

Figure S1. SDS-PAGE analysis of Ldt_{Cd1} , Ldt_{Cd2} and Ldt_{Cd3} purified recombinant proteins used for *in vitro* assays.

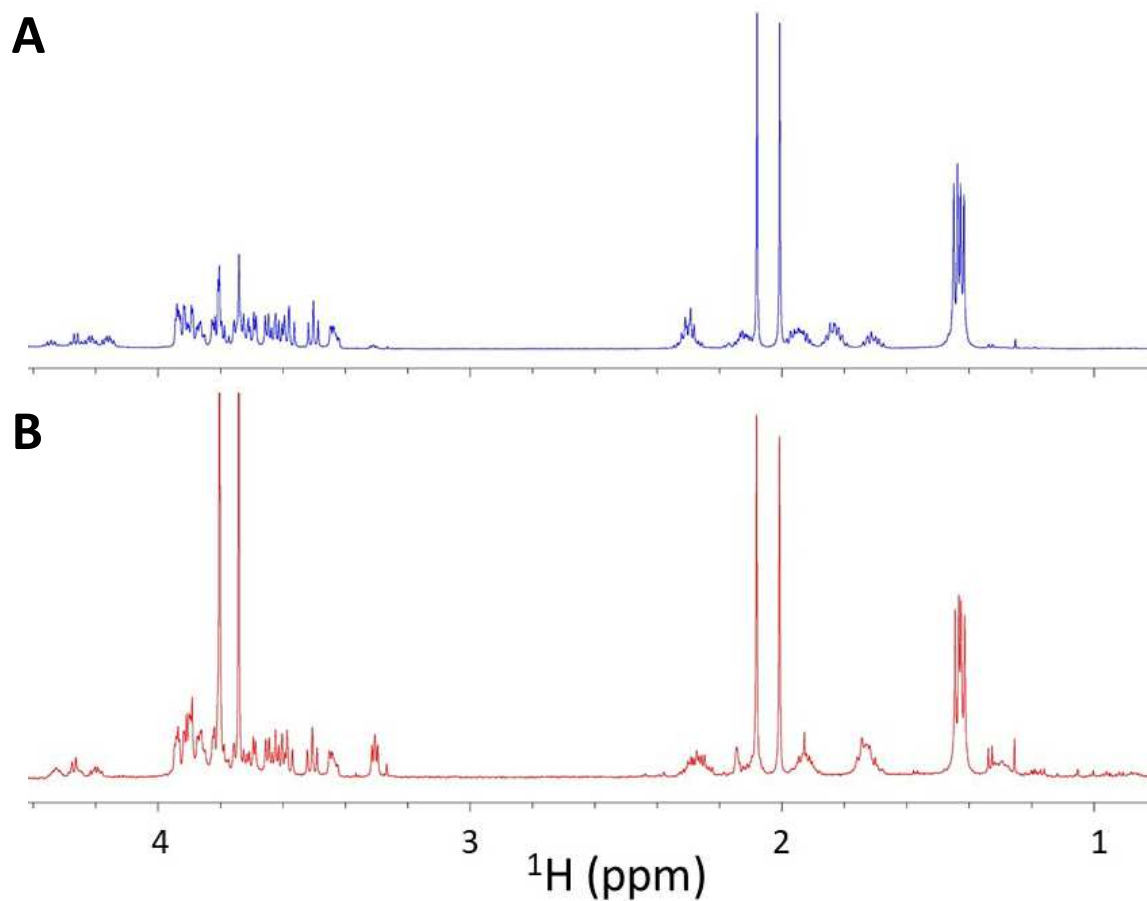


Figure S2. One-dimensional ^1H NMR spectra of (A) gm-AEJ monomer (peak 1 in Figure 1) and (B) gm-AEJ=gm-AEJ (-H₂O) dimer (peak a in Figure 1). The two singlet *N*-acetyl methyl signals are at around 2 ppm, and the two methyl doublets are at around 1.4 ppm.

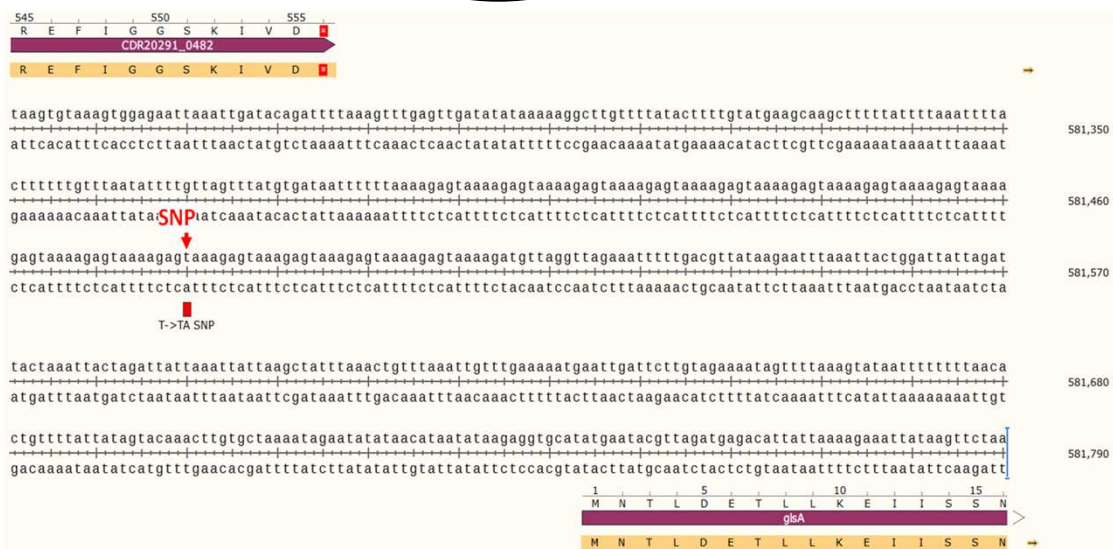
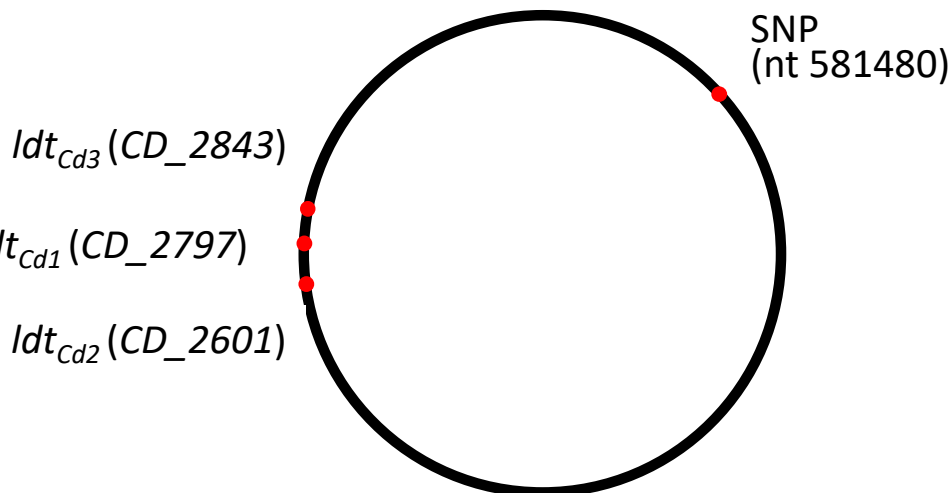
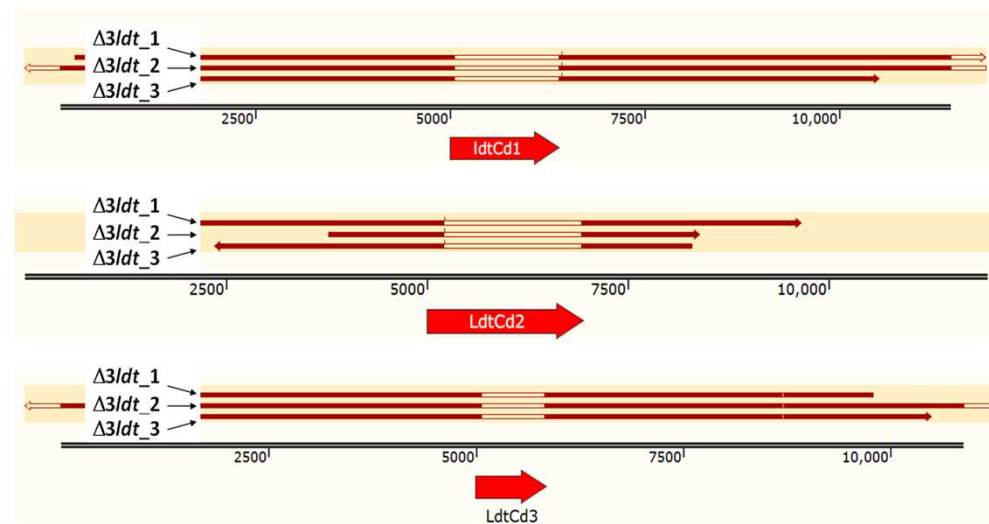
A**B**

Figure S3. Genome analysis of *C. difficile* WT and $\Delta 3ldt$ derivative. **A**, schematic representation of the R20291 chromosome depicting the localisation of the 3 *ldt_{Cd}* genes and the SNP detected in the triple mutant in position 581480 (T→TA). The sequence in figure A shows the position of the mutation between the two adjacent genes. **B**, sequence alignments of the contigs assembled from the 3 independent genomes sequenced. Each DNA was purified from the culture that was used for peptidoglycan analysis.

