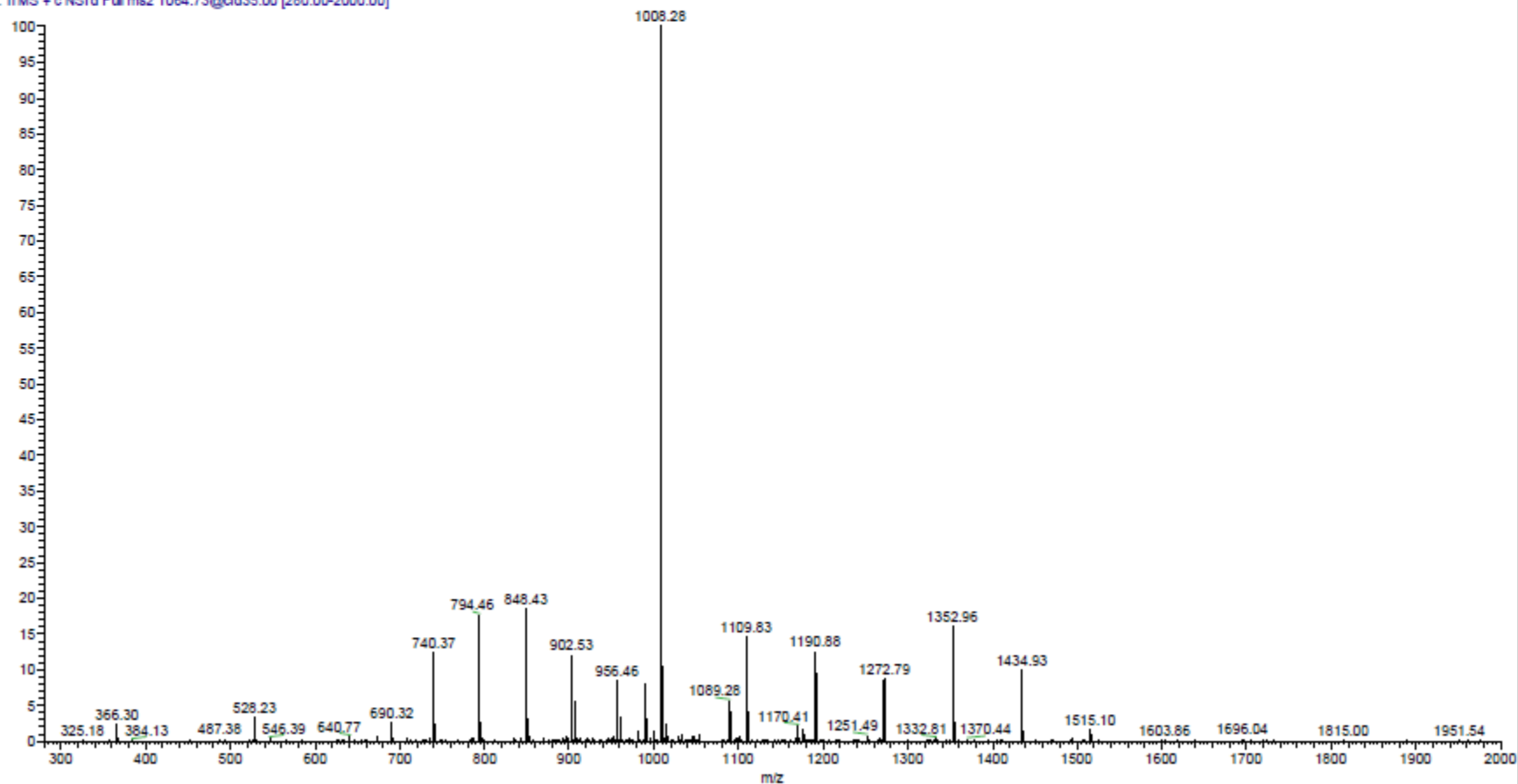


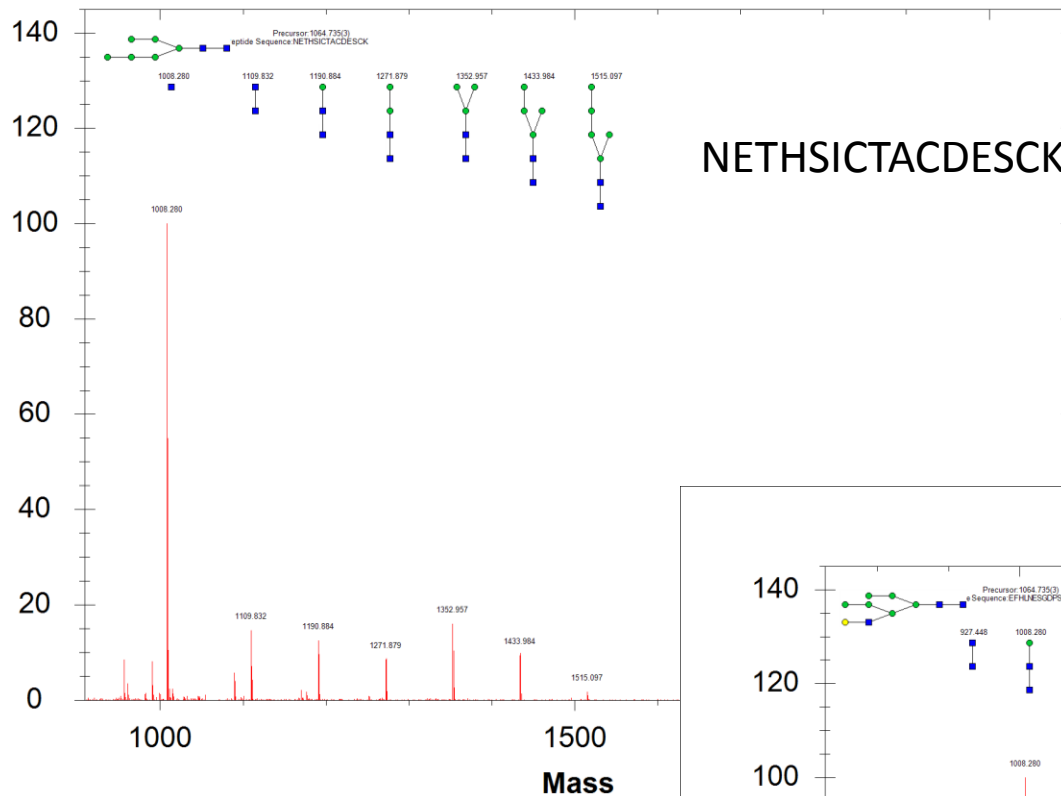
Software: EFHLNESGDPSSK+37000

Manually process: NETHSICTACDESCK+26000

