

Mass spectrometry: forming ions, to identifying proteins and their modifications

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Introduction to mass spectrometry

- **Class 1 - Biology and mass spectrometry**
 - Why is mass spectrometry so important?
 - Short history of mass spectrometry
 - Ionization and measurement of ions
- **Class 2 - The mass spectrum**
 - What is a mass spectrum?
 - Interpreting ESI and MALDI-TOF spectra
 - Combining peptide separation with mass spectrometry
 - MALDI mass fingerprinting
 - Tandem mass spectrometry and peptide sequencing

Goals of research on proteins

- **To know which proteins are expressed in each cell, preferably one cell at a time**
- **Major analytical challenges**
 - **Sensitivity - no PCR reaction for proteins**
 - **Larger number of protein forms than open reading frames**
 - **Huge dynamic range (10^9)**
 - **Spatial and time-dependent issues**

Changes at the protein level

- **To know how proteins are modified, information that cannot necessarily be deduced from the nucleotide sequence of individual genes.**
- **Modification may take the form of**
 - **specific deletions (leader sequences),**
 - **enzymatically induced additions and subsequent deletions (e.g., phosphorylation and glycosylation),**
 - **intended chemical changes (e.g., alkylation of sulfhydryl groups),**
 - **and unwanted chemical changes (e.g., oxidation of sulfhydryl groups, nitration, etc.).**

Proteins once you have them

Protein structure and protein-protein interaction

- to determine how proteins assemble in solution
- how they interact with each other
- Transient structural and chemical changes that are part of enzyme catalysis, receptor activation and transporters

So, what you need to know about mass spec

- Substances have to be ionized to be detected.
- The net charge can be either positive or negative.
- The mass-to-charge ratio of an ion (m/z) is the most important parameter.
- The mass spectrometer is a selective detector (based on mass differences), but all the substances that are present in a sample and can be ionized are measured.

Important things to know

- **Polyionic buffer salts, particularly phosphate, interfere with ion formation in the electrospray ionization interface.**
- **Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) is very tolerant of the biomedical scientist.**
- **The mass spectrometer is always right.**

Where did mass spectrometry come from?

- 1803** Dalton proposes atomic theory of matter
- 1886** Discovery of “canal rays” by Goldstein
- 1905** J.J. Thompson introduces the use of low pressure
- 1919** Francis Aston establishes isotopes of neon (20/22)
- 1931** Aston discovers U-235/U238 isotopes
- 1937** Aston notes the mass defect of elements up to fluorine - $e = mc^2$
- 1938** Hahn/Strassman observe uranium fission
- 1940** Nier begins isolation of U235 by mass spec
- 1943** Army takes over - Manhattan project (Lawrence)

Postwar - modern mass spectrometry begins

- 1952** First meeting of the ASMS

Biomedical Mass Spectrometry

Early work in mass spec concentrated on isotopes and isotope ratios ($^2\text{H}/^1\text{H}$, $^{13}\text{C}/^{12}\text{C}$ and $^{15}\text{N}/^{14}\text{N}$)

Rittenberg and Schoenheimer established many of the pathways of metabolism using these isotopes

The combination of gas chromatography and mass spectrometry was good for small molecules

BUT what about proteins, peptides and other heat labile molecules?



David
Rittenberg

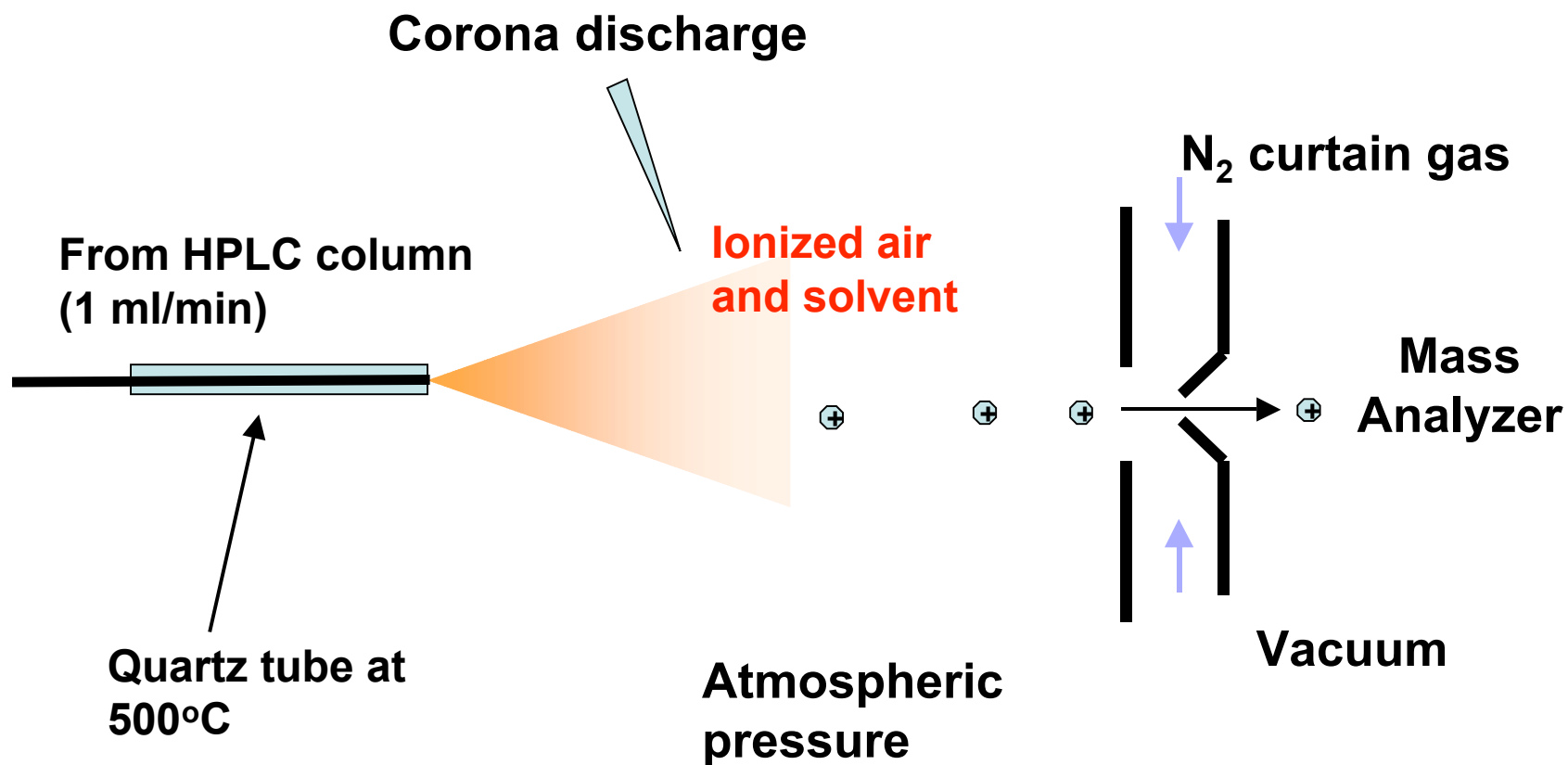
Outline

- **Interfaces and ion sources**
 - Heated nebulizer atmospheric pressure chemical ionization
 - Electrospray ionization (ESI)
 - » conventional and nanospray
 - Matrix assisted laser desorption ionization
- **Types of MS analyzers**
 - Magnetic sector
 - Quadrupole
 - Time-of-flight
 - Ion trap/FT-ICR
 - Hybrid

Interfaces and ion sources

- **Direct insertion probe - probe heated**
- **GC-MS (Ryhage, Biemann) volatile derivatives, thermal decomposition, not good for either peptides or proteins**
- **Field desorption - on carbon fibers**
- **Sputtering - glycerol matrix for fast atom bombardment (FAB)**
- **Matrix-assisted laser desorption**
- **Spraying**
 - **Thermospray ionization**
 - **Heated nebulizer atmospheric pressure chemical ionization**
 - **Electrospray ionization**

HN-APCI interface

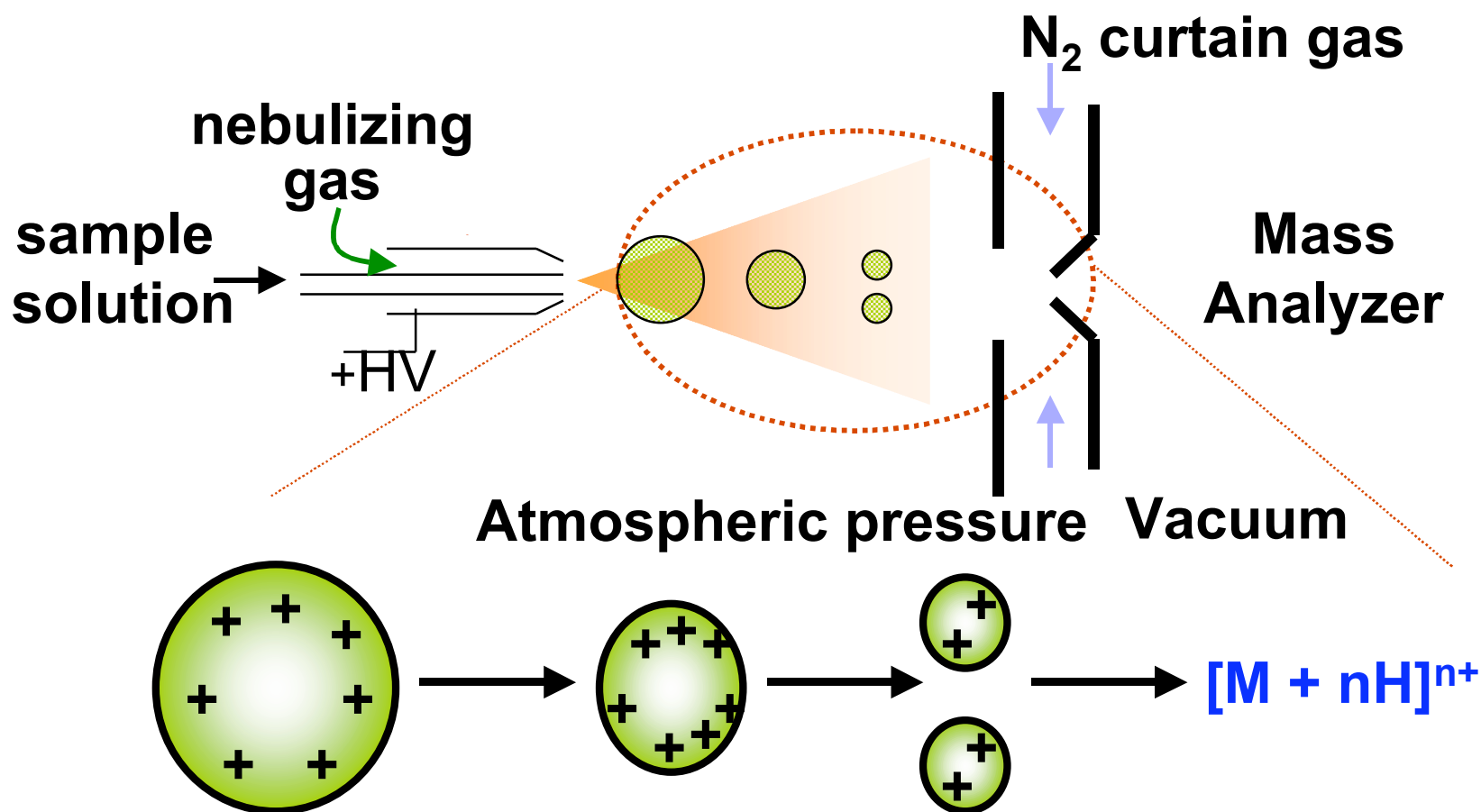


Electrospray ionization

Peptides and proteins can be transferred from solution into the gas phase without degradation by forming a nebulized spray of droplets (a **Taylor cone**) which are subject to rapid evaporation by warm nitrogen “curtain” gas. Typically, the nebulizing solution contains 30% acetonitrile which lowers the surface tension (and decreases droplet size) and facilitates the evaporation. The solutes are ejected from the surface of the droplet probably by coulombic repulsion. This occurs at atmospheric pressure.

