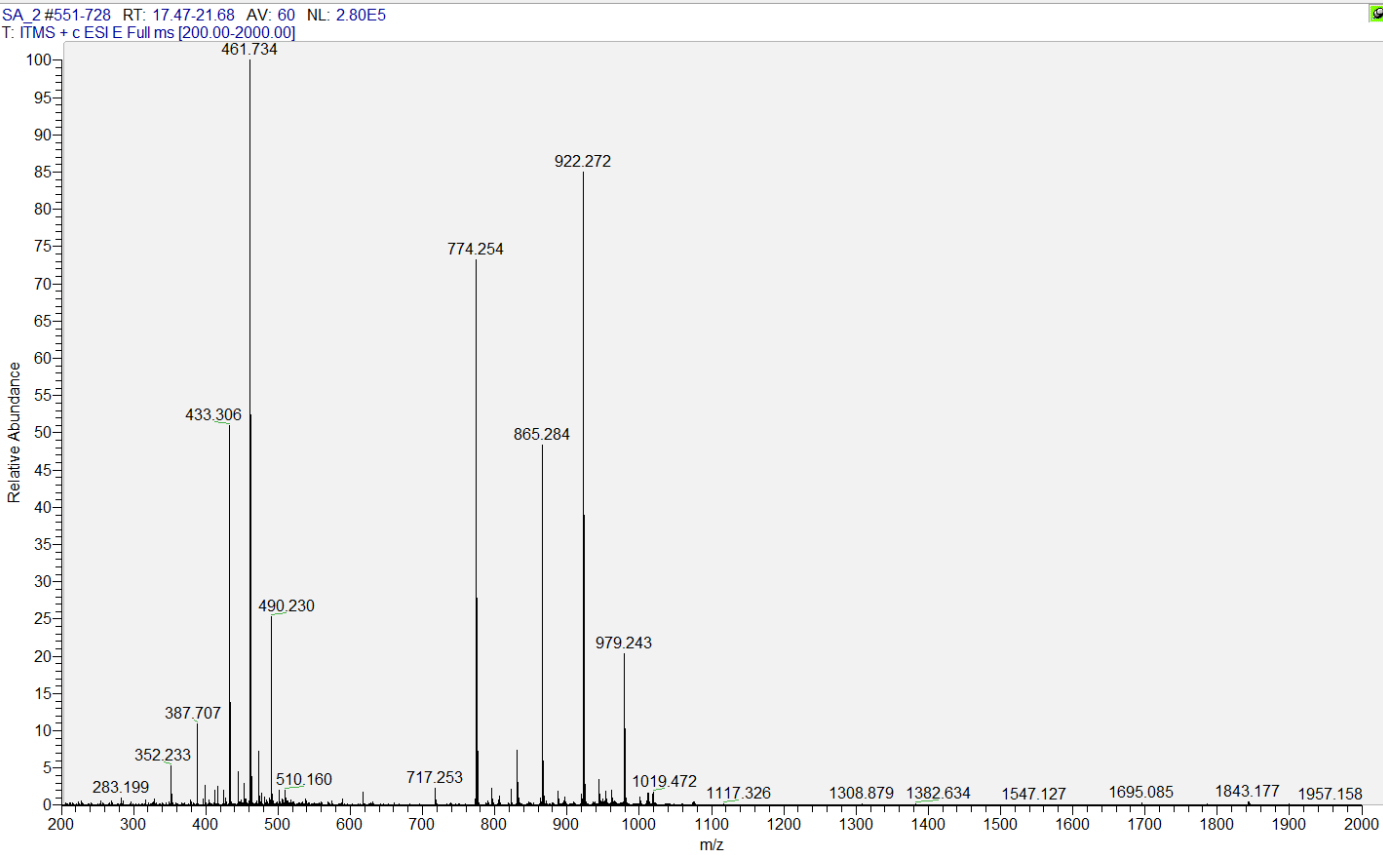
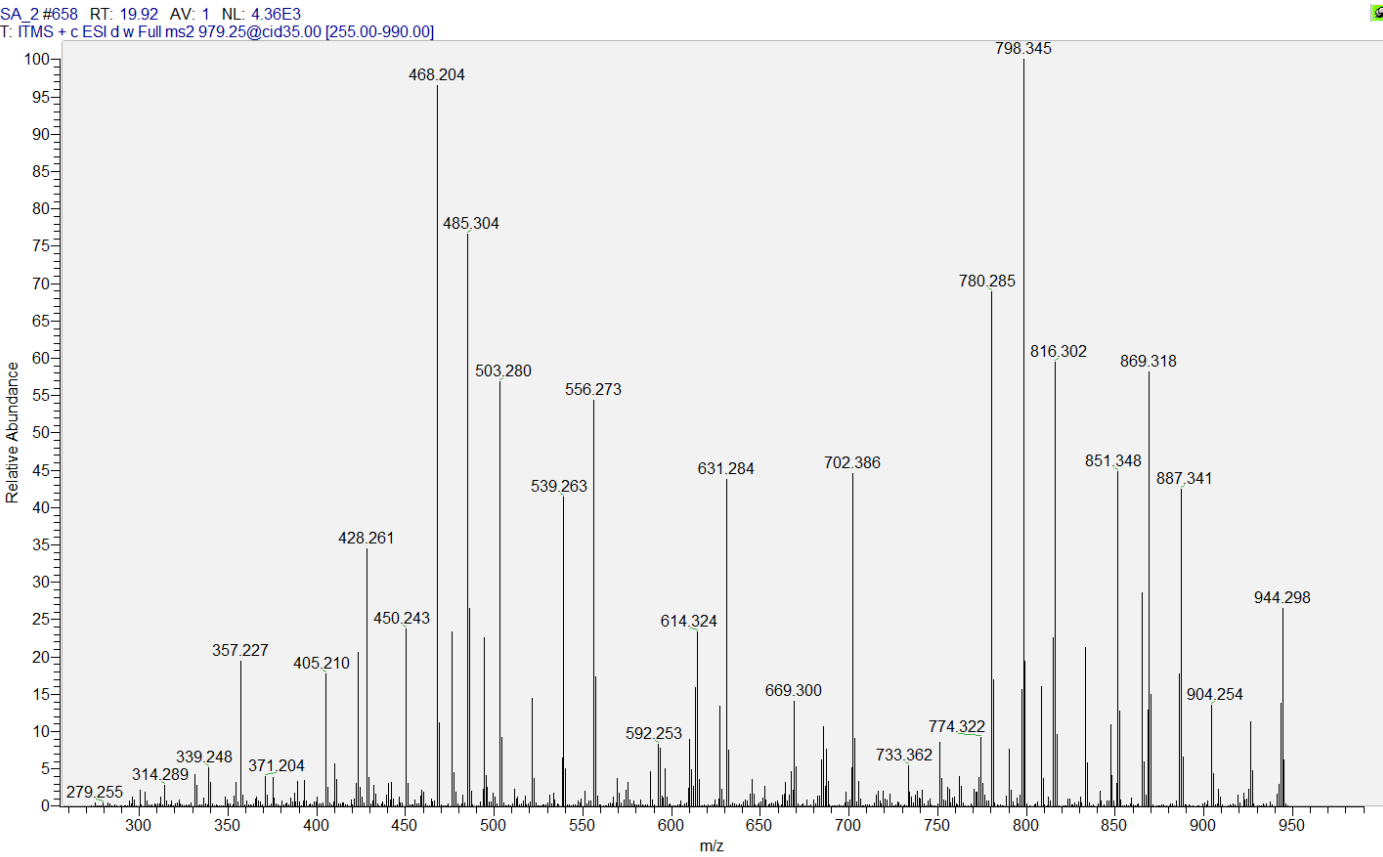


