



University of  
Zurich UZH

**SIAF**  
Swiss Institute of Allergy &  
Asthma Research

## Proteomics

**BIO390 “Introduction to Bioinformatics”**

**1.11.2022**

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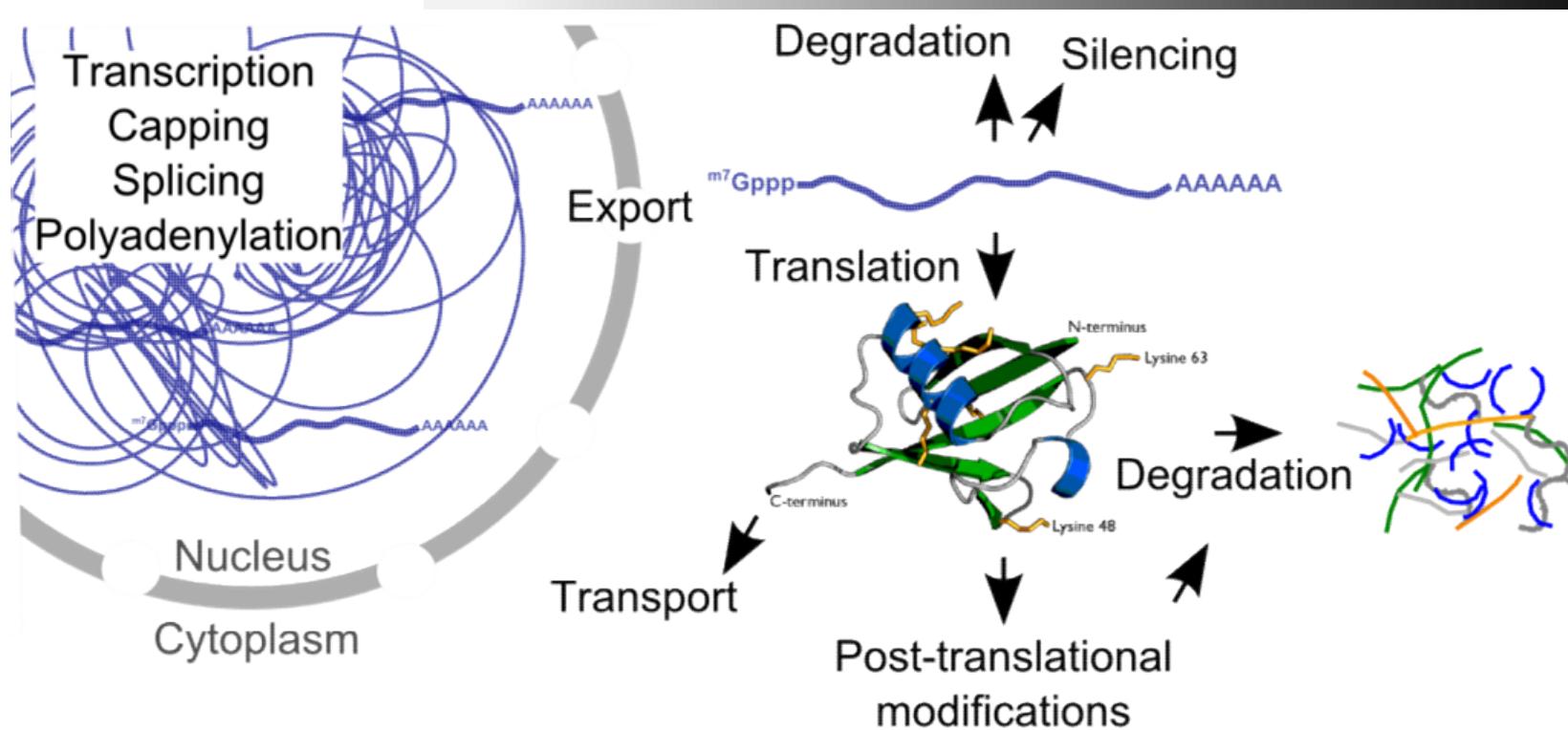
Swiss Institute of  
Bioinformatics

In proteomics one of the important bioinformatics tasks is to generate lists of reliably identified peptides and proteins in mass spectrometry-based experiments. For this, amino acid sequences are assigned to measured tandem mass spectra. The quality of the peptide spectrum assignments are scored and criteria are applied that allow to distinguish the good from the bad hits and to estimate the quality of the dataset.

In the context of this lecture, you will need to learn and understand:

- what information can be gained in a proteomics experiment
- what's the principle of assigning an amino acid sequence to a tandem mass spectrum
- how *de novo* and database-dependent peptide identifications work
- one way of how the accuracy of peptide identifications can be estimated
- how the number of wrong hits in a dataset can be estimated
- current proteomic approaches

## Various processes determine protein levels and activities



- Not only the genome, but in particular the proteins present and their activities, their sub-cellular localisation, and their protein-protein or protein-DNA/RNA interactions determine the appearance and state of a biological organism
- Gene expression is regulated on many different levels, including also enhanced or reduced translational efficiency, increased or decreased protein degradation, triggering of signalling cascades, e.g. through protein phosphorylation

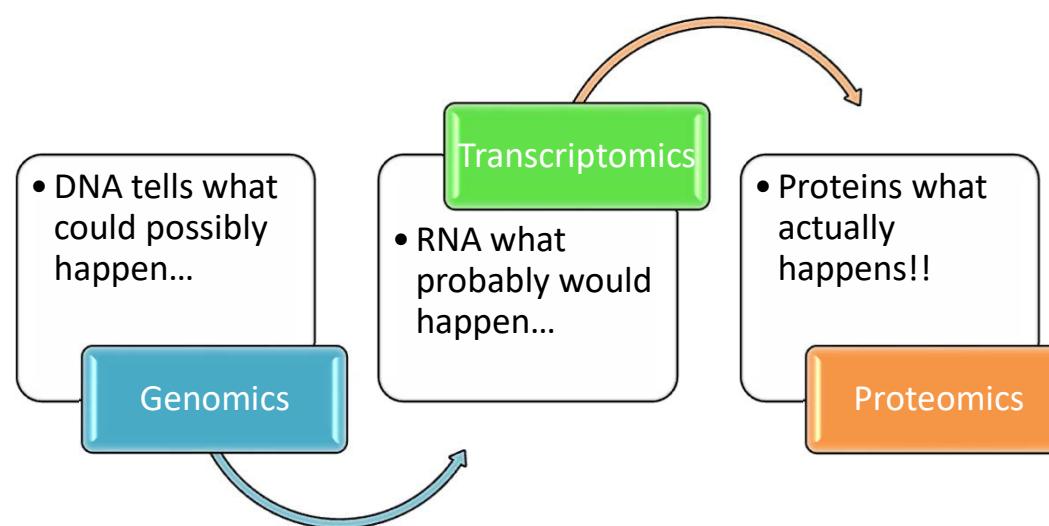
Why proteome research?

Proteomics is the large-scale study of proteins and the proteome, which is the entire set of proteins produced or modified by an organism or system.

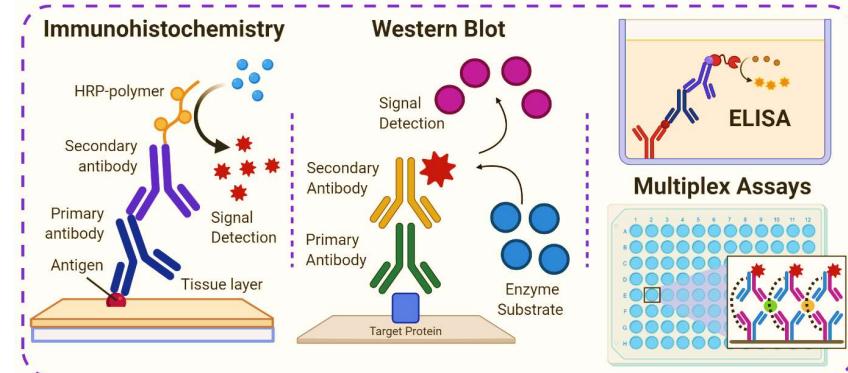
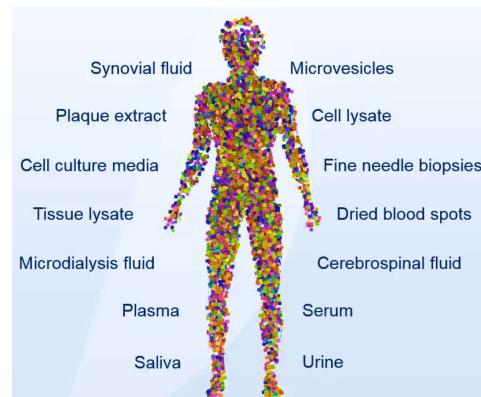
Proteomics includes the study of:

- protein roles, structures, quantities, localization, and functions
- post-translational modifications (and their change)
- protein interactions with DNA, RNA, other proteins, etc.

and how all these change in time, between conditions or in response to stimuli



## Examples of non mass spectrometry-based proteomics approaches

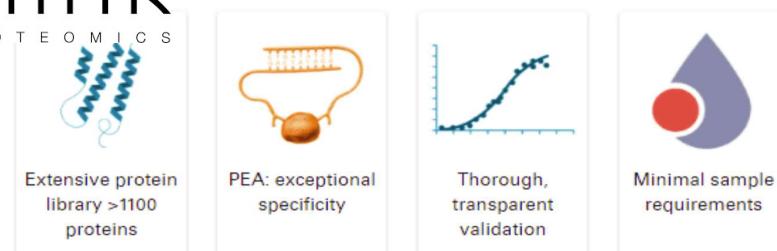


Olink: Targeted proteomics:

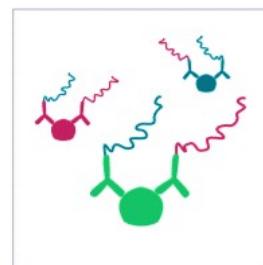


High-throughput, multiplex immunoassays:  
1µl → 92 proteins across 88 samples

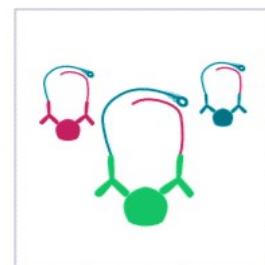
Proximity Extension Assay technology:



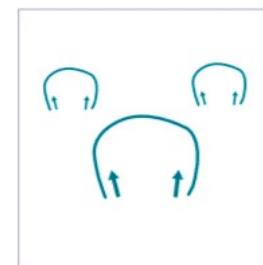
(A) Immunoassay



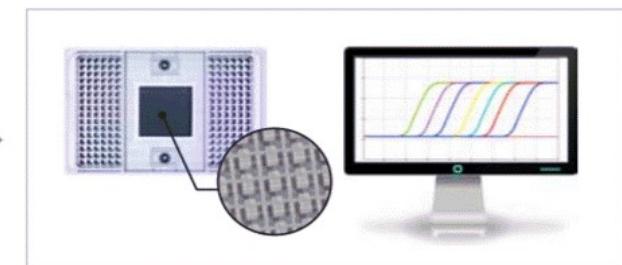
(B) Extension



(C) Preamplification

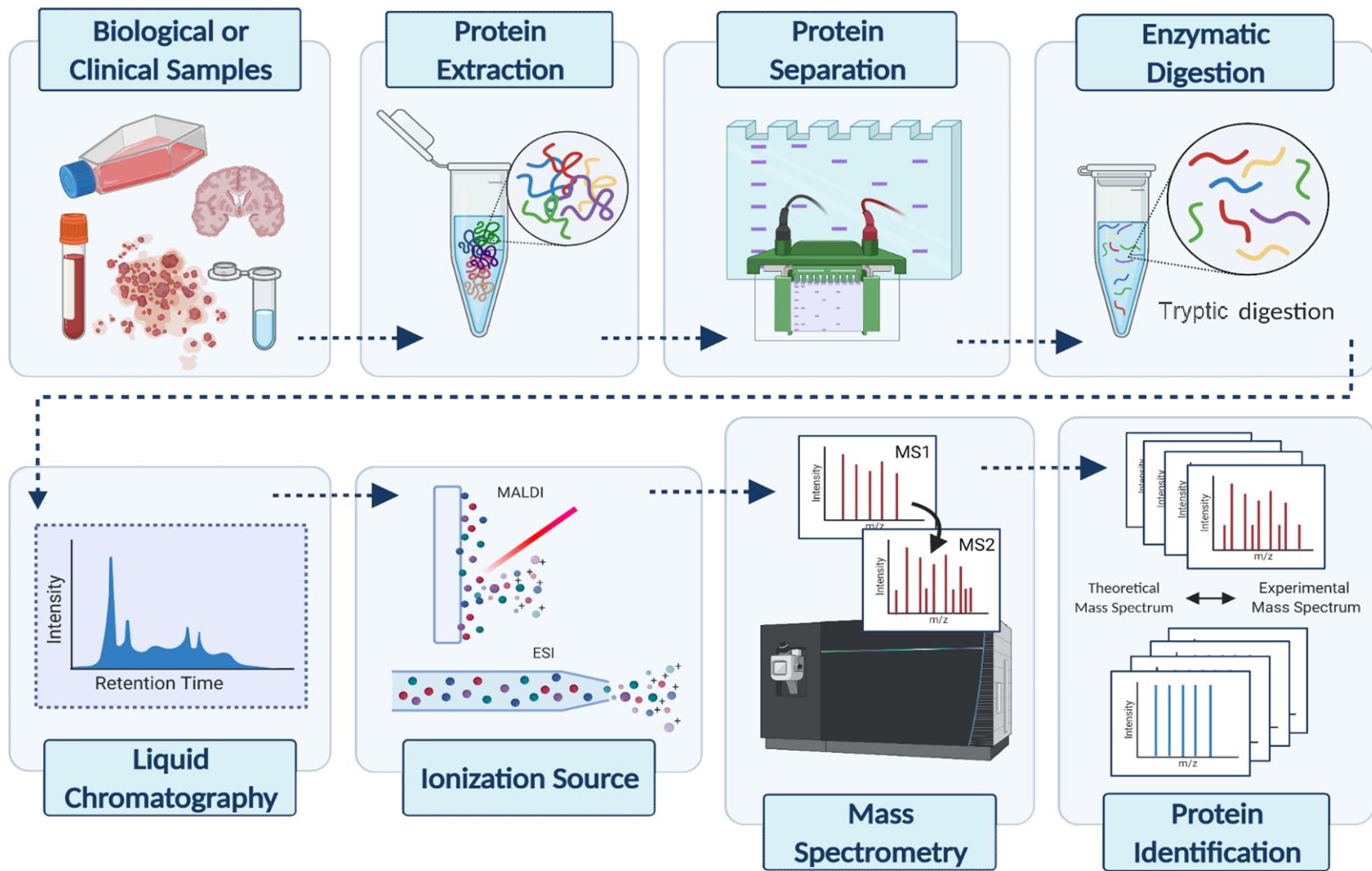


(D) Detection by microfluidic qPCR



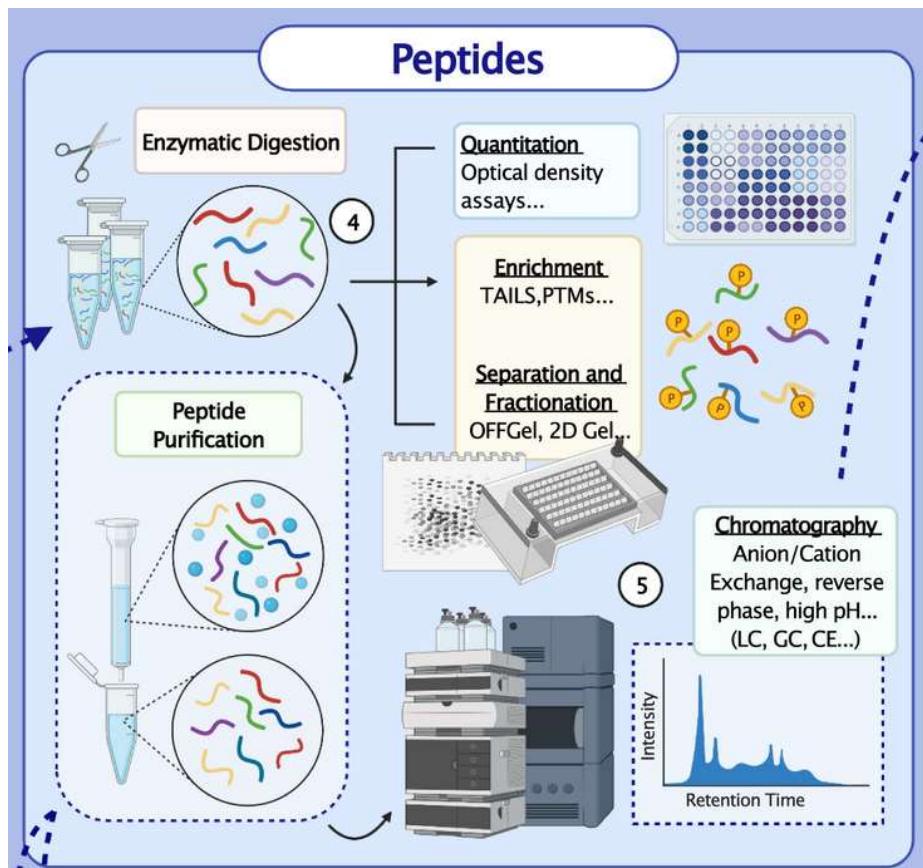
Mass spectrometry

# Generic mass spectrometry-based proteomics experiment



Mass spectrometry

# Enzymatic digestion



Radzikowska et al., *Omics technologies in allergy and asthma research: An EAACI position paper*, Allergy, 2022

- Before analysis, the proteins are typically digested with a site specific protease, most of the time with trypsin.
- Trypsin cuts after arginine or lysine, except when the cutting site is followed by proline, which leads to limited cleavage.



