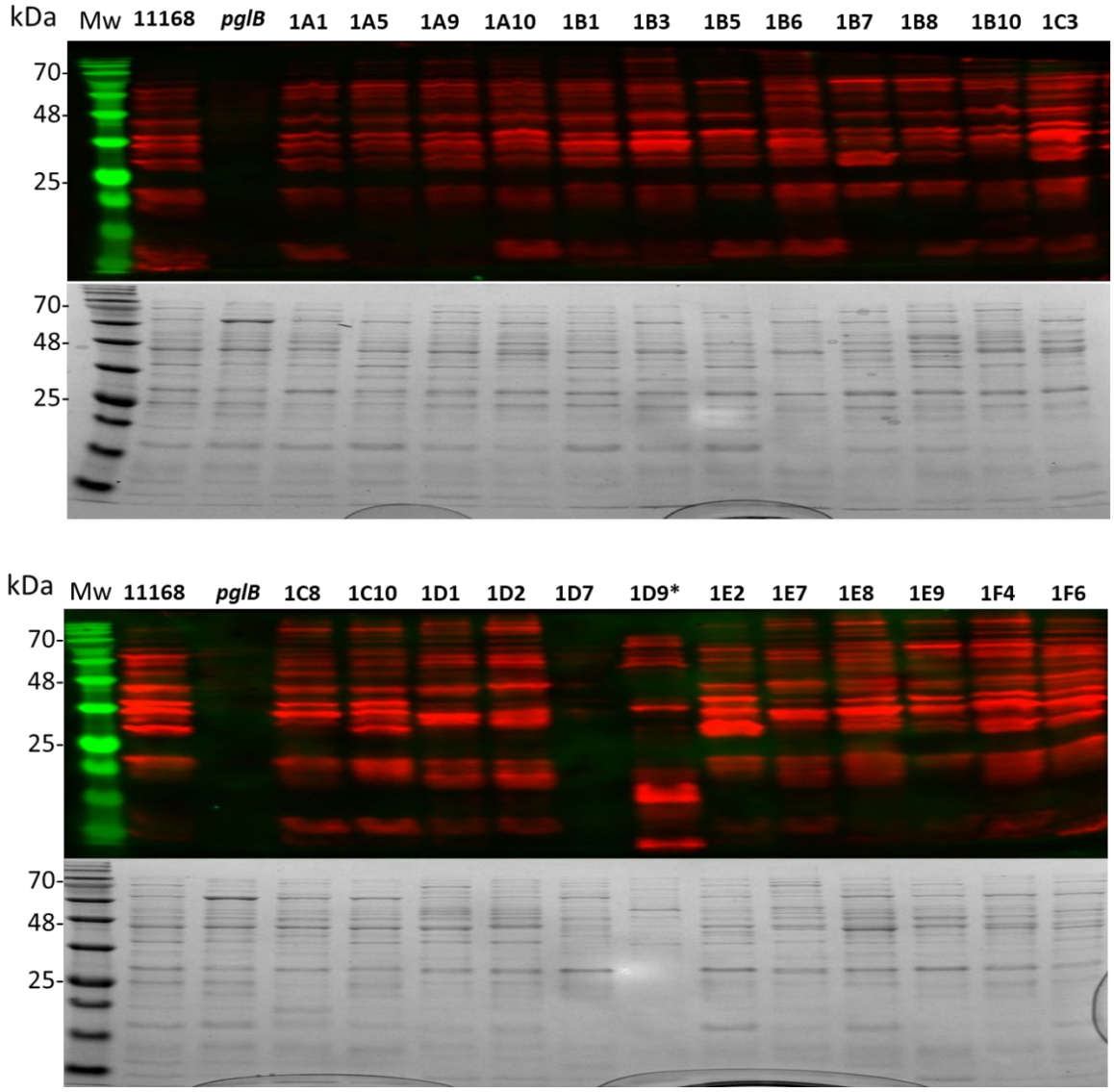


Figure S1 cont.

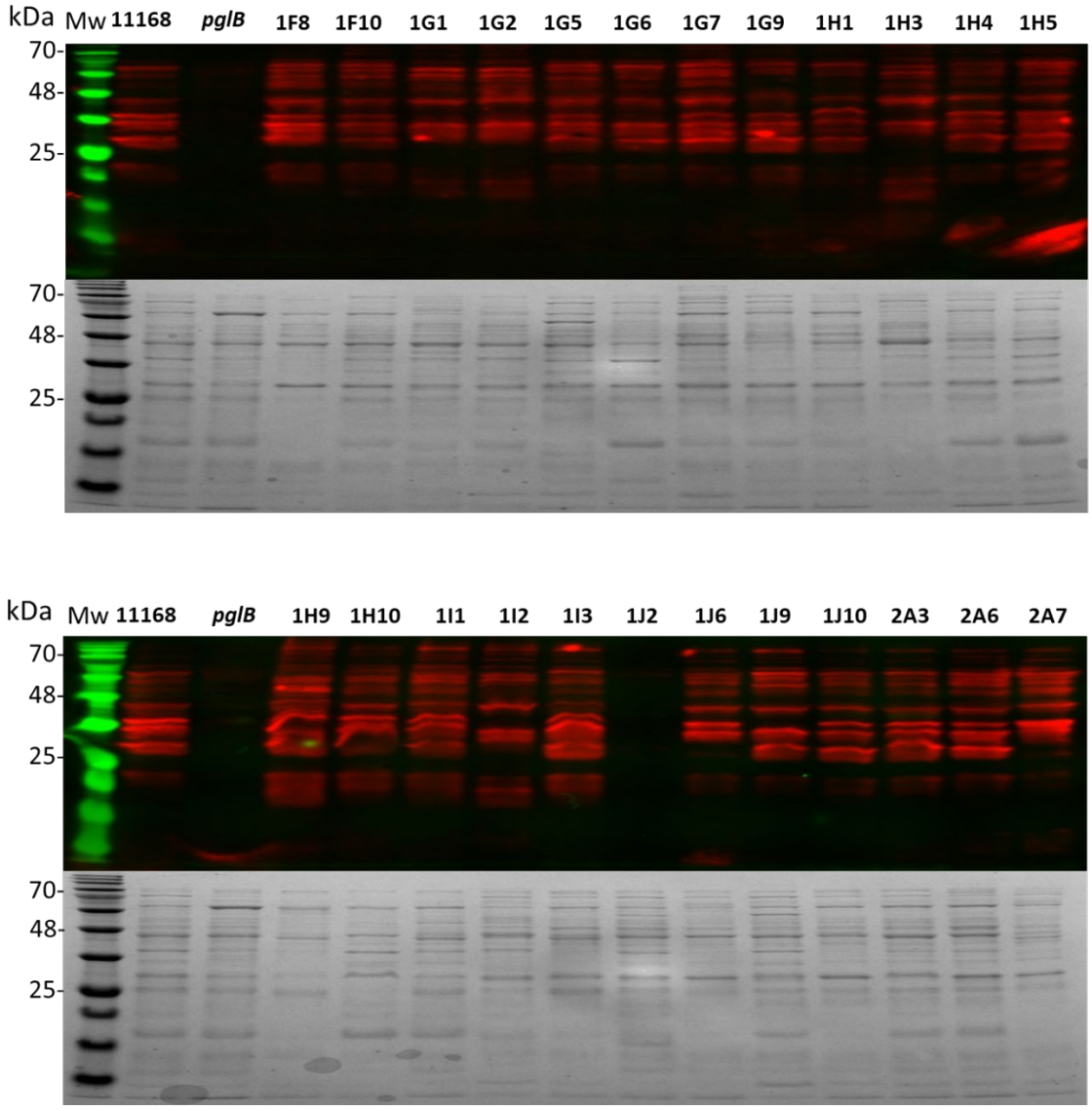


Figure S1 cont.

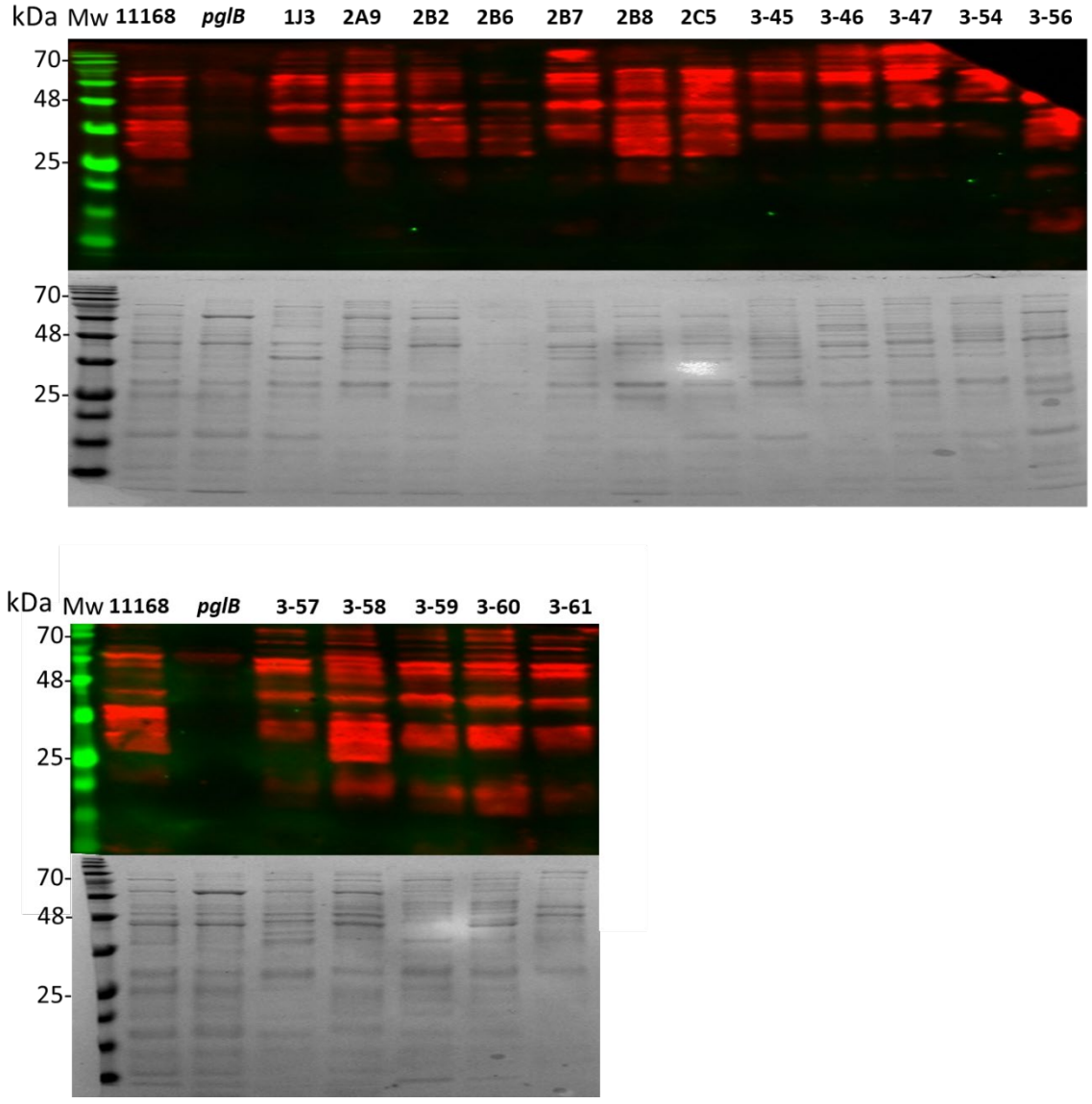


Figure S1. Western Blots and Coomassie-stained gels for all GEMS isolates included in this study. Reactivity with *Cj*-N-glycan specific R1 antiserum of equal amounts of whole cell lysates (3 µg) of *C. jejuni* WT (11168), the isogenic *pglB* mutant (*pglB*) and other *C. jejuni* and *C. coli* isolates is shown (upper panels). Coomassie-stained gels were run in parallel as loading as controls (lower panel). *Western blot signals in samples 1A4 and 1D9 are due to cross-reactivity of the R1 serum with *E. coli* protein since no *Campylobacter* was present in the preparation; presence of *E. coli* was confirmed 16S rRNA sequencing. A full list of strains is provided in **Table S3.**

Figure S2

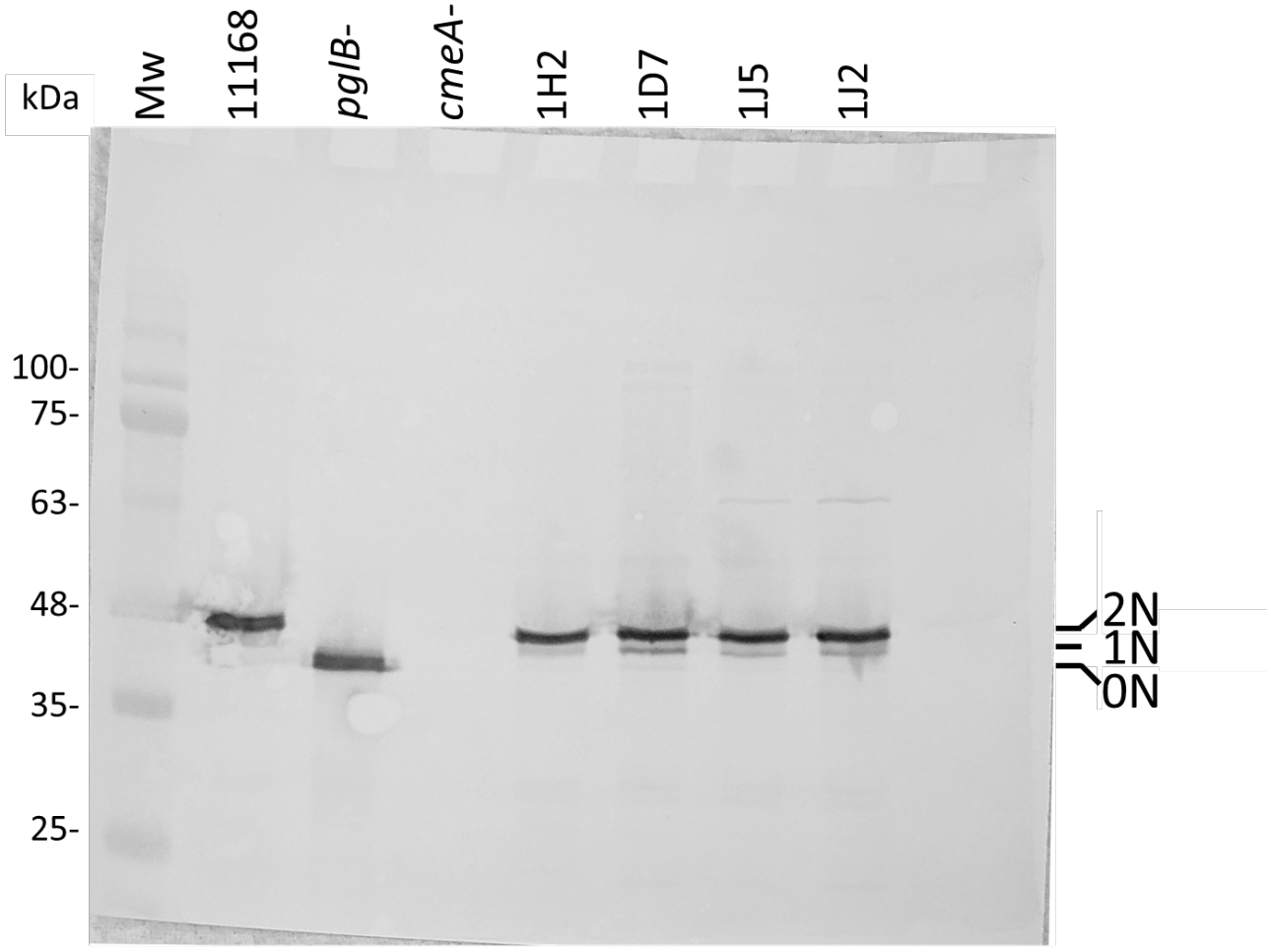
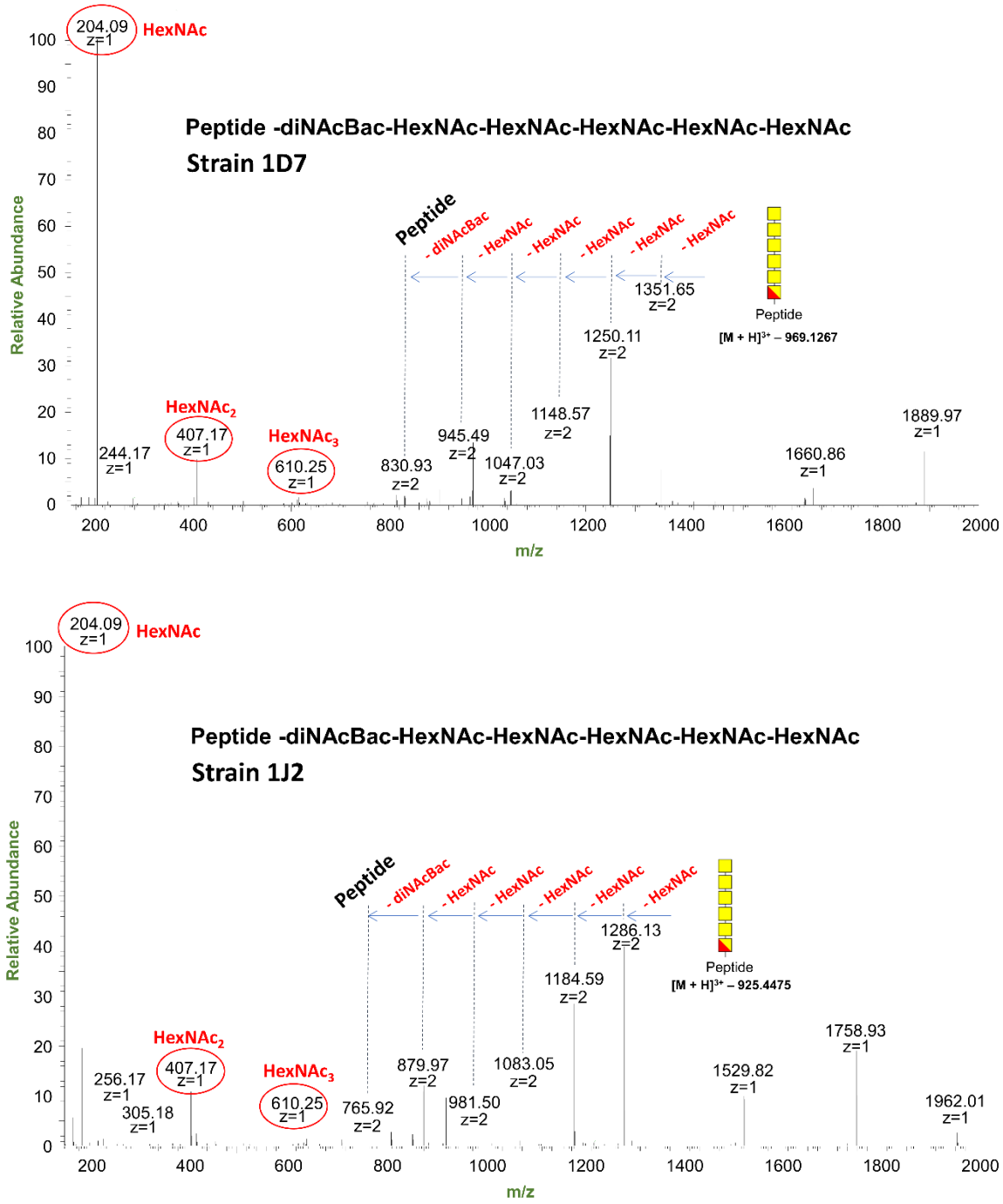


Figure S2. Full (top-to-bottom) scan of the original western blot shown in Figure 1B. Western blot with *Cj*-CmeA-specific antiserum of *C. jejuni* WT (11168), the isogenic *pglB* (*pglB*-) and *cmeA* mutants (*cmeA*-, background control) and the GEMS strains (as indicated) that did not react with *Cj*-N-glycan-specific (R1) serum. Non-mono-and di-glycosylated CmeA proteins are indicated as 0N, 1N and 2N. Note that mono-glycosylated CmeA cannot be detected in the *Cj*-WT since it produces only di-glycosylated (2N) CmeA while the N-glycan is absent in the *pglB* mutant (0N). Molecular weight markers (Mw in kDa) are indicated on the left.

Figure S3


204.09
z=1
HexNAc
Peptide -diNAcBac-HexNAc-HexNAc-HexNAc-HexNAc-HexNAc
Strain 1D7
Relative Abundance
m/z
Peptide
- diNAcBac
- HexNAc
- HexNAc
- HexNAc
- HexNAc
- HexNAc
1351.65
z=2
Peptide
[M + H]3+ – 969.1267
1250.11
z=2
HexNAc2
407.17
z=1
HexNAc3
610.25
z=1
244.17
z=1
830.93
z=2
945.49
z=2
1047.03
z=2
1148.57
z=2
1660.86
z=1
1889.97
z=1
204.09
z=1
HexNAc
Peptide -diNAcBac-HexNAc-HexNAc-HexNAc-HexNAc-HexNAc
Strain 1J2
Relative Abundance
m/z
Peptide
- diNAcBac
- HexNAc
- HexNAc
- HexNAc
- HexNAc
- HexNAc
1286.13
z=2
Peptide
[M + H]3+ – 925.4475
1184.59
z=2
HexNAc2
407.17
z=1
HexNAc3
610.25
z=1
256.17
z=1
305.18
z=1
765.92
z=2
879.97
z=2
981.50
z=2
1083.05
z=2
1529.82
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z=1
1962.01
z=1

Figure S3 cont.