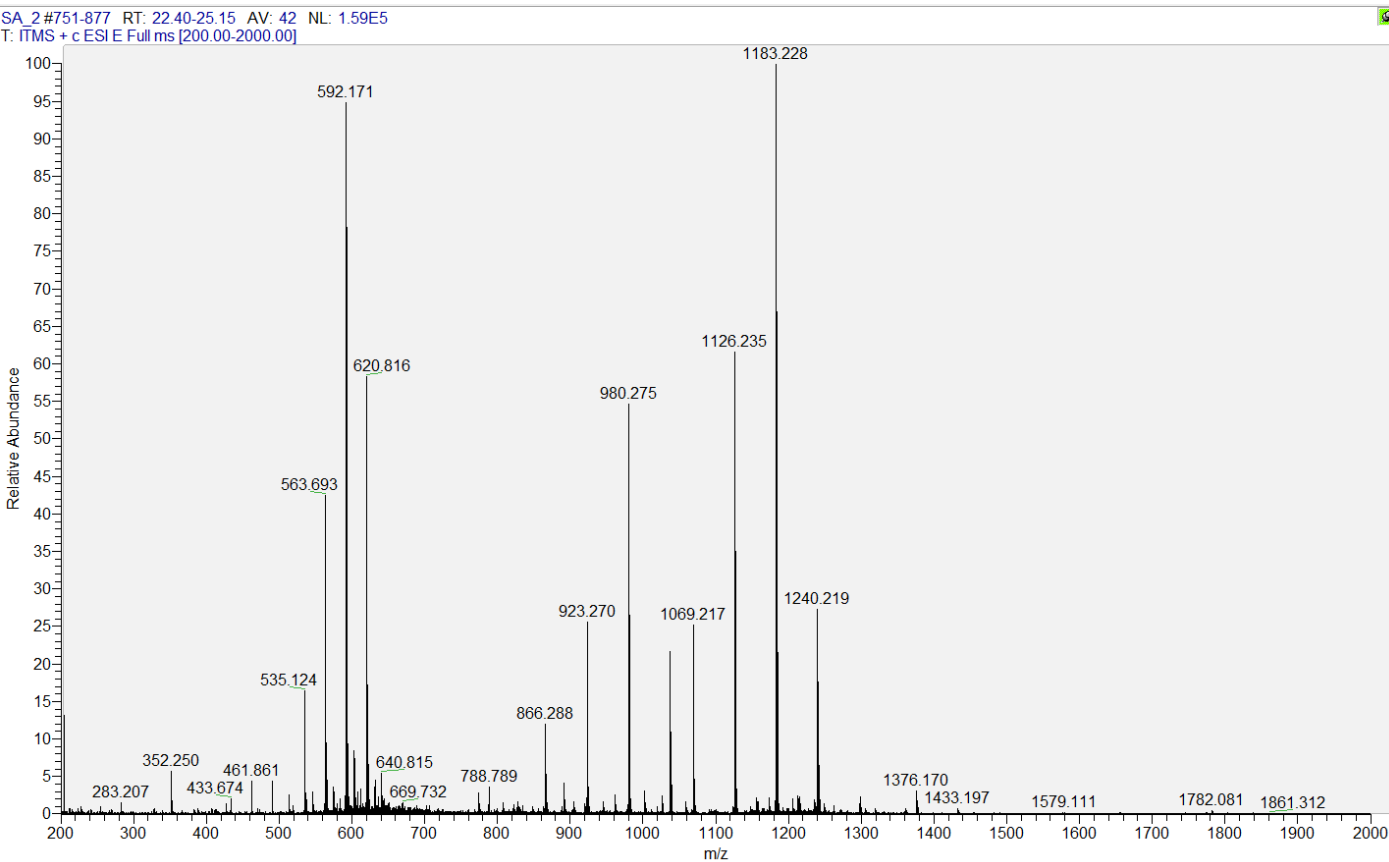
A LC-MS Peak 1



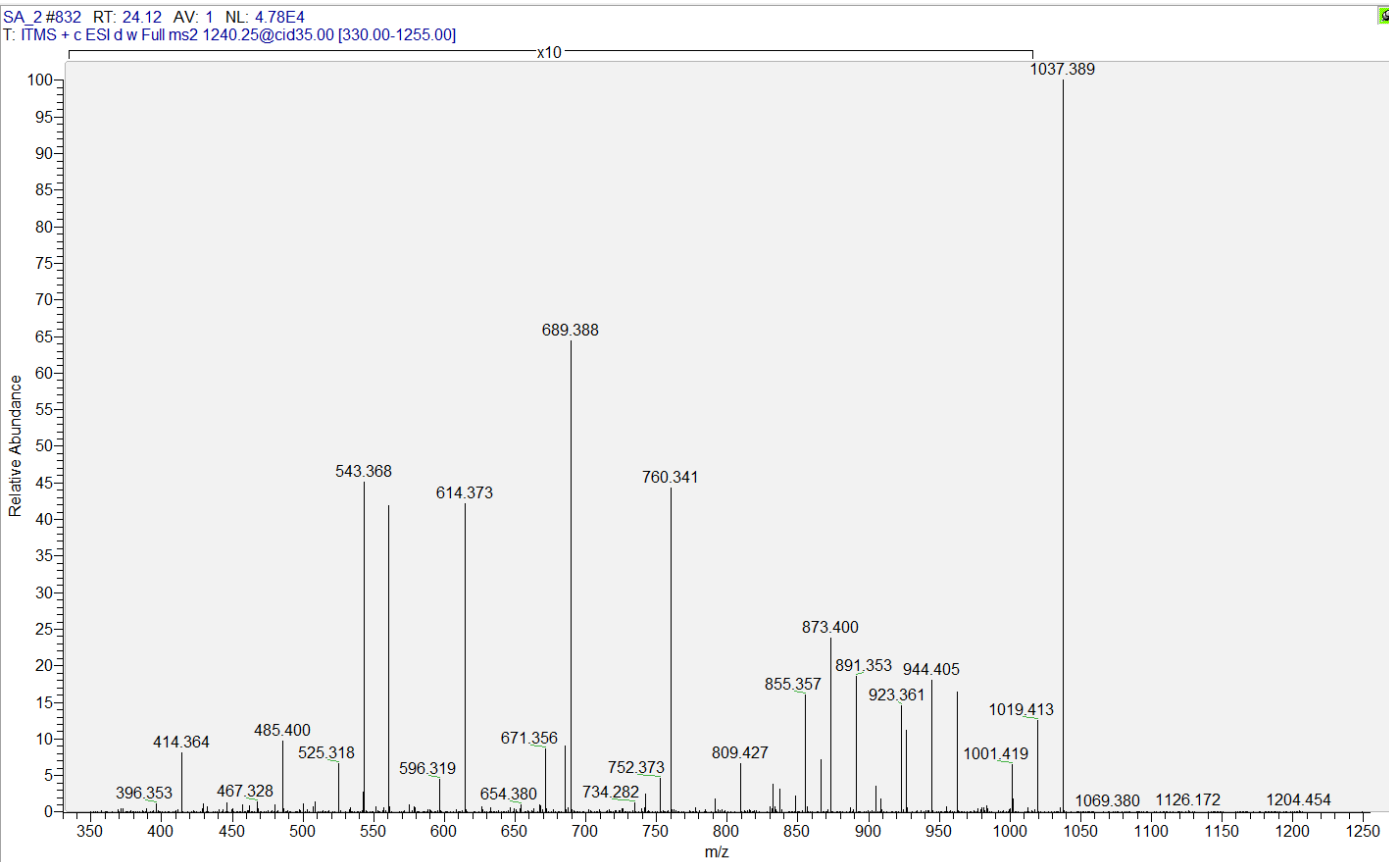
B LC-MS/MS Peak 1



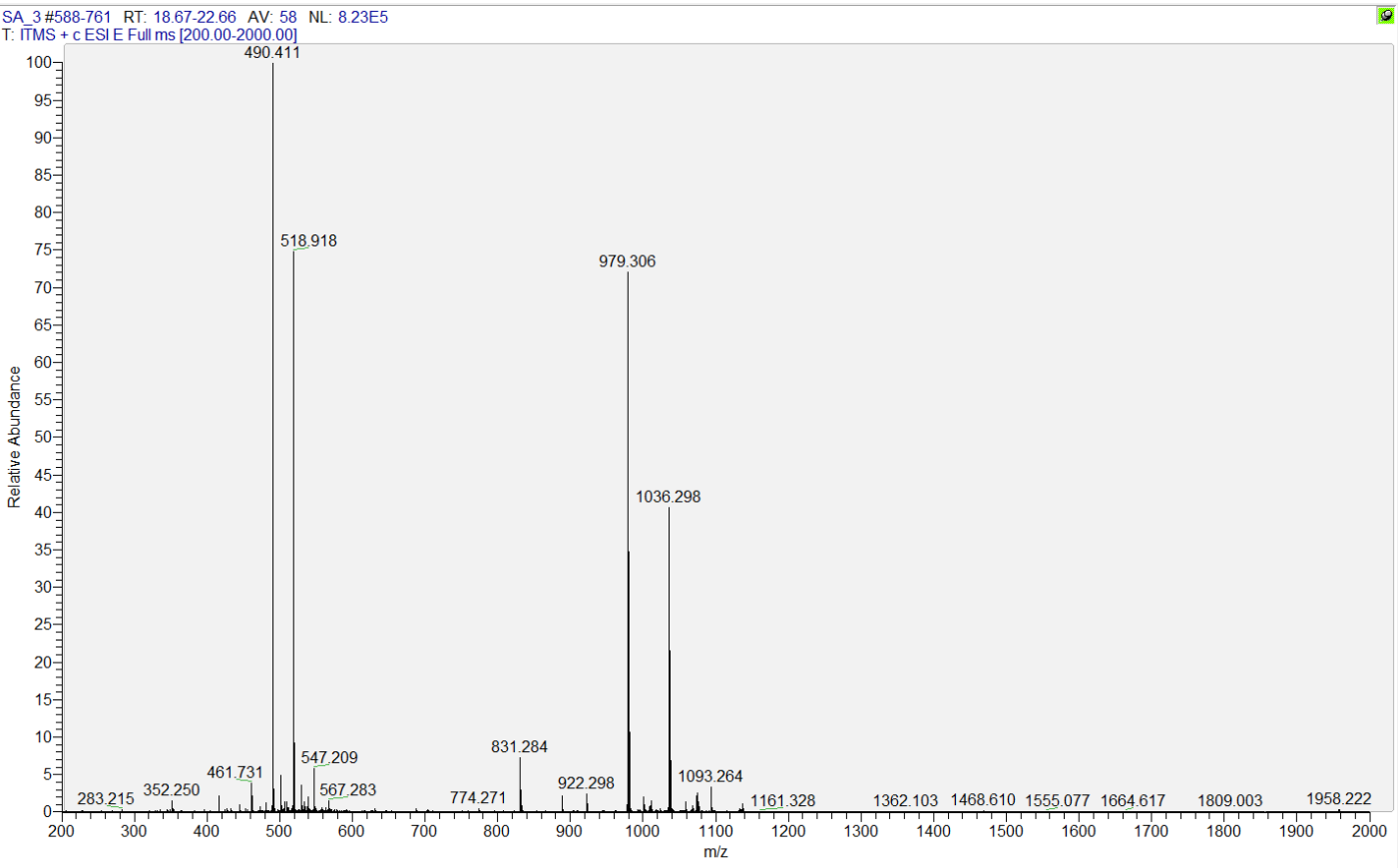
A LC-MS Peak 2



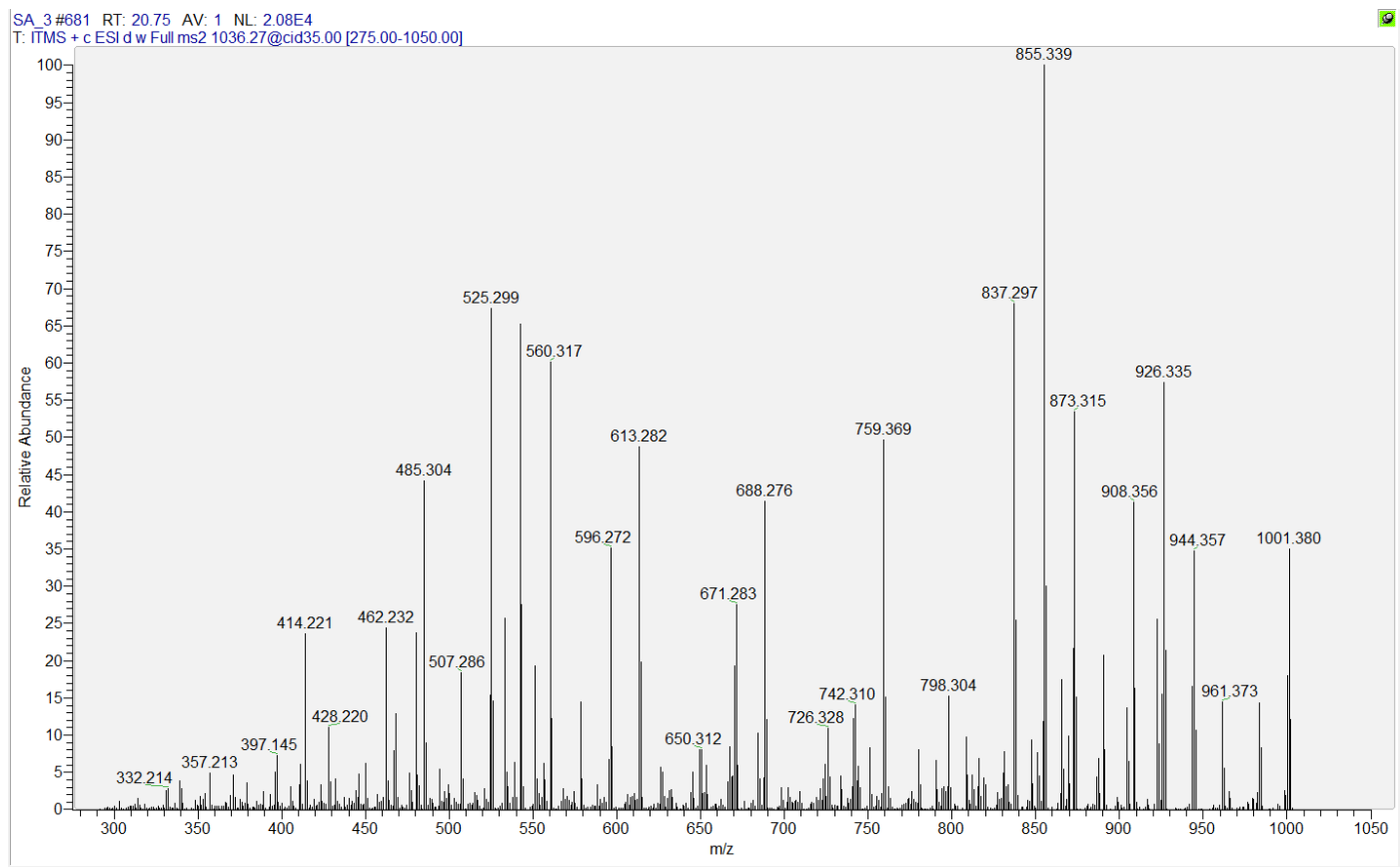
B LC-MS/MS Peak 2