131 HILIC 091614 01 #424 RT: 15.65 AV: 1 NL: 6.86E4
T: ITMS + c NSI d Full ms2 1064.73 @cid35.00 [280.00-2000.00]



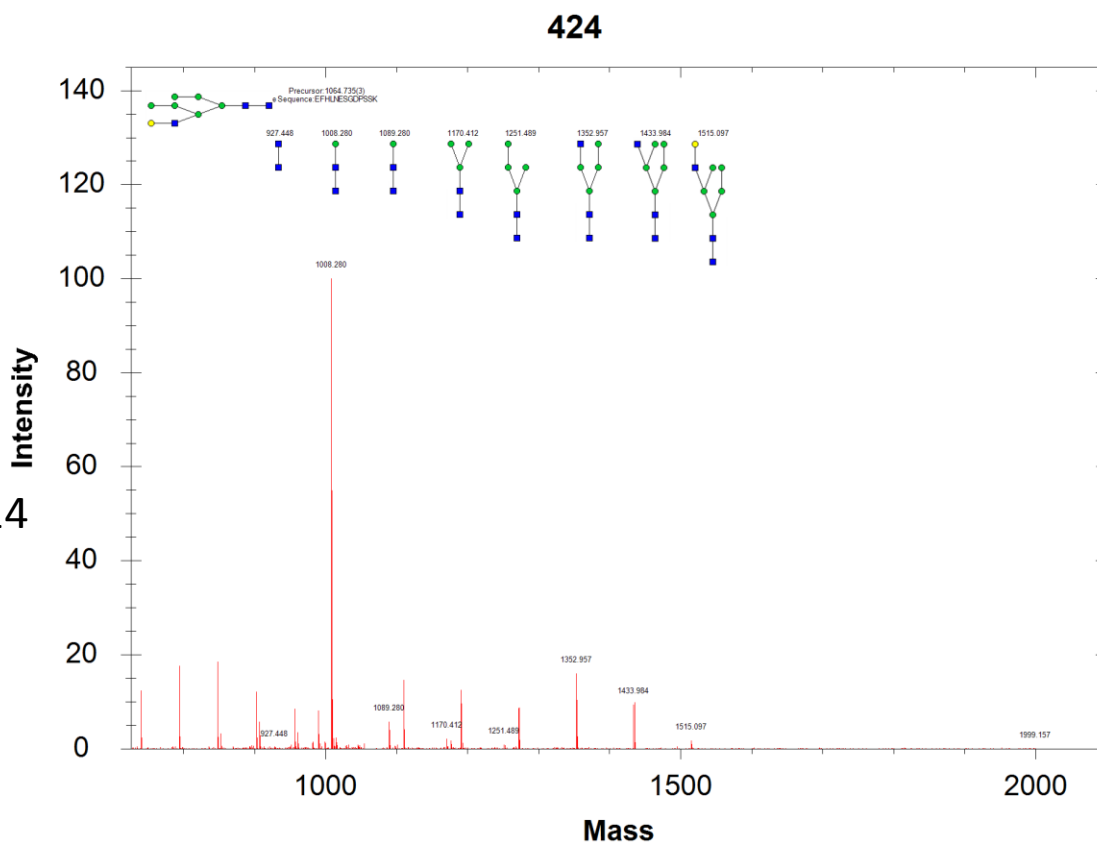
424



NETHSICTACDESK + 26000 Score:16.59

This peptide has Mascot score 14, so didn't include in csv file. If I include this peptide, the sequencing result is correct.