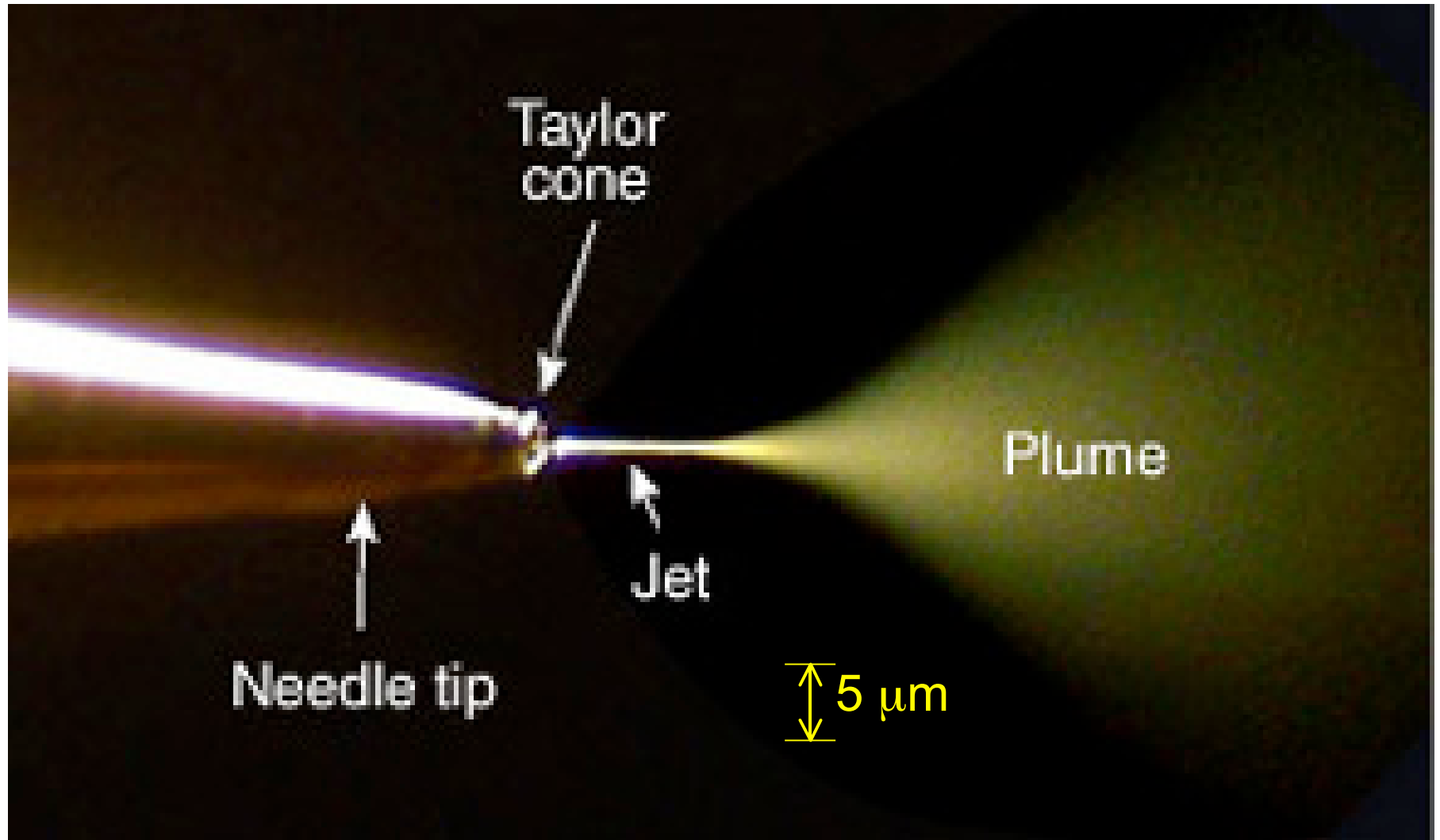
The flow rates that are suitable for ESI interfaces vary from 10 nl/min up to 1 ml/min (latter requires turbo heating). Samples can be introduced by flow injection (no chromatography) or following chromatographic separation.

Electrospray Ionization (ESI)

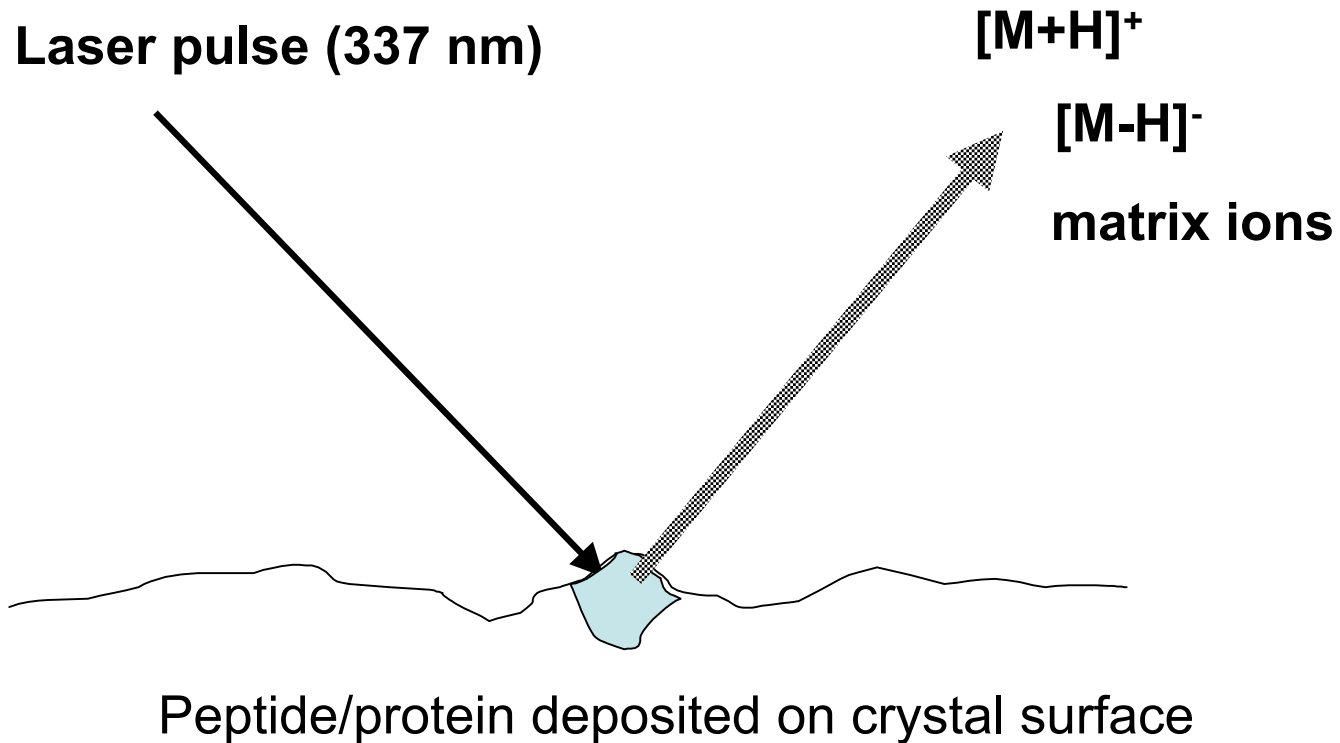


1. Solvent evaporation
2. Coulombic repulsion

NanoElectrospray



MALDI generation of ions



Sample mixed with a UV-absorbing matrix and is allowed to co-crystallize on the metal target.

Matrices for MALDI analysis

Peptides/proteins

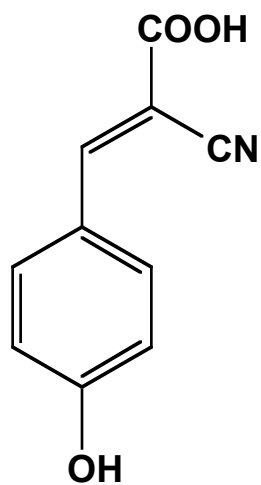
- 3,5-dimethoxy-4-hydroxycinnamic acid (sinapinic acid)
- α -cyano-4-hydroxycinnamic acid (CHCA)
- 2,5-dihydroxybenzoic acid (DHB)
- 2-(4-hydroxyphenylazo)-benzoic acid (HABA)

Oligonucleotides

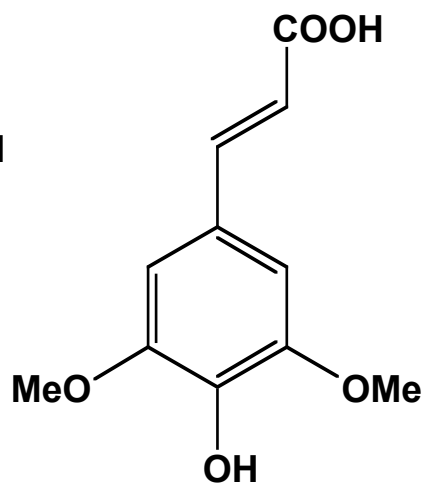
- 2-aminobenzoic acid
- 3-hydroxypicolinic acid (3-HPA)
- 2,4,6-trihydroxyacetophenone (THAP)

The choice of matrix depends greatly on the solute to be analyzed.

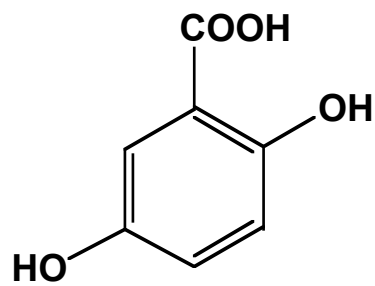
Matrices for MALDI analysis



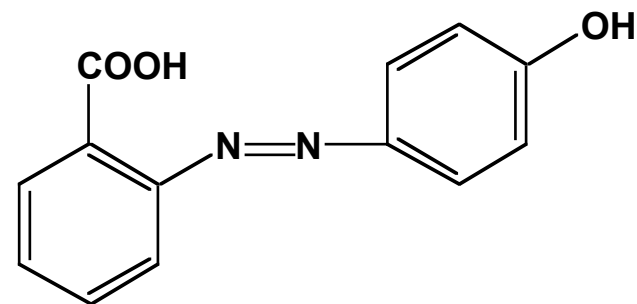
CHCA



Sinapinic acid

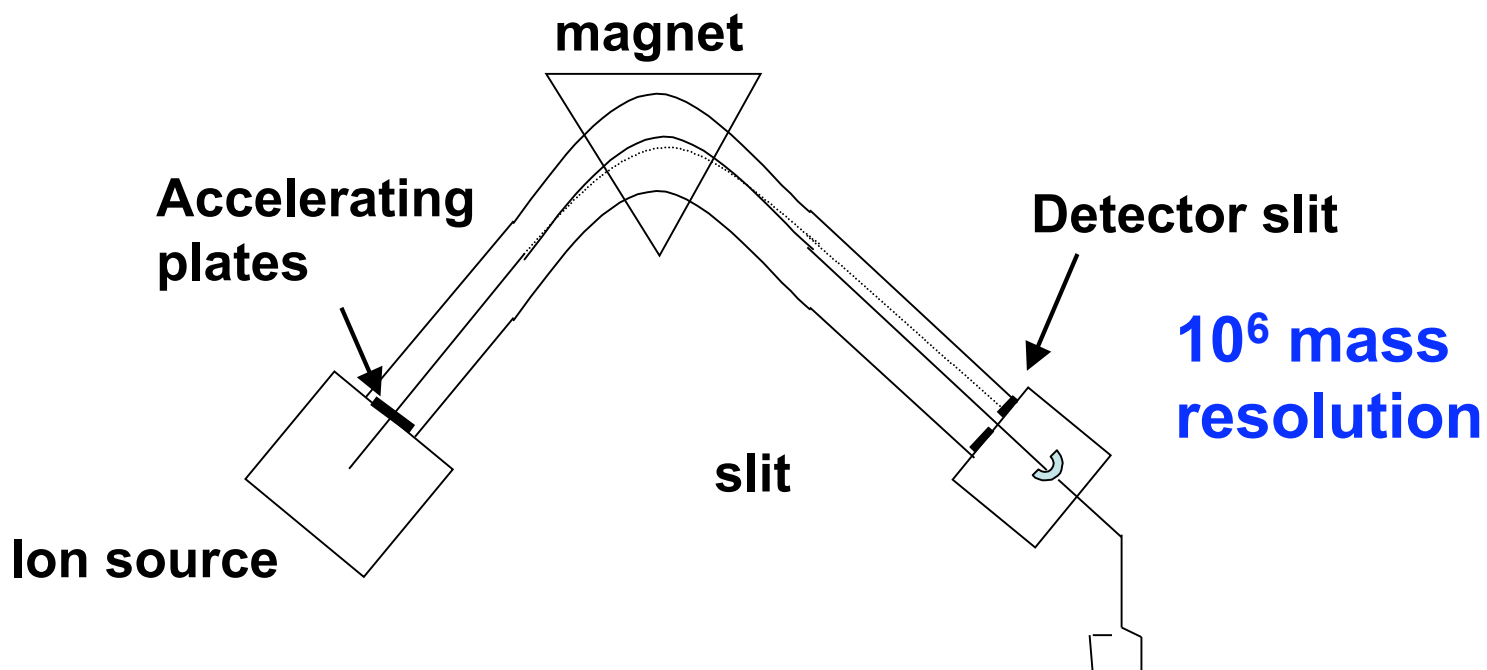


DHB



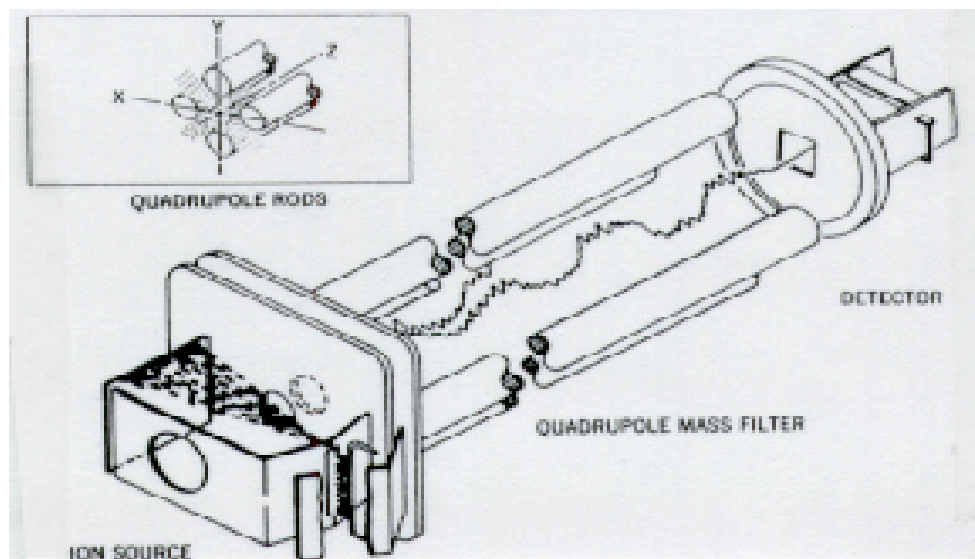
HABA

Magnetic sector analyzer



Generated ions are accelerated and are passed around a curved track (the sector) leading to a detector. By increasing the magnetic field applied to the ions, heavier ions with higher momentum can be induced to follow the curved track. A mass spectrum is obtained by applying a magnetic field gradient. Scanning is somewhat slower than in a quadrupole analyzer due to “magnetic reluctance”.