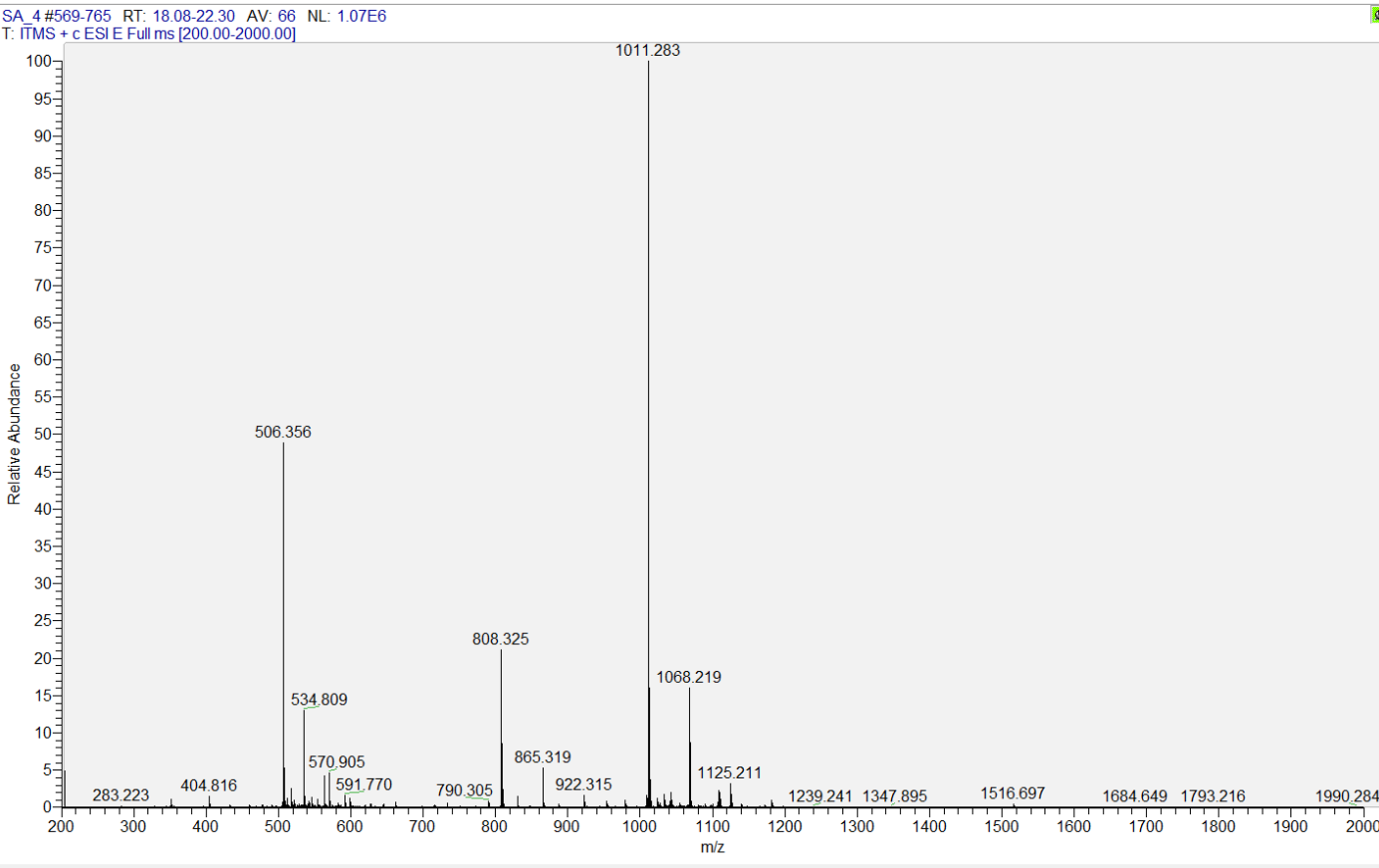
A LC-MS Peak 3



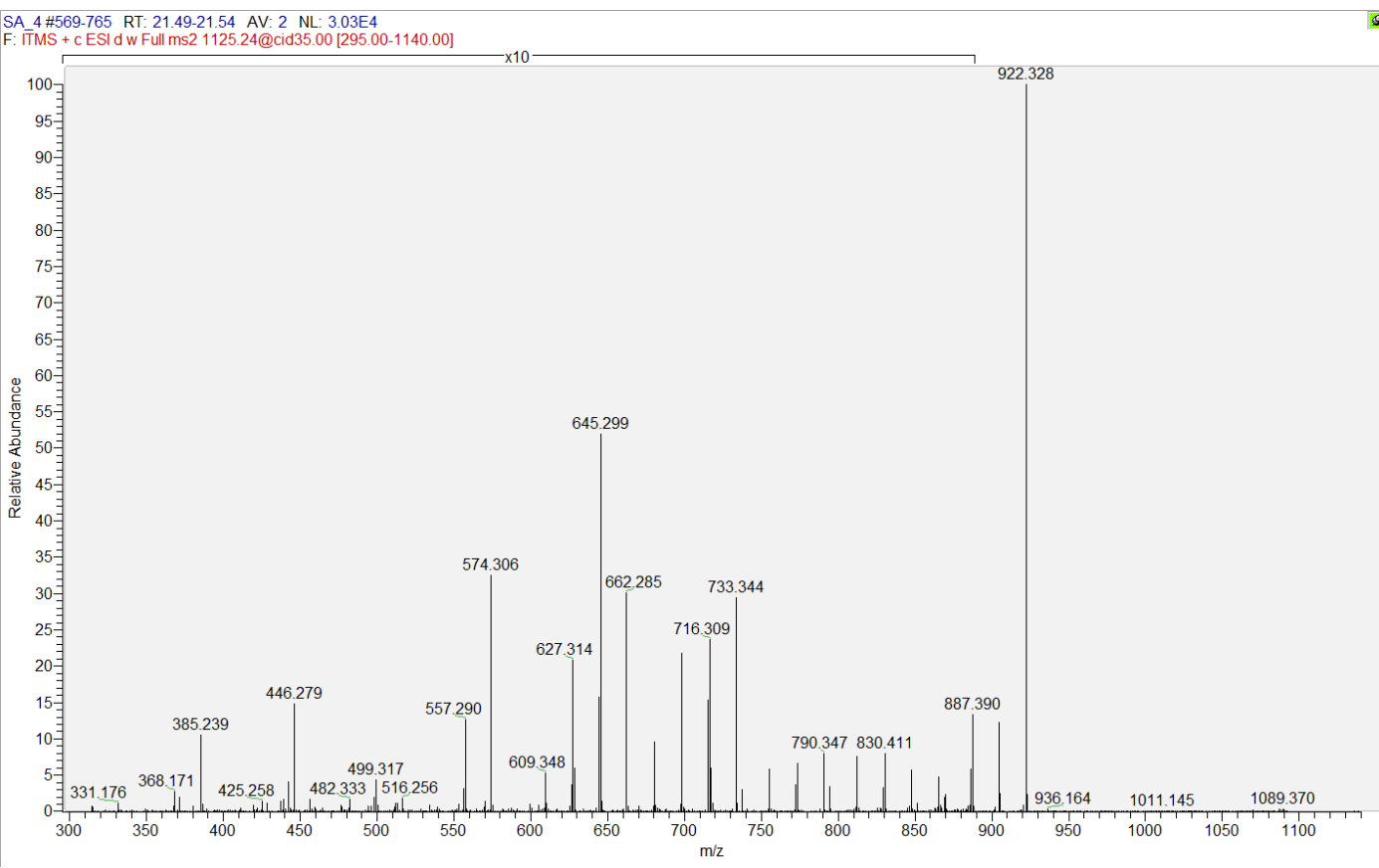
B LC-MS/MS Peak 3



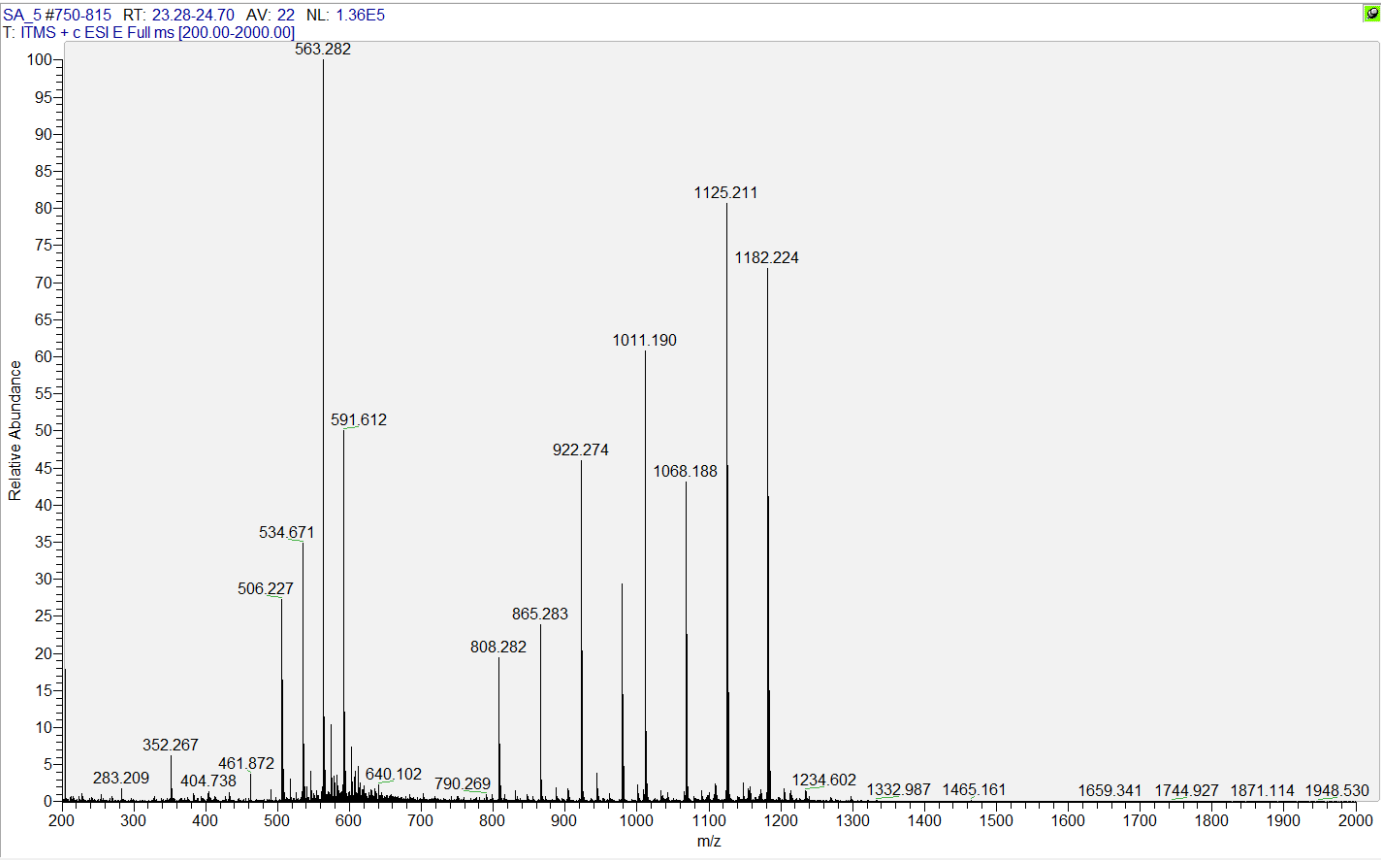
A LC-MS Peak 4



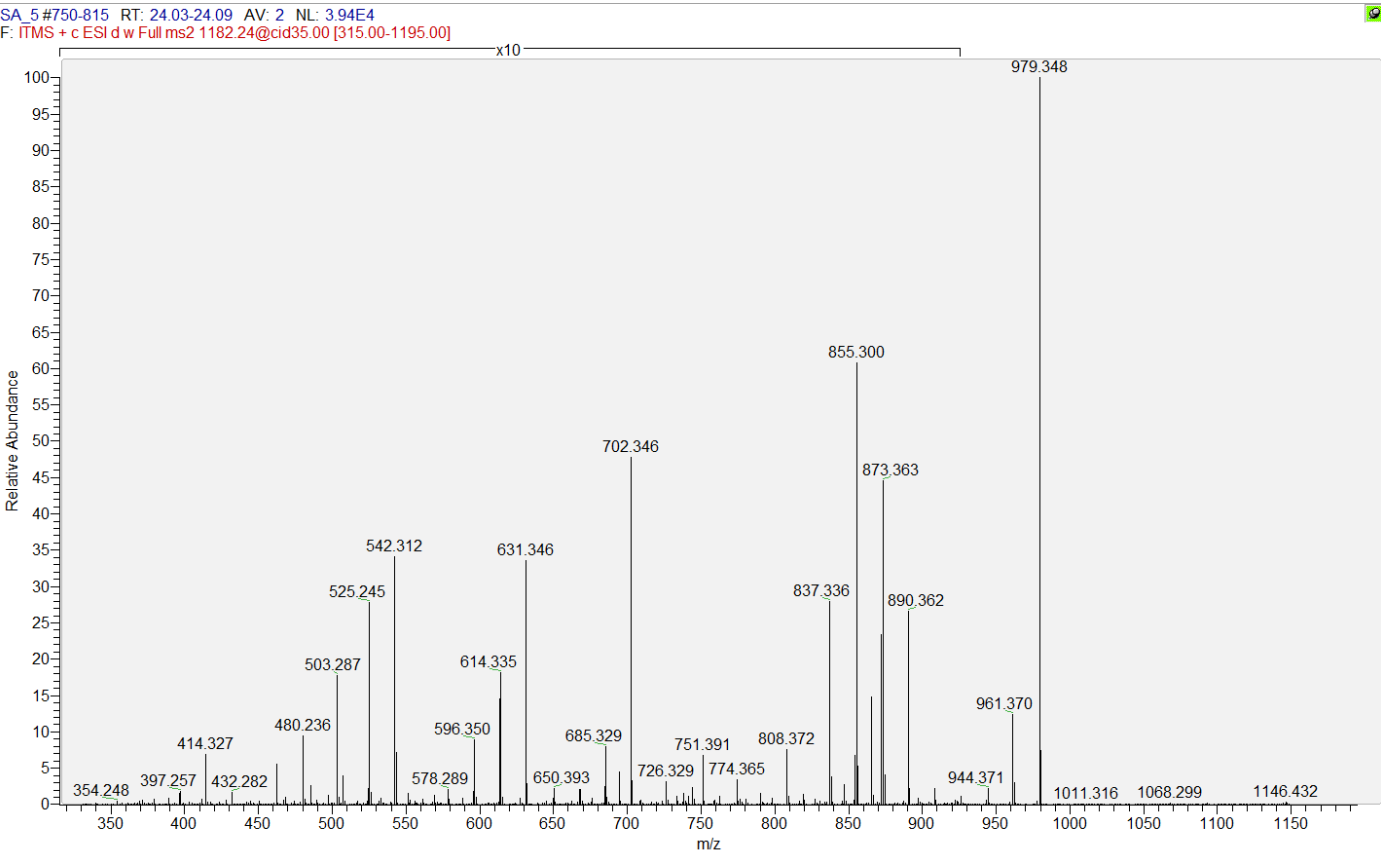
B LC-MS/MS Peak 4