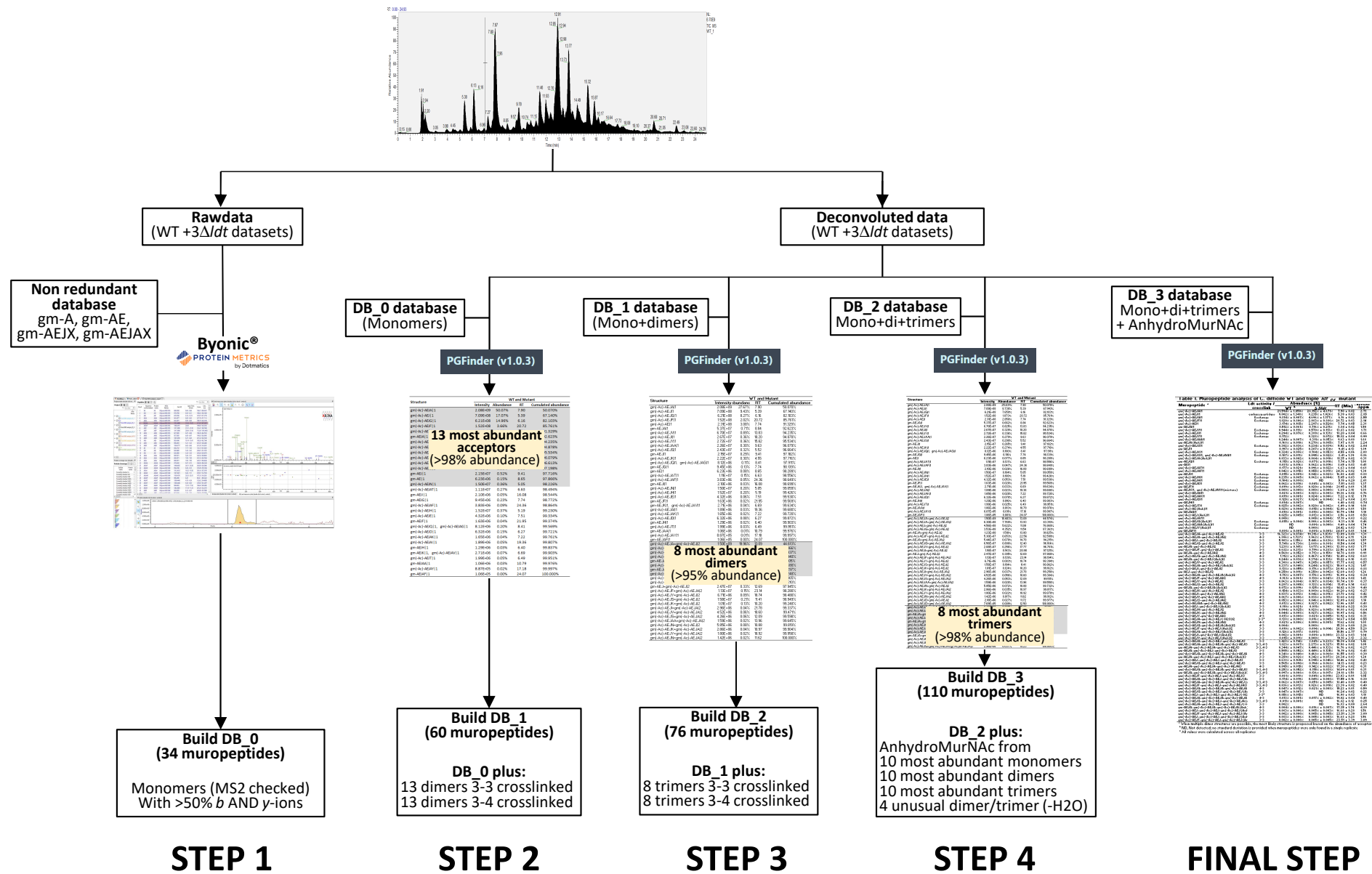
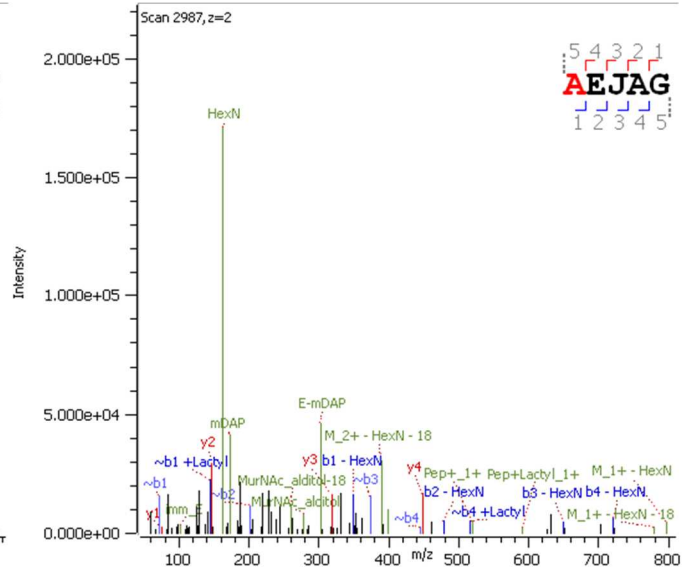
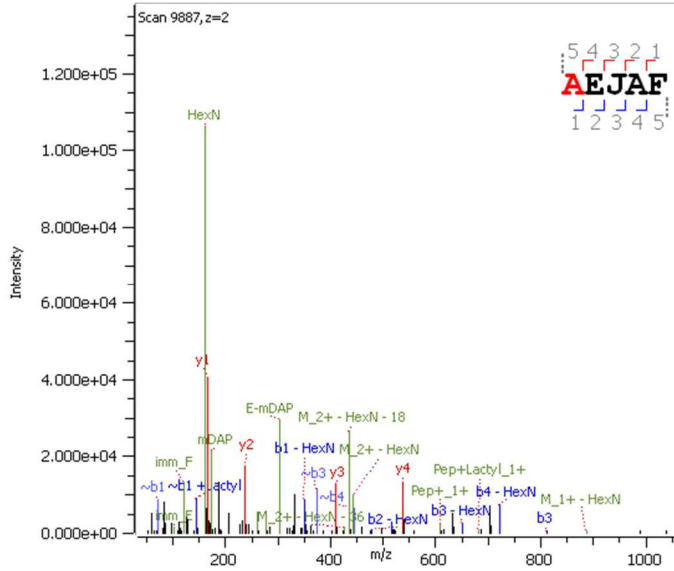
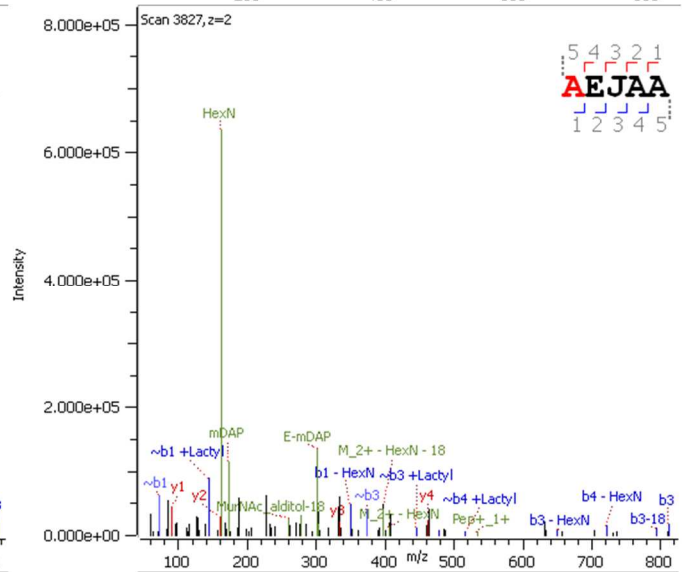
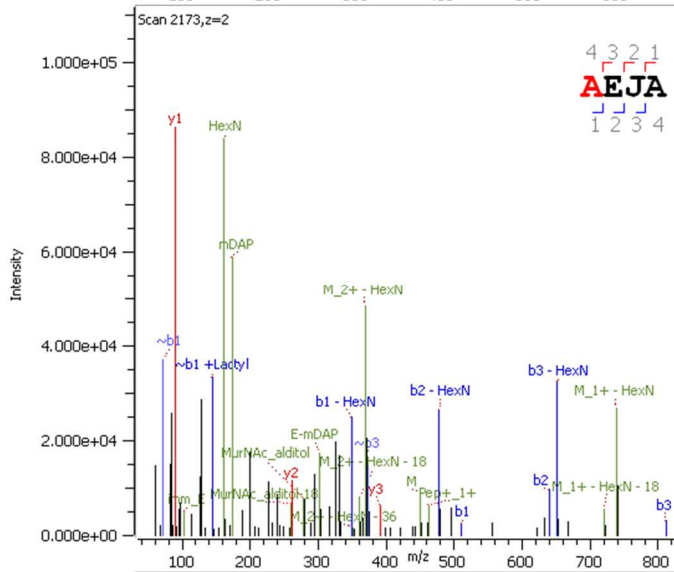
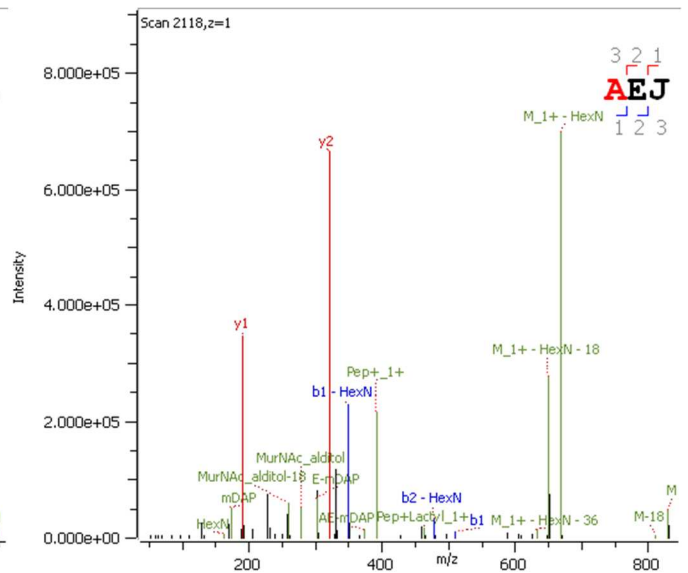
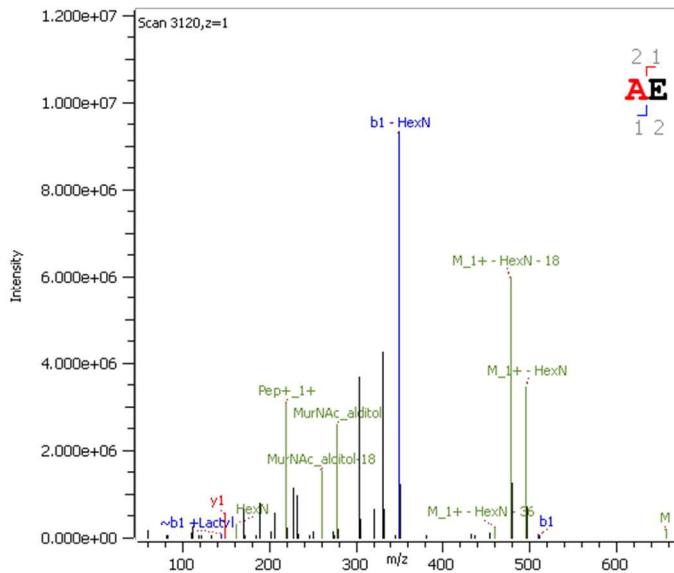
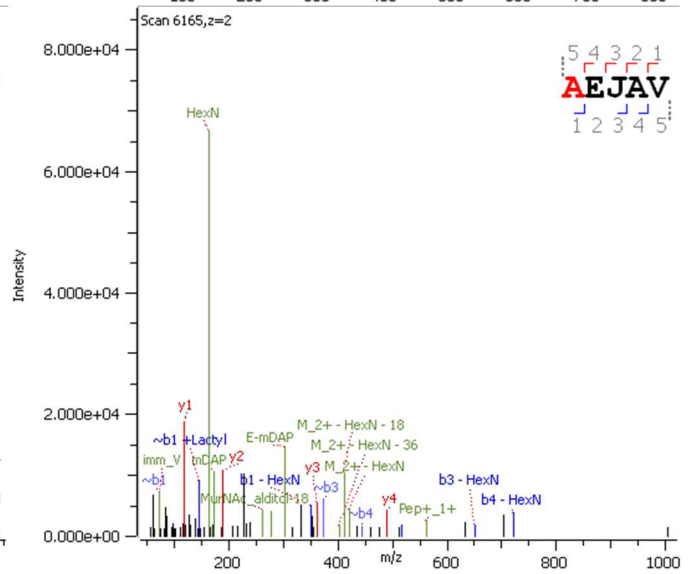
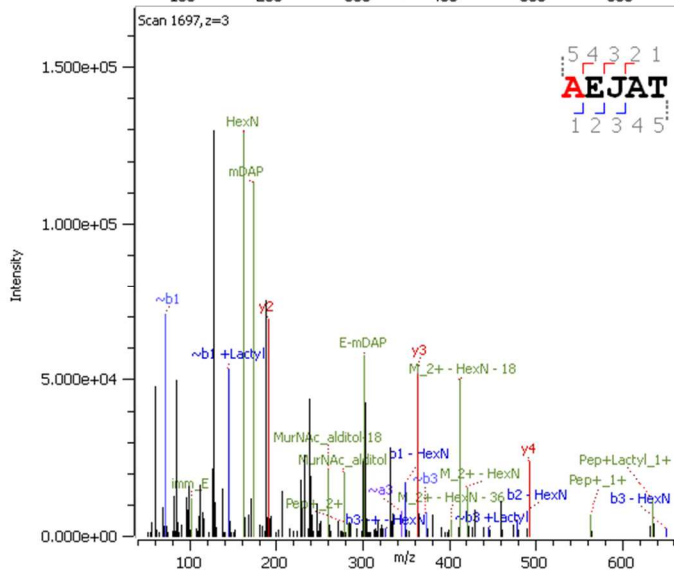
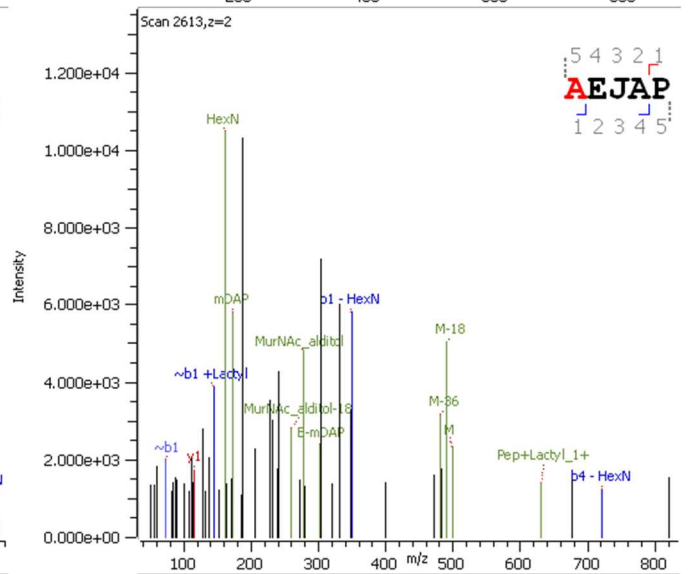
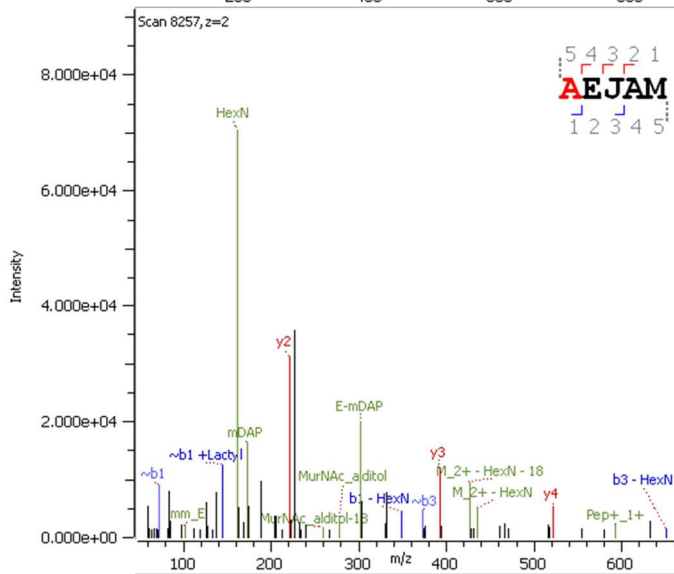
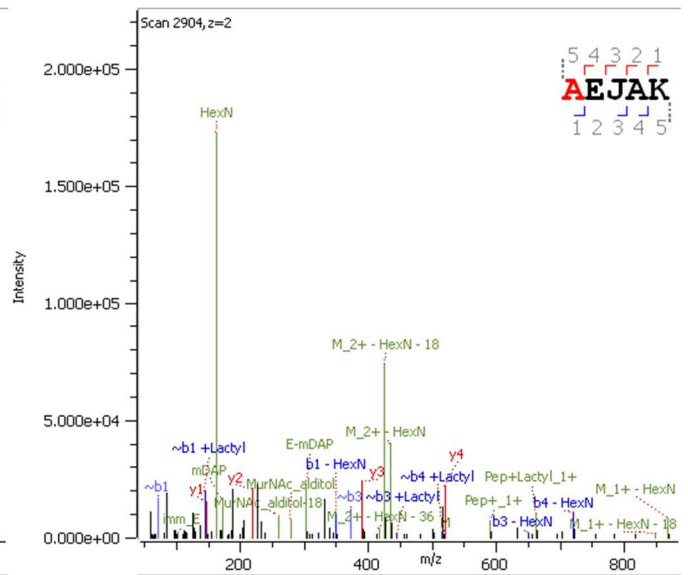