Quadrupole analyzer



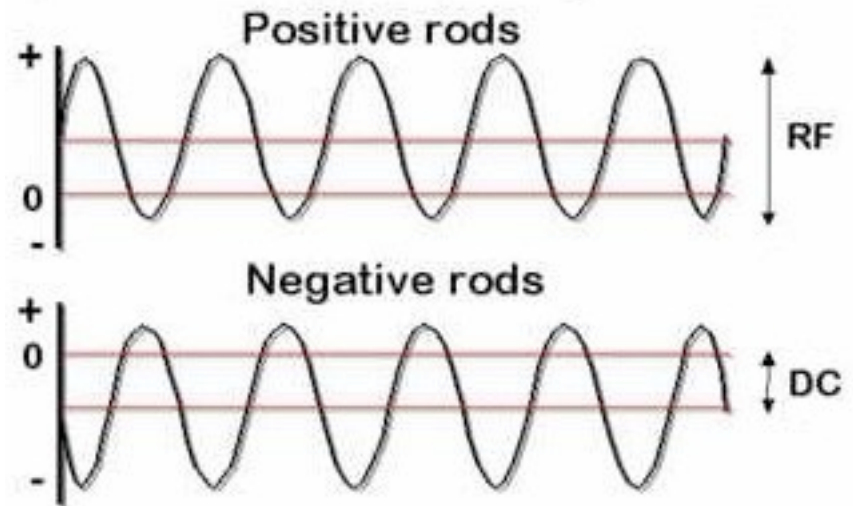
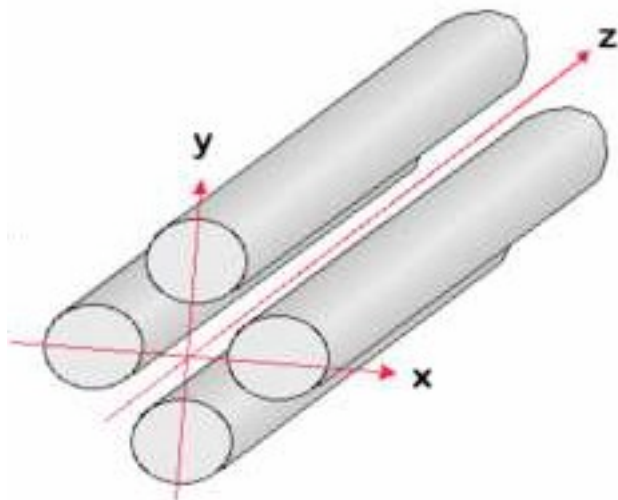
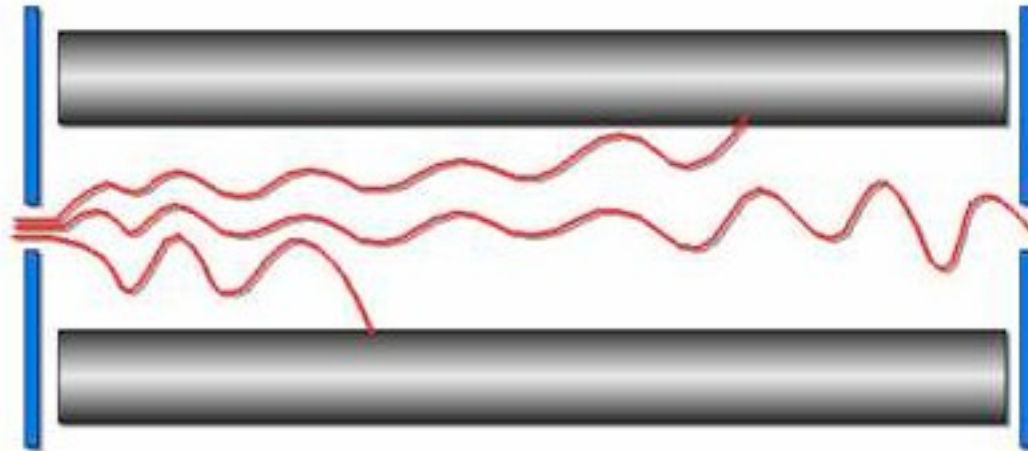
Mass resolution 2×10^3

Tolerant of relatively high pressure (10^{-4} torr)

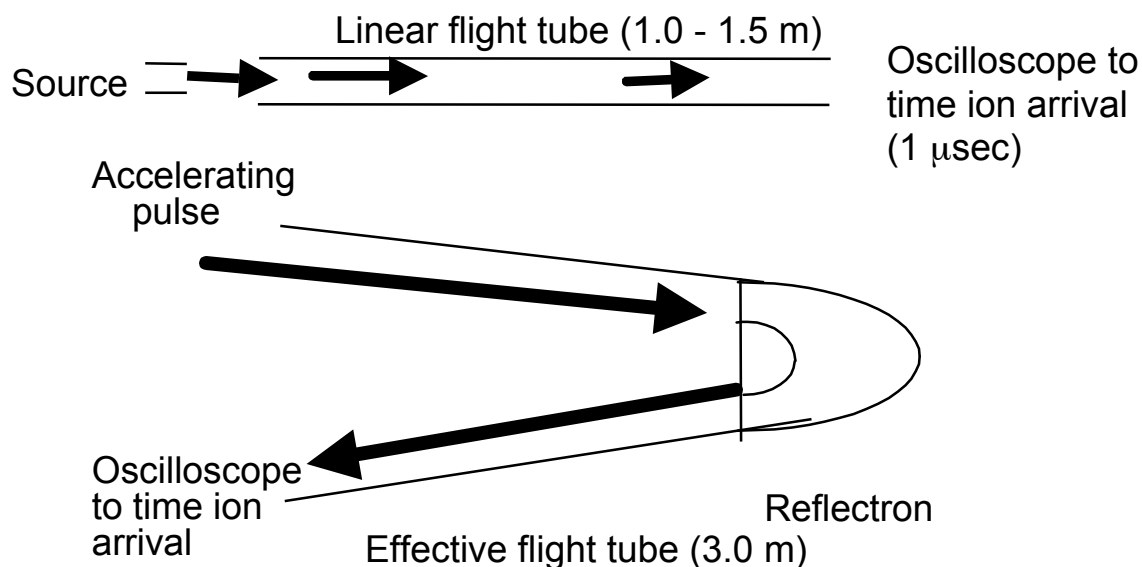
Upper limit for m/z is 3,000-4,000

Generated ions are accelerated electrically (5-15V) and passed along the long central axis of four rods arranged symmetrically. By applying combined DC and oscillating RF potentials, the ions drift along irregular flight paths along the rod axis. The DC/RF ratio is held constant and the absolute values of DC and RF are varied. Only ions with a particular m/z value have stable trajectories for a given value of DC and RF. If DC is set to 0, then all ions have stable trajectories. *A scan can be accomplished over a period of 10-1000 msec.*

Elements of a quadrupole analyzer



Time-of-flight (TOF) analyzer



Resolution 2×10^4

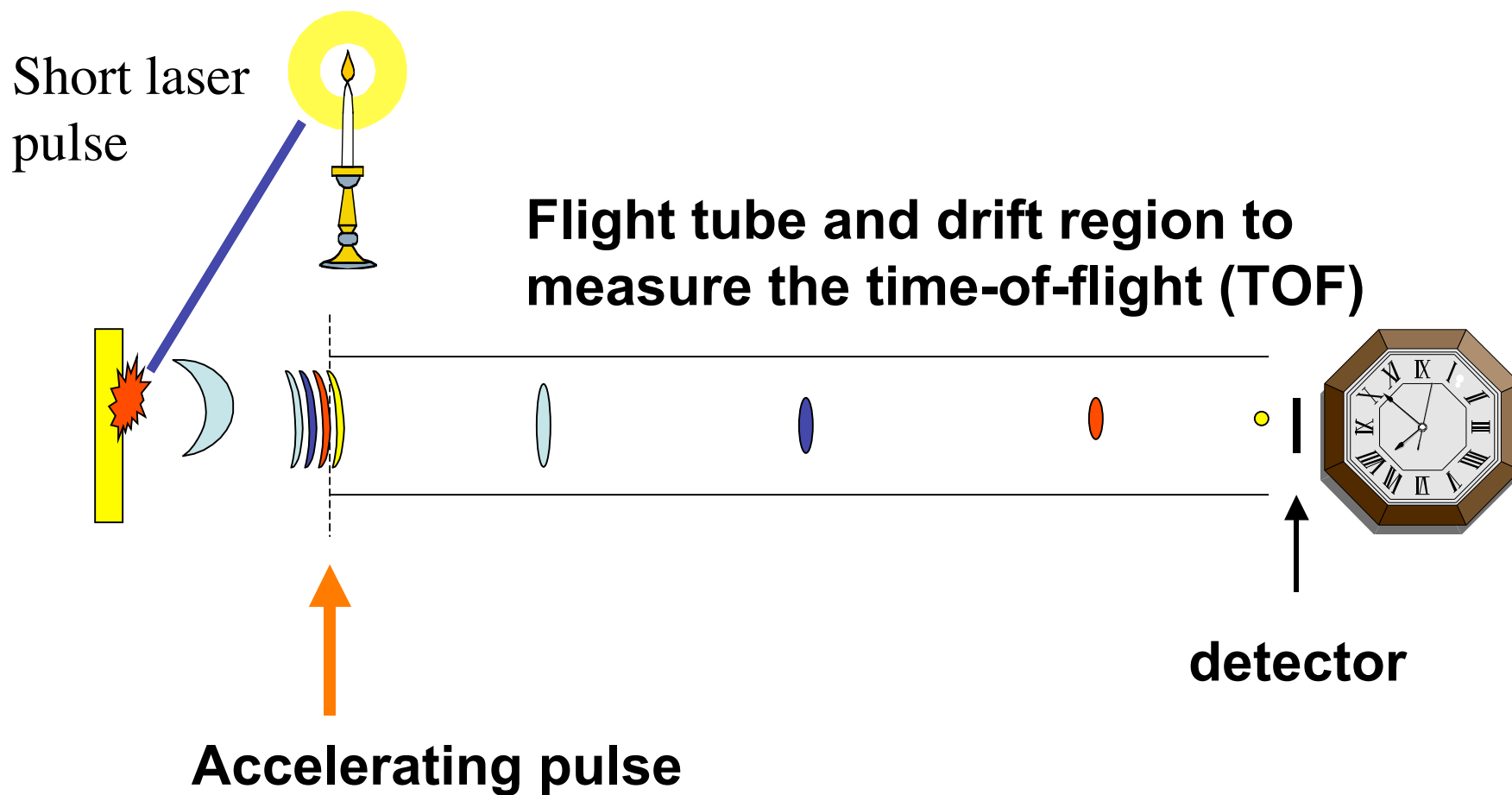
No upper limit of mass

Scan times $\sim 1 \mu\text{sec}$, good for LC-MSMS

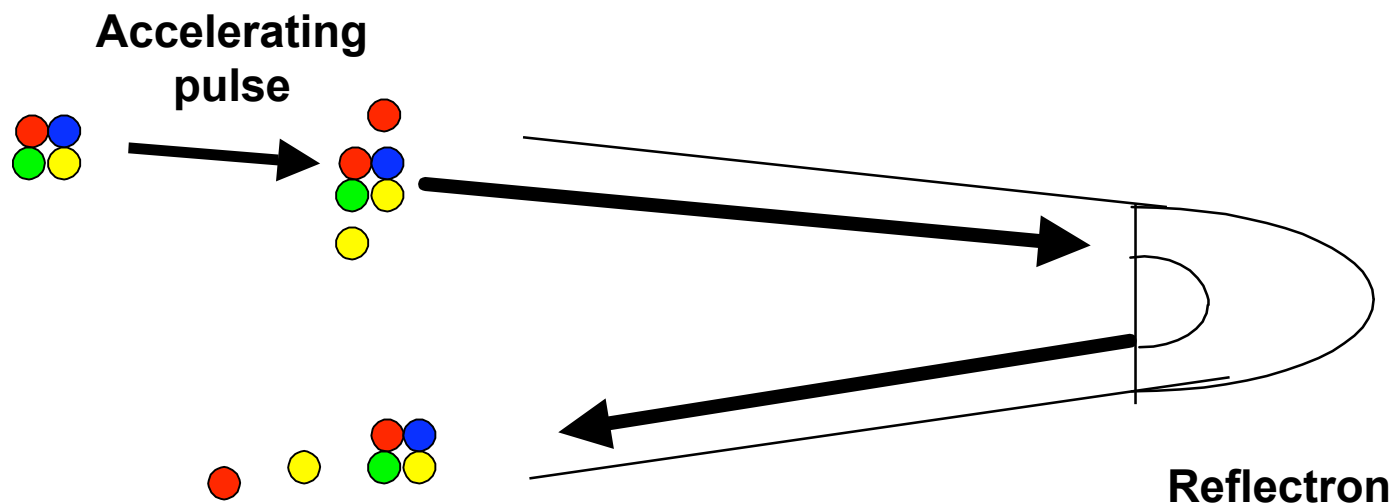
Generated ions are accelerated so that they have equal kinetic energy. They are allowed to “drift” down a 1 - 1.5 meter tube before striking a photomultiplier detector. The “time of flight” (t) depends on the mass of the ion (m), where $t = (m/2eV)^{1/2} \cdot D$

V is the applied potential and D is the flight tube distance. For a given instrument, the flight time varies as the square root of the mass of the ion.