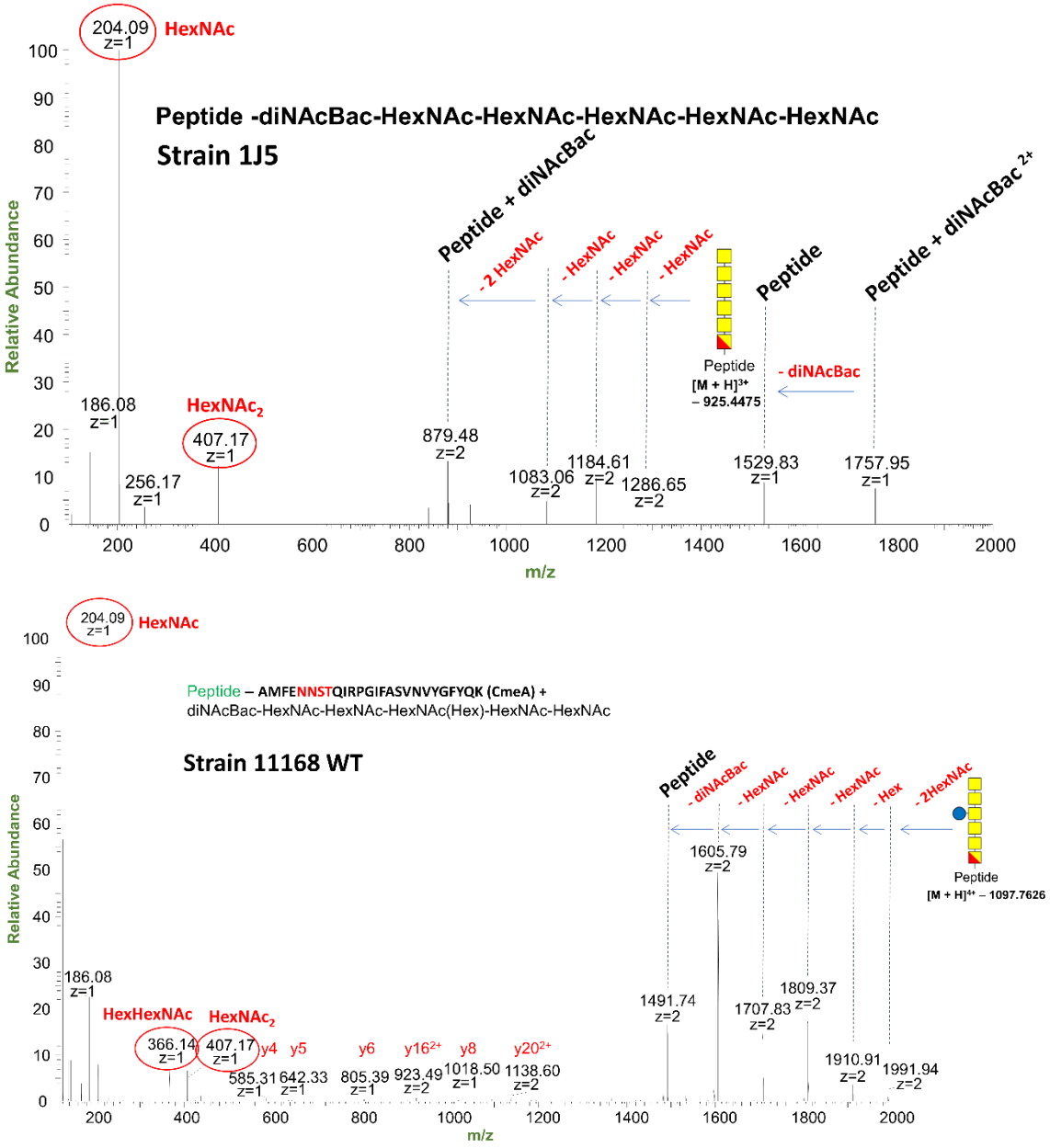


Figure S3. Liquid chromatography mass spectrometric (LC-MS)-based analyses of glycopeptides. HCD MS^2 spectrum showing the fragmentation pattern of the carbohydrate portion on an isolated glycopeptide resulted in the identification of a $HexNAc_5$-diNAcBac N-glycan to a glycopeptide of *C. jejuni* 1D7, 1J2 and 1J5 (as indicated). Since the exact sequence of the protein amino acid sequence from the GEMS strain was not available, only the attached glycan was sequenced. A similar analysis of the full-length *C. jejuni* heptasaccharide N-glycan (HexNAc-HexNAc-HexNAc(Hex)-HexNAc-HexNAc-diNAcBac) attached to CmeA of 11168 WT is shown for comparison.

Figure S4. Alignment of 700 *pglI* alleles (nt 228 to nt 328) from *C. jejuni* and *C. coli*. Color coded in green indicates that nt residues at that position are invariant throughout the alignment, light green to orange highlighting indicates the amino acids with lower conservation, the deduced amino acid sequence for the DDDDE motif is indicated above the nucleotide sequence; (-) indicates nt deletion(s) at this position.

Figure S5. Alignment of 400 unique PglI sequences from *C. jejuni* and *C. coli*. Color coded in green indicates that residues at that position are invariant throughout the alignment, orange highlighting indicates the amino acids with lower conservation, the DDDD motif is highlighted by asterisks, (-) indicates an amino acid deletion at this position.

Figure S6. Position-specific iterative (PSI)-BLAST comparing PglI of *Cj*- 81116 with 1000 non-*Campylobacter* related GTases. The alignment of *Cj*-PglI with other (non-*Campylobacter*) GTases obtained after position-specific iterative (PSI)-BLAST was obtained with PHYRE2 and displayed with MView (https://desmid.github.io/mview/). The DxDD motif is highlighted by asterisks.

Identity
D D D D E

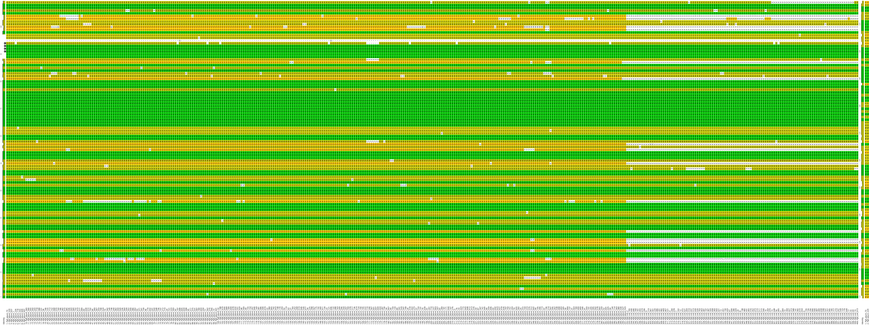
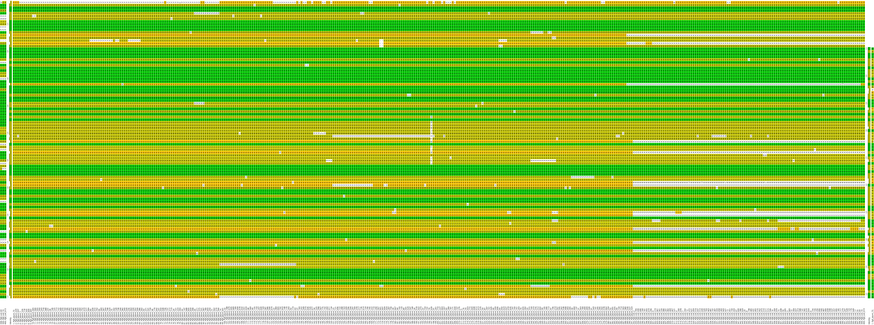
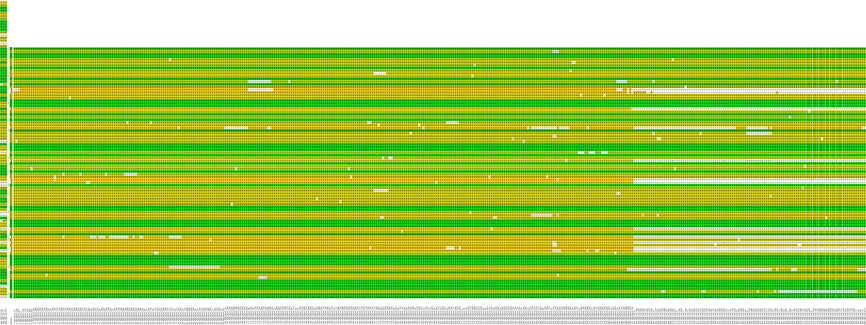
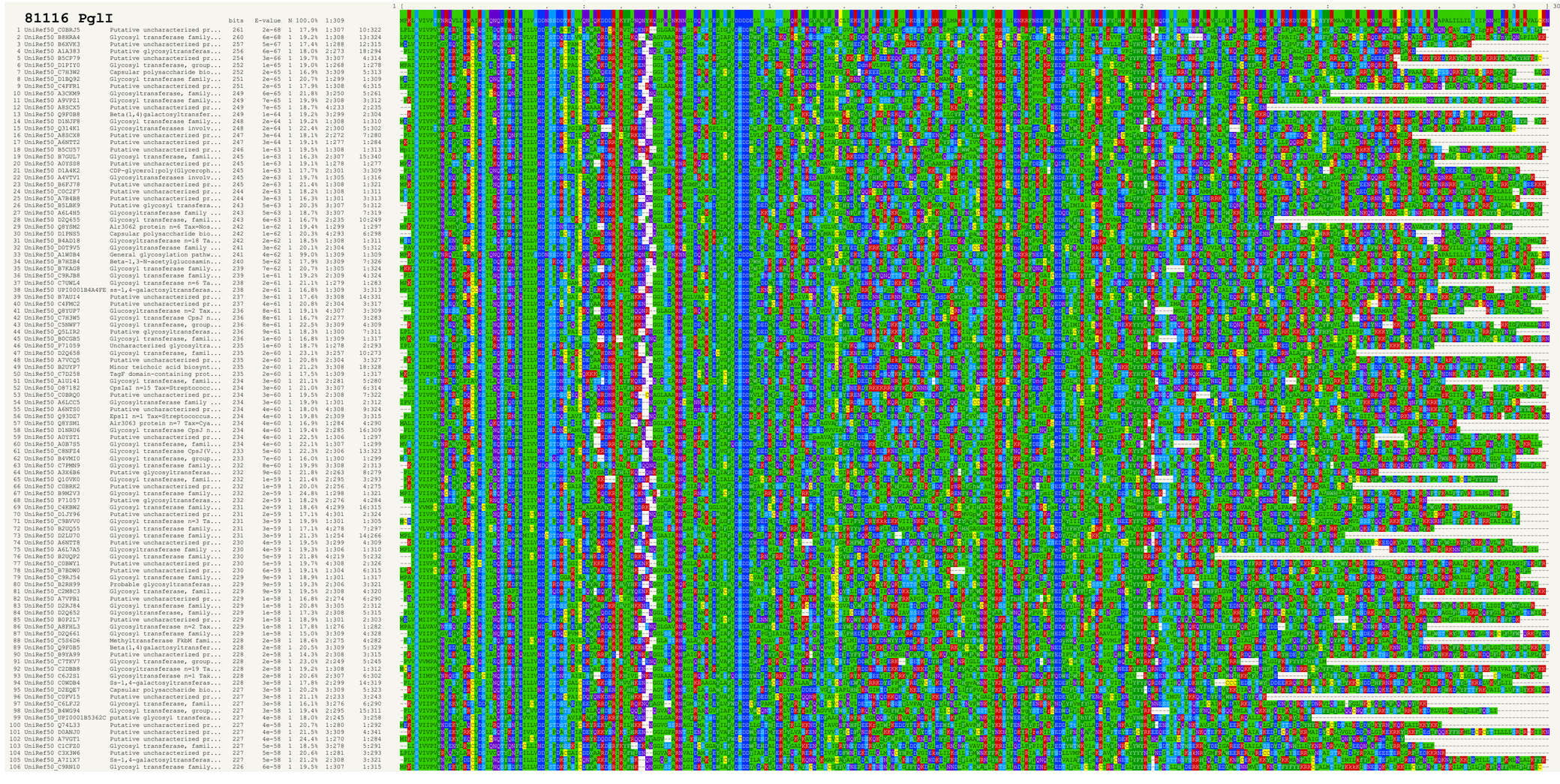
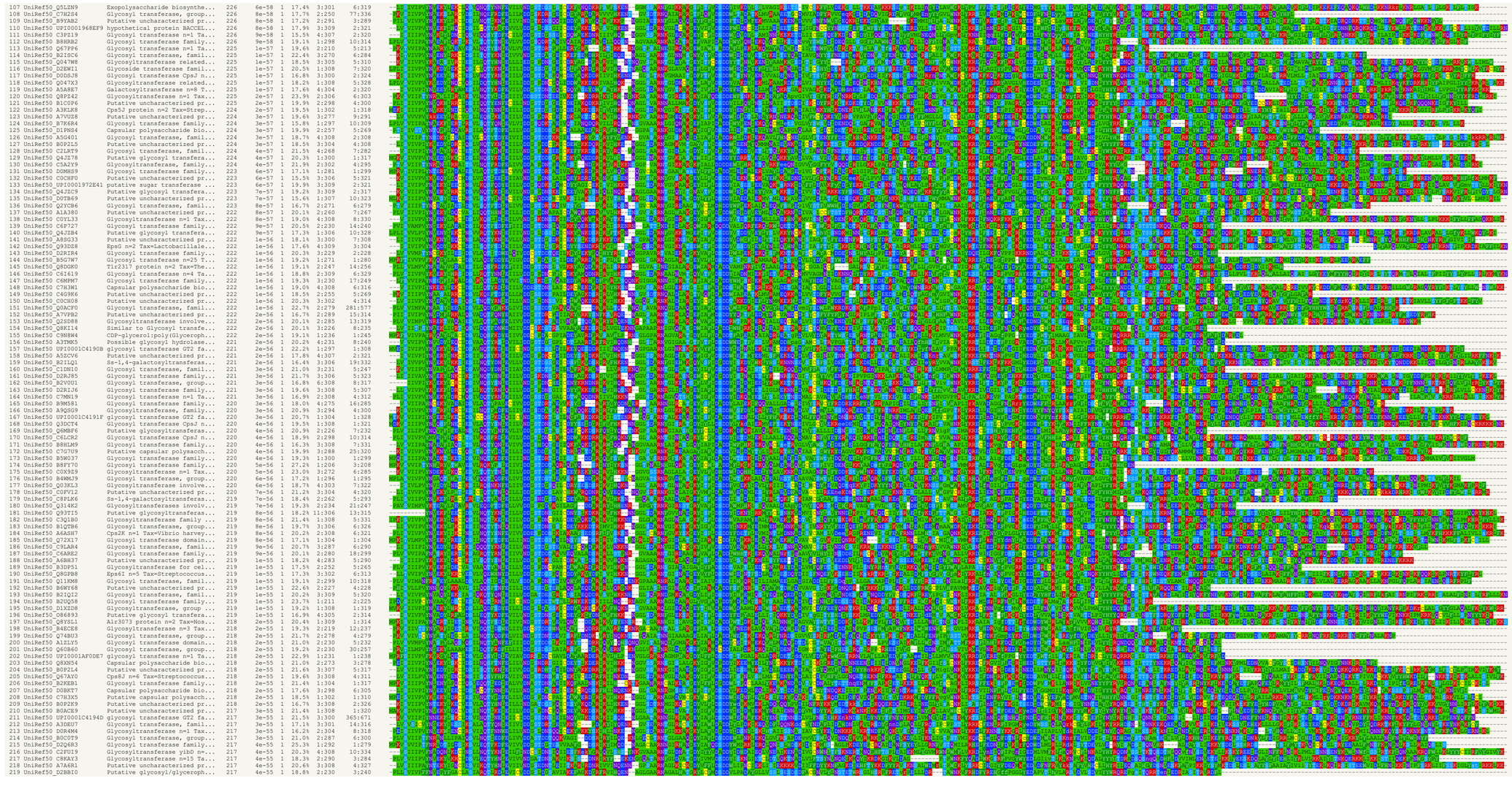




Figure S6. PSI-BLAST (Zoom in for details)




