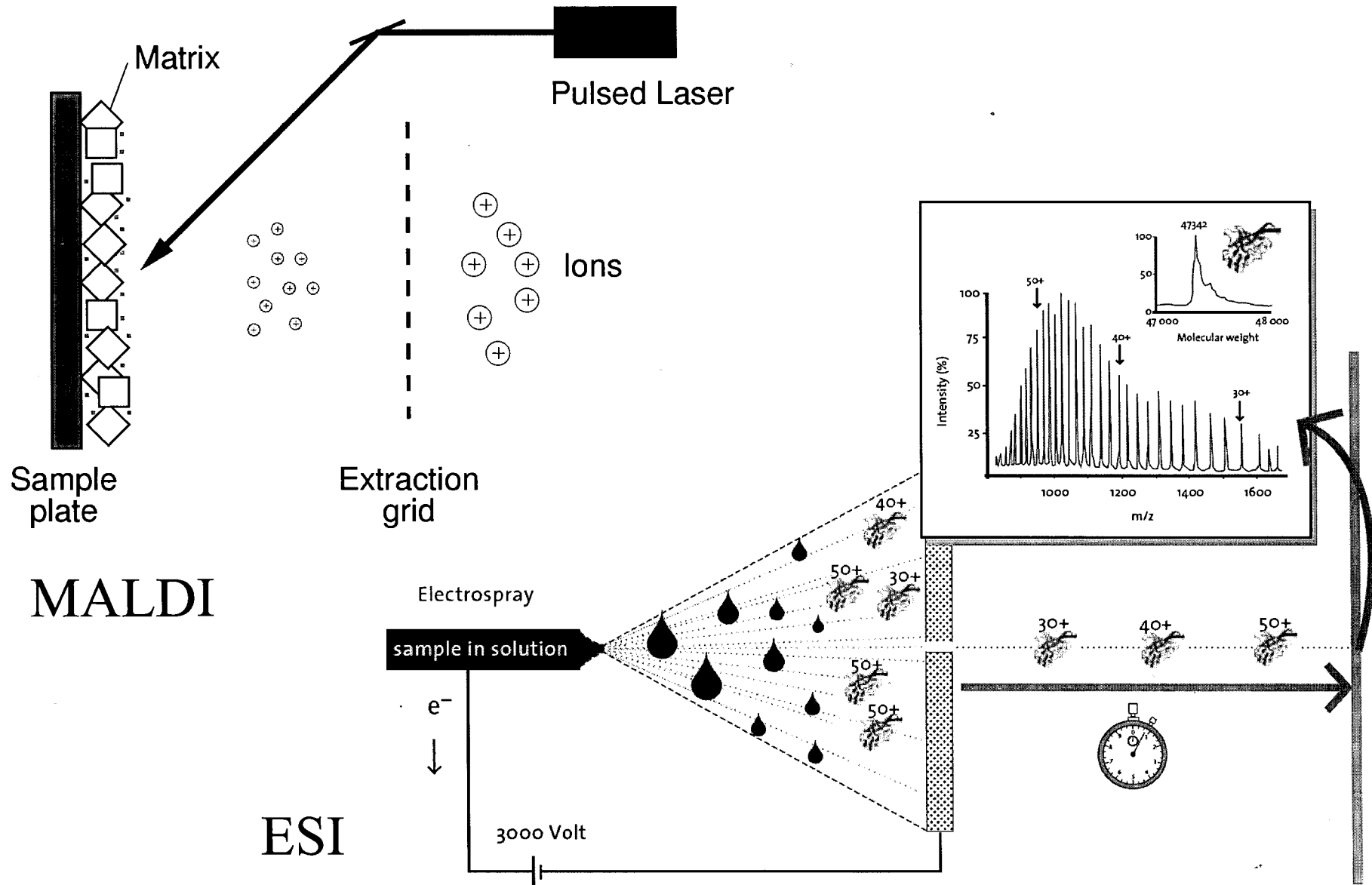