Matrix-Assisted Laser Desorption Ionization (MALDI)



Post-source decay experiments in a TOF-mass spectrometer



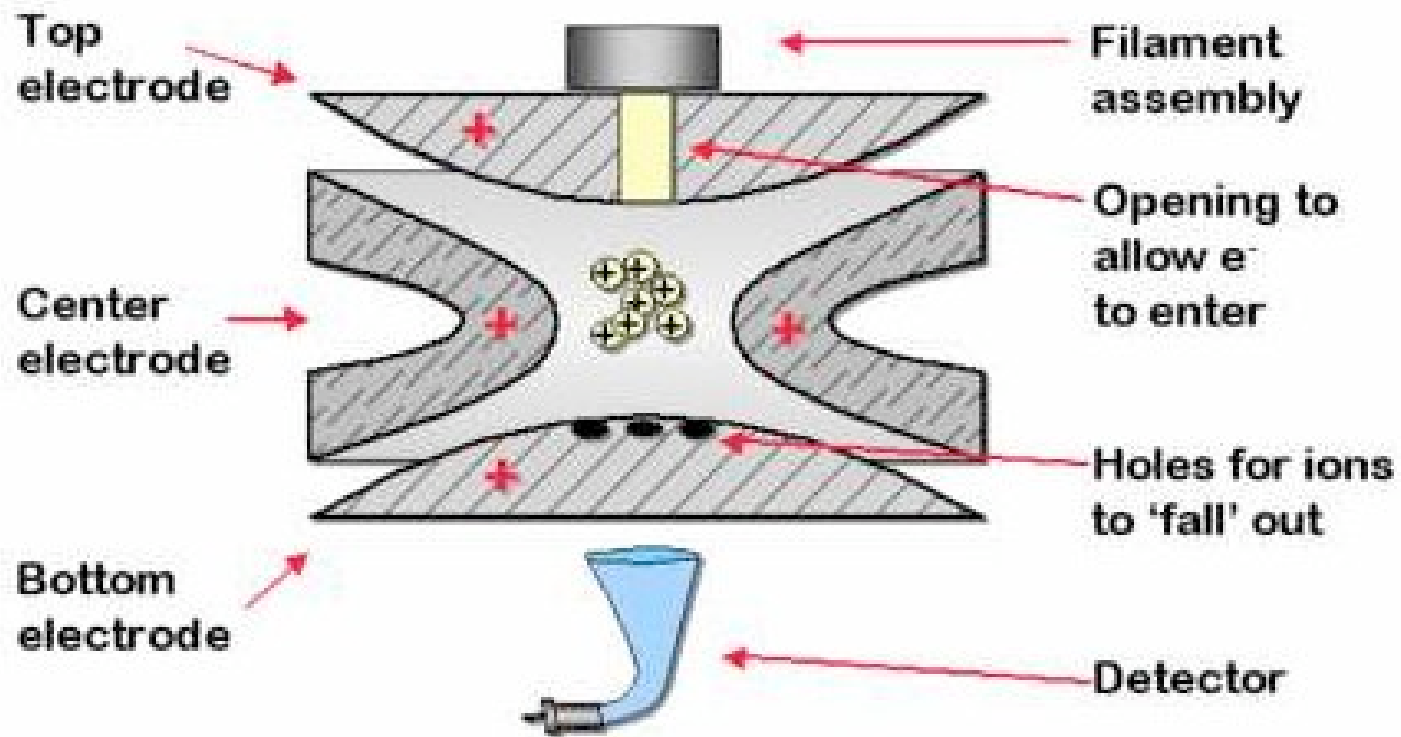
Daughter fragment ions formed in the drift region are separated by the reflectron. Suitable resolution only occurs over a limited range of m/z values. This can be overcome by recording individual spectra over a wide range of voltage settings (10-12) for the reflectron. Alternatively, a curved applied voltage can be used to obtain the daughter ion spectrum in a single experiment.

Ion Traps

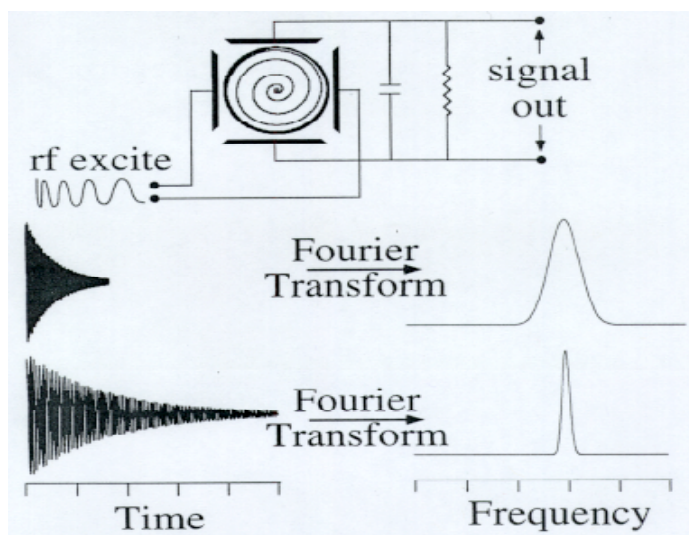


The ion trap is an energy well - ions with sufficient energy to enter the trap are retained by an energy barrier on the exit side of the trap. The advantage of the ion trap is that it accumulates selected ions prior to their analysis giving it high initial sensitivity (detection limit of approx. 20 fmol). Ions are fragmented by collision with helium gas and their daughter ions analyzed within the trap. Selected daughter ions can undergo further fragmentation, thus allowing MS^n . This is important for structural experiments such as in peptide sequencing. The ion trap has a high efficiency of transfer of fragment ions to the next stage of fragmentation (unlike the triple quadrupole instrument).

Expanded view of ion trap



Ion trap and FT-ICR MS



By placing the ion trap within a superconducting magnet, the trapped ions undergo cyclotron gyration and are radially confined. The frequency of the cyclotron radiation is inversely proportional to the m/z ratio for an ion and directly proportional to the magnetic field. If an ion is excited at its natural cyclotron frequency, it moves to a higher energy level.

A range of rf components are used to excite a sample. The ions clouds then induce an image current at two or more detection electrodes. The resulting signal when subjected to FT analysis yields an extremely precise measure of ion cyclotron frequencies, and hence m/z values, and molecular weights. The sensitivity is substantially enhanced and a 1 to 10^6 mass resolution can be achieved using a 9.4 tesla magnet.

ThermoFinnigan LTQ-FT

Linear Ion Trap MS

- MS, MS/MS and MSⁿ Analysis
- AGC Control
- Secondary Electron Multiplier **Detector**

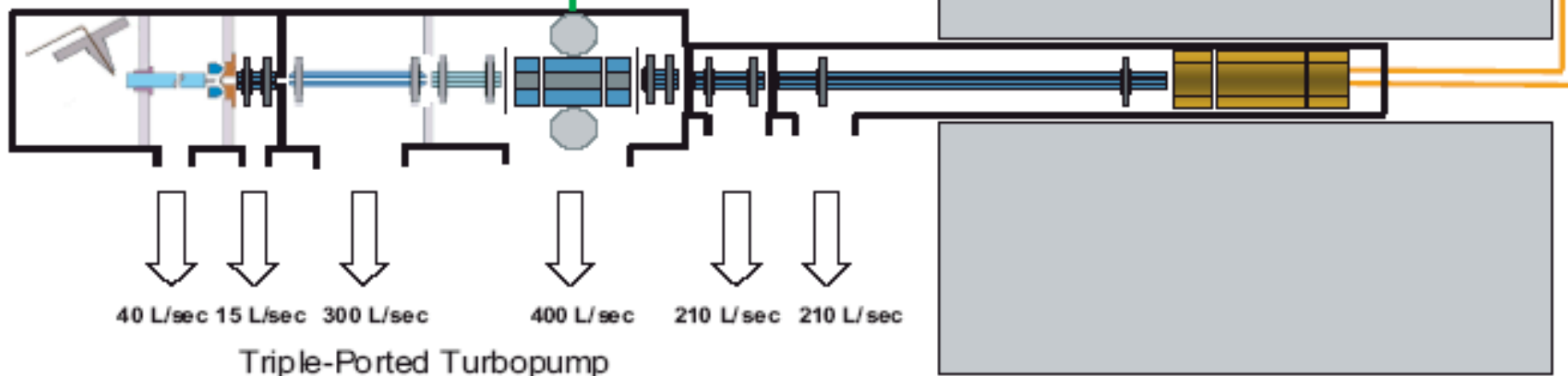
Linear Ion Trap Data

FTICR MS

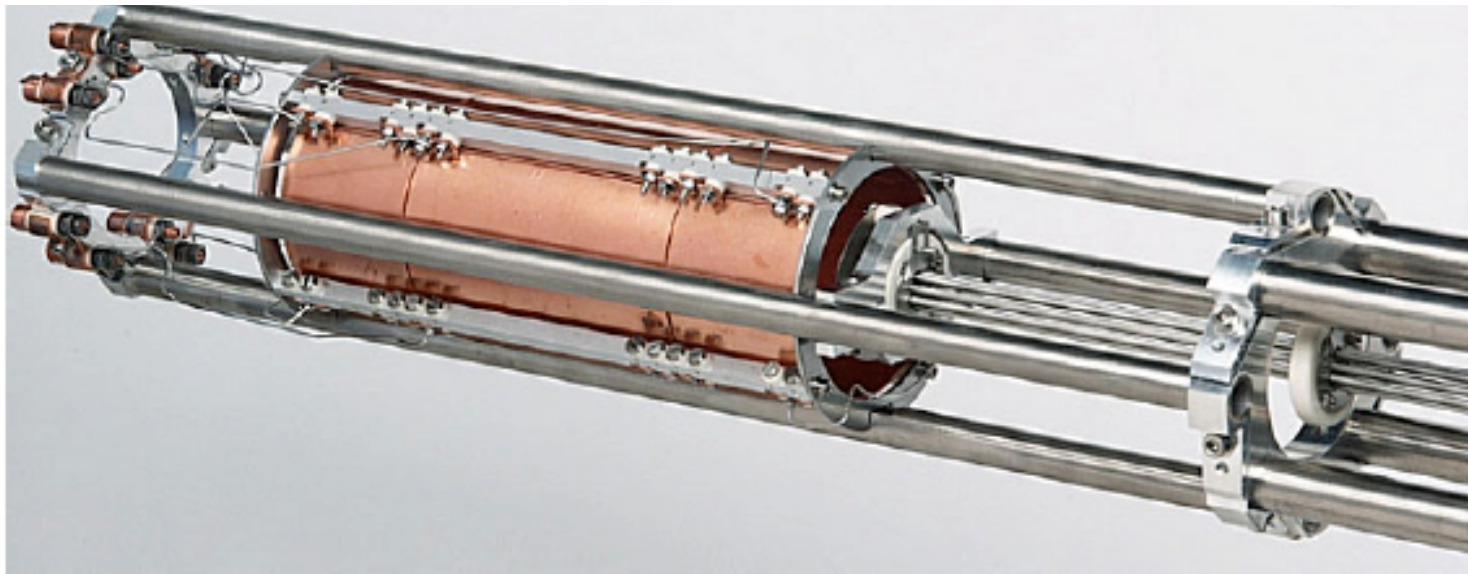
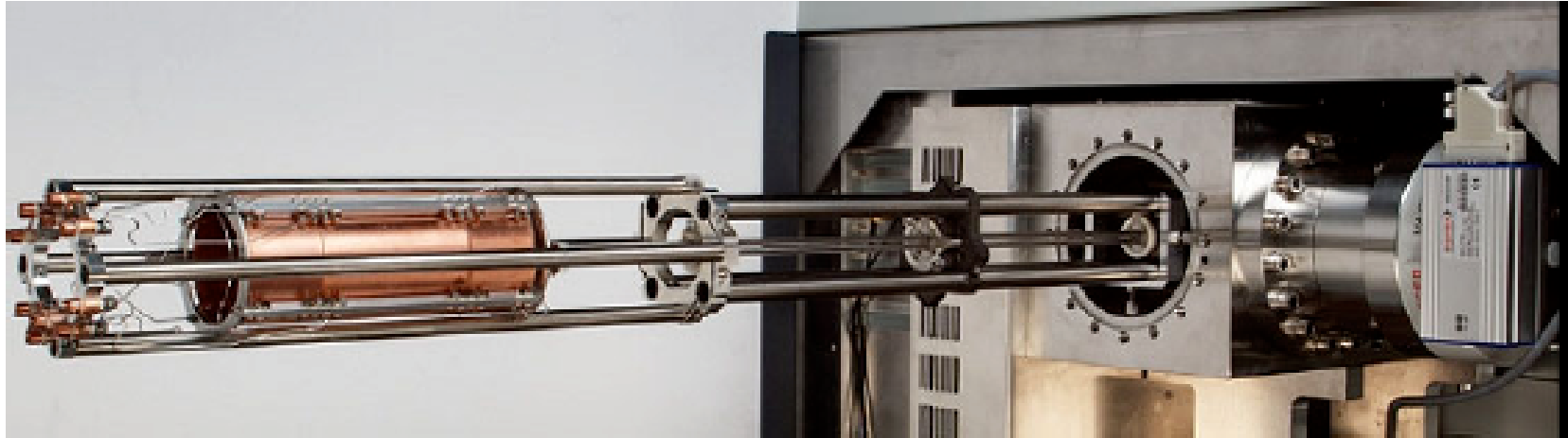
- Ion Image Current **Detector**
- Accurate Mass
- High Resolution