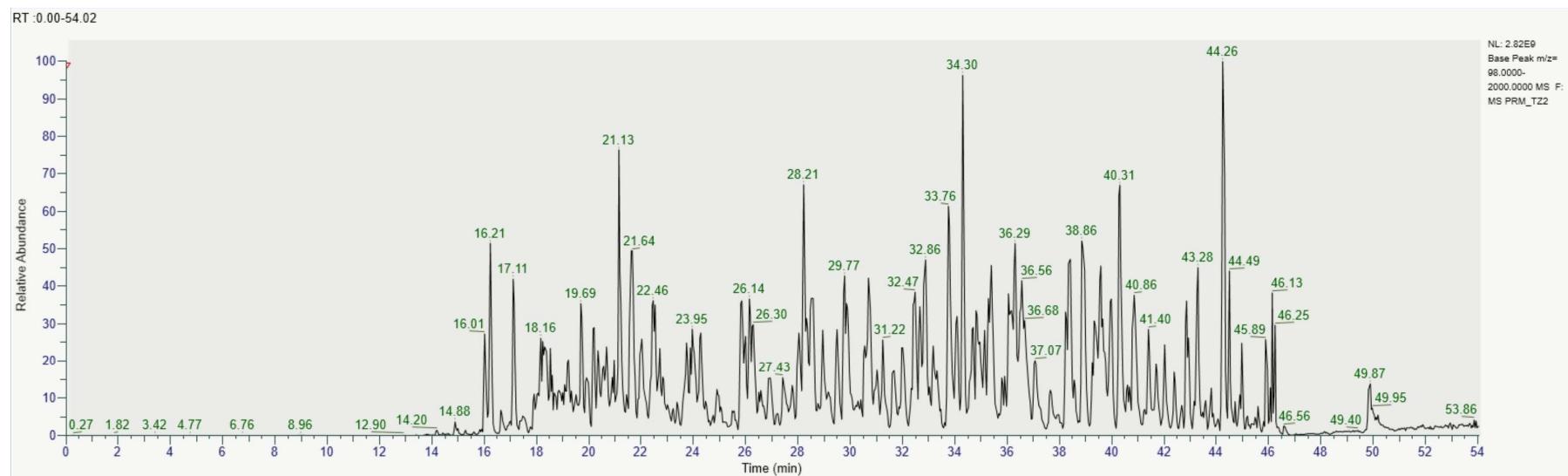
- After protein cleavage, the peptides need to be purified.
- The peptides are often fractionated or enriched for specific features such as specific post-translational modifications, internal cleavage sites, etc.

## Liquid chromatography

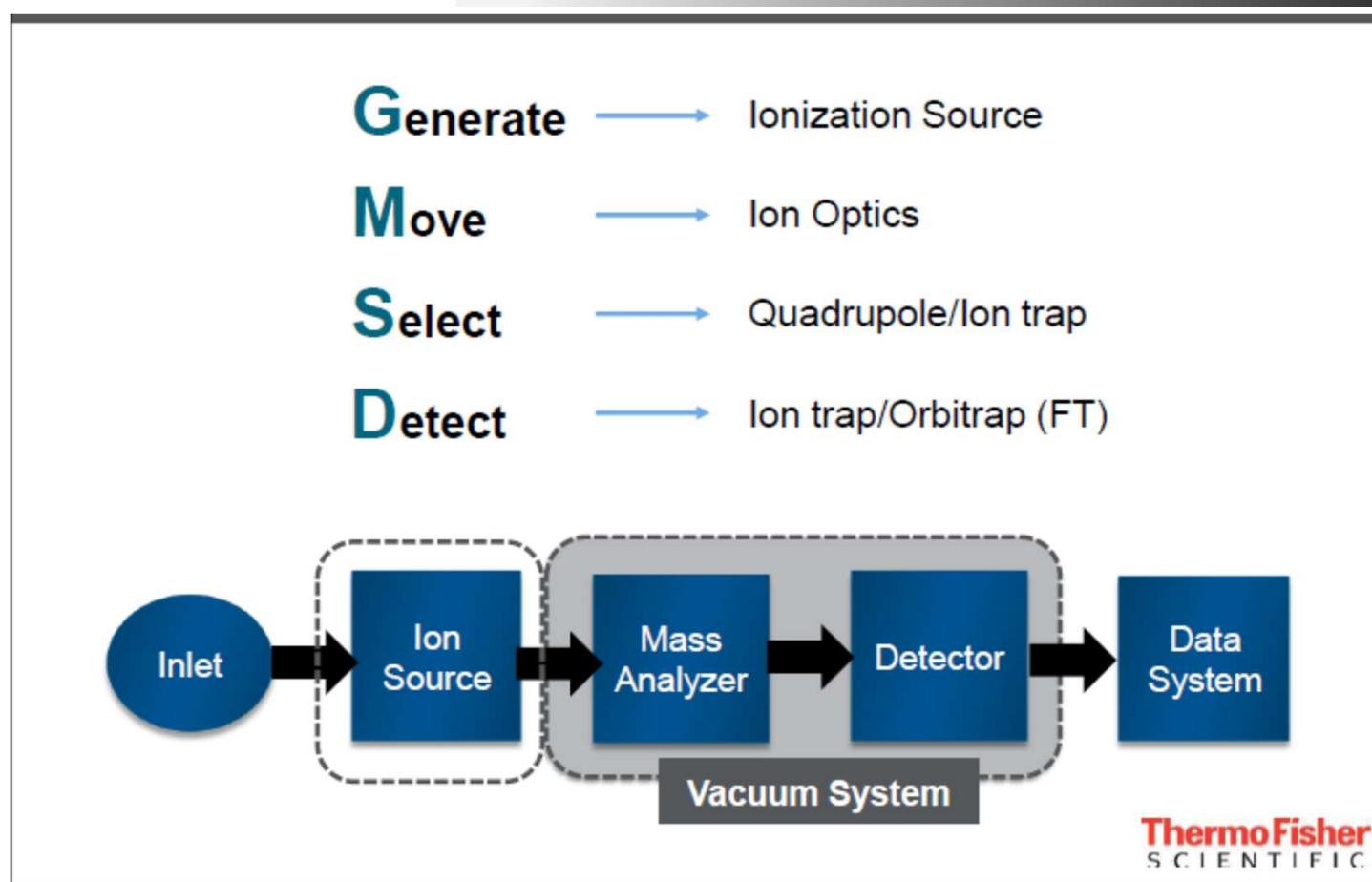
Liquid chromatography separates the mixture of peptides based on the principle of partitioning of solutes between two phases.

In reverse phase (RP) chromatography, the separation uses a column (non-polar stationary phase) and solvent (gradient of a mixture of a polar and a non-polar mobile phase); the components are separated from each other based on their affinity for the stationary phase depending on the polarity of the mobile phase that is changing over time.

The goal of the separation is to find the best compromise between resolving the components over time and having sharp and intense elution peaks.



## Simplified Mass Spectrometer



Mass spectrometer types:

TOF = Time of Flight

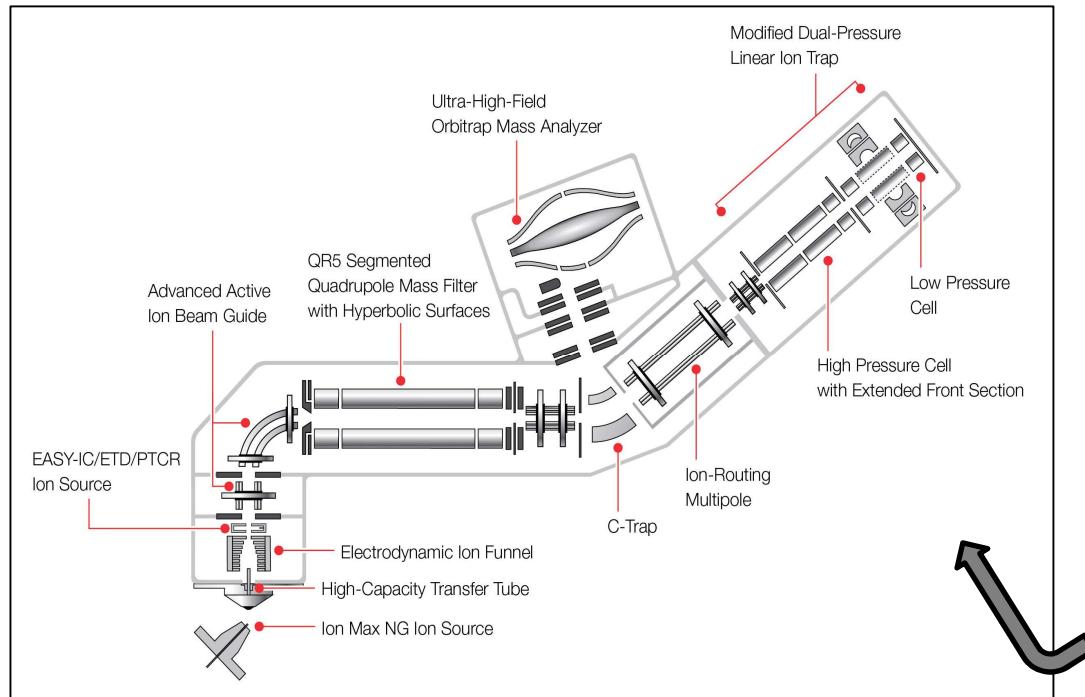
Quadrupole (Q)

Ion Trap

Orbitrap

FT-ICR = Fourier Transform Ion Cyclotron Resonance

# Mass Spectrometry

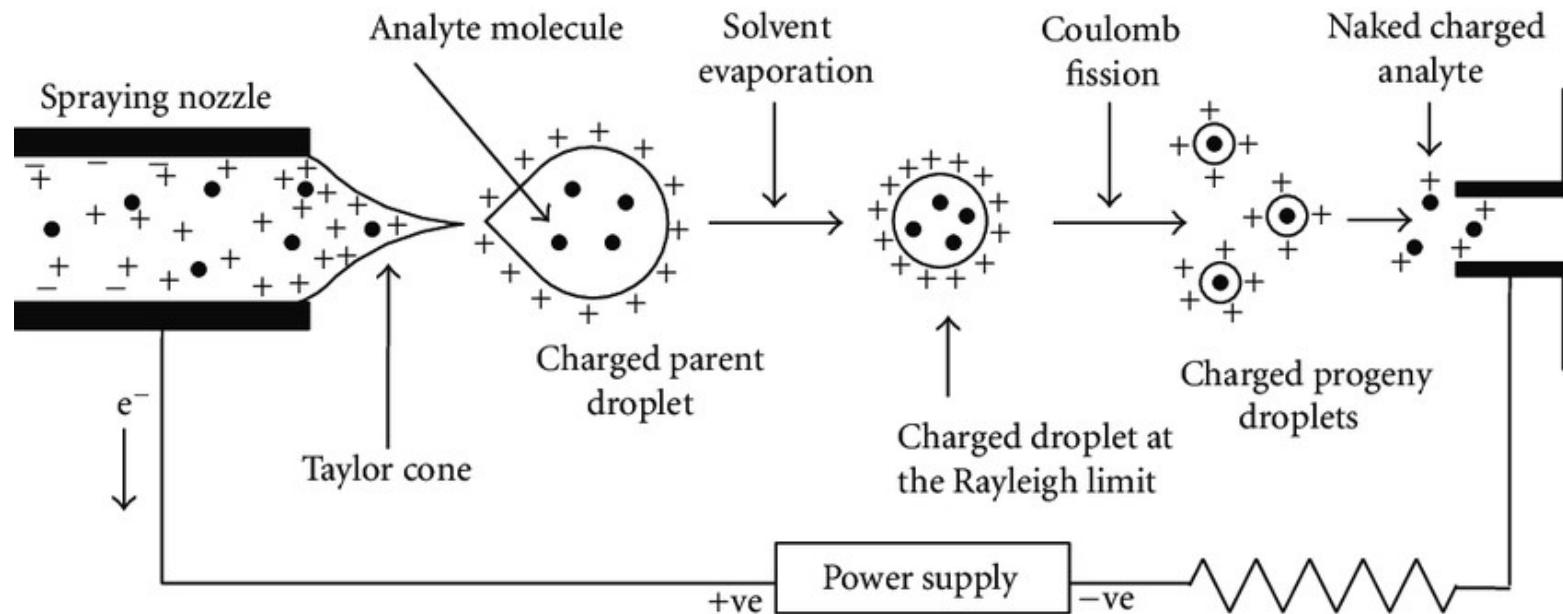


G**e**n**e**r**a**t**e**  
M**o**v**e**  
S**e**l**e**c**t**  
D**e**te**c**t

©Thermo Fisher Scientific - Orbitrap Eclipse™ Tribrid™ Mass Spectrometer



## Ion Generation - Electrospray Ionization (ESI)

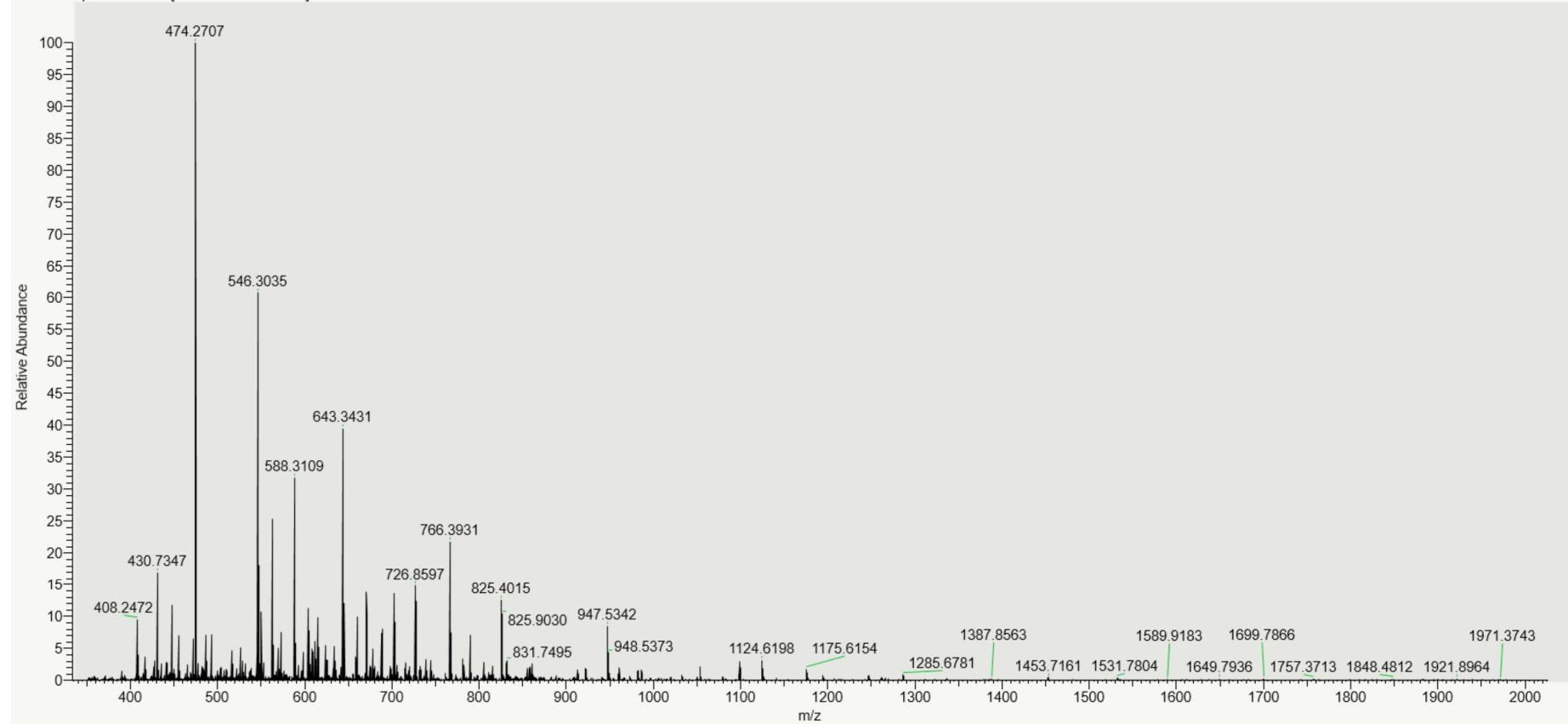


Banerjee and Mazumdar S. IJAC, 2012

- Ionization types:
- ESI = Electrospray Ionization (from solution)
  - APCI = Atmospheric Pressure Chemical Ionization (from gas phase)
  - APPI = Atmospheric Pressure Photoionization (from gas phase)
  - MALDI = Matrix-Assisted Laser Desorption Ionization (from solid phase)

