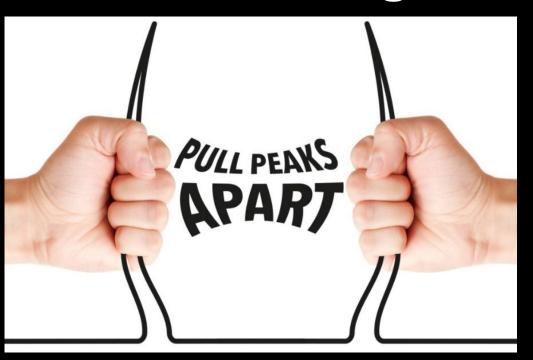




#### 28èmes Journées Scientifiques de ccCTA

## Ultra-High-Resolution (UHR) MS: The Blessing, The Curse, The Data Overload



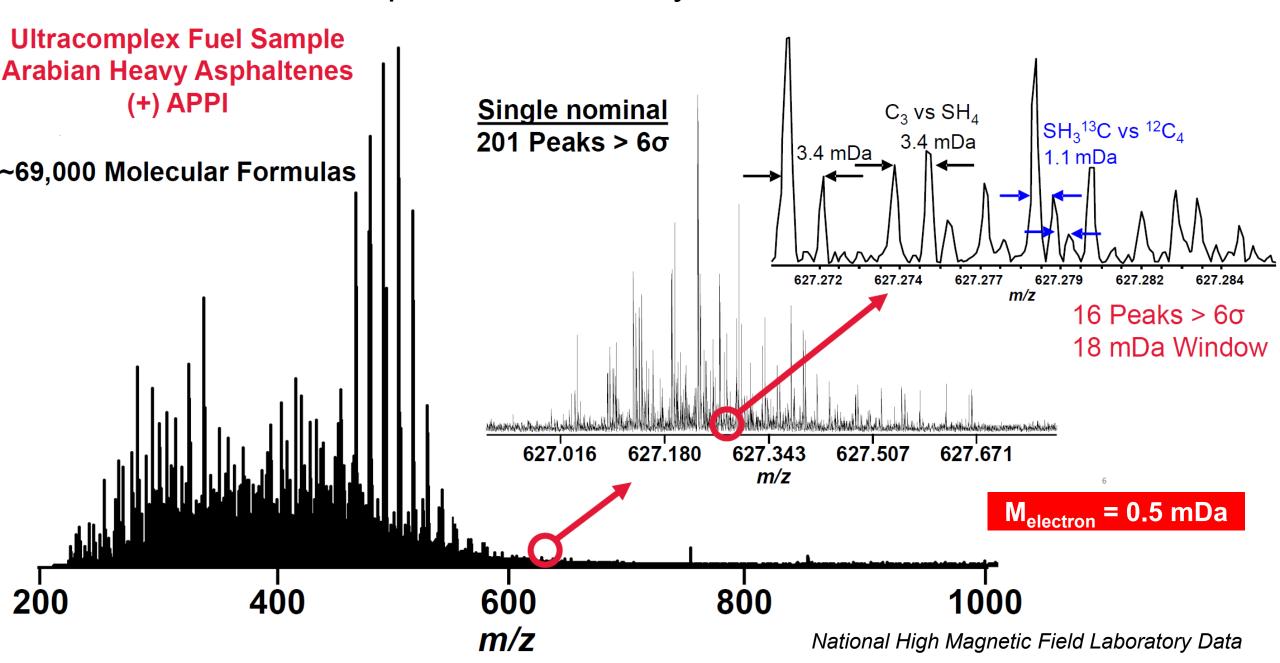
On the use, possibilities, & limitations of UHR MS (FT-ICR MS & Orbitraps)

Yury Tsybin tsybin@spectroswiss.ch

Spectroswiss Sàrl Lausanne, Switzerland Villars-sur-Ollon, Near home October 2, 2025; 15:10-15:40