FTMS Data

7 T Actively Shielded
Superconductive Magnet



Penning Trap (ICR cell)



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Penning Trap (ICR cell)

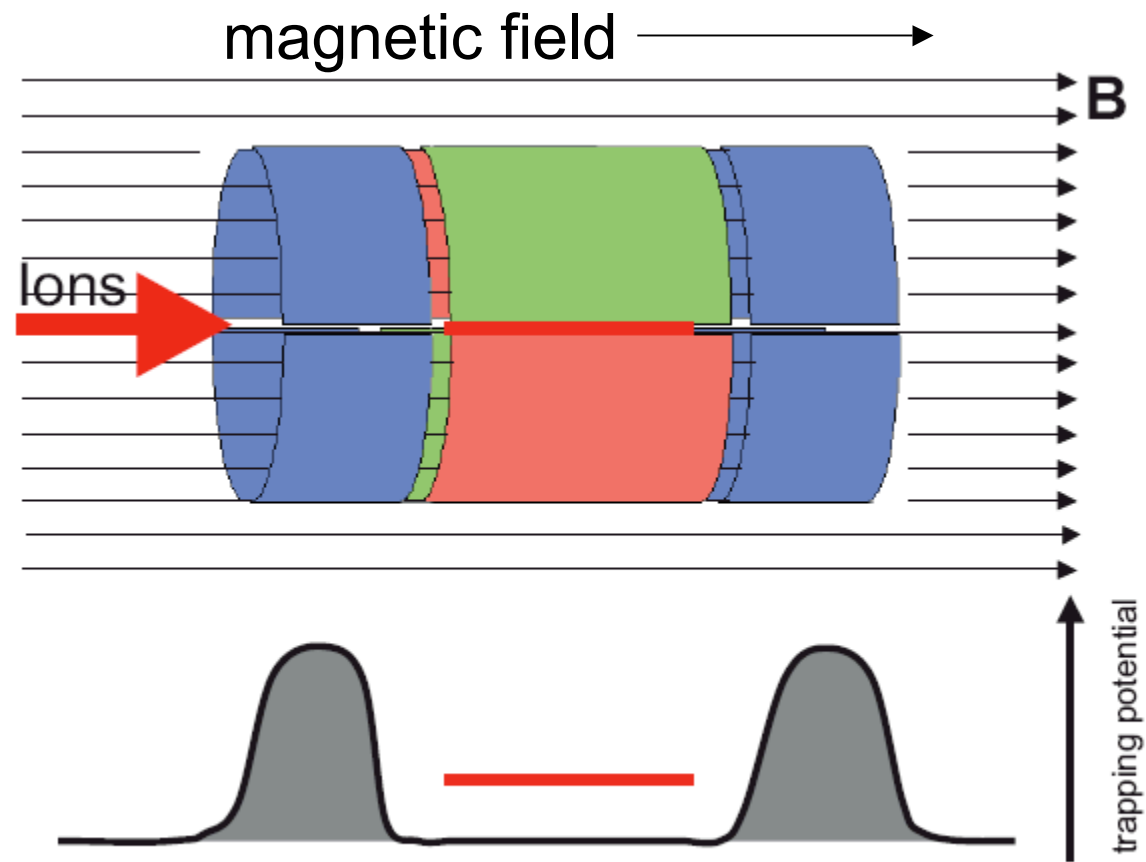
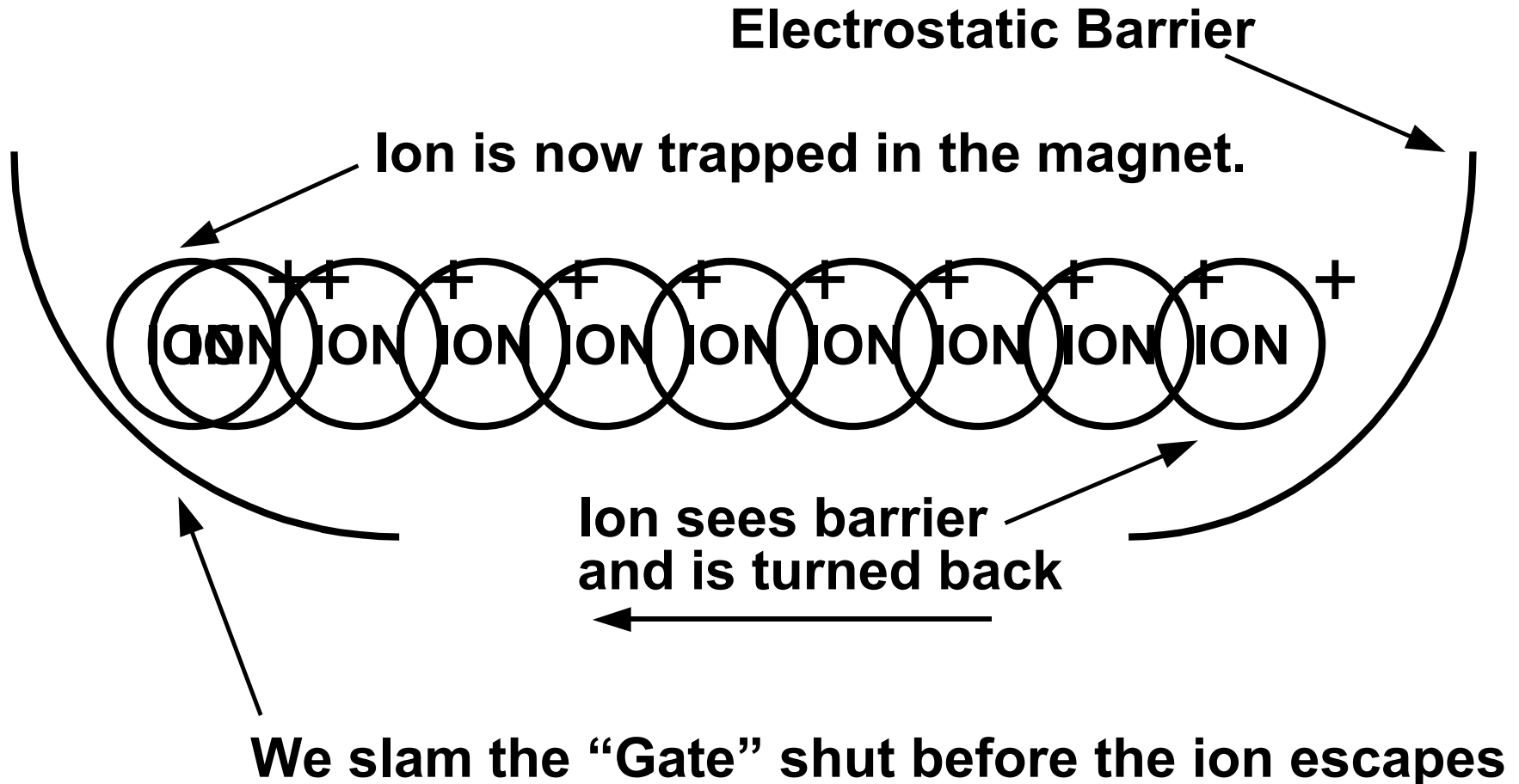


Figure 1-14. Operating principle of the Penning trap

Once we make an ion, we move **Moving and Trapping Ions**
it into the center of the Magnet.
Then, we trap it before it can escape.



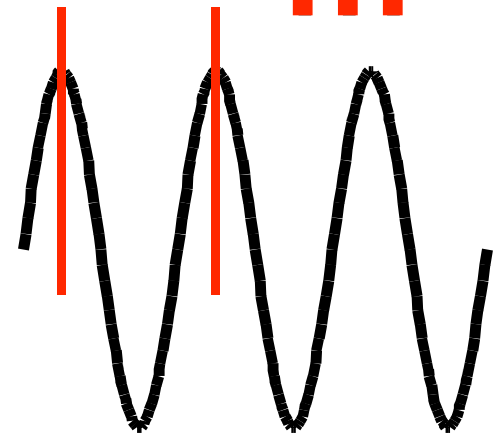
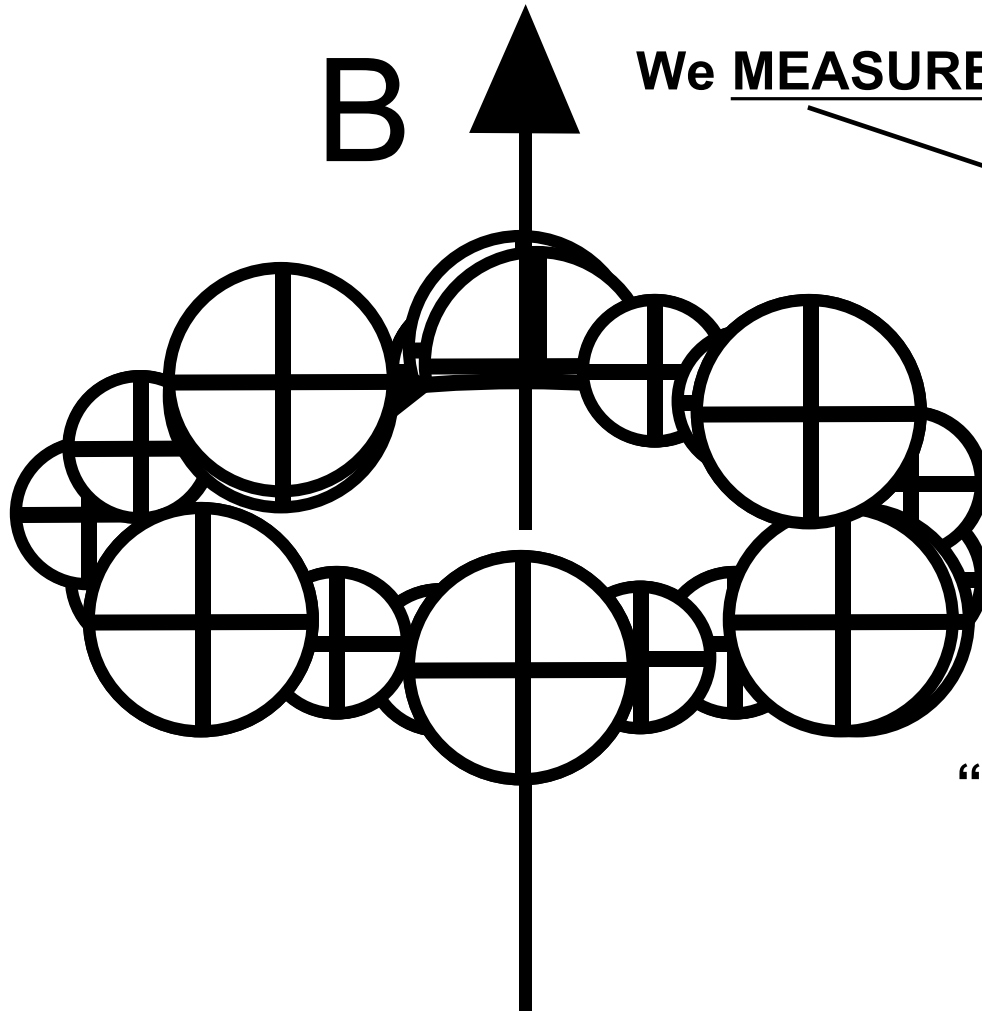
Once the ion is trapped, the magnet bends it into a circular path.