# MS Spectrum

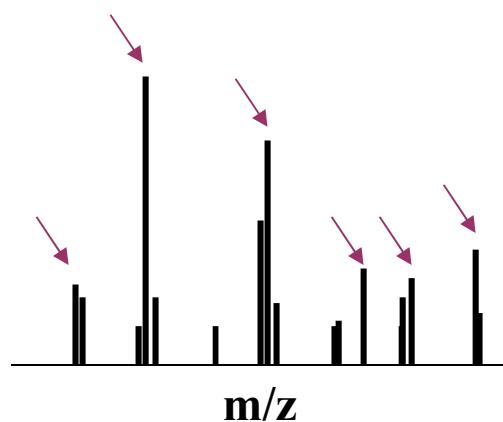
PRM\_TZ2 #43407 RT: 32.27 AV: 1 NL: 2.22E+008  
T: FTMS + p NSI Full ms [350.0000-2000.0000]



## Peptide Mass Fingerprint

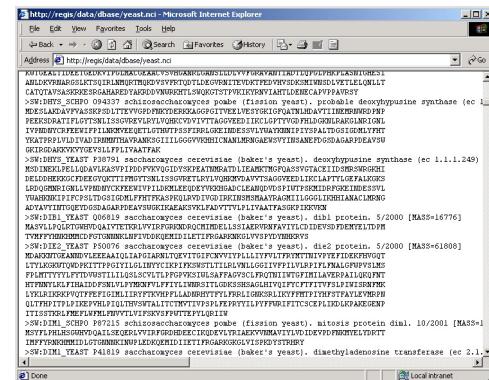
## Identifying peptides using an MS spectrum:

# List of peptide masses from MS scan



# Search algorithm

# Sequence database

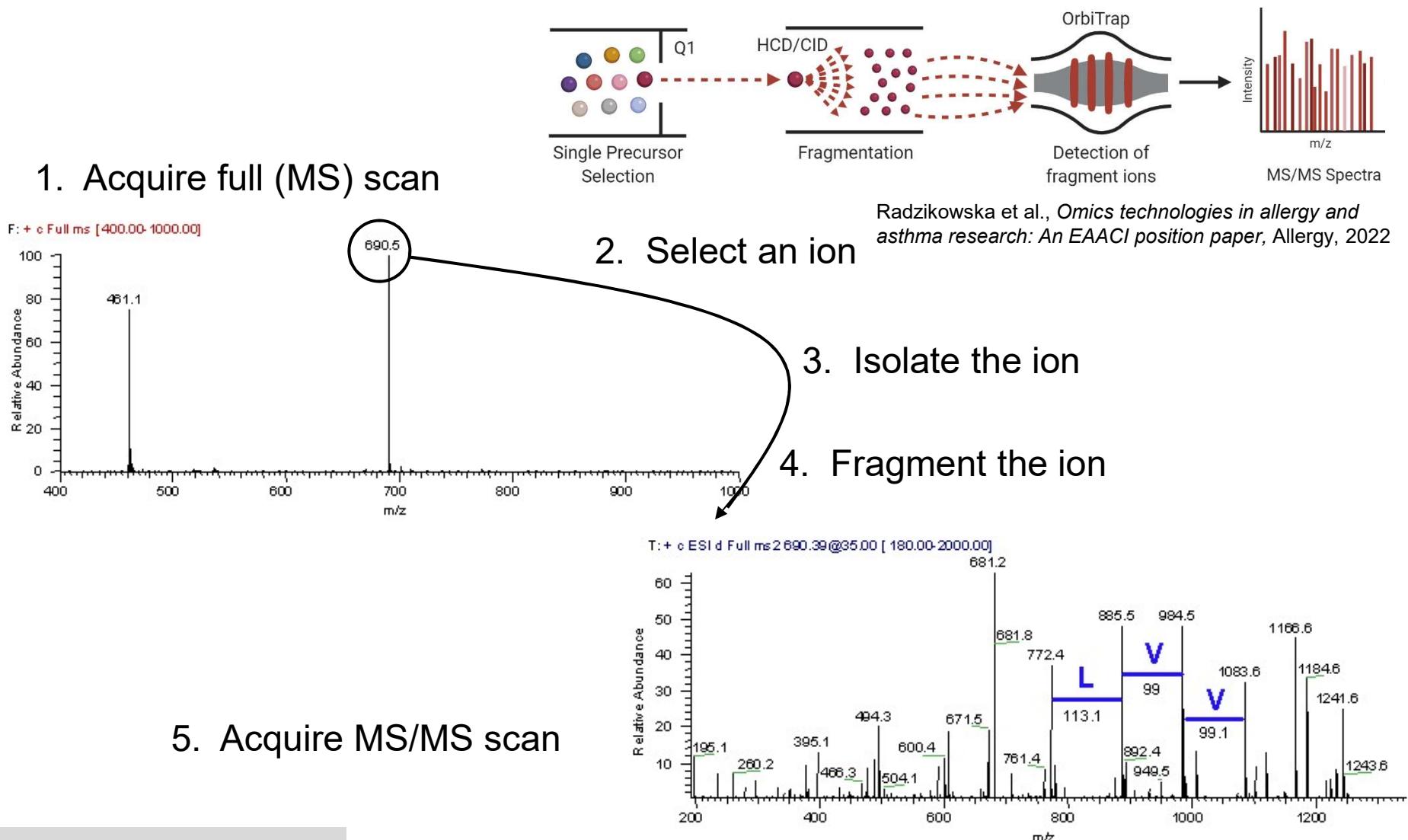


## Identified peptide/protein

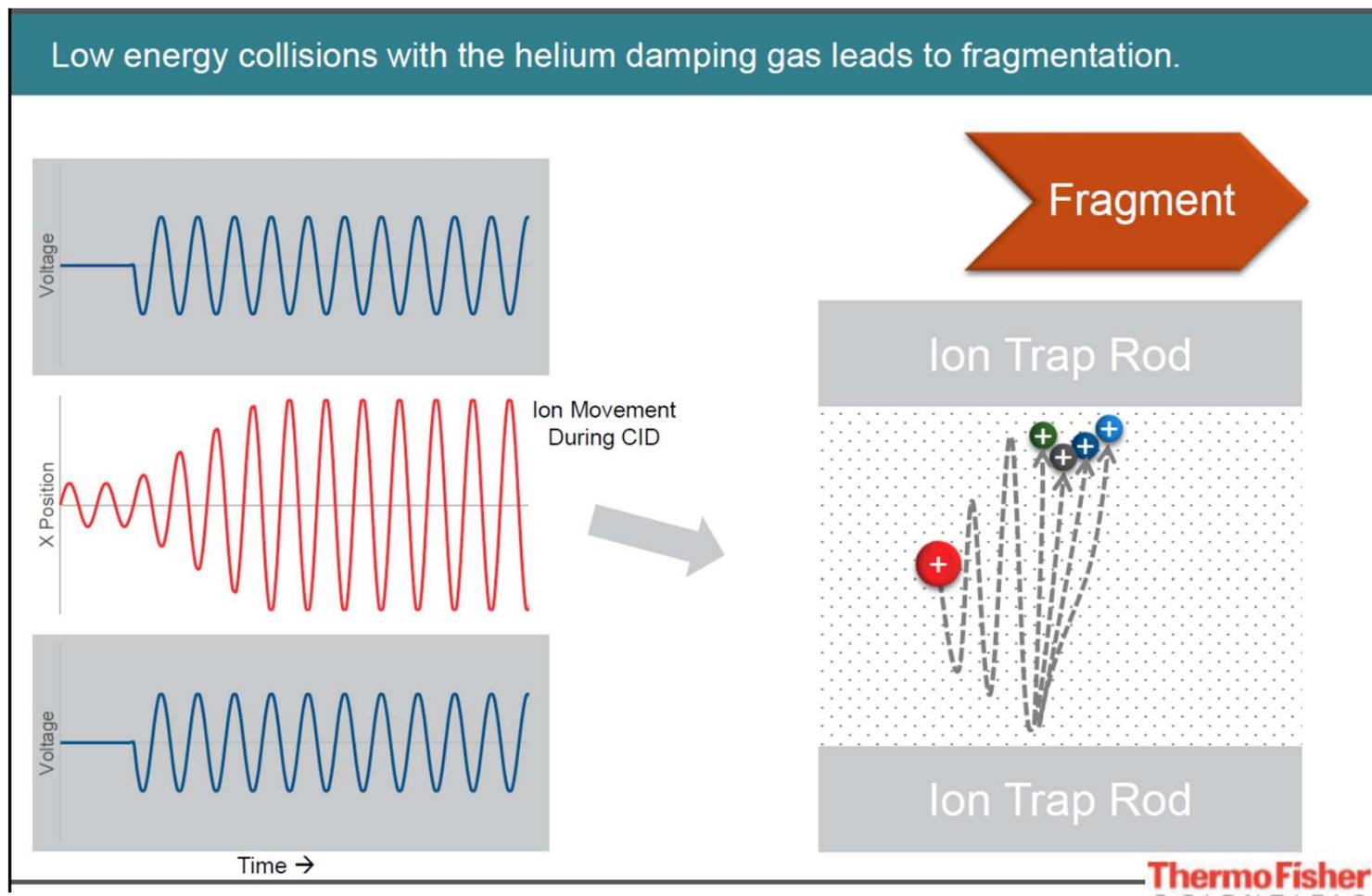
- Peptide spectrum assignment with Peptide Mass Fingerprinting is only advisable with samples of low complexity and small sequence databases, as the number of all possible peptides with a given mass over charge is huge in large sequence databases.

# Tandem Mass Spectrometry (MS/MS)

- Obtaining **sequence information** for a peptide ion:

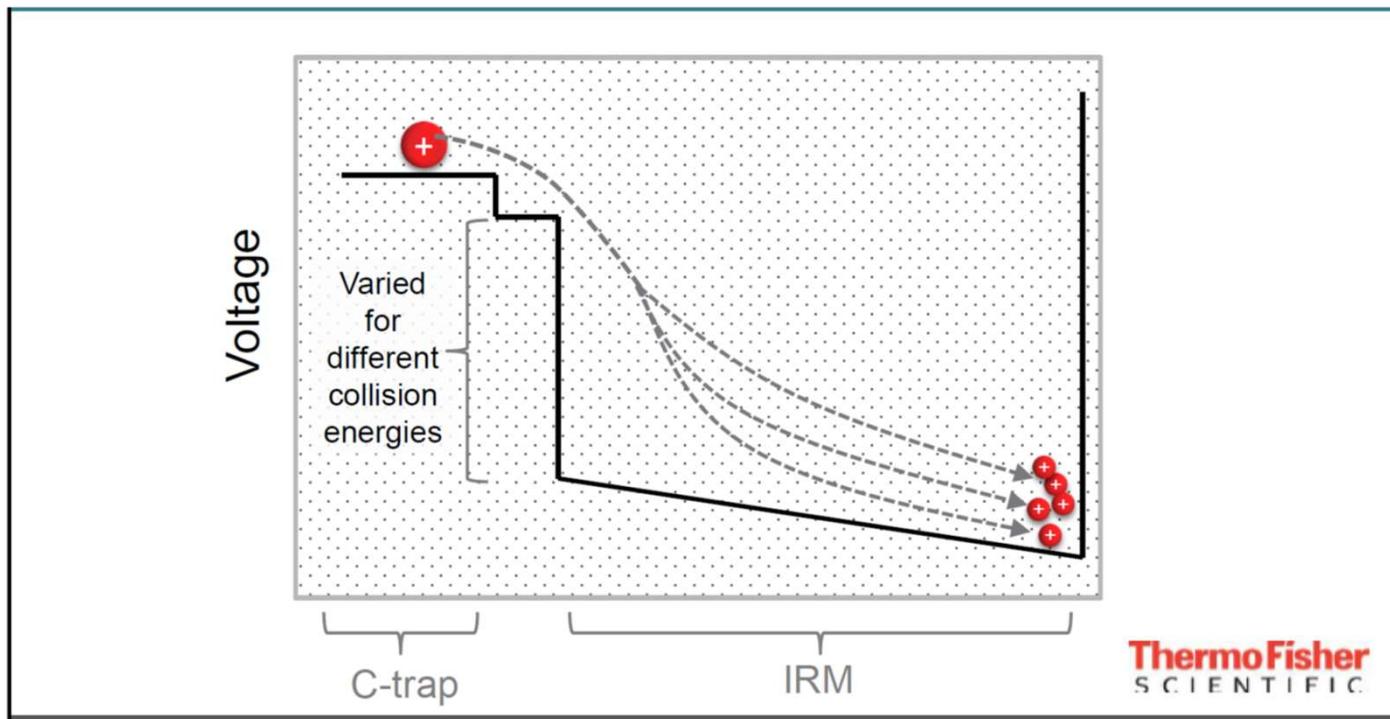


## Ion Fragmentation – Collision-Induced Dissociation (CID)



CID uses resonance excitation so that the ion of interest is excited (and moves faster). This additional movement of the ion of interest leads to additional higher energy collisions with the helium gas, which leads to fragmentation.