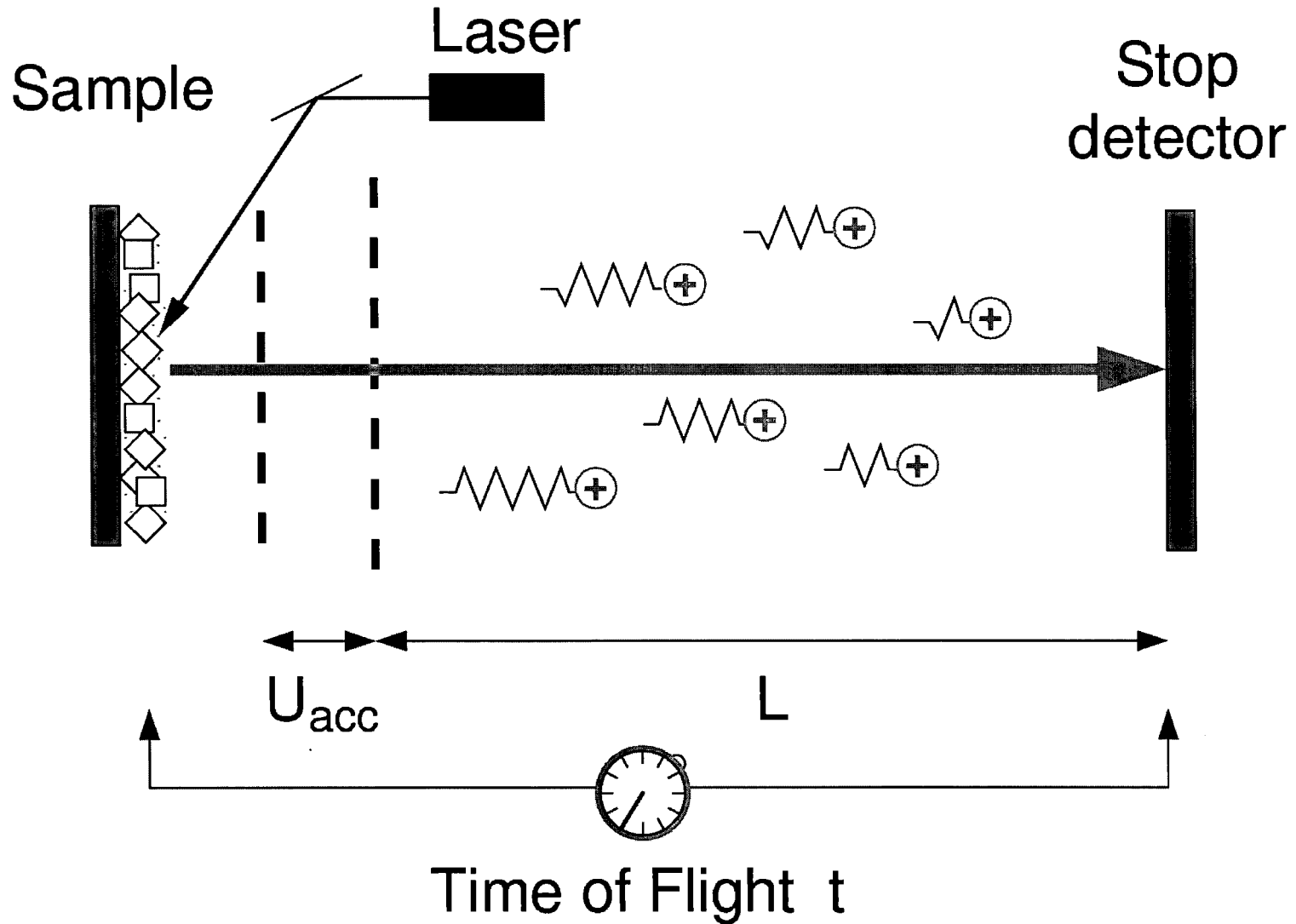