#### Spectroswiss

#### Complex Mixture Analysis with UHR MS





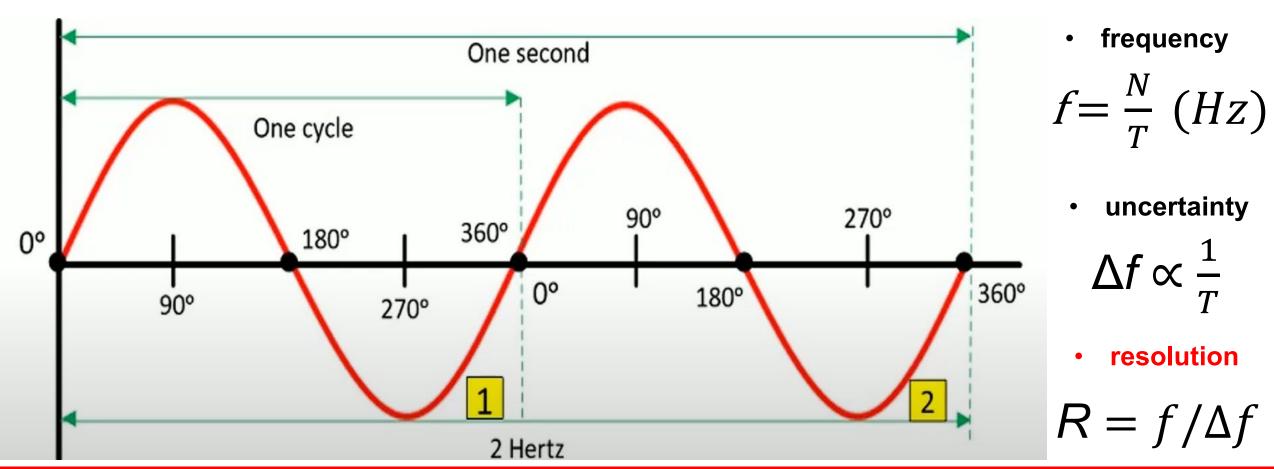
#### Core Scientific Question UHR MS Answers:

### Which exact elemental compositions are in this peak? by separating what other (LRMS & HRMS) mass spectra blur together

- Single vs. composite peak? Distinguish a lone species from a superposition of near-isobars.
- Unambiguous formula assignment. Use exact mass + isotopic fine structure (e.g., <sup>34</sup>S vs <sup>13</sup>C2; Cl/Br patterns) to pin down elemental composition, especially at higher *m/z*.
- **Heteroatom counting.** Determine the number of S/Cl/Br (and sometimes N/O) directly from isotopic fine structure.
- Adduct/charge state clarity. Separate overlapping adducts/charge states that would otherwise
  masquerade as one feature.
- Deconvolution of congested mixtures. In complex matrices (PFAS, environmental DOM, unknowns), map compositional space rather than a blur.
  - BUT... UHR MS won't resolve constitutional/positional/stereo isomers need MS/MS, chromatography, ion mobility, or all of the above.

#### How to Achieve Ultra-High-Resolution (UHR) MS?

- Measure frequency of ion oscillations, not an arrival time on a detector (a single-shot measurement)
- Measure thousands to millions of oscillations over the detection time (can be seconds)
- Each oscillation contributes another "vote" for the true frequency, reducing uncertainty



How to establish an oscillation motion of ions and how to measure the frequency?



#### FTMS: Fourier Transform Mass Spectrometry

- Ion identity (m/z) is encoded as a frequency of ion oscillations in an ion trap
- Frequencies of ion oscillations are measured as time-domain signals (transients)
- Each transient comprises hundreds of thousands to millions of oscillations
- Fourier transform (FT) decodes transients to reveal frequencies (m/z) values

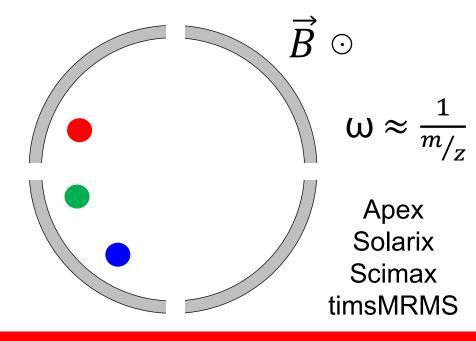
#### **Electrostatic field-based**

# Orbitrap $\omega \approx \sqrt{\frac{k}{m_{/z}}}$

Orbitrap<sup>TM</sup> families: LTQ Orbitrap; Exactive; Q Exactive; Exploris; Excedion; Fusion; Lumos; Eclipse, Ascend, Astral