EFHLNESGDPSSK+37000 Score:11.14

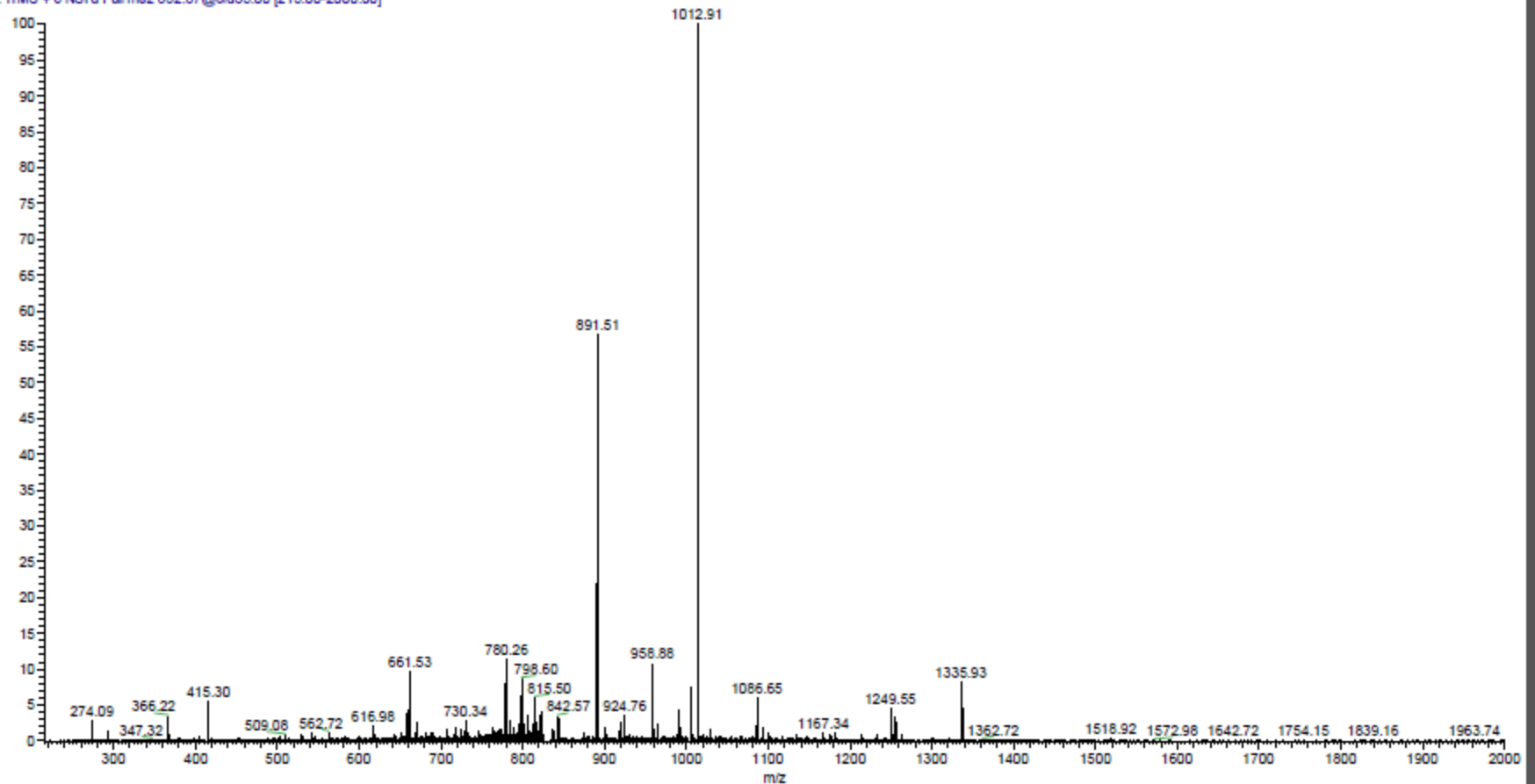


Both glycopeptides are completed.