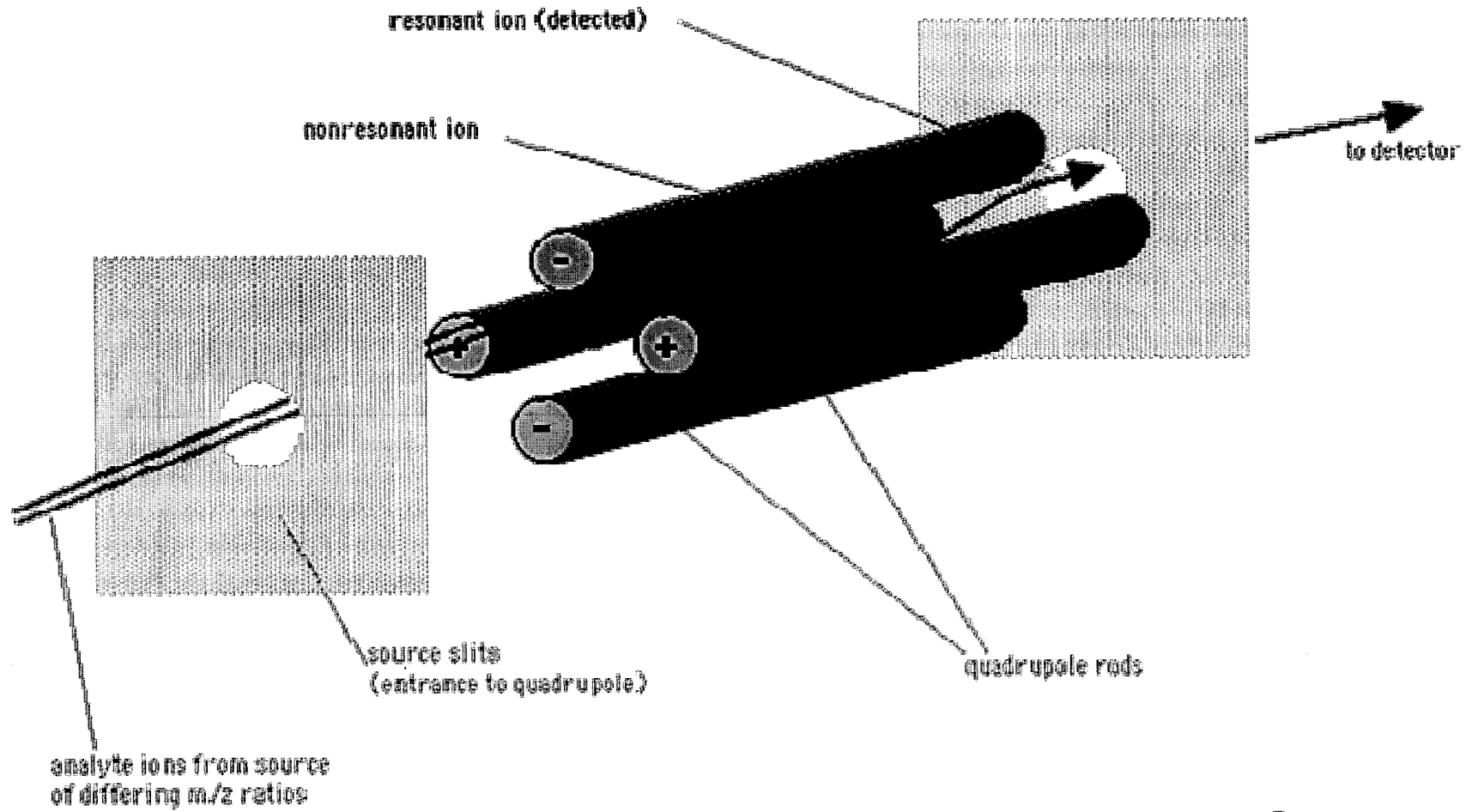
Ionisierung durch ESI und MALDI



Time Of Flight (TOF)