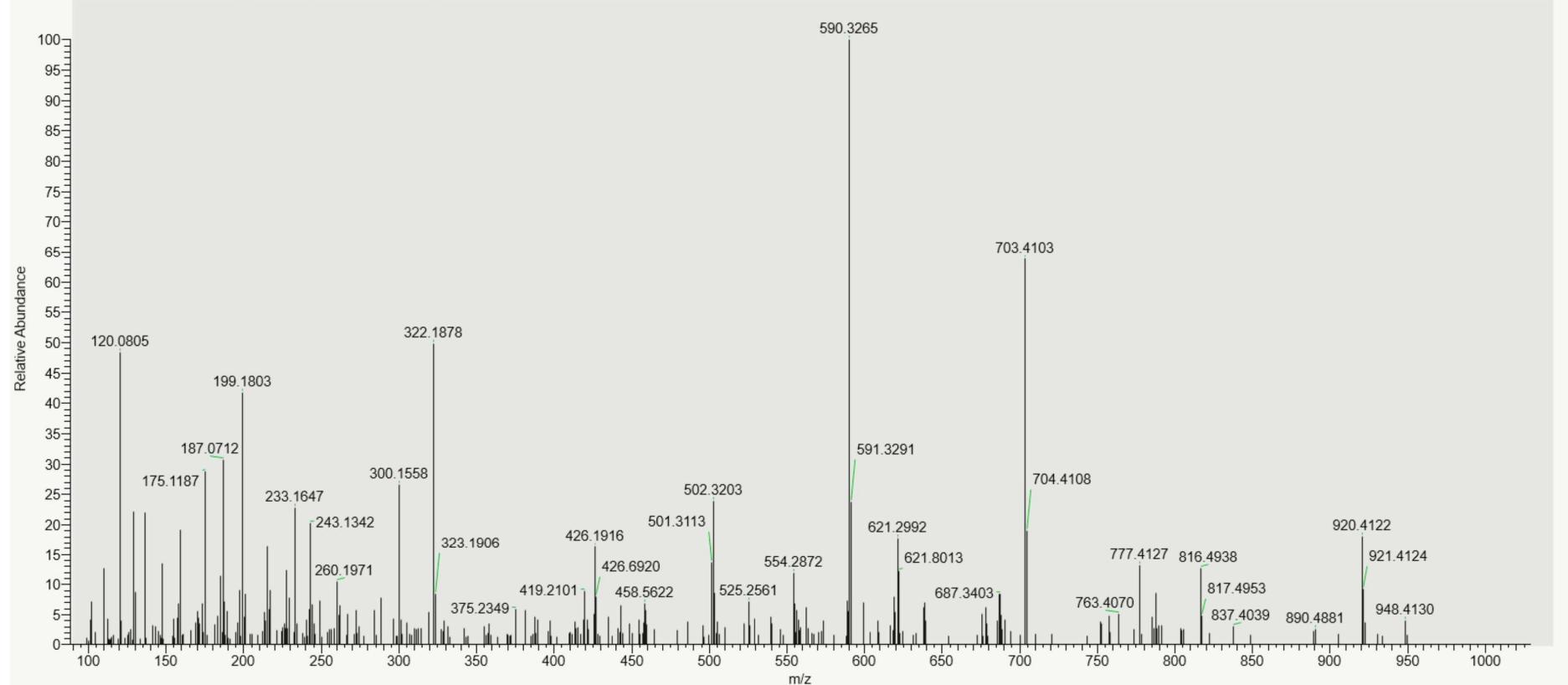
## Ion Fragmentation – Higher-Energy Collisional Dissociation (HCD)



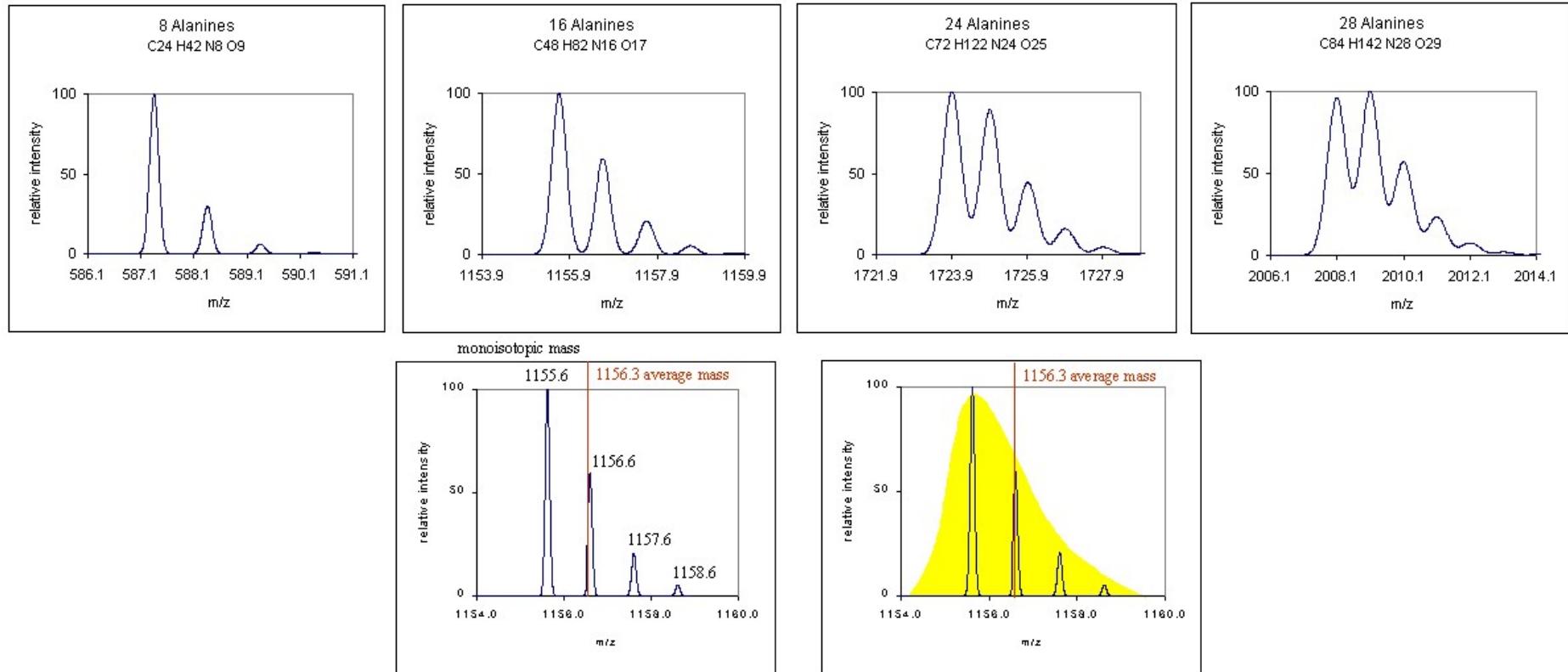
In HCD, ions are accelerated as they enter the routing multipole (IRM) via a large voltage offset between the C-trap and the IRM. The higher velocity of the ions results in higher energy collisions with the nitrogen, which leads to fragmentation of the ions. The amount of fragmentation that results is dependent on the velocity of the ions.

# MS/MS spectrum

PRM\_TZ2 #43405 RT: 32.27 AV: 1 NL: 7.59E+005  
T: FTMS + c NSI Full ms2 501.7769@hcd30.00 [98.0000-1014.0000]

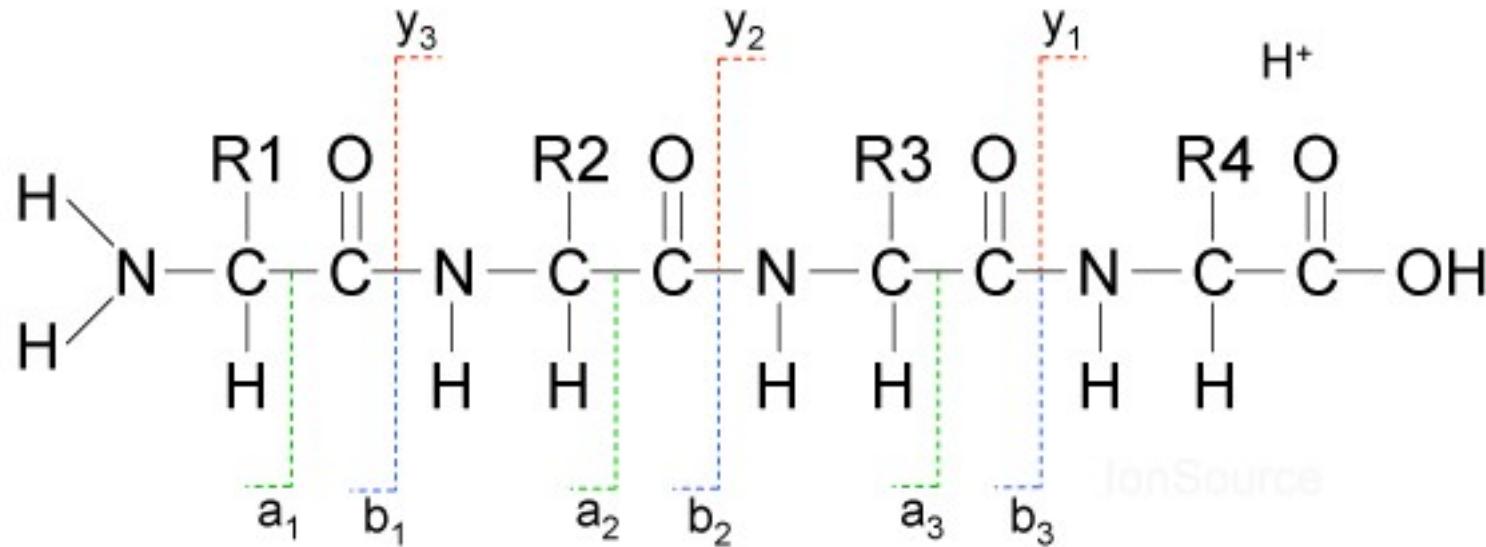


## The isotope issue



- 1/100 C atoms is C13
- The more atoms a peptide contains, the more probably it is that one to several C atoms are C13

a, b and y ions after CID



- The most common peptide fragments observed in low energy collisions are **a**, **b** and **y** ions.
- The **b** ions appear to extend from the amino terminus (N-terminus), and **y** ions appear to extend from the carboxyl terminus (C-terminus).
- **a** ions occur at a lower frequency and abundance in relation to **b** ions.

adjusted from <http://www.ionsource.com/>

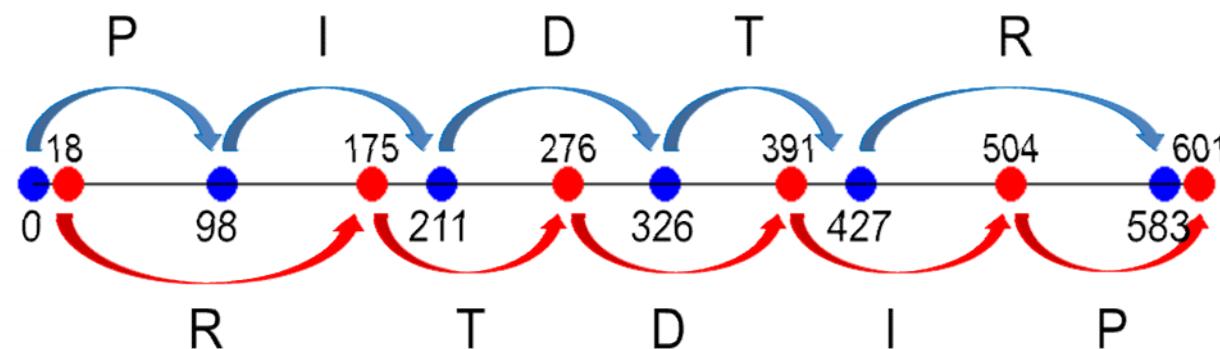
## Fragmenting a peptide

P – I – D – T – R  
 $m/z = 601.31$

Masses of b- and y- ions:

	b-ions			y-ions
		PIDTR	601.31	$\gamma 5$
b1	98.05	P ----- IDTR	504.26	$\gamma 4$
b2	211.14	PI ----- DTR	391.18	$\gamma 3$
b3	326.16	PID ----- TR	276.15	$\gamma 2$
b4	427.21	PIDT ----- R	175.10	$\gamma 1$
b5	583.31	PIDTR		

Fragment masses aligned along a spectrum graph:

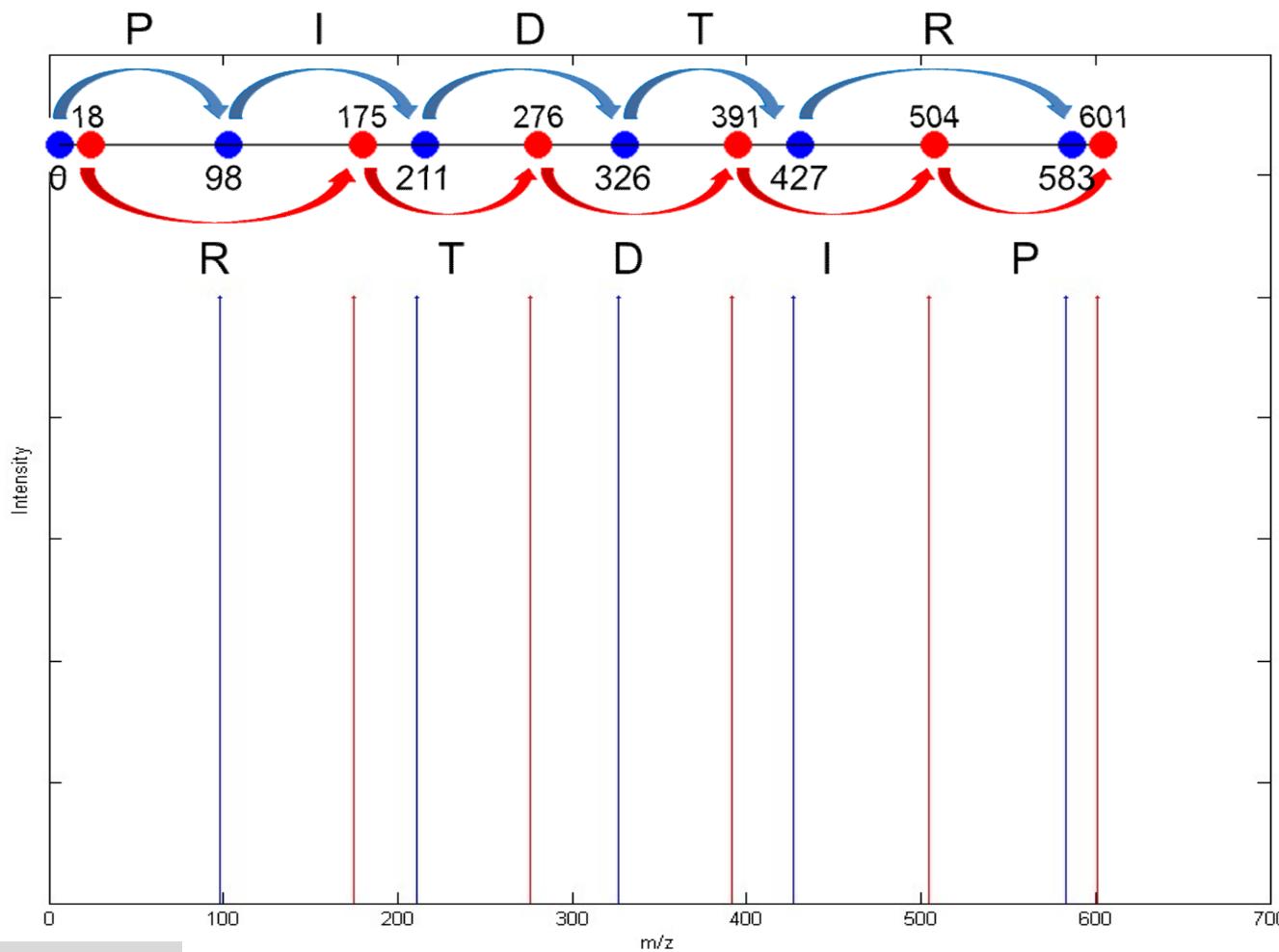


Peptide spectrum assignment

## Hypothetical fragment spectrum

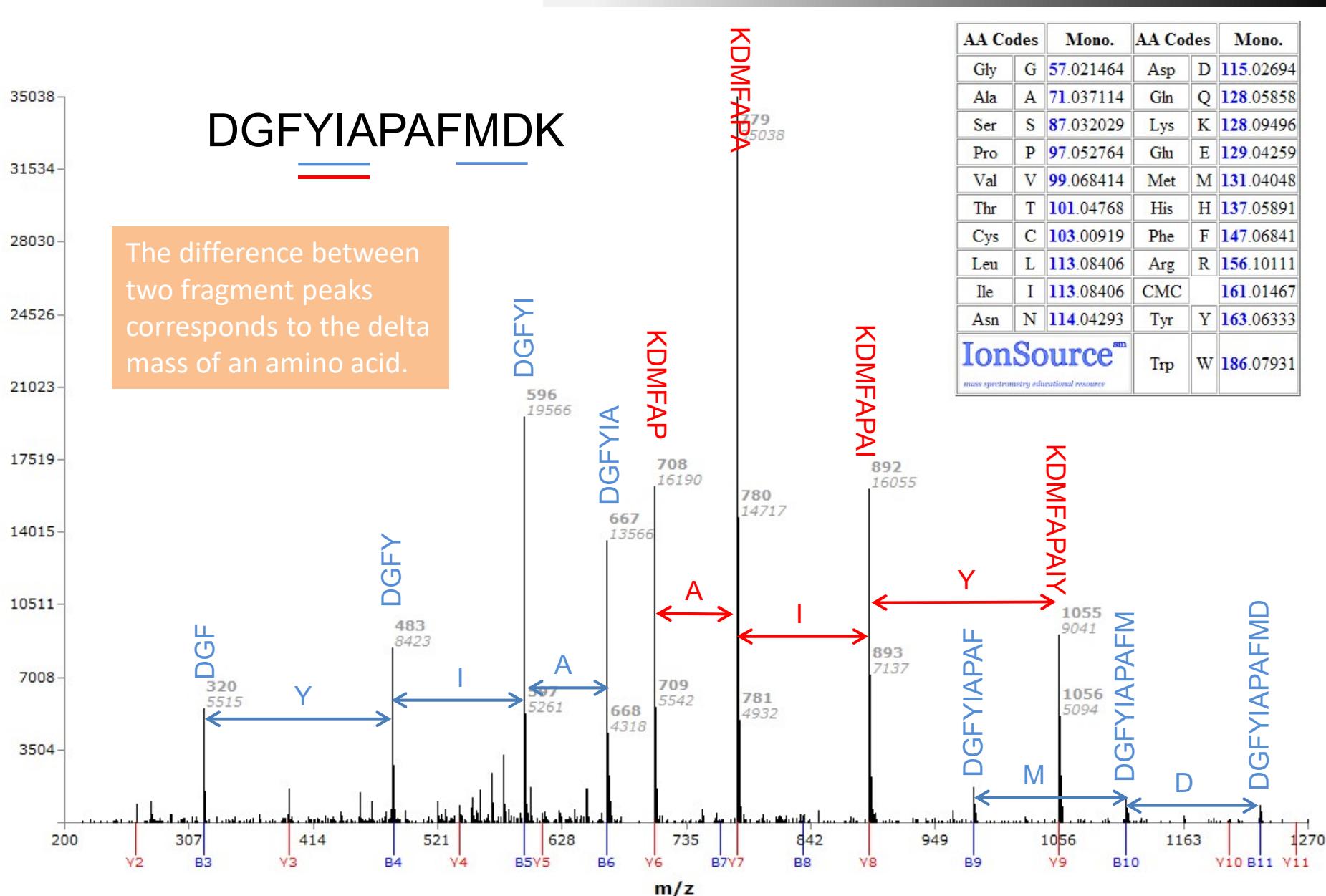
P - I - D - T - R

$m/z = 601.31$



Peptide spectrum assignment

## Analysing a spectrum for the fragments



## *De novo* peptide sequencing

In *de novo* peptide sequencing, all information about the peptide sequence resides in the MS/MS spectrum itself. It is therefore database-independent and can be done manually or with algorithms.

Manual *de novo* peptide sequencing:

- M = Mass of the peptide

- **Precursor ion**  $M_{\text{Precursor}} \equiv \frac{(M + 2H)^2^+}{2}$

- **Parent ion**  $M_{\text{Parent}} \equiv (M+H)^+$

$$M_{\text{Parent}} = M_{\text{Precursor}} * 2 - 1 = \frac{(M+2H)^2^+}{2} * 2 - 1$$

- Monoisotopic mass of the parent ion

$$M_{\text{Parent mono}} = M_{\text{Parent average}} - \frac{M_{\text{Parent average}}}{1463}$$

- b- and y- ions:

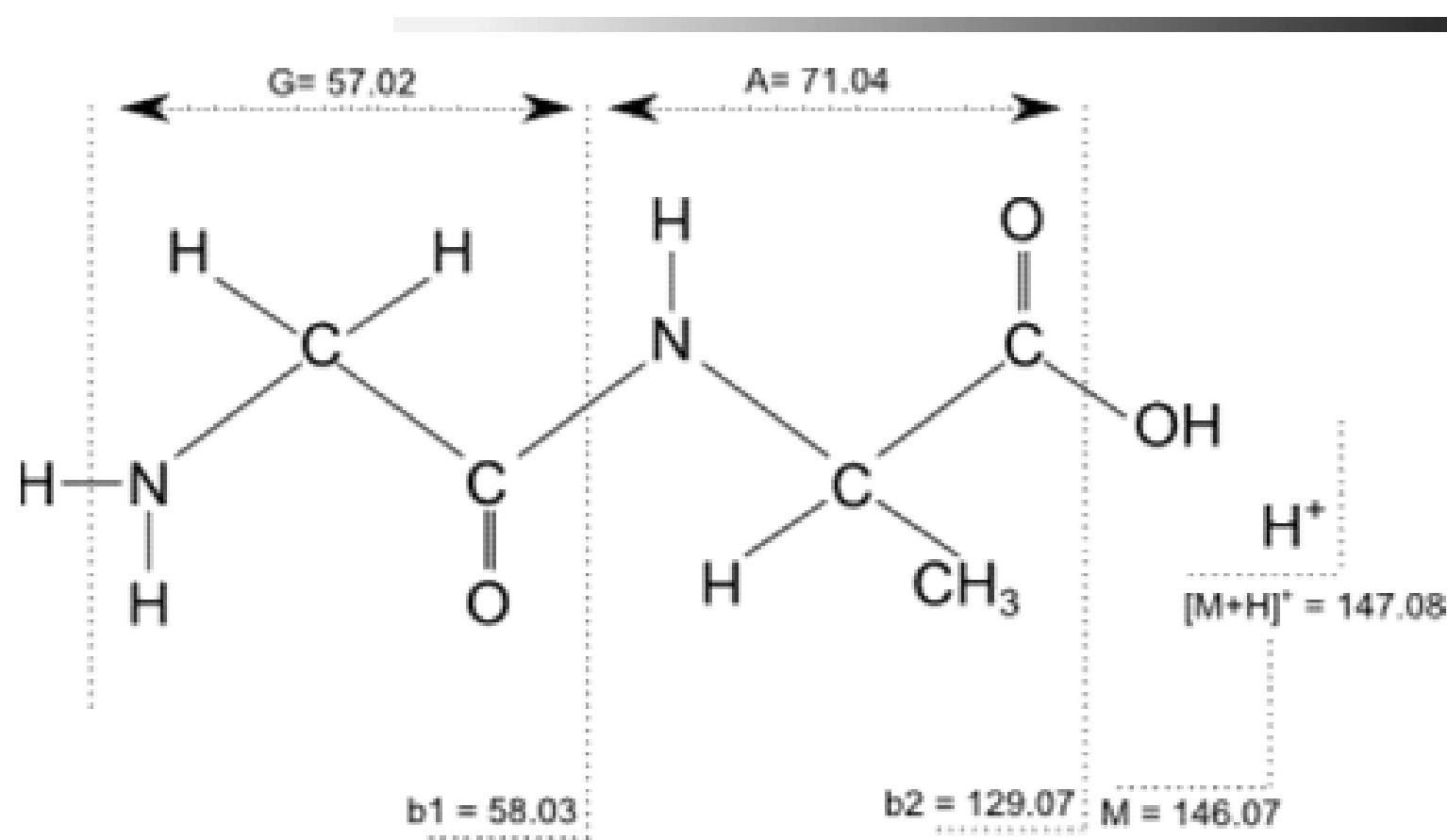
$$y = (M+H)^+ - b + 1 ; b = (M+H)^+ - y + 1$$

Zubarev and Bondarenko, 1991

- Find the b-ion without the C-terminal K or R:  $(M+H)^+ - 18$  ('lost' oxygen) – [KR]

AA Codes	Mono.	AA Codes	Mono.
Gly G	57.021464	Asp D	115.02694
Ala A	71.037114	Gln Q	128.05858
Ser S	87.032029	Lys K	128.09496
Pro P	97.052764	Glu E	129.04259
Val V	99.068414	Met M	131.04048
Thr T	101.04768	His H	137.05891
Cys C	103.00919	Phe F	147.06841
Leu L	113.08406	Arg R	156.10111
Ile I	113.08406	CMC	161.01467
Asn N	114.04293	Tyr Y	163.06333
<b>IonSource™</b> <small>mass spectrometry educational resource</small>		Trp W	186.07931

'Lost' oxygen



- Upon peptide bond formation,  $H_2O$  gets released and this mass is therefore not included in the  $\Delta$  mass for the individual amino acids
- The largest b-ion is mass of the parent ion – 18, because  $H_2O$  gets released and the positive charge resides at the C-terminus

20070130\_11\_ppi1\_B1 #1321 RT: 38.25 AV: 1 NL: 1.57E6  
T: + c d Full ms2 946.76 @35.00 [ 250.00-1905.00]

$$M_{\text{Precursor}} = \frac{(M + 2H)^2}{2} = 946.76$$

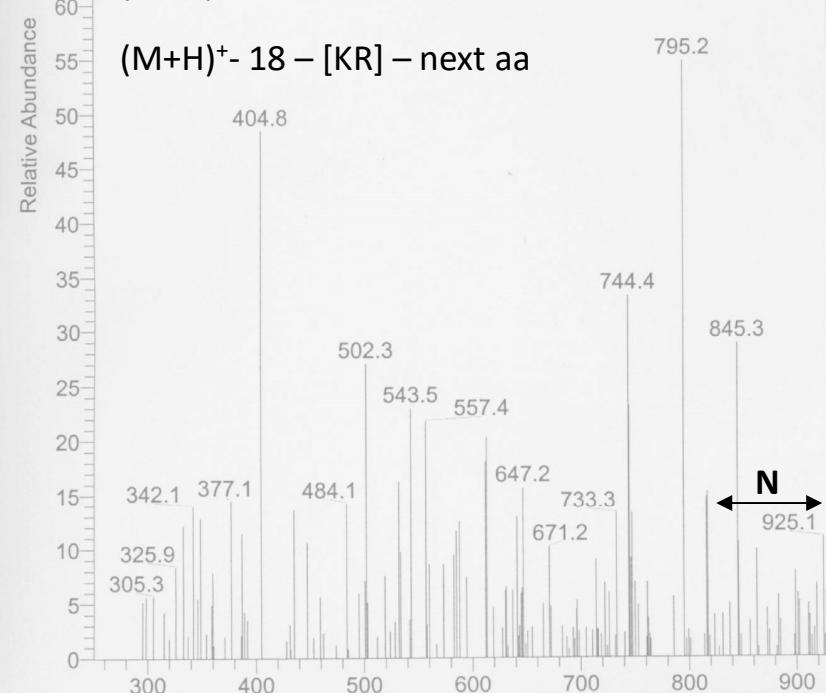
$$M_{\text{Parent average}} = (M+H)^+ = 1892.52$$

$$M_{\text{Parent mono}} = (M+H)^+ \sim 1892$$

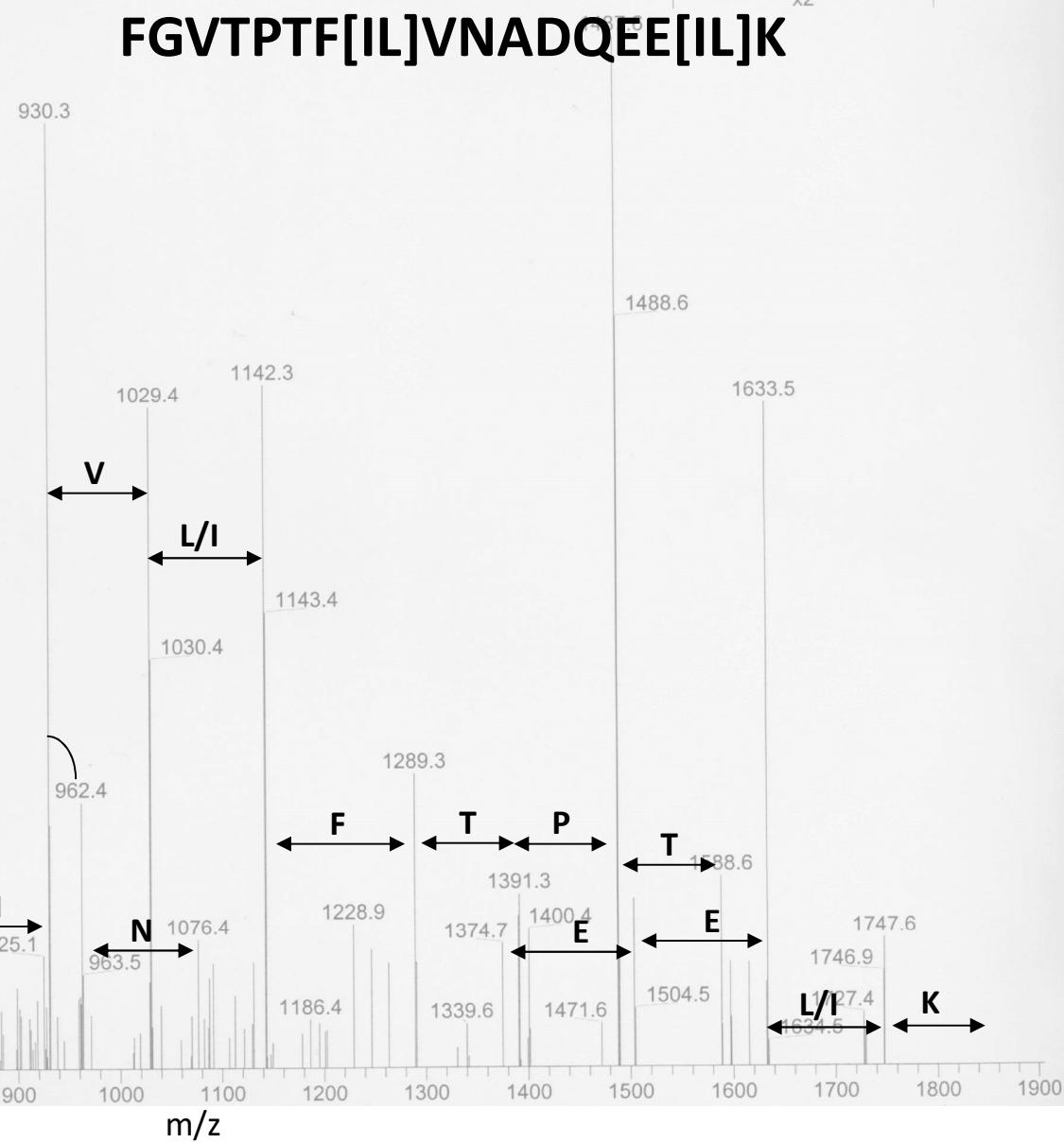
$$y = (M+H)^+ - b + 1 ; b = (M+H)^+ - y + 1 ;$$

$(M+H)^+ - 18 - [\text{KR}]$

$(M+H)^+ - 18 - [\text{KR}] - \text{next aa}$



**FGVTPTF[IL]VNADQEE[IL]K**



## Peptide fragmentation

ion	offset <sup>b</sup>	$\Delta^c$	no. peaks <sup>d</sup>	no. spectra <sup>e</sup>	probability
y	19.020	0.002	2245	2792	0.804
b	1.006	-0.002	1934	2806	0.689
<i>b</i> -H <sub>2</sub> O	-17.005	-0.002	777	2744	0.283
y/2 <sup>f</sup>	9.508	-0.001	508	2359	0.215
y-H <sub>2</sub> O	1.005	-0.003	312	2360	0.132
y <sup>+2</sup>	10.012	-0.001	316	2448	0.129
<i>b</i> -NH <sub>3</sub>	-16.021	-0.002	253	2746	0.092
<i>a</i>	-26.988	-0.001	205	2706	0.076
[y-H <sub>2</sub> O] <sup>+2</sup>	1.006	-0.002	156	2246	0.070
[y-H <sub>2</sub> O-H <sub>2</sub> O] <sup>+2</sup>	-7.998	0.000	142	2189	0.065
<i>b</i> -H <sub>2</sub> O-H <sub>2</sub> O	-35.015	-0.002	119	2661	0.045
y-NH <sub>3</sub>	1.989	-0.003	110	2689	0.041
[y-H <sub>2</sub> O-NH <sub>3</sub> ] <sup>+2</sup>	-7.507	-0.001	75	2192	0.034
<i>b</i> /2 <sup>f</sup>	0.503	-0.001	64	2139	0.030
<i>b</i> -H <sub>2</sub> O-NH <sub>3</sub>	-34.031	-0.002	71	2663	0.027
<i>a</i> -NH <sub>3</sub>	-44.015	-0.002	42	2652	0.016
<i>a</i> -H <sub>2</sub> O	-44.999	-0.001	32	2650	0.012
[y-NH <sub>3</sub> ] <sup>+2</sup>	1.498	-0.001	23	2248	0.010
<i>b</i> <sup>+2</sup>	1.006	-0.002	14	2146	0.007
<i>b</i> -NH <sub>3</sub> -NH <sub>3</sub>	-33.047	-0.002	17	2664	0.006
y-H <sub>2</sub> O-H <sub>2</sub> O	-17.007	-0.004	12	2673	0.005
y-H <sub>2</sub> O-NH <sub>3</sub>	-16.022	-0.003	10	2676	0.004
Internal+H	1.005	-0.003	227	10841	0.021
Internal+H-H <sub>2</sub> O	-17.005	-0.002	125	10345	0.012
Internal+NH <sub>2</sub> +H <sub>2</sub> O	34.027	0.002	112	11633	0.010