Magnetic field-based

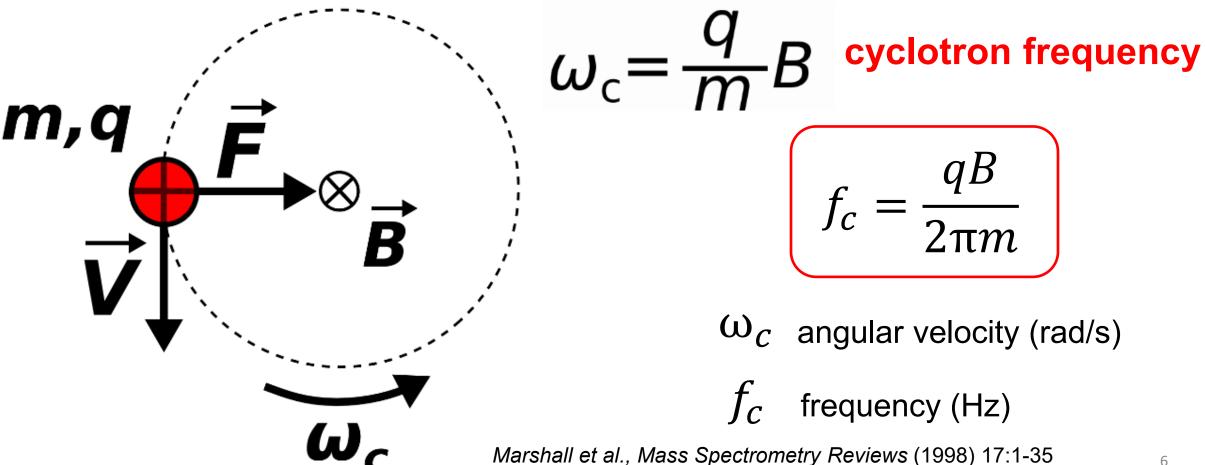
#### Ion Cyclotron Resonance (ICR)





#### FT-ICR MS Concept: Ion Cyclotron Frequency use of the magnetic field

- Cyclotron frequency is independent of the radius and velocity and therefore independent of the ion's kinetic energy
- All ions with the same charge-to-mass ratio rotate around magnetic field lines with the same cyclotron frequency



Ion Dete

Ion packet inject



Ion trapping (on-



Ion excitation to a radius with an RF (compact clou



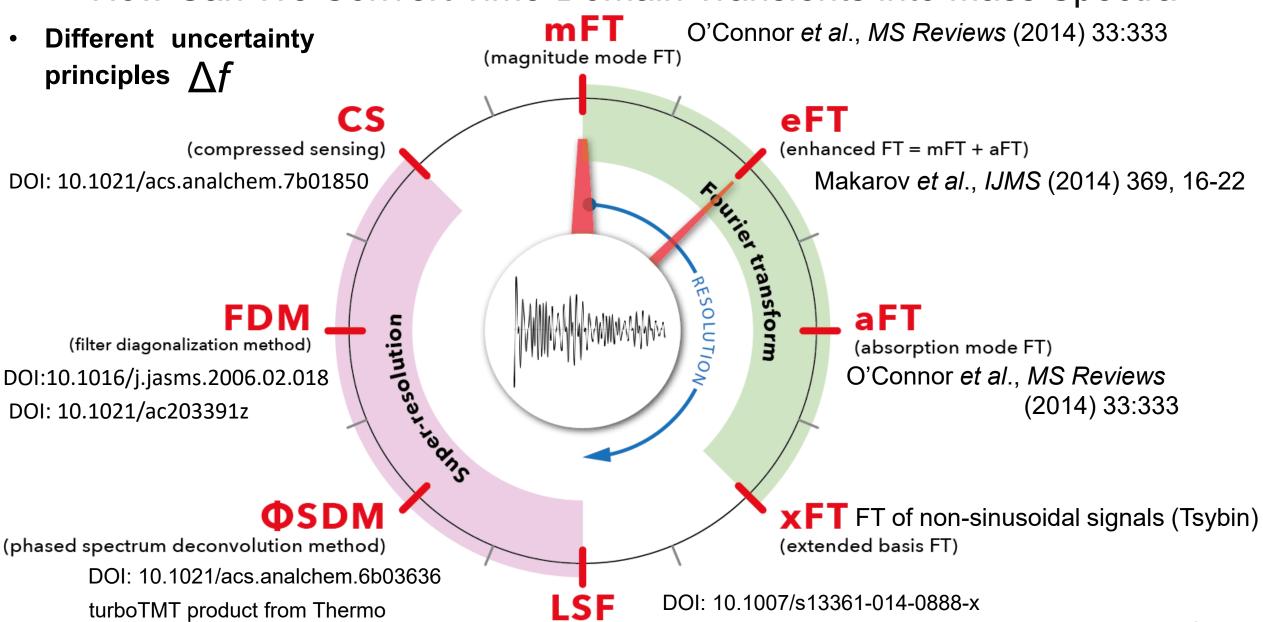
Ion detection (induced ion curr



Quench of ion (ion ejection)



