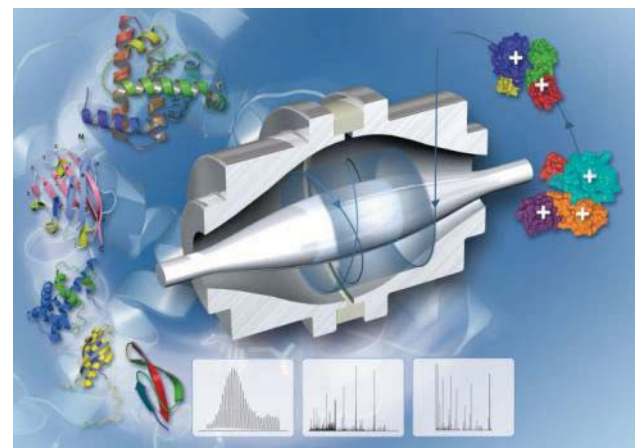


Orbitrap Mass Spectrometry: Ultra-high Resolution for Every Lab

Alexander Makarov

March 14, 2012



What is Orbitrap™ analyzer?

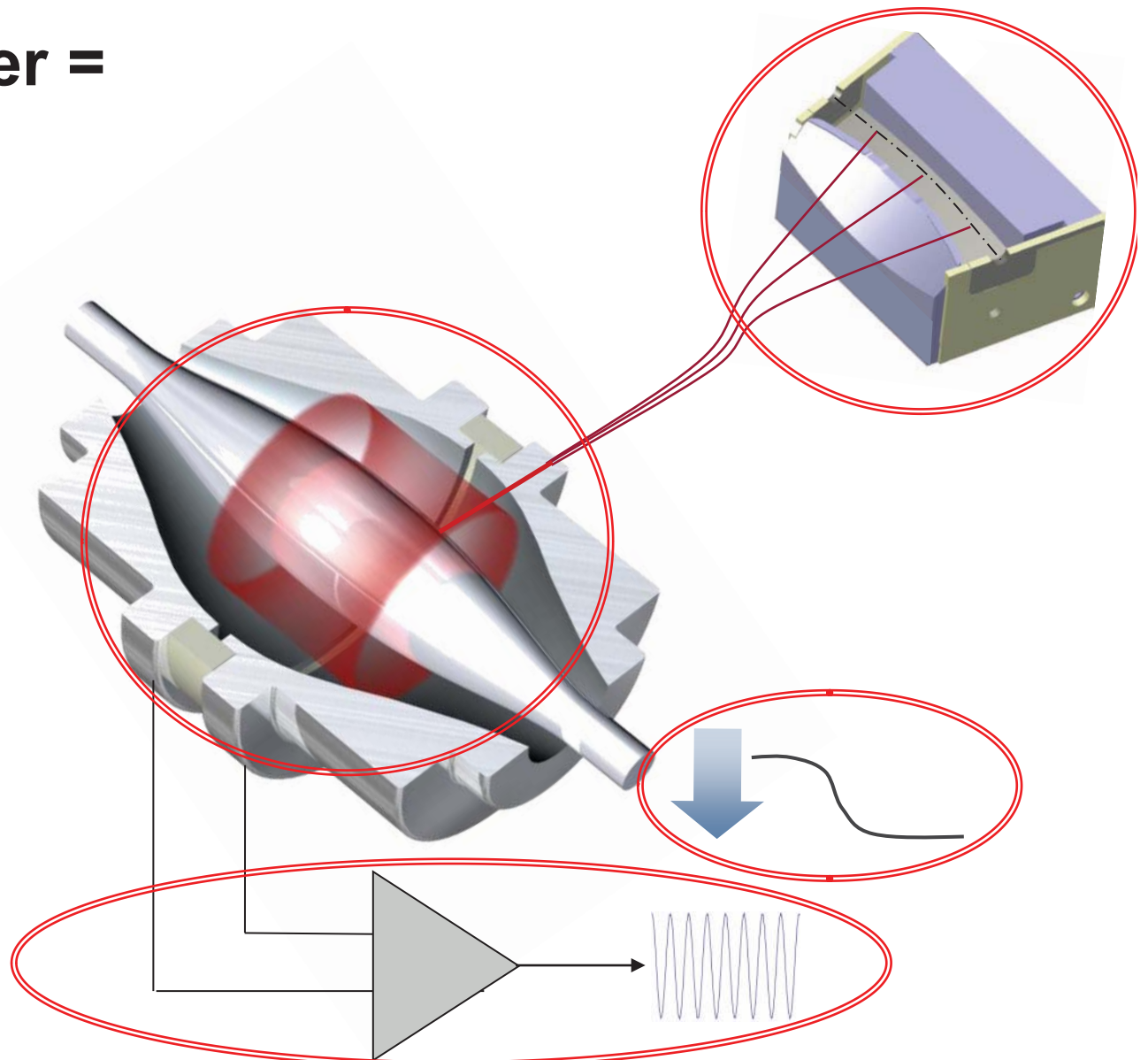
Orbitrap analyzer =

= Orbital trapping

+ Image current detection

+ Electrodynamics squeezing

+ External pulsed ion source

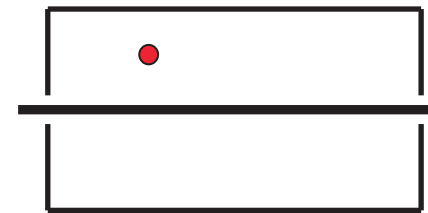


The unstable world of electrostatic trapping

Earnshaw's theorem (1842):

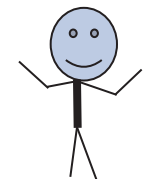
“A collection of point charges cannot be maintained in a stable stationary equilibrium configuration solely by electrostatic interaction of the charges”

...but
moving
charges
could be
stable!



Orbital traps
Kingdon (1923)

No promise?

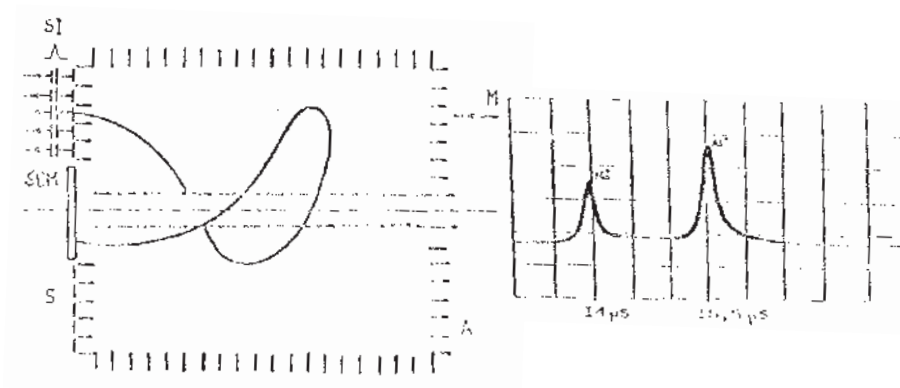


TOF Adventures: Prelude to the Orbitrap analyzer

$$U(r, z) = \frac{k}{2} \cdot \left\{ z^2 - r^2 / 2 + R_m^2 \cdot \ln(r / R_m) \right\}$$

Gall L.N., Golikov Y.K., Aleksandrov M.L.,
Pechalina Y.E., Holin N.A. *SU Pat. 1247973*, 1986.

1st implementation of quadro-
logarithmic potential in mass
spectrometry (1989)

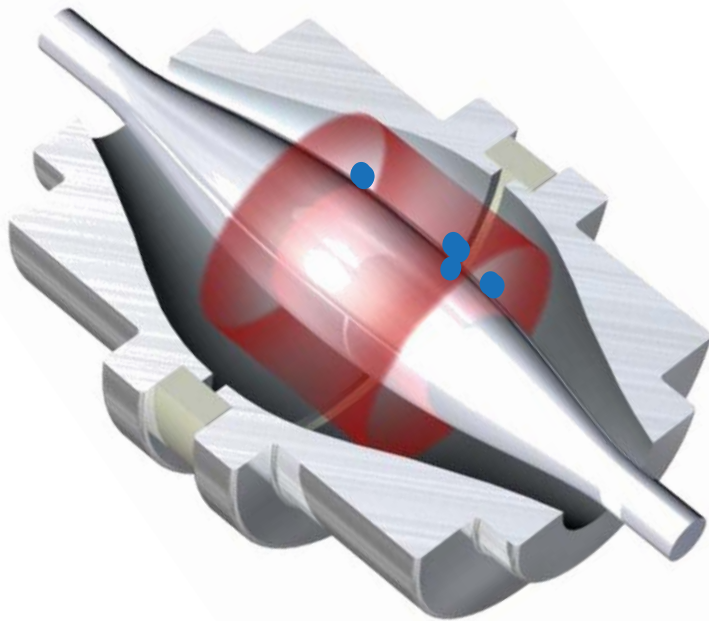


“A mosquito-
catcher”

Orbital trapping

“Ideal Kingdon trap”:
Quadro-logarithmic potential

$$U(r, z) = \frac{k}{2} \cdot \left\{ z^2 - r^2 / 2 + R_m^2 \cdot \ln(r / R_m) \right\}$$



Characteristic frequencies:

- Frequency of rotation ω_ϕ
- Frequency of radial oscillations ω_r
- Frequency of axial oscillations ω_z

$$\omega_\phi = \frac{\omega_z}{\sqrt{2}} \sqrt{\left(\frac{R_m}{R}\right)^2 - 1}$$

$$\omega_r = \omega_z \sqrt{\left(\frac{R_m}{R}\right)^2 - 2}$$

$$\omega_z = \sqrt{\frac{k}{m/q}}$$

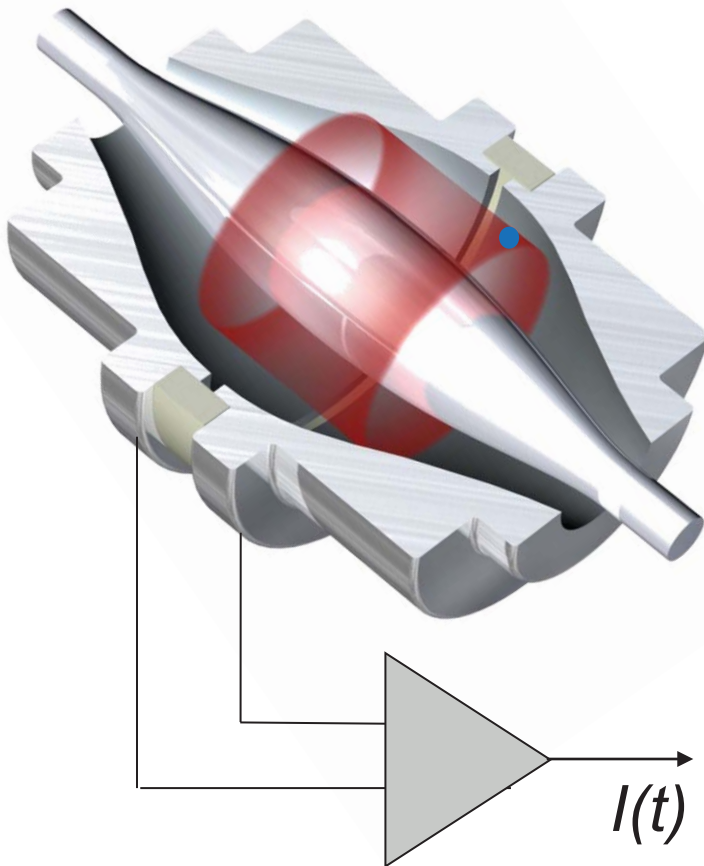
“Beauty will save the world.”- F.M. Dostoevsky

Only this frequency does not depend on energy, angle, etc. and is used for mass analysis

Detection of Ions in the Orbitrap analyzer

Image current detection

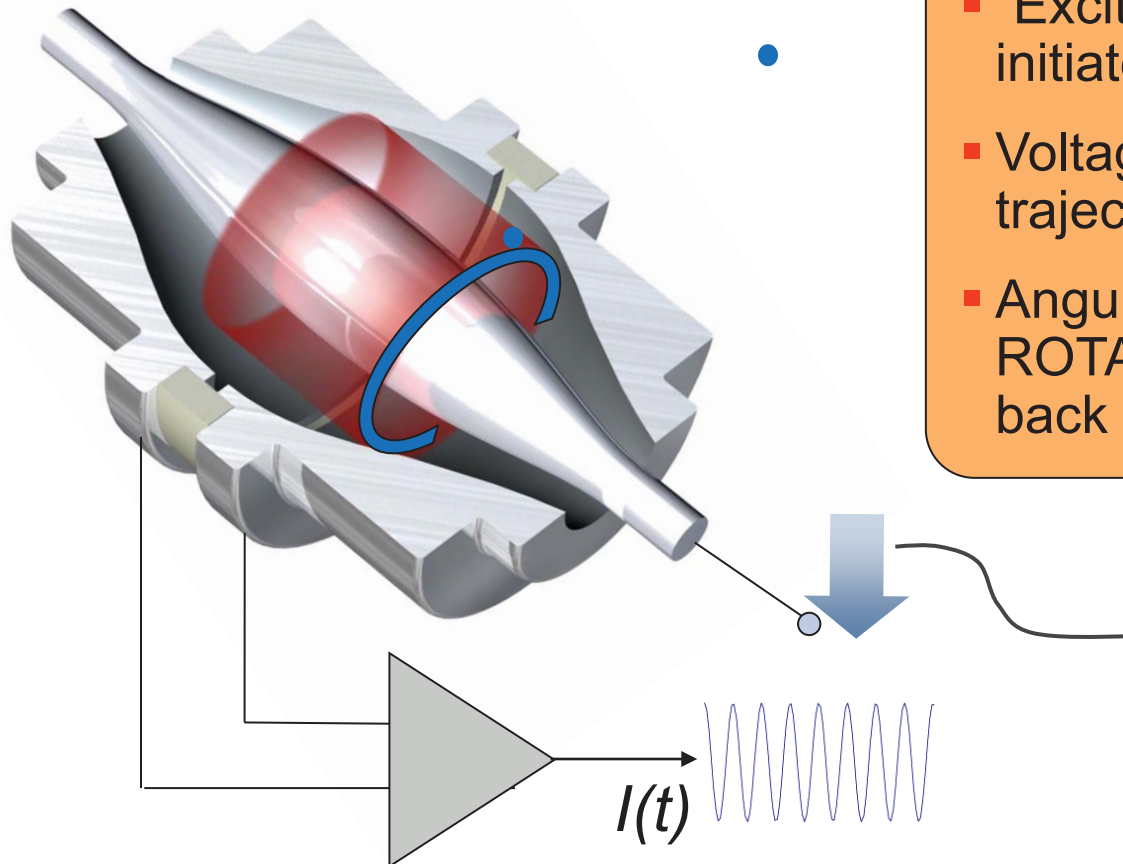
- All-mass detection
- Noise equivalent to $<10 \bar{e}/\sqrt{\text{Hz}}$



- Frequency of axial oscillations of each ring induces an image current on split outer electrodes
- Multiple ions in the Orbitrap generate a complex signal with frequencies determined using a Fourier Transformation

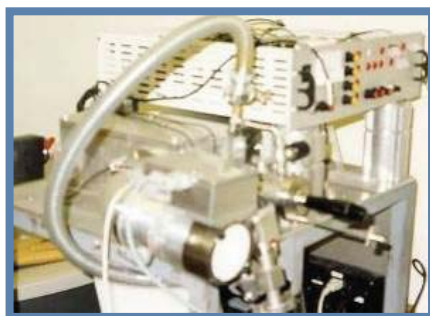
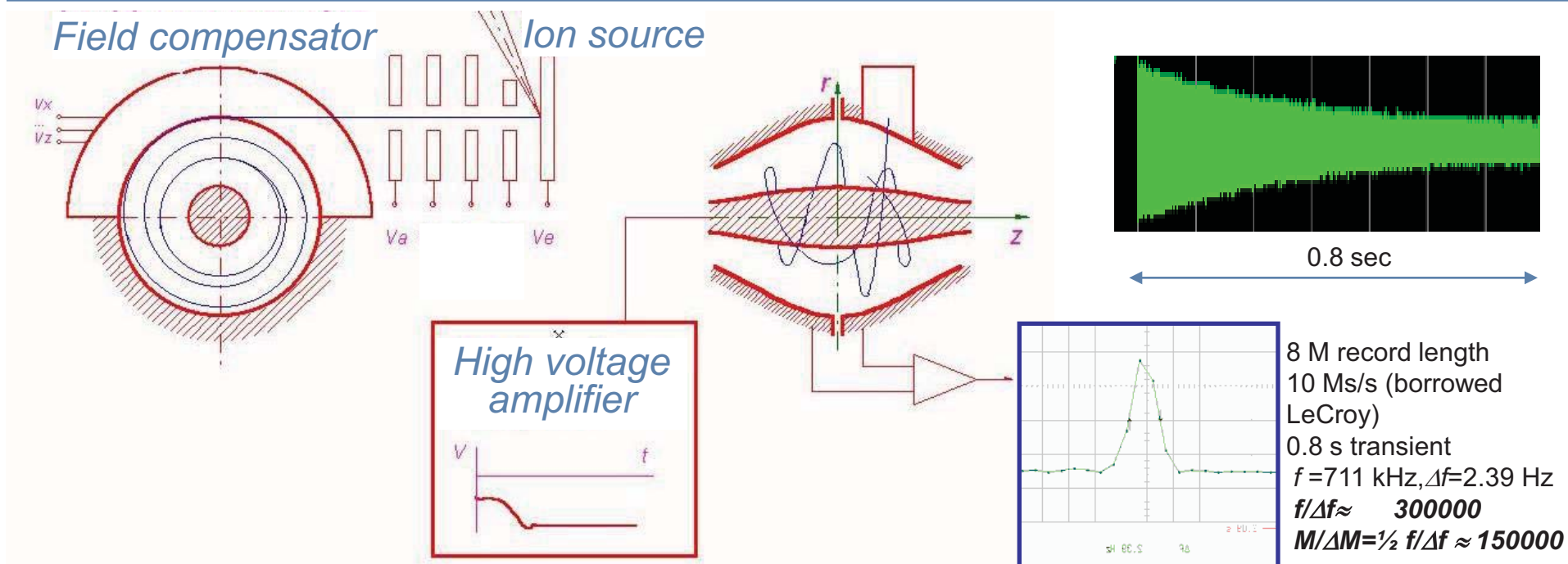


Injection of Ions into the Orbitrap analyzer



- A short ion packet of one m/z enters the field
- Increasing voltage squeezes ions
- “Excitation by injection” is initiated
- Voltage stabilises and ion trajectories are also stabilized
- Angular spreading forms ROTATING RINGS bouncing back and forth