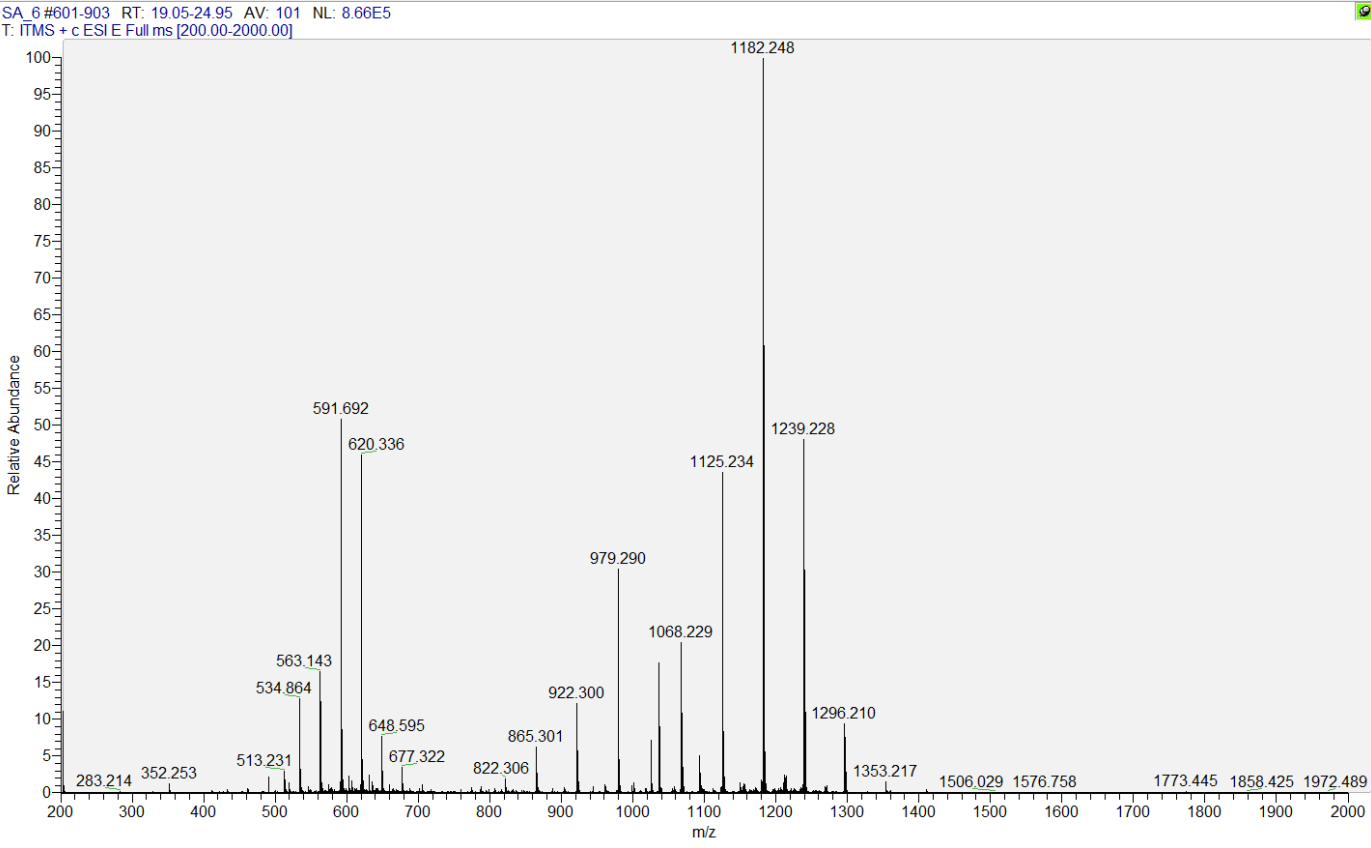
A LC-MS Peak 5



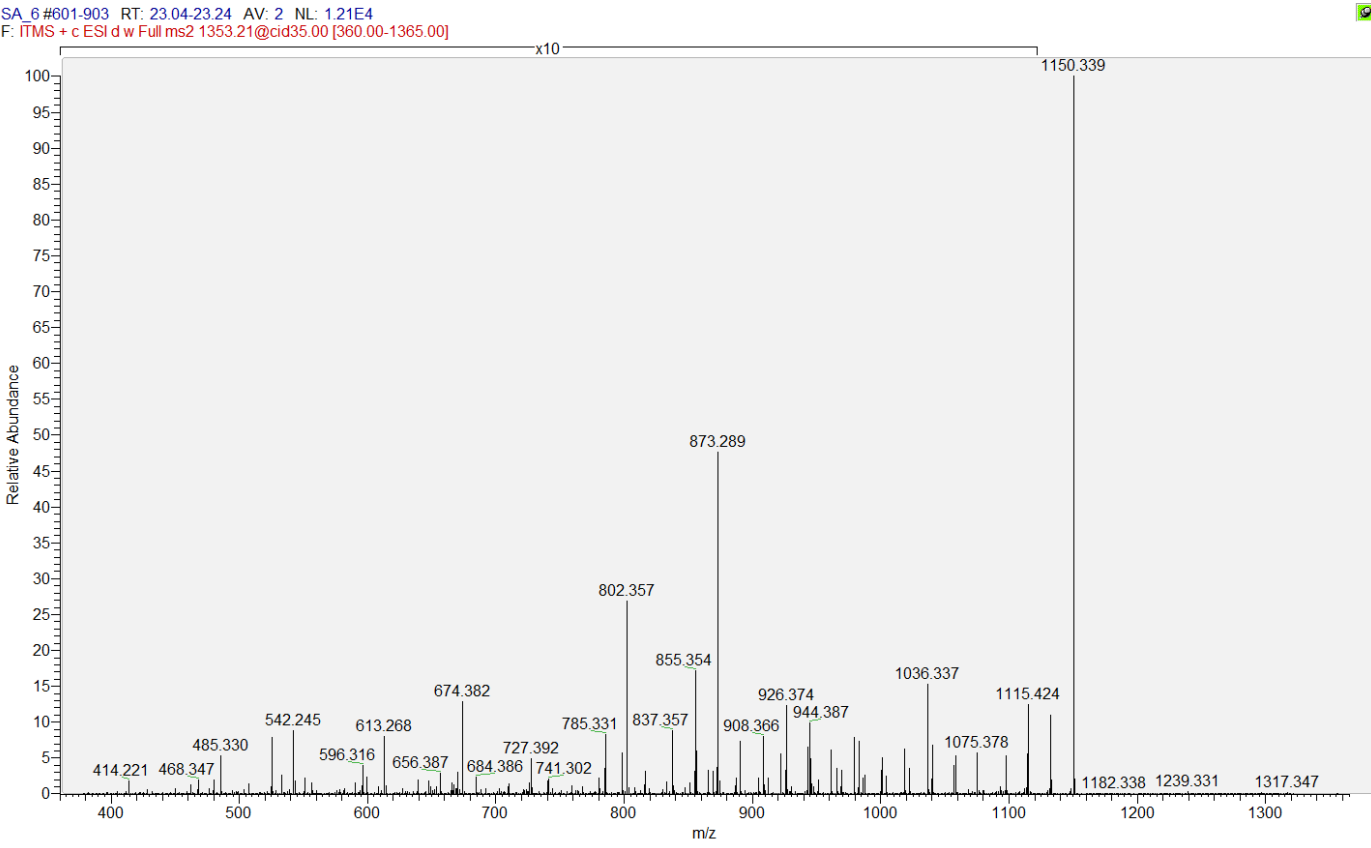
B LC-MS/MS Peak 5



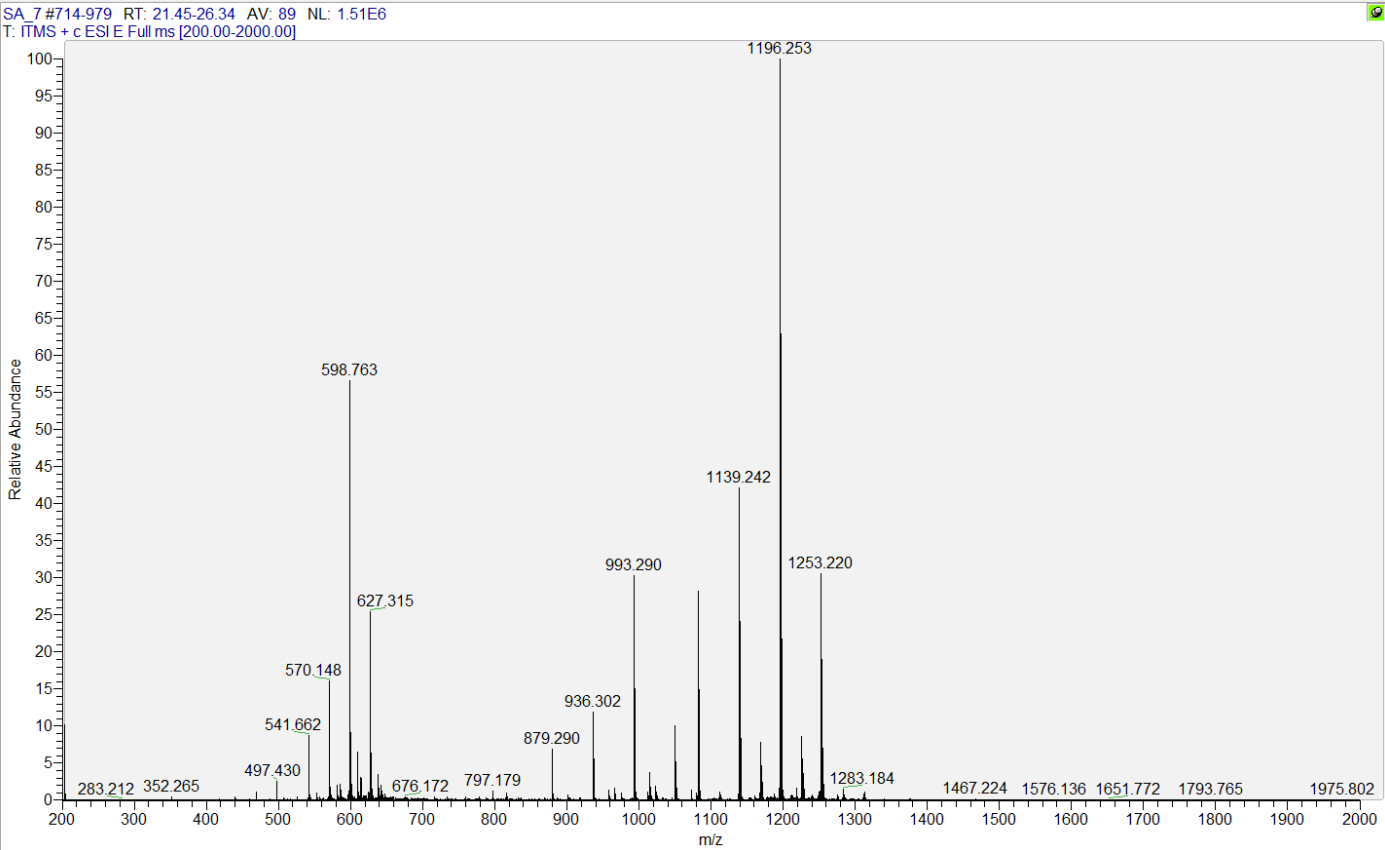
A LC-MS Peak 6



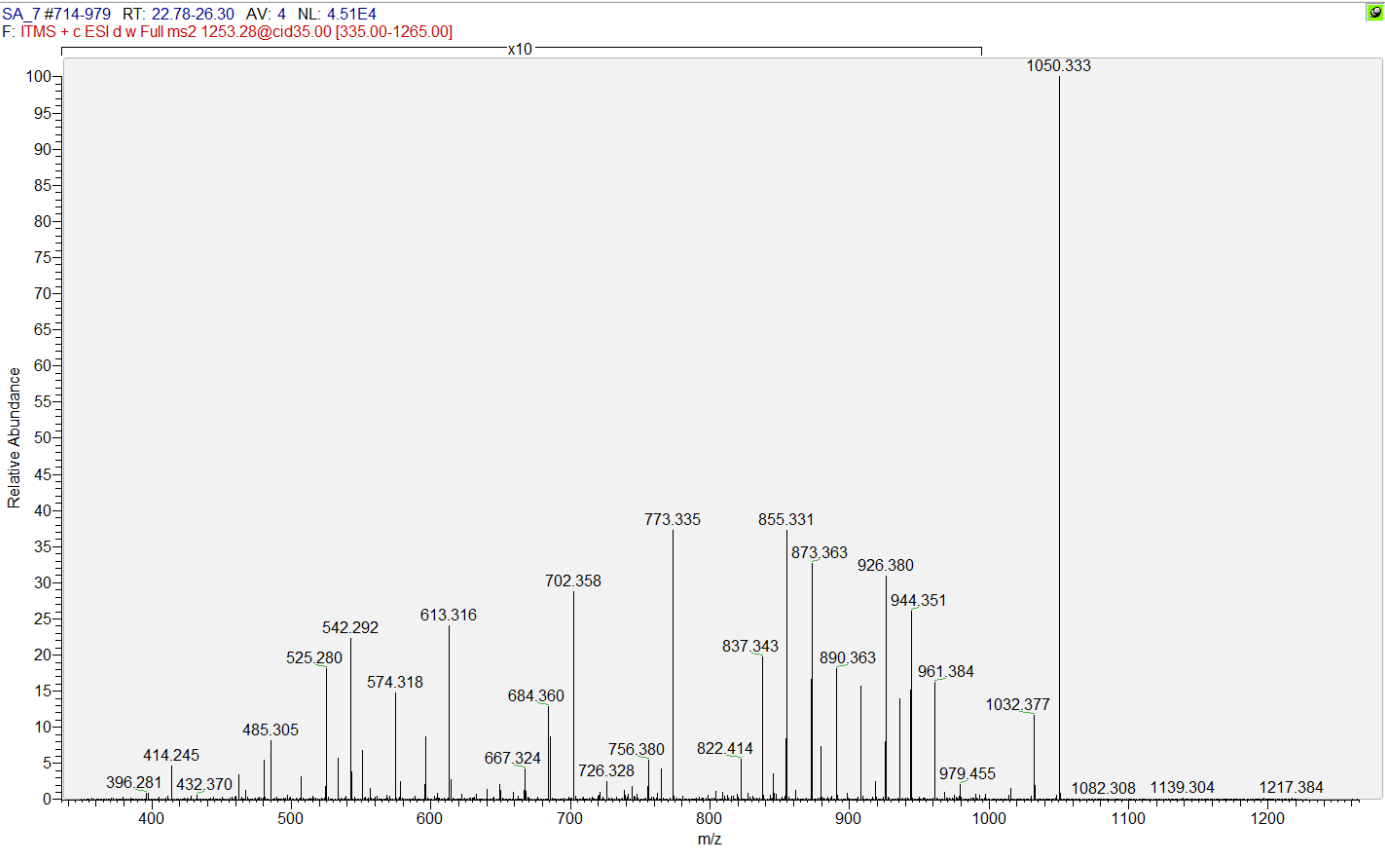
B LC-MS/MS Peak 6