Software: SYSTTYEERNITGTR+34010

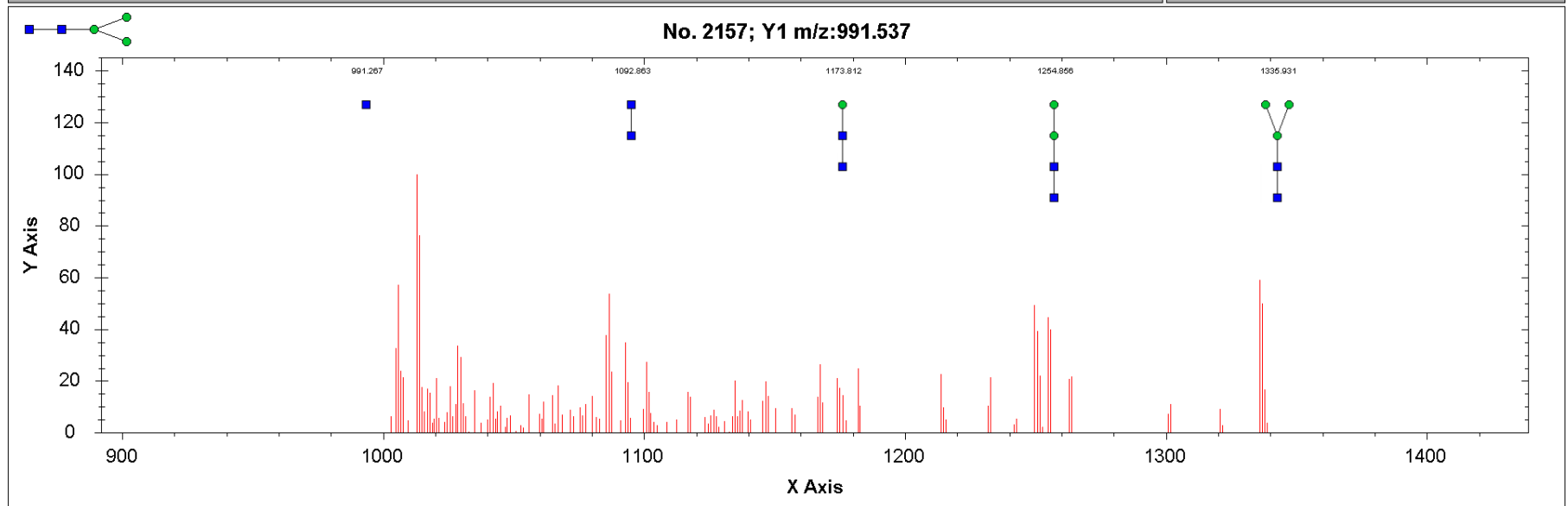
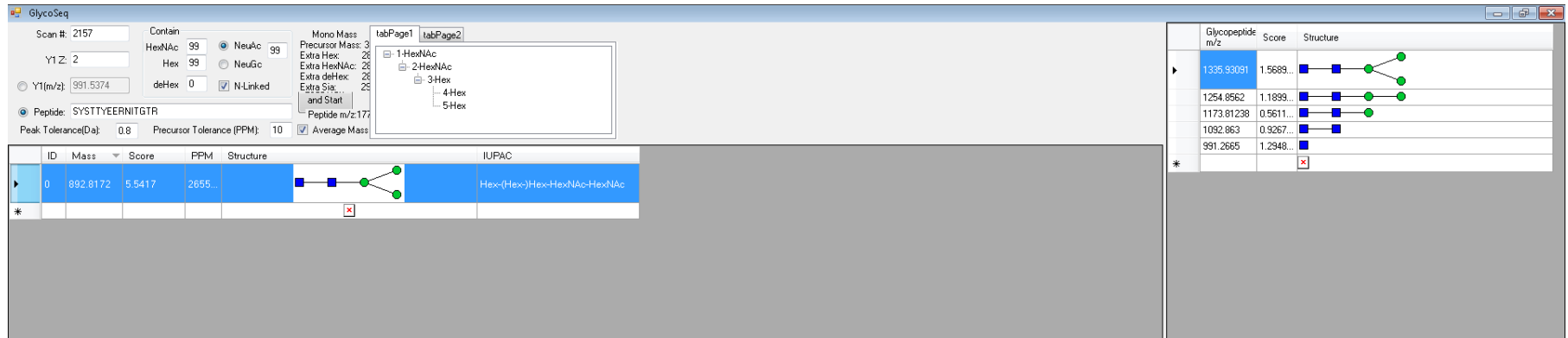
Manually process: Not a N-linked glycopeptide

131_HILIC_091614_01#2157 RT: 26.86 AV: 1 NL: 3.83E4
T: ITMS + c NSI d Full ms2 832.87@cid35.00 [215.00-2000.00]



I can't find the result that you refer.