Proof of Principle: Orbitrap MS with Laser Ion Source



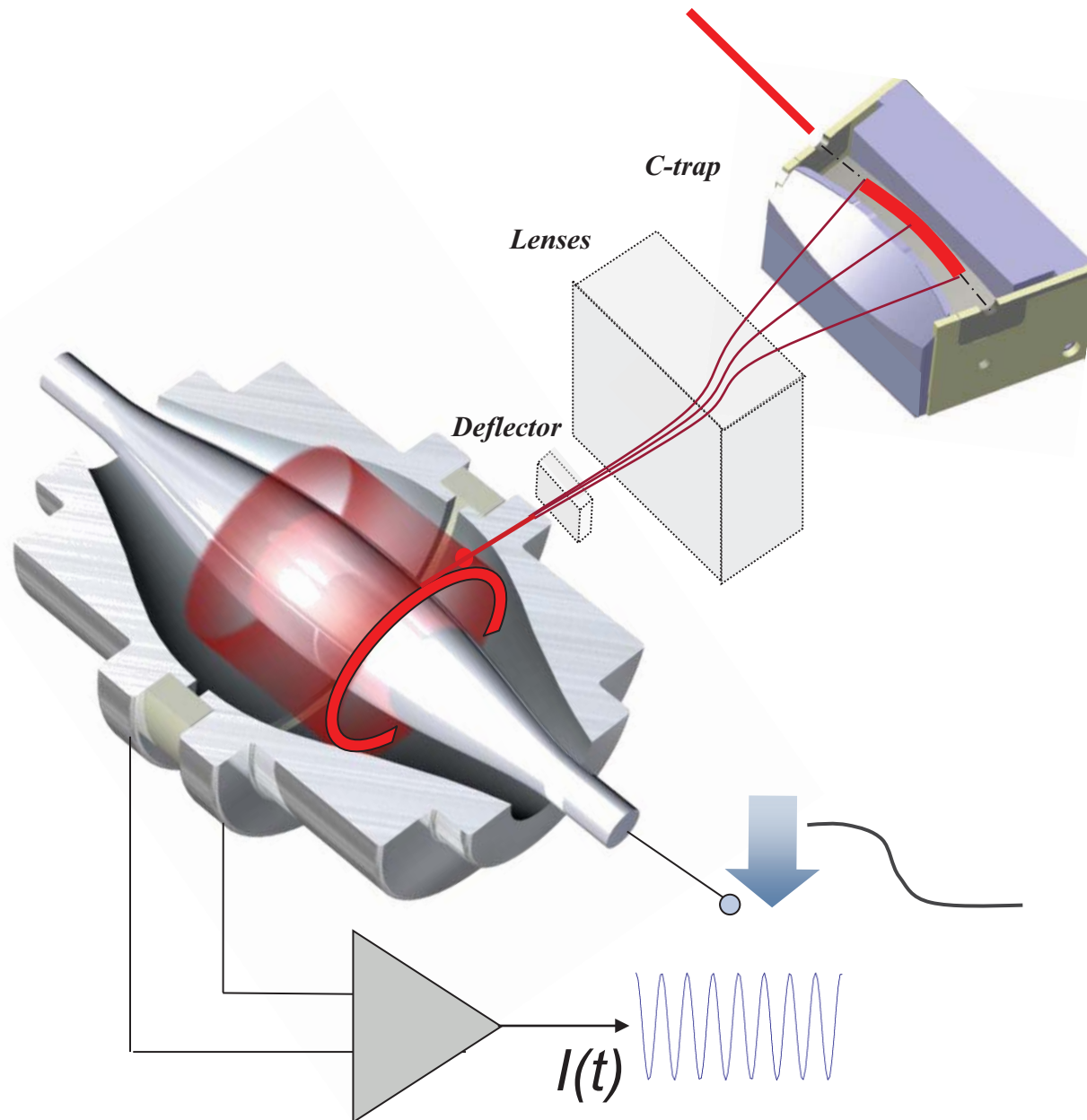
HD Technologies Ltd
 From Jan. 25, 2000- within Thermo Inc.
 (in Thermo Masslab, Manchester, UK)

Reasons Why Orbitrap Would Never Work

- Not possible to provide ion packets with required spatial and temporal parameters for continuous ion sources
- Tolerance requirements on electrodes are not realistic
- Injection and central slots ruin resolving power and mass accuracy
- Vacuum requirements are ridiculously high and can not be met
- Ions can not be injected with high efficiency
- Wide mass range can not be injected and captured
- Image current preamplifier will be destroyed by pick-up during injection
- Noise from high voltage power supply will overwhelm preamplifier
- Surface potentials would disturb and scatter ions
- Mass accuracy will be poor because of voltage drift & noise
- Large ion numbers cannot be properly injected or analyzed
- Electrodes shape, rotational and radial frequencies will cause unmanageable mass-dependent harmonics

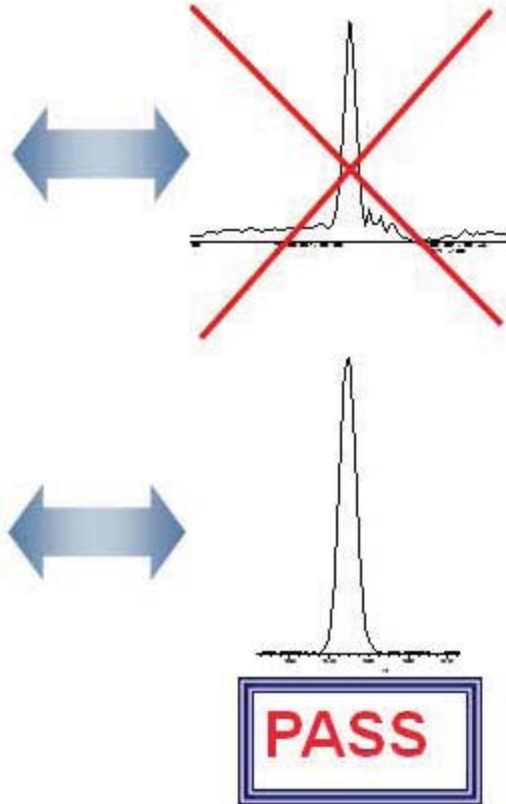
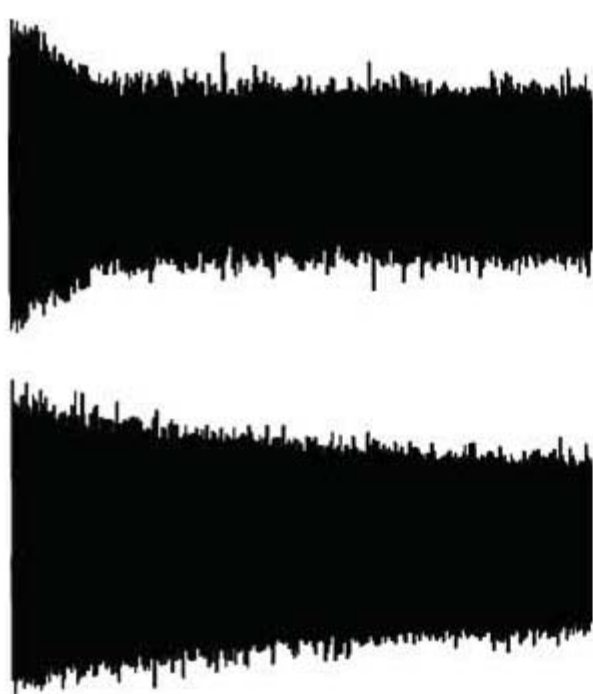
All these reasons are valid and require a lot of work!

Injection of Ions into the Orbitrap analyzer



- Ions are stored and cooled in a curved RF-only quadrupole (C-trap)
- RF is ramped down, radial DC is applied
- Ions are ejected along lines converging on the orbitrap entrance).
- As ions enter orbitrap, they are picked up and squeezed by its electric field
- All ions start simultaneously, but light ions enter Orbitrap analyzer earlier than heavy ions

Influence of (in) Correct Electrode Shape



De-focusing +
self-bunching =
bad peak shape



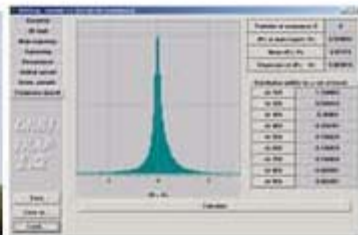
Correct tolerances =
High resolution &
good peak shape



M. Monastyrski



D. Grinfeld



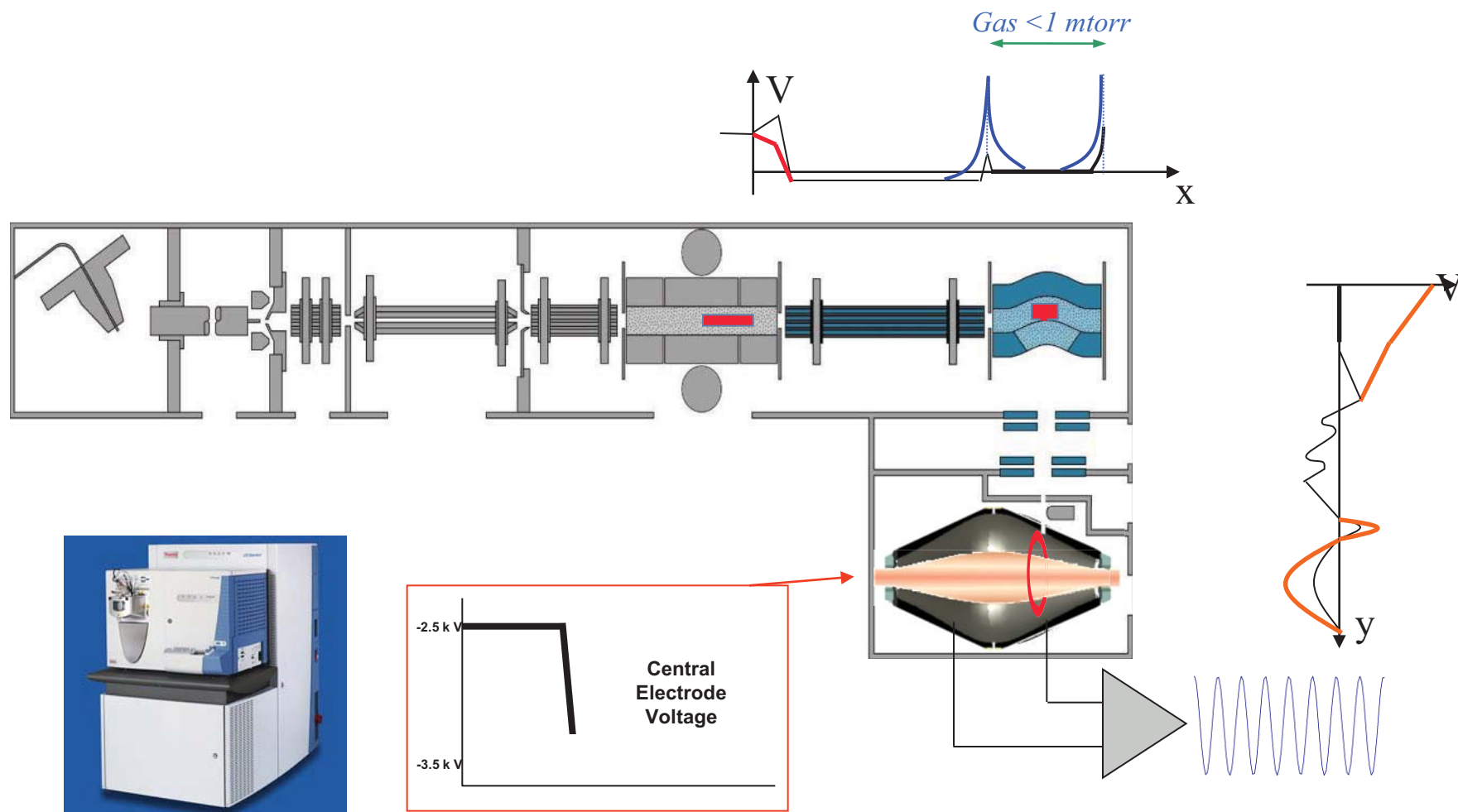
B. Laser



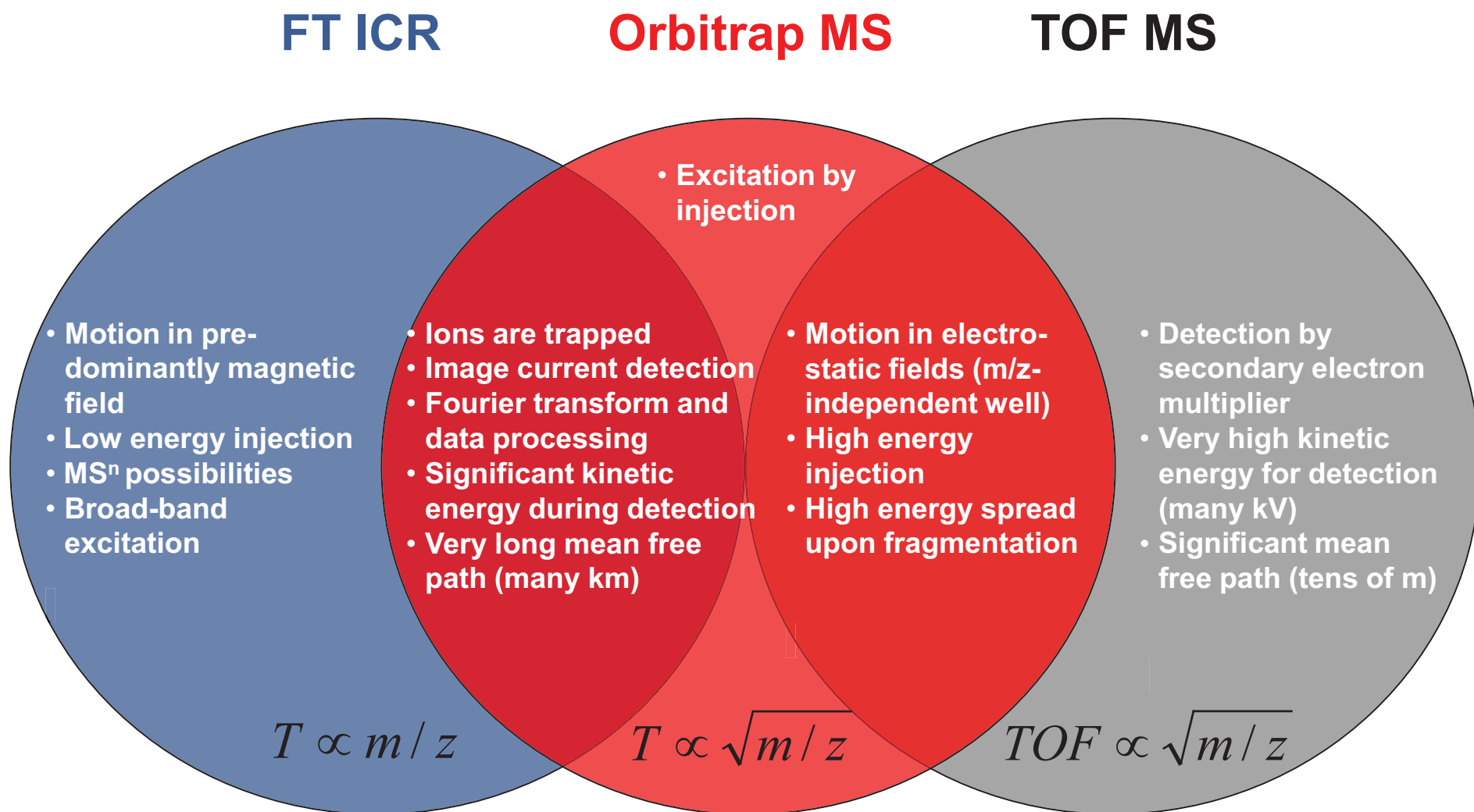
F. Schaefer

LTQ-Orbitrap: All Technologies Come Together

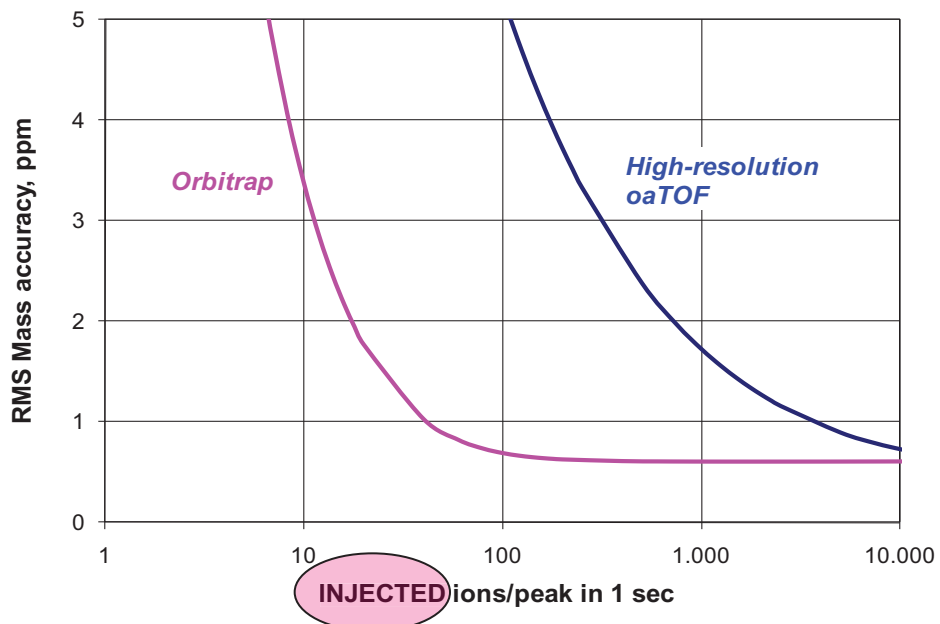
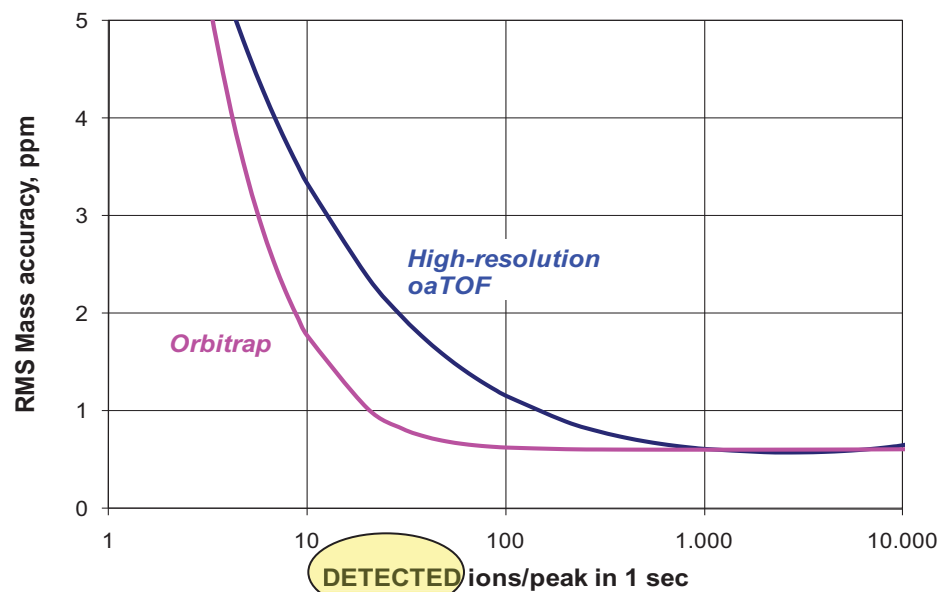
1. Ions are stored in the linear trap of LTQ