107 UniRef50_Q5LZN9 Exopolysaccharide biosynthe... 226 6e-58 1 17.4% 3:301 6:319
108 UniRef50_C7HZS4 Glycosyl transferase, group... 226 8e-58 1 17.7% 2:250 77:336
109 UniRef50_B9YAB2 Putative uncharacterized pr... 226 8e-58 1 17.2% 2:291 3:289
110 UniRef50_UPI0001968EF9 hypothetical protein BACCEL... 226 8e-58 1 17.9% 3:309 2:321
111 UniRef50_C3P219 Glycosyltransferase n=1 Ta... 226 9e-58 1 15.5% 4:307 2:320
112 UniRef50_B8HRB2 Glycosyl transferase family... 226 9e-58 1 19.1% 1:298 10:314
113 UniRef50_Q67PP6 Glycosyl transferase n=1 Ta... 225 1e-57 1 19.6% 2:210 5:213
114 UniRef50_B2IEC6 Glycosyl transferase, famil... 225 1e-57 1 22.4% 3:270 6:284
115 UniRef50_Q047W8 Glycosyltransferase related... 225 1e-57 1 18.5% 3:305 5:310
116 UniRef50_D2EWI1 Glycoside transferase famil... 225 1e-57 1 20.5% 1:308 7:320
117 UniRef50_D0DSJ8 Glycosyl transferase CpsJ n... 225 1e-57 1 16.8% 3:300 2:324
118 UniRef50_Q047X3 Glycosyltransferase related... 225 1e-57 1 18.2% 1:308 5:328
119 UniRef50_A5A8E7 Galactosyltransferase n=8 T... 225 1e-57 1 17.6% 4:304 2:320
120 UniRef50_Q8F242 Glycosyltransferase n=1 Tax... 225 1e-57 1 23.9% 2:306 6:303
121 UniRef50_B1C0P6 Putative uncharacterized pr... 225 2e-57 1 19.9% 2:298 4:300
122 UniRef50_A3KLK8 CpsSJ protein n=2 Tax=Strep... 224 2e-57 1 19.5% 1:302 1:318
123 UniRef50_A7VUZ8 Putative uncharacterized pr... 224 3e-57 1 19.6% 3:277 9:291
124 UniRef50_B7K6R4 Glycosyl transferase family... 224 3e-57 1 15.8% 1:297 10:309
125 UniRef50_D1PNS4 Capsular polysaccharide bio... 224 3e-57 1 19.9% 2:257 5:269
126 UniRef50_A5G401 Glycosyl transferase, famil... 224 3e-57 1 18.7% 4:308 2:308
127 UniRef50_B0P2L5 Putative uncharacterized pr... 224 3e-57 1 18.5% 3:304 4:308
128 UniRef50_C2LRT9 Glycosyl transferase, famil... 224 4e-57 1 21.5% 4:268 7:282
129 UniRef50_Q4JZ78 Putative glycosyl transfera... 224 4e-57 1 20.3% 1:300 1:317
130 UniRef50_C5A2Y9 Glycosyltransferase, family... 224 4e-57 1 21.9% 2:302 4:295
131 UniRef50_D0MSH9 Glycosyl transferase family... 223 6e-57 1 17.1% 1:281 1:299
132 UniRef50_C0CHF0 Putative uncharacterized pr... 223 6e-57 1 15.5% 3:306 5:321
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134 UniRef50_Q4JZC9 Putative glycosyl transfera... 223 7e-57 1 19.2% 3:309 2:317
135 UniRef50_D0TB69 Putative uncharacterized pr... 223 7e-57 1 15.6% 1:307 10:320
136 UniRef50_Q2YCB6 Glycosyl transferase, famil... 223 8e-57 1 16.7% 2:271 6:279
137 UniRef50_A1A38G Putative uncharacterized pr... 222 8e-57 1 20.1% 2:260 7:267
138 UniRef50_C0YL33 Glycosyltransferase n=1 Tax... 222 9e-57 1 19.0% 4:308 8:330
139 UniRef50_C6P727 Glycosyl transferase family... 222 9e-57 1 20.5% 2:230 14:240
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145 UniRef50_Q8DGK0 T1r2317 protein n=2 Tax=The... 222 1e-56 1 19.1% 2:247 14:256
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148 UniRef50_C7H3W1 Capsular polysaccharide bio... 222 1e-56 1 19.0% 4:308 6:316
149 UniRef50_C4G9K6 Putative uncharacterized pr... 222 1e-56 1 18.5% 2:255 5:269
150 UniRef50_C0CH08 Putative uncharacterized pr... 222 1e-56 1 20.3% 3:302 4:314
151 UniRef50_Q0ACF0 Glycosyl transferase, famil... 222 1e-56 1 22.7% 2:279 281:577
152 UniRef50_A7VPB2 Putative uncharacterized pr... 222 2e-56 1 16.7% 2:289 15:314
153 UniRef50_Q2SDS8 Glycosyltransferase involve... 222 2e-56 1 20.1% 2:285 13:310
154 UniRef50_Q8KI14 Similar to Glycosyl transfe... 222 2e-56 1 20.1% 3:226 8:235
155 UniRef50_C9N8W4 CDP-glycerol:poly(Glyceroph... 222 2e-56 1 19.1% 1:236 1:245
156 UniRef50_A3TMK5 Possible glycosyl hydrolase,... 221 2e-56 1 20.2% 4:231 8:240
157 UniRef50_UPI0001C4190B glycosyl transferase GT2 fa... 221 2e-56 1 22.2% 1:297 1:308
158 UniRef50_A5ZCV6 Putative uncharacterized pr... 221 2e-56 1 17.8% 4:307 2:321
159 UniRef50_B2IQ1 Ss-1,4-galactosyltransferas... 221 2e-56 1 16.4% 3:306 19:332
160 UniRef50_C1DN10 Glycosyl transferase, famil... 221 3e-56 1 21.0% 3:231 5:247
161 UniRef50_D2RJ85 Glycosyl transferase family... 221 3e-56 1 21.7% 3:306 5:323
162 UniRef50_B2VUU1 Glycosyltransferase, group... 221 3e-56 1 16.8% 6:308 8:317
163 UniRef50_D2RIJ6 Glycosyl transferase family... 221 3e-56 1 19.6% 3:308 5:307
164 UniRef50_C7MN19 Glycosyl transferase n=1 Ta... 221 3e-56 1 16.9% 2:308 4:312
165 UniRef50_B9MSB1 Glycosyltransferase family... 220 3e-56 1 18.0% 4:275 16:285
166 UniRef50_A9QSG9 Glycosyltransferase, family... 220 3e-56 1 20.9% 3:294 4:300
167 UniRef50_UPI0001C4191F glycosyl transferase GT2 fa... 220 3e-56 1 20.7% 1:304 1:328
168 UniRef50_Q3UCT4 Glycosyltransferase CpsJ n... 220 4e-56 1 19.5% 1:308 1:321
169 UniRef50_Q6MBF6 Putative glycosyltransferas... 220 4e-56 1 20.9% 2:226 7:232
170 UniRef50_C6LCR2 Glycosyl transferase CpsJ n... 220 4e-56 1 18.9% 2:298 10:314
171 UniRef50_B8HLM9 Glycosyl transferase family... 220 4e-56 1 16.3% 3:308 7:331
172 UniRef50_C7G7U9 Putative capsular polysacch... 220 4e-56 1 19.9% 3:288 25:320
173 UniRef50_B5W037 Glycosyl transferase family... 220 4e-56 1 19.3% 1:300 1:299
174 UniRef50_B8F770 Glycosyl transferase family... 220 5e-56 1 27.2% 1:206 3:208
175 UniRef50_C0X929 Glycosyltransferase n=1 Tax... 220 5e-56 1 23.0% 3:272 6:285
176 UniRef50_B4WMJ9 Glycosyl transferase, group... 220 6e-56 1 17.2% 1:296 1:295
177 UniRef50_Q03KL3 Glycosyltransferase involve... 220 6e-56 1 18.7% 4:303 7:322
178 UniRef50_C0FV12 Putative uncharacterized pr... 220 7e-56 1 21.2% 3:304 4:320
179 UniRef50_C8P1K6 Ss-1,4-galactosyltransferas... 219 7e-56 1 18.4% 2:262 5:293
180 UniRef50_Q3L4K2 Glycosyltransferase involv... 219 7e-56 1 19.3% 2:234 21:247
181 UniRef50_Q93TI5 Putative glycosyltransferas... 219 8e-56 1 18.2% 11:306 13:315
182 UniRef50_C3Q1B0 Glycosyltransferase family ... 219 8e-56 1 21.4% 1:308 5:331
183 UniRef50_B1QTB6 Glycosyltransferase, group... 219 8e-56 1 19.7% 3:306 6:326
184 UniRef50_A6ASH7 Cps2K n=1 Tax=Vibrio harvey... 219 8e-56 1 20.2% 2:308 6:321
185 UniRef50_Q72XI7 Glycosyl transferase domain... 219 8e-56 1 17.1% 1:304 1:304
186 UniRef50_C9LAB4 Glycosyl transferase, famil... 219 9e-56 1 20.7% 3:287 6:290
187 UniRef50_C6ARE2 Glycosyl transferase family... 219 9e-56 1 20.1% 2:280 18:299
188 UniRef50_A6BH37 Putative uncharacterized pr... 219 1e-55 1 18.2% 4:283 5:290
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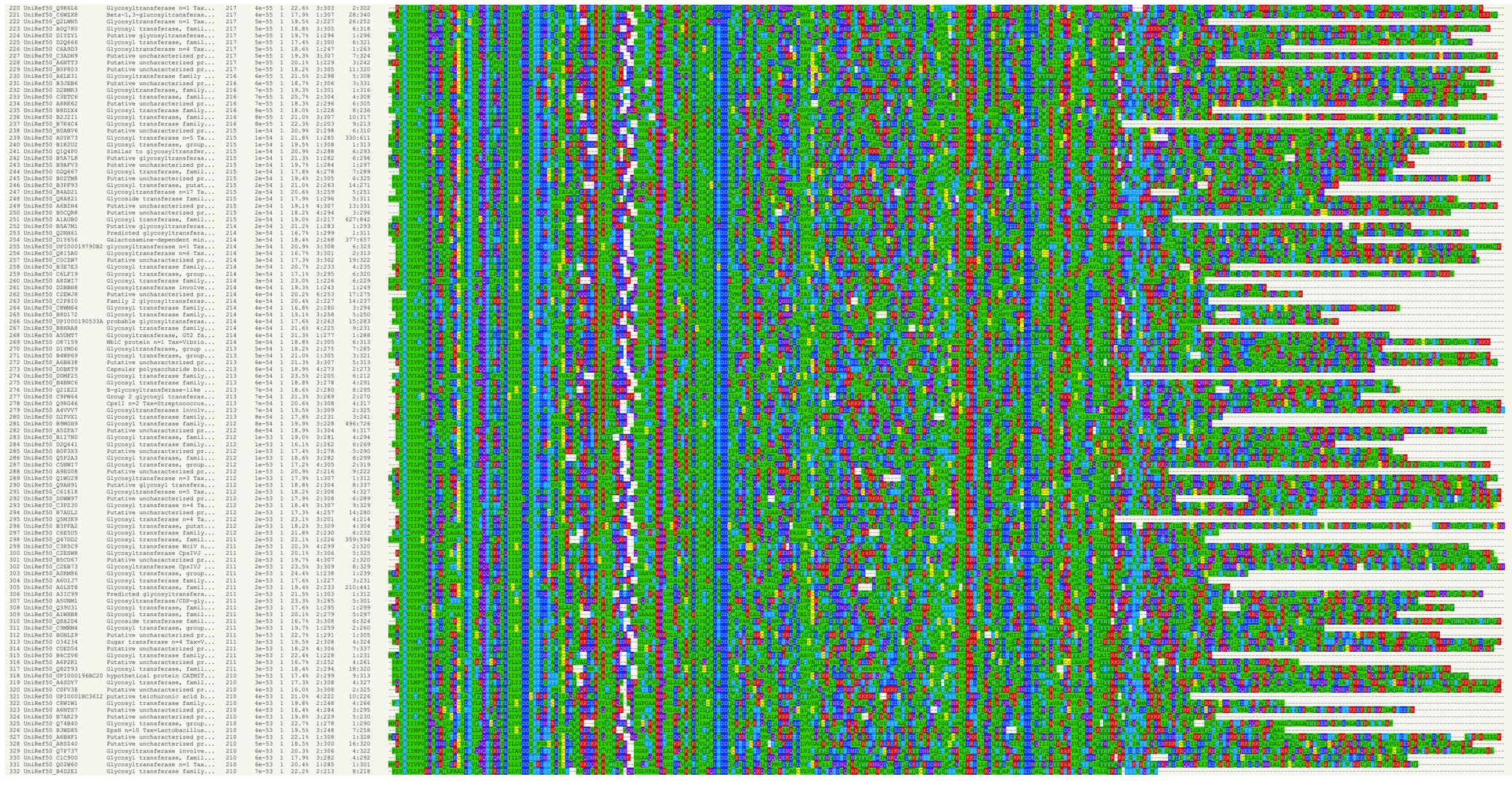
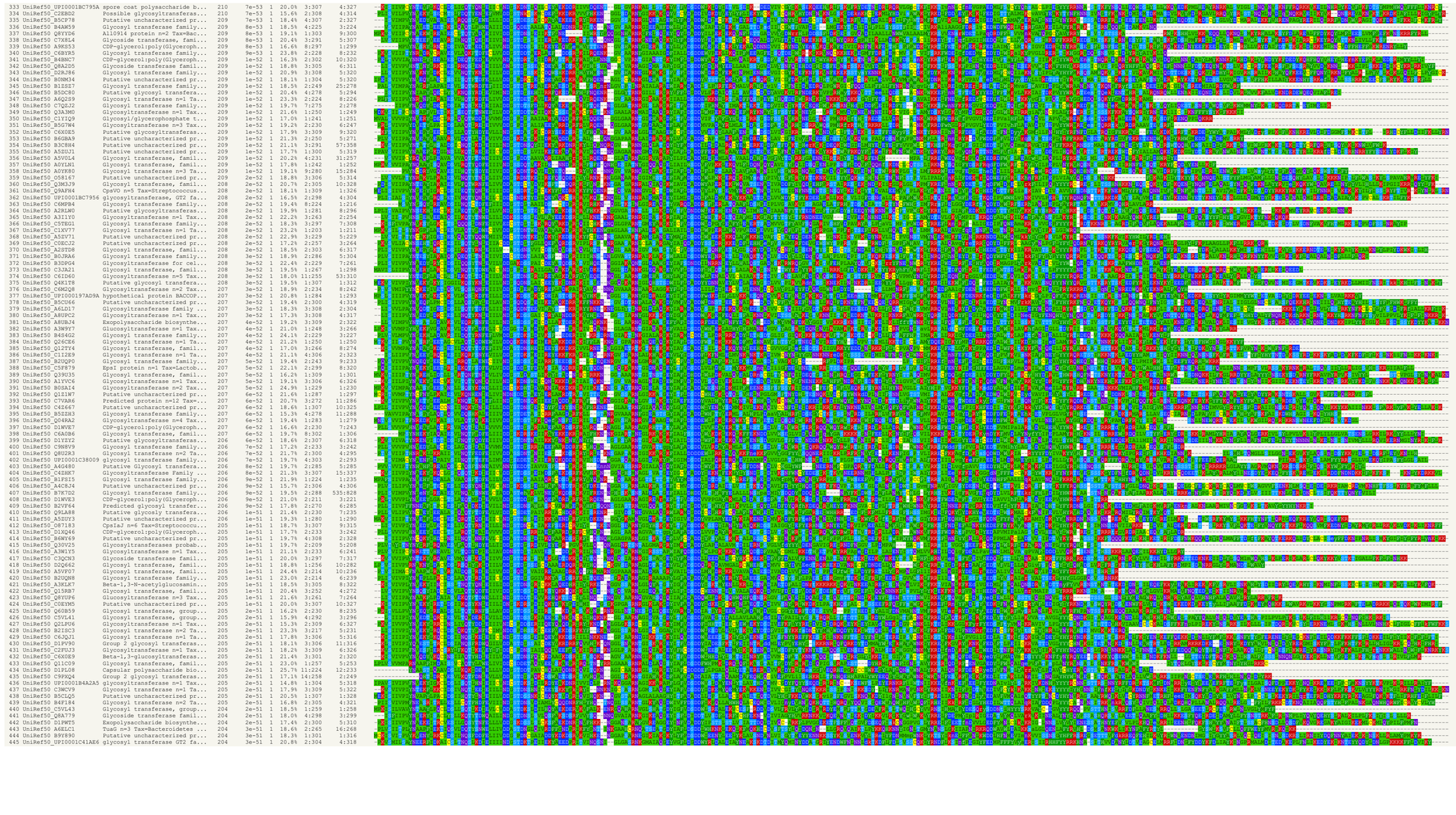
193 UniRef50_B2IQI2 Glycosyl transferase, famil... 219 1e-55 1 20.2% 3:309 5:320
194 UniRef50_B2UQS8 Glycosyl transferase family... 219 1e-55 1 23.7% 1:211 2:225
195 UniRef50_D1XZD8 Glycosyltransferase, group ... 219 1e-55 1 19.2% 1:308 1:319
196 UniRef50_Q86B93 Putative glycosyl transfera... 219 1e-55 1 16.9% 4:305 2:314
197 UniRef50_Q8YSL1 Alr3073 protein n=2 Tax=Nos... 218 2e-55 1 20.4% 1:309 1:314
198 UniRef50_B4ECE8 Glycosyltransferase n=3 Tax... 218 2e-55 1 19.3% 2:219 12:237
199 UniRef50_Q74BU3 Glycosyl transferase, group... 218 2e-55 1 21.7% 2:278 4:279
200 UniRef50_A1ZLY5 Glycosyl transferase domain... 218 2e-55 1 21.0% 2:230 5:232
201 UniRef50_Q60B60 Glycosyl transferase, group... 218 2e-55 1 21.0% 2:230 30:257
202 UniRef50_UPI0001AF0DE7 glycosyl transferase n=1 Ta... 218 2e-55 1 22.9% 1:231 1:238
203 UniRef50_Q8XN54 Capsular polysaccharide bio... 218 2e-55 1 21.0% 2:273 3:278
204 UniRef50_B0P2L4 Putative uncharacterized pr... 218 2e-55 1 21.6% 2:307 5:317
205 UniRef50_Q67AY0 CpsSJ n=6 Tax=Streptococcus... 218 2e-55 1 19.6% 3:308 4:311
206 UniRef50_B2KEB1 Glycosyl transferase family... 218 2e-55 1 21.4% 1:304 1:317
207 UniRef50_D0BKT7 Glycosyltransferase family... 218 2e-55 1 17.6% 1:298 6:305
208 UniRef50_C7H3X5 Putative capsular polysacch... 218 2e-55 1 18.5% 1:302 1:310
209 UniRef50_B0P2K9 Putative uncharacterized pr... 218 2e-55 1 16.7% 3:308 2:326
210 UniRef50_B0AC89 Putative uncharacterized pr... 217 3e-55 1 21.4% 1:308 1:320
211 UniRef50_UPI0001C4194D glycosyl transferase GT2 fa... 217 3e-55 1 21.5% 3:300 365:671
212 UniRef50_A3DEU7 Glycosyl transferase, famil... 217 3e-55 1 17.1% 3:301 14:316
213 UniRef50_D0R4M4 Glycosyltransferase n=1 Tax... 217 3e-55 1 16.2% 2:304 8:318
214 UniRef50_B0C0T9 Glycosyl transferase, group... 217 3e-55 1 21.0% 2:287 6:300
215 UniRef50_D2Q6R3 Glycosyl transferase family... 217 4e-55 1 25.3% 1:292 1:279
216 UniRef50_C2FU19 Glycosyltransferase yibD n=... 217 4e-55 1 20.3% 4:308 10:334
217 UniRef50_C8KAY3 Glycosyltransferase n=15 Ta... 217 4e-55 1 18.3% 2:290 3:284
218 UniRef50_A7A6R1 Putative uncharacterized pr... 217 4e-55 1 20.6% 3:308 4:327
219 UniRef50_D2BBI0 Putative glycosyl/glyceroph... 217 4e-55 1 18.8% 2:230 3:240