#### How Can We Convert Time-Domain Transients into Mass Spectra



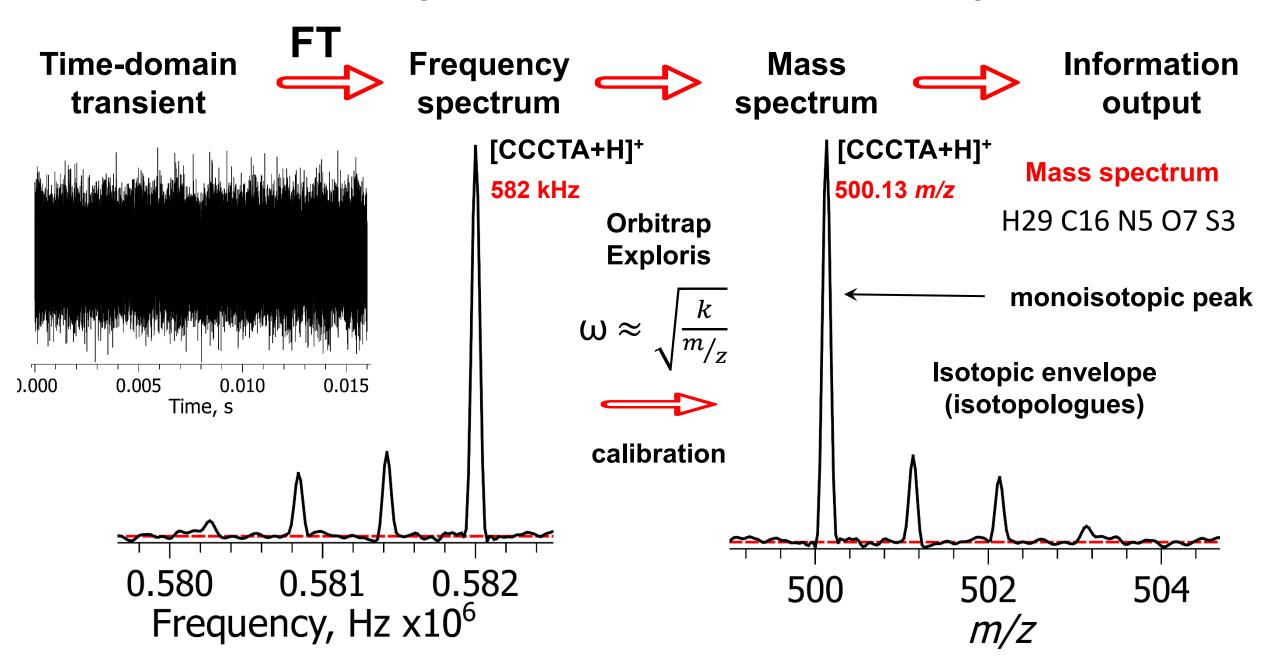
(least-squares fitting)