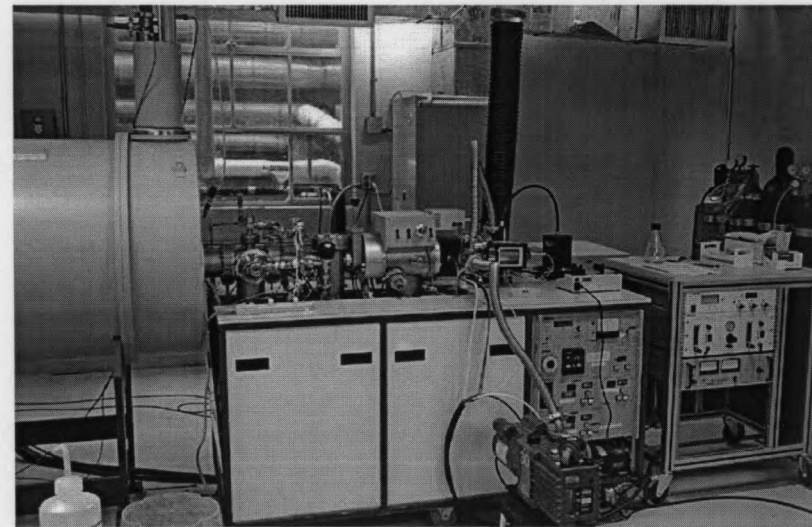
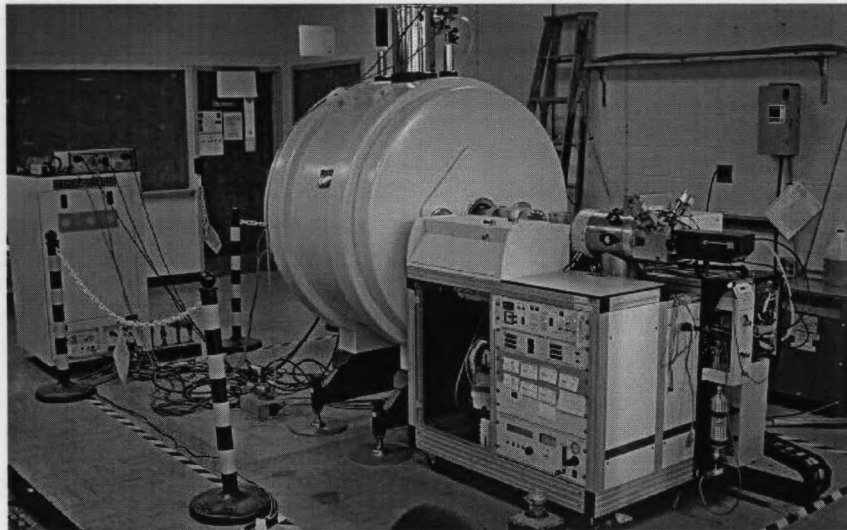
Quadrupole



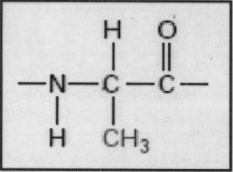
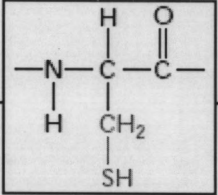
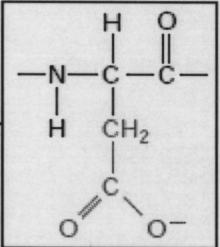
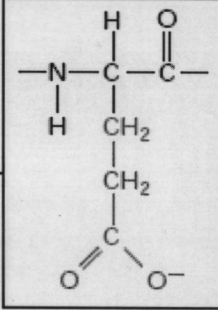
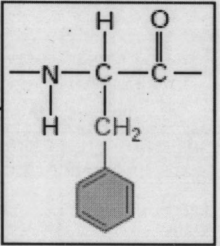
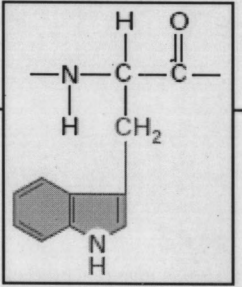
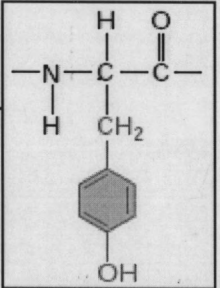
Hochauflösende Massenspektrometrie