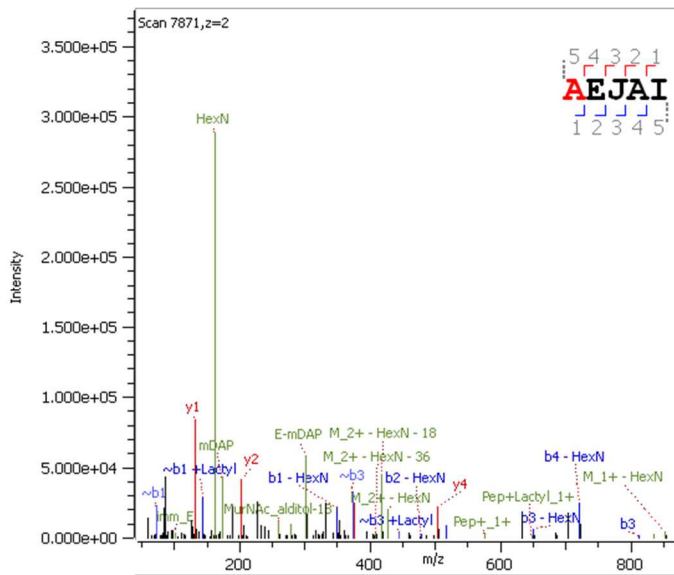
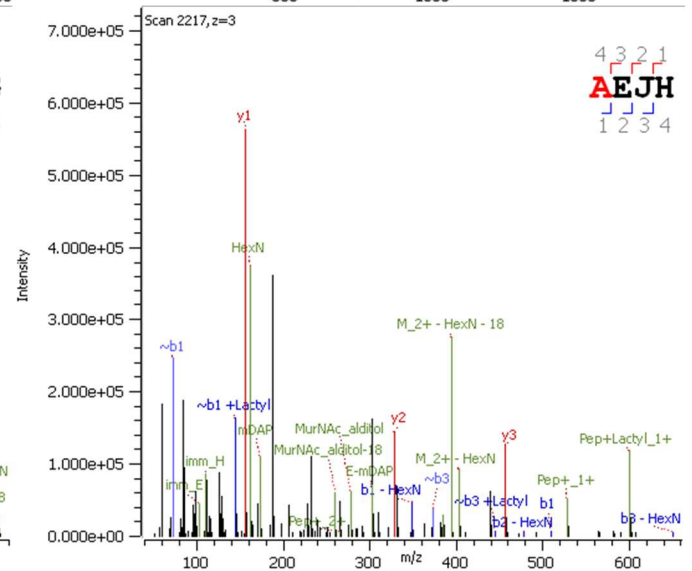
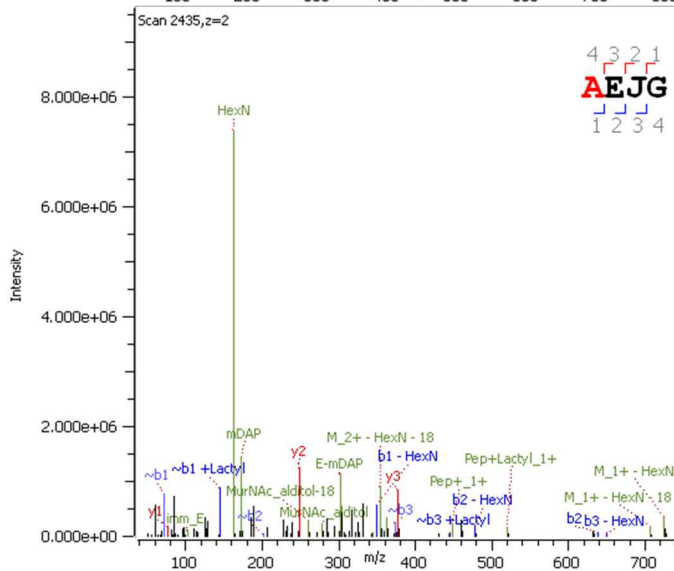
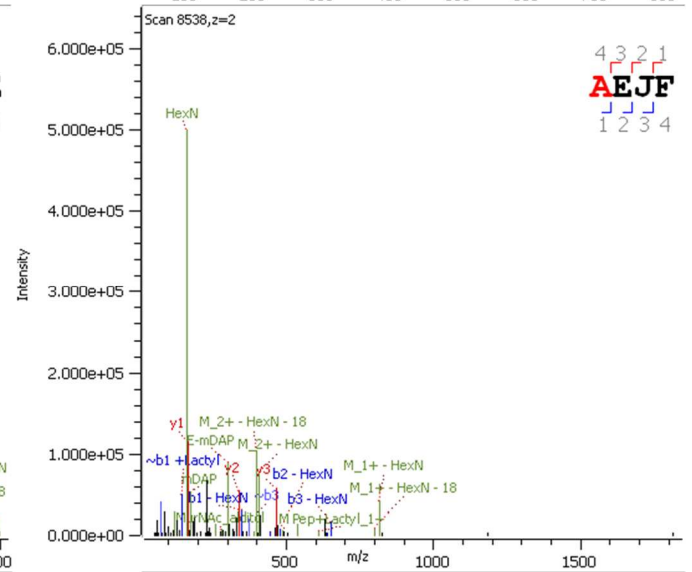
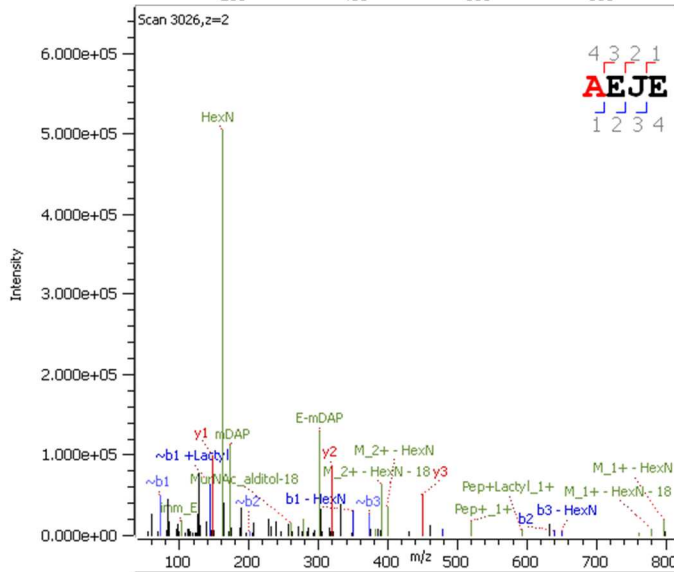
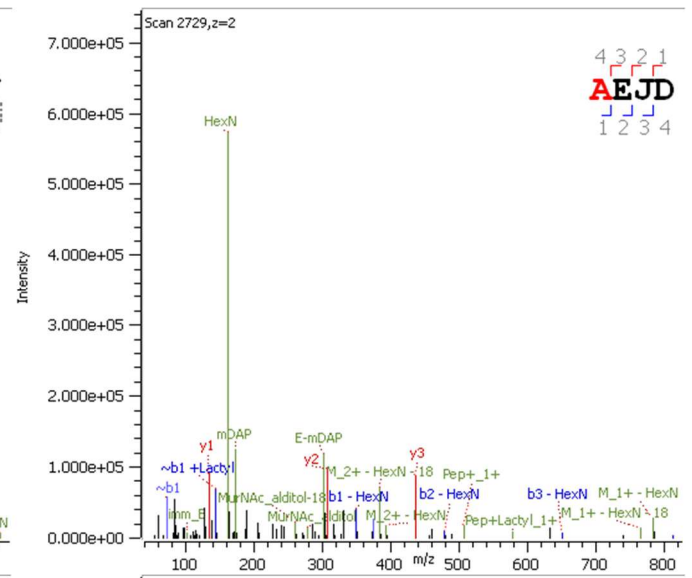
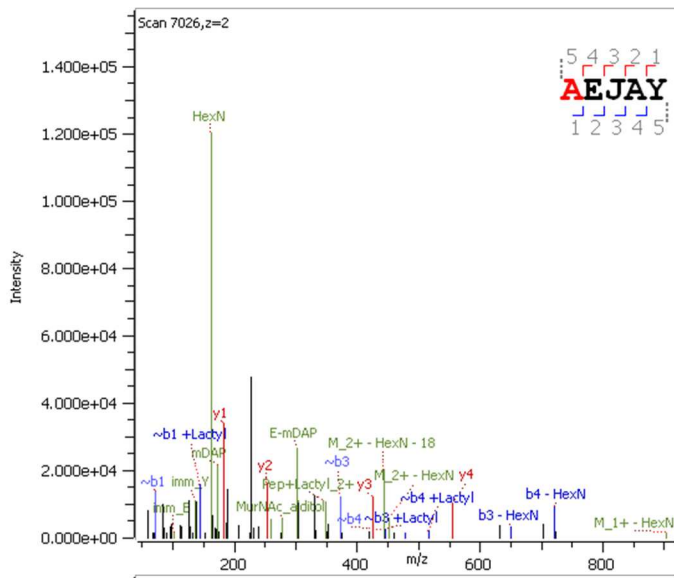
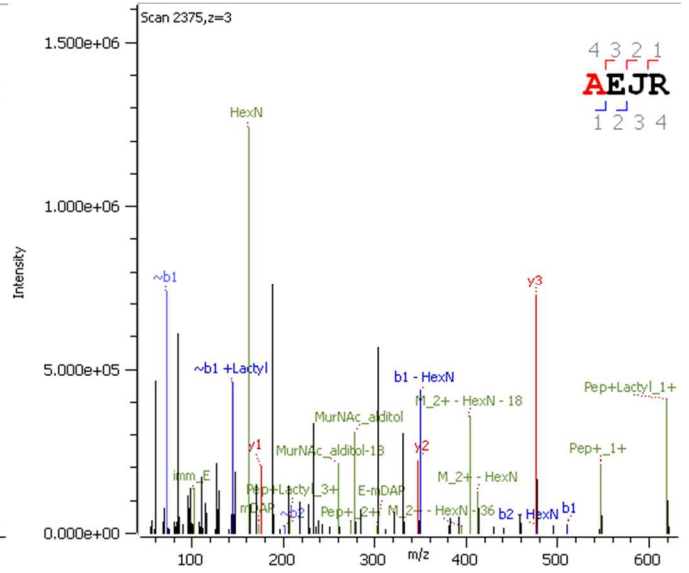
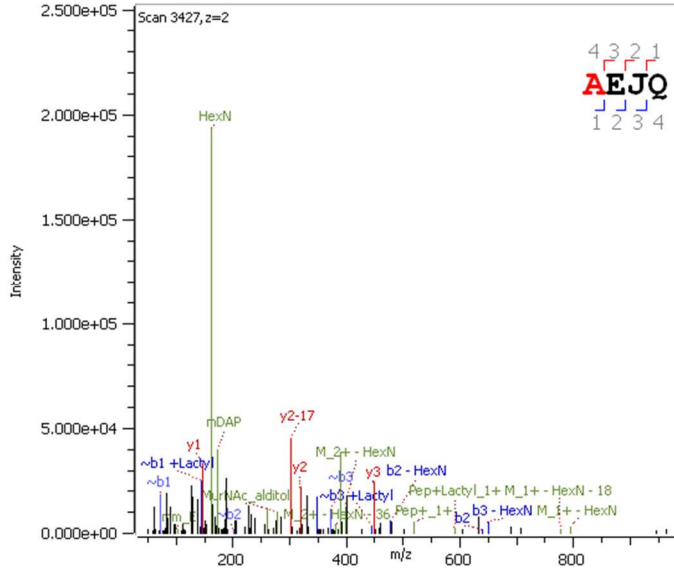
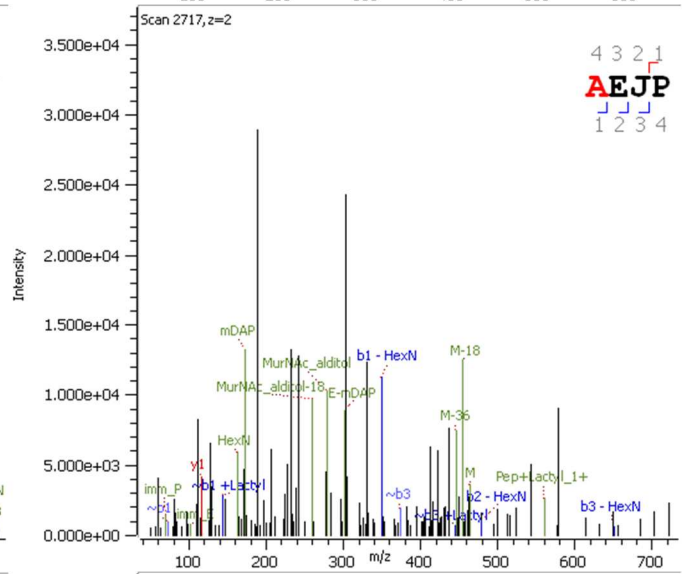
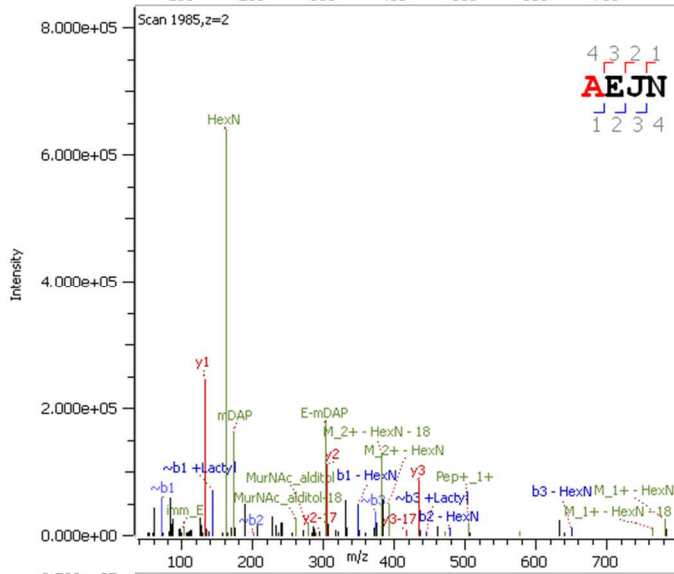
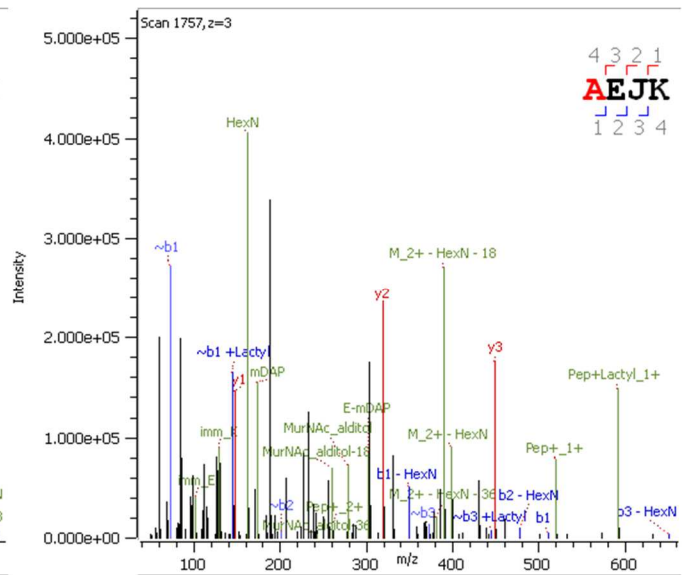
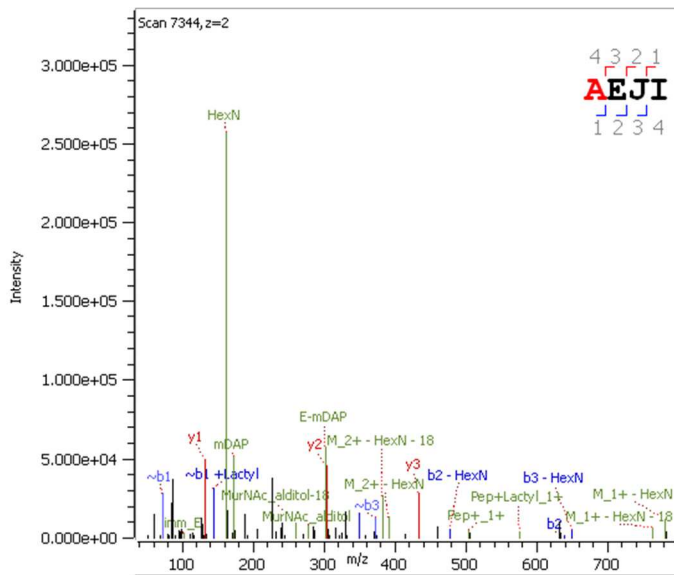