- Peptides do not fragment sequentially, but fragmentation events are somewhat random
- Some fragmentations are preferred over others as noted by the variation in the abundance of observed peaks
- The mess of peaks normally observed in a fragment spectrum are a reflection of the population of fragment ions produced in the collision cell of a mass spectrometer

## Neutral losses and peptide modifications

- Neutral losses
  - H<sub>2</sub>O (-18 Da)
  - NH<sub>2</sub> (-17 Da)
  - CO (-28 Da)
  - H<sub>3</sub>PO<sub>4</sub> (-98 Da)

- Modifications

Oxidation: M +16 Da

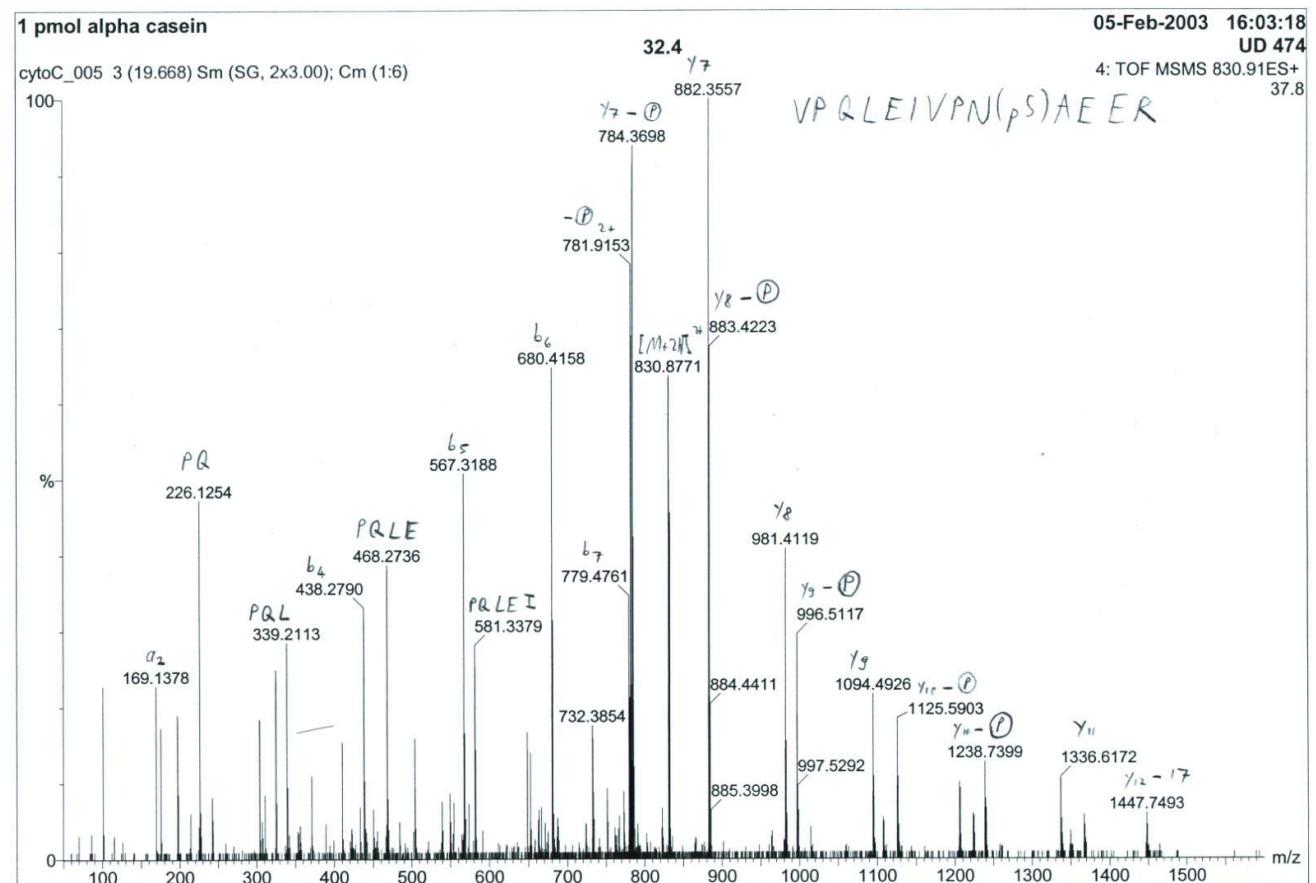
Deamidation: N → Q, -1 Da

Methylation: R +14 Da

Phosphorylation: S, T, Y +80 Da

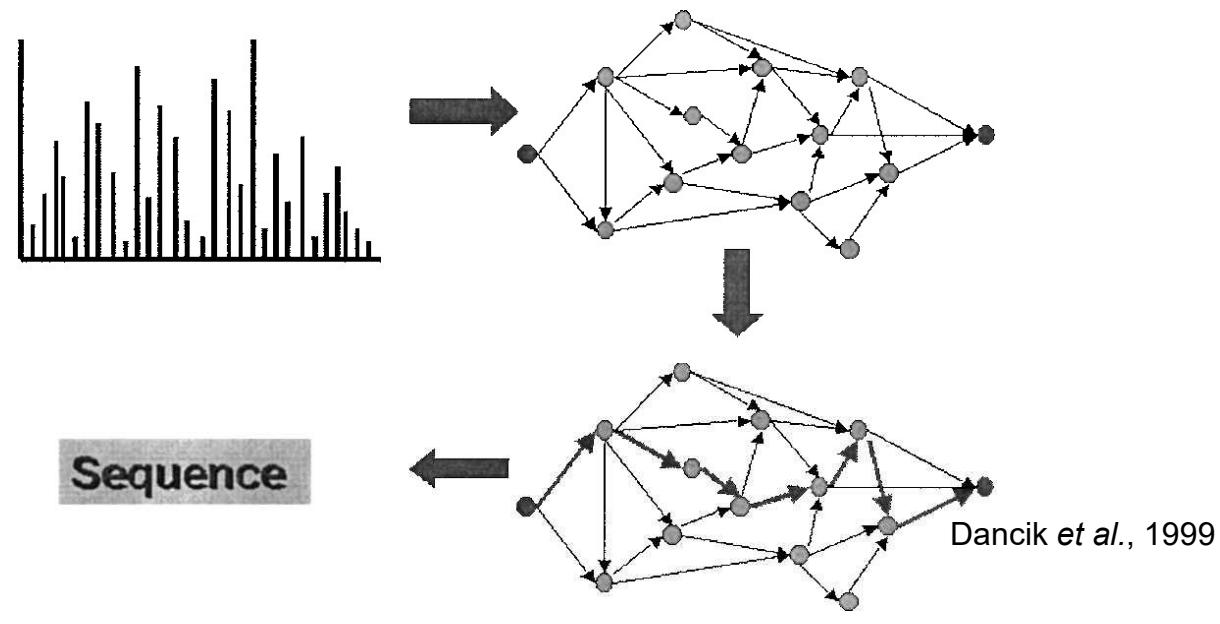
Acetylation: K, R, N-terminus +42 Da

Carboxyamidomethylation: C +57 Da



## Dynamic programming in *de novo* sequencing

- In *de novo* sequencing with dynamic programming, the peaks in a spectrum are transformed to a spectrum graph representation. In the spectrum graph representation, the peaks in the spectrum serve as nodes in the graph, while the edges of the graph link nodes differing by the mass of an amino acid.
- Each peak in an experimental spectrum is transformed into several nodes in a spectrum graph, and each node represents a possible fragment type assignment for a peak
- Sequence reconstructions correspond to paths in the spectrum graphs
- In correct reconstructions the nodes in the path correspond to cleavages in the peptide



# Use of Hidden Markov Models in *de novo* sequencing

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*JAnal. Chem.* 2005, 77, 7265–7273

## **NovoHMM: A Hidden Markov Model for de Novo Peptide Sequencing**

**Bernd Fischer,<sup>†</sup> Volker Roth,<sup>†</sup> Franz Roos,<sup>§</sup> Jonas Grossmann,<sup>‡</sup> Sacha Baginsky,<sup>‡</sup> Peter Widmayer,<sup>§</sup> Wilhelm Gruissem,<sup>‡</sup> and Joachim M. Buhmann<sup>†</sup>**

- In the NovoHMM model, the observable random variables correspond to the observed mass peaks, whereas the hidden variables represent the unknown underlying sequence

### 1. Dynamic programming

- The algorithms suffer from 'real life issues' of peptide mass spectrometry, e.g. they are sensitive against noisy data
- Requires pre-processing of the information in an MS/MS spectrum

### 2. Hidden Markov Models

- Fully probabilistic
- Can deal with noisy data

- Studies comparing the performance of *de novo* sequencing algorithms revealed that the rate of exact peptide sequence identification is low with high error rate
- Problems for *de novo* sequencing are limited mass accuracy of the mass spectrometers, missing ions, unknown identity of the peaks and additional, sequence-independent peaks

Different database-dependent peptide identification search algorithms:

- Sequest
- Mascot
- PepSplice
- OMSSA
- X!Tandem
- Phenyx
- ProteinPilot
- SpectrumMill
- ProbID
- PepFrag
- InSpect
- ...

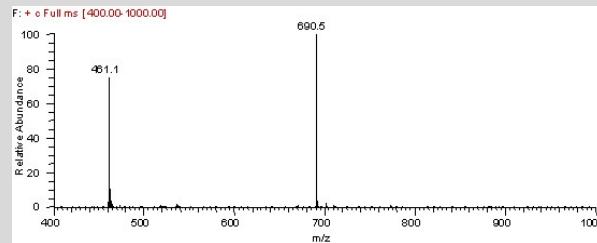
- 
- Peptide sequences with one or more scores with which to evaluate the likelihood that the resulting sequence is correct.
  - Even though each implementation is different, they operate under the same general principle.

# Database-dependent peptide identification

## Experimental

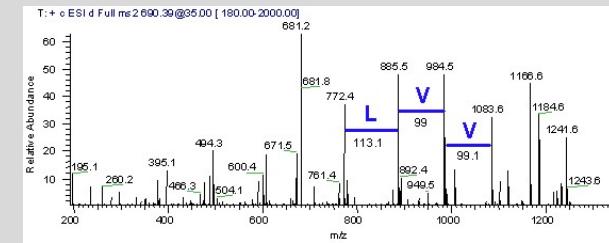
Protein sample

tryptic digest



**Full Scan [MS]:**  
Mass measurement of full peptides

fragmentation



**MS/MS-Scan:**  
Measurement of peptide fragments

1) Peptides from a protein database are matched to the measured mass

2) Theoretical spectrum is cross-correlated to the measured one

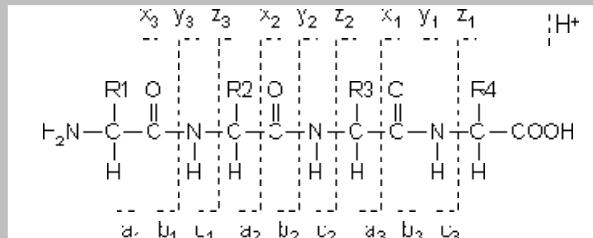
Protein database

in silico digest

Peptide database

in silico dissociation

Theoretical tryptic peptides  
from a protein database



Theoretical spectra  
assuming peptide bond breakage

In silico

Peptide spectrum assignment

- The goal is to identify the best sequence match to the spectrum
- The details of this implementation differ among the algorithms. In addition, the methods used to assign scores are very different.
- Four basic approaches have been developed to model matches to the sequences: descriptive models, interpretative models, stochastic models and statistical and probability models (Sadygov, Cociorva and Yates, 2004 )

Descriptive algorithms are based on a mechanistic prediction of how peptides fragment in a tandem mass spectrometer, which is then quantified to determine the quality of the match between the prediction and the experimental spectrum. Mathematical methods such as correlation analysis have been used to assess match quality.

- Sequest is an example of a program using a descriptive model:
  - $S_p$ , sums the peak intensity of fragment ions matching the predicted sequence ions and accounts for the continuity of an ion series and the length of a peptide
  - Xcorr, is a cross-correlation score of the experimental and theoretical spectra
  - $\Delta Cn$  gives the normalised difference of Xcorr values between the best sequence and lower-scoring matches and is useful to determine the uniqueness of the match

Sadygov, Cociorva and Yates, 2004

Interpretative approaches are based on manual or automated interpretation of a partial sequence from a tandem mass spectrum and incorporation of that sequence into a database search. Matches between the sequence and the spectrum have been scored using probabilities or correlation methods.

- PeptideSearch and InSpect belong to the programs using sequence tagging:
  - The program identifies a continuous series of fragment ions (sequence tag)
  - Every candidate peptide is divided into three parts: m1, sequence tag = m2, m3
  - The sequence tag can be from the b- or y-ion series and therefore both possibilities have to be considered by the algorithm
  - The algorithm searches the database for matches using the masses of m1, m2 and m3, as well as information from protease specificity
  - The sequence match is then scored by calculating the probability of the match being non-random

Stochastic models are based on probability models for the generation of tandem mass spectra and the fragmentation of peptides. Basic probabilities of fragment ion matches are obtained from training sets of spectra of known sequence identity. Stochastic models use statistical limits on the measurement and fragmentation process to create a likelihood that the match is correct.

- SCOPE is an example of a program using a stochastic model:
  - First, the fragmentation probabilities are estimated with assumptions on fragmentation patterns and/or with collections of annotated spectra
    - probability of obtaining the fragmentation pattern F from CID of peptide p
  - Second, the probability of observing a collection of spectral peaks given a particular peptide fragmentation is computed
    - probability of fragmentation pattern F to generate spectrum S
  - Finally, the probability of obtaining spectrum S from peptide b is computed

Statistical and probability models determine the relationship between the tandem mass spectrum and sequences. The probability of peptide identification and its significance are then derived from the model.