Major accurate-mass analyzers for Life Science



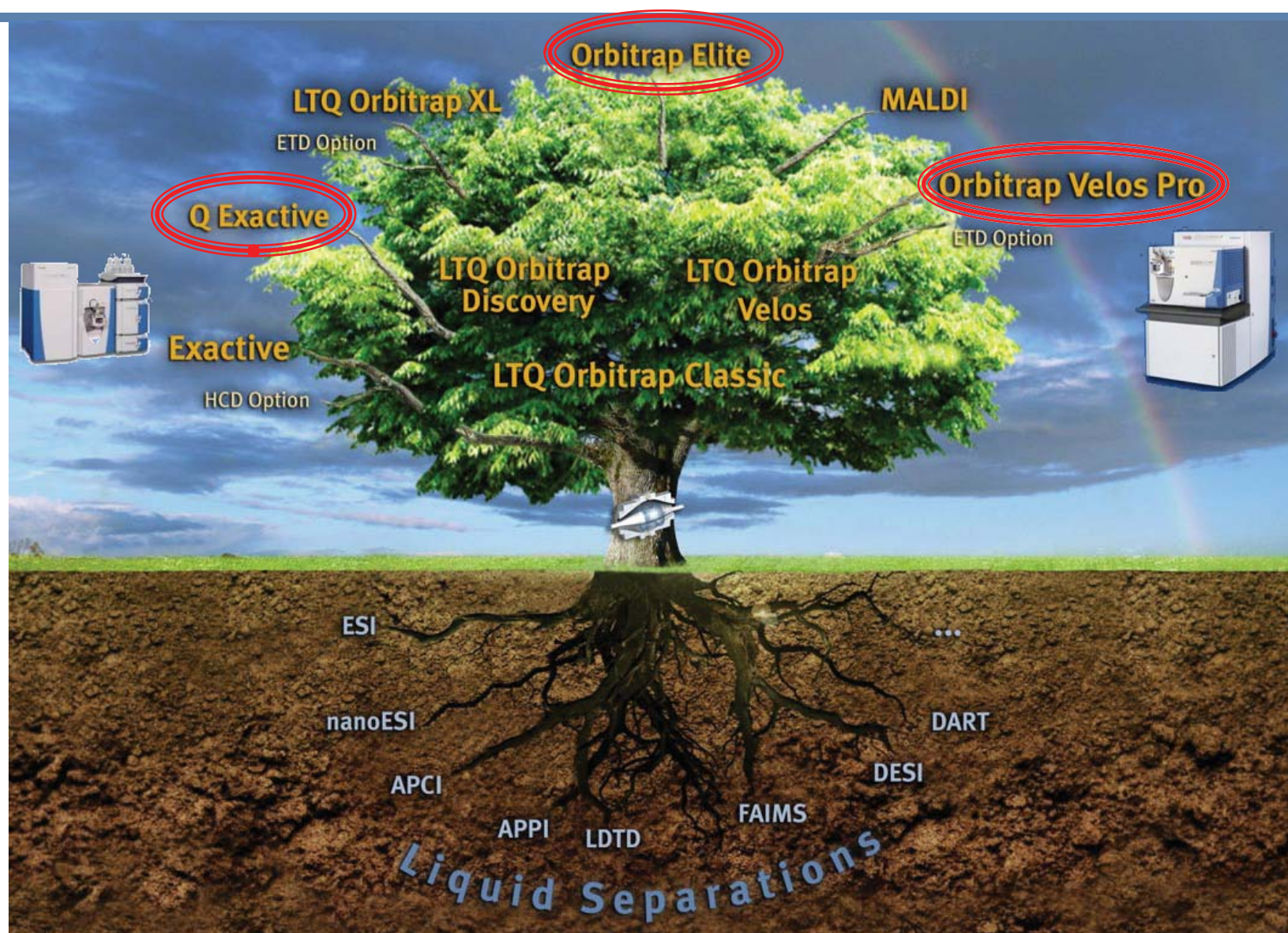
Importance of high transmission



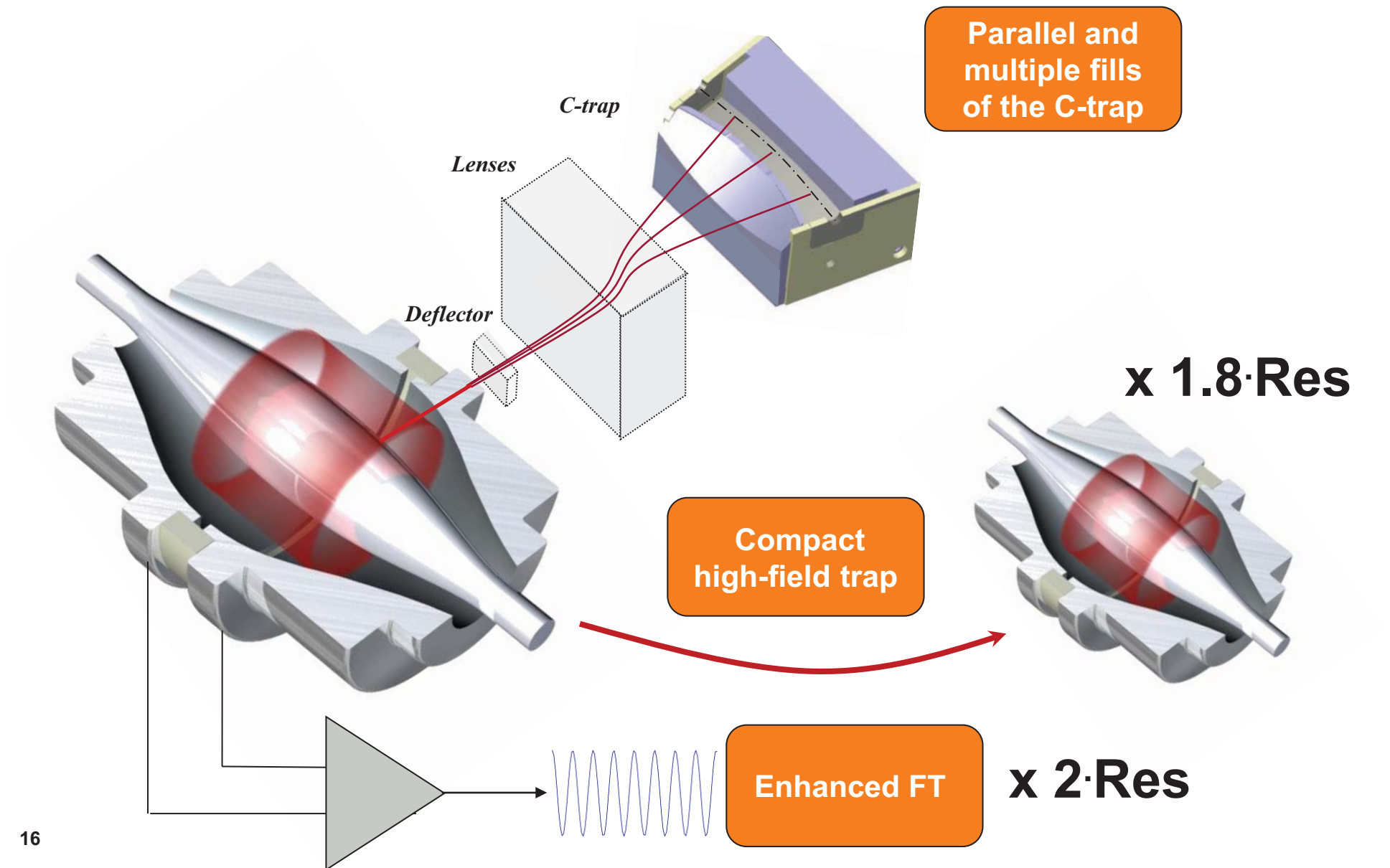
Assumptions:

- oaTOF: resolving power 40,000, transmission 4% (grids x duty cycle x angular scattering on grids)
- Orbitrap transmission 50%

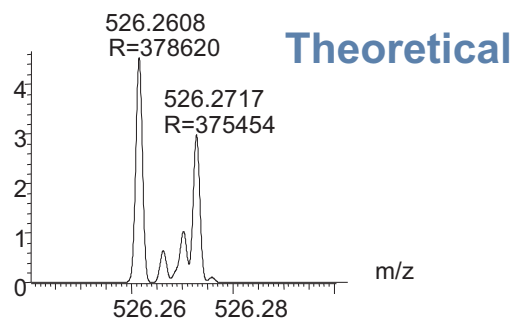
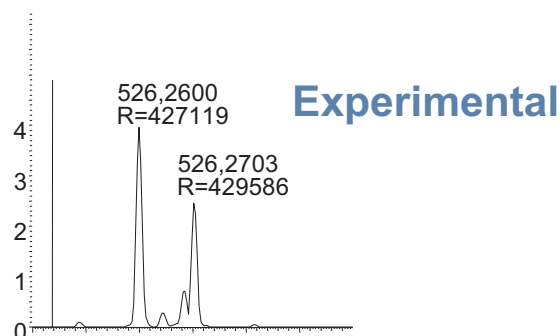
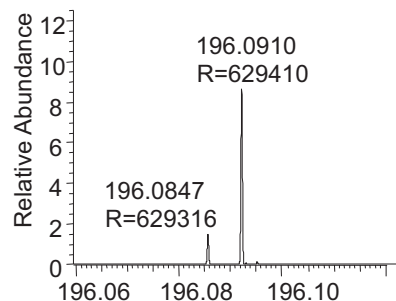
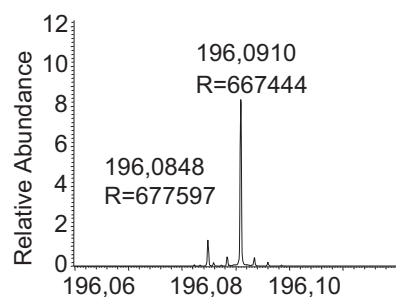
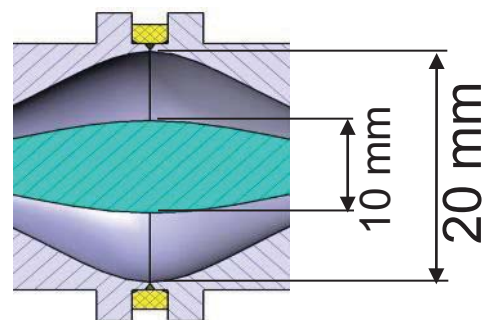
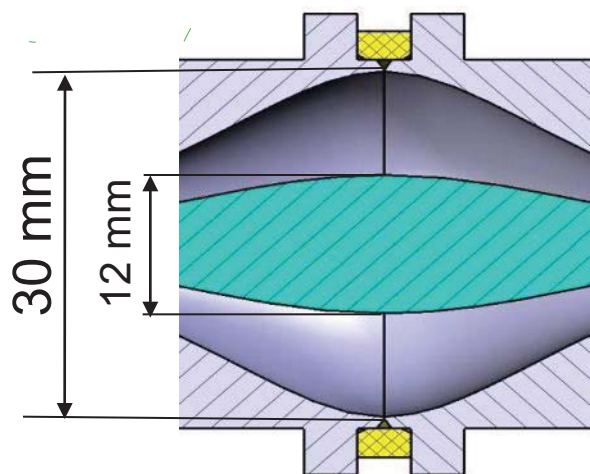
2011: A new season in life of Orbitrap mass spectrometry



Recent developments of the Orbitrap analyzer

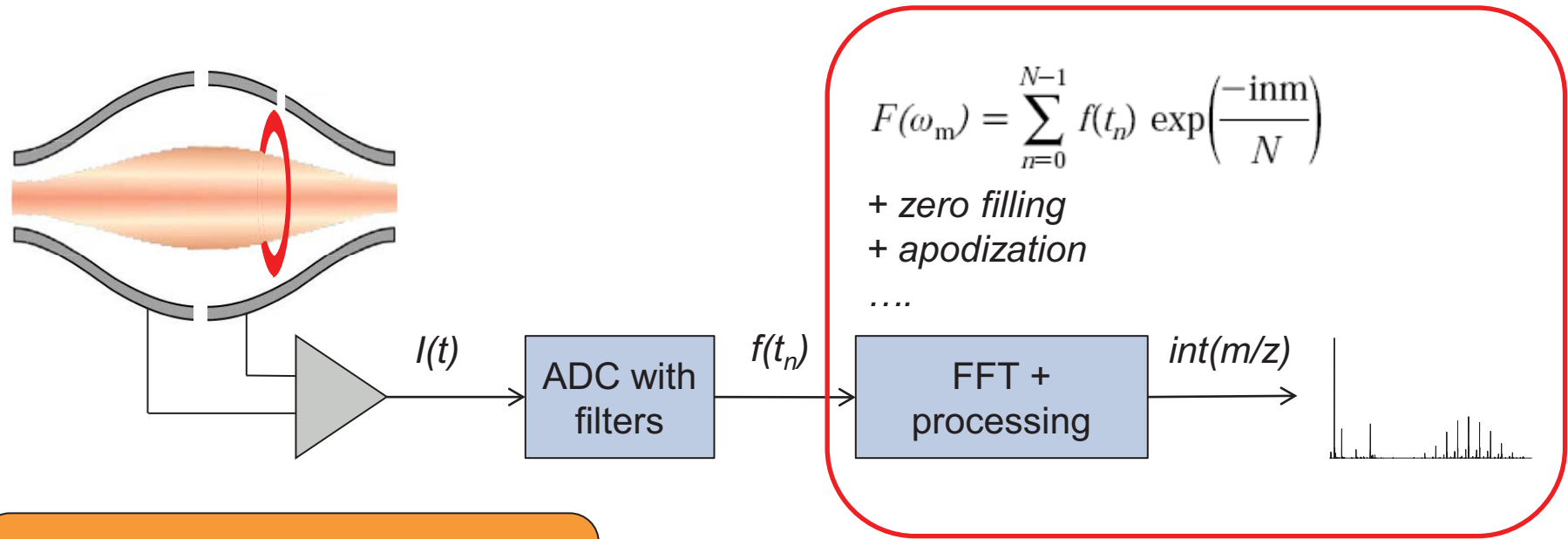


Improvements in orbital trapping: Compact high-field analyzer



- Smaller size- 1.8x frequency at the same voltage, 2.1x at higher voltage
- New miniature lenses for focusing onto Orbitrap entrance
- Higher tolerance requirements
- Lower capacitance and new preamplifier transistors bring increased sensitivity.
- Space charge shift: ca. 70% rel. to the standard trap at the same target

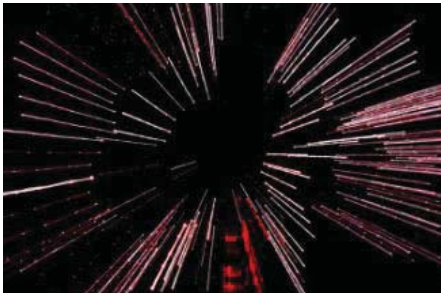
Detection process in the Orbitrap analyzer



All ions are ejected from the C-trap at the same moment

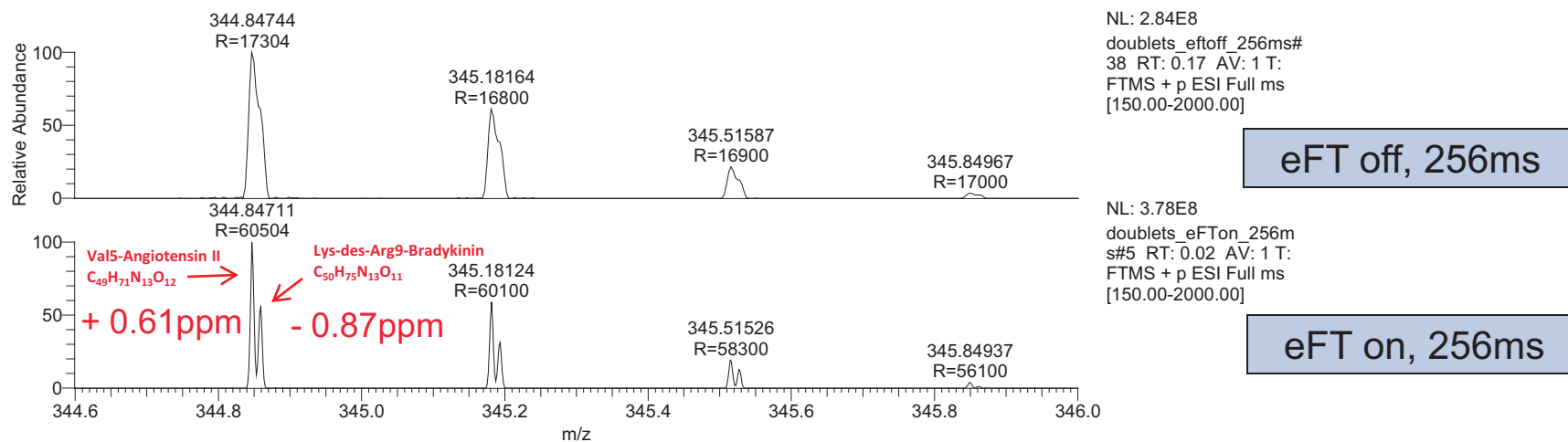
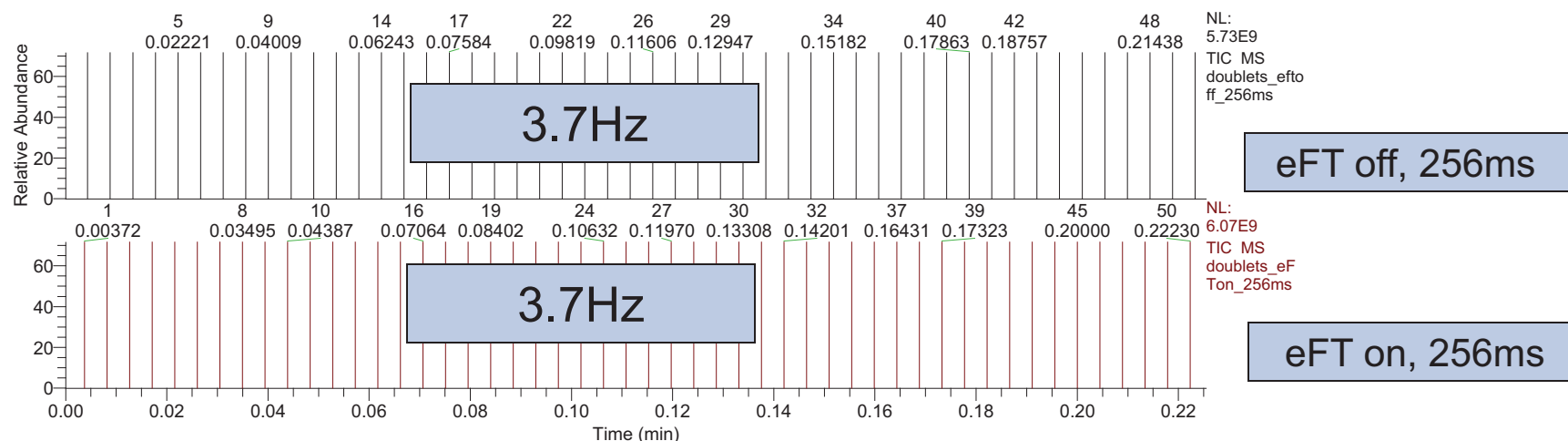
Coherent nature of ion packets allows for a new advanced signal processing procedure