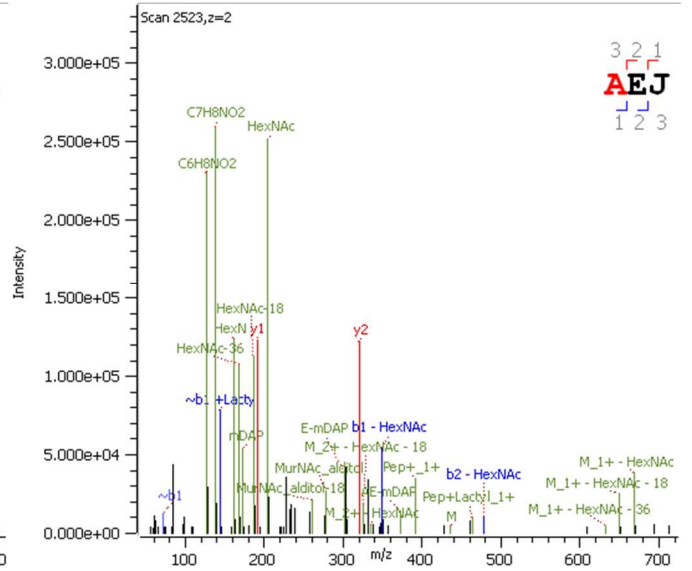
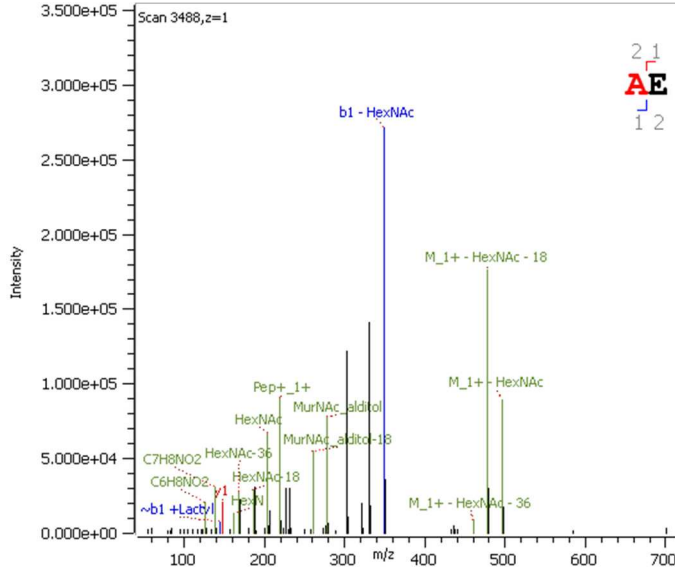
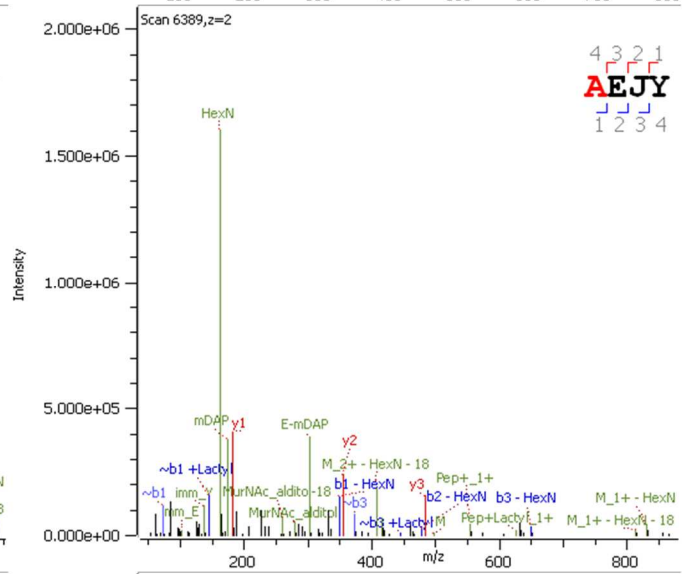
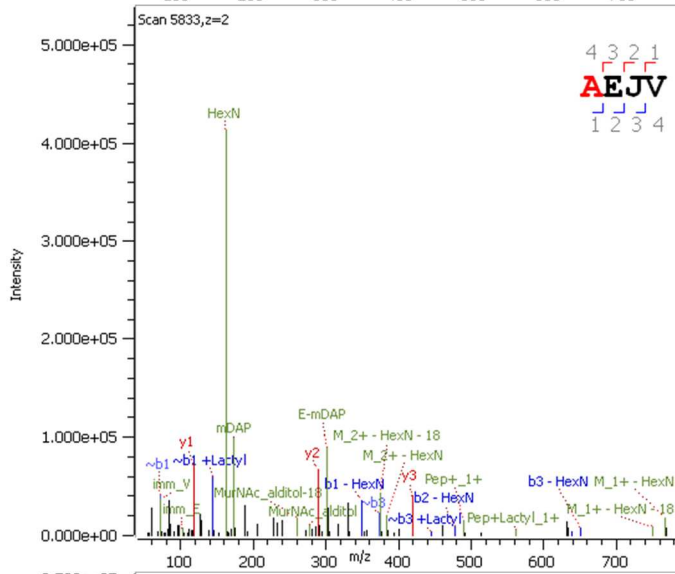
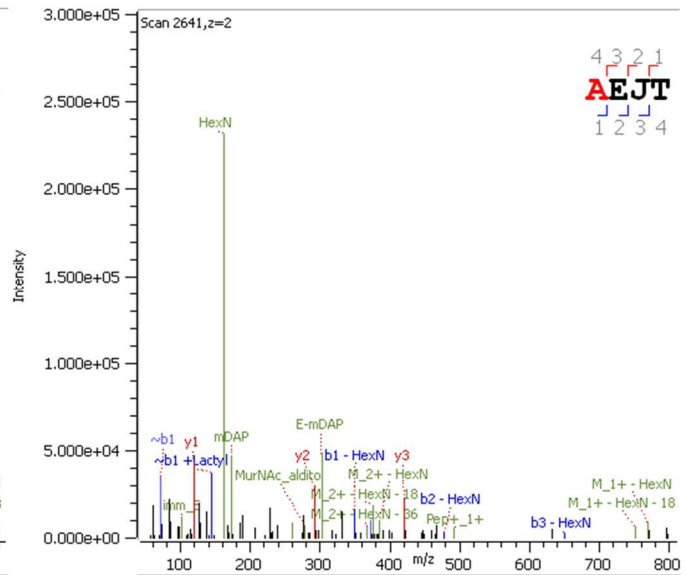
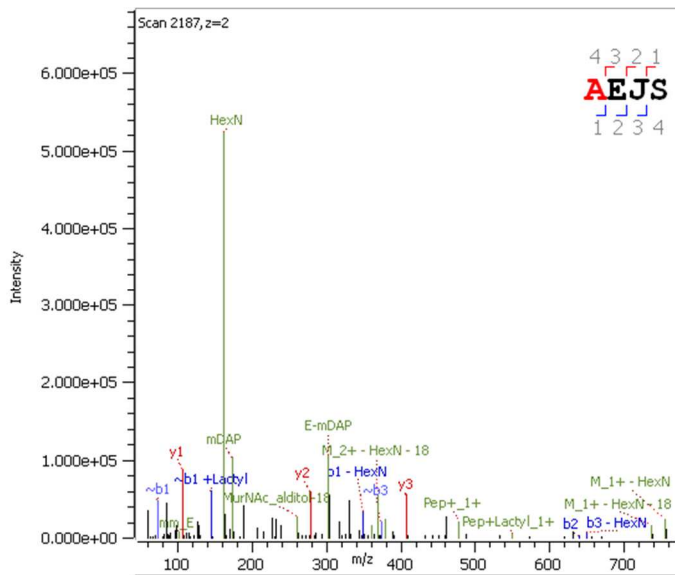
Figure S4. Strategy for peptidoglycan structural analysis. Sequential searches were performed using the Byonic[™] and PGFinder software. The monomer database DB_0 was built based on the MS/MS analysis carried out with Byonic[™]. The identification of