DOI: 10.1002/mas.21681

8

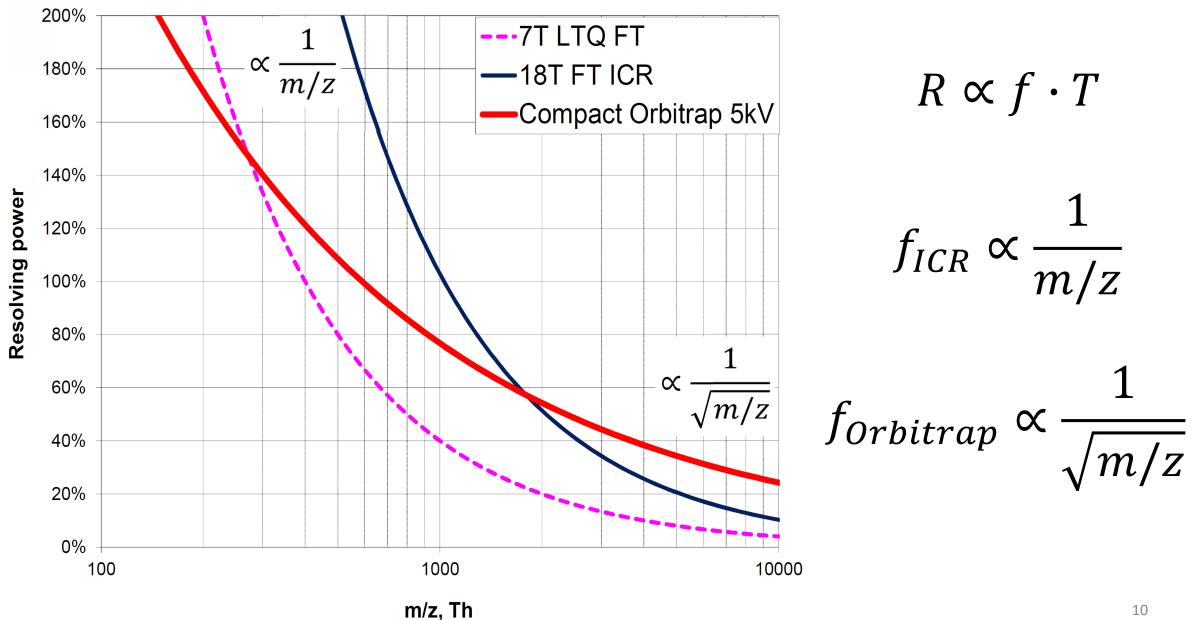


#### Data Processing in FTMS: from time to **frequency**, to *m/z*



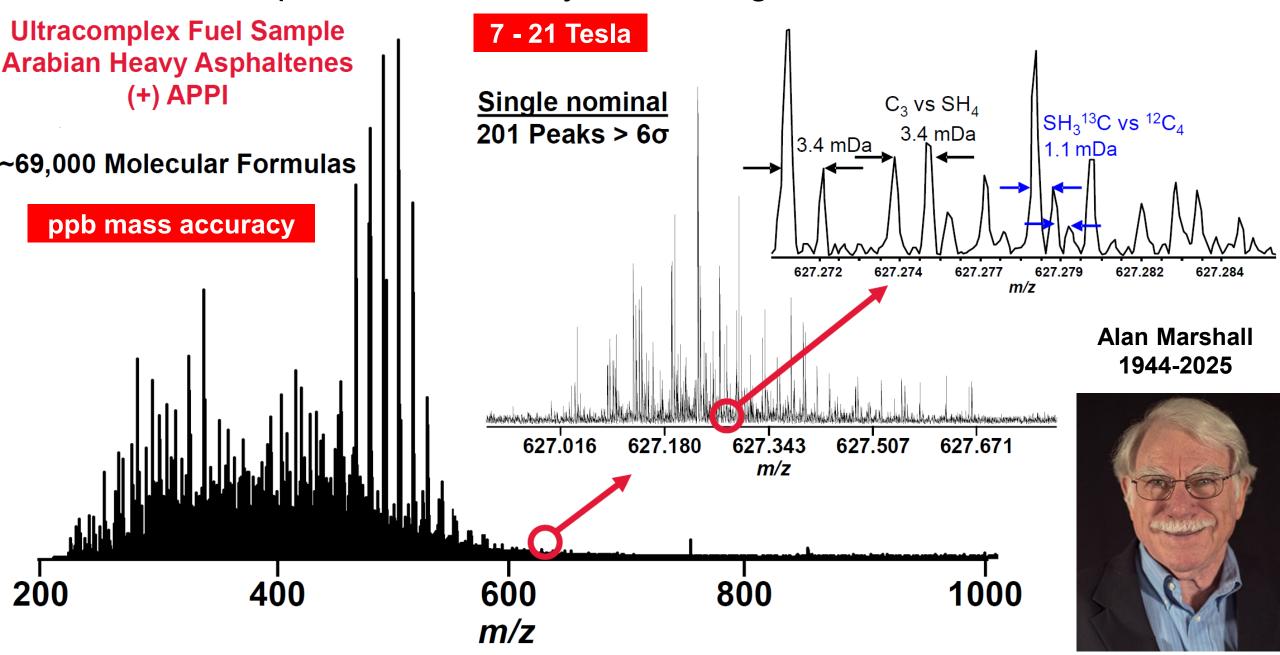


#### Resolution = function of frequency or m/z





#### Complex Mixture Analysis with High-Field FT-ICR MS



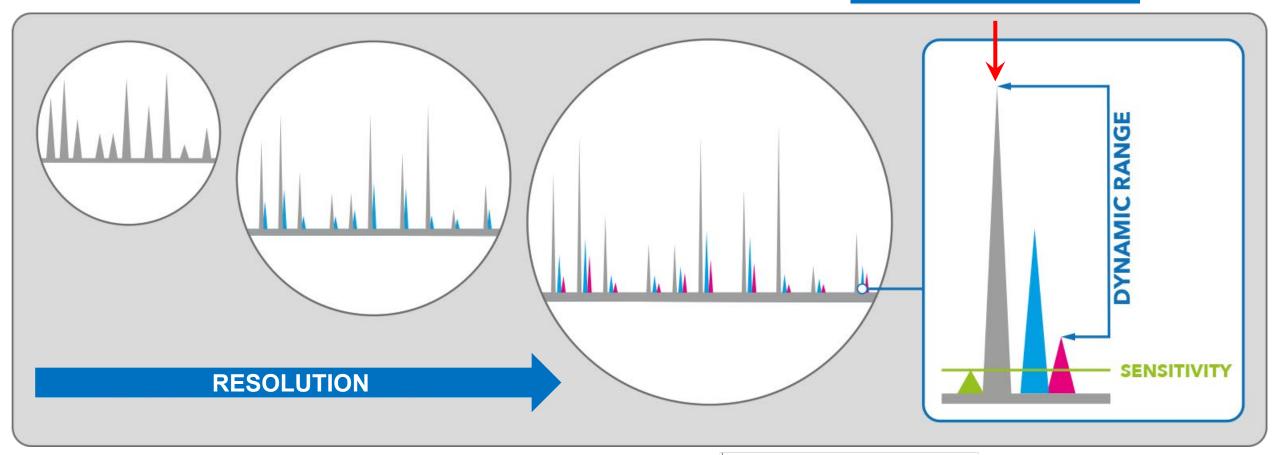
#### **FTMS Analytical Characteristics**

Spectroswiss

- the highest resolution
- the highest mass accuracy

#### ABUNDANCE ACCURACY

**MASS ACCURACY** 



**DATA ACQUISITION SPEED (THROUGHPUT)** 

induced current ion detection (transients)

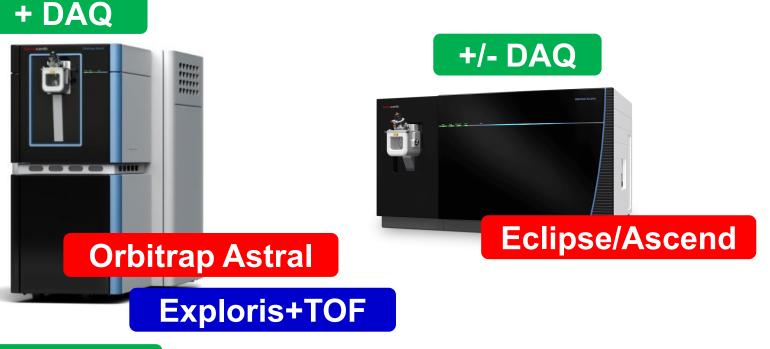


 $R \propto f \cdot T$ 

#### Spectroswiss

Kozhinov et al.,