Narrow peaks in Enhanced FT



Enhanced FT as a tool for increasing resolving power

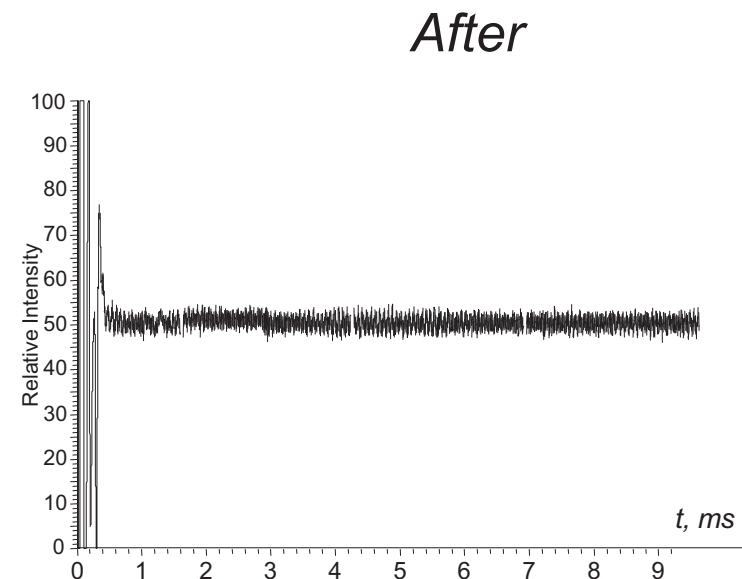
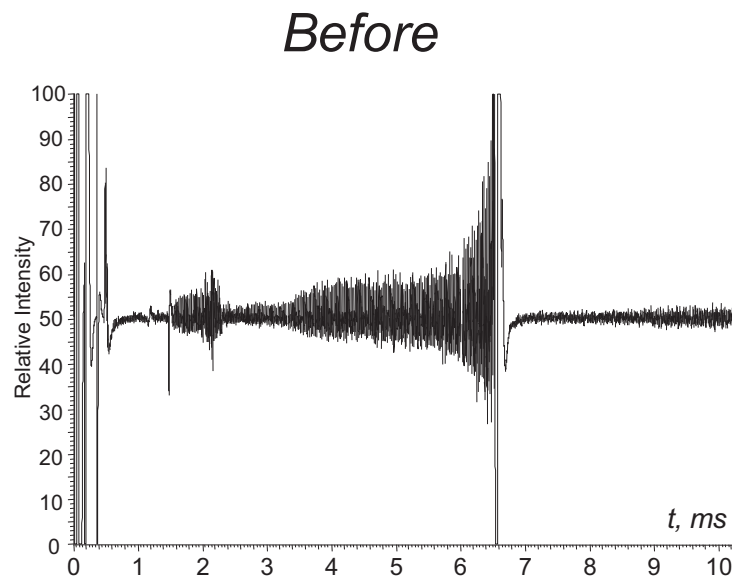
- MS analysis of two peptides (Val5-Angiotensin II and Lys-des-Arg9-Bradykinin) differing in mass by 12.1 mmu (triple charged ions)



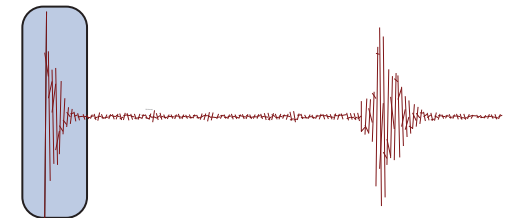
Please see: O. Lange; E. Damoc; A. Wieghaus; A. Makarov. "Enhanced FT for Orbitrap Mass Spectrometry". Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011.

Enhanced FT is not just a software!

- Improved stabilization and filtering of voltages
- Special dielectric materials
- Improved preamplifier



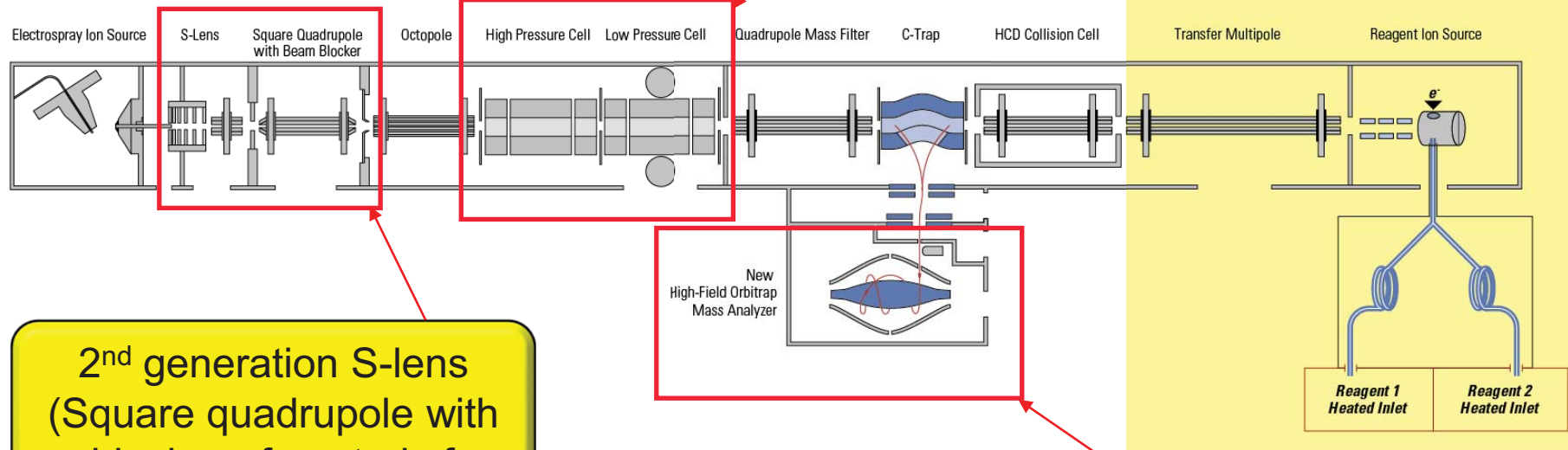
Conclusion: detection of the first beat is very important for heavy intact proteins



Orbitrap Elite instrument



Faster Dual trap electronics:
>12 scans/sec



2nd generation S-lens
(Square quadrupole with
a blocker of neutrals for
improved ruggedness)

Compact high-field
Orbitrap analyzer+ eFT

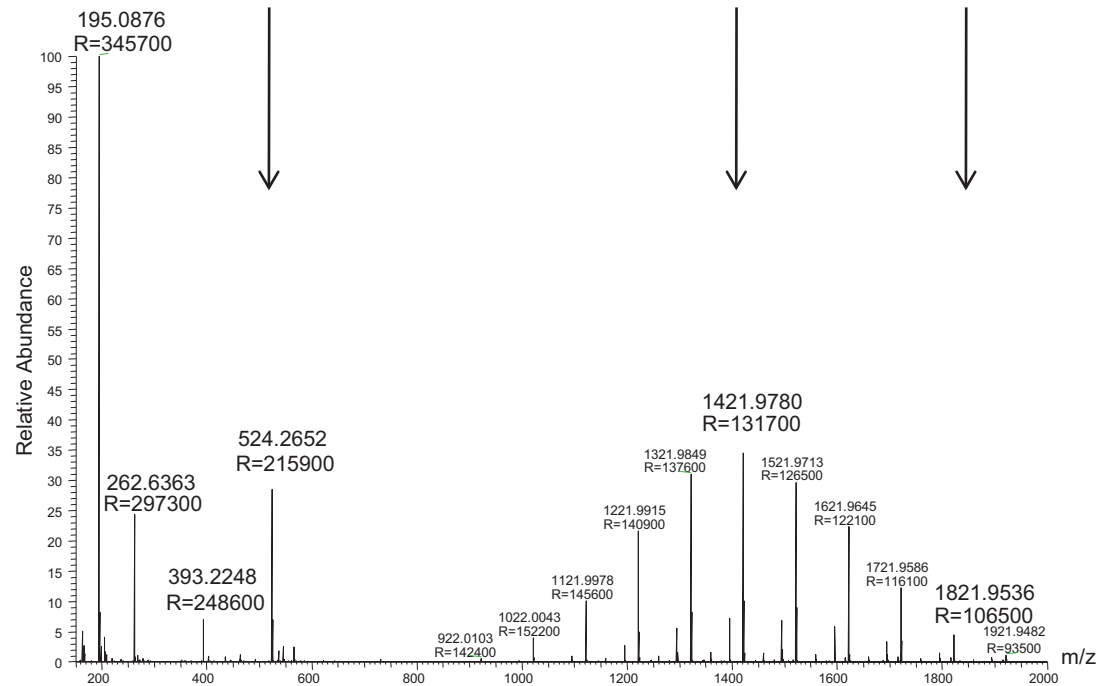
Resolving power of Orbitrap Elite

0.76 sec acquisition
 (std for R=60,000)
 Hamming apodization,
 T=5e5

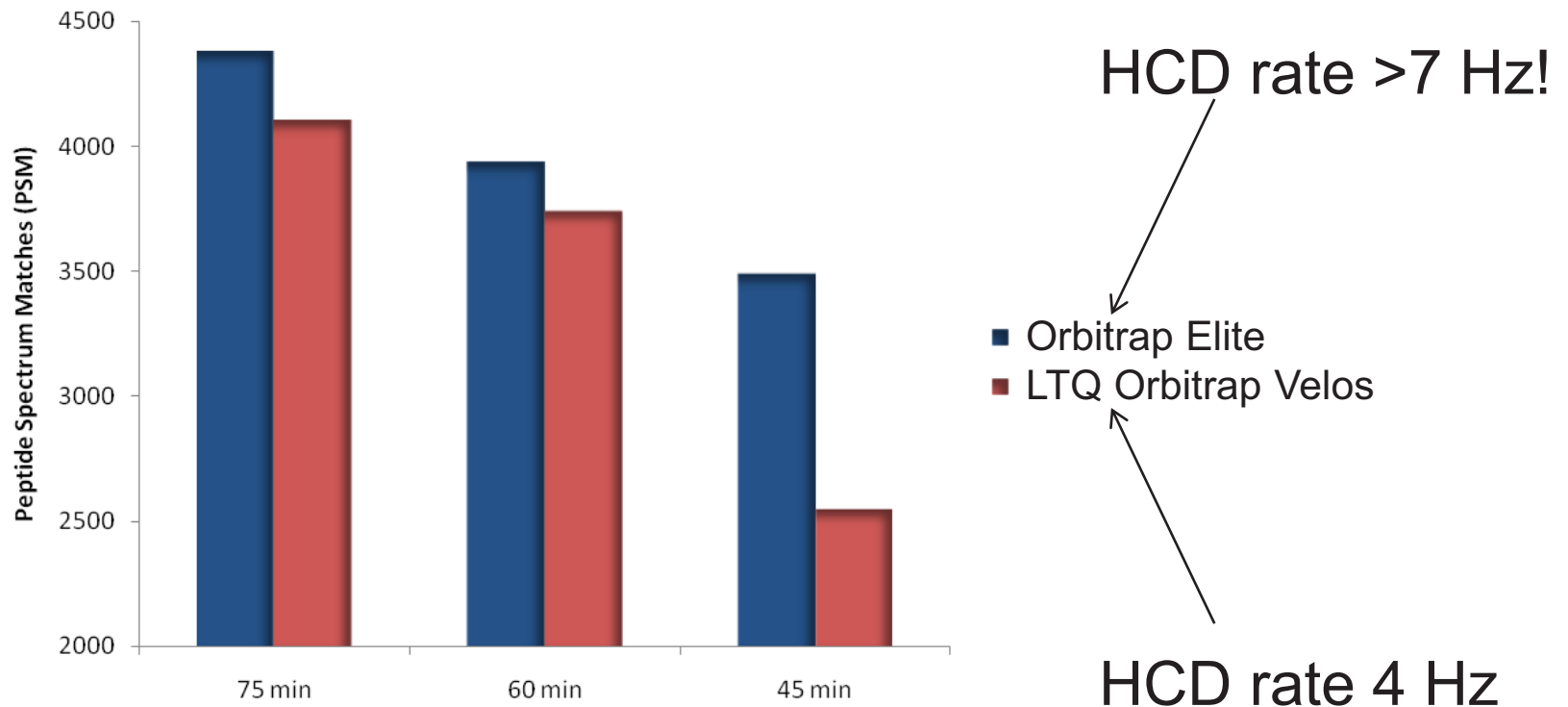
R=60,000 \longleftrightarrow

m/z	R _{FWHM} in 0.76s
195	345,000
393	248,000
524	215,000
1222	140,000
1822	106,000

LTQ FT equivalent: 12T 20T 32T 34T



Number of peptide spectrum matches for different LC gradients

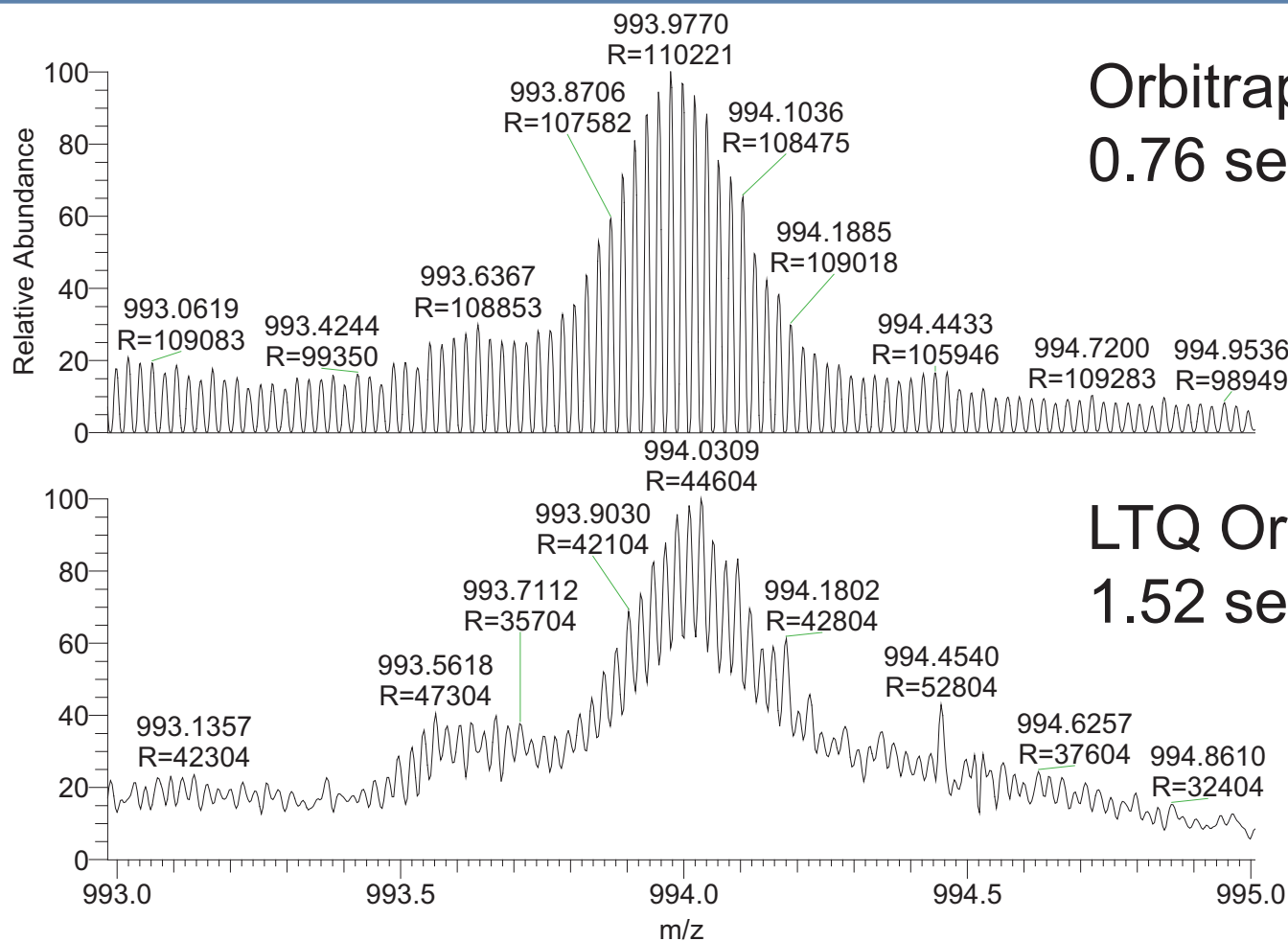


Sample: *E.coli*, HCD top 15 method

Slide courtesy
M.Zeller

Please see also: M. Zeller; C. Crone; M. Mueller; E. Damoc; E. Denisov; A. Makarov; D. Nolting; T. Moehring. "Increased analytical performance on a hybrid iontrap-FTMS mass spectrometer with a compact Orbitrap mass analyzer", Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011.

Protein performance



Slide courtesy
E. Damoc, M.Zeller

Please see also: E. Damoc, E. Denisov, O. Lange, T. Moehring, A. Makarov. "Improving protein analysis in Orbitrap mass spectrometry", Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011.

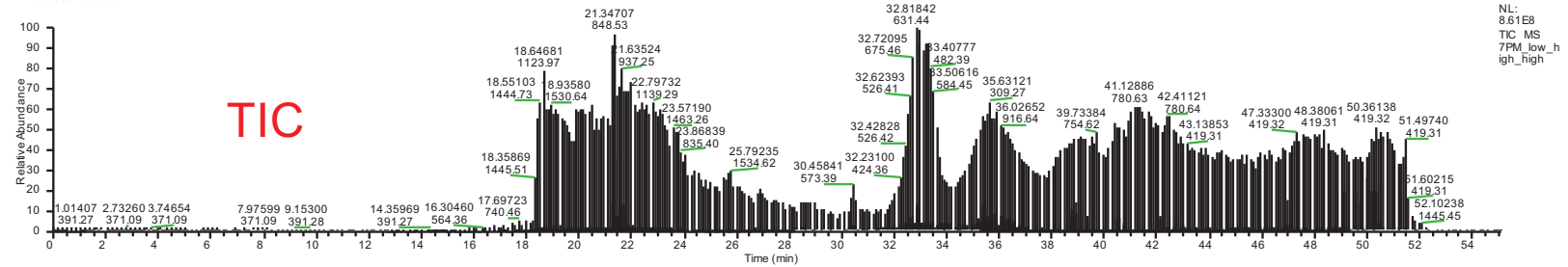
Please see also: P. Compton; E. Damoc; E. Denisov; J.C. Tran; A. Wieghaus; M.W. Senko; S.R. Horning; A.Makarov; N.L. Kelleher. "Top-Down Proteomics on Orbitrap-Based Mass Spectrometers" Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011.