220 UniRef50_Q9K6L6 Glycosyltransferase n=1 Tax... 217 4e-55 1 22.6% 3:303 2:302
221 UniRef50_C6WZX8 Beta-1,3-glucosyltransferas... 217 4e-55 1 17.9% 1:307 28:340
222 UniRef50_Q2LWN5 Glycosyltransferase n=1 Tax... 217 5e-55 1 19.5% 2:227 26:252
223 UniRef50_A0Q780 Glycosyl transferase, famil... 217 5e-55 1 18.8% 3:305 6:318
224 UniRef50_D1YZY1 Putative glycosyltransferas... 217 5e-55 1 19.7% 1:294 1:296
225 UniRef50_D2Q666 Glycosyl transferase, famil... 217 5e-55 1 17.4% 2:300 6:321
226 UniRef50_C6A9D3 Glycosyltransferase n=4 Tax... 217 5e-55 1 18.6% 1:247 1:263
227 UniRef50_C3AUH9 Putative uncharacterized pr... 217 5e-55 1 19.3% 3:307 7:324
228 UniRef50_A6NTT3 Putative uncharacterized pr... 217 5e-55 1 20.1% 1:229 3:242
229 UniRef50_B0P803 Putative uncharacterized pr... 217 5e-55 1 18.2% 3:305 11:320
230 UniRef50_A6LE31 Glycosyl transferase family ... 216 6e-55 1 21.5% 2:298 5:308
231 UniRef50_B3JEB6 Putative uncharacterized pr... 216 6e-55 1 18.7% 2:306 3:331
232 UniRef50_D2BMR3 Glycosyltransferase, family... 216 7e-55 1 19.3% 1:301 1:316
233 UniRef50_C3ETC6 Glycosyl transferase, famil... 216 7e-55 1 25.7% 1:304 4:308
234 UniRef50_A8RK62 Putative uncharacterized pr... 216 7e-55 1 18.3% 2:296 6:305
235 UniRef50_B8DIX4 Glycosyl transferase family... 216 8e-55 1 18.0% 1:228 8:236
236 UniRef50_B2J2I1 Glycosyl transferase, famil... 216 8e-55 1 21.0% 3:307 10:317
237 UniRef50_B7K4C4 Glycosyl transferase family... 216 8e-55 1 22.3% 2:203 9:213
238 UniRef50_B0ABV6 Putative uncharacterized pr... 215 1e-54 1 20.9% 2:298 6:310
239 UniRef50_A0YKF3 Glycosyl transferase n=5 Ta... 215 1e-54 1 21.8% 1:285 330:611
240 UniRef50_B1R2U2 Glycosyl transferase, group... 215 1e-54 1 19.5% 1:308 1:313
241 UniRef50_Q1Q4P0 Similar to glycosyltransfer... 215 1e-54 1 20.9% 2:288 6:293
242 UniRef50_B5A7L8 Putative glycosyltransferas... 215 1e-54 1 21.3% 1:282 4:296
243 UniRef50_B9AFV3 Putative uncharacterized pr... 215 1e-54 1 19.7% 1:284 1:297
244 UniRef50_D2Q667 Glycosyl transferase, famil... 215 1e-54 1 17.8% 4:278 7:289
245 UniRef50_B0ZTM8 Putative uncharacterized pr... 215 2e-54 1 19.4% 2:305 6:325
246 UniRef50_B3PF93 Glycosyl transferase, putat... 215 2e-54 1 21.0% 2:263 14:271
247 UniRef50_B4AD21 Glycosyltransferase n=17 Ta... 215 2e-54 1 20.6% 3:259 5:251
248 UniRef50_Q8A821 Glycoside transferase famil... 215 2e-54 1 17.9% 1:296 5:311
249 UniRef50_A6BIH4 Putative uncharacterized pr... 215 2e-54 1 19.1% 4:307 13:331
250 UniRef50_B5CQR8 Putative uncharacterized pr... 215 2e-54 1 18.2% 4:294 3:296
251 UniRef50_A1AUB0 Glycosyl transferase, famil... 215 2e-54 1 19.0% 2:217 627:842
252 UniRef50_B5A7M1 Putative glycosyltransferas... 214 2e-54 1 21.2% 1:283 1:293
253 UniRef50_Q2NH61 Predicted glycosyltransfera... 214 3e-54 1 16.7% 1:299 1:311
254 UniRef50_D1Y656 Galactosamine-dependent mix... 214 3e-54 1 18.6% 2:268 377:657
255 UniRef50_UPI000197790B2 glycosyltransferase n=1 Tax... 214 3e-54 1 20.9% 3:308 6:323
256 UniRef50_Q815A0 glycosyltransferase n=6 Tax... 214 3e-54 1 16.7% 3:301 2:313
257 UniRef50_C0C2W7 Putative uncharacterized pr... 214 3e-54 1 17.3% 3:302 19:322
258 UniRef50_B3E7E3 Glycosyl transferase family... 214 3e-54 1 20.7% 2:233 4:235
259 UniRef50_C6LFI9 Glycosyl transferase, group... 214 3e-54 1 17.1% 3:295 6:320
260 UniRef50_A8XM17 Glycosyl transferase family ... 214 3e-54 1 23.0% 1:226 6:229
261 UniRef50_D2BBH8 Glycosyltransferase involve... 214 4e-54 1 19.3% 1:243 1:249
262 UniRef50_C2EWJ8 Putative uncharacterized pr... 214 4e-54 1 20.2% 6:253 17:275
263 UniRef50_C2FBI0 Family 2 glycosyltransferase 214 4e-54 1 20.4% 2:227 14:237
264 UniRef50_C8WM64 Glycosyl transferase family... 214 4e-54 1 16.8% 2:280 3:294
265 UniRef50_B8D172 Glycosyl transferase family... 214 4e-54 1 19.1% 3:258 5:250
266 UniRef50_UPI000190533A probable glycosyltransferase... 214 4e-54 1 17.6% 2:263 15:283
267 UniRef50_B8HRA8 Glycosyltransferase family... 214 4e-54 1 21.6% 4:225 9:231
268 UniRef50_A5UMT7 Glycosyltransferase, GT2 fa... 214 4e-54 1 21.3% 1:277 1:288
269 UniRef50_Q87159 Wbic2 protein n=1 Tax=Vibrio... 214 5e-54 1 18.8% 2:305 6:313
270 UniRef50_D1YMO6 Glycosyltransferase, group ... 213 5e-54 1 18.2% 2:275 7:285
271 UniRef50_B4WP69 Glycosyl transferase, group... 213 5e-54 1 21.0% 1:305 3:321
272 UniRef50_A6BH38 Putative uncharacterized pr... 213 6e-54 1 21.3% 1:307 5:313
273 UniRef50_D0BKT9 Capsular polysaccharide bio... 213 6e-54 1 18.9% 4:273 2:273
274 UniRef50_D0MF25 Glycosyl transferase family... 213 6e-54 1 23.5% 2:205 6:212
275 UniRef50_B4BNC6 Glycosyl transferase family... 213 6e-54 1 18.8% 3:278 4:291
276 UniRef50_Q21E22 B-glycosyltransferase-like ... 213 7e-54 1 18.6% 2:280 8:295
277 UniRef50_C9PW64 Group 2 glycosyl transferas... 213 7e-54 1 21.3% 3:269 2:270
278 UniRef50_Q9RG46 Cps1I n=2 Tax=Streptococcus... 213 7e-54 1 20.6% 3:308 4:317
279 UniRef50_A4VVV7 Glycosyltransferases involv... 213 7e-54 1 19.5% 3:309 2:325
280 UniRef50_D2PVX1 Glycosyl transferase family... 213 8e-54 1 17.8% 2:231 3:241
281 UniRef50_B9MUH9 Glycosyl transferase family ... 212 8e-54 1 19.9% 3:228 496:726
282 UniRef50_A5ZFA7 Putative uncharacterized pr... 212 8e-54 1 18.9% 3:304 6:317
283 UniRef50_B1I7N0 Glycosyl transferase, famil... 212 1e-53 1 19.0% 3:281 4:294
284 UniRef50_D2Q641 Glycosyl transferase family... 212 1e-53 1 16.1% 2:262 6:269
285 UniRef50_B0P3X3 Putative uncharacterized pr... 212 1e-53 1 17.4% 3:278 5:290
286 UniRef50_Q5P2A3 Glycosyl transferase, famil... 212 1e-53 1 18.6% 3:282 6:299
287 UniRef50_C5NMI7 Glycosyl transferase, group... 212 1e-53 1 17.2% 4:305 2:319
288 UniRef50_A9EG08 Putative uncharacterized pr... 212 1e-53 1 20.9% 2:216 9:222
289 UniRef50_Q1WUZ9 Glycosyltransferase n=3 Tax... 212 1e-53 1 17.9% 1:307 1:312
290 UniRef50_Q9AN91 Putative glycosyl transfera... 212 1e-53 1 18.8% 2:304 8:337
291 UniRef50_C6I618 Glycosyltransferase n=5 Tax... 212 2e-53 1 18.2% 2:308 4:327
292 UniRef50_D0WW97 Putative uncharacterized pr... 212 2e-53 1 17.9% 2:308 6:289
293 UniRef50_C3PZ30 Glycosyl transferase n=4 Ta... 212 2e-53 1 18.4% 3:307 9:329
294 UniRef50_B7AUL2 Putative uncharacterized pr... 212 2e-53 1 17.3% 4:257 14:280
295 UniRef50_Q5M3K9 Glycosyl transferase n=4 Ta... 212 2e-53 1 23.1% 3:201 4:214
296 UniRef50_B3FPA2 Glycosyl transferase, putat... 212 2e-53 1 18.2% 3:309 4:304
297 UniRef50_C6E5U5 Glycosyl transferase family... 212 2e-53 1 21.8% 2:230 6:232
298 UniRef50_Q47DD2 Glycosyl transferase, famil... 211 2e-53 1 22.1% 1:226 359:594
299 UniRef50_C3H5C9 Glycosyltransferase WcLV n... 211 2e-53 1 20.3% 4:299 2:320
300 UniRef50_C2ESW8 Glycosyltransferase CpsIVJ ... 211 2e-53 1 20.1% 3:306 5:325
301 UniRef50_B5CUD7 Putative uncharacterized pr... 211 2e-53 1 19.7% 4:307 2:320
302 UniRef50_C2EB73 Glycosyltransferase CpsIVJ ... 211 2e-53 1 23.5% 3:309 8:329
303 UniRef50_A0KM86 Glycosyl transferase, group... 211 2e-53 1 24.4% 1:238 1:239
304 UniRef50_A6UIJ7 Glycosyl transferase family... 211 2e-53 1 17.6% 1:227 1:231
305 UniRef50_A0LST8 Glycosyl transferase, famil... 211 2e-53 1 19.4% 2:233 210:441
306 UniRef50_A3IC99 Predicted glycosyltransfera... 211 2e-53 1 21.5% 1:303 1:312
307 UniRef50_A5UNM1 Glycosyltransferase/CDP-gly... 211 2e-53 1 23.3% 3:285 5:301
308 UniRef50_Q39U31 Glycosyl transferase, famil... 211 3e-53 1 17.6% 1:295 1:299
309 UniRef50_A1WCB8 Glycosyl transferase, famil... 211 3e-53 1 20.1% 2:279 5:297
310 UniRef50_Q8A2D4 Glycoside transferase famil... 211 3e-53 1 16.7% 3:308 6:324
311 UniRef50_C9MBM4 Glycosyl transferase, group... 211 3e-53 1 19.7% 1:259 2:260
312 UniRef50_B0NLZ9 Putative uncharacterized pr... 211 3e-53 1 22.7% 1:291 1:305
313 UniRef50_O34234 Sugar transferase n=4 Tax=V... 211 3e-53 1 19.5% 2:308 4:324
314 UniRef50_C0E254 Putative uncharacterized pr... 211 3e-53 1 18.2% 4:306 7:327
315 UniRef50_B4C2V6 Glycosyl transferase family... 211 3e-53 1 22.4% 1:228 1:231
316 UniRef50_A6P2R1 Putative uncharacterized pr... 211 3e-53 1 16.7% 2:252 4:261
317 UniRef50_Q8Z793 Glycosyl transferase, famil... 210 3e-53 1 18.6% 2:294 18:320
318 UniRef50_UPI0001968BC20 hypothetical protein CATMIT... 210 3e-53 1 17.4% 2:299 9:313
319 UniRef50_A4SDY7 Glycosyl transferase, famil... 210 3e-53 1 17.3% 2:308 4:327
320 UniRef50_C0FY38 Putative uncharacterized pr... 210 3e-53 1 16.0% 3:308 2:325
321 UniRef50_UPI0001BC3612 putative teichuronic acid b... 210 4e-53 1 21.0% 4:222 10:226
322 UniRef50_C8WIW1 Glycosyl transferase family... 210 4e-53 1 19.8% 2:248 4:266
323 UniRef50_A6NTS7 Putative uncharacterized pr... 210 4e-53 1 16.4% 4:284 3:295
324 UniRef50_B7AK29 Putative uncharacterized pr... 210 4e-53 1 19.8% 3:229 5:230
325 UniRef50_Q74B40 Glycosyl transferase, group... 210 4e-53 1 22.7% 1:278 1:290
326 UniRef50_B3WD85 EpsH n=10 Tax=Lactobacillus... 210 4e-53 1 19.5% 3:248 7:258
327 UniRef50_A6BHF1 Putative uncharacterized pr... 210 5e-53 1 22.1% 1:308 1:328
328 UniRef50_A8SZ40 Putative uncharacterized pr... 210 5e-53 1 18.5% 3:300 16:320
329 UniRef50_Q7F737 Glycosyltransferase involve... 210 6e-53 1 20.3% 2:306 4:322
330 UniRef50_C1C900 Glycosyl transferase, famil... 210 6e-53 1 17.9% 3:282 4:292
331 UniRef50_Q02W60 Glycosyltransferase n=1 Tax... 210 6e-53 1 20.4% 1:285 1:301
332 UniRef50_B4D2E1 Glycosyl transferase family... 210 7e-53 1 22.2% 2:213 8:218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335 UniRef50_B5CP78 Putative uncharacterized pr... 209 7e-53 1 18.4% 4:307 2:327
336 UniRef50_B4AW59 Glycosyl transferase family... 209 8e-53 1 18.5% 4:225 3:224
337 UniRef50_Q8YYD6 All0914 protein n=2 Tax=Nost... 209 8e-53 1 19.1% 1:303 9:300
338 UniRef50_C7X8L4 Glycoside transferase, fami... 209 8e-53 1 20.4% 3:291 5:307
339 UniRef50_A9KS53 CDP-glycerol:poly(Glyceroph... 209 8e-53 1 16.6% 8:297 1:299
340 UniRef50_C6BYR5 Glycosyl transferase family... 209 9e-53 1 23.8% 2:228 8:232
341 UniRef50_B4BNC7 CDP-glycerol:poly(Glyceroph... 209 1e-52 1 16.3% 2:302 10:320
342 UniRef50_Q8A2D5 Glycoside transferase famil... 209 1e-52 1 18.8% 3:305 6:311
343 UniRef50_D2RJR6 Glycosyl transferase family... 209 1e-52 1 20.9% 3:308 5:320
344 UniRef50_B0NM34 Putative uncharacterized pr... 209 1e-52 1 18.1% 1:304 5:320
345 UniRef50_B1ZSZ7 Glycosyl transferase family... 209 1e-52 1 18.5% 2:249 25:278
346 UniRef50_B5DC80 Putative glycosyl transfera... 209 1e-52 1 20.4% 4:278 5:294
347 UniRef50_A6Q2S9 Glycosyl transferase n=1 Ta... 209 1e-52 1 23.3% 2:224 8:226
348 UniRef50_C7Q2J2 Glycosyl transferase family... 209 1e-52 1 19.7% 7:275 2:278
349 UniRef50_Q3AJM0 Glycosyltransferase n=1 Tax... 209 1e-52 1 21.6% 1:250 1:249
350 UniRef50_C1YIQ9 Glycosyl/glycerophosphate t... 209 1e-52 1 17.0% 1:241 1:251
351 UniRef50_B5G7W4 Glycosyltransferase n=3 Tax... 209 1e-52 1 19.2% 2:230 6:247
352 UniRef50_C6X0E5 Putative glycosyltransferas... 209 1e-52 1 17.9% 3:309 9:320
353 UniRef50_B6GBA9 Putative uncharacterized pr... 209 1e-52 1 21.3% 2:250 5:271
354 UniRef50_B3C8H4 Putative uncharacterized pr... 209 1e-52 1 21.1% 3:291 57:358
355 UniRef50_A5ZUJ1 Putative uncharacterized pr... 209 1e-52 1 17.7% 1:300 5:319
356 UniRef50_A5V0L4 Glycosyl transferase, famil... 209 1e-52 1 20.2% 4:231 31:257
357 UniRef50_A0YLN1 Glycosyl transferase, famil... 209 1e-52 1 17.8% 1:242 1:252
358 UniRef50_A0YKH0 Glycosyl transferase n=3 Ta... 209 1e-52 1 19.1% 9:280 15:284
359 UniRef50_O58167 Putative uncharacterized pr... 209 2e-52 1 18.8% 3:306 5:314
360 UniRef50_Q3MJJ9 Glycosyl transferase, famil... 208 2e-52 1 20.7% 2:305 10:328
361 UniRef50_Q9AFH4 cpsVD n=5 Tax=Streptococcus... 208 2e-52 1 18.1% 1:309 1:326
362 UniRef50_UPI0001BC7956 glycosyltransferase, GT2 fa... 208 2e-52 1 16.5% 2:298 4:304
363 UniRef50_C6MPB4 Glycosyl transferase family... 208 2e-52 1 19.4% 8:224 1:216
364 UniRef50_A2NLW0 Putative glycosyltransferas... 208 2e-52 1 19.9% 1:281 8:296
365 UniRef50_A3I1Y0 Glycosyltransferase n=1 Tax... 208 2e-52 1 22.2% 3:263 2:254
366 UniRef50_C5TEG1 Glycosyl transferase family... 208 2e-52 1 18.3% 3:297 7:308
367 UniRef50_C1XV77 Glycosyl transferase n=1 Ta... 208 2e-52 1 23.2% 1:203 1:211
368 UniRef50_A5EV71 Putative uncharacterized pr... 208 2e-52 1 22.9% 3:229 5:229
369 UniRef50_C0ECJ2 Putative uncharacterized pr... 208 2e-52 1 17.2% 2:257 3:264
370 UniRef50_A2STD8 Glycosyl transferase, famil... 208 2e-52 1 18.5% 2:303 6:317
371 UniRef50_B0JRA6 Glycosyl transferase family... 208 3e-52 1 18.9% 2:286 5:304
372 UniRef50_B3DPG4 Glycosyltransferase for cel... 208 3e-52 1 22.4% 2:229 7:261
373 UniRef50_C3JA21 Glycosyl transferase, famil... 208 3e-52 1 19.5% 1:267 1:298
374 UniRef50_C6ID60 Glycosyltransferase n=5 Tax... 208 3e-52 1 18.0% 11:255 53:310
375 UniRef50_Q4K1T8 Putative glycosyl transfera... 208 3e-52 1 19.5% 1:307 1:312
376 UniRef50_C6MQP8 Glycosyltransferase n=2 Tax... 207 3e-52 1 18.9% 2:234 8:242
377 UniRef50_UPI0001979AD9A hypothetical protein BACCOP... 207 3e-52 1 20.8% 1:284 1:293
378 UniRef50_B5CU66 Putative uncharacterized pr... 207 3e-52 1 19.4% 2:300 4:319
379 UniRef50_A6LDI7 Glycosyltransferase family ... 207 3e-52 1 18.3% 3:308 2:304
380 UniRef50_A8UPC2 Glycosyltransferase n=1 Tax... 207 3e-52 1 17.3% 3:308 4:317
381 UniRef50_A8UBJ4 Exopolysaccharide biosynthe... 207 4e-52 1 19.2% 3:309 2:322
382 UniRef50_A3W9Y7 Glucosyltransferase n=1 Tax... 207 4e-52 1 21.0% 1:248 3:266
383 UniRef50_B4S4G2 Glycosyl transferase family... 207 4e-52 1 24.1% 2:229 3:227
384 UniRef50_Q26CE6 Glycosyl transferase n=1 Ta... 207 4e-52 1 21.2% 1:250 1:250
385 UniRef50_Q12TY4 Glycosyl transferase, famil... 207 4e-52 1 17.0% 3:266 8:274
386 UniRef50_C1IZE9 Glycosyl transferase n=1 Ta... 207 4e-52 1 21.1% 4:306 2:323
387 UniRef50_B2UQP0 Glycosyl transferase family... 207 5e-52 1 19.4% 2:243 9:233
388 UniRef50_C5FBT9 Rpsl protein n=1 Tax=Actob... 207 5e-52 1 22.1% 2:299 8:320
389 UniRef50_Q39U35 Glycosyl transferase, famil... 207 5e-52 1 16.2% 1:309 1:301
390 UniRef50_A1YVC6 Glycosyltransferase n=1 Tax... 207 5e-52 1 19.1% 3:306 6:326
391 UniRef50_B0SAI4 Glycosyltransferase n=2 Tax... 207 5e-52 1 24.8% 1:229 1:230
392 UniRef50_Q1Z1W7 Putative uncharacterized pr... 207 6e-52 1 21.6% 1:287 1:297
393 UniRef50_C7VAR6 Predicted protein n=12 Tax=... 207 6e-52 1 20.7% 3:272 11:286
394 UniRef50_C4Z667 Putative uncharacterized pr... 207 6e-52 1 18.6% 1:307 10:325
395 UniRef50_B5ZZH3 Glycosyl transferase family... 207 6e-52 1 15.3% 4:278 11:288
396 UniRef50_Q04RA2 Glycosyltransferase n=4 Tax... 207 6e-52 1 19.4% 1:283 1:279
397 UniRef50_D1WVE7 CDP-glycerol:poly(Glyceroph... 207 6e-52 1 16.6% 2:230 7:243
398 UniRef50_C6AQB6 Glycosyl transferase, famil... 207 6e-52 1 19.7% 8:302 1:306
399 UniRef50_D1YZY2 Putative glycosyltransferas... 206 6e-52 1 18.6% 2:307 6:318
400 UniRef50_C9NBV9 Glycosyl transferase family... 206 7e-52 1 17.2% 2:233 3:242
401 UniRef50_Q8UZR3 Glycosyl transferase n=2 Ta... 206 7e-52 1 21.7% 2:300 4:295
402 UniRef50_UPI0001C38009 glycosyl transferase family... 206 7e-52 1 19.7% 4:303 2:293
403 UniRef50_A4G480 Putative Glycosyl transfera... 206 8e-52 1 19.7% 2:285 5:285
404 UniRef50_C4ZHK7 Glycosyltransferase Family ... 206 8e-52 1 21.3% 3:307 15:337
405 UniRef50_B1FSI5 Glycosyl transferase family... 206 9e-52 1 21.9% 1:224 1:235
406 UniRef50_A4C8J4 Putative uncharacterized pr... 206 9e-52 1 15.7% 2:306 4:306