#### What Instruments Offer UHR MS: ICRs & Orbitraps







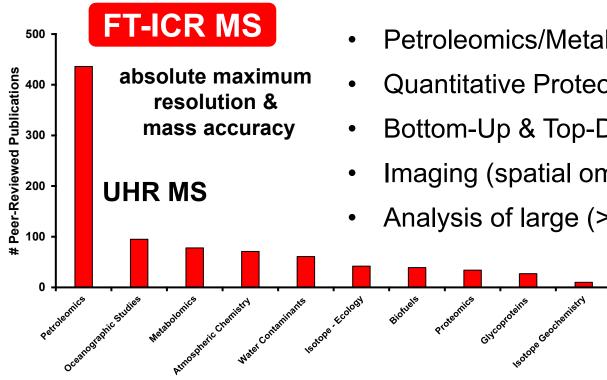




DAQ: high-performance Data Acquisition (DAQ) system



#### FTMS Applications: ICRs & Orbitraps



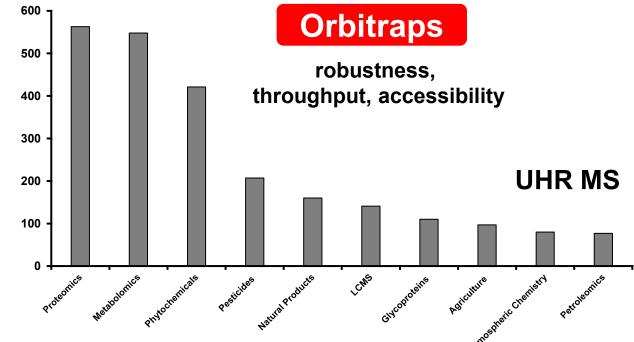
- Petroleomics/Metabolomics: isobars, isotopic fine structure (IFS)
- Quantitative Proteomics/Lipidomics: multiplexing with labeling
- Bottom-Up & Top-Down: higher sequence coverage, confidence
- Imaging (spatial omics): more IDs, higher confidence
- Analysis of large (> 1 MDa) biomolecules: individual (single) ion counting

#### FT-ICR MS:

Unmatched in resolution (>10,000,000), mass accuracy, & spectral complexity handling (better space charge control).