One of workflows for top-down analysis

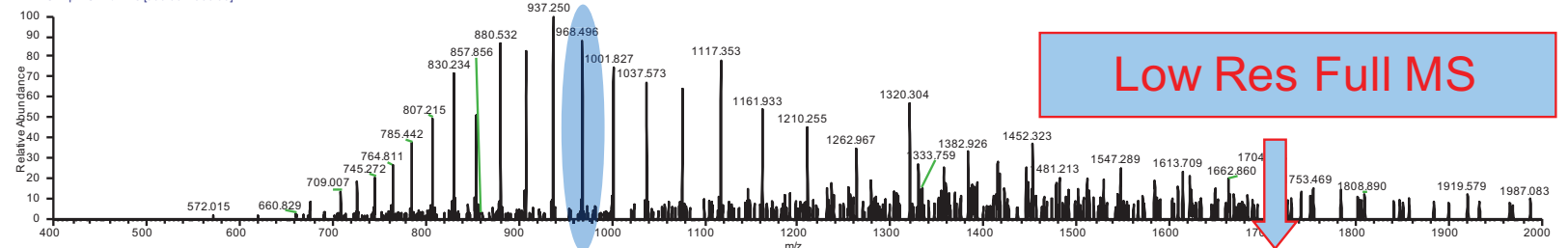
D:\Nike_ASMS201117PM_low_high_high

4/1/2011 3:31:37 PM

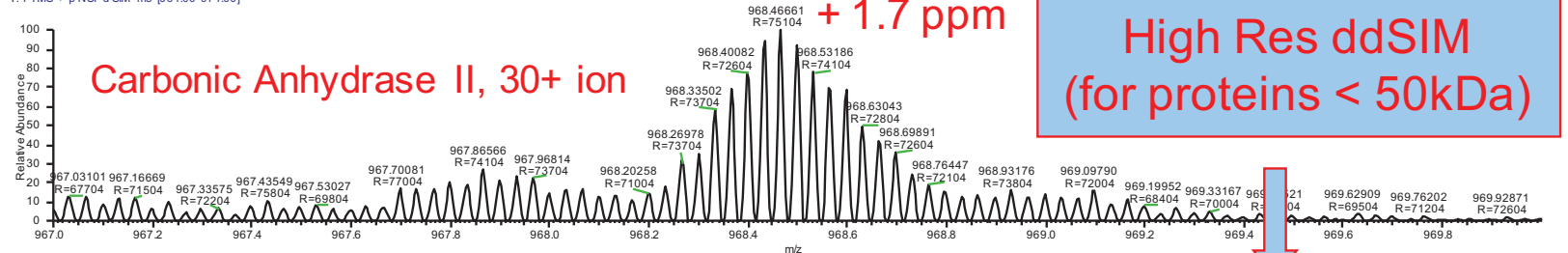
RT: 0.00000 - 55.05627



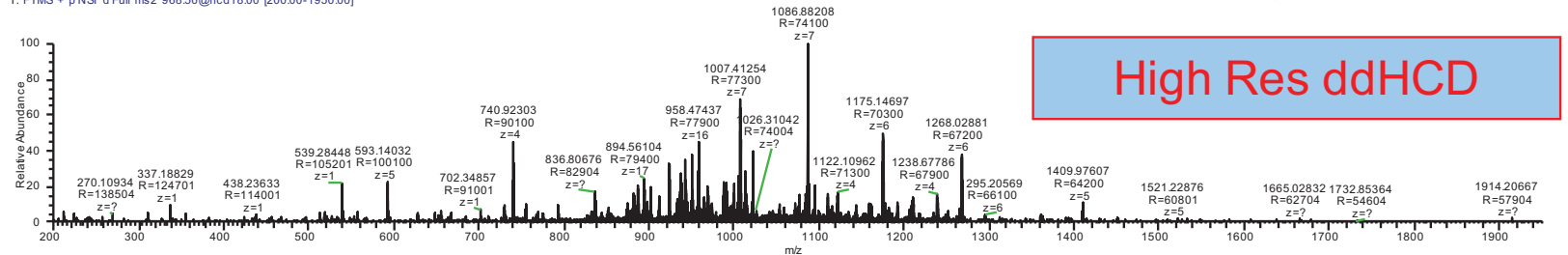
7PM_low_high_high#439 RT: 21.73 AV: 1 NL: 1.41E7
T: FTMS + p NSI Full ms [300.00-4000.00]



7PM_low_high_high#440 RT: 21.76 AV: 1 NL: 8.69E5
T: FTMS + p NSI d SIM ms [964.00-974.00]

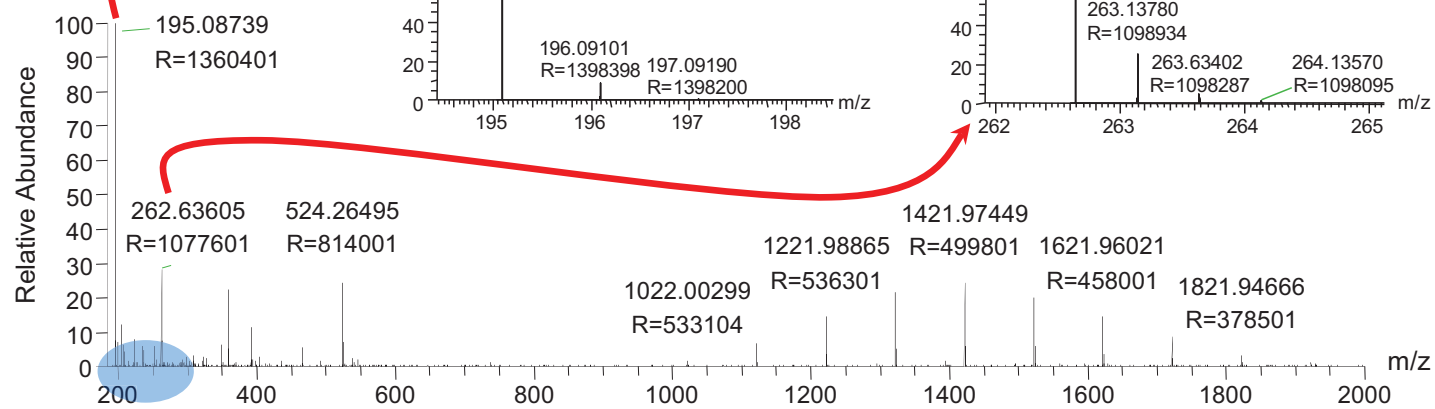
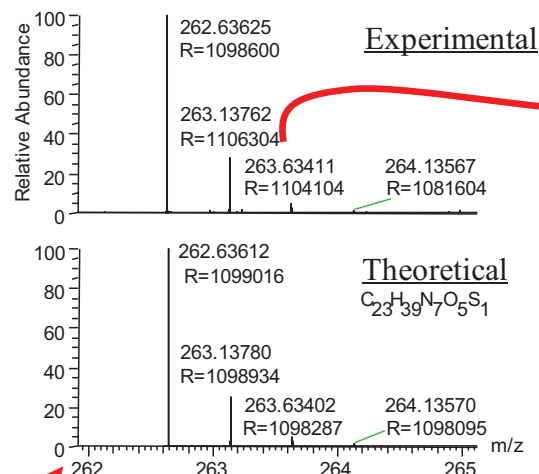
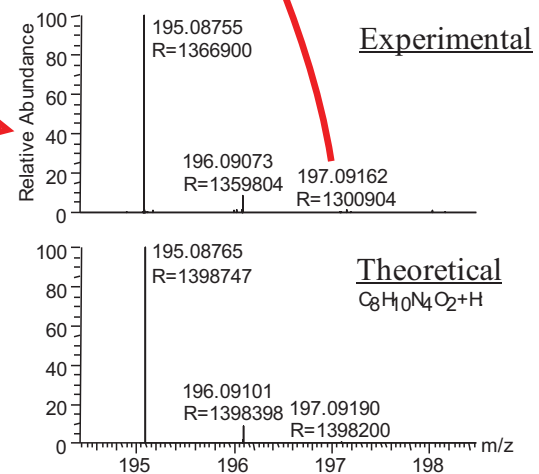
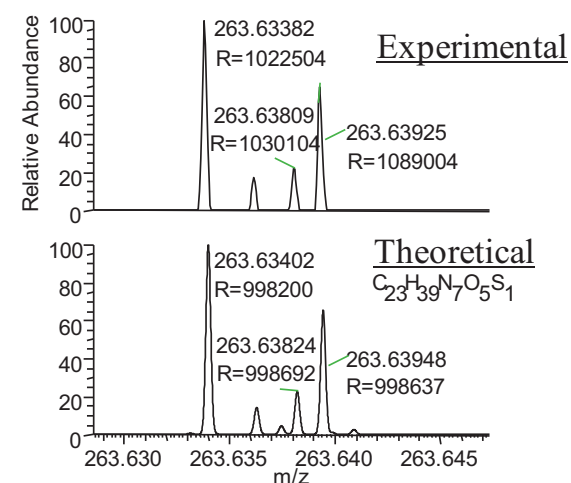
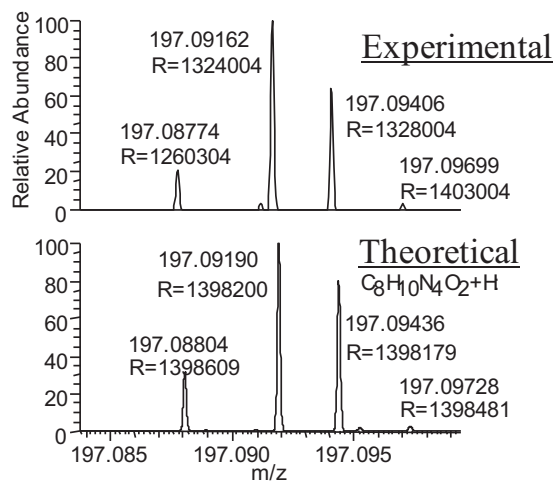


7PM_low_high_high#441 RT: 21.79 AV: 1 NL: 2.78E5
T: FTMS + p NSI d Full ms2 968.50@hcd18.00 [200.00-1950.00]



Some records...

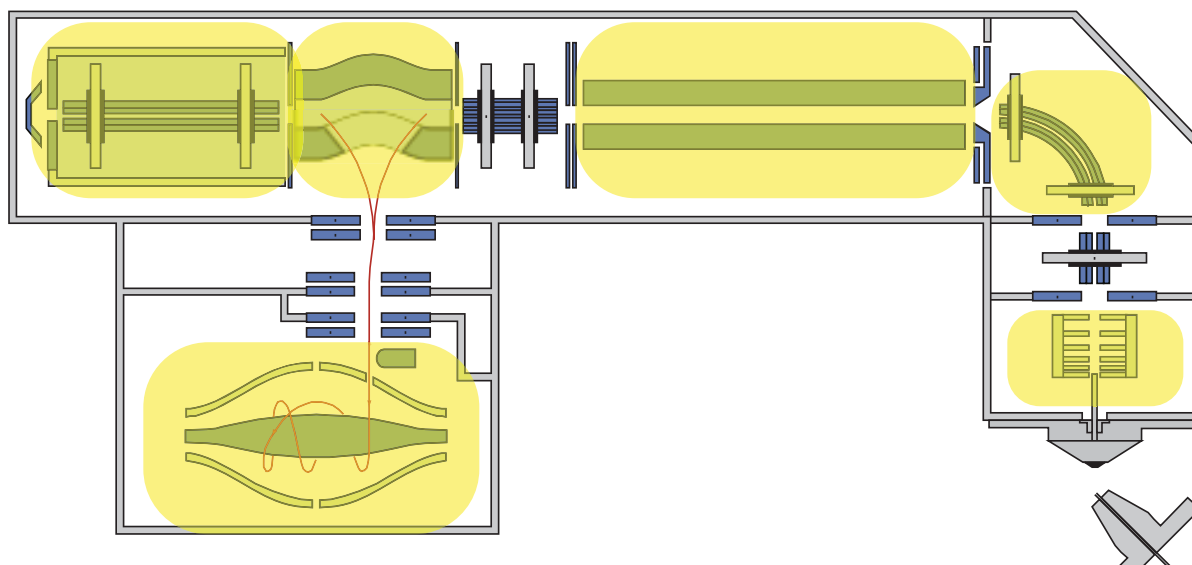
Hand-selected manually-tuned Orbitrap analyzer, 3 sec transients



Slide courtesy E. Damoc, E. Denisov

Q Exactive: new features relatively to Exactive

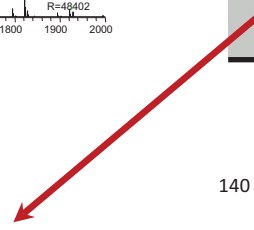
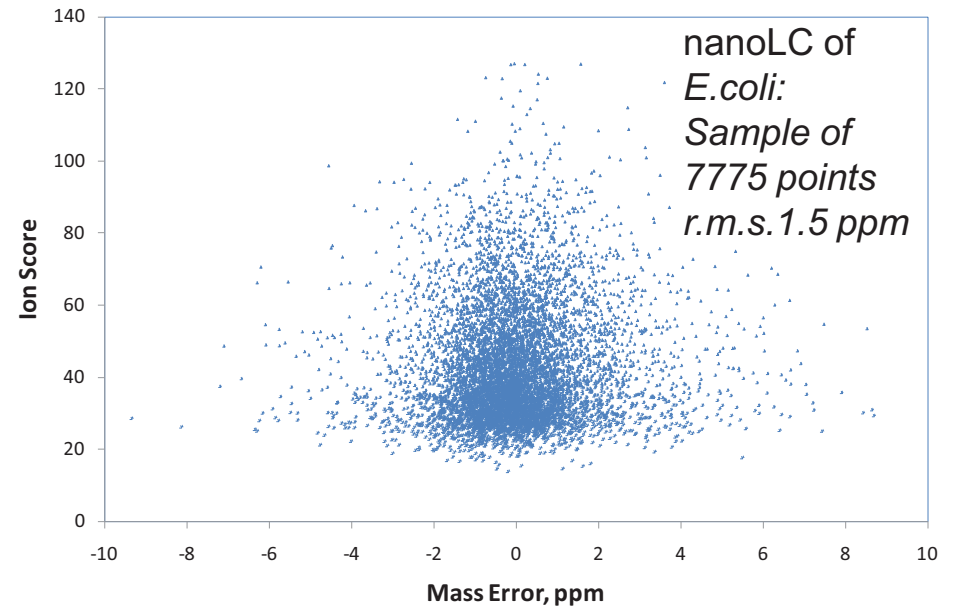
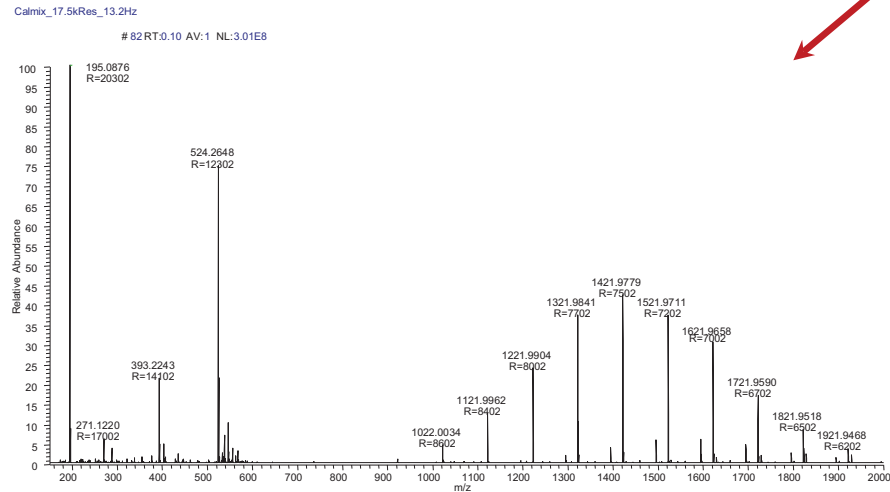
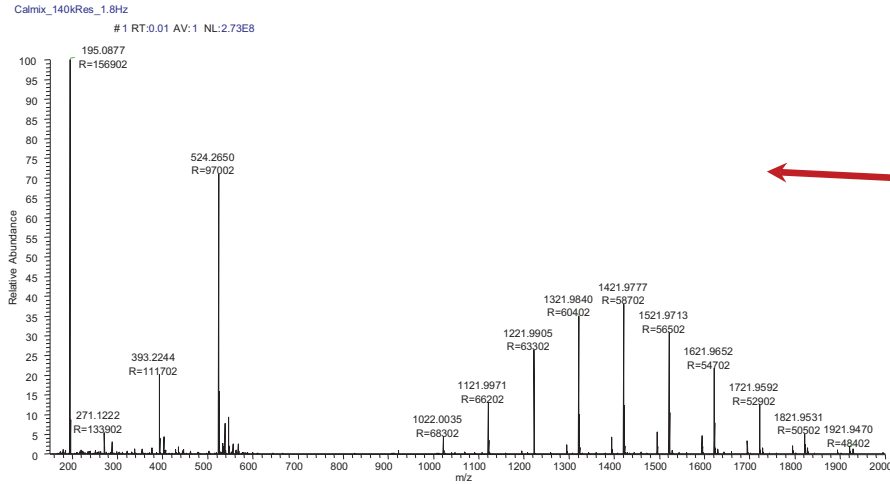
- Quadrupole mass filter
- Enhanced Fourier transform (eFT™) for Orbitrap data processing
- Predictive automatic gain control (pAGC) and parallel filling & detection
- Possibility of multiple fills for spectrum multiplexing
- S-lens for higher transmission (like in LTQ Orbitrap Velos) with rugged optics
- C-trap directly interfaced to HCD (like in LTQ Orbitrap Velos)