407 UniRef50_B7K7D2 Glycosyl transferase family... 206 9e-52 1 19.5% 2:288 535:828
408 UniRef50_D1WVE3 CDP-glycerol:poly(Glyceroph... 206 9e-52 1 21.0% 2:211 3:221
409 UniRef50_B2VPE4 Predicted glycosyl transfer... 206 9e-52 1 17.8% 2:270 6:285
410 UniRef50_Q9LAB8 Putative glycosly transfera... 206 1e-51 1 21.4% 2:230 7:235
411 UniRef50_A5ZUY3 Putative uncharacterized pr... 206 1e-51 1 19.3% 1:280 1:290
412 UniRef50_Q87183 Cps1B1 n=6 Tax=Streptococcu... 205 1e-51 1 18.7% 3:307 9:315
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414 UniRef50_B6WY69 Putative uncharacterized pr... 205 1e-51 1 19.7% 4:308 2:328
415 UniRef50_Q30V25 Glycosyltransferases probab... 205 1e-51 1 19.7% 2:209 5:208
416 UniRef50_A3W1Y5 Glycosyltransferase n=1 Tax... 205 1e-51 1 21.1% 2:233 6:241
417 UniRef50_C3QCN3 Glycoside transferase famil... 205 1e-51 1 20.0% 3:297 7:317
418 UniRef50_D2Q642 Glycosyl transferase, famil... 205 1e-51 1 18.8% 1:256 10:282
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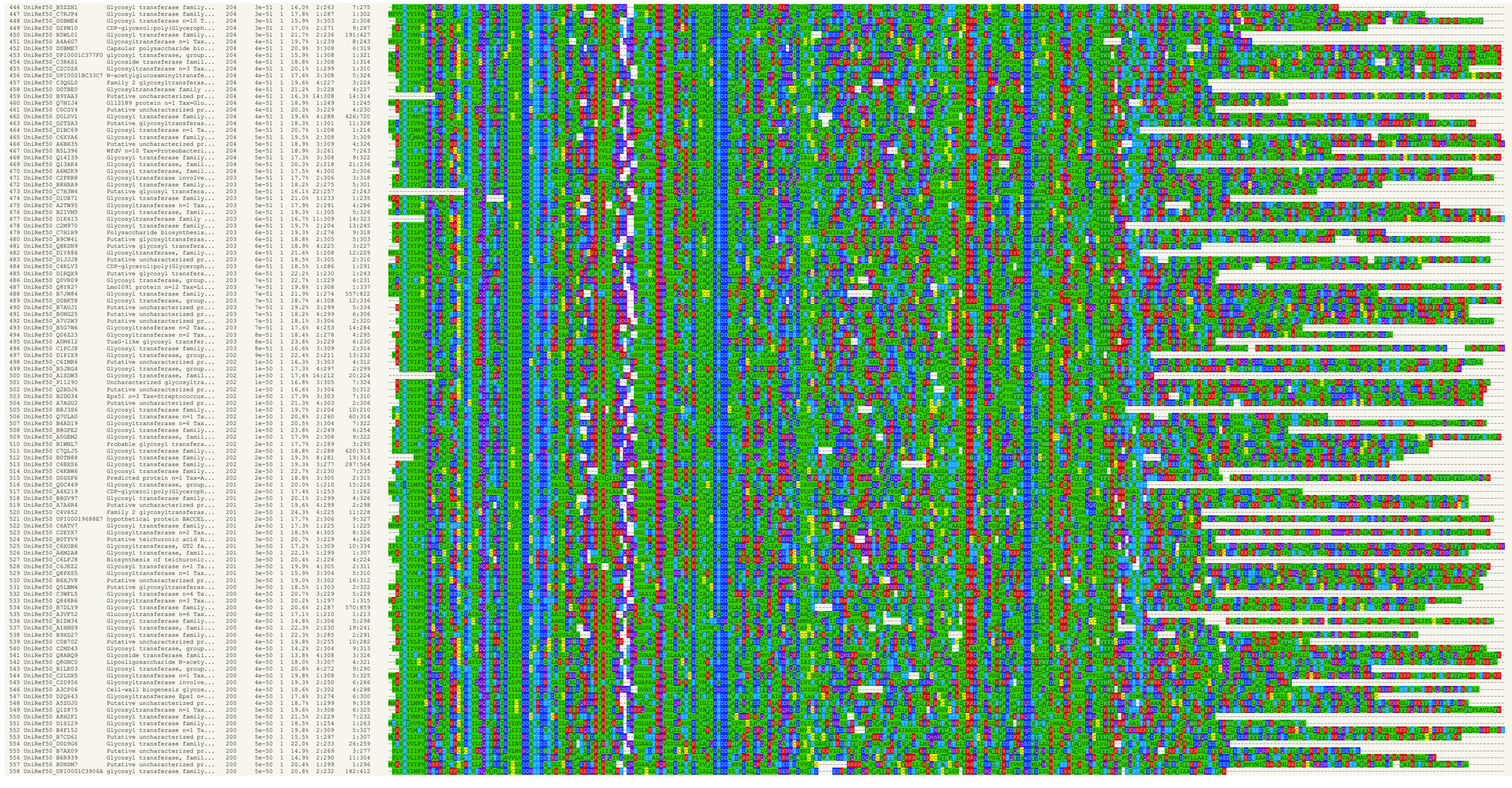
421 UniRef50_A3KLK7 Beta-1,3-N-acetylglucosamin... 205 1e-51 1 18.5% 3:305 8:322
422 UniRef50_Q15RB7 Glycosyl transferase, famil... 205 1e-51 1 20.4% 3:252 4:272
423 UniRef50_Q8YUP6 Glucosyltransferase n=3 Tax... 205 1e-51 1 21.6% 3:261 7:264
424 UniRef50_C0EIM5 Putative uncharacterized pr... 205 1e-51 1 20.0% 1:307 10:327
425 UniRef50_Q60B59 Glycosyl transferase, group... 205 2e-51 1 16.2% 2:230 8:235
426 UniRef50_C5VL41 Glycosyl transferase, group... 205 2e-51 1 15.9% 4:292 3:296
427 UniRef50_Q2LPU6 Glycosyltransferase n=1 Tax... 205 2e-51 1 15.3% 2:309 6:327
428 UniRef50_B2ISC3 Glycosyl transferase n=2 Ta... 205 2e-51 1 23.3% 3:217 5:231
429 UniRef50_C6JQJ1 Glycosyl transferase n=1 Ta... 205 2e-51 1 17.8% 3:306 5:316
430 UniRef50_D1F9P0 Group 2 glycosyl transferas... 204 2e-51 1 18.1% 3:306 11:316
431 UniRef50_C2FUJ3 Glycosyltransferase n=1 Tax... 205 2e-51 1 18.2% 3:309 6:326
432 UniRef50_C6X0E9 Beta-1,3-glucosyltransferas... 205 2e-51 1 21.4% 3:301 2:320
433 UniRef50_Q11C09 Glycosyl transferase, famil... 204 2e-51 1 23.0% 1:257 5:253
434 UniRef50_D1PLO8 Capsular polysaccharide bio... 205 2e-51 1 25.7% 11:224 12:233
435 UniRef50_C9PXQ4 Group 2 glycosyl transferas... 205 2e-51 1 17.1% 14:258 2:249
436 UniRef50_UPI0001B4A2A5 glycosyltransferase n=1 Tax... 205 2e-51 1 14.8% 1:304 5:318
437 UniRef50_C3WCV9 Glycosyl transferase n=1 Ta... 205 2e-51 1 17.9% 3:309 5:322
438 UniRef50_B5CLQ5 Putative uncharacterized pr... 205 2e-51 1 20.5% 1:307 1:328
439 UniRef50_B4F184 Glycosyl transferase n=2 Ta... 204 2e-51 1 16.8% 2:305 4:321
440 UniRef50_C5VL43 Glycosyl transferase, group... 204 2e-51 1 18.5% 1:259 1:258
441 UniRef50_Q8A779 Glycoside transferase famil... 204 2e-51 1 18.0% 4:298 3:299
442 UniRef50_D1PWT5 Exopolysaccharide biosynthe... 204 2e-51 1 17.4% 2:300 5:310
443 UniRef50_A6ELC1 TuaG n=3 Tax=Bacteroidetes ... 204 3e-51 1 18.6% 2:265 16:268
444 UniRef50_B9Y890 Putative uncharacterized pr... 204 3e-51 1 18.3% 1:301 1:316
445 UniRef50_UPI0001C41AE6 glycosyl transferase GT2 fa... 204 3e-51 1 20.8% 2:304 4:318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447 UniRef50_C7RJP4 Glycosyl transferase family... 204 3e-51 1 17.8% 1:287 1:302
448 UniRef50_D0BME4 Glycosyl transferase n=10 T... 204 3e-51 1 15.9% 3:303 2:308
449 UniRef50_D2PW10 CDP-glycerol:poly(Glyceroph... 204 3e-51 1 17.0% 2:271 9:287
450 UniRef50_B5WLG1 Glycosyl transferase family... 204 3e-51 1 21.7% 2:236 191:427
451 UniRef50_A4A6G7 Glycosyltransferase n=1 Tax... 204 4e-51 1 19.7% 1:239 8:243
452 UniRef50_D0BME7 Capsular polysaccharide bio... 204 4e-51 1 20.9% 3:308 6:319
453 UniRef50_UPI0001C377F0 glycosyl transferase, group... 204 4e-51 1 15.9% 1:308 1:321
454 UniRef50_C3R6S1 Glycoside transferase famil... 204 4e-51 1 18.8% 1:308 1:314
455 UniRef50_C2C0Z6 Glycosyltransferase n=3 Tax... 204 4e-51 1 20.1% 1:299 1:310
456 UniRef50_UPI0001BC33C7 N-acetylglucosaminyltransfera... 204 4e-51 1 17.6% 1:308 5:324
457 UniRef50_C3QGL0 Family 2 glycosyltransferas... 204 4e-51 1 19.6% 4:227 3:224
458 UniRef50_D0TBE0 Glycosyltransferase family ... 204 4e-51 1 21.2% 3:228 4:227
459 UniRef50_B9YAA3 Putative uncharacterized pr... 204 4e-51 1 16.3% 14:308 14:314
460 UniRef50_Q7NIJ4 Gll2189 protein n=1 Tax=Glo... 204 4e-51 1 18.9% 1:249 1:245
461 UniRef50_C0CGY4 Putative uncharacterized pr... 204 4e-51 1 20.3% 3:229 4:230
462 UniRef50_D0LGV1 Glycosyl transferase family... 204 4e-51 1 19.6% 4:288 426:720
463 UniRef50_D2TSA3 Putative glycosyltransferas... 204 4e-51 1 18.3% 1:301 11:328
464 UniRef50_D1BC69 Glycosyl transferase n=1 Ta... 204 5e-51 1 20.7% 1:208 1:214
465 UniRef50_C6XYA6 Glycosyl transferase family... 204 5e-51 1 19.5% 2:308 3:309
466 UniRef50_A6BH35 Putative uncharacterized pr... 204 5e-51 1 18.9% 3:309 4:326
467 UniRef50_B5L396 WfdV n=10 Tax=Proteobacteri... 204 5e-51 1 18.9% 3:261 7:263
468 UniRef50_Q14I39 Glycosyl transferase family... 204 5e-51 1 17.3% 3:308 9:322
469 UniRef50_Q13AK4 Glycosyl transferase, famil... 204 5e-51 1 20.3% 2:218 21:236
470 UniRef50_A6MZK9 Glycosyl transferase, famil... 204 5e-51 1 17.5% 4:300 2:306
471 UniRef50_C2FPK8 Glycosyltransferase involve... 203 5e-51 1 17.7% 2:306 3:318
472 UniRef50_B8HRA9 Glycosyl transferase family... 203 5e-51 1 18.2% 2:275 5:301
473 UniRef50_C7HJW4 Putative glycosyl transfera... 203 5e-51 1 16.1% 22:257 2:243
474 UniRef50_D1UB71 Glycosyl transferase family... 203 5e-51 1 21.0% 1:233 1:235
475 UniRef50_A2TW95 Glycosyltransferase n=1 Tax... 203 5e-51 1 17.9% 2:291 4:286
476 UniRef50_B2IVM5 Glycosyl transferase, famil... 203 5e-51 1 19.3% 1:305 5:326
477 UniRef50_D1K413 Glycosyl transferase family ... 203 6e-51 1 16.7% 11:309 14:322
478 UniRef50_C2M970 Glycosyl transferase family... 203 6e-51 1 19.7% 2:204 13:245
479 UniRef50_C7H1H9 Polysaccharide biosynthesis... 203 6e-51 1 19.3% 2:276 9:318
480 UniRef50_B9CW41 Putative glycosyltransferas... 203 6e-51 1 18.8% 2:305 5:303
481 UniRef50_Q8RSN9 Putative glycosyl transfera... 203 6e-51 1 18.9% 4:225 3:227
482 UniRef50_D1Y886 Glycosyltransferase, family... 203 6e-51 1 21.6% 1:208 12:229
483 UniRef50_D1JJJ8 Putative uncharacterized pr... 203 6e-51 1 18.5% 3:305 2:310
484 UniRef50_C4RLV3 CDP-glycerol:poly(Glyceroph... 203 6e-51 1 18.5% 1:286 1:291
485 UniRef50_D1RQX9 Putative glycosyl transfera... 203 6e-51 1 22.2% 1:230 1:243
486 UniRef50_Q0VR09 Glycosyl transferase, group... 203 7e-51 1 22.7% 1:229 4:231
487 UniRef50_Q8Y827 Lmo1091 protein n=12 Tax=Li... 203 7e-51 1 19.8% 1:308 1:337
488 UniRef50_B7JW84 Glycosyl transferase family... 203 7e-51 1 21.9% 1:274 557:822
489 UniRef50_D0BKT8 Glycosyl transferase, group... 203 7e-51 1 18.7% 4:308 12:336
490 UniRef50_B7AUJ1 Putative uncharacterized pr... 203 7e-51 1 19.2% 3:299 5:334
491 UniRef50_B0NGZ5 Putative uncharacterized pr... 203 7e-51 1 18.2% 4:299 6:306
492 UniRef50_A7VZW3 Putative uncharacterized pr... 203 7e-51 1 18.1% 3:306 2:320
493 UniRef50_B5GTW6 Glycosyltransferase n=2 Tax... 203 7e-51 1 17.6% 4:253 14:284
494 UniRef50_Q06Z23 Glycosyltransferase n=2 Tax... 203 8e-51 1 18.4% 2:278 4:295
495 UniRef50_A0MEI2 TuaG-like glycosyl transfer... 203 8e-51 1 23.8% 3:229 6:230
496 UniRef50_C1PCJ8 Glycosyl transferase family... 203 8e-51 1 16.6% 3:309 2:314
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498 UniRef50_C6IMK6 Putative uncharacterized pr... 202 1e-50 1 16.3% 3:303 4:312
499 UniRef50_B5JRG4 Glycosyl transferase, group... 202 1e-50 1 17.3% 4:297 2:299
500 UniRef50_A1SDW3 Glycosyl transferase, famil... 202 1e-50 1 17.6% 14:212 20:224
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503 UniRef50_B2DG34 Eps5I n=3 Tax=Streptococcus... 202 1e-50 1 17.9% 3:303 7:310
504 UniRef50_A7AGU2 Putative uncharacterized pr... 202 1e-50 1 21.3% 4:303 2:306
505 UniRef50_B8J3S6 Glycosyl transferase family... 202 1e-50 1 19.7% 2:204 10:210
506 UniRef50_Q7ULA0 Glycosyl transferase n=1 Ta... 202 1e-50 1 20.8% 2:260 60:314
507 UniRef50_B4AD19 Glycosyl transferase n=6 Tax... 202 1e-50 1 20.5% 4:304 7:322
508 UniRef50_B8GFE2 Glycosyl transferase family... 202 1e-50 1 23.8% 2:249 6:254
509 UniRef50_A5GEM2 Glycosyl transferase, famil... 202 1e-50 1 17.9% 2:308 9:322
510 UniRef50_B1WNL7 Probable glycosyl transfera... 202 1e-50 1 17.7% 2:289 3:295
511 UniRef50_C7QLJ5 Glycosyl transferase family... 202 2e-50 1 18.8% 2:288 620:913
512 UniRef50_B0TN88 Glycosyl transferase family... 202 2e-50 1 19.3% 8:281 19:314
513 UniRef50_C6BXS6 Glycosyl transferase family... 202 2e-50 1 19.3% 3:277 287:564
514 UniRef50_C4KBW6 Glycosyl transferase family... 202 2e-50 1 22.7% 2:230 7:235
515 UniRef50_D0SXP6 Predicted protein n=1 Tax=A... 202 2e-50 1 18.8% 3:305 2:315
516 UniRef50_Q0C449 Glycosyl transferase, group... 201 2e-50 1 20.0% 1:210 15:226
517 UniRef50_A4X219 CDP-glycerol:poly(Glyceroph... 201 2e-50 1 17.4% 1:253 1:262
518 UniRef50_B8GV97 Glycosyl transferase family... 201 2e-50 1 20.1% 2:299 4:326
519 UniRef50_A7AER4 Putative uncharacterized pr... 201 2e-50 1 19.6% 4:299 2:298
520 UniRef50_C4V652 Family 2 glycosyltransferas... 201 2e-50 1 24.3% 4:225 11:228
521 UniRef50_UPI000196888E7 hypothetical protein BACCEL... 201 2e-50 1 17.7% 2:306 9:327
522 UniRef50_C6AFV7 Glycosyl transferase family... 201 2e-50 1 17.3% 1:225 1:225
523 UniRef50_C2EYX7 Glycosyltransferase n=2 Tax... 201 3e-50 1 18.5% 4:305 8:326
524 UniRef50_B0TYV9 Putative teichuronic acid b... 201 3e-50 1 20.7% 3:229 4:226
525 UniRef50_C6XDB6 Glycosyltransferase, GT2 fa... 201 3e-50 1 17.2% 1:309 10:334
526 UniRef50_A6M2A8 Glycosyl transferase, famil... 201 3e-50 1 22.1% 1:299 1:307
527 UniRef50_C6LFJ8 Biosynthesis of teichuronic... 201 3e-50 1 20.4% 2:226 4:224
528 UniRef50_C6JKZ2 Glycosyl transferase n=1 Ta... 201 3e-50 1 19.9% 4:305 2:311
529 UniRef50_Q8PXS5 Glycosyltransferase n=1 Tax... 201 3e-50 1 15.9% 3:304 5:310
530 UniRef50_B6XJV8 Putative uncharacterized pr... 201 3e-50 1 19.0% 3:302 16:312
531 UniRef50_Q5LBM4 Putative glycosyltransferas... 200 3e-50 1 18.5% 1:303 2:322
532 UniRef50_C3WFL5 Glycosyltransferase n=4 Ta... 200 4e-50 1 20.7% 3:229 5:229
533 UniRef50_Q848R6 Glycosyltransferase n=3 Tax... 200 4e-50 1 20.2% 1:297 1:315
534 UniRef50_B7DLY9 Glycosyl transferase family... 200 4e-50 1 20.6% 2:287 570:859
535 UniRef50_A3VF52 Glucosyltransferase n=6 Tax... 200 4e-50 1 17.1% 1:210 1:213
536 UniRef50_B1ZW34 Glycosyl transferase family... 200 4e-50 1 14.8% 2:306 5:298
537 UniRef50_A1HN89 Glycosyl transferase, famil... 200 4e-50 1 22.3% 2:230 19:241
538 UniRef50_B9XD27 Glycosyl transferase family... 200 4e-50 1 22.3% 3:285 2:291
539 UniRef50_C0B702 Putative uncharacterized pr... 200 4e-50 1 19.8% 3:255 10:282
540 UniRef50_C2MG43 Glycosyl transferase, group... 200 4e-50 1 14.2% 2:304 9:313
541 UniRef50_Q8ABQ9 Glycoside transferase famil... 200 4e-50 1 13.8% 4:308 3:326
542 UniRef50_Q8GNC0 Lipooligosaccharide N-acety... 200 4e-50 1 18.0% 3:307 4:321
543 UniRef50_B1LEG3 Glycosyl transferase, group... 200 4e-50 1 20.8% 4:272 9:290
544 UniRef50_C2LDX5 Glycosyltransferase n=1 Tax... 200 4e-50 1 19.8% 1:308 5:325
545 UniRef50_C2D956 Glycosyltransferase involve... 200 4e-50 1 19.3% 2:250 6:266
546 UniRef50_A3CP06 Cell-wall biogenesis glycos... 200 4e-50 1 18.6% 2:302 4:298
547 UniRef50_D2Q643 Glycosyltransferase Eps1 n=... 200 4e-50 1 17.6% 3:274 6:300
548 UniRef50_A5ZUJ0 Putative uncharacterized pr... 200 4e-50 1 18.7% 1:299 9:318
549 UniRef50_Q1E875 Glycosyl transferase n=1 Tax... 200 5e-50 1 19.6% 3:308 6:325
550 UniRef50_A8H2F1 Glycosyl transferase family... 200 5e-50 1 21.5% 2:229 7:232
551 UniRef50_D1S129 Glycosyl transferase family... 200 5e-50 1 18.5% 1:254 1:263
552 UniRef50_B4F152 Glycosyl transferase n=1 Ta... 200 5e-50 1 19.8% 2:309 5:327
553 UniRef50_B7CD61 Putative uncharacterized pr... 200 5e-50 1 15.5% 1:297 1:307
554 UniRef50_D0D9G6 Glycosyl transferase family... 200 5e-50 1 22.0% 2:233 26:259
555 UniRef50_B7AX09 Putative uncharacterized pr... 200 5e-50 1 14.9% 2:269 3:277
556 UniRef50_B6R939 Glycosyl transferase, famil... 200 5e-50 1 14.9% 2:290 11:304
557 UniRef50_B0NSM7 Putative uncharacterized pr... 200 5e-50 1 20.4% 1:299 1:296
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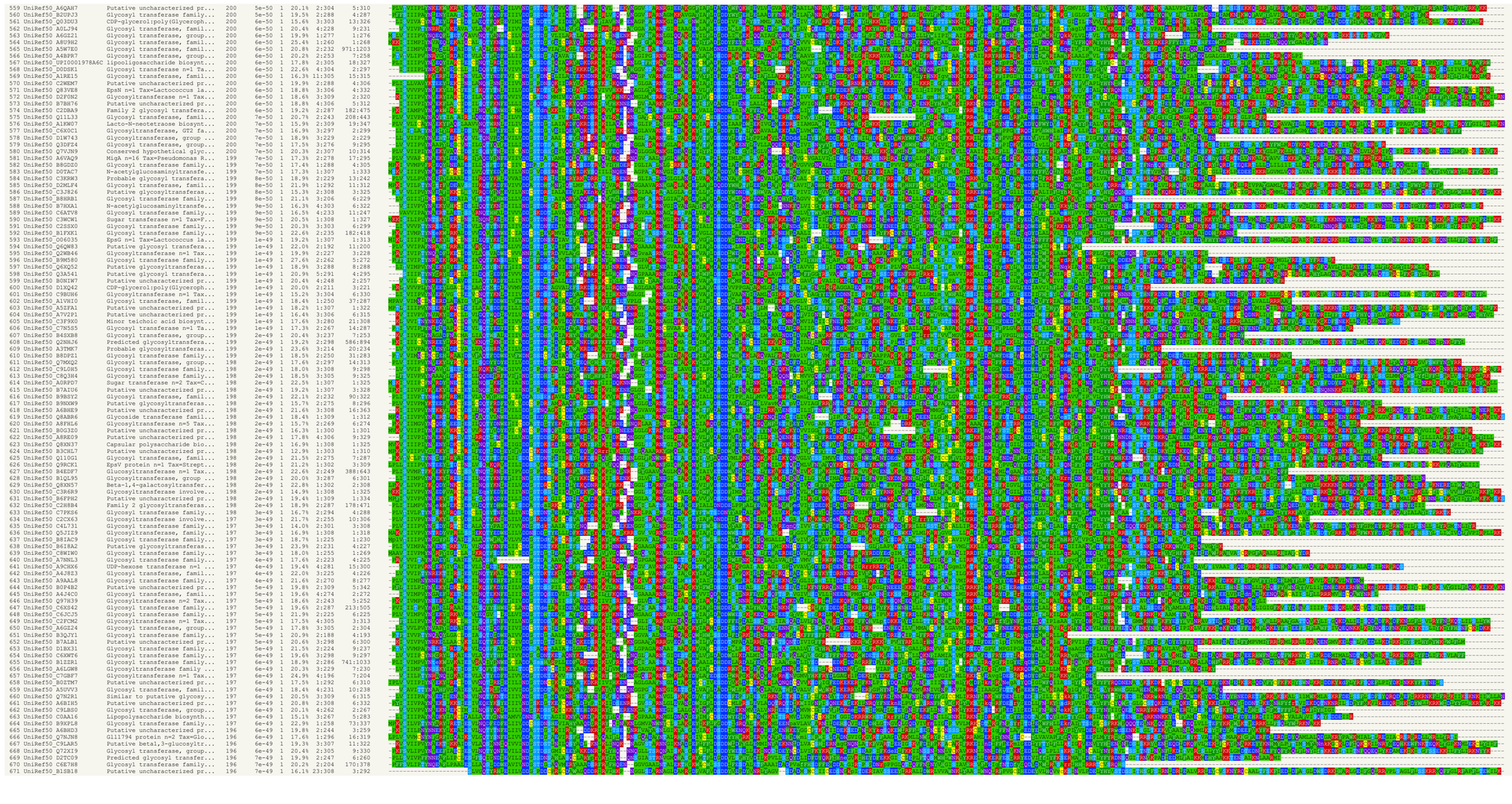
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562 UniRef50_A0LJ94 Glycosyl transferase, famil... 200 6e-50 1 20.4% 4:228 9:231
563 UniRef50_A6GZ21 Glycosyl transferase, group... 200 6e-50 1 19.9% 1:277 1:276
564 UniRef50_A8U9H2 Glycosyl transferase, famil... 200 6e-50 1 25.4% 1:260 1:268
565 UniRef50_A5W7E0 Glycosyl transferase, famil... 200 6e-50 1 20.8% 2:232 971:1203
566 UniRef50_A4BPR7 Glycosyl transferase, group... 200 6e-50 1 20.2% 2:253 7:258
567 UniRef50_UPI0001978A6C lipooligosaccharide biosynt... 200 6e-50 1 17.8% 2:305 18:327
568 UniRef50_D0DSK1 Glycosyl transferase n=1 Ta... 200 6e-50 1 22.6% 4:304 2:297
569 UniRef50_A1RE15 Glycosyl transferase, famil... 200 6e-50 1 16.3% 11:305 15:315
570 UniRef50_C2WEM7 Putative uncharacterized pr... 200 6e-50 1 19.9% 2:288 4:306
571 UniRef50_Q83VE8 EpsN n=1 Tax=Lactococcus la... 200 6e-50 1 18.8% 3:306 4:332
572 UniRef50_D2F0N2 Glycosyltransferase n=1 Tax... 200 6e-50 1 18.6% 3:309 2:320
573 UniRef50_B7BH76 Putative uncharacterized pr... 200 6e-50 1 18.8% 4:306 5:312
574 UniRef50_C2DBA9 Family 2 glycosyl transfera... 200 6e-50 1 19.2% 2:287 182:475
575 UniRef50_Q11L33 Glycosyl transferase, famil... 200 7e-50 1 20.7% 2:243 208:443
576 UniRef50_A1KW07 Lacto-N-neotetraose biosynt... 200 7e-50 1 15.9% 2:309 19:347
577 UniRef50_C6X0C1 Glycosyltransferase, GT2 fa... 200 7e-50 1 16.9% 3:297 2:299
578 UniRef50_D1W743 Glycosyltransferase, group ... 200 7e-50 1 18.9% 3:229 2:229
579 UniRef50_Q3DFZ4 Glycosyl transferase, group... 200 7e-50 1 17.5% 3:276 9:295
580 UniRef50_Q7VJN9 Conserved hypothetical glyc... 200 7e-50 1 20.3% 2:307 10:314
581 UniRef50_A6VAQ9 MigA n=16 Tax=Pseudomonas a... 199 7e-50 1 17.3% 2:278 17:295
582 UniRef50_B8GDZ0 Glycosyl transferase family... 199 7e-50 1 17.4% 1:288 4:305
583 UniRef50_D0TAC7 N-acetylglucosaminyltransfe... 199 7e-50 1 17.3% 1:307 1:333
584 UniRef50_C3KRW3 Probable glycosyl transfera... 199 8e-50 1 18.9% 2:229 13:242
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587 UniRef50_B8HRB1 Glycosyl transferase family... 199 8e-50 1 21.1% 3:206 6:229
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589 UniRef50_C6ATV8 Glycosyl transferase family... 199 9e-50 1 16.5% 4:233 11:247
590 UniRef50_C3WCW1 Sugar transferase n=1 Tax=F... 199 9e-50 1 20.5% 1:308 1:327
591 UniRef50_C2SSX0 Glycosyl transferase family... 199 9e-50 1 20.3% 3:303 6:299
592 UniRef50_B1FXK1 Glycosyl transferase family... 199 9e-50 1 22.6% 2:235 182:418
593 UniRef50_C0G635 EpsG n=1 Tax=Lactococcus la... 199 1e-49 1 19.2% 1:307 1:313
594 UniRef50_Q6QW83 Putative glycosyl transfera... 199 1e-49 1 22.0% 2:192 11:200
595 UniRef50_Q2WB46 Glycosyltransferase n=1 Tax... 199 1e-49 1 19.9% 2:227 3:228
596 UniRef50_B9M580 Glycosyl transferase family... 199 1e-49 1 27.6% 2:262 5:272
597 UniRef50_Q6XQ52 Putative glycosyltransferas... 199 1e-49 1 18.9% 3:288 8:288
598 UniRef50_Q3A541 Putative glycosyl transfera... 199 1e-49 1 20.9% 5:291 4:295