the most abundant monomers was used to build the following databases containing dimers (DB_1), trimers (DB_2) and anhydroMurNAC groups (DB_3). DB_3 was used for a final « one off » search.

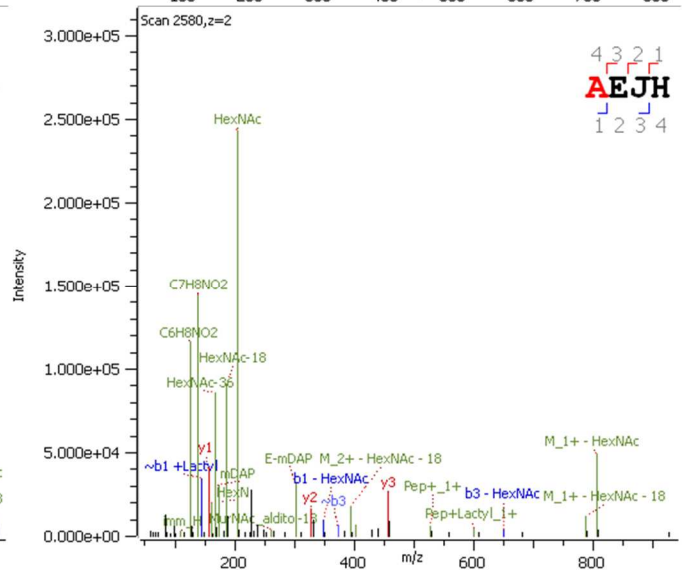
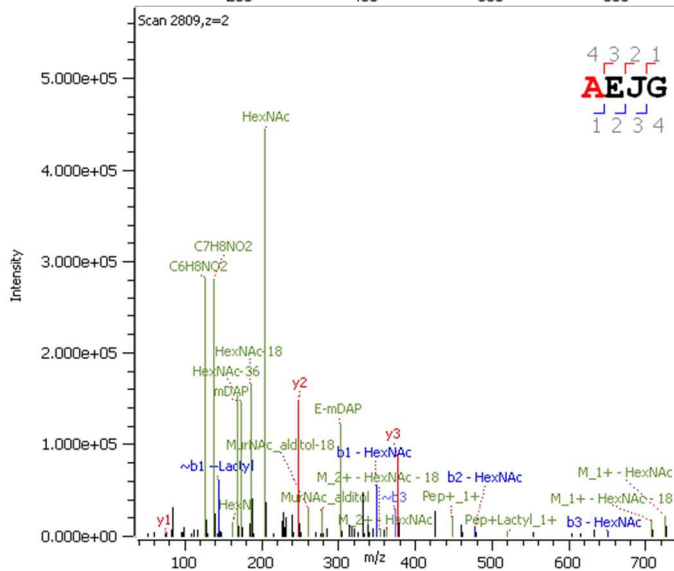
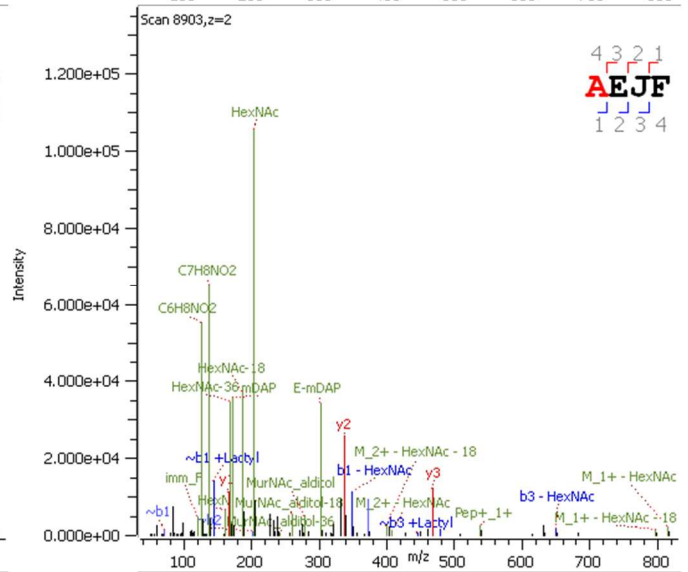
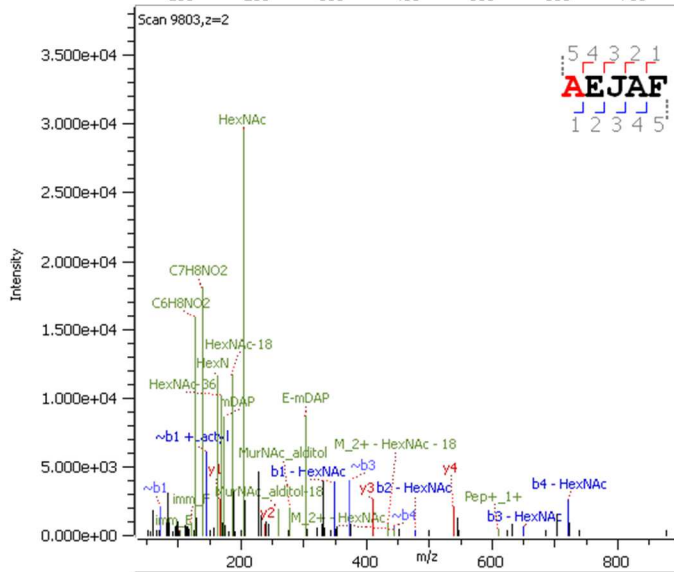
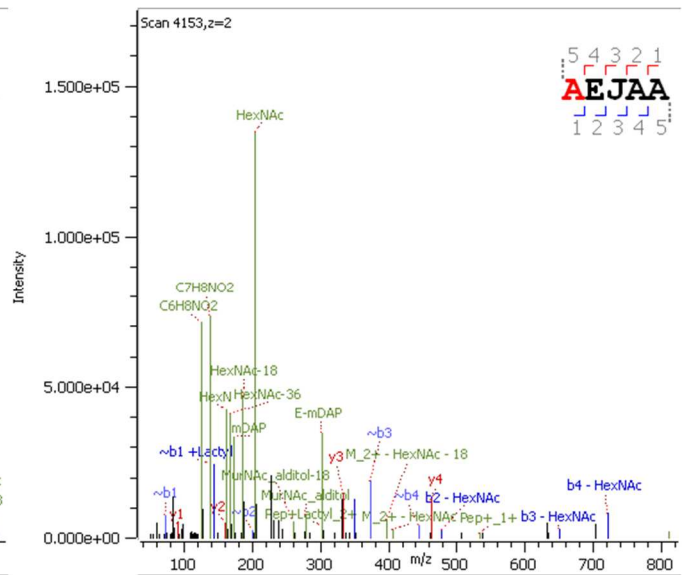
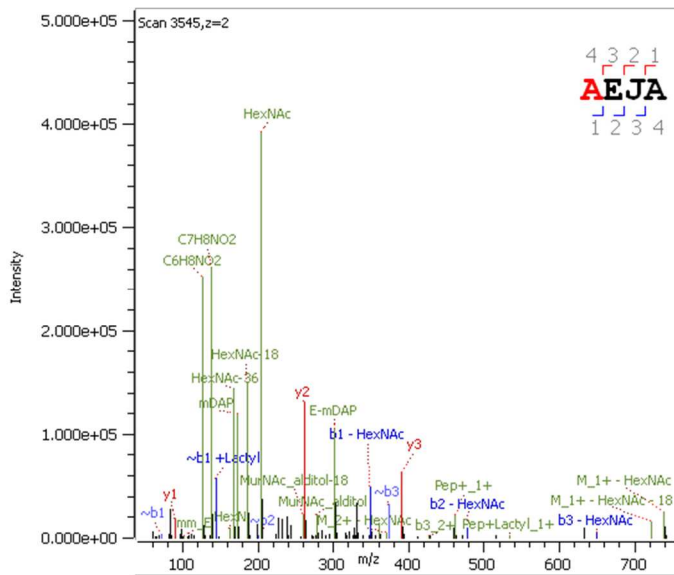












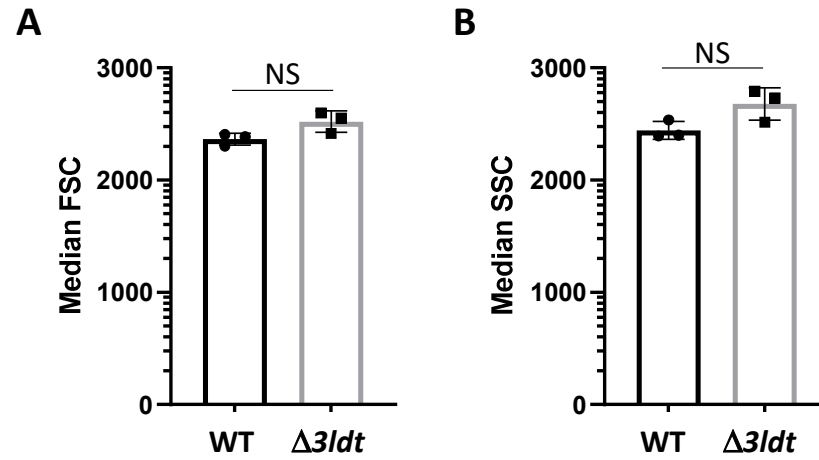