- A hypergeometric probability models the frequencies of database peptides based on the number of matches. The significance of a peptide match is defined as a rejection of the null hypothesis that all fragment matches are random
- In Mascot, the score is the probability-based MOWSE (MOlecular Weight SEarch) score given as  $s = -10 \cdot \log(P)$  where P is the probability that the observed match between experimental data and a peptide sequence is a random event
- The correct match, which is a not a random event, has a very low probability

**Expect value** = the number of times you could expect to get this score or better by chance

- A completely random match has a score of 1 or higher
- The better the match the lower the expect value

# Empirical statistical model to estimate the accuracy of peptide identifications

#	File	MH+	XCorr	dCn	Sp	RSp	Ions	Ref	Sequence
325	./sergei digest A full 01.1001.1003.3	2511.7 (-0.6)	7.5863	0.450	4546.1	✓ 1	42/ 84	sp P00921 CAH2_BOVIN	R. MVNNNGHSFNVEYDDSDQDKAVLK.D
462	./sergei digest A full 01.1239.1241.3	2584.7 (+2.0)	6.1808	0.382	3126.2	✓ 1	39/ 84	sp P00921 CAH2_BOVIN	R. LVQFHFHWGSSBBQGSEHTVDR.K
1070	./sergei digest A full 01.2335.2337.3	2254.5 (+0.5)	6.0682	0.491	2166.9	✓ 1	37/ 84	sp P00921 CAH2_BOVIN	K. YGDFGTAAQQPDGLAVVGVFLK.V
1105	./sergei digest A full 01.2405.2407.3	2254.5 (+0.8)	6.0041	0.511	1873.6	✓ 1	35/ 84	sp P00921 CAH2_BOVIN	K. YGDFGTAAQQPDGLAVVGVFLK.V
510	./sergei digest A full 01.1317.1323.3	2584.7 (+1.5)	5.9521	0.403	2488.3	✓ 1	38/ 84	sp P00921 CAH2_BOVIN	R. LVQFHFHWGSSBBQGSEHTVDR.K
1219	./sergei digest A full 01.2617.2619.3	2187.6 (-0.1)	5.7343	0.502	2282.1	✓ 1	33/ 72	sp P02666 CASP_BOVIN	R. DMPIQAFLLYQEPVLGPV.R
894	./sergei digest A full 01.2013.2015.3	2314.7 (+0.0)	5.5636	0.418	1260.3	✓ 1	33/ 76	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
812	./sergei digest A full 01.1873.1875.3	2314.7 (+0.5)	5.5466	0.428	1407.6	✓ 1	35/ 76	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
1142	./sergei digest A full 01.2471.2473.2	2254.5 (-0.8)	5.5372	0.526	771.0	✓ 1	24/ 42	sp P00921 CAH2_BOVIN	K. YGDFGTAAQQPDGLAVVGVFLK.V
856	./sergei digest A full 01.1943.1945.3	2314.7 (+0.9)	5.4579	0.426	1581.3	✓ 1	34/ 76	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
1289	./sergei digest A full 01.2765.2771.2	2709.1 (+0.4)	5.3678	0.495	1654.1	✓ 1	24/ 50	sp P02754 LACB_BOVIN	K. VAGTWYSLAMAASDISLLDAQSAPLR.V
1220	./sergei digest A full 01.2621.2623.2	2187.6 (-0.5)	5.3391	0.461	1646.5	✓ 1	22/ 36	sp P02666 CASP_BOVIN	R. DMPIQAFLLYQEPVLGPV.R
1153	./sergei digest A full 01.2491.2493.3	2219.5 (+2.1)	5.3167	0.276	1640.4	✓ 1	31/ 72	sp P00921 CAH2_BOVIN	R. TLNFNAEGEPEELLMLANW.P
1102	./sergei digest A full 01.2401.2403.2	2254.5 (-0.6)	5.1675	0.495	1009.0	✓ 1	24/ 42	sp P00921 CAH2_BOVIN	K. YGDFGTAAQQPDGLAVVGVFLK.V
1067	./sergei digest A full 01.2329.2333.2	2254.5 (-0.9)	5.1492	0.546	688.2	✓ 1	23/ 42	sp P00921 CAH2_BOVIN	K. YGDFGTAAQQPDGLAVVGVFLK.V
125	./sergei digest A full 01.0681.0681.2	2100.2 (+0.8)	4.9146	0.481	1779.2	✓ 1	22/ 34	sp P00921 CAH2_BOVIN	R. MVNNNGHSFNVEYDDSDQDK.A
1020	./sergei digest A full 01.2237.2239.2	1568.7 (-0.1)	4.8921	0.413	1764.0	✓ 1	19/ 24	sp P02769 ALBU_BOVIN	K. DAFLGSFLYEYSR.R
981	./sergei digest A full 01.2163.2165.2	2147.3 (-0.7)	4.8738	0.452	1515.4	✓ 1	26/ 38	sp P02666 CASP_BOVIN	E. LNVPGEIVESLSSSEESITR.I
533	./sergei digest A full 01.1361.1367.3	2906.0 (+0.7)	4.8712	0.301	655.0	✓ 1	29/ 92	sp P02666 CASP_BOVIN	K. FQSEEQQQTDELQDKIHPFAQTQ.S
815	./sergei digest A full 01.1879.1883.2	2314.7 (-0.6)	4.7827	0.419	438.7	X 1	19/ 38	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
760	./sergei digest A full 01.1771.1773.2	2034.2 (-0.1)	4.7587	0.465	1047.9	✓ 1	26/ 36	sp P02666 CASP_BOVIN	L. NVPGEIVESLSSSEESITR.I
1048	./sergei digest A full 01.2289.2291.2	2804.0 (+0.5)	4.7564	0.433	1497.0	✓ 1	26/ 48	sp P02666 CASP_BOVIN	A. RELEELNVPGEIVESLSSSEESITR.I
157	./sergei digest A full 01.0735.0737.3	2100.2 (-0.5)	4.7471	0.300	1496.2	✓ 1	32/ 68	sp P00921 CAH2_BOVIN	R. MVNNNGHSFNVEYDDSDQDK.A
91	./sergei digest A full 01.0607.0609.2	1983.0 (-0.4)	4.6602	0.358	3224.6	X 1	24/ 30	sp P02666 CASP_BOVIN	K. FQSEEQQQTDELQDK.I
625	./sergei digest A full 01.1523.1525.3	2046.3 (-0.7)	4.6539	0.307	1901.4	✓ 1	29/ 60	sp P02769 ALBU_BOVIN	R. RPHPYFYAPELLYYANK.Y
117	./sergei digest A full 01.0663.0665.3	2100.2 (+0.0)	4.5901	0.286	1627.3	X 1	36/ 68	sp P00921 CAH2_BOVIN	R. MVNNNGHSFNVEYDDSDQDK.A
712	./sergei digest A full 01.1675.1681.2	1832.0 (-0.3)	4.5772	0.393	1148.8	X 1	21/ 34	sp Q29443 TRFE_BOVIN	K. GEADAMSLLGGYLYIAGK.C
651	./sergei digest A full 01.1569.1571.3	3106.3 (+0.4)	4.5737	0.362	537.5	X 1	26/100	sp P02666 CASP_BOVIN	K. FQSEEQQQTDELQDKIHPFAQTQ.S
942	./sergei digest A full 01.2085.2089.3	2314.7 (+1.4)	4.5707	0.299	1348.2	X 1	32/ 76	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
1045	./sergei digest A full 01.2277.2279.3	2804.0 (-0.5)	4.5012	0.352	1236.7	✓ 1	31/ 96	sp P02666 CASP_BOVIN	A. RELEELNVPGEIVESLSSSEESITR.I
861	./sergei digest A full 01.1951.1953.2	2314.7 (-0.4)	4.4874	0.348	482.4	X 1	20/ 38	sp P02754 LACB_BOVIN	R. VYVEELKPTPEGDLEILLQK.W
626	./sergei digest A full 01.1529.1531.2	1480.7 (-0.5)	4.4192	0.315	1731.6	X 1	20/ 24	sp P02769 ALBU_BOVIN	K. LGEYGFQNALIVR.Y
176	./sergei digest A full 01.0767.0767.2	1983.0 (+0.7)	4.4109	0.414	1966.2	X 1	22/ 30	sp P02666 CASP_BOVIN	K. FQSEEQQQTDELQDK.I
328	./sergei digest A full 01.1009.1011.3	1440.7 (+0.8)	4.4102	0.302	2269.3	X 1	28/ 44	sp P02769 ALBU_BOVIN	R. PHPEYAVSVLL.R

Peptide spectrum assignment

## Empirical statistical model to estimate the accuracy of peptide identifications

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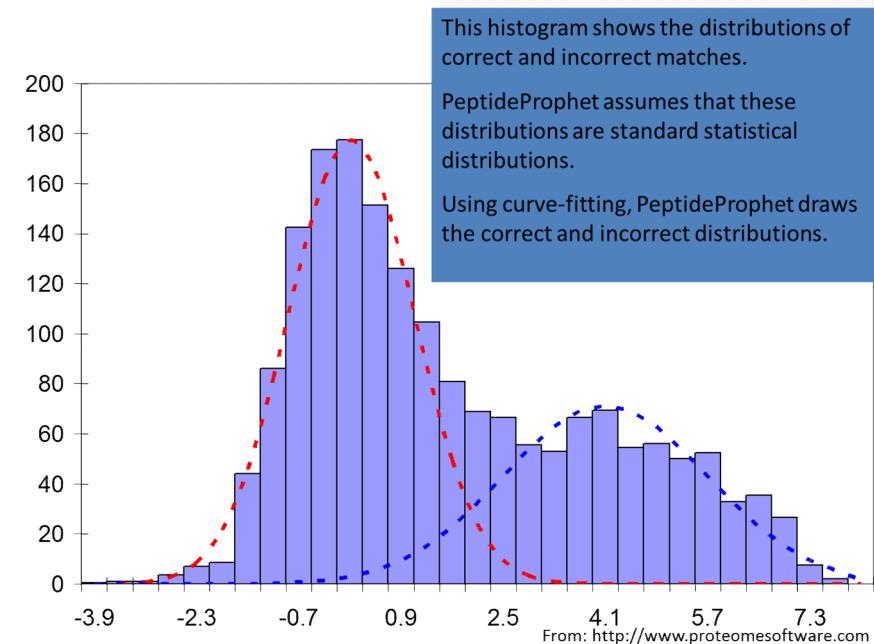
### Task:

Derive a list of identified peptides from database search results carried out with a large number of MS/MS spectra.

- This entails distinguishing correct peptide assignments from false identifications. For small datasets, this can be achieved by researchers with expertise manually verifying the peptide assignments made by database search programs.
- For high-throughput analysis and consistent data analysis a statistical model is needed to assess the validity of peptide identifications made by MS/MS database searches.

Keller et al., 2002

- **PeptideProphet** computes for each peptide assignment to a spectrum a probability of being correct.
- A discriminant function analysis is used to combine together any number of database search scores into a single discriminant score that best separates training data into correct and incorrect identifications. The discriminant score F is a weighted combination of the database search scores.



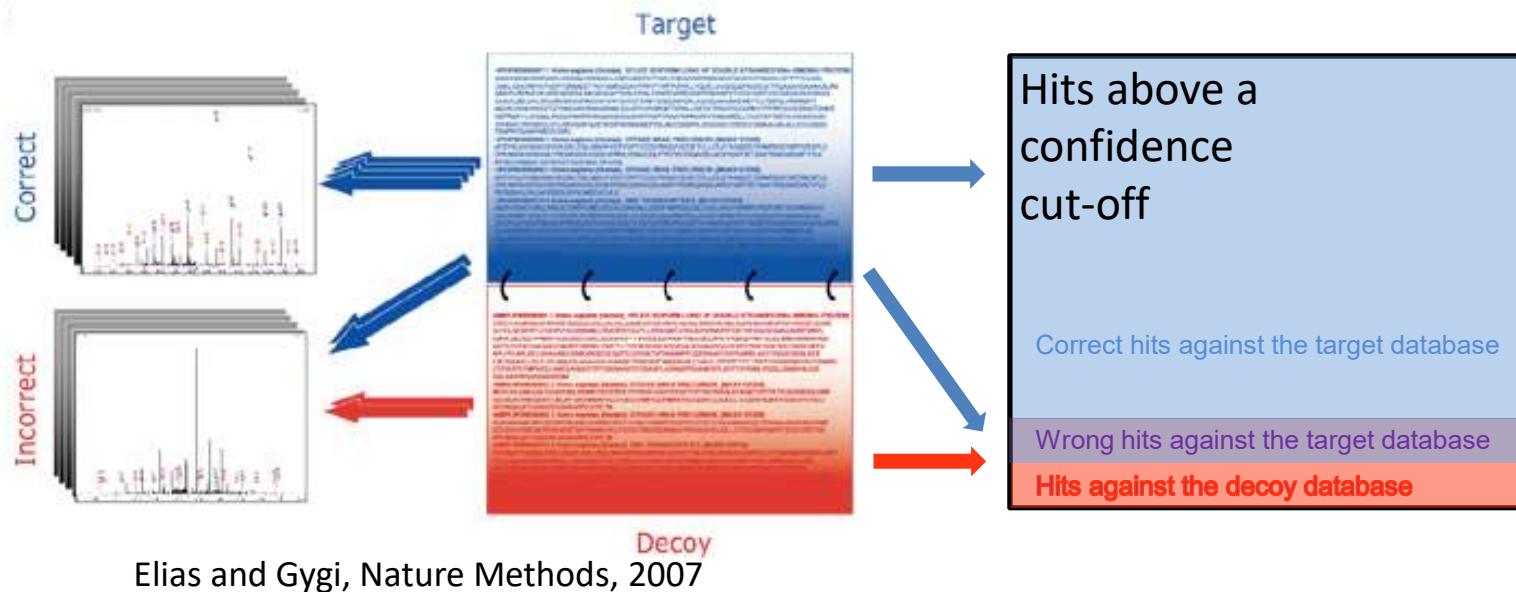
- Bayes' theorem gives the probability that a particular peptide assignment with a specific discriminant score is correct:
- $$p(+|F) = p(F|+)p(+) / (p(F|+)p(+) + p(F|-)p(-))$$
- where  $p(+|F)$  = probability that the peptide assignment with discriminant score F is correct

### **False positives are a concern and can occur because:**

- Spectra can be single peptide ions, chemical noise, non-peptide molecules for mixtures of co-eluting isobaric peptides
- Peptides are often present at a wide range of concentrations in a sample, and peptides present at the limit of detection can produce poor quality spectra
- Chemistry of peptide fragmentation is not completely understood
- There are amino acid sequences that do not produce a unique fragmentation pattern but share enough of the same fragment ions to be indistinguishable from one another

## Target-decoy search strategy

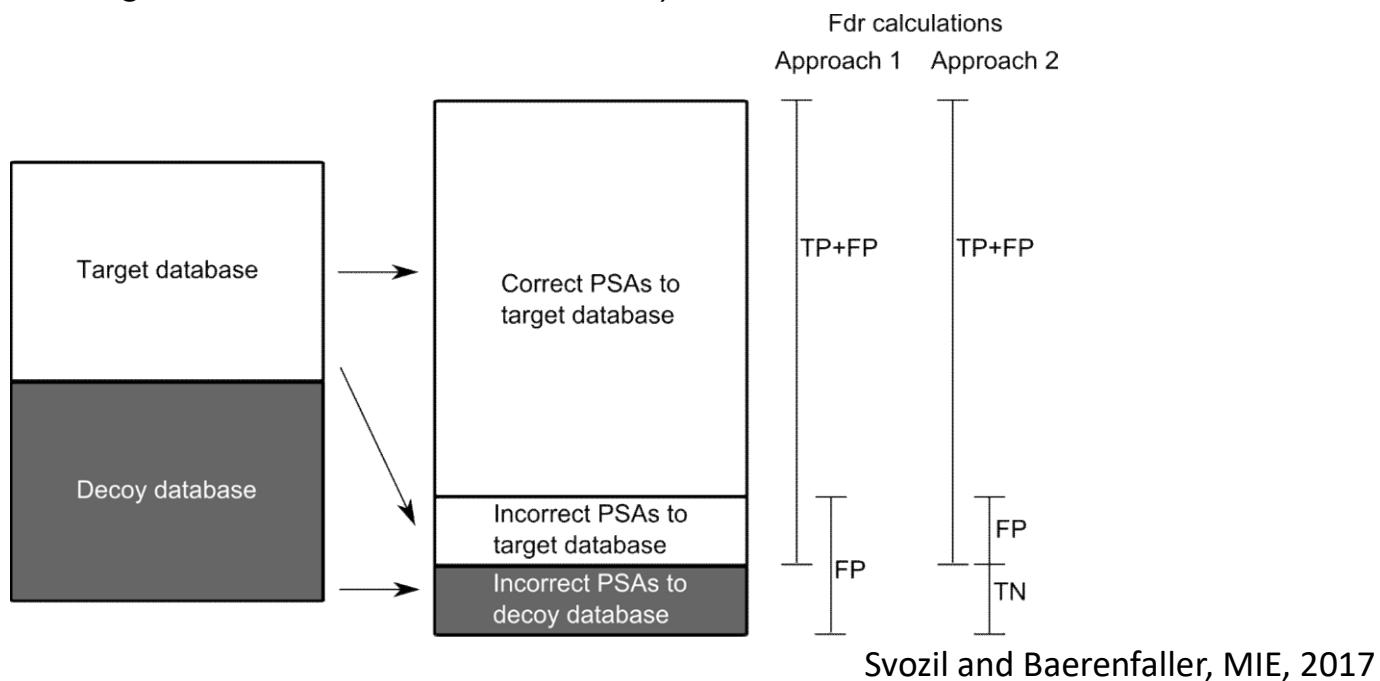
1. All the spectra are searched against a database that consists of the target database concatenated to a decoy database (either randomized or reversed target database)



1. The hits against the decoy database are clearly wrong as these sequences don't exist
2. It can then be assumed that the number of noticeable wrong hits against the decoy database equals the number of non-noticeable wrong hits against the target database