So we can calculate the **mass** of the ion

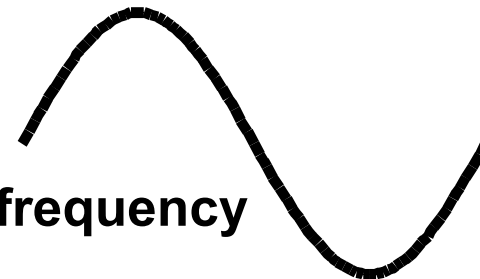
We know the Magnetic Field

We MEASURE the frequency

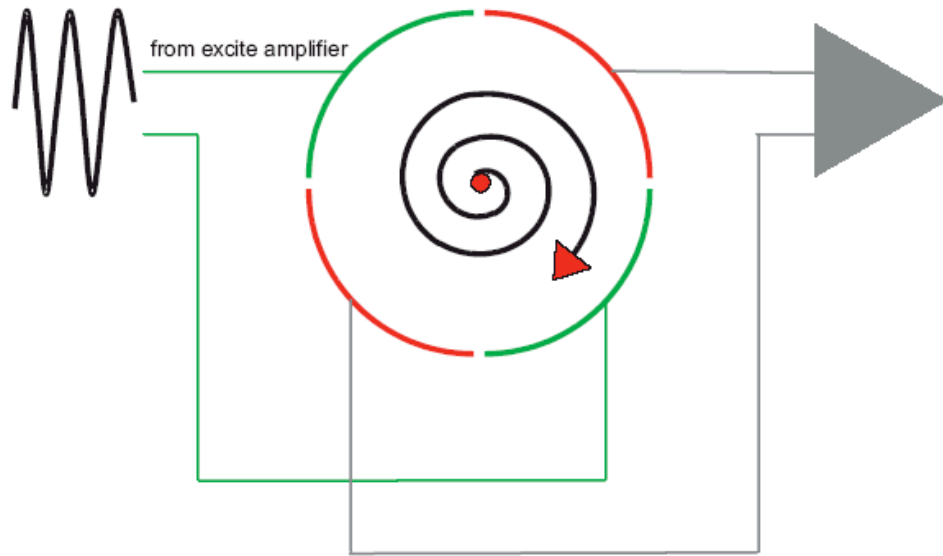
$$\omega = \frac{q B}{m}$$



“Light” ions have a High frequency



“Heavy” ions have a Low frequency



Two of the sides of the cylinder that make up the trap are **excitation plates**.

Figure 1-15. Excitation of the trapped ions

The other two sides of the cylinder **detection plates**.

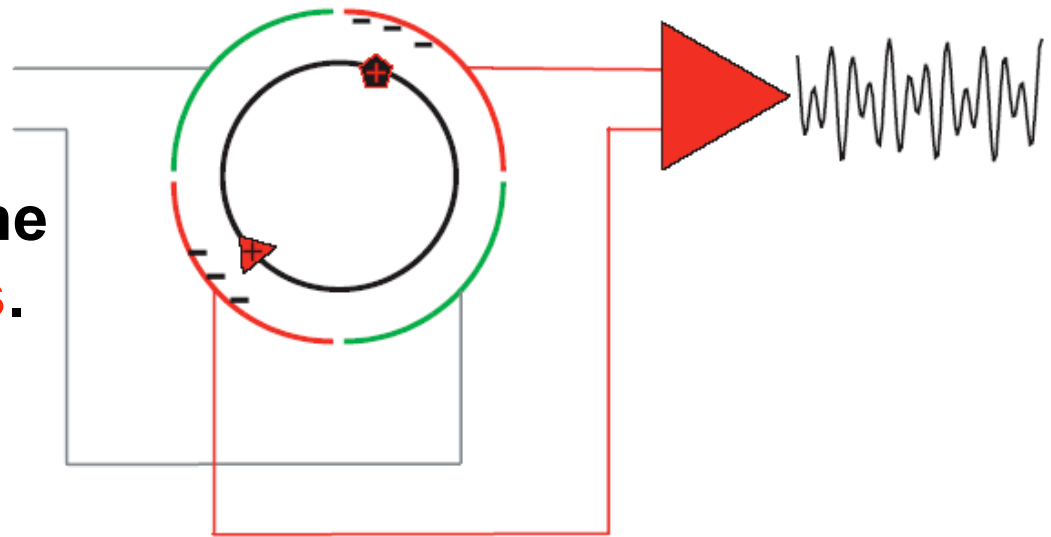


Figure 1-16. Recording the image current

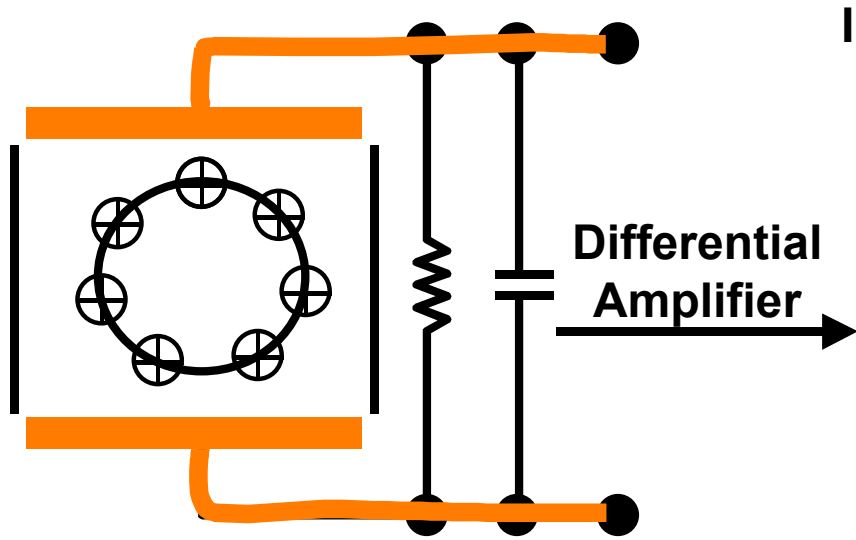
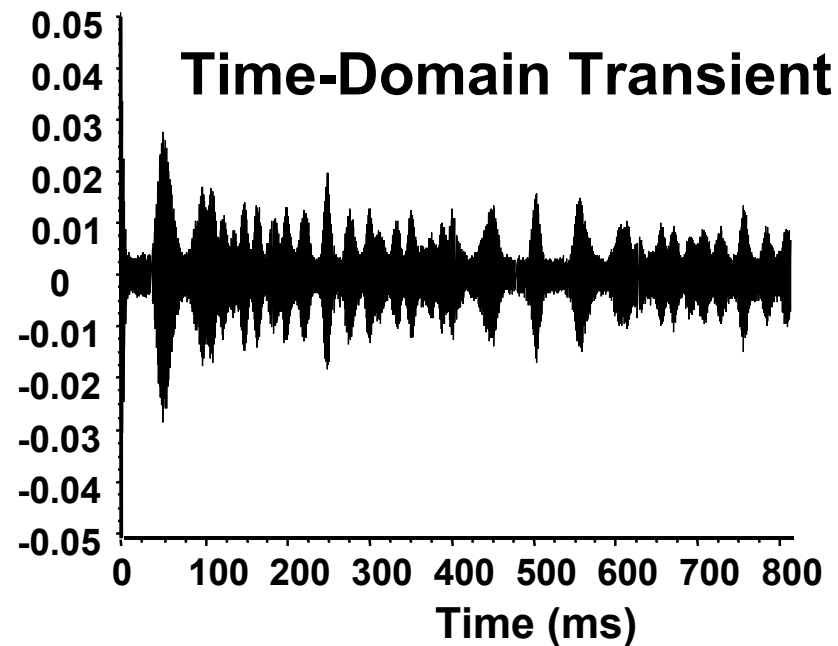


Image Current

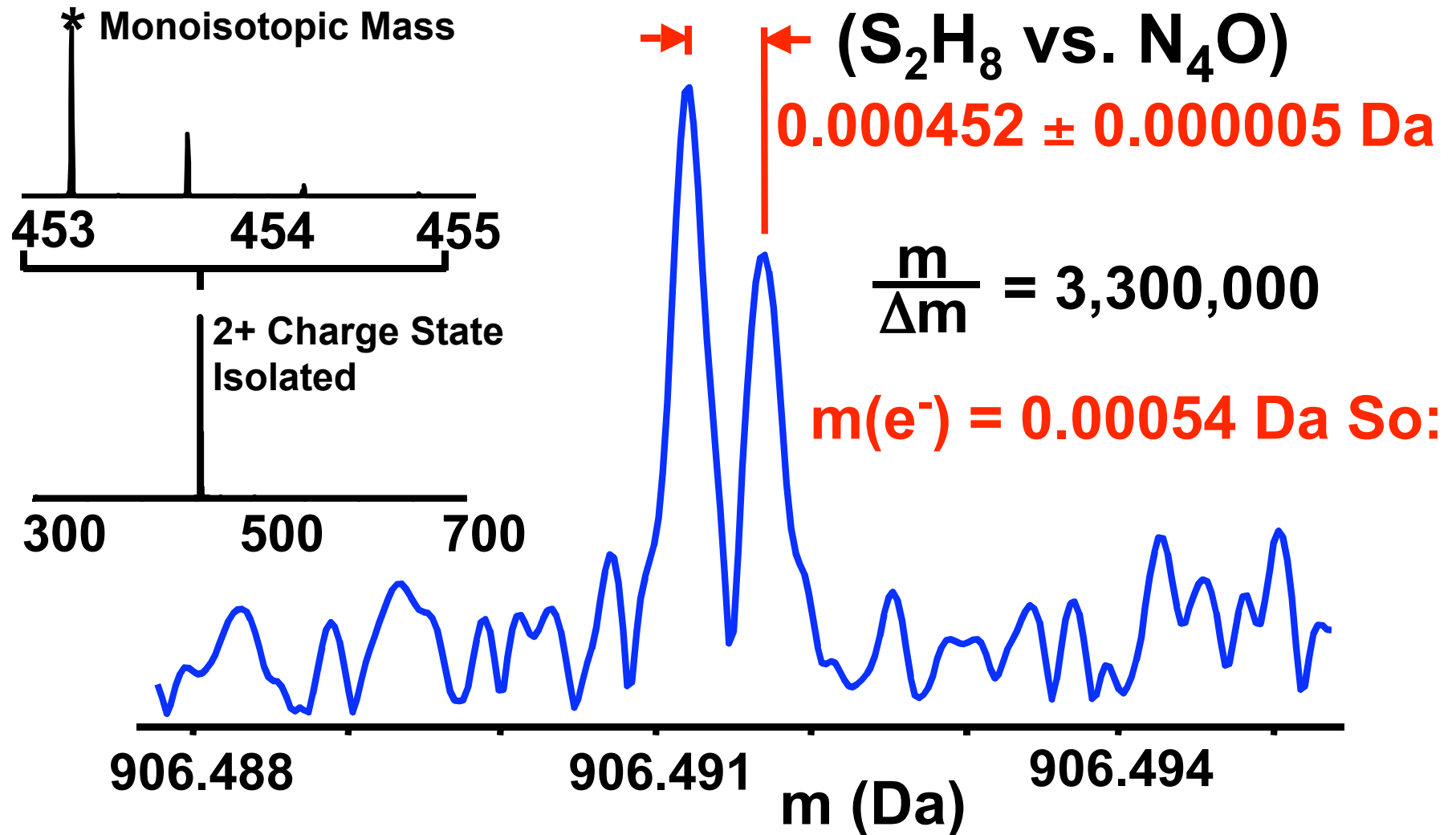


As the spiraling ion gets near a detect plate, it induces a current that is detected by the instrument.