Figure S6. Comparative analysis of WT and $\Delta 3ldt$ cell size by flow cytometry. Comparison of median forward scattered (FSC) (A) and side scattered (SSC) light values (B) corresponding to WT and $\Delta 3ldt$ mutant; NS, $P > 0.05$; $n = 3$ (Student unpaired t -test with Welch's correction).

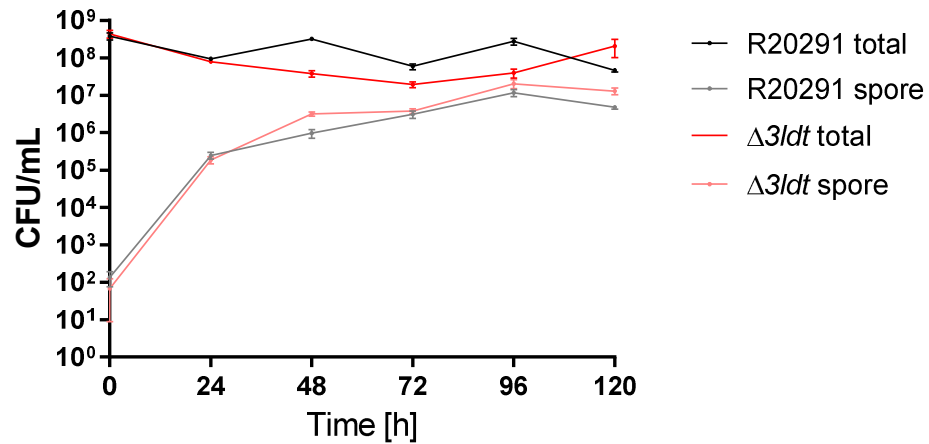


Figure S7. Comparative analysis of WT and $\Delta 3ldt$ sporulation efficiency. Stationary-phase cultures were incubated anaerobically for 5 days, and samples were taken at 24-h