A LC-MS Peak 7

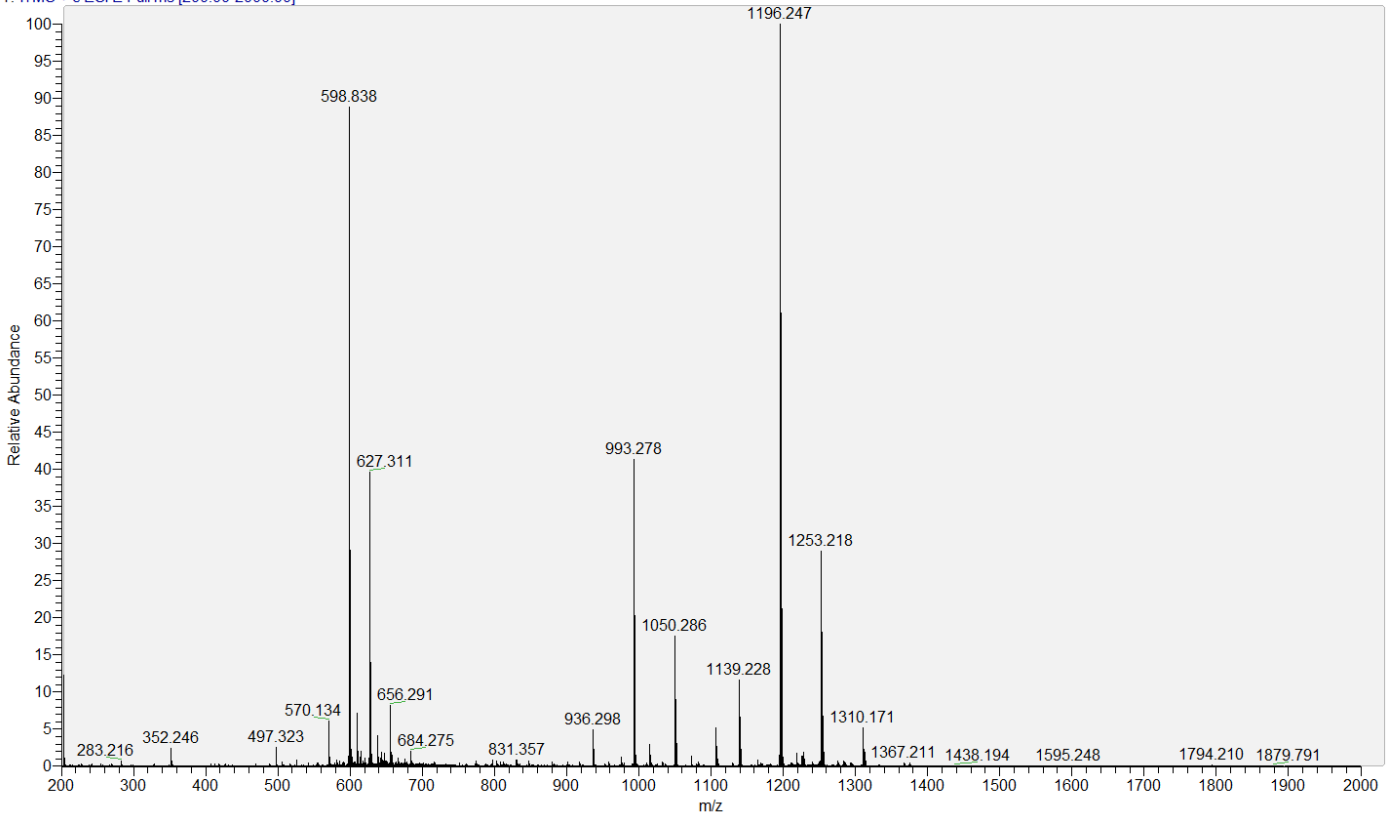


B LC-MS/MS Peak 7



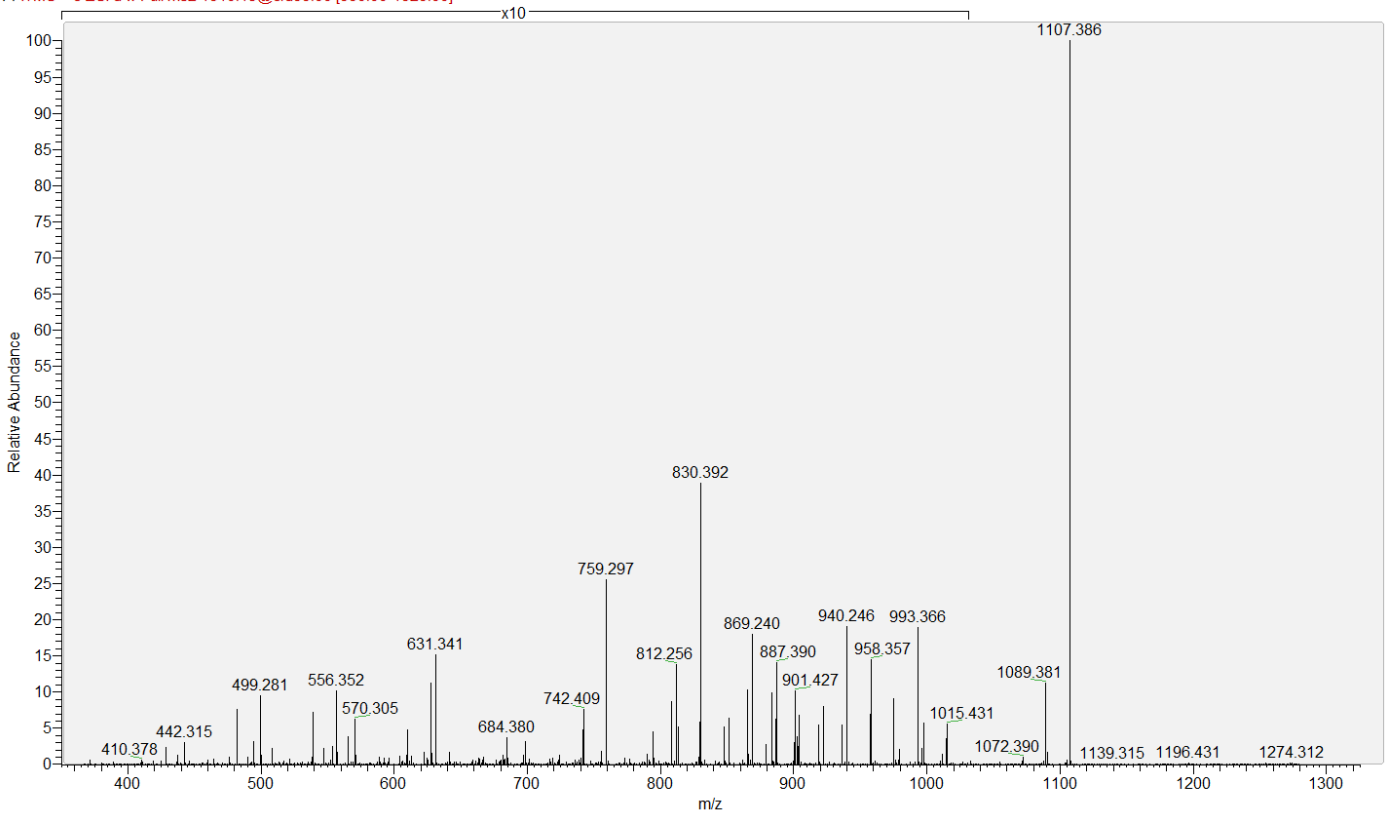
A LC-MS Peak 8

SA_8 #705-861 RT: 22.70-26.21 AV: 52 NL: 3.88E5
T: ITMS + c ESI E Full ms [200.00-2000.00]