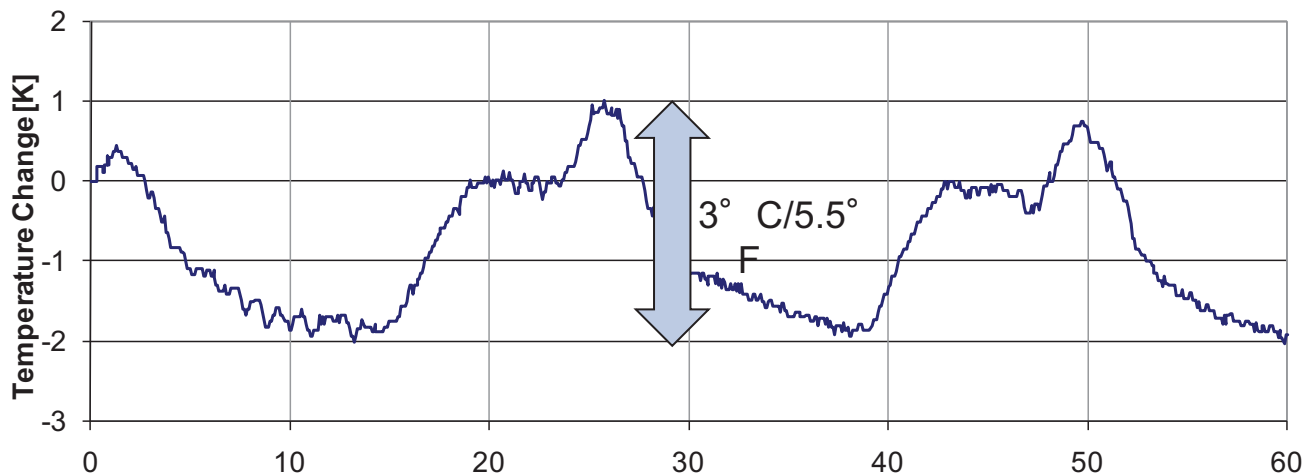
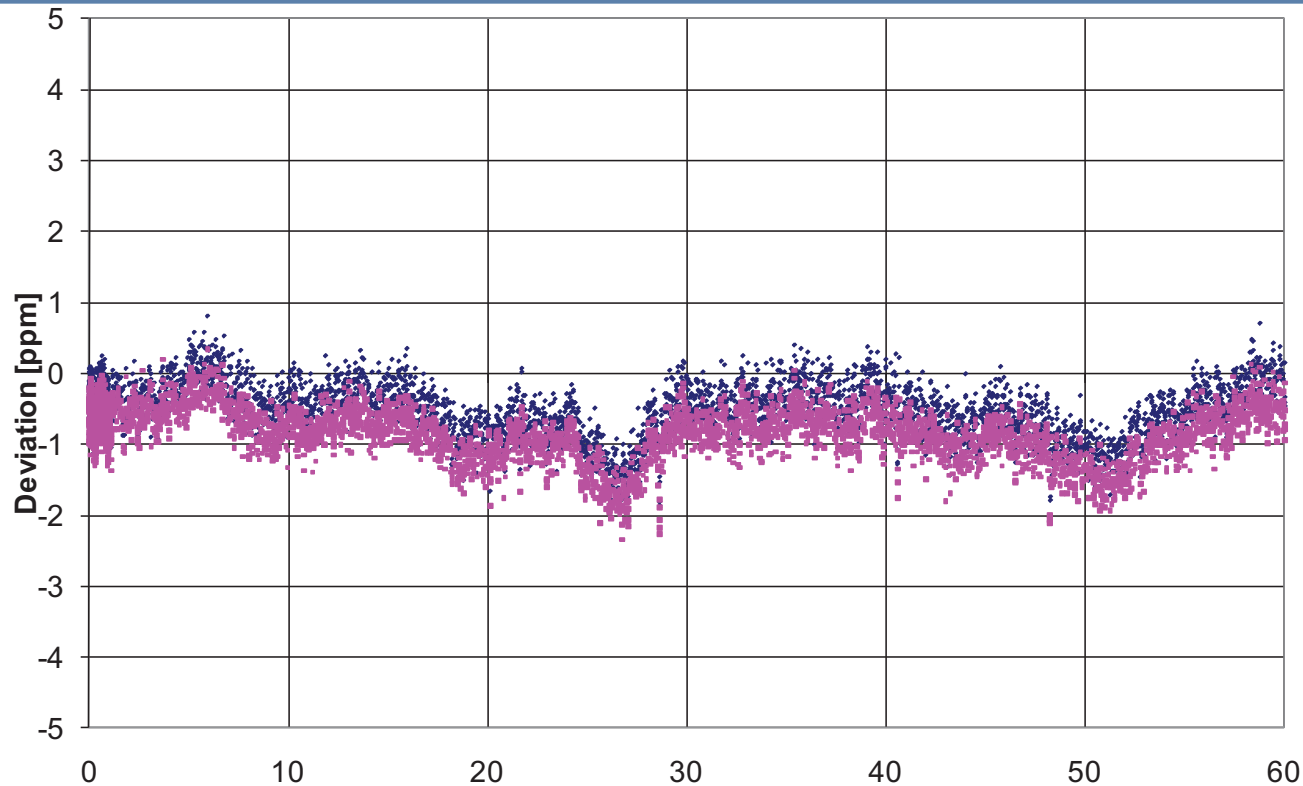
Michalski, A; Damoc, E; Hauschild, JP; Lange, O; Wieghaus, A; Makarov, A; Nagaraj, N; Cox, J; Mann, M; Horning, S
"Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer". *Mol. Cell Proteomics* **10**, (2011)

Resolving power and mass accuracy of the Orbitrap analyzer

Res setting @ m/z 200	Transient length, ms	Max. scan speed, Hz
140,000	512	1.5
70,000	256	3
35,000	128	7
17,500	64	12



Long-term mass accuracy with external calibration

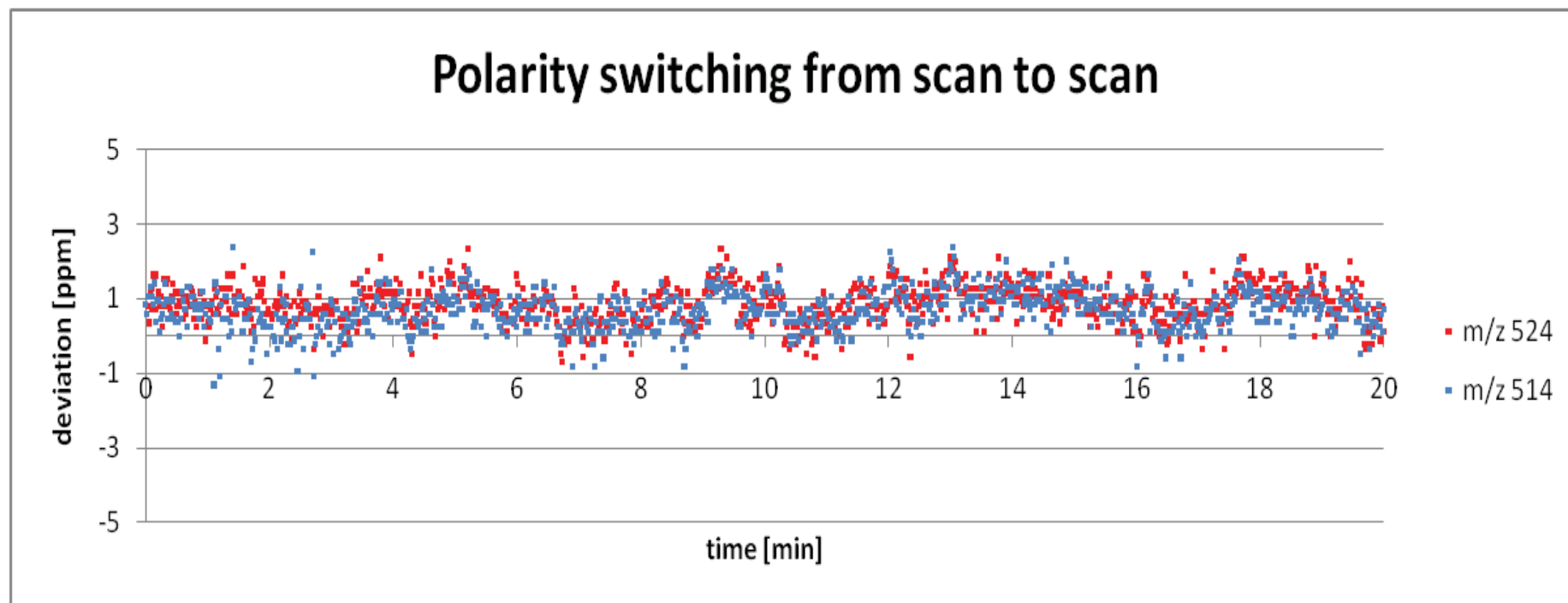


Time [h]

- Realistic conditions of an average lab
- Air cooling only!
- Experiment was carried out with temperature variations up to 3°C peak-to-peak, up to 1°C/hour

Time [h]

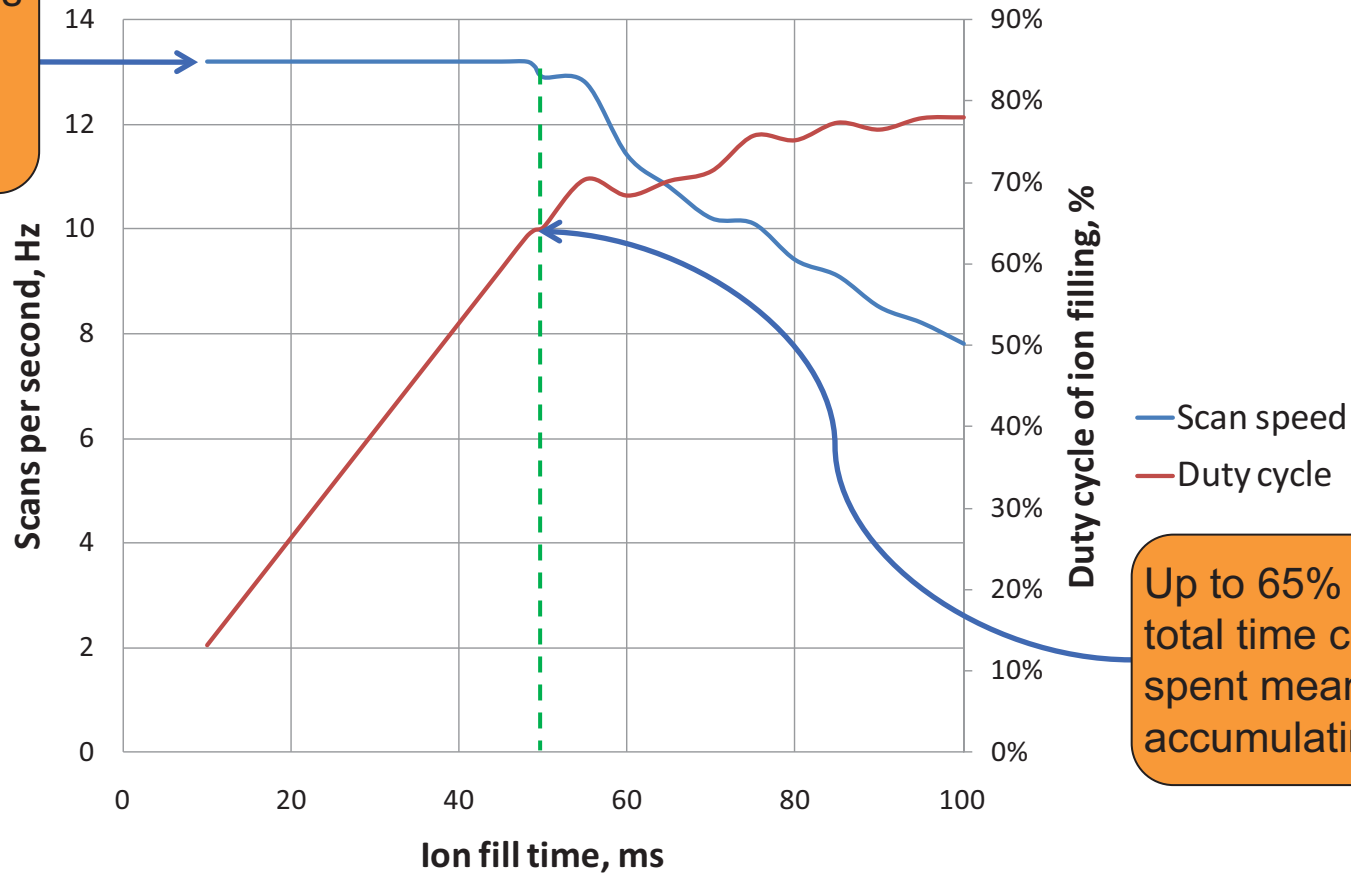
Mass accuracy with polarity switching and external calibration



1 positive + 1 negative scan in 1 second

Spectral acquisition speed with predictive AGC and parallel filling/detection

Scan speed does not change until ion fill time reaches 50 ms

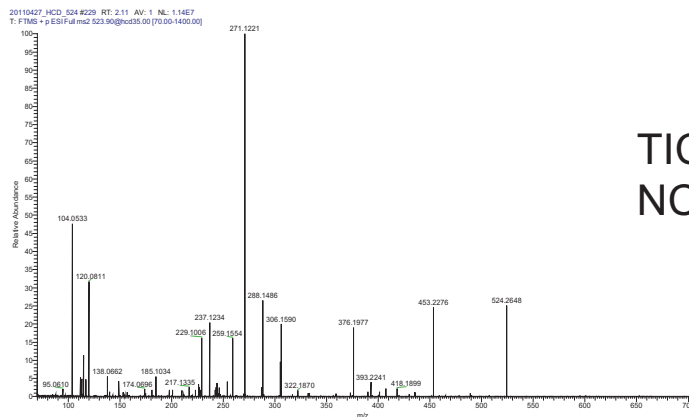
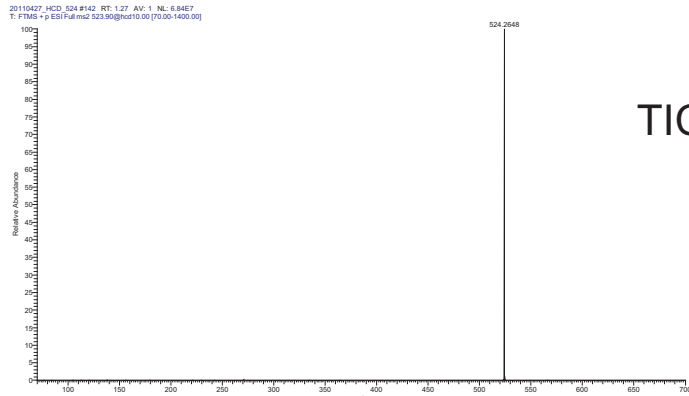


Up to 65% of the total time could be spent meanwhile on accumulating ions!

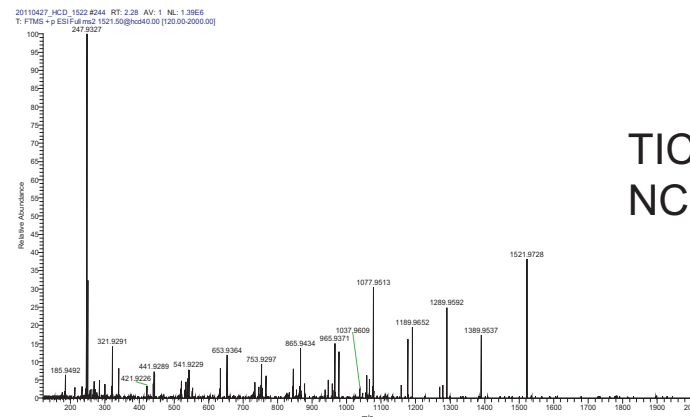
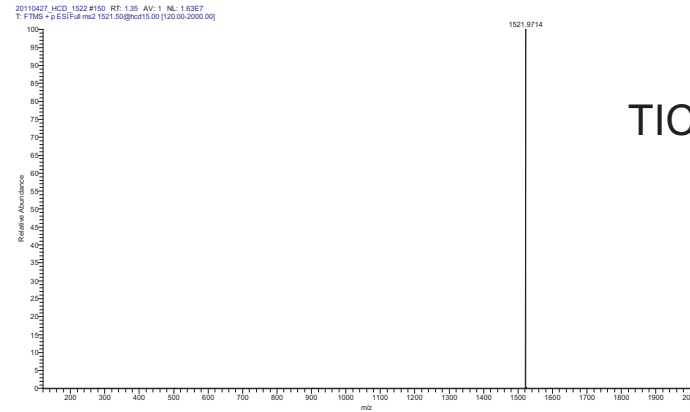
Resolving power setting: 17,500 (min.)
At higher resolving powers, ion fill times and duty cycles are even longer!

HCD performance

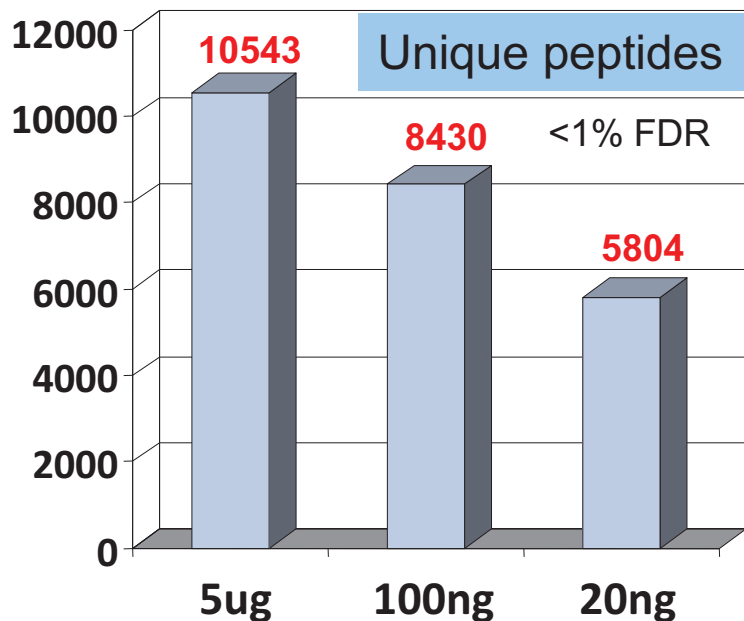
m/z 524 (MRFA peptide)



m/z 1522 (Ultramark)