599 UniRef50_B0NIW7 Putative uncharacterized pr... 199 1e-49 1 20.4% 4:248 2:257
600 UniRef50_D1KQ42 CDP-glycerol:poly(Glyceroph... 199 1e-49 1 20.0% 2:211 3:221
601 UniRef50_C9BUH6 Glycosyltransferase n=1 Tax... 199 1e-49 1 15.2% 3:304 6:330
602 UniRef50_A1VHI0 Glycosyl transferase, famil... 199 1e-49 1 18.4% 1:250 37:287
603 UniRef50_A5ZFA1 Putative uncharacterized pr... 199 1e-49 1 18.2% 1:307 1:322
604 UniRef50_A7V2P1 Putative uncharacterized pr... 199 1e-49 1 16.4% 3:306 6:315
605 UniRef50_C3F9X0 Minor teichoic acid biosynt... 199 1e-49 1 17.6% 3:280 21:308
606 UniRef50_C7NSS5 Glycosyl transferase n=1 Ta... 199 1e-49 1 17.3% 2:267 14:287
607 UniRef50_B4SXB8 Glycosyl transferase, group... 199 2e-49 1 20.4% 3:237 7:253
608 UniRef50_Q2NHJ6 Predicted glycosyltransfera... 199 2e-49 1 19.2% 2:298 586:894
609 UniRef50_A3TMK7 Probable glycosyltransferas... 199 2e-49 1 23.6% 3:214 20:234
610 UniRef50_B8DPZ1 Glycosyl transferase family... 199 2e-49 1 18.5% 2:250 31:283
611 UniRef50_Q7MQQ2 Glycosyl transferase, group... 198 2e-49 1 17.6% 2:297 14:313
612 UniRef50_C9LOH5 Glycosyl transferase family... 198 2e-49 1 18.0% 3:308 9:298
613 UniRef50_C8Q3H4 Glycosyl transferase family... 198 2e-49 1 18.5% 3:305 9:325
614 UniRef50_A0RFD7 Sugar transferase n=2 Tax=C... 198 2e-49 1 22.5% 1:307 1:325
615 UniRef50_B7AIU6 Putative uncharacterized pr... 198 2e-49 1 19.2% 1:307 3:328
616 UniRef50_B9BSY2 Glycosyl transferase, famil... 198 2e-49 1 22.1% 2:232 90:322
617 UniRef50_B9NXW9 Putative glycosyltransferas... 198 2e-49 1 15.7% 2:275 8:296
618 UniRef50_A6BHE9 Putative uncharacterized pr... 198 2e-49 1 21.6% 3:308 16:363
619 UniRef50_Q8ABR6 Glycoside transferase famil... 198 2e-49 1 18.4% 1:309 1:312
620 UniRef50_A8FHL6 Glycosyltransferase n=5 Tax... 198 2e-49 1 15.7% 2:269 6:274
621 UniRef50_B0G3Z0 Putative uncharacterized pr... 198 2e-49 1 16.3% 1:300 1:301
622 UniRef50_A8REO9 Putative uncharacterized pr... 198 2e-49 1 17.8% 4:306 9:329
623 UniRef50_Q8XM37 Capsular polysaccharide bio... 198 2e-49 1 16.8% 1:308 1:325
624 UniRef50_B3CHL7 Putative uncharacterized pr... 198 2e-49 1 12.9% 1:303 1:310
625 UniRef50_Q11GG1 Glycosyl transferase, famil... 198 2e-49 1 21.5% 2:275 7:287
626 UniRef50_Q9RCK1 EpsV protein n=1 Tax=Strept... 198 2e-49 1 21.2% 1:302 1:309
627 UniRef50_B4EDF7 Glycosyltransferase n=1 Tax... 198 2e-49 1 22.6% 2:249 388:643
628 UniRef50_B1QL95 Glycosyltransferase, group ... 198 2e-49 1 20.0% 3:287 6:301
629 UniRef50_Q8XM57 Beta-1,4-galactosyltransfer... 198 2e-49 1 22.8% 1:302 2:308
630 UniRef50_C3R6R9 Glycosyltransferase involve... 198 2e-49 1 14.9% 1:308 1:325
631 UniRef50_B6FPH2 Putative uncharacterized pr... 198 2e-49 1 19.4% 1:309 1:334
632 UniRef50_C2HBB4 Family 2 glycosyltransferas... 198 2e-49 1 18.9% 2:287 178:471
633 UniRef50_C7PKS6 Glycosyl transferase family... 198 3e-49 1 16.7% 2:294 4:288
634 UniRef50_C2CX63 Glycosyltransferase involve... 197 3e-49 1 21.7% 2:255 10:306
635 UniRef50_C4L731 Glycosyl transferase family... 197 3e-49 1 14.0% 2:301 3:308
636 UniRef50_Q5JIZ9 Glycosyltransferase, family... 197 3e-49 1 16.9% 1:308 1:318
637 UniRef50_B8IAC9 Glycosyl transferase family... 197 3e-49 1 18.7% 1:225 1:230
638 UniRef50_B6I8A2 Putative glycosyltransferas... 197 3e-49 1 23.9% 2:231 4:227
639 UniRef50_C8WIW0 Glycosyl transferase family... 197 3e-49 1 18.0% 1:255 1:269
640 UniRef50_A7NNL3 Glycosyl transferase family... 197 4e-49 1 17.6% 2:223 4:225
641 UniRef50_A9CHX6 UDP-hexose transferase n=1 ... 197 4e-49 1 19.4% 4:281 15:300
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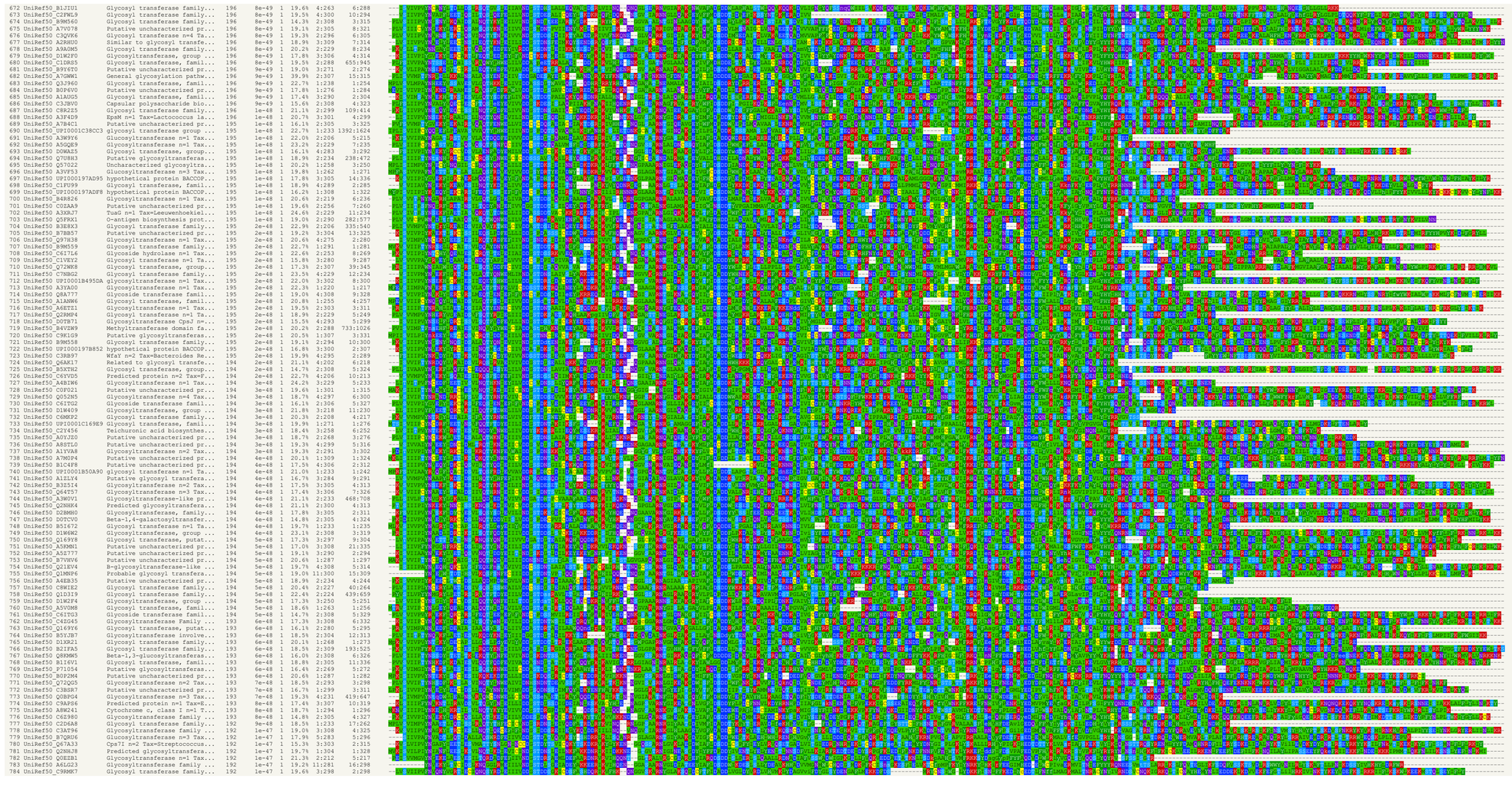
645 UniRef50_A4J4C0 Glycosyl transferase, famil... 197 5e-49 1 19.6% 4:274 2:272
646 UniRef50_Q97H39 Glycosyltransferase n=2 Tax... 197 5e-49 1 18.6% 2:243 5:252
647 UniRef50_C6X542 Glycosyl transferase family... 197 5e-49 1 19.6% 2:287 213:505
648 UniRef50_C6JCJ5 Glycosyl transferase family... 197 5e-49 1 21.9% 2:225 6:225
649 UniRef50_C2FCM2 Glycosyltransferase n=1 Tax... 197 5e-49 1 17.5% 4:305 3:313
650 UniRef50_A6GZ24 Glycosyl transferase, group... 197 5e-49 1 17.8% 3:305 2:304
651 UniRef50_B3QJY1 Glycosyl transferase family... 197 5e-49 1 20.9% 2:188 4:193
652 UniRef50_B7ALB1 Putative uncharacterized pr... 197 5e-49 1 20.6% 3:298 6:300
653 UniRef50_D1BX31 Glycosyl transferase family... 197 6e-49 1 21.5% 2:224 9:237
654 UniRef50_C6XWT6 Glycosyl transferase family... 197 6e-49 1 19.6% 3:298 9:297
655 UniRef50_B1Z2R1 Glycosyl transferase family... 197 6e-49 1 18.9% 2:286 741:1033
656 UniRef50_A6LQW8 Glycosyltransferase family ... 197 6e-49 1 20.3% 3:229 7:230
657 UniRef50_C7GBF7 Glycosyltransferase n=1 Tax... 197 6e-49 1 24.9% 4:196 7:204
658 UniRef50_B0ZTM7 Putative uncharacterized pr... 197 6e-49 1 17.5% 1:292 6:310
659 UniRef50_A5UVV3 Glycosyl transferase, famil... 197 6e-49 1 18.6% 4:231 10:238
660 UniRef50_Q7N2R1 Similar to putative glycosy... 197 6e-49 1 20.5% 3:309 6:315
661 UniRef50_A6B1H5 Putative uncharacterized pr... 197 6e-49 1 20.8% 2:308 6:332
662 UniRef50_C9LA80 Glycosyl transferase, group... 197 6e-49 1 20.1% 4:262 2:267
663 UniRef50_C0AA16 Lipopolysaccharide biosynth... 197 6e-49 1 15.1% 3:267 5:283
664 UniRef50_B9XPL8 Glycosyl transferase family... 197 6e-49 1 22.9% 1:258 73:337
665 UniRef50_A6BHD3 Putative uncharacterized pr... 196 6e-49 1 19.8% 2:244 3:259
666 UniRef50_Q7NJN8 Gll1794 protein n=2 Tax=Glo... 196 6e-49 1 17.6% 1:296 16:319
667 UniRef50_C9LAR5 Putative beta1,3-glucosyltr... 196 6e-49 1 19.3% 3:307 11:322
668 UniRef50_Q72XI9 Glycosyl transferase, group... 196 7e-49 1 20.4% 2:305 9:330
669 UniRef50_D2TCO9 Predicted glycosyl transfer... 196 7e-49 1 19.9% 2:247 6:260
670 UniRef50_C6E7H8 Glycosyl transferase family... 196 7e-49 1 20.2% 2:204 170:378
671 UniRef50_B1SB18 Putative uncharacterized pr... 196 7e-49 1 16.1% 23:308 3:292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673 UniRef50_C2FWL9 Glycosyl transferase family... 196 8e-49 1 19.5% 4:300 10:294
674 UniRef50_B9M560 Glycosyl transferase family... 196 8e-49 1 14.3% 2:308 3:315
675 UniRef50_A7VO78 Putative uncharacterized pr... 196 8e-49 1 19.1% 2:305 8:321
676 UniRef50_C5QVK6 Glycosyl transferase n=4 Ta... 196 8e-49 1 19.3% 2:296 6:305
677 UniRef50_A2RHU0 Similar to glycosyl transfe... 196 8e-49 1 18.9% 3:309 7:314
678 UniRef50_A9A0M5 Glycosyl transferase family... 196 8e-49 1 20.2% 2:229 8:234
679 UniRef50_D1W2F0 Glycosyltransferase, group ... 196 8e-49 1 17.8% 3:306 4:314
680 UniRef50_C1DRS5 Glycosyl transferase, famil... 196 8e-49 1 19.5% 2:288 655:945
681 UniRef50_B9Y6T0 Putative uncharacterized pr... 196 9e-49 1 19.0% 3:271 2:274
682 UniRef50_A7GWW1 General glycosylation pathw... 196 9e-49 1 39.8% 2:307 15:315
683 UniRef50_Q3J960 Glycosyl transferase, famil... 196 9e-49 1 22.7% 1:238 1:254
684 UniRef50_B0P6V0 Putative uncharacterized pr... 196 9e-49 1 17.8% 1:276 1:284
685 UniRef50_A1AUG5 Glycosyl transferase, famil... 196 9e-49 1 17.4% 2:290 2:304
686 UniRef50_C3JBV0 Capsular polysaccharide bio... 196 9e-49 1 15.6% 2:308 4:323
687 UniRef50_C8R2Z5 Glycosyl transferase family... 196 1e-48 1 21.1% 2:299 109:414
688 UniRef50_A3F4D9 GpaM n=1 Tax=Lactococcus pa... 195 1e-48 1 20.7% 3:301 4:299
689 UniRef50_A7B4C1 Putative uncharacterized pr... 195 1e-48 1 16.1% 2:305 3:325
690 UniRef50_UPI0001C38CC3 Glycosyl transferase group ... 195 1e-48 1 22.7% 1:233 1392:1624
691 UniRef50_A3W9Y6 Glucosyltransferase n=1 Tax... 195 1e-48 1 22.0% 2:206 5:215
692 UniRef50_A5GQE9 Glycosyltransferase n=1 Tax... 195 1e-48 1 23.2% 2:229 7:235
693 UniRef50_D0WAZ5 Glycosyl transferase, group... 195 1e-48 1 16.1% 4:283 3:292
694 UniRef50_Q7UBH3 Putative glycosyltransferase... 195 1e-48 1 18.8% 2:234 238:472
695 UniRef50_Q57022 Uncharacterized glycosyltra... 195 1e-48 1 20.2% 1:258 3:250
696 UniRef50_A3VF53 Glucosyltransferase n=3 Tax... 195 1e-48 1 19.8% 1:262 1:271
697 UniRef50_UPI0001970AD95 hypothetical protein BACCOP... 195 1e-48 1 17.8% 2:305 14:336
698 UniRef50_C1FU99 Glycosyl transferase, famil... 195 1e-48 1 18.9% 4:289 2:285
699 UniRef50_UPI0001970ADF8 hypothetical protein BACCOP... 195 1e-48 1 16.2% 1:308 1:322
700 UniRef50_B4R826 Glycosyltransferase n=1 Tax... 195 1e-48 1 20.6% 2:219 6:236
701 UniRef50_C0ZAA9 Putative uncharacterized pr... 195 1e-48 1 19.6% 2:256 7:260
702 UniRef50_A3XRJ7 TuaG n=1 Tax=Leeuwenhoekiel... 195 1e-48 1 24.6% 2:229 11:234
703 UniRef50_Q5FRX1 O-antigen biosynthesis prot... 195 1e-48 1 19.0% 2:290 282:577
704 UniRef50_B3E8X3 Glycosyl transferase family... 195 1e-48 1 22.9% 2:206 335:540
705 UniRef50_B7B8S7 Putative uncharacterized pr... 195 2e-48 1 19.2% 3:304 13:325
706 UniRef50_Q97H38 Glycosyltransferase n=1 Tax... 195 2e-48 1 20.6% 4:275 2:280
707 UniRef50_B9M559 Glycosyl transferase family... 195 2e-48 1 22.7% 1:291 1:281
708 UniRef50_C6I7L6 Glycoside hydrolase n=1 Tax... 195 2e-48 1 22.6% 2:253 8:269
709 UniRef50_C1VEY2 Glycosyltransferase n=1 Tax... 195 2e-48 1 15.8% 3:280 9:287
710 UniRef50_Q72WK8 Glycosyl transferase, group... 195 2e-48 1 17.3% 2:307 39:345
711 UniRef50_C7NBG2 Glycosyl transferase family... 195 2e-48 1 23.5% 4:229 12:234
712 UniRef50_UPI0001B495DA glycosyltransferase n=1 Tax... 195 2e-48 1 22.0% 3:302 8:300
713 UniRef50_A3VA00 Glycosyltransferase n=1 Tax... 195 2e-48 1 22.3% 1:220 1:217
714 UniRef50_Q8A777 Glycoside transferase famil... 195 2e-48 1 19.0% 4:308 9:328
715 UniRef50_A1AMW6 Glycosyl transferase, famil... 195 2e-48 1 20.8% 1:255 4:257
716 UniRef50_A6ETZ1 Glycosyltransferase n=1 Tax... 195 2e-48 1 19.5% 2:303 3:311
717 UniRef50_Q2RMP4 Glycosyl transferase n=1 Ta... 195 2e-48 1 18.9% 2:229 5:249
718 UniRef50_D0TBT1 Glycosyltransferase CpsJ n=... 195 2e-48 1 15.5% 4:293 5:299
719 UniRef50_B4VZW9 Methyltransferase domain fa... 195 2e-48 1 20.2% 2:288 733:1026
720 UniRef50_C9K1G9 Putative glycosyltransferas... 195 2e-48 1 20.5% 1:307 3:331
721 UniRef50_B9M558 Glycosyl transferase family... 195 2e-48 1 19.1% 2:294 10:300
722 UniRef50_UPI0001970B852 hypothetical protein BACCOP... 195 2e-48 1 16.8% 3:300 2:307
723 UniRef50_C3RB97 WfaY n=2 Tax=Bacteroides Re... 195 2e-48 1 19.9% 4:295 2:289
724 UniRef50_Q6AK17 Related to glycosyl transfe... 194 2e-48 1 21.1% 4:202 6:218
725 UniRef50_B5XTH2 Glycosyl transferase, group... 194 2e-48 1 14.7% 2:308 5:324
726 UniRef50_C6YVD5 Predicted protein n=2 Tax=F... 194 2e-48 1 22.7% 4:206 10:213
727 UniRef50_A4B1W6 Glycosyltransferase n=1 Tax... 194 3e-48 1 24.2% 3:229 5:233
728 UniRef50_C0FQ21 Putative uncharacterized pr... 194 3e-48 1 19.6% 1:301 1:315
729 UniRef50_Q052N5 Glycosyltransferase n=4 Tax... 194 3e-48 1 18.7% 4:297 6:300
730 UniRef50_C6I7G2 Glycoside transferase famil... 194 3e-48 1 16.1% 2:306 5:327
731 UniRef50_D1W409 Glycosyltransferase, group ... 194 3e-48 1 21.8% 3:218 11:230
732 UniRef50_C6MKP2 Glycosyl transferase family... 194 3e-48 1 20.3% 2:208 4:217
733 UniRef50_UPI0001C169E9 Glycosyl transferase, famil... 194 3e-48 1 19.9% 1:271 1:276
734 UniRef50_C2Y456 Teichuronic acid biosynthes... 194 3e-48 1 18.4% 3:258 6:252
735 UniRef50_A0YJZ0 Putative uncharacterized pr... 194 3e-48 1 18.7% 2:268 3:276
736 UniRef50_A8STL0 Putative uncharacterized pr... 194 3e-48 1 19.3% 4:299 5:316
737 UniRef50_A1YVA8 Glycosyltransferase n=2 Tax... 194 3e-48 1 19.3% 2:291 3:302
738 UniRef50_A7M0P4 Putative uncharacterized pr... 194 4e-48 1 20.1% 1:309 1:324
739 UniRef50_B1C4F8 Putative uncharacterized pr... 194 4e-48 1 17.5% 2:306 2:312
740 UniRef50_UPI0001B50A90 glycosyl transferase n=1 Ta... 194 4e-48 1 21.0% 1:233 1:242
741 UniRef50_A1ZLY4 Putative glycosyl transfera... 194 4e-48 1 16.7% 3:284 9:291
742 UniRef50_B3ES14 Glycosyltransferase n=2 Tax... 194 4e-48 1 17.5% 3:305 4:313
743 UniRef50_Q64T57 Glycosyltransferase n=3 Tax... 194 4e-48 1 17.4% 3:306 7:326
744 UniRef50_A3W0V1 Glycosyltransferase-like pr... 194 4e-48 1 21.1% 2:233 468:708
745 UniRef50_Q2NHK4 Predicted glycosyltransfera... 194 4e-48 1 21.1% 2:300 4:313
746 UniRef50_D2BMH0 Glycosyltransferase, family... 194 4e-48 1 17.8% 3:305 2:311
747 UniRef50_D0TCV0 Beta-1,4-galactosyltransfer... 194 4e-48 1 14.8% 2:305 4:324
748 UniRef50_B5I672 Glycosyl transferase n=1 Ta... 194 4e-48 1 19.7% 1:233 1:235
749 UniRef50_D1W6W2 Glycosyltransferase, group ... 194 4e-48 1 23.1% 2:308 3:319
750 UniRef50_Q169Y8 Glycosyl transferase, putat... 194 5e-48 1 17.3% 3:297 9:304
751 UniRef50_A5WDM1 Putative uncharacterized pr... 194 5e-48 1 17.0% 3:308 21:335
752 UniRef50_A5Z777 Putative uncharacterized pr... 194 5e-48 1 19.1% 3:290 2:294
753 UniRef50_B7VHV6 Putative uncharacterized pr... 194 5e-48 1 20.6% 1:287 1:297
754 UniRef50_Q21EV4 B-glycosyltransferase-like ... 194 5e-48 1 19.7% 4:308 5:314
755 UniRef50_Q1MNP6 Probable glycosyl transfera... 194 5e-48 1 19.0% 11:300 15:309
756 UniRef50_A4EB35 Putative uncharacterized pr... 194 5e-48 1 18.9% 2:234 4:244
757 UniRef50_C8WIE2 Glycosyl transferase family... 194 5e-48 1 20.4% 2:227 40:264
758 UniRef50_Q1D3I9 Glycosyl transferase family... 194 5e-48 1 22.4% 2:224 439:659
759 UniRef50_D1W2F4 Glycosyltransferase, group ... 194 5e-48 1 17.3% 3:250 5:251
760 UniRef50_A5VDM8 Glycosyl transferase, famil... 194 5e-48 1 18.6% 1:263 1:256
761 UniRef50_C6ITG3 Glycoside transferase famil... 194 5e-48 1 14.7% 2:308 5:329
762 UniRef50_C4ZG45 Glycosyltransferase family ... 193 6e-48 1 17.3% 3:308 6:332
763 UniRef50_Q169Y6 Glycosyl transferase, putat... 193 6e-48 1 16.1% 2:280 5:295
764 UniRef50_B5YJB7 Glycosyltransferase involve... 193 6e-48 1 18.5% 2:304 12:313
765 UniRef50_D1XR21 Glycosyl transferase family... 193 6e-48 1 20.1% 1:268 1:273
766 UniRef50_B2IFA5 Glycosyl transferase family... 193 6e-48 1 18.5% 2:309 193:525
767 UniRef50_Q8KMW5 Beta-1,3-glucosyltransferas... 193 6e-48 1 16.0% 2:308 6:326
768 UniRef50_B1I6V1 Glycosyl transferase, famil... 193 6e-48 1 18.8% 2:305 11:336
769 UniRef50_F7105A Glycosyltransferase family ... 193 6e-48 1 16.4% 2:269 5:272
770 UniRef50_B0P2M4 Putative uncharacterized pr... 193 6e-48 1 20.6% 1:287 1:282
771 UniRef50_Q72QG5 Glycosyltransferase n=2 Tax... 193 7e-48 1 18.5% 2:293 3:298
772 UniRef50_C3B3R7 Putative uncharacterized pr... 193 7e-48 1 16.7% 1:299 3:311
773 UniRef50_Q0BPG4 Glycosyltransferase n=3 Tax... 193 7e-48 1 19.3% 4:231 419:647
774 UniRef50_C9APS6 Predicted protein n=1 Tax=E... 193 8e-48 1 17.4% 3:307 10:319
775 UniRef50_A4HE41 Cytochrome c, class I n=1 T... 193 8e-48 1 18.7% 1:294 1:296
776 UniRef50_C6Z980 Glycosyltransferase family ... 193 8e-48 1 14.8% 2:305 4:327
777 UniRef50_C2D6A8 Glycosyl transferase family... 192 9e-48 1 18.5% 1:233 17:262
778 UniRef50_C3AT96 Glycosyltransferase family ... 192 1e-47 1 19.0% 3:308 4:325
779 UniRef50_B7QKU6 Glucosyltransferase n=3 Tax... 192 1e-47 1 17.9% 5:283 5:296
780 UniRef50_Q67A33 Cps7I n=2 Tax=Streptococcus... 192 1e-47 1 15.3% 3:303 2:315
781 UniRef50_Q2NNJ8 Predicted glycosyltransfera... 192 1e-47 1 19.7% 1:304 1:328
782 UniRef50_Q0EZB1 Glycosyltransferase n=1 Tax... 192 1e-47 1 21.3% 2:212 5:217
783 UniRef50_A6LG23 Glycosyltransferase family ... 192 1e-47 1 19.2% 11:281 16:298
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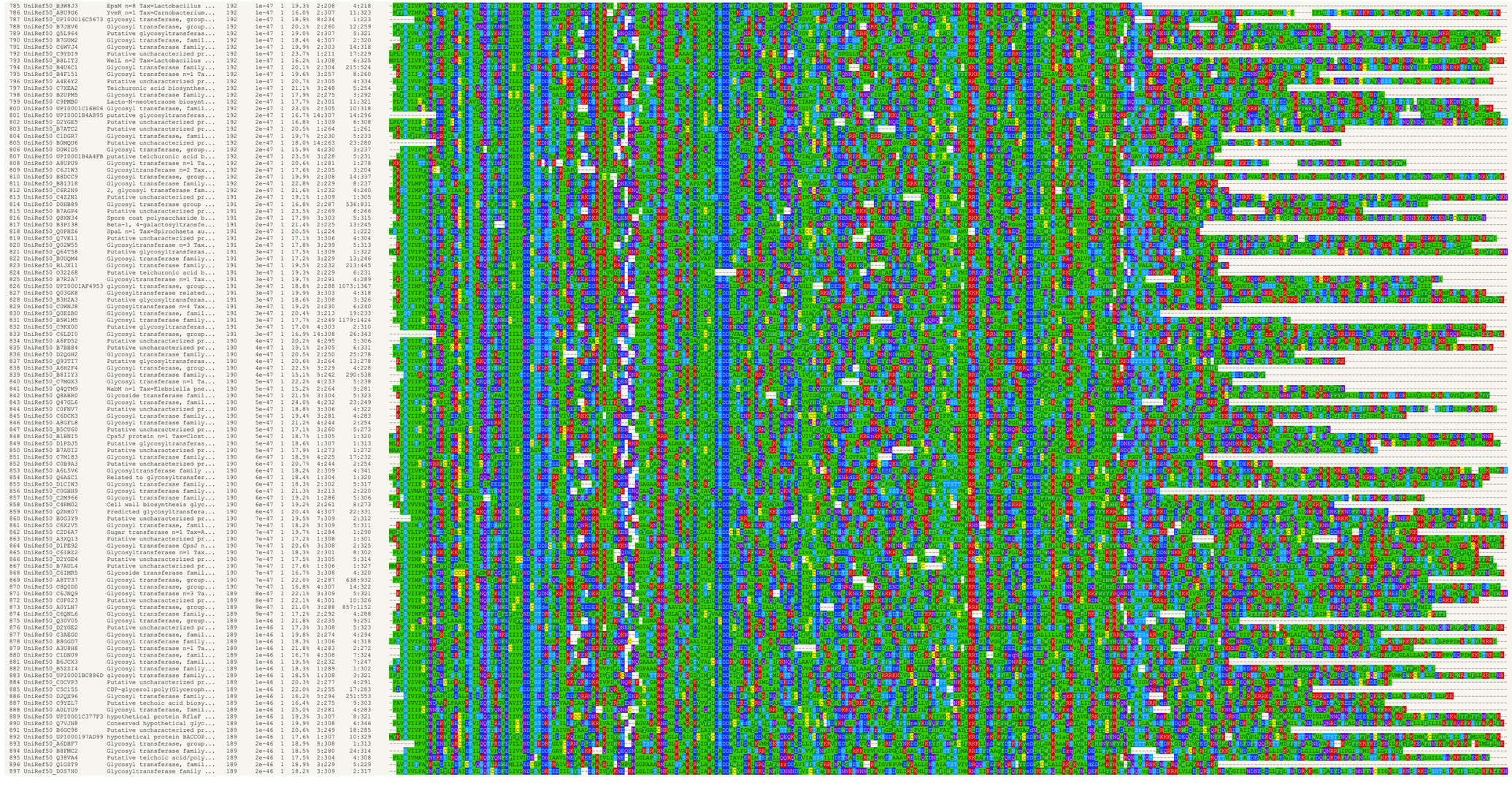
