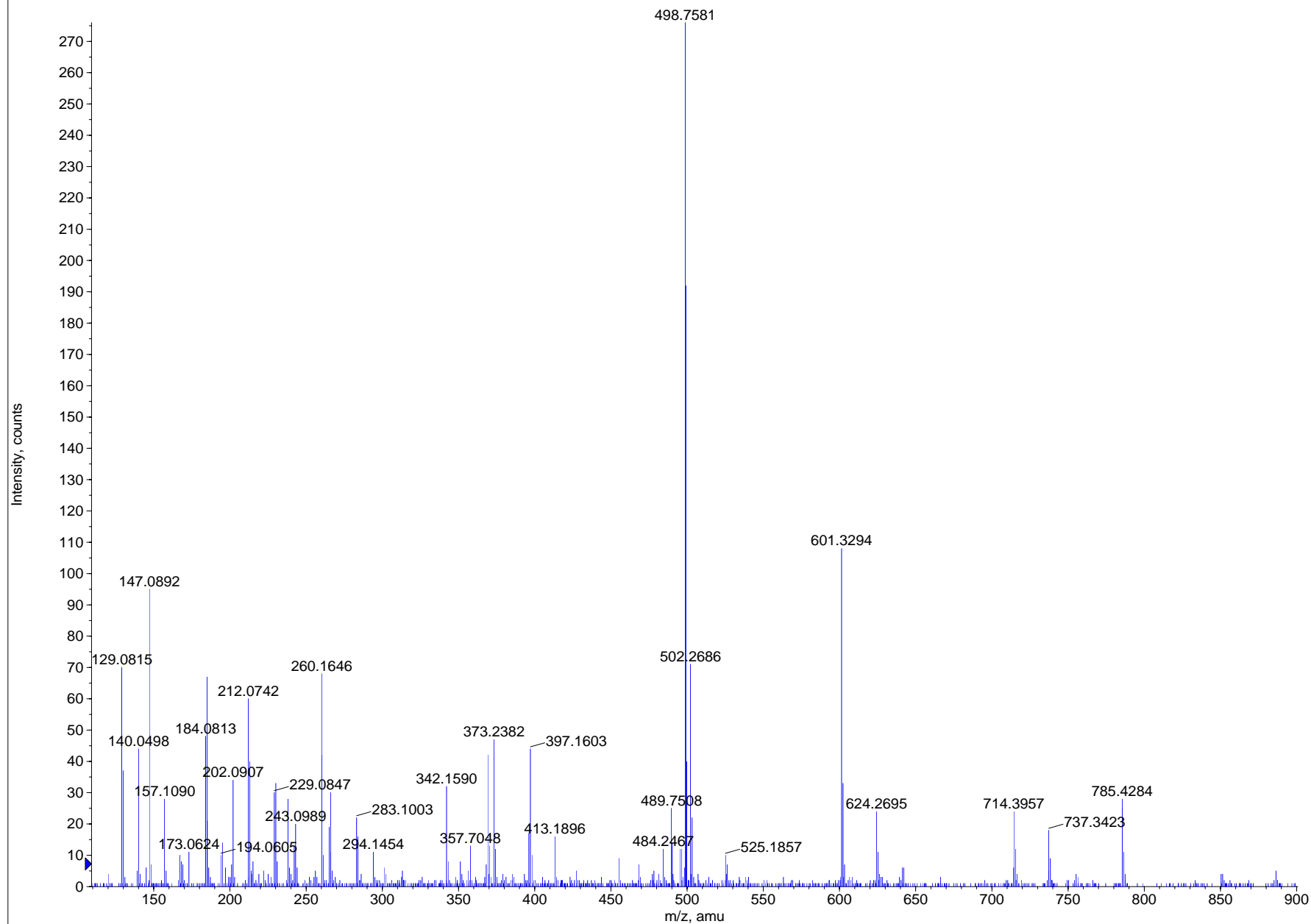


+TOF Product (507.8): Experiment 2, 22.141 min from Sample 2 (060605_BSA-Verdau) of BSA.wiff
a=3.56542312359049760e-004, t0=3.25081628932020980e+001

Max. 276.0 counts.



Fragmented ion: m/z 507.76; $z = 2$

Found masses, recalibrated

(Noise peaks were filtered, every ion can be assigned!)

129.07	147.11	(212.10)	230.11
260.20	(283.14)	(369.21 ($z = 2$))	373.28
(397.21)	414.23	(434.76 ($z = 2$))	502.32
601.39	(624.34)	642.35	714.48
737.42	785.51	868.51	886.56
1014.61			

Help: (Only) one of the series (a, b, c, x, y or z) is complete!

All ions except the marked ones have ($z = 1$).

Tasks:

- 1) What is the sequence of the peptide, which was formed after tryptic digestion of a protein?

2. Can you assign all the ions according to the nomenclature (e.g. a, b, c, x, y or z, loss of water/ammonia?)

3. Are there problems when assigning the peptide sequence? When can these problems be seen?

4. Which method was used for ionization, which one for fragmentation?
Explanatory statement!

- 5) Why are there fragment ions with a higher value for m/z than the precursor ion has?