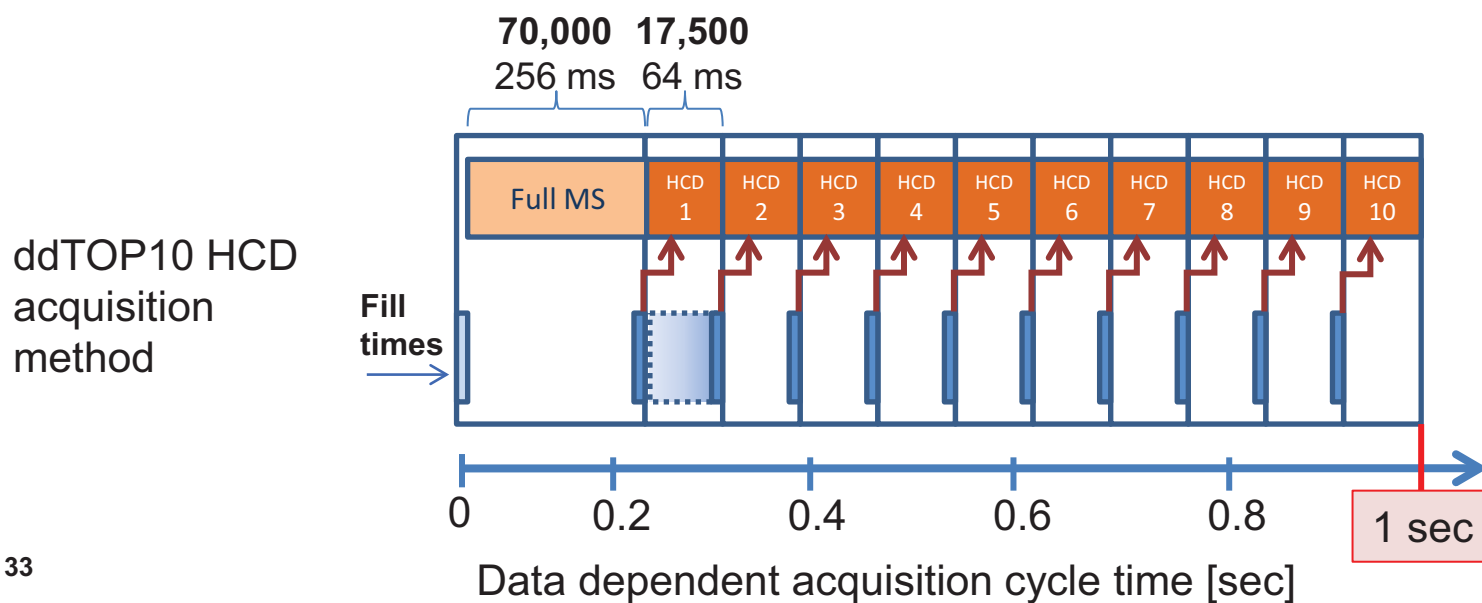
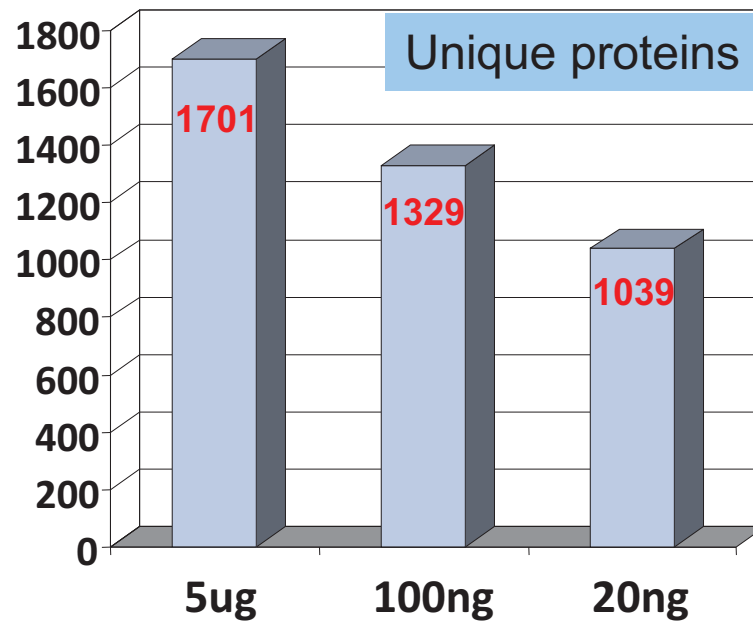


- Fill times are similar to those in LTQ Orbitrap Velos instrument
- Direct interfacing of the C-trap to HCD cell minimizes losses during fragmentation

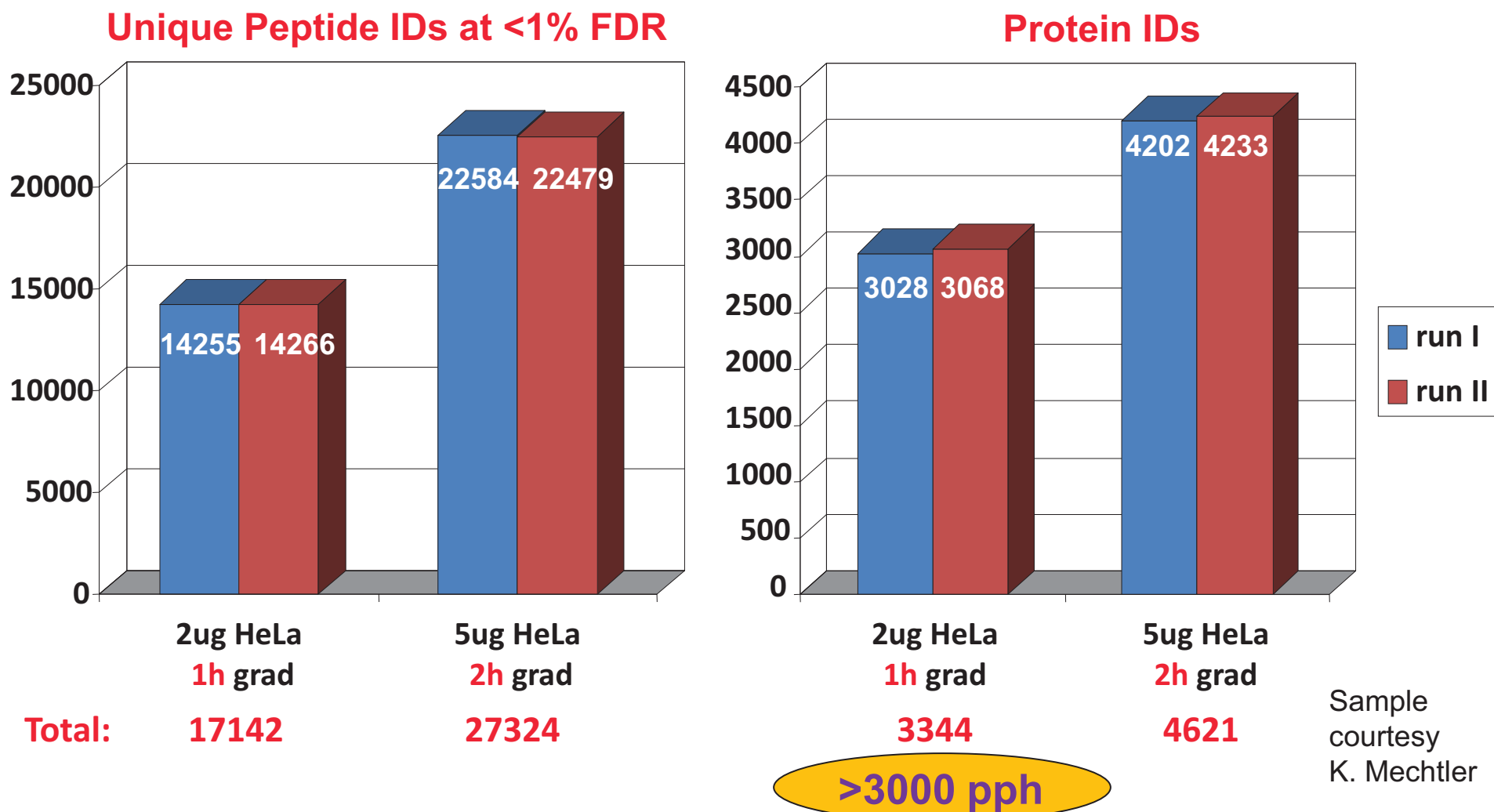


E. Coli digest

2h gradient,
Proxeon
NanoUPLC
3 search engines



Q Exactive LC-MS/MS in action: *HeLa* digest

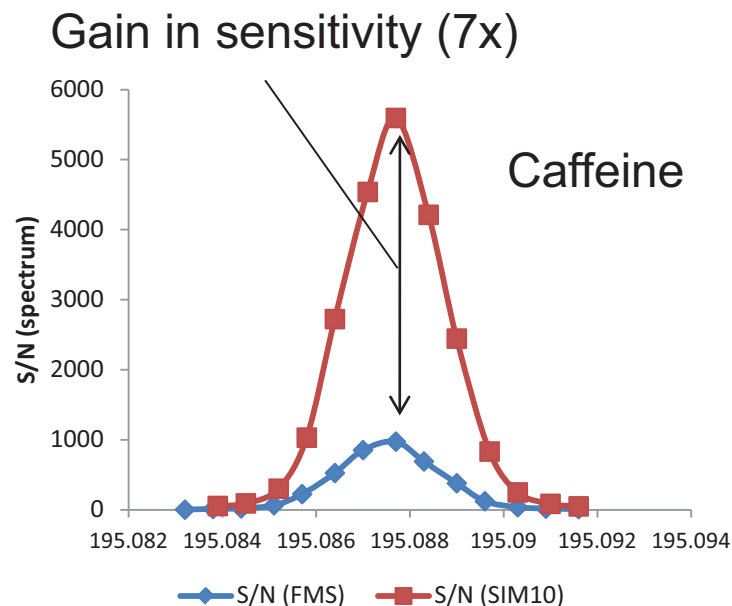
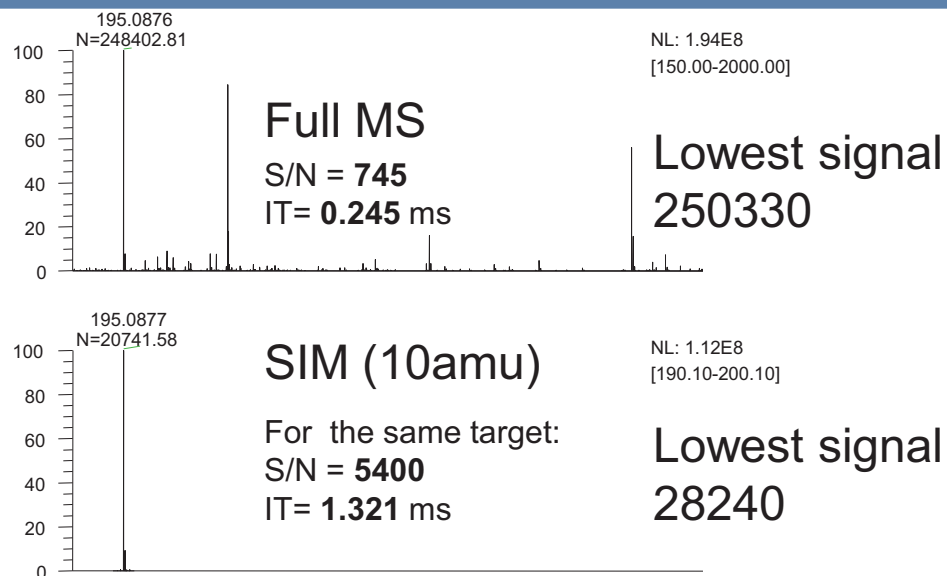


Please see also: C. Paschke; Y. Xuan; E. Damoc; T. Ueckert; U. Comberg; H. Grensemann; M. Kellmann; B. Delanghe. "Breaking the 2000 proteins barrier in a standard LC run using a new benchtop Orbitrap instrument and multiple search engines.". Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011.

What do we gain by selected ion monitoring?

- In Full MS, total C-trap charge capacity is shared between multiple signals of different intensity
- Signal-to-noise ratio becomes dependent on the ratio of compound of interest to other analytes- much less so in SIM!
- In Orbitrap instruments, SIM could become MRM without any additional overhead!

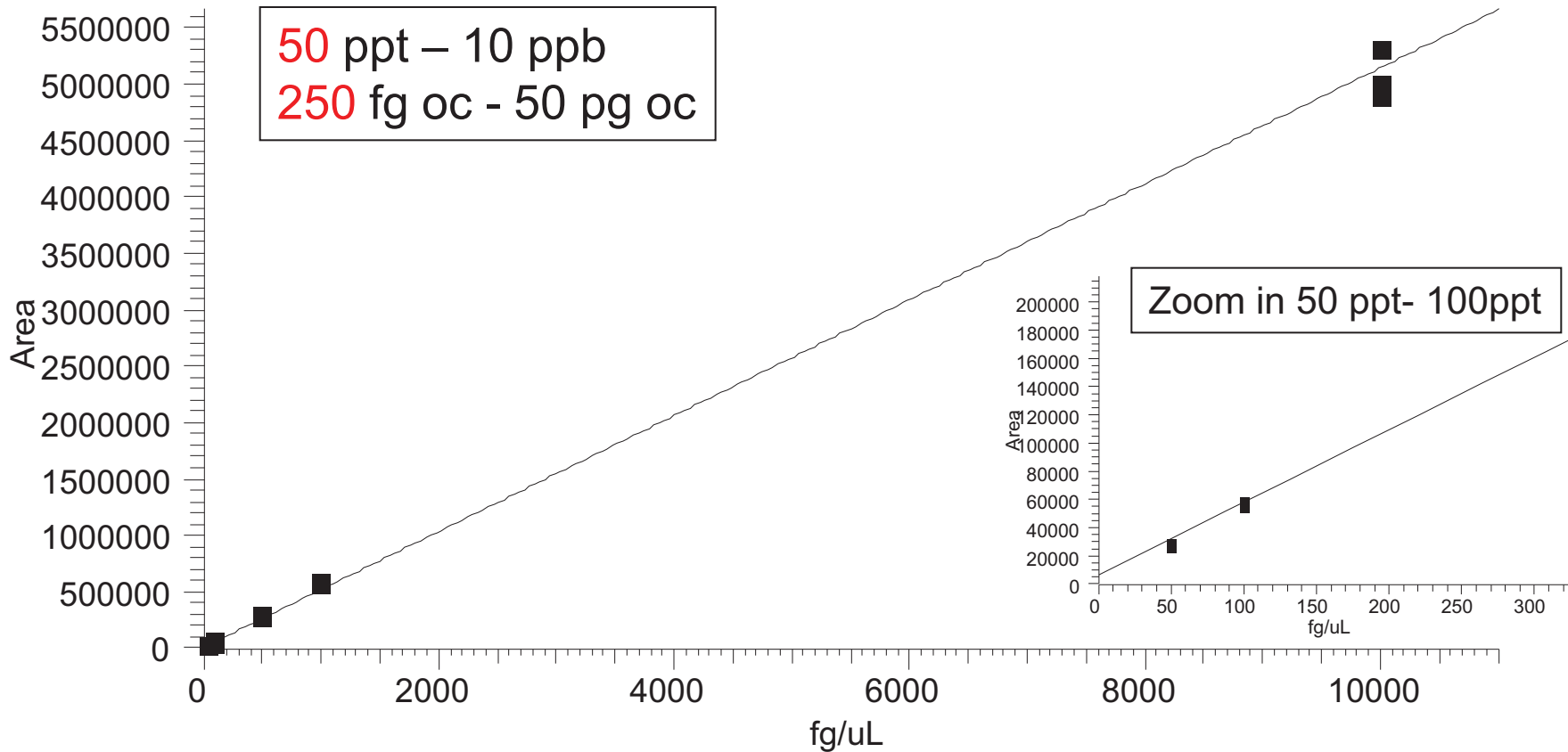
- Sensitivity gain 5 – 10 x with SIM mode
- The gain will be higher in more complex matrices



Alprazolam, Full-Scan Experiment

Alprazolam

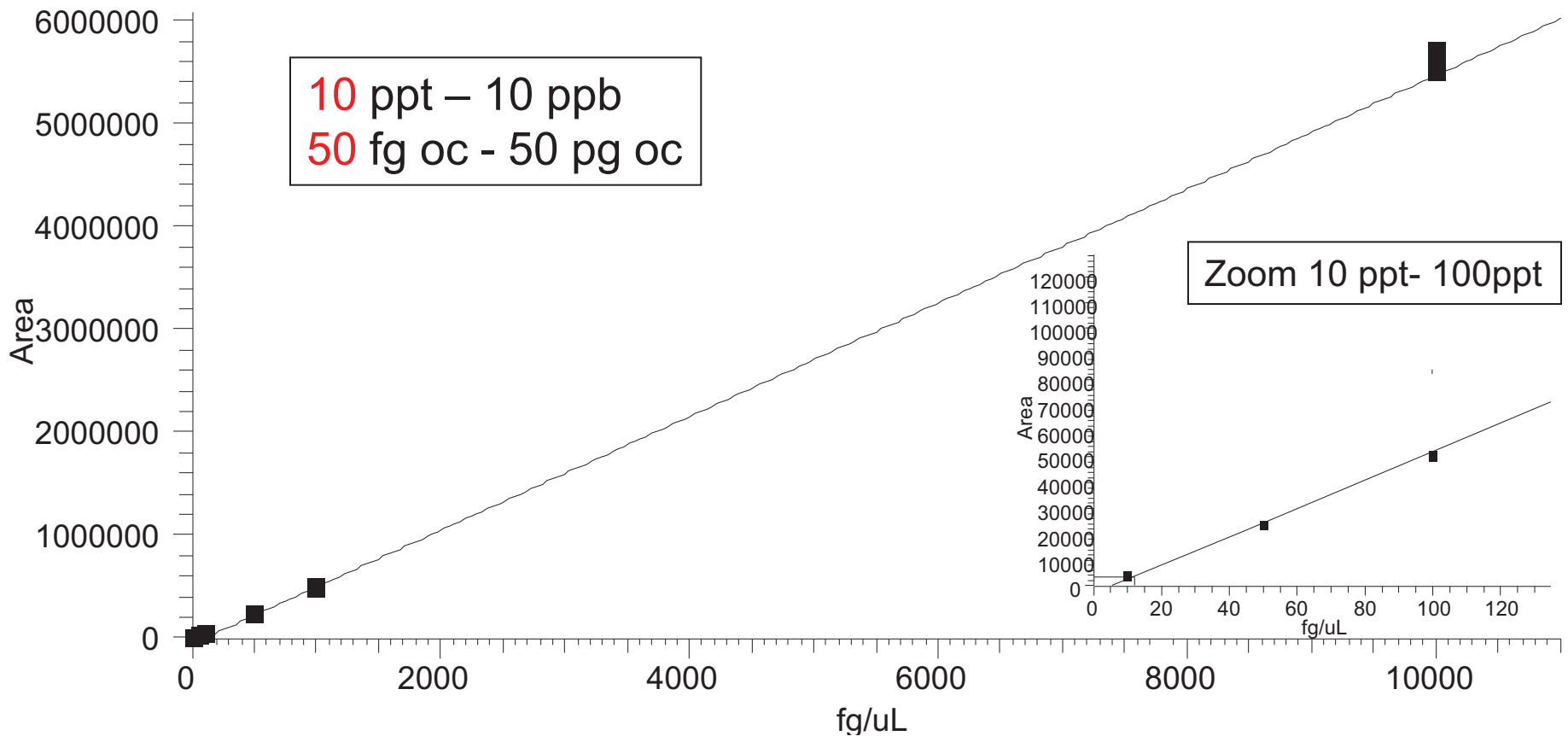
$$Y = 6366.31 + 514.015 * X \quad R^2 = 0.9967 \quad W: 1/X$$



Alprazolam SIM Experiment

Alprazolam

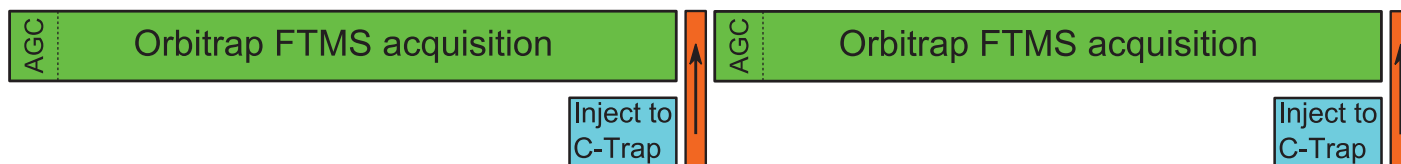
$$Y = -3135.8 + 552.216 * X \quad R^2 = 0.9982 \quad W: 1/X$$



See also: X. He; M. Kozak. "Evaluation of quantitative performance for testosterone analysis in plasma on a novel quadrupole Orbitrap mass spectrometer". Proc. 59th Conf. Amer. Soc. Mass Spectrom., Denver June 5-9, 2011, **Poster WP077**.