- Fourier Transform MS kann die Masse eines Moleküls mit sehr hoher Genauigkeit bestimmen:

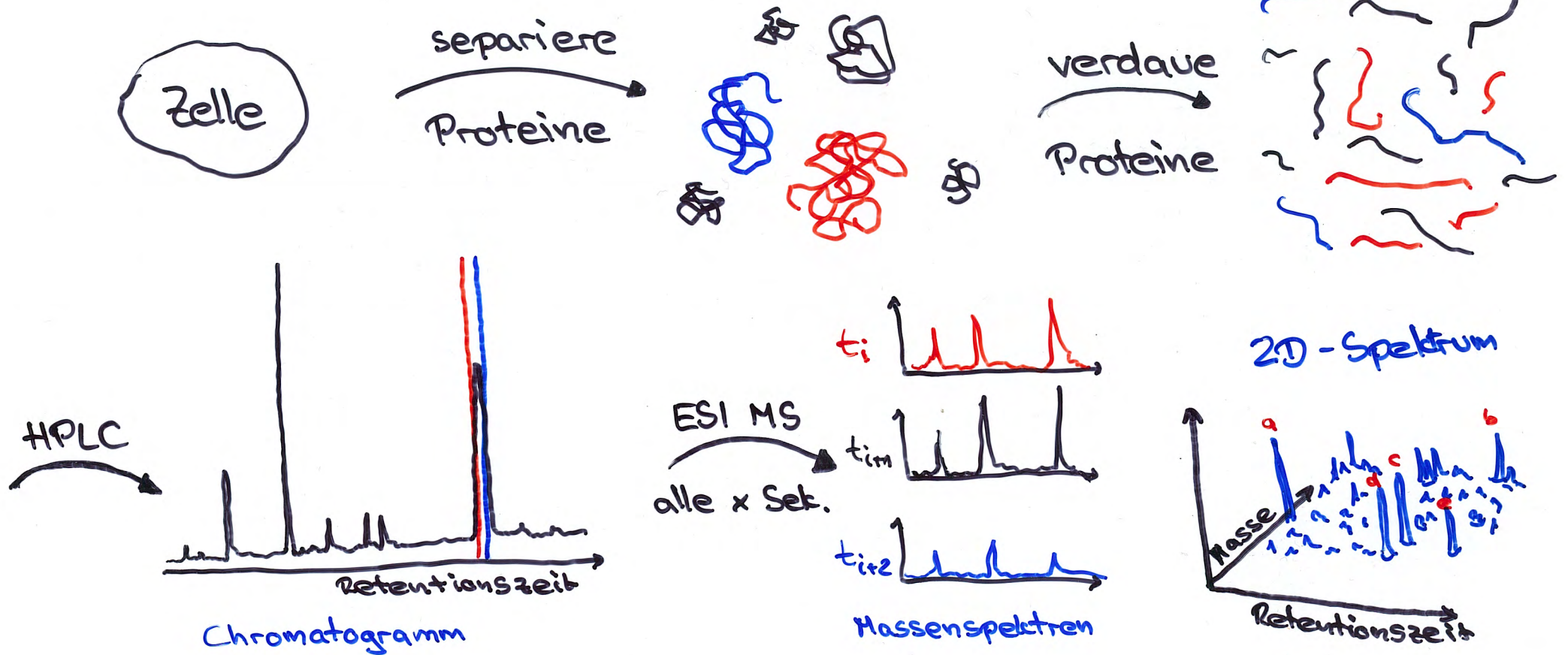
Messungengenauigkeit ist **ein Tausendstel**
der Masse eines **einzelnen Neutrons!**