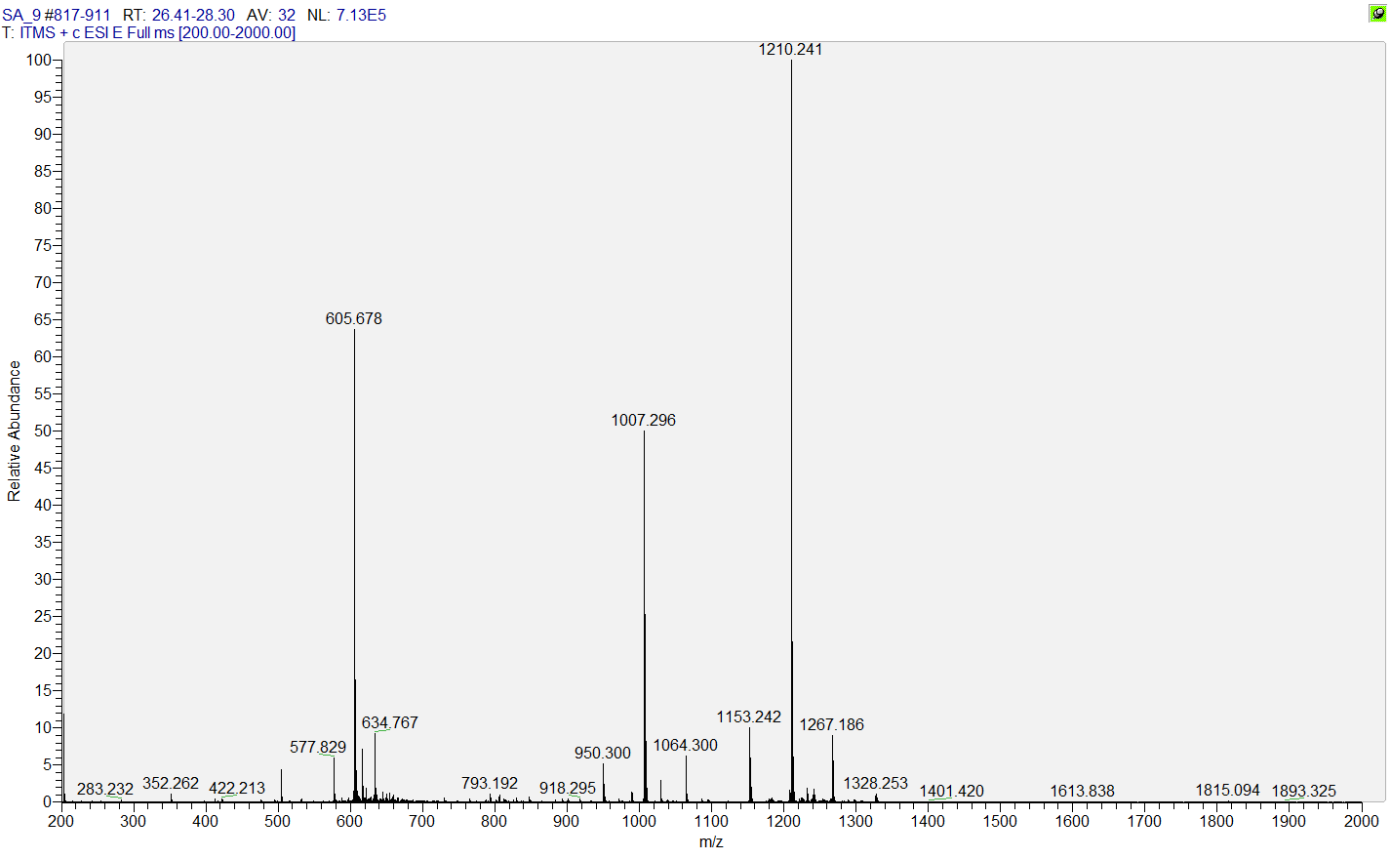


B LC-MS/MS Peak 8

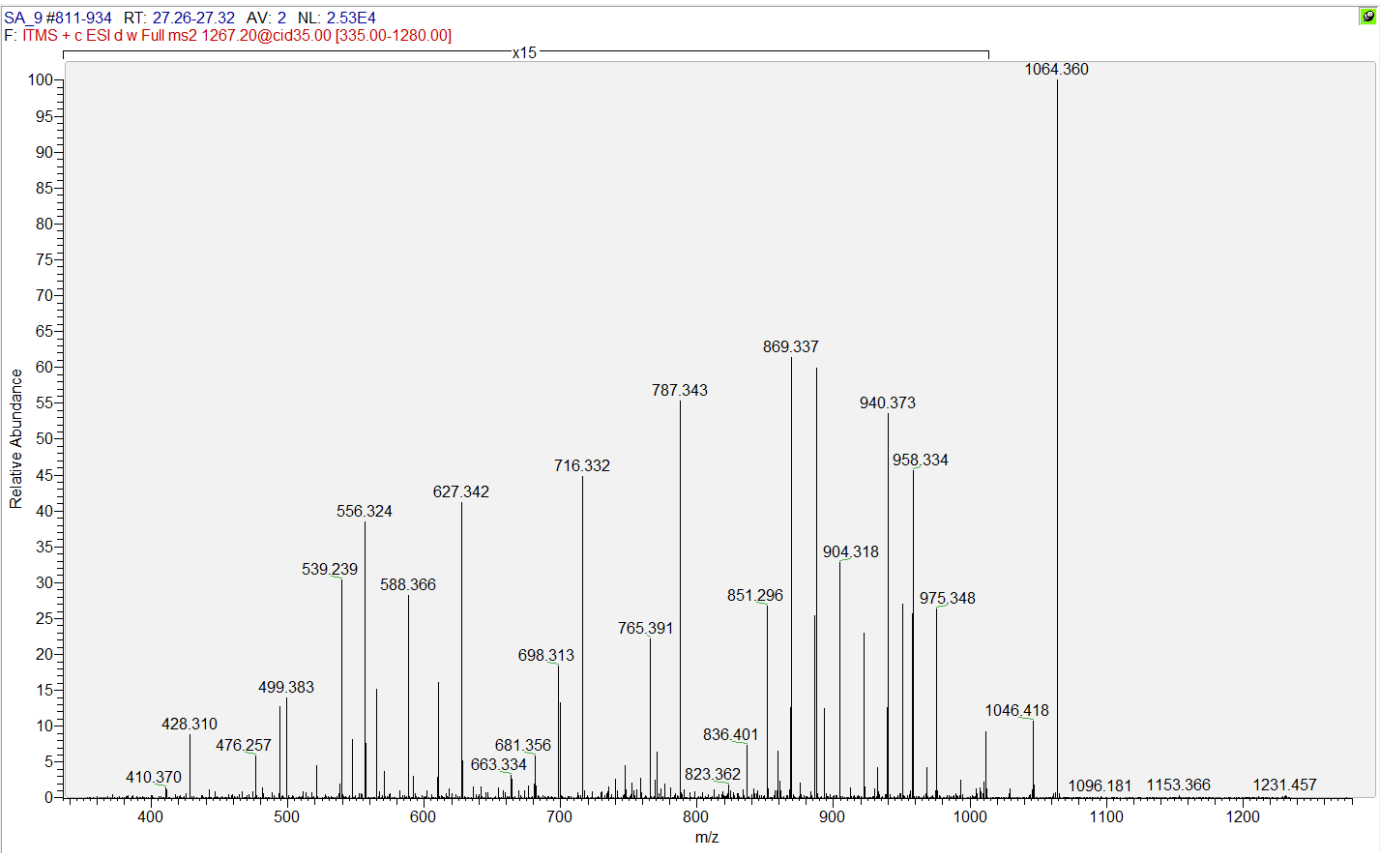
SA_8 #705 RT: 25.59 AV: 1 NL: 2.72E4
F: ITMS + c ESI d w Full ms2 1310.19@cid35.00 [350.00-1325.00]