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788 UniRef50_B7JHV6 Glycosyl transferase, group... 192 1e-47 1 20.1% 2:260 12:259
789 UniRef50_Q5L9K4 Putative glycosyltransferas... 192 1e-47 1 19.0% 2:307 5:321
790 UniRef50_B7GUM2 Glycosyl transferase, famil... 192 1e-47 1 18.4% 4:307 2:320
791 UniRef50_C6WVJ4 Glycosyl transferase family... 192 1e-47 1 19.9% 2:303 14:318
792 UniRef50_C9YDI9 Putative uncharacterized pr... 192 1e-47 1 23.7% 1:211 17:229
793 UniRef50_B8LIT3 Weil n=2 Tax=Lactobacillus ... 192 1e-47 1 16.2% 1:308 6:325
794 UniRef50_B4U6C1 Glycosyl transferase family... 192 1e-47 1 20.1% 2:304 215:524
795 UniRef50_B4F1S1 Glycosyl transferase n=1 Ta... 192 1e-47 1 19.6% 2:257 8:260
796 UniRef50_A4E6Y2 Putative uncharacterized pr... 192 1e-47 1 20.7% 2:305 4:334
797 UniRef50_C7XEA2 Teichuronic acid biosynthes... 192 1e-47 1 21.1% 3:248 5:254
798 UniRef50_B2UPM5 Glycosyl transferase family... 192 1e-47 1 17.9% 2:275 3:292
799 UniRef50_C9PMB0 Lacto-N-neotetraose biosynt... 192 1e-47 1 17.7% 2:301 11:321
800 UniRef50_UPI0001C16B06 Glycosyl transferase, famil... 192 2e-47 1 23.0% 2:305 10:318
801 UniRef50_UPI0001B4A895 putative glycosyltransferase... 192 2e-47 1 16.7% 14:307 14:296
802 UniRef50_D2YGE5 Putative uncharacterized pr... 192 2e-47 1 16.8% 1:309 6:308
803 UniRef50_B7ATC2 Putative uncharacterized pr... 192 2e-47 1 20.5% 1:264 1:261
804 UniRef50_C1DGR7 Glycosyl transferase, famil... 192 2e-47 1 19.7% 2:230 5:233
805 UniRef50_B0MQU6 Putative uncharacterized pr... 192 2e-47 1 18.0% 14:263 23:280
806 UniRef50_D0WID5 Glycosyl transferase, group... 192 2e-47 1 15.9% 4:230 3:237
807 UniRef50_UPI0001B4A4FB putative teichuronic acid b... 192 2e-47 1 23.5% 3:228 5:231
808 UniRef50_A8UPU9 Glycosyltransferase n=1 Ta... 192 2e-47 1 20.6% 1:281 1:278
809 UniRef50_C6J1W3 Glycosyltransferase n=2 Tax... 192 2e-47 1 17.6% 2:205 3:204
810 UniRef50_B8DCC9 Glycosyl transferase, group... 192 2e-47 1 19.9% 2:308 14:337
811 UniRef50_B8I318 Glycosyl transferase family... 192 2e-47 1 22.8% 2:229 8:237
812 UniRef50_C6RZN9 2, glycosyl transferase fam... 192 2e-47 1 21.6% 1:232 4:240
813 UniRef50_C4Z2N1 Putative uncharacterized pr... 191 2e-47 1 19.1% 1:309 1:305
814 UniRef50_D0HB89 Glycosyl transferase group ... 191 2e-47 1 16.8% 2:287 536:831
815 UniRef50_B7AGP4 Putative uncharacterized pr... 191 2e-47 1 23.5% 2:269 6:266
816 UniRef50_Q8KM34 Spore coat polysaccharide b... 191 2e-47 1 17.9% 3:303 5:315
817 UniRef50_B3PI38 Beta-1, 4-galactosyltransfe... 191 2e-47 1 21.4% 2:225 13:245
818 UniRef50_Q0PHZ6 SpaI n=1 Tax=Spirochaeta au... 191 2e-47 1 20.5% 1:224 1:222
819 UniRef50_Q7VPI1 Putative uncharacterized pr... 191 2e-47 1 17.1% 2:306 4:304
820 UniRef50_Q02W55 Glycosyltransferase n=3 Tax... 191 2e-47 1 17.8% 3:299 5:313
821 UniRef50_Q64T58 Putative glycosyltransferas... 191 3e-47 1 17.5% 1:309 1:322
822 UniRef50_B0UQM4 Glycosyl transferase family... 191 3e-47 1 17.2% 3:229 13:246
823 UniRef50_B1JX11 Glycosyl transferase family... 191 3e-47 1 19.5% 2:232 213:445
824 UniRef50_O32268 Putative teichuronic acid b... 191 3e-47 1 19.3% 2:229 6:231
825 UniRef50_B7RZA7 Glycosyltransferase n=1 Tax... 191 3e-47 1 19.7% 2:291 4:289
826 UniRef50_UPI0001AF4953 glycosyl transferase, group... 191 3e-47 1 18.8% 2:288 1073:1367
827 UniRef50_Q03GK8 Glycosyltransferase related... 191 3e-47 1 19.9% 3:303 4:318
828 UniRef50_B3HZA3 Putative glycosyltransferas... 191 3e-47 1 18.6% 2:308 3:326
829 UniRef50_C0WNJ8 Glycosyltransferase n=4 Tax... 191 3e-47 1 19.2% 2:230 6:240
830 UniRef50_Q0EZB0 Glycosyl transferase, famil... 191 3e-47 1 20.4% 3:213 19:233
831 UniRef50_B5W1M5 Glycosyl transferase family... 191 3e-47 1 17.7% 2:249 1179:1424
832 UniRef50_C9KX00 Putative glycosyltransferas... 191 3e-47 1 17.0% 4:303 2:310
833 UniRef50_C6LDI0 Glycosyl transferase, group... 191 3e-47 1 16.9% 14:308 26:343
834 UniRef50_A6TD52 Putative uncharacterized pr... 190 4e-47 1 20.2% 4:295 5:306
835 UniRef50_B7BH84 Putative uncharacterized pr... 190 4e-47 1 19.1% 2:305 6:331
836 UniRef50_D2QGH2 Glycosyl transferase family... 190 4e-47 1 20.5% 2:250 25:278
837 UniRef50_Q93TI7 Putative glycosyltransferase... 190 4e-47 1 20.6% 3:264 13:278
838 UniRef50_A6H2F4 Glycosyl transferase, group... 190 4e-47 1 22.5% 3:229 4:228
839 UniRef50_B8I1Y3 Glycosyl transferase family... 190 4e-47 1 15.1% 5:242 290:538
840 UniRef50_C7MGX3 Glycosyl transferase n=1 Ta... 190 5e-47 1 22.2% 4:233 5:238
841 UniRef50_Q4QTM9 WabM n=1 Tax=Klebsiella pne... 190 5e-47 1 15.2% 2:264 9:281
842 UniRef50_Q8ABR0 Glycoside transferase famil... 190 5e-47 1 21.5% 3:304 5:323
843 UniRef50_Q47GL6 Glycosyl transferase, famil... 190 5e-47 1 24.0% 4:232 23:249
844 UniRef50_C0FNV7 Putative uncharacterized pr... 190 5e-47 1 18.8% 3:306 4:322
845 UniRef50_C6DCK3 Glycosyl transferase family... 190 5e-47 1 19.4% 3:281 4:283
846 UniRef50_A8GFL8 Glycosyl transferase family... 190 5e-47 1 21.2% 4:244 2:254
847 UniRef50_B5CU60 Putative uncharacterized pr... 190 5e-47 1 17.1% 3:260 5:273
848 UniRef50_B1BNI5 Cps5J protein n=1 Tax=Clost... 190 5e-47 1 18.7% 1:305 1:320
849 UniRef50_D1PDJ5 Putative glycosyltransferase... 190 5e-47 1 18.6% 1:307 1:313
850 UniRef50_B7AUI2 Putative uncharacterized pr... 190 5e-47 1 17.9% 1:273 1:272
851 UniRef50_C7M183 Glycosyl transferase family... 190 6e-47 1 18.5% 4:225 17:232
852 UniRef50_C0B9A3 Putative uncharacterized pr... 190 6e-47 1 20.7% 4:244 2:254
853 UniRef50_A6L5V6 Glycosyltransferase family ... 190 6e-47 1 18.2% 2:309 4:341
854 UniRef50_Q6A3C1 Related to glycosyltransfer... 190 6e-47 1 18.4% 1:304 1:320
855 UniRef50_D1C1W3 Glycosyl transferase family... 190 6e-47 1 18.3% 2:302 5:317
856 UniRef50_C0GHH9 Glycosyl transferase family... 190 6e-47 1 21.3% 3:213 2:220
857 UniRef50_C2M966 Glycosyl transferase family... 190 6e-47 1 19.2% 1:286 5:306
858 UniRef50_C4KMG2 Cell wall biosynthesis glyc... 190 6e-47 1 19.2% 2:261 8:273
859 UniRef50_Q2NH07 Predicted glycosyltransfera... 190 6e-47 1 20.4% 4:307 22:331
860 UniRef50_B0G3Y9 Putative uncharacterized pr... 190 7e-47 1 19.5% 7:309 2:312
861 UniRef50_C6XZV5 Glycosyl transferase, famil... 190 7e-47 1 18.2% 3:309 5:311
862 UniRef50_C2D6A7 Sugar transferase n=1 Tax=A... 190 7e-47 1 19.7% 1:284 1:290
863 UniRef50_A3XQ13 Putative uncharacterized pr... 190 7e-47 1 17.2% 1:308 1:301
864 UniRef50_D1PER2 Glycosyl transferase CpaJ n... 190 7e-47 1 20.6% 3:308 2:325
865 UniRef50_C6IBZ2 Glycosyltransferase n=1 Tax... 190 7e-47 1 18.3% 2:301 8:302
866 UniRef50_D2YGE4 Putative uncharacterized pr... 190 7e-47 1 17.5% 3:305 5:314
867 UniRef50_B7AIL4 Putative uncharacterized pr... 190 7e-47 1 17.6% 1:306 1:327
868 UniRef50_C6IMR5 Glycoside transferase famil... 190 7e-47 1 16.7% 3:308 4:320
869 UniRef50_A8TT37 Glycosyl transferase, group... 190 7e-47 1 22.0% 2:287 638:932
870 UniRef50_C8QD00 Glycosyl transferase, group... 190 7e-47 1 16.8% 4:307 14:322
871 UniRef50_C6JNQ9 Glycosyl transferase n=3 Ta... 189 8e-47 1 22.1% 3:309 5:321
872 UniRef50_C0F023 Putative uncharacterized pr... 189 8e-47 1 22.1% 4:301 10:326
873 UniRef50_A0YLN7 Glycosyl transferase, group... 189 9e-47 1 21.0% 3:288 857:1152
874 UniRef50_C6QNL6 Glycosyl transferase family... 189 9e-47 1 17.2% 2:292 4:288
875 UniRef50_Q30V05 Glycosyl transferase, group... 189 1e-46 1 21.8% 2:235 9:251
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877 UniRef50_C3AEG0 Glycosyl transferase, famil... 189 1e-46 1 19.8% 2:274 4:294
878 UniRef50_B8GGD7 Glycosyl transferase family... 189 1e-46 1 18.3% 1:306 4:318
879 UniRef50_A3UH88 Glycosyl transferase n=1 Ta... 189 1e-46 1 21.8% 4:283 2:272
880 UniRef50_C1DNO9 Glycosyl transferase, famil... 189 1e-46 1 16.7% 4:308 7:324
881 UniRef50_B6JCX3 Glycosyl transferase, famil... 189 1e-46 1 19.5% 2:232 7:247
882 UniRef50_B5Z2I4 Glycosyl transferase, famil... 189 1e-46 1 18.3% 1:289 1:302
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887 UniRef50_C9YZL7 Putative techoic acid biosy... 189 1e-46 1 16.4% 2:275 9:303
888 UniRef50_A0LVU9 Glycosyl transferase, famil... 189 1e-46 1 25.0% 2:281 4:283
889 UniRef50_UPI0001C377F3 hypothetical protein RflaF ... 189 1e-46 1 19.3% 3:307 8:321
890 UniRef50_Q7VJN8 Conserved hypothetical glyc... 189 1e-46 1 19.9% 2:308 6:346
891 UniRef50_B6QC98 Putative uncharacterized pr... 189 1e-46 1 20.6% 3:249 18:285
892 UniRef50_UPI000197AD99 hypothetical protein BACCOP... 189 1e-46 1 17.6% 1:307 10:329
893 UniRef50_A6DHF7 Glycosyl transferase, group... 189 2e-46 1 18.9% 8:308 1:313
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895 UniRef50_Q3BVA4 Putative teichoic acid/poly... 189 2e-46 1 17.5% 2:304 4:308
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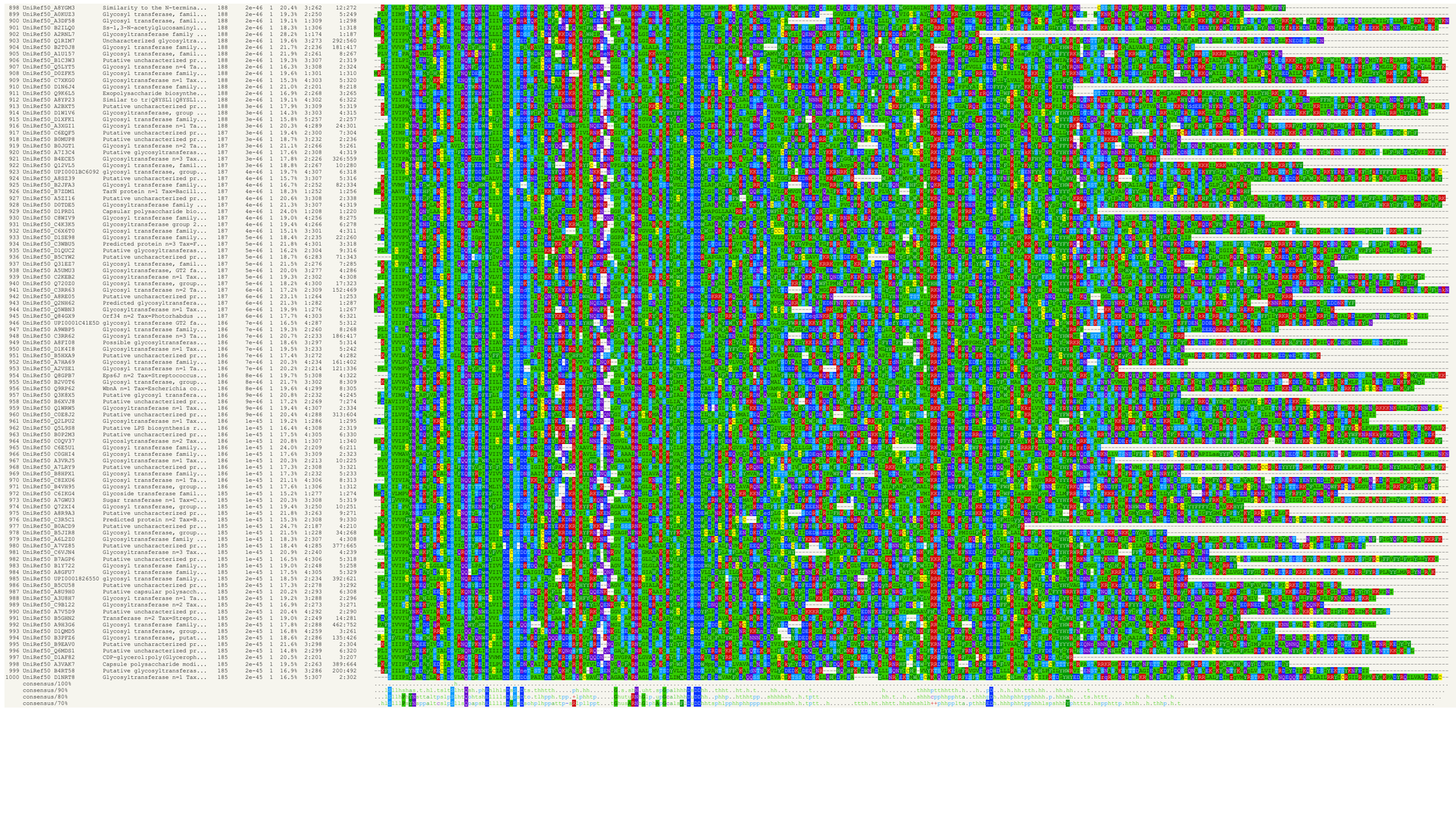
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899 UniRef50_A0KUZ3 Glycosyl transferase, famil... 188 2e-46 1 19.3% 2:250 5:249
900 UniRef50_A3DF58 Glycosyl transferase, famil... 188 2e-46 1 19.1% 1:309 1:298
901 UniRef50_B2ILQ0 Ss-1,3-N-acetylglucosaminyl... 188 2e-46 1 18.3% 1:306 1:318
902 UniRef50_A2RML7 Glycosyltransferase family ... 188 2e-46 1 28.2% 1:174 1:187
903 UniRef50_Q1RIM7 Uncharacterized glycosyltra... 188 2e-46 1 19.6% 3:273 292:560
904 UniRef50_B2TOJ8 Glycosyl transferase family... 188 2e-46 1 21.7% 2:236 181:417
905 UniRef50_A1UI57 Glycosyl transferase, famil... 188 2e-46 1 21.9% 2:261 8:267
906 UniRef50_B1C3W3 Putative uncharacterized pr... 188 2e-46 1 19.3% 3:307 2:319
907 UniRef50_Q5LYT5 Glycosyl transferase n=4 Ta... 188 2e-46 1 16.3% 3:308 2:324
908 UniRef50_D0ZEF5 Glycosyl transferase family... 188 2e-46 1 19.6% 1:301 1:310
909 UniRef50_C7XKG0 Glycosyltransferase n=1 Tax... 188 2e-46 1 15.3% 4:303 5:320
910 UniRef50_D1N6J4 Glycosyl transferase family... 188 2e-46 1 21.0% 2:201 8:218
911 UniRef50_Q9K6L5 Exopolysaccharide biosynthes... 188 2e-46 1 16.9% 2:268 3:265
912 UniRef50_A8YP23 Similar to tr|Q8YSL1|Q8YSL1... 188 2e-46 1 19.1% 4:302 6:322
913 UniRef50_A2BXT5 Putative uncharacterized pr... 188 3e-46 1 17.9% 3:309 5:319
914 UniRef50_D1W1V6 Glycosyltransferase, group ... 188 3e-46 1 14.3% 3:303 4:315
915 UniRef50_D1XFK1 Glycosyl transferase family... 188 3e-46 1 15.8% 5:257 2:257
916 UniRef50_A3XG11 Glycosyl transferase n=1 Ta... 188 3e-46 1 20.3% 4:289 24:301
917 UniRef50_C6EQF5 Putative uncharacterized pr... 187 3e-46 1 19.4% 2:300 7:304
918 UniRef50_B0MUP8 Putative uncharacterized pr... 187 3e-46 1 18.7% 3:232 2:236
919 UniRef50_B0JGT1 Glycosyl transferase n=2 Ta... 187 3e-46 1 21.1% 2:266 5:261
920 UniRef50_A7I3C4 Putative glycosyltransferas... 187 3e-46 1 17.6% 2:308 4:319
921 UniRef50_B4ECE5 Glycosyltransferase n=3 Tax... 187 3e-46 1 17.8% 2:226 326:559
922 UniRef50_Q12VL5 Glycosyl transferase, famil... 187 3e-46 1 18.8% 2:267 10:280
923 UniRef50_UPI0001BC6092 glycosyl transferase, group... 187 4e-46 1 19.7% 4:307 6:318
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925 UniRef50_B2JFA3 Glycosyl transferase family... 187 4e-46 1 16.7% 2:252 82:334
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928 UniRef50_D0TDE5 Glycosyltransferase family ... 187 4e-46 1 21.3% 3:307 4:319
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930 UniRef50_C8WIV9 Glycosyl transferase family... 187 4e-46 1 19.0% 4:256 8:275
931 UniRef50_C4K3K5 Glycosyltransferase group 2... 187 4e-46 1 19.4% 4:266 6:278
932 UniRef50_C6X6T0 Glycosyl transferase family... 187 4e-46 1 15.1% 3:301 4:311
933 UniRef50_D1SE98 Glycosyl transferase family... 187 5e-46 1 18.4% 2:235 22:260
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935 UniRef50_D1QDC2 Putative glycosyltransferas... 187 5e-46 1 16.2% 2:304 9:316
936 UniRef50_B5CYW2 Putative uncharacterized pr... 187 5e-46 1 18.7% 6:283 71:343
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938 UniRef50_A5UMU3 Glycosyltransferase, GT2 fa... 187 5e-46 1 20.0% 3:277 4:286
939 UniRef50_C2KEB2 Glycosyltransferase n=1 Tax... 187 5e-46 1 19.3% 2:302 4:308
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946 UniRef50_UPI0001C41E5D glycosyl transferase GT2 fa... 186 7e-46 1 16.5% 4:287 5:312
947 UniRef50_A9WBP5 Glycosyl transferase family... 186 7e-46 1 19.3% 2:260 8:268
948 UniRef50_C3RR62 Glycosyl transferase n=3 Ta... 186 7e-46 1 20.7% 2:233 186:417
949 UniRef50_A8F108 Possible glycosyltransferas... 186 7e-46 1 18.6% 3:297 5:314
950 UniRef50_D1K4I8 Glycosyltransferase n=1 Tax... 186 7e-46 1 19.5% 3:233 5:242
951 UniRef50_B5HXA9 Putative uncharacterized pr... 186 7e-46 1 17.4% 3:272 4:282
952 UniRef50_A7HA69 Glycosyl transferase family... 186 7e-46 1 20.3% 4:234 161:402
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956 UniRef50_Q9RP62 WbnA n=1 Tax=Escherichia co... 186 8e-46 1 19.4% 4:299 8:305
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958 UniRef50_B6XVJ8 Putative uncharacterized pr... 186 9e-46 1 17.2% 2:269 7:274
959 UniRef50_Q1WRW5 Glycosyltransferase n=1 Tax... 186 9e-46 1 19.4% 4:307 2:334
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964 UniRef50_C0QV37 Glycosyltransferase n=2 Tax... 186 1e-45 1 20.8% 1:307 1:340
965 UniRef50_C6ES01 Glycosyl transferase family... 186 1e-45 1 24.0% 2:209 6:211
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967 UniRef50_A3VRJ5 Glycosyltransferase n=1 Tax... 186 1e-45 1 20.3% 2:213 10:225
968 UniRef50_A7LKY9 Putative uncharacterized pr... 186 1e-45 1 17.3% 2:308 3:321
969 UniRef50_B8HPX1 Glycosyl transferase family... 186 1e-45 1 17.3% 2:232 5:233
970 UniRef50_C8ZXU6 Glycosyl transferase n=1 Ta... 186 1e-45 1 21.1% 4:306 8:313
971 UniRef50_B4VW95 Glycosyltransferase, group... 186 1e-45 1 17.6% 1:306 1:312
972 UniRef50_C6IKG4 Glycoside transferase famil... 185 1e-45 1 15.2% 1:277 1:274
973 UniRef50_A7GWU3 Sugar transferase n=1 Tax=C... 185 1e-45 1 20.3% 3:308 5:319
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978 UniRef50_B5JIR8 Glycosyl transferase, group... 185 1e-45 1 21.5% 1:228 34:268
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983 UniRef50_B1Y722 Glycosyl transferase family... 185 1e-45 1 19.0% 2:248 5:258
984 UniRef50_A8GFU7 Glycosyl transferase family... 185 1e-45 1 17.5% 4:305 5:329
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988 UniRef50_A3U8H7 Glycosyl transferase n=1 Ta... 185 2e-45 1 19.2% 3:288 2:296
989 UniRef50_C9B122 Glycosyltransferase n=2 Tax... 185 2e-45 1 16.9% 2:273 3:271
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991 UniRef50_B5GHN2 Transferase n=2 Tax=Strepto... 185 2e-45 1 19.0% 2:249 14:281
992 UniRef50_A9H3G6 Glycosyl transferase family... 185 2e-45 1 17.8% 2:288 462:752
993 UniRef50_D1QMD5 Glycosyl transferase, group... 185 2e-45 1 16.8% 4:259 3:261
994 UniRef50_B3PZF6 Glycosyl transferase, putat... 185 2e-45 1 18.6% 2:286 135:426
995 UniRef50_B9EAV0 Putative uncharacterized pr... 185 2e-45 1 21.6% 3:298 2:304
996 UniRef50_Q6MDS1 Putative uncharacterized pr... 185 2e-45 1 14.8% 2:299 6:320
997 UniRef50_D1AF82 CDP-glycerol:poly(Glyceroph... 185 2e-45 1 20.5% 2:201 3:207
998 UniRef50_A3VAK7 Capsular polysaccharide modi... 185 2e-45 1 19.5% 2:263 389:664
999 UniRef50_B4RT58 Putative glycosyltransferas... 185 2e-45 1 16.9% 3:286 200:492
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consensus/100%
consensus/90%
consensus/80%
consensus/70%