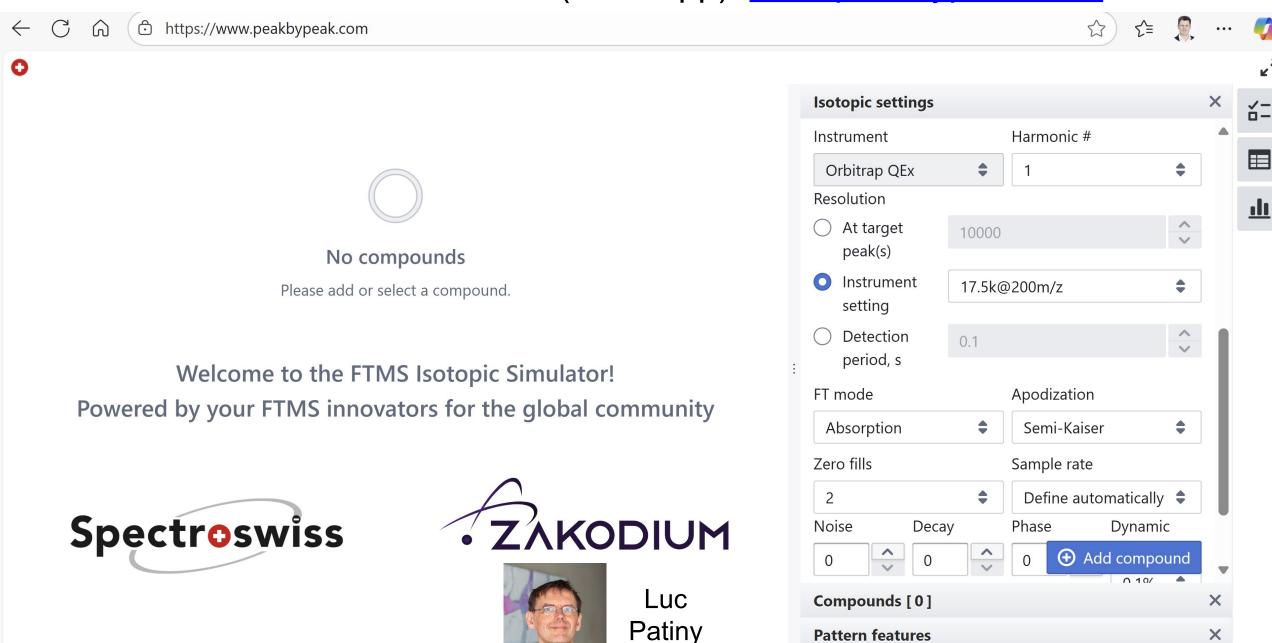
#### **Orbitraps:**

Sufficient for most HRMS & UHR MS needs (<1,000,000 resolution). Ideal for routine proteomics, biopharma, and clinical labs (easier LC-MS operation).