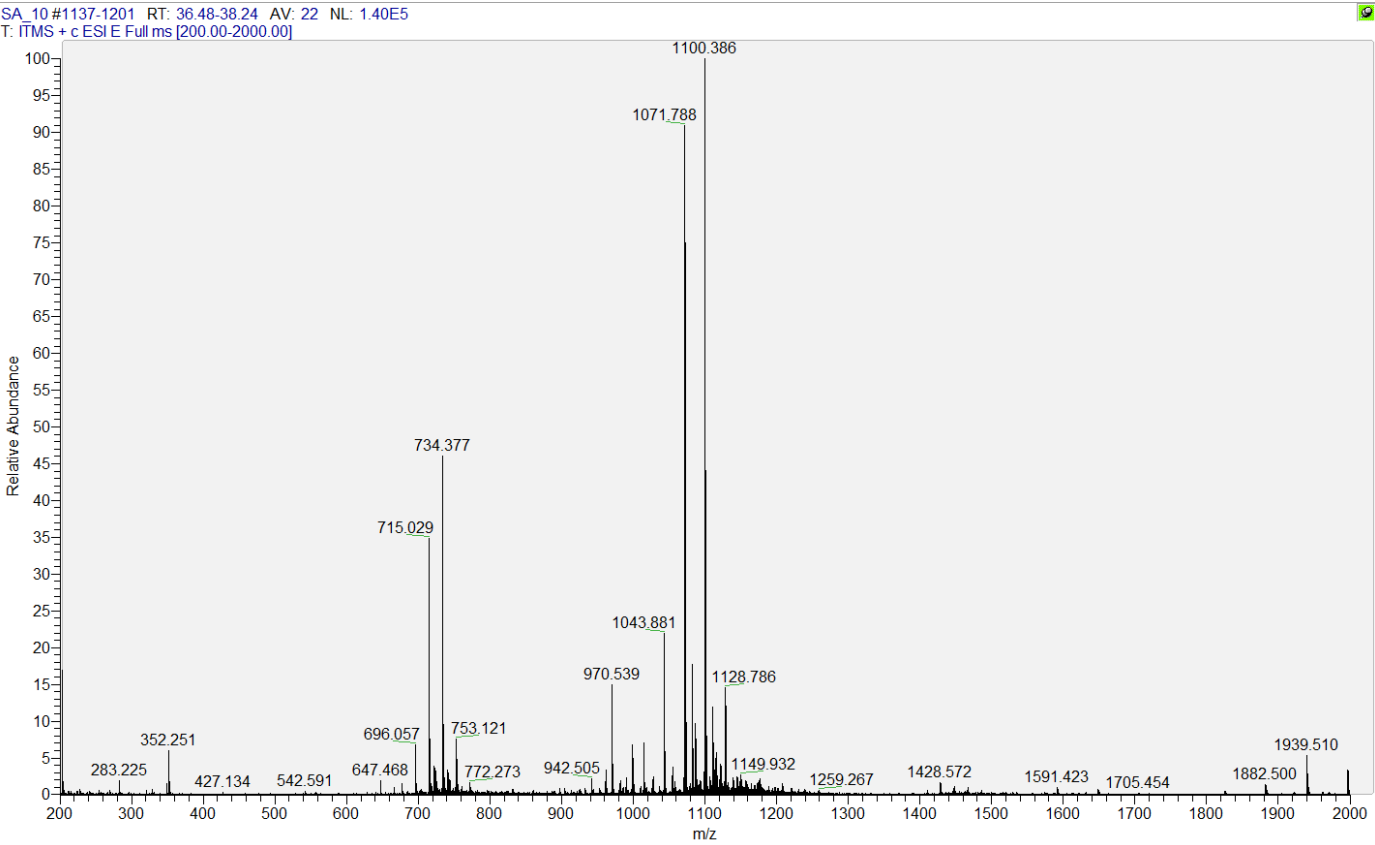
A LC-MS Peak 9



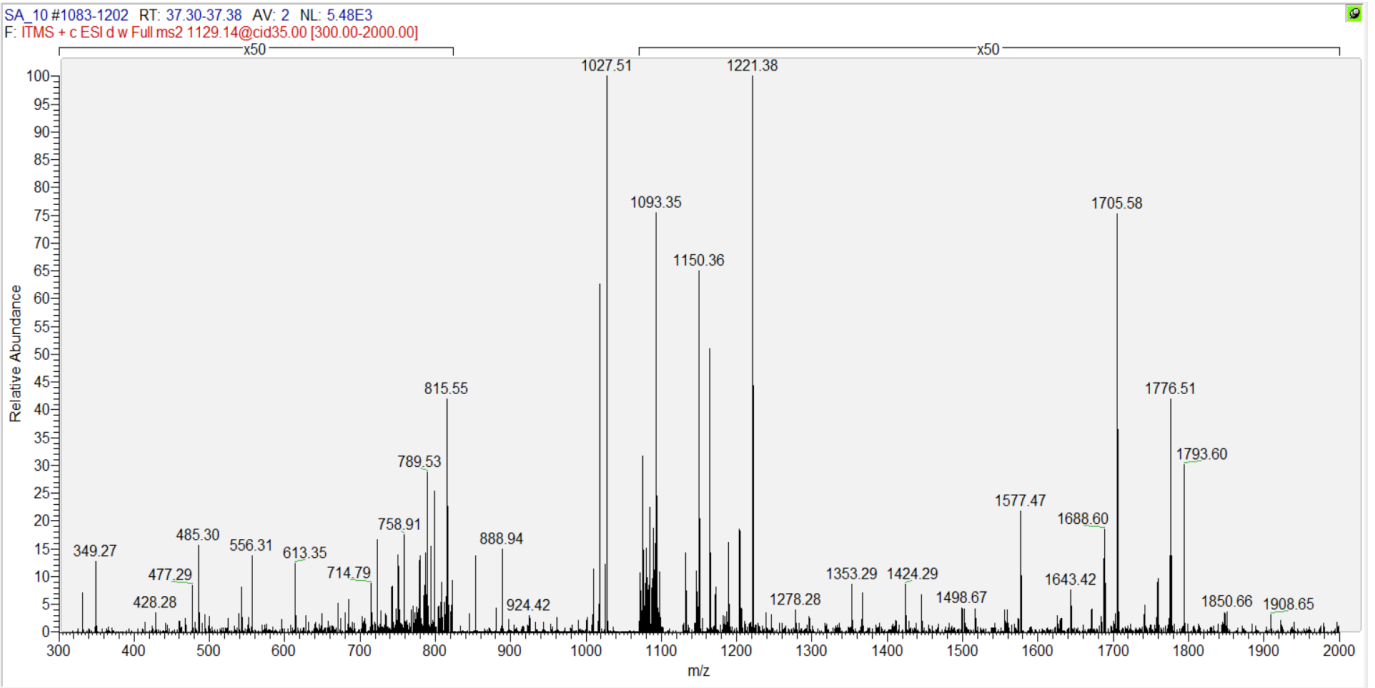
B LC-MS/MS Peak 9



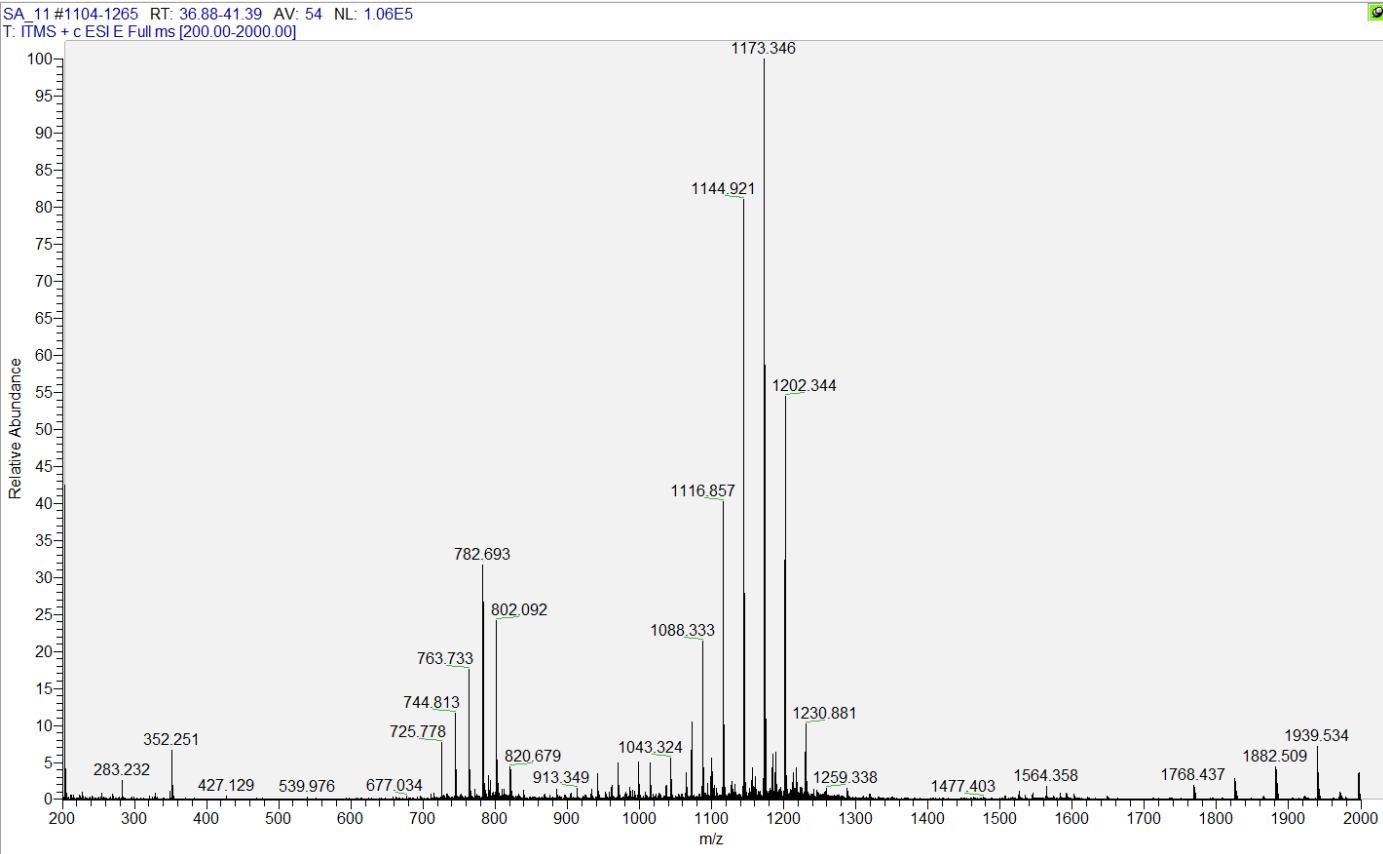
A LC-MS Peak 10



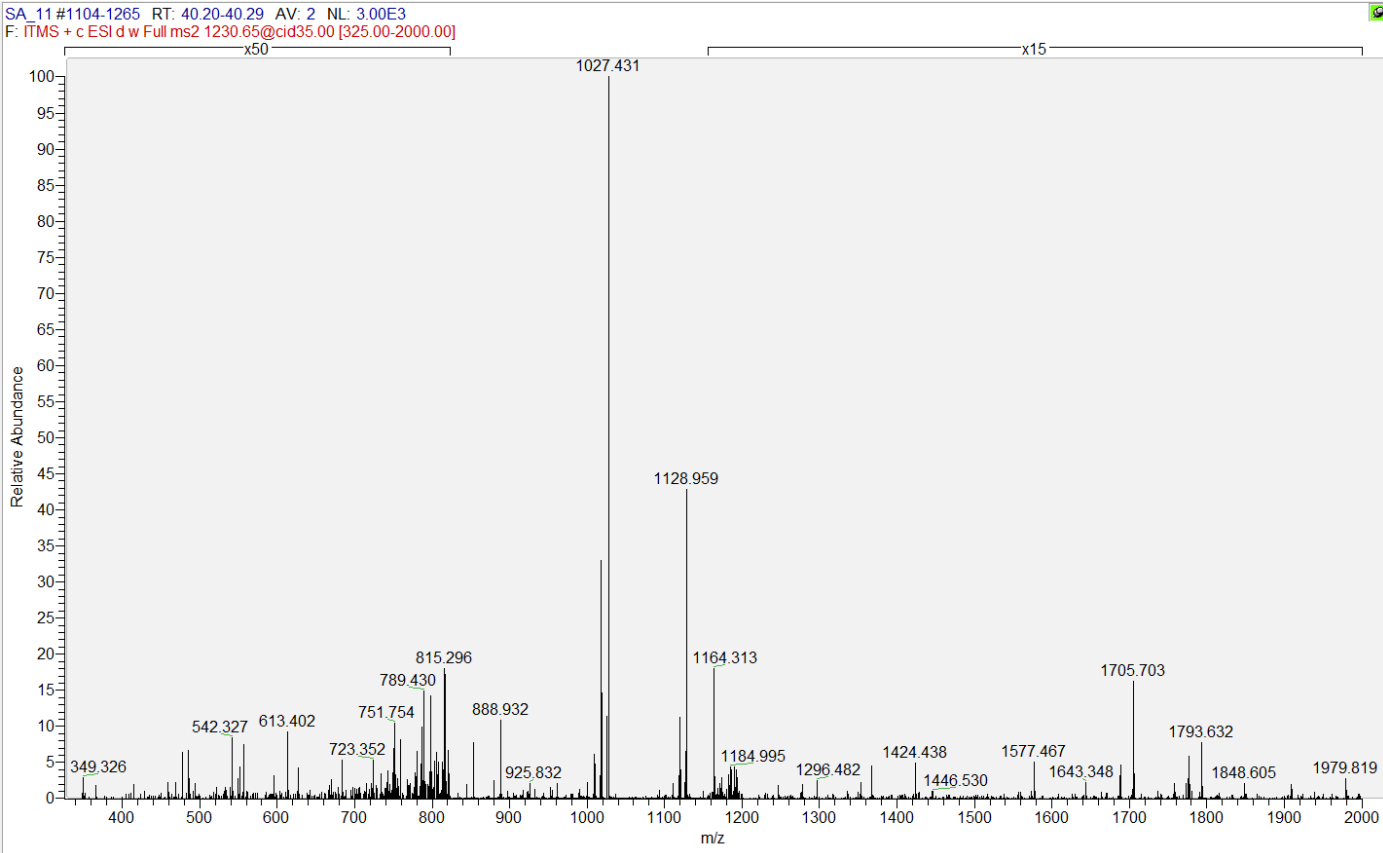
B LC-MS/MS Peak 10



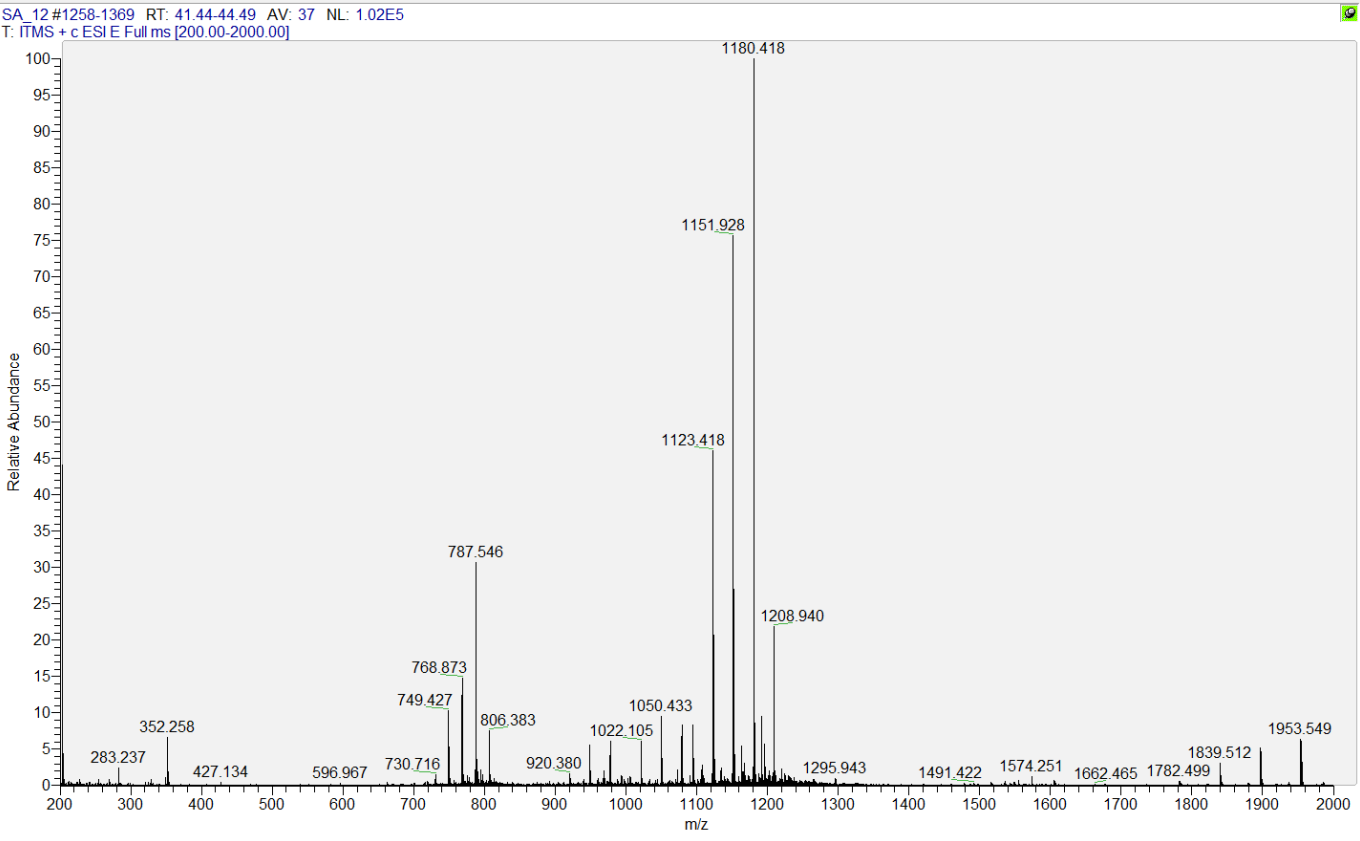
A LC-MS Peak 11



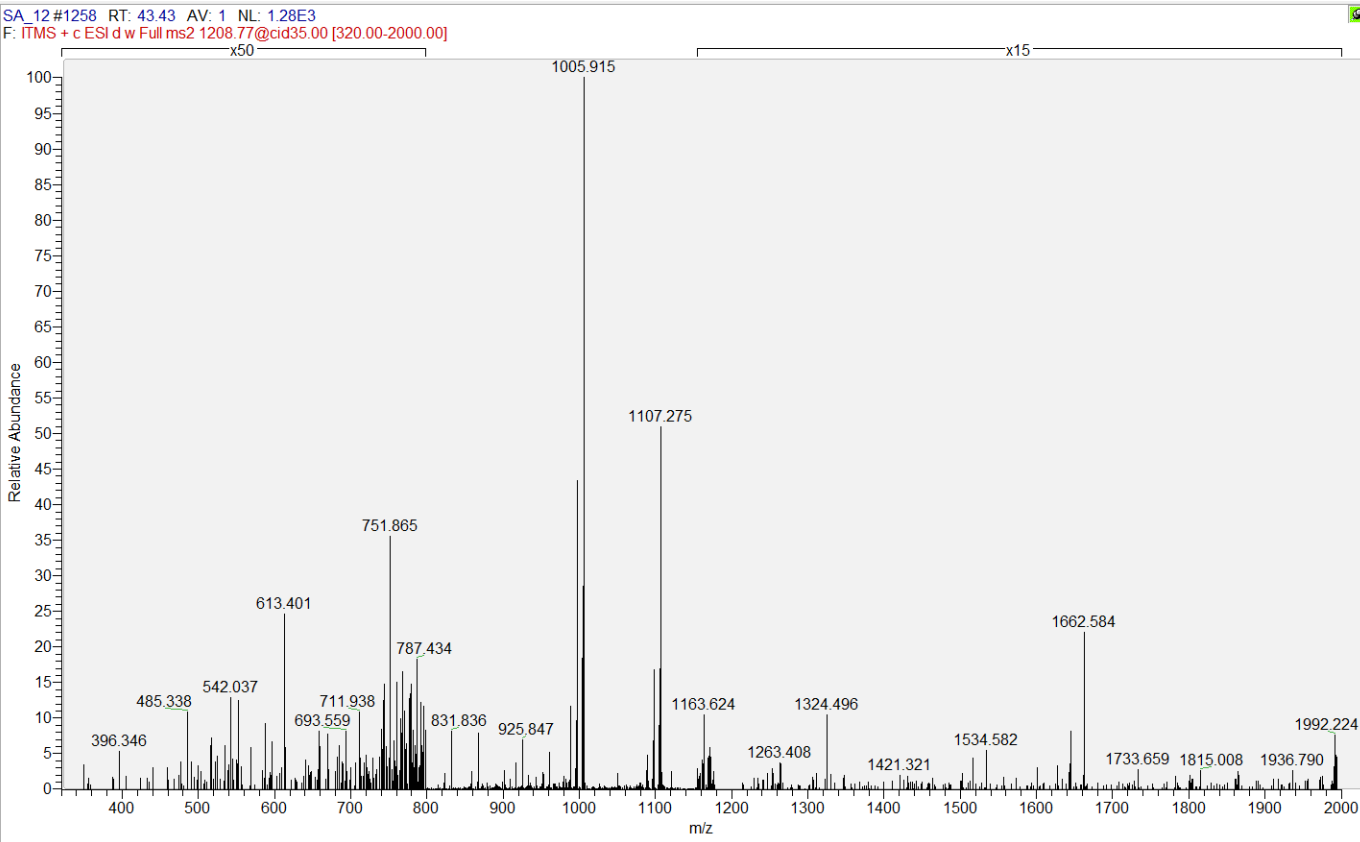
B LC-MS/MS Peak 11



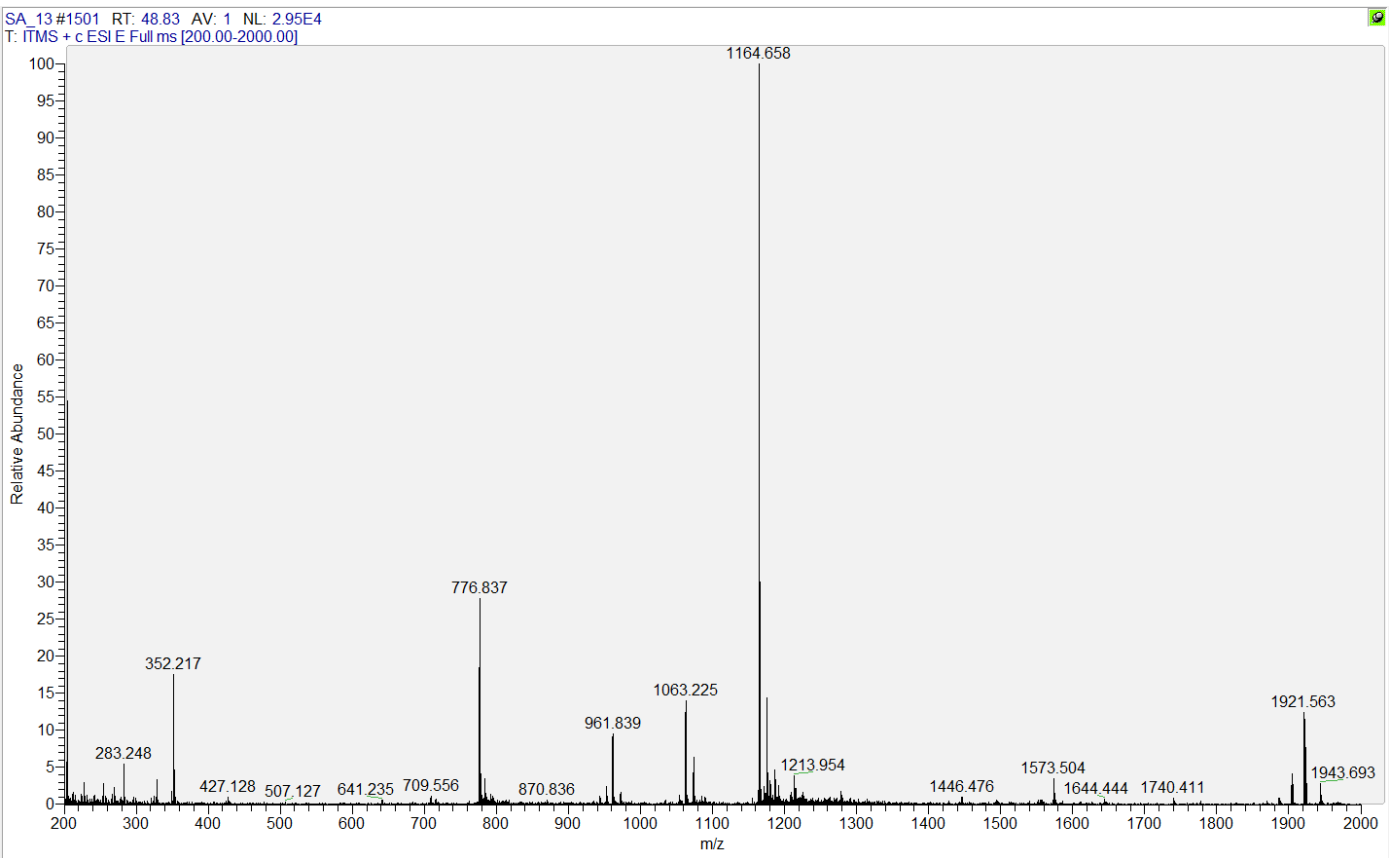
A LC-MS Peak 12



B LC-MS/MS Peak 12