Figure S7

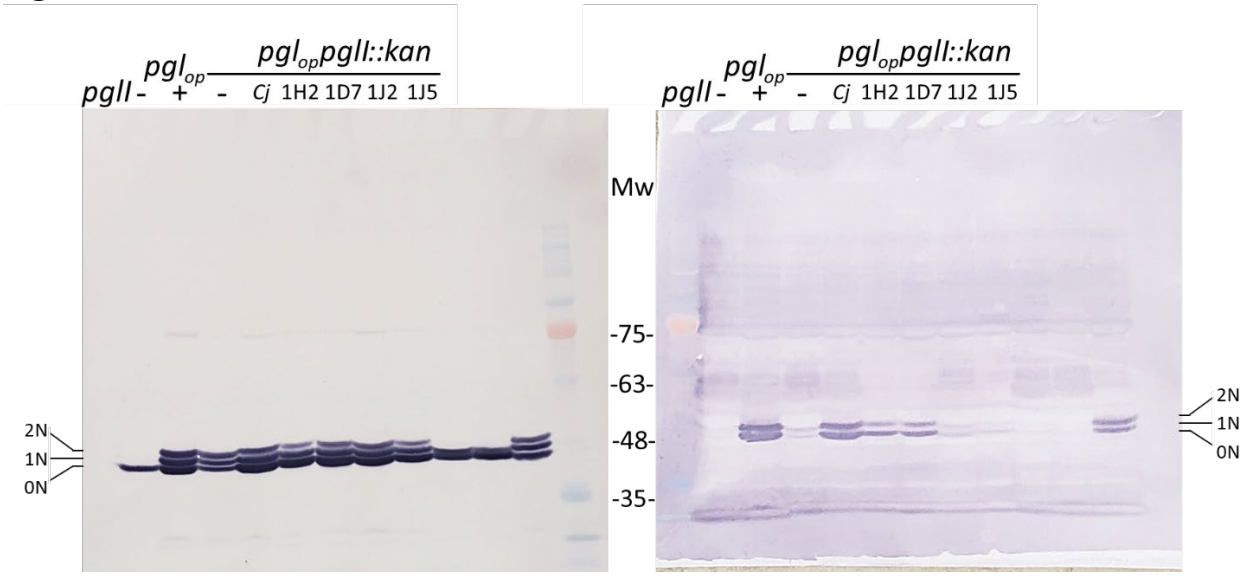

Figure S7. Functional analysis of PglI GTases in the heterologous *E. coli* glycosylation system. Full scans (top to bottom) of the original western blots shown in Figure 3 A and B are provided. Unrelated lanes are not labelled. GTase-activities of GEMS PglIs in the *E. coli* 3-plasmid complementation system were analysed in whole cell extracts of *E. coli* CLM24 (5 µg) by western blotting. **(A)** His-tag specific antibodies detect the glycosylation status of the glycan acceptor protein CmeA-His_6; **(B)** *Cj*-N-glycan-specific antibodies (R1) detect the full-length *Cj*-N-glycan on CmeA-His_6 that is only formed upon expression of an active PglI protein. Gene/plasmid combinations present in the underlying strains are indicated on top of each lane. Non, -mono, -and di-glycosylated CmeA-His_6 proteins are indicated as 0N, 1N, and 2N. Molecular weight markers (Mw) in kDa are indicated for both blots.

Figure S8A

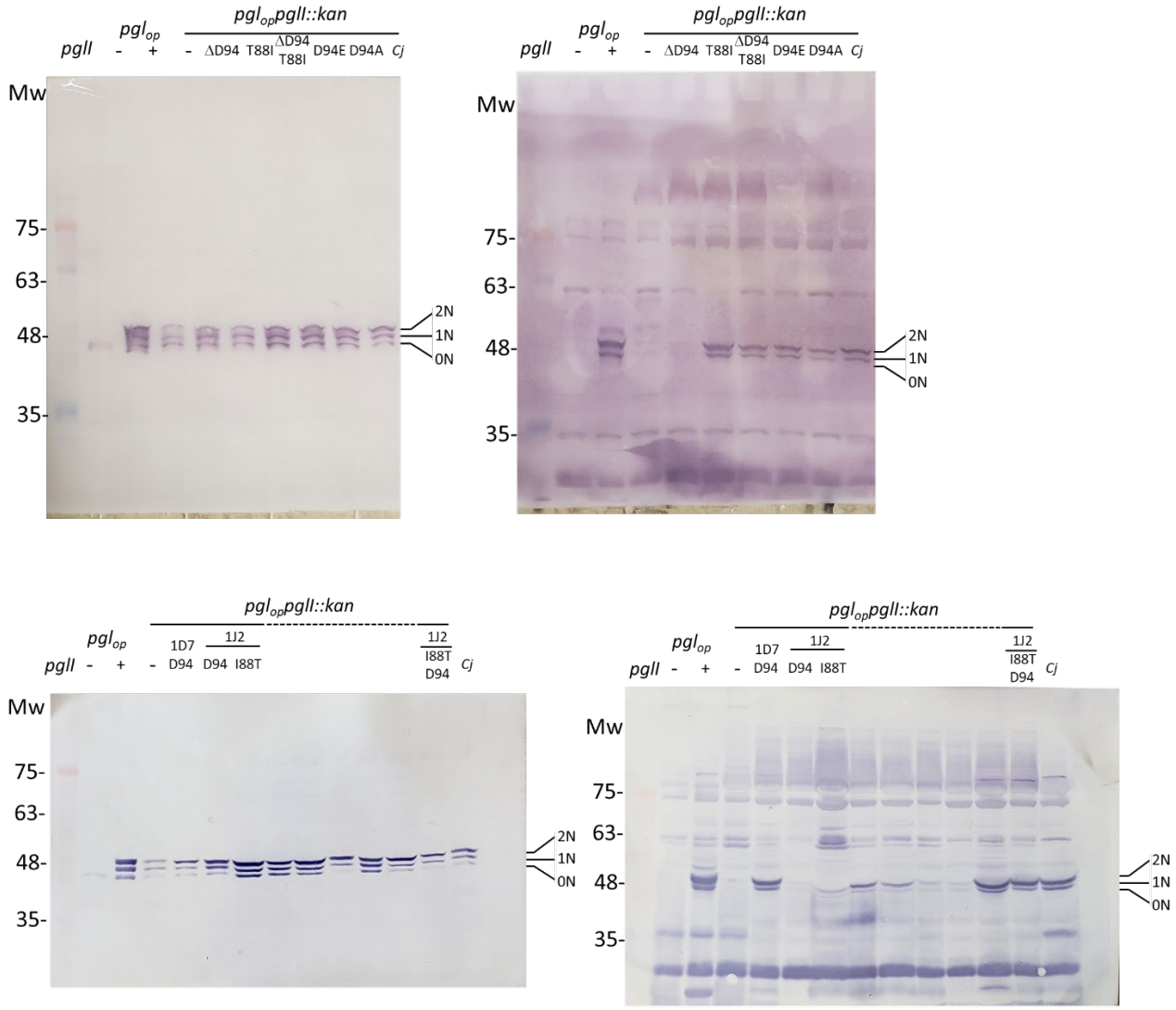

Figure S8. Functional analysis of PglI variants and active site point mutants in the heterologous *E. coli* glycosylation system. Full scans (top to bottom) of the original western blots shown in Figure 4 A and B are provided. Unrelated lanes are not labelled. (A) The GTase-activities of active site point mutants in the PglI of 81116 and (B) in select GEMS PglIs (lower panel) were analyzed by western blotting. The glycan acceptor, CmeA-His_6, was detected with His_6-tag antibodies, the formation of the full length *Cj*-N-glycan was followed with R1 serum. Whole cell extracts of *E. coli* CLM24 (5 µg) containing and expressing the indicated gene/plasmid combinations are indicated on top of each lane. Non, -mono, -and di-glycosylated CmeA-His_6 proteins are indicated as 0N, 1N, and 2N. Molecular weight markers (Mw) in kDa are indicated on the left.

Figure S9

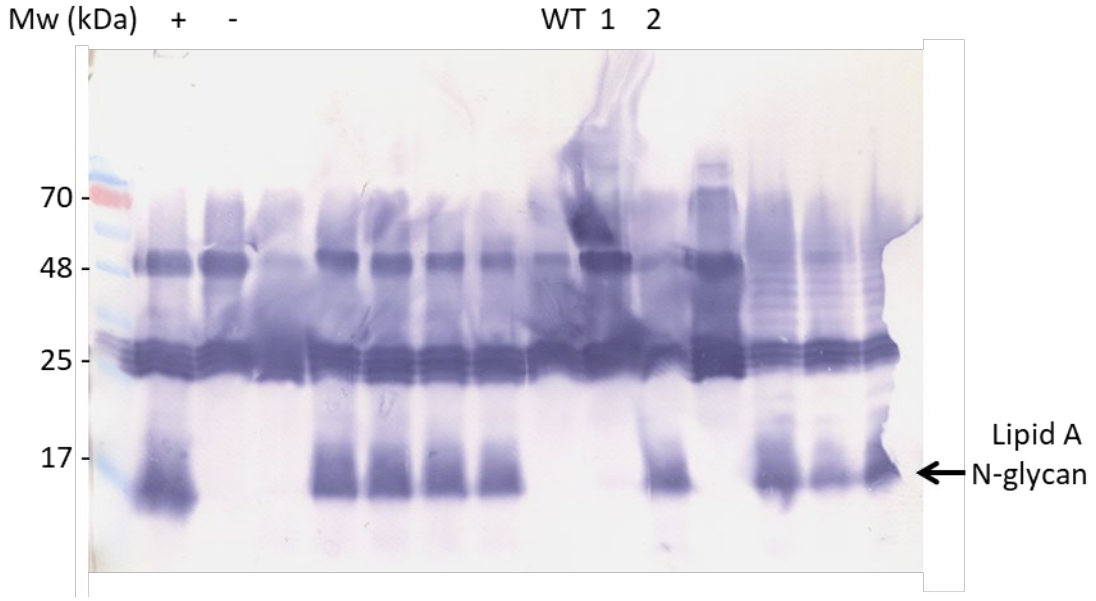

Figure S9. The ACAM2025 strain with integrated *Cj-pgl* genes expresses the lipid A-N-glycan compound at levels comparable to a previously described live *E. coli* strain. Western blot (top to bottom scan) shows the expression of the lipid A N-glycan compound in ACAM2025 (only relevant lanes of the blot are labelled) after integration of the *C. jejuni pgl* locus into the O-antigen polymerase locus, *wzy.* The lipid A-N-glycan compound was detected with R1 (rabbit-derived, *Cj*-N-glycan-specific serum, alkaline phosphatase anti-rabbit-AP served as secondary antibody) in Proteinase K digested whole cell lysates separated by 12.5% PAGE and transferred to a PVDF membrane. The lipid A-N-glycan compound is indicated by an arrow. *E. coli (pgl)* was included as a positive control sample (+); *E. coli* not expressing *pgl* (-) as well as the unmodified ACAM2025 (WT) were included as negative controls. The candidate in lane 2 was used for further studies. Molecular weight markers (MW in kDa) are indicated on the left.

Figure S10

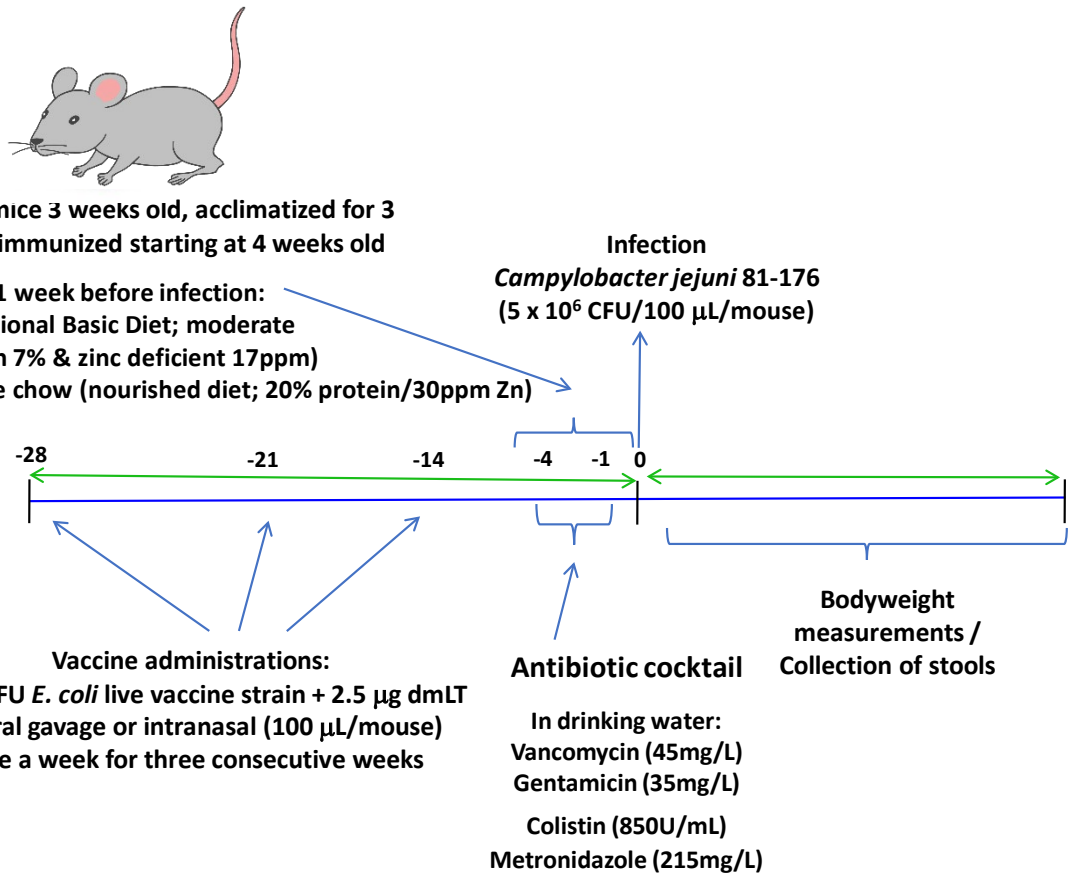

Figure S10. Timeline for mouse vaccination and *Campylobacter* challenge

Author contributions

HN, XB and CMS designed the experiments; XB performed the initial GEMS strain screening and *pglI* identification; HN performed all the *E. coli*-based work and the immunological assays, AS and PA designed and performed the MS/N-glycan analyses; WGM analyzed the *pglI* sequences; KKSN performed the molecular modelling and interpretation; DTB and RLG designed and carried-out the mouse studies. HN and CMS wrote the initial draft of the manuscript. All authors read, edited and approved the final manuscript.

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