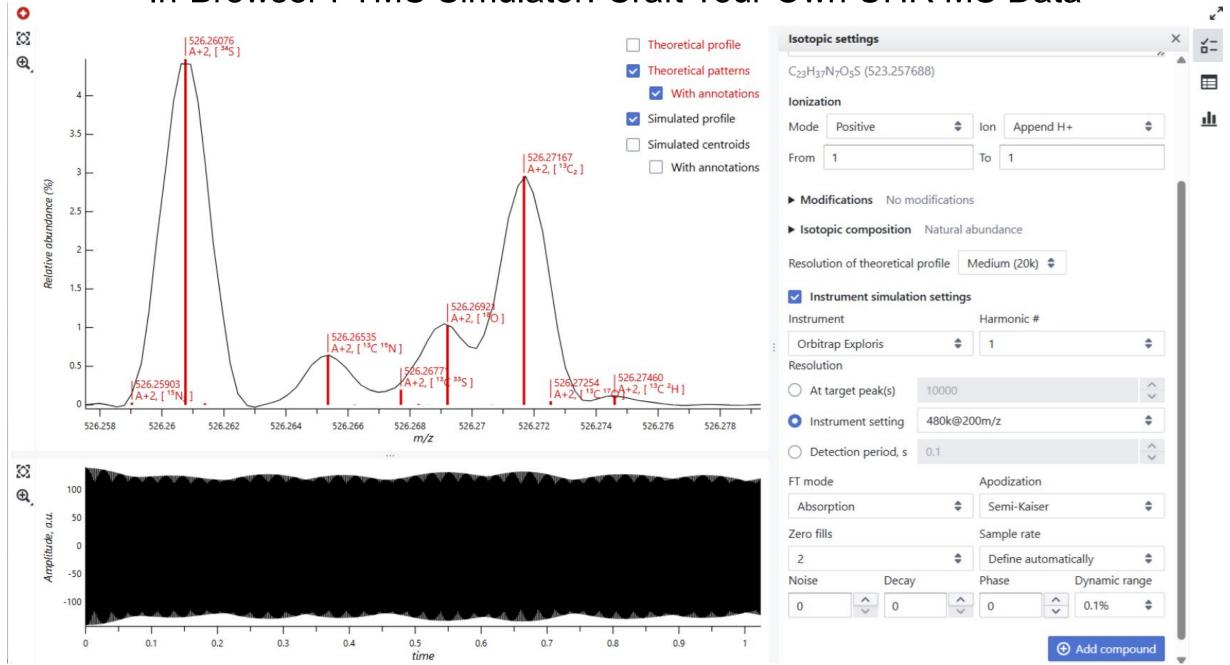
#### In-Browser FTMS Simulator (Web-App): www.peakbypeak.com

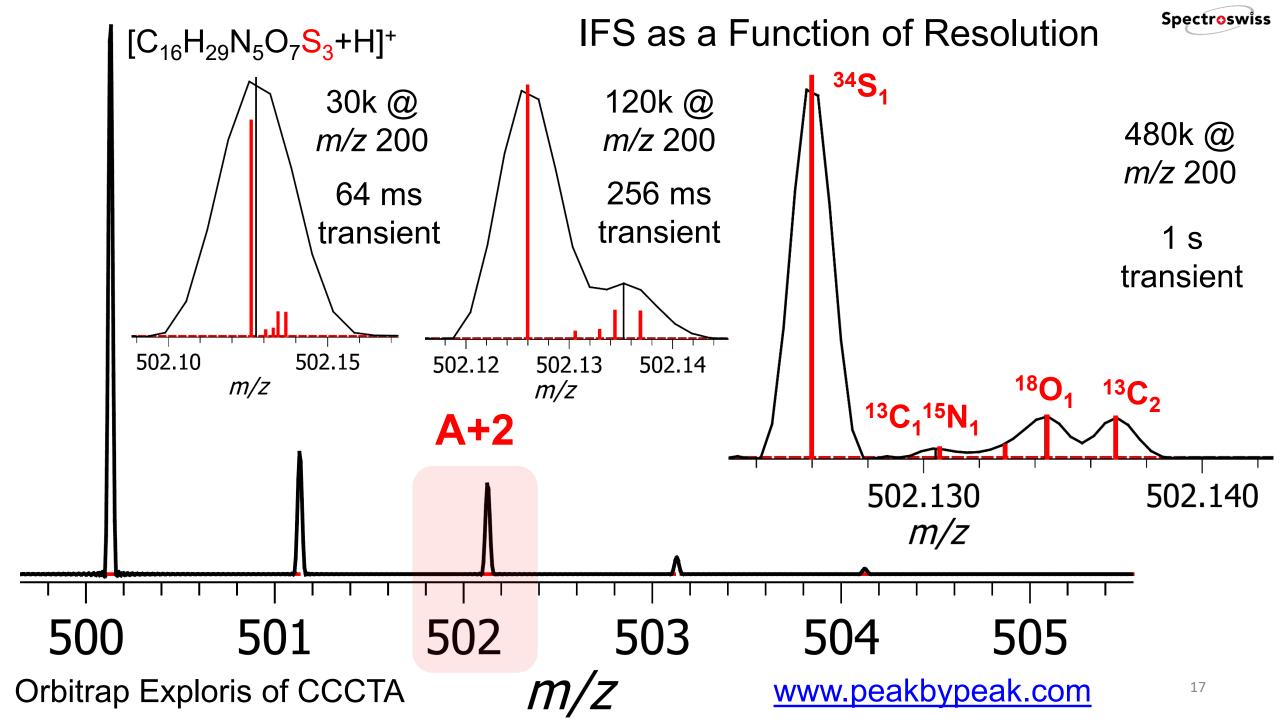