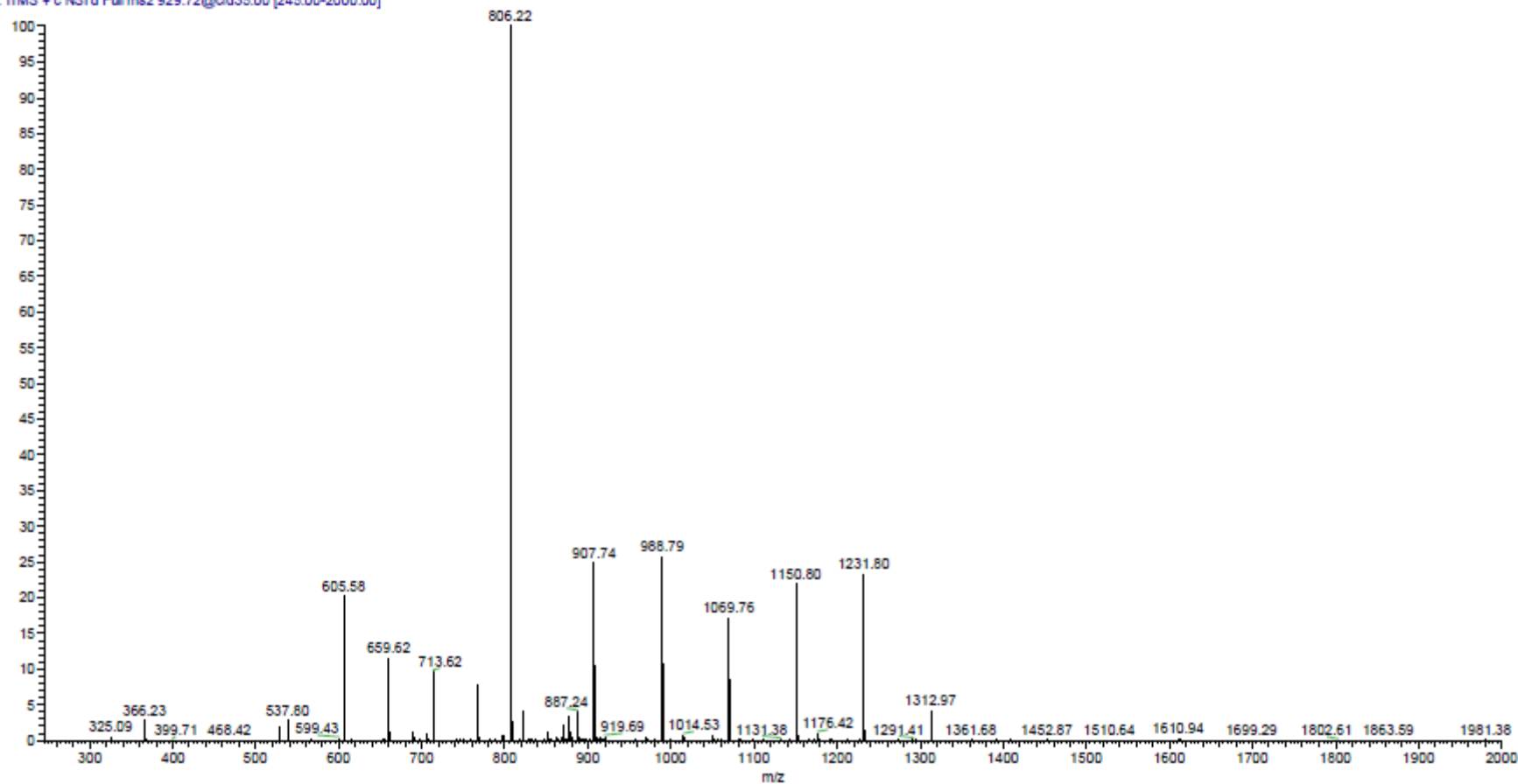
SYSTTYEERNITGTR+34010



Software: Not a glycopeptide

Manually process: YNCTATNHIGTR+26000

131 HILIC 091614 01#567 RT: 16.56 AV: 1 NL: 1.72E5
T: ITMS + c NSI d Full ms2 929.72@cid35.00 [245.00-2000.00]



I can't get completed sequencing for this one, so if you check "completed only" it won't show in result.

This one has very high sequencing score 16.7.