The signal is recorded for a period of time and then displayed by the software

High Resolution by FT-ICR MS

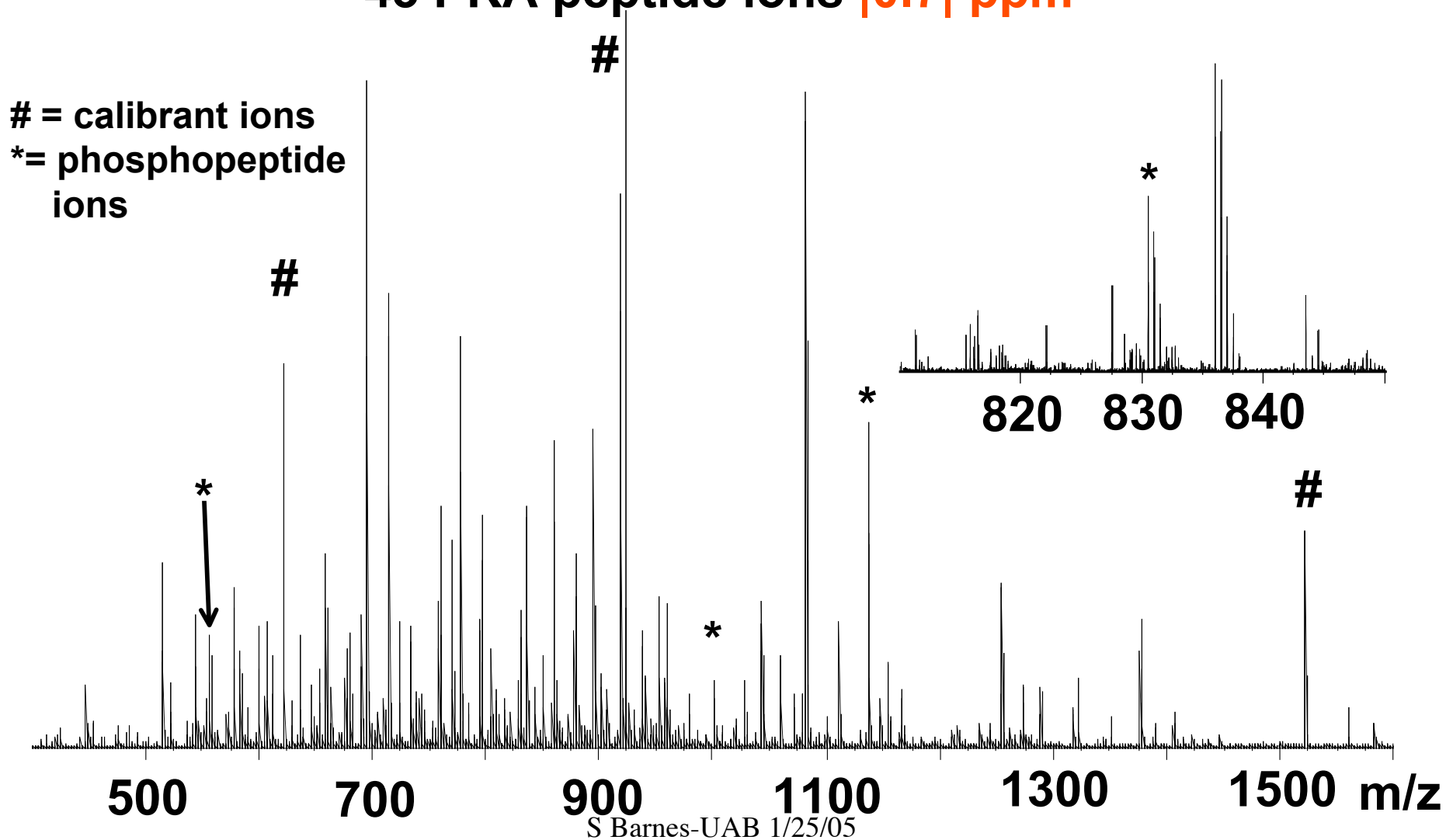
RVMRGMR vs. RSHRGHR (MW \approx 904 Da)



Protein kinase A

9.4 T Passively Shielded Magnet

43 PKA peptide ions |0.7| ppm



Advantages of High Field FTMS

Which FTMS Performance Factors Increase With Increasing Field?

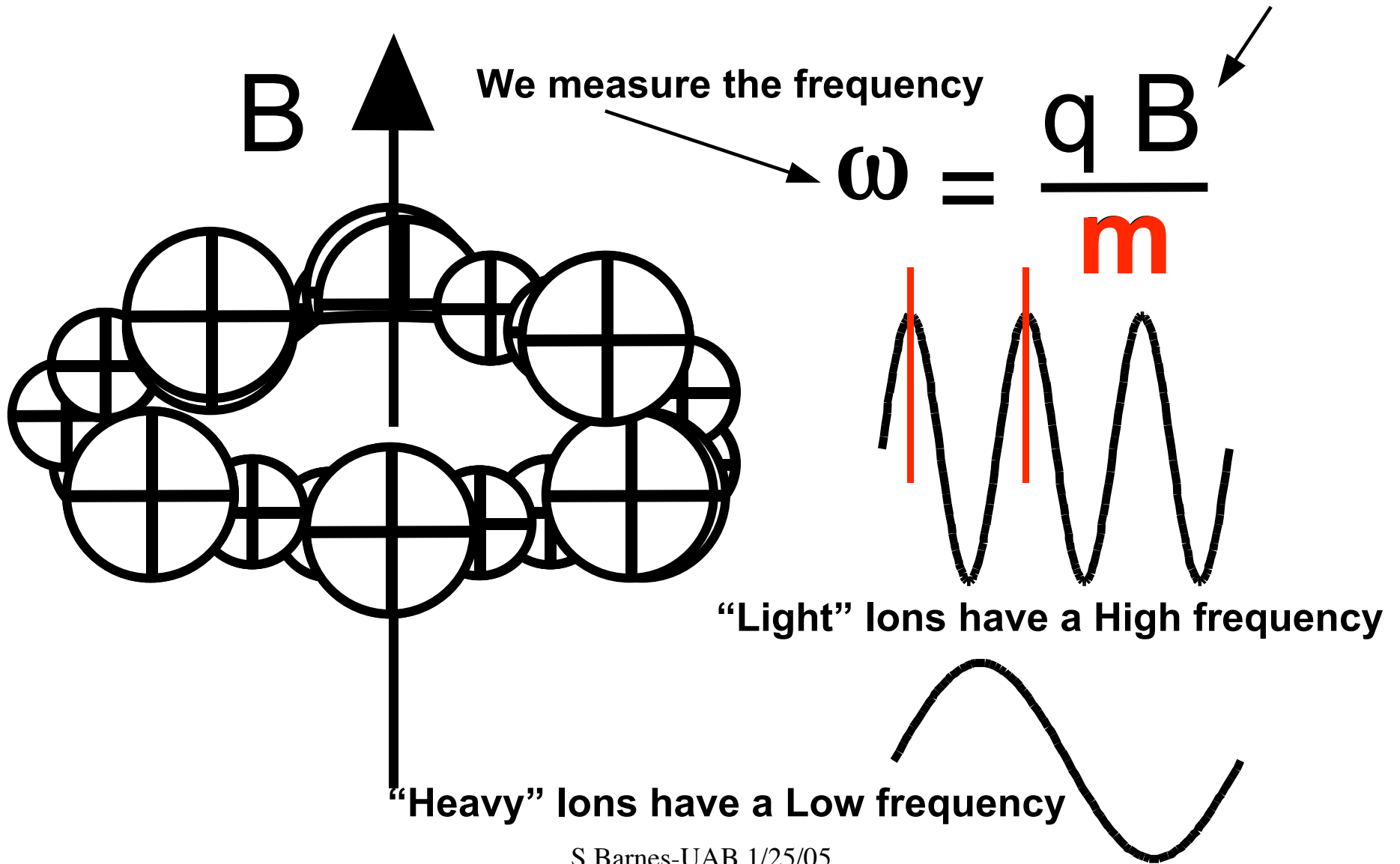
- Resolution (B)
- Acquisition Speed (1/B)
- Maximum Ion Kinetic Energy (B^2)
- Radius for a given kinetic energy ($1/B^2$)
- Upper mass limit (B^2)
- Maximum ion trapping duration (B^2)
- Maximum number of trapped ions (B^2)
- Quadrupolar axialization efficiency (B^2)
- Peak Coalescence (B^2)

Comparison of mass spectrometers performances

Instrument	Mass resolution	Mass accuracy	Sensitivity
Quadrupole	1×10^3	0.1 Da*	0.5-1.0 pmol
DE-MALDI	2×10^4	20 ppm	1-10 fmol peptide 1-5 pmol protein
Ion trap	1×10^3	0.1 Da*	10-20 fmol
FT-ICR	1×10^6	<1 ppm	20 amole

***depends on the mass window being used**

The Lure of The Increased B



The Lure of The Increased B

While many performance factors increase with

B,

NEVER FORGET for FT-ICR MS

We **MEASURE** the frequency $\longrightarrow \omega = \frac{q B}{m}$

MEASURE = Making Ions

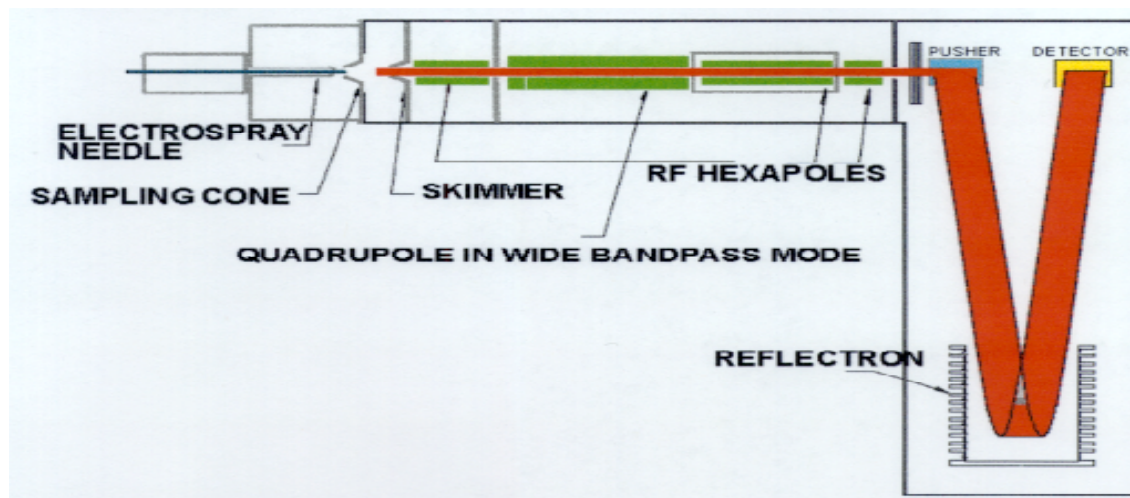
+ Moving Ions

+ Trapping Ions

+ Detecting Ions

B only affects Detecting Ions

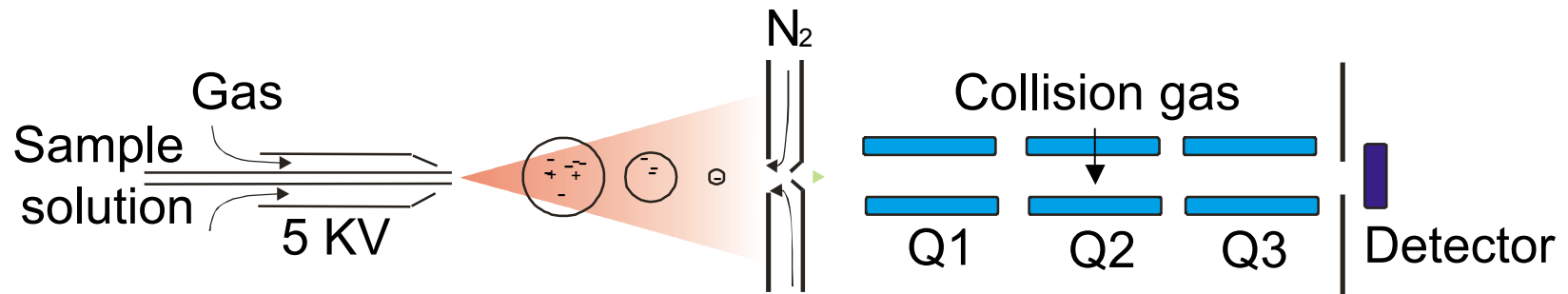
Another hybrid Instrument - Qtof (hybrid quadrupole-orthogonal time-of-flight)



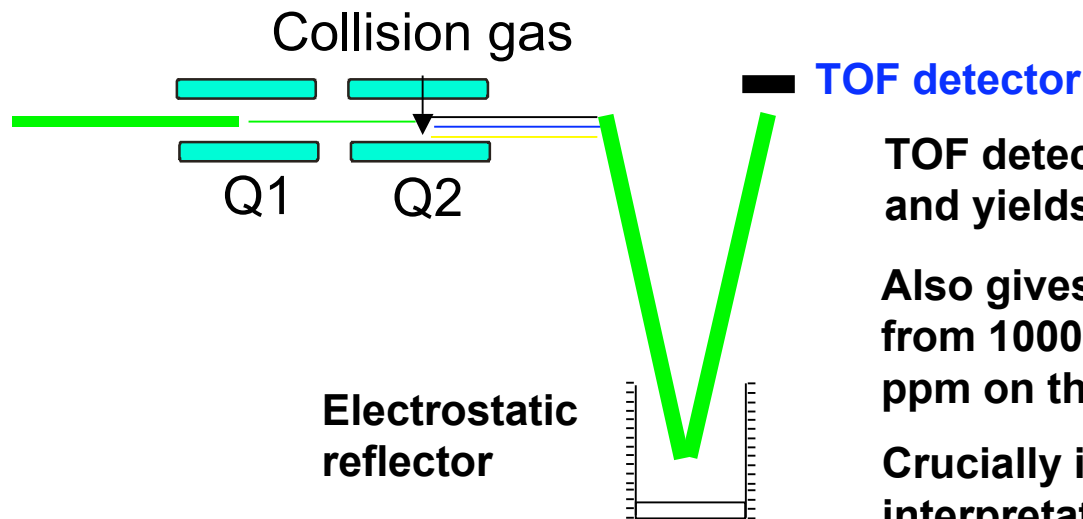
A limitation of the magnetic sector and quadrupole analyzers is that only one ion is measured at a time. Thus while analyzing ions over a mass range of m/z 1-1000 at unit mass resolution, **at any one m/z value all the ions at other ions are ignored.** This results in discarding 99.9% of the available information.