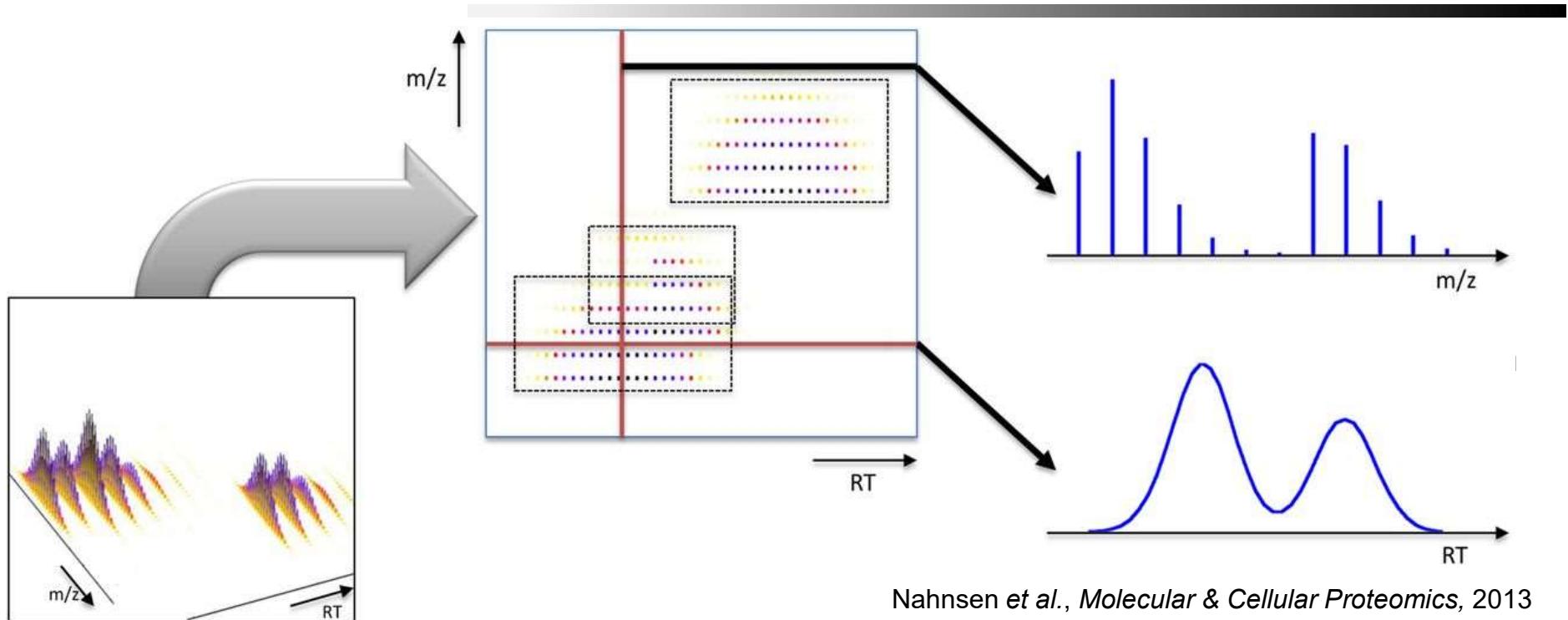
## Calculation of false discovery rates (fdrs)

- The estimation of the fdr is a requirement for the analysis and documentation of mass spectrometry data according to the Paris guidelines of Molecular and Cellular Proteomics (Bradshaw, Burlingame, Carr & Aebersold, 2006)



- Global fdrs are calculated for the full dataset
- Local false discovery rates (lfdrs) can be calculated for a subset of the peptide spectrum matches, e.g. the spectra assigned to peptides carrying specific post-translational modifications, or spectra assigned to peptides in an alternative search database, etc.

## Label-free quantification (data dependent analysis DDA)

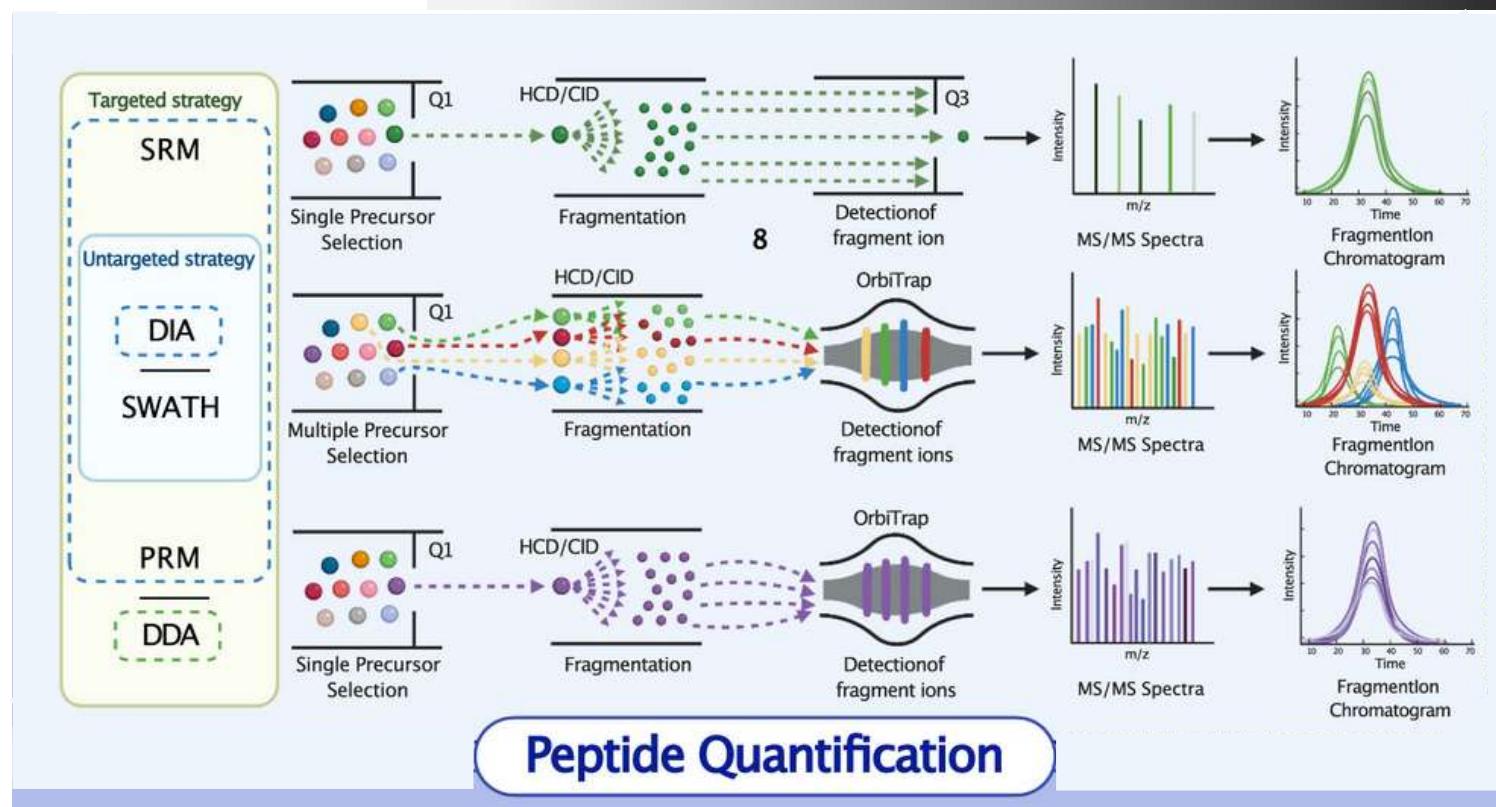


Nahnsen et al., *Molecular & Cellular Proteomics*, 2013

LC/MS data consist of individual MS spectra accumulated over (retention) time. Stacked side by side, these spectra form two-dimensional maps.

- In spectral counting the basic assumption is that protein abundance is proportional to the number of spectra (after normalization)
- Quantification can also be based on the comparison of features, which can be defined as all mass-spectrometric signals (peaks) caused by the same peptide

# Hypothesis-driven, targeted bottom-up proteomics approaches



Radzikowska et al., *Omics technologies in allergy and asthma research: An EAACI position paper*, Allergy, 2022

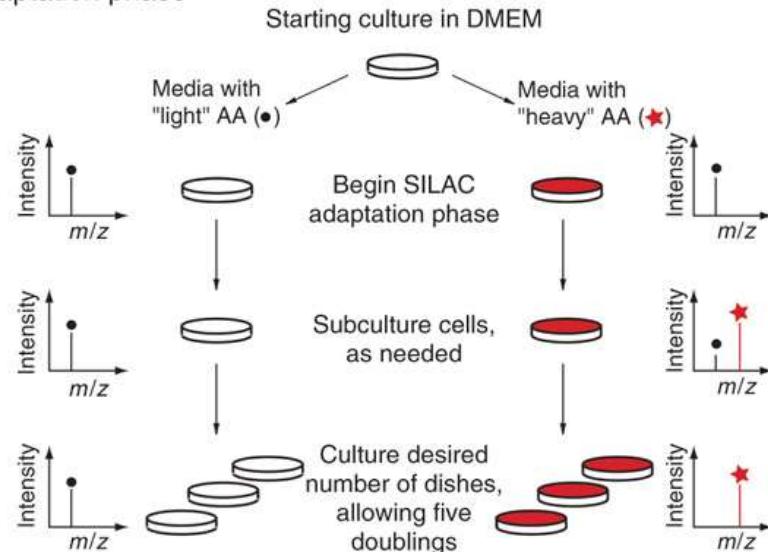
S/MRM: Selected/Multiple Reaction Monitoring; the proteins are pre-selected and provide information on the characteristic peptide precursor and fragment ion signals (transitions)

DIA/SWATH: Data Independent Acquisition/Sequential Windowed Acquisition of All Theoretical Mass Spectra

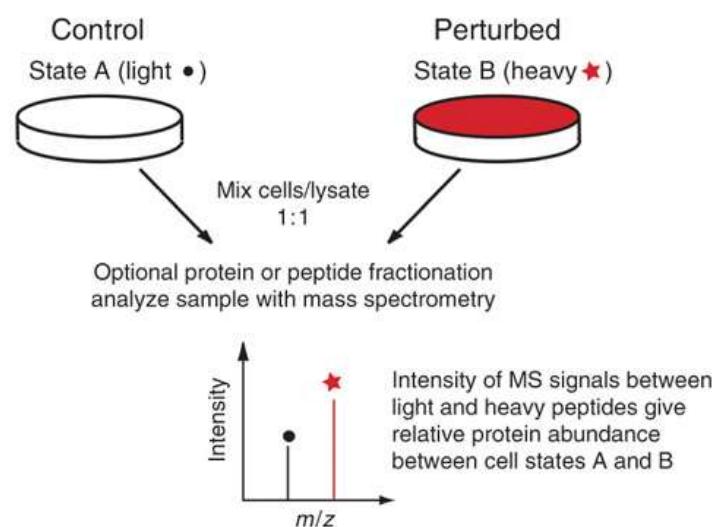
PRM: Parallel Reaction Monitoring; similar to S/MRM, but all resulting fragment ion signals from a precursor ion are monitored

## Quantification with labelling: SILAC

### a Adaptation phase



### b Experiment phase



SILAC = stable isotope labeling by amino acids in cell culture

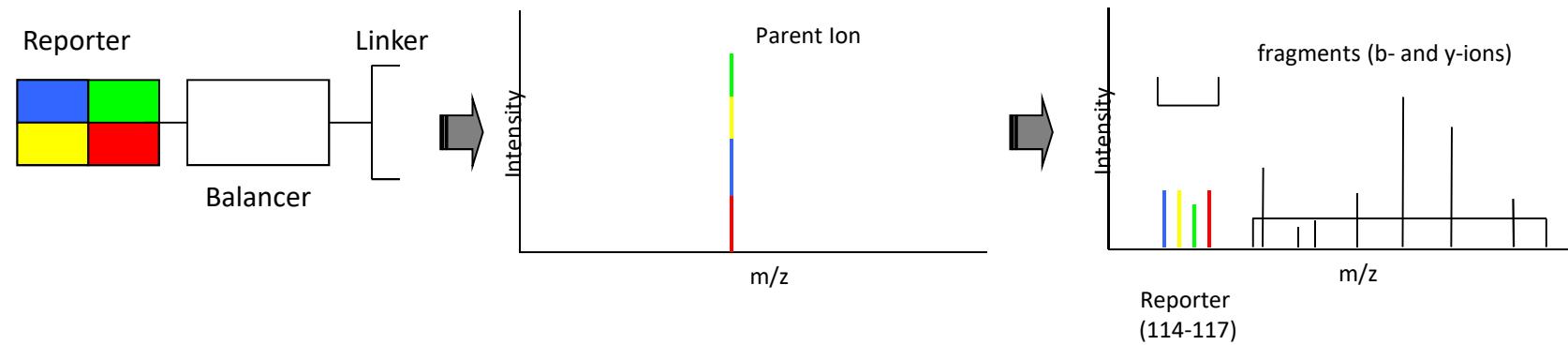
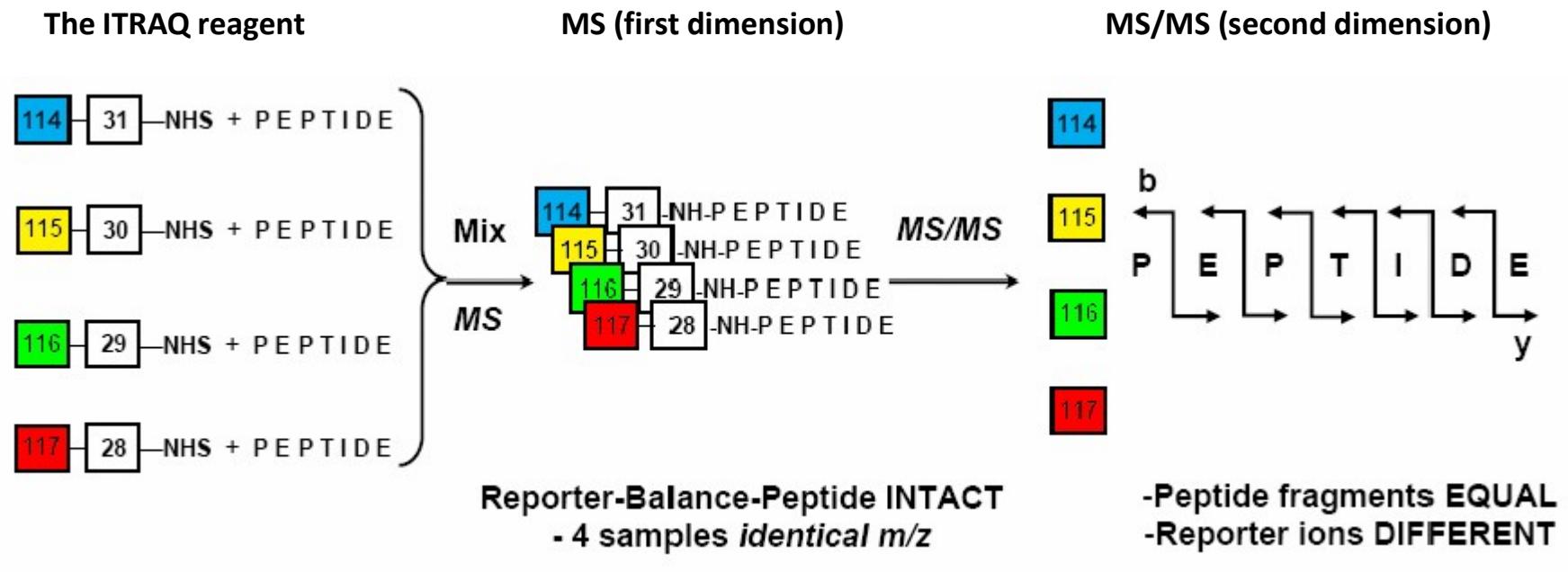
- In the adaptation phase, cells are grown in light and heavy SILAC media until full incorporation of heavy amino acids
- In the experimental phase, the two populations are treated differentially to induce changes in the proteome

Afterwards, the samples are mixed and processed; the peptide are analyzed by MS for protein identification and quantification

Ong and Mann, *Nature Protocols*, 2007

Quantitative proteomics

# Quantification with labelling: iTRAQ



# Quantification with labelling: TMT

