Vorschau

test

Datum: Mi 29 Okt 2014 14:47:52 CET Maximale Punktezahl: 100

1. tandem MS (easy) *(10 Punkte)*

Please find the matching pairs:

Auswählbare Terme

specifies mass range for fragmentation

most intense peaks are scheduled for fragmentation

schedules mass peaks for fragmentation

allows for broader coverage of peptides

Auswahl

data dependent acquisition	passt zu
precursor isolation window	passt zu
dynamic exclusion list	passt zu
inclusion list	passt zu

2. mass accuracy (easy) *(5 Punkte)*

Suppose the mass of a peptide is measured to 2500 Da. The error is 0.01 Da. What is the error in ppm?

3. mass resolution (medium) *(10 Punkte)*

Download the mass spectrometry data. Open it in TOPPView and (roughly) estimate the mass resolution at m/z = 400.

4. cofragmentation (medium) *(10 Punkte)*

Consider two peptides with similar m/z (e.g. 463.2 and 464.4). By chance, they elute at the same time. The instrument operates in data dependent aquisition mode. At some point, one of the two peptide masses is scheduled for fragmentation. Briefly explain why the tandem spectrum might be difficult to analyse.

5. Size-exclusion chromatography *(10 Punkte)*

Will larger or smaller molecules elute earlier when using size-exclusion chromatography (SEC)? Please explain why.

6. Chromatography - Multiple Choice *(10 Punkte)*

Please select **all** correct statements from the following list and do not select any incorrect statement:

   The number of theoretical plates increases as HETP decreases.
   Reverse phase chromatography uses a polar stationary phase.
   When using HPLC the mobile phases moves through the column due to capillary forces.
   The van Deemter equation can be used to find the optimal column length.
   The term longitudinal diffusion in the chromatographic column depends on the flow rate.

7. Time-of-flight *(30 Punkte)*

You have a mass spectrometer with a short flight tube (0.6 m), and you are measuring ions that flew 14.397408926795598 microseconds. You had your fieldstrength at 9000V and you know the ions detected are singly charged. Now what is the mass (in u) of the measured peptide?

Note: please use the NIST definitions for the constants of elementary charge (coulomb) and the unified atomic mass unit (u): http://physics.nist.gov/cuu/Constants/index.html

Note: the kinetic energy of a mass is $E\_k = 1/2 \, m \, v^2$, the potential energy of a charged analyte $E\_P = qU$, $E\_k = E\_p$ and the velocity $v = d/t$

()

8. DDA *(5 Punkte)*

You are a mass spectrometer running DDA with a Top-5 setting. Please mark the respective peak tips you select for fragmentation.
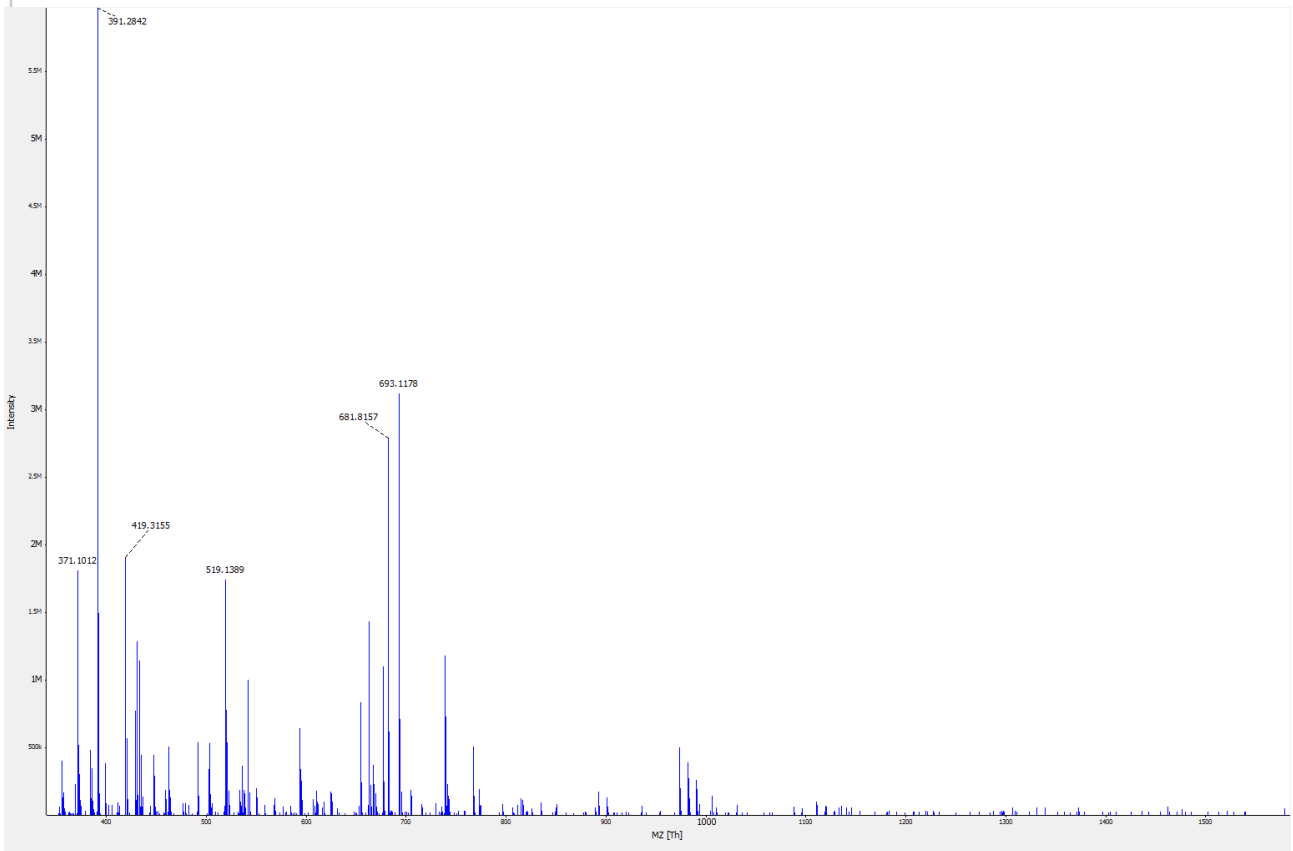
9. HPLC *(10 Punkte)*

Please explain briefly the main components of an HPLC system and the general principles of HPLC analyses.