For the Qtof, the fragment ions are accelerated orthogonally and **all of them** are detected by the TOF analyzer.

Triple quad versus Q-tof and sensitivity



The quadrupole analyzer (Q3) is slow and insensitive - it's a filter - thus throws away large amounts of data



TOF detector collects all ions generated and yields fmol rather than pmol sensitivity

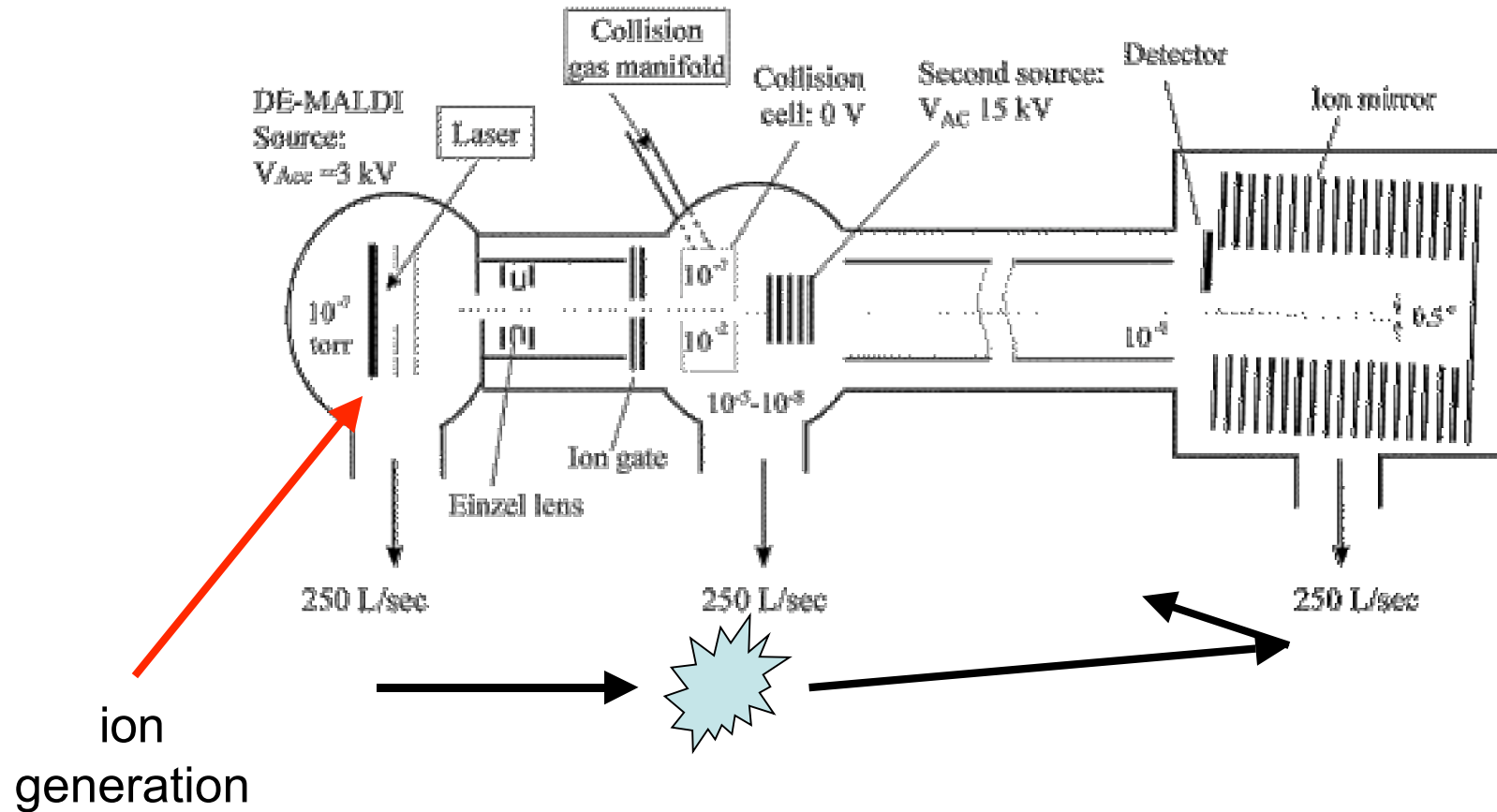
Also gives far greater mass accuracy - from 1000 ppm on the triple quad to <20 ppm on the Q-tof

Crucially important for automated interpretation of MS-MS spectra to yield amino acid sequence

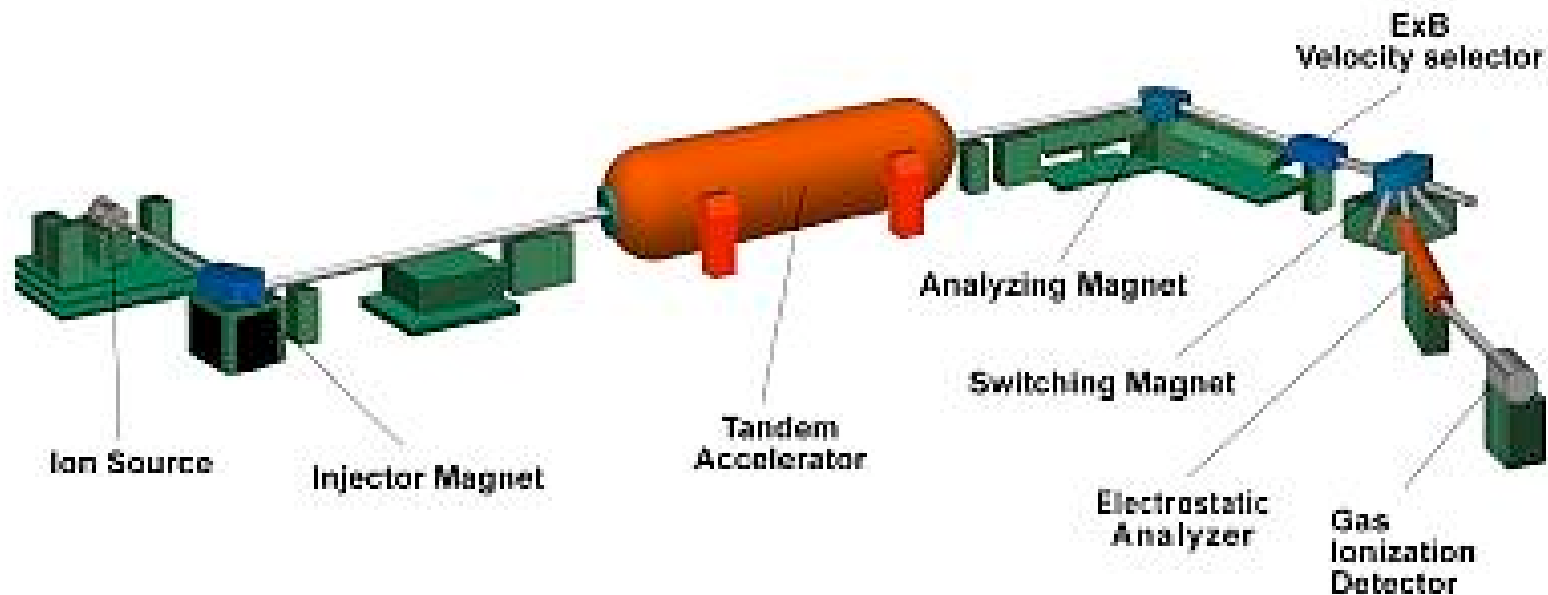
Other hybrid instruments

- **MALDI-FT-ICR**
 - Generates singly charged ions
- **MALDI-quadrupole trap**
 - High sensitivity and high throughput
- **MALDI-TOF-TOF**
 - 200-1000 Hz laser leads to highest rate of MS analysis (3,000-4,000 spectra/hr)
 - Also can record novel MS-MS spectra (500/hr)

TOF-TOF - high speed MSMS

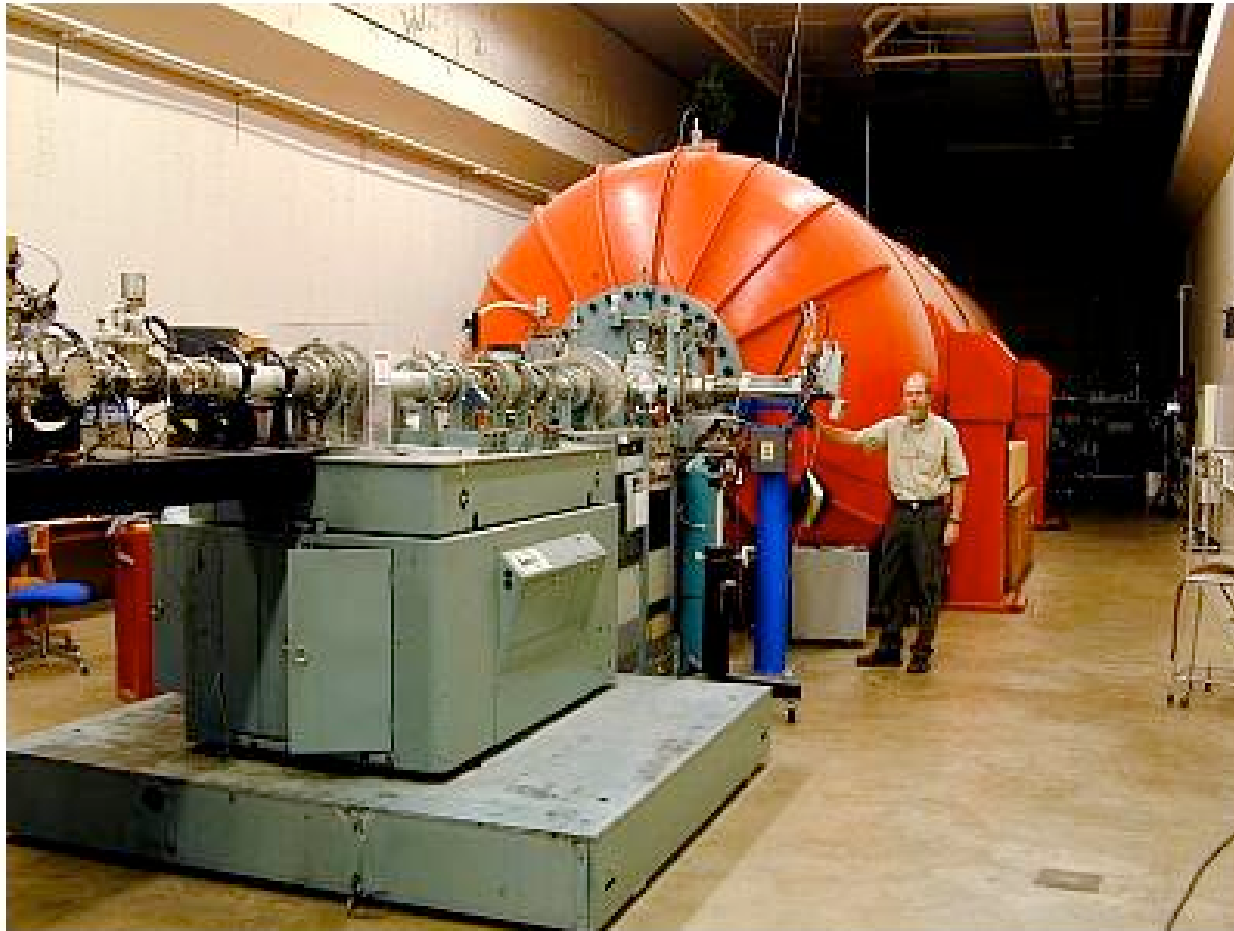


Purdue Rare Isotope Measurement Lab



Accelerator mass spectrometry for rare isotopes, ^{10}Be , ^{14}C , ^{26}Al , ^{36}Cl , ^{41}Ca , ^{129}I

Accelerator in PRIME Lab



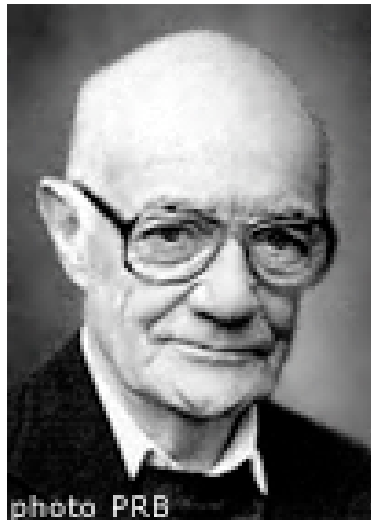
**Dr. David
Elmore next to
10 MV
accelerator**

Inside Accelerator in PRIME Lab



If an animal is given 50 nCi of a ^{14}C -labeled compound and 0.01% is absorbed and reaches the brain, then 20 mg of tissue is sufficient to provide enough signal to give a 1000:1 signal-to-noise ratio

Congratulations to the Nobel Laureates - 2002



John Fenn



Koichi Tanaka

"for the development of methods for identification and structure analyses of biological macromolecules"

and

"for their development of soft desorption ionisation methods for mass spectrometric analyses of biological macromolecules"