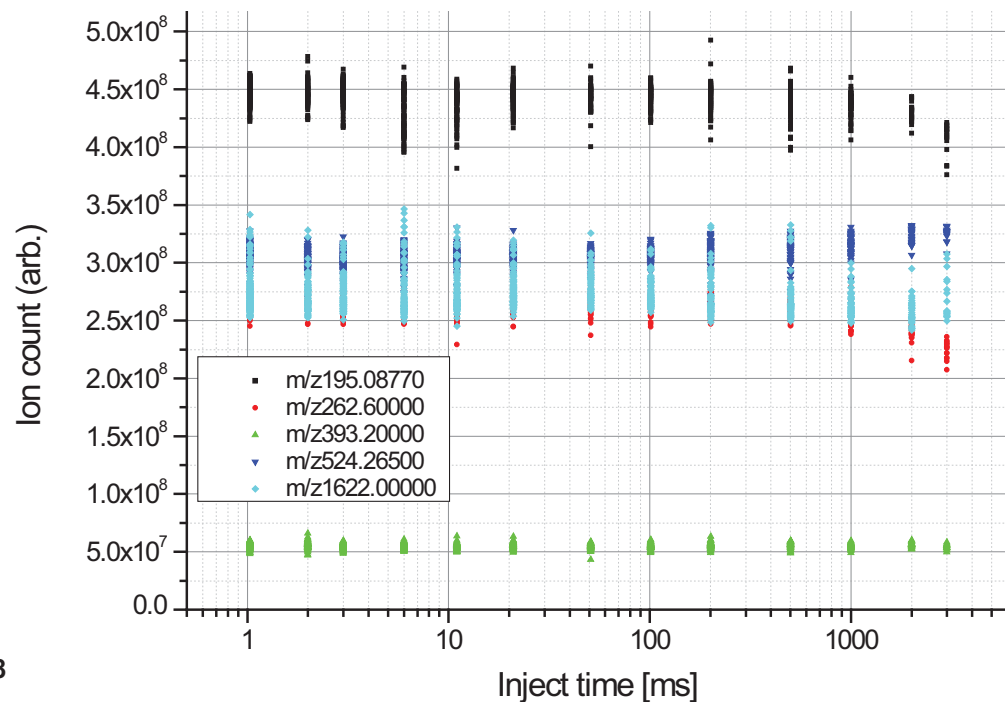
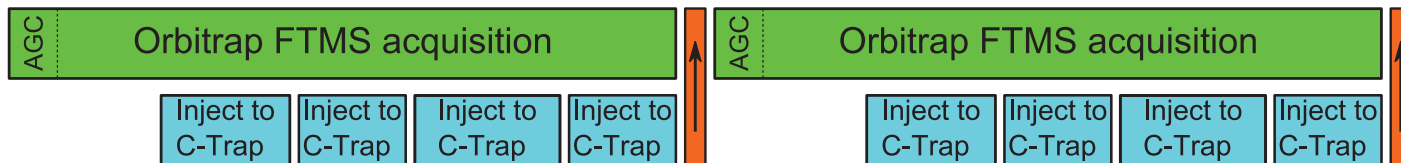
Spectrum multiplexing: principle of operation

Standard operation mode



vs

Spectrum multiplexing



C-Trap storage: No ion loss over a broad range of storage times!

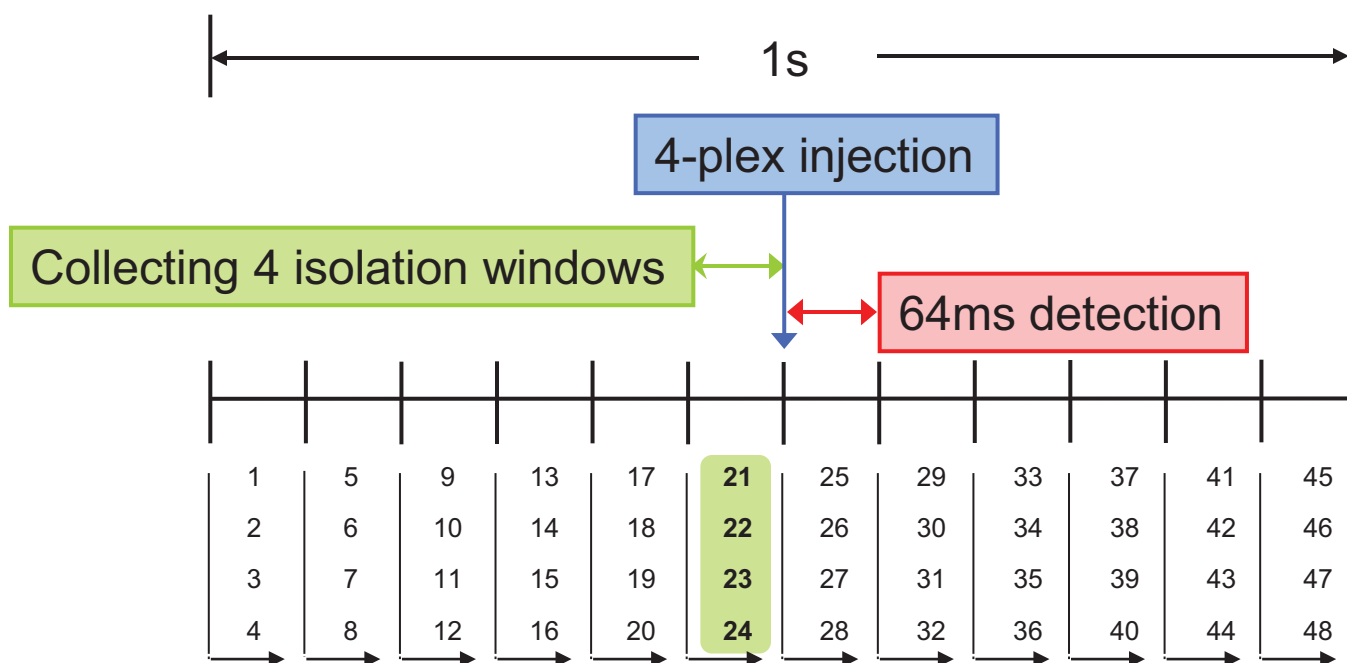
(St. Steel, fused silica, ceramics)

Spectrum multiplexing: example of 4-plex SIM

Experimental Setup: 1 Cycle

12 Hz Acquisition Rate

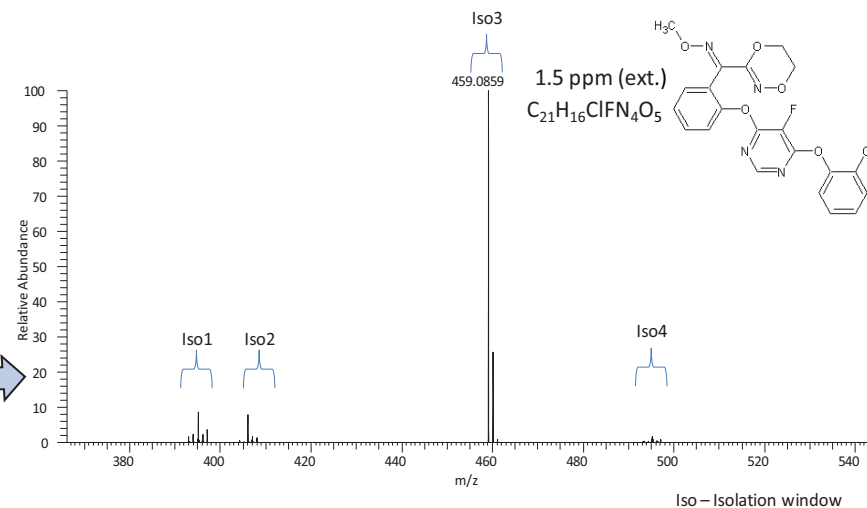
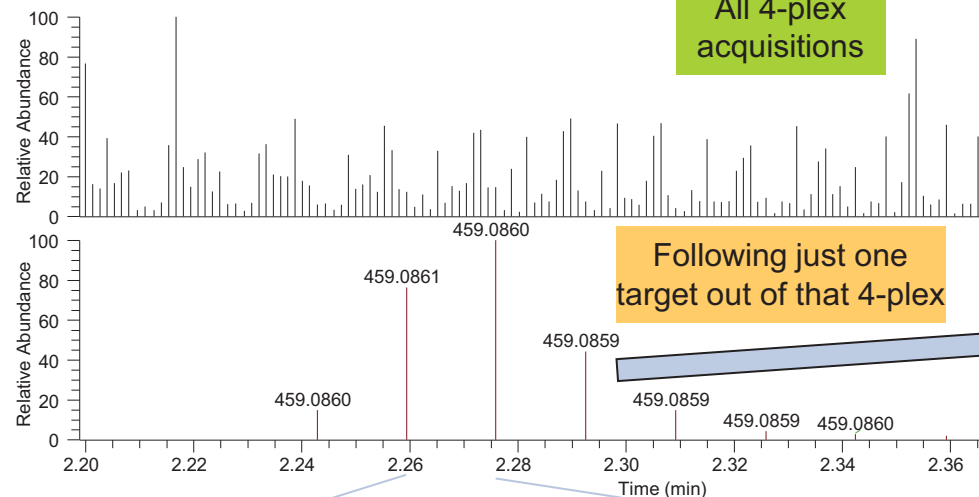
48 Precursors / second



Please see: O. Lange; J.-P. Hauschild; A. Makarov; U. Fröhlich; C. Crone; Y. Xuan; M. Kellmann; A. Wiegand. "Multiple C-Trap Fills as a Tool for Massive Parallelization of Orbitrap Mass Spectrometry- a new Concept for Targeted Mass Analysis".

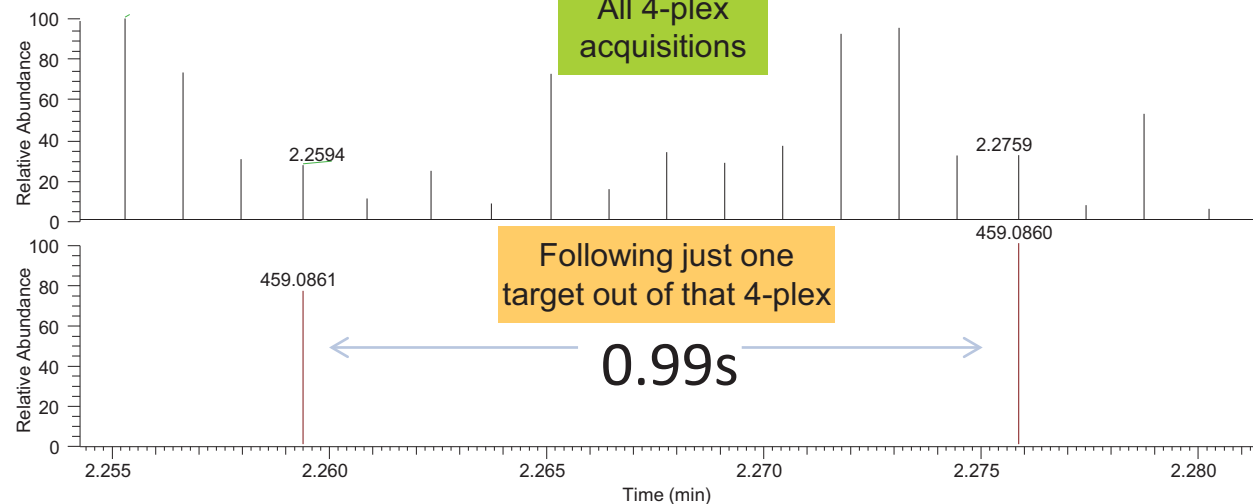
Example Fluoxastrobin, [M+H]⁺ calc. 459.0866

RT: 2.1989 - 2.4164



zoom

RT: 2.2543 - 2.2815



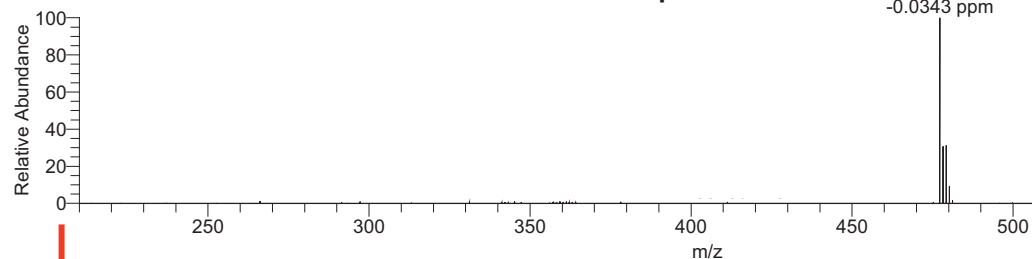
- If we were doing this by conventional SIM, we would have had 4 times less data points across the peak!
- At high resolution and mass accuracy, fragmentation is frequently not needed!

Boosting dynamic range by multiple fills

20110509 JPH JG DEP2 DynRangeTest Sol2_2_70k #520 RT: 2.48 AV: 1 NL: 1.44E9
T: FTMS + p ESI Full ms [210.00-600.00]

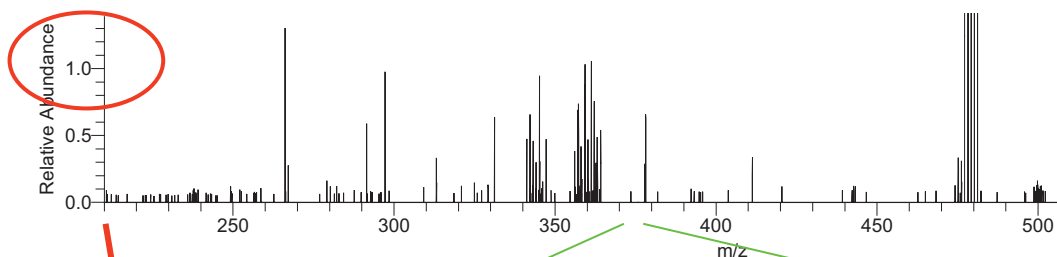
Research only!

Loperamide
477.2303
R=51306
N=881374.69
C₂₉H₃₄O₂N₂Cl
-0.0343 ppm



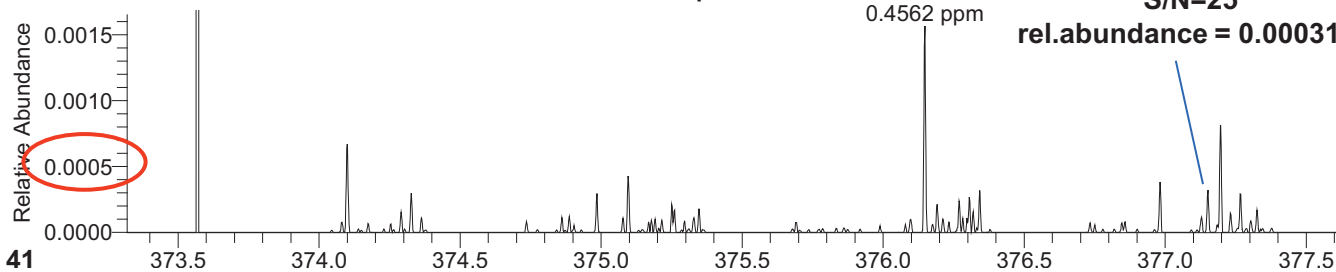
[m/z 200..600]@ 0.1ms &
[m/z 374..378]@ 250ms

↓ zoom



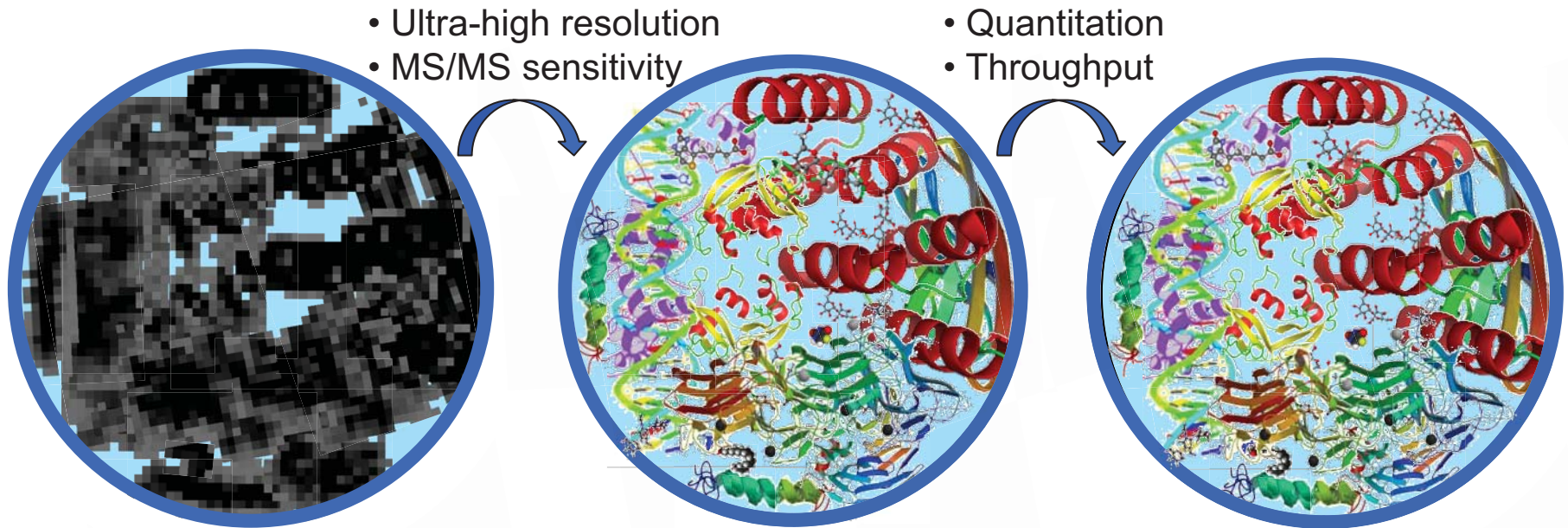
zoom

Haloperidol
376.1476
R=56802
N=169.29
C₂₁H₂₄O₂N Cl F
0.4562 ppm
(A+1) Isotope: 377.1513
R=53502
N=169.13
S/N=25



rel.abundance = 0.00031% ← DR>320.000

Conclusion



- The Orbitrap Mass Analyzer is a new type of mass analyzers with its own unique combination of analytical parameters
- Orbitraps are still evolving...
 - Higher speed
 - Higher resolving power and mass accuracy
 - Higher sensitivity
 - More routine applications
- Exciting new applications continue to emerge

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