Aminosäure-Reste

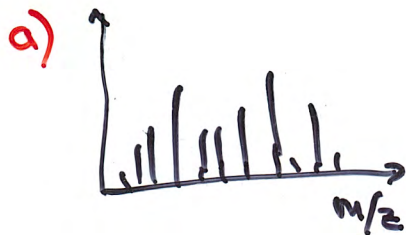
A: Alanin	(Ala)		$C_3H_5N_1O_1$	71.037
C: Cystein	(Cys)		$C_3H_5N_1O_1S_1$	103.009
D: Asparaginsäure (Asp)			$C_4H_5N_1O_3$	115.026
E: Glutaminsäure (Glu)			$C_5H_7N_1O_3$	129.042
F: Phenylalanin	(Phe)		$C_9H_9N_1O_1$	147.068
...
W: Tryptophan	(Trp)		$C_{11}H_{10}N_2O_1$	186.079
Y: Tyrosin	(Tyr)		$C_9H_9N_1O_2$	163.063

Shotgun Proteomics, LC/MS

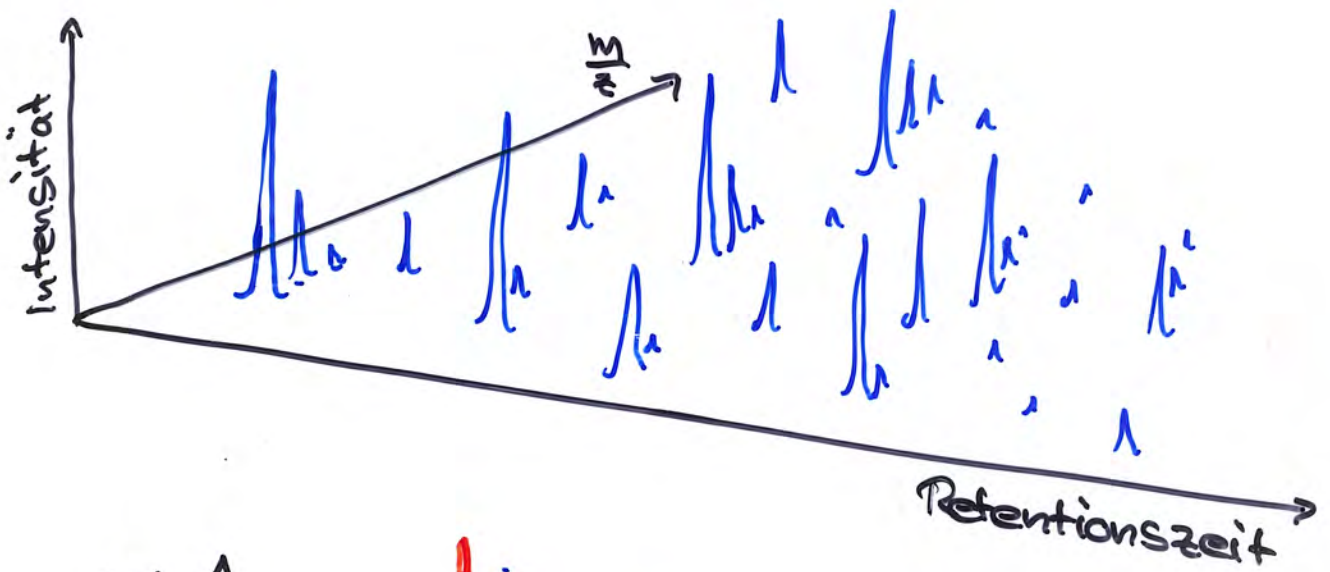


Tandem MS

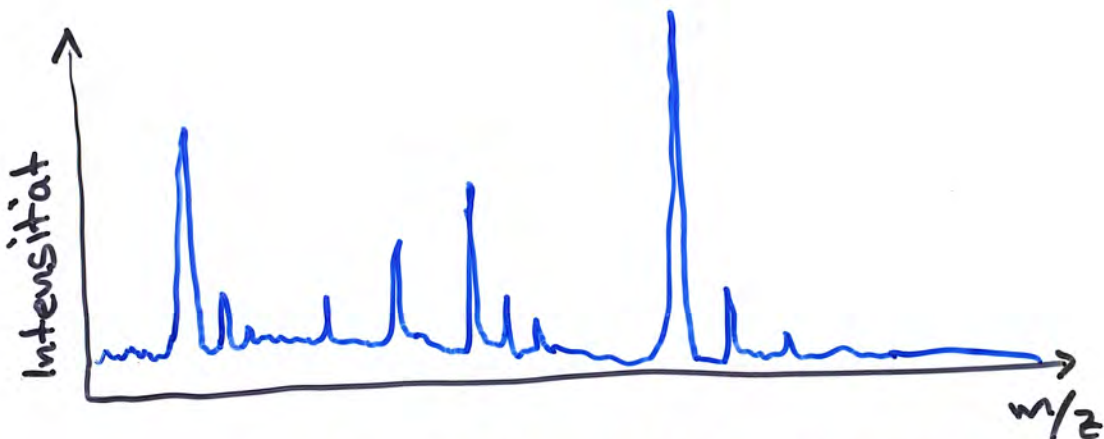
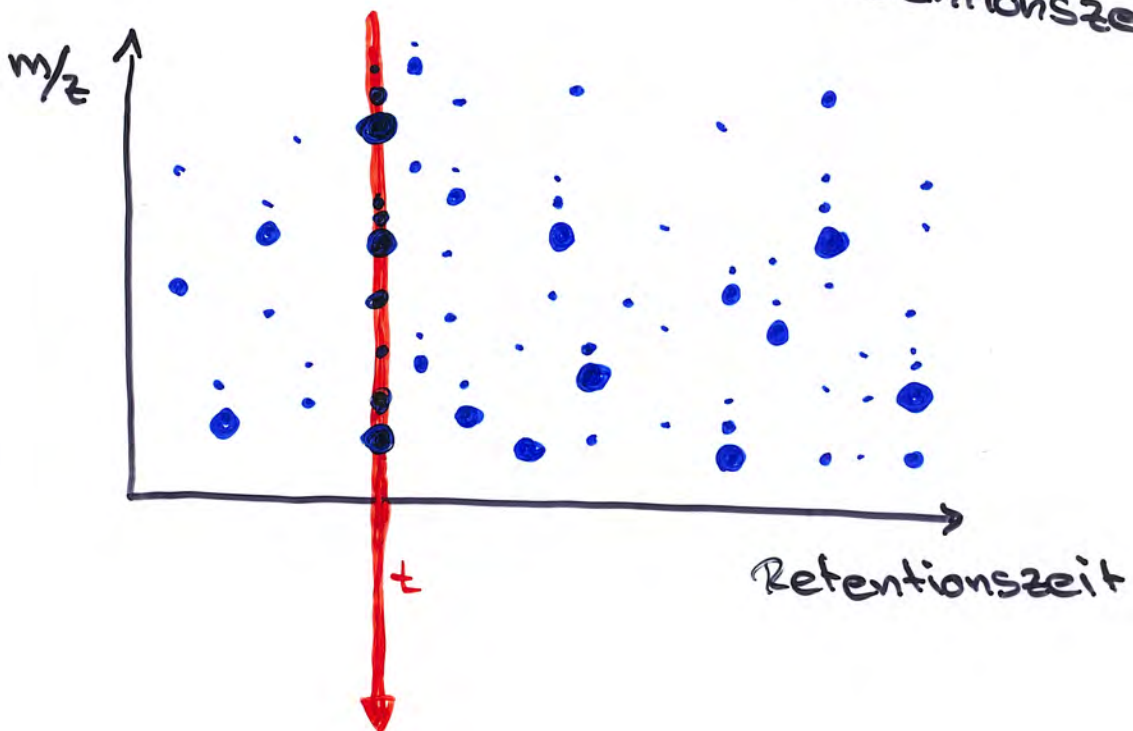
für aus-
gewählte
Peaks



2D LC/MS Spektrum



Draufsicht



Zu jedem diskreten Zeitpunkt t gibt es ein gemessenes Massenspektrum.

Peptid - String AWCYW

Masse 709

Vorsicht:
In der Realität
sind Massen
noch mod.

	Masse
A	71
AW	257
AWC	360
AWCY	523

	Masse
WCYW	638
CYW	452
YW	349
W	186