intervals for analysis. Total cell numbers were determined by counting the number of CFU on BHIS agar containing the germinant taurocholate. Spore numbers were determined by the same method following incubation at 70°C for 30 min. Experiments were carried out in triplicate on biological duplicate samples. The means \pm standard deviations (error bars) are shown.

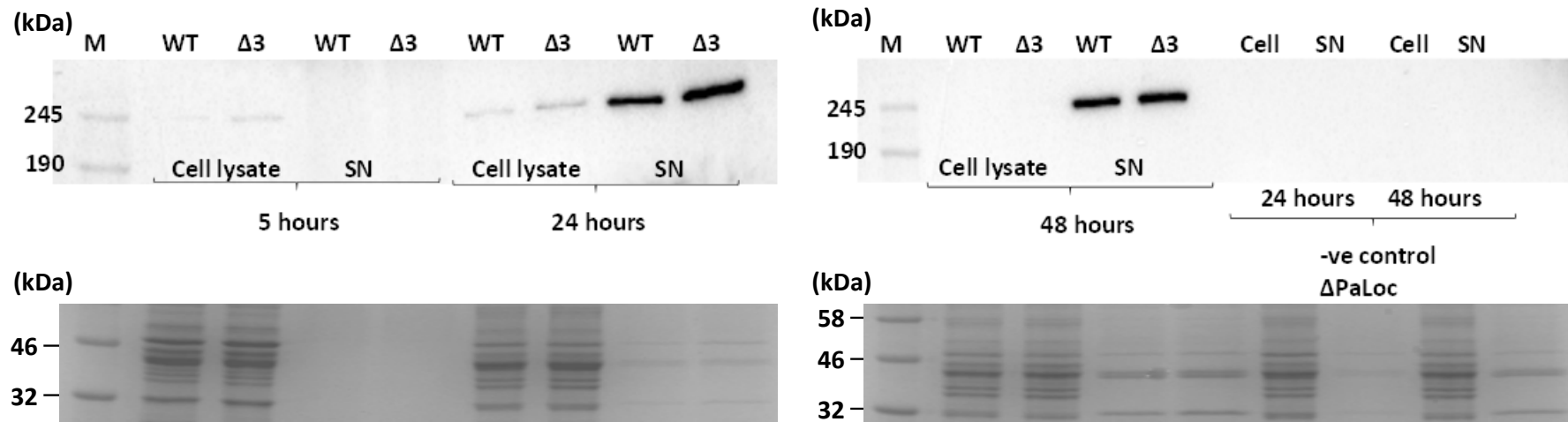


Figure S8. Analysis of toxin release by *C. difficile* R20291 and the $\Delta 3ldt$ mutant. Cells were grown overnight and inoculated in TY broth at a 1/100 dilution. Cultures were harvested at different time points to prepare cell lysates and concentrated culture supernatants (SN). Toxin B was detected by Western blot (chemiluminescence) using a mouse monoclonal Anti toxin B antibody (MA1-7413) and a secondary rabbit anti-mouse antibody conjugated to horseradish peroxidase. A strain with a deletion in the gene encoding toxin B ($\Delta PaLoc$) was used as a negative control. M, Molecular weight marker.