A LC-MS Peak 13



B LC-MS/MS Peak 13

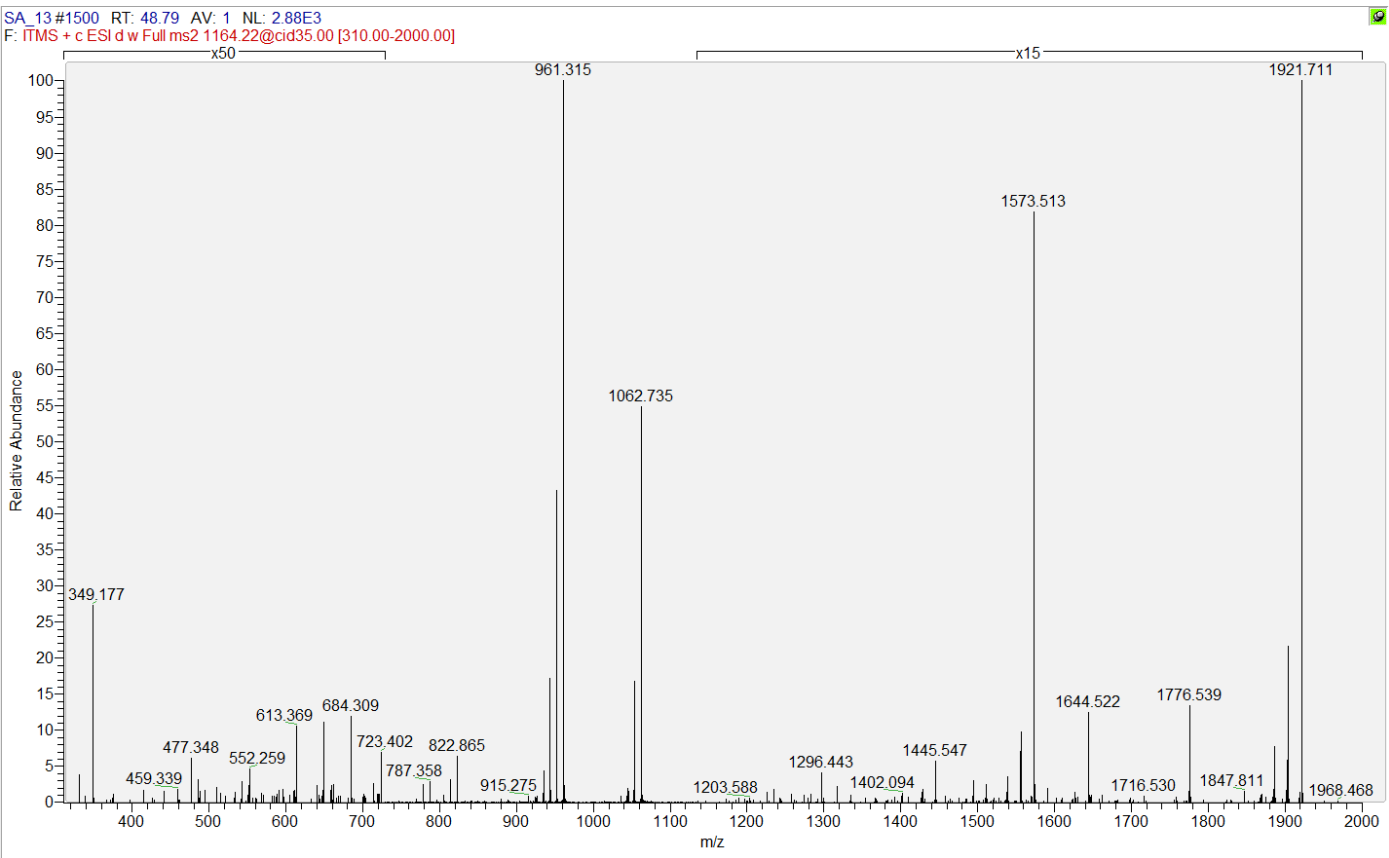


Figure S4: Identification of JE2 Δ *mpsABC* PG fragments by LC-MS and LC-MS/MS. The collected peaks from the lysostaphin-cellosyl double-digested Δ *mpsABC* PG profile (Fig. 4a) were analyzed by LC-MS (A) and LC-MS/MS (B). The determined masses of fragmented PG are summarized in Table S3, while the corresponding identified fragments are illustrated in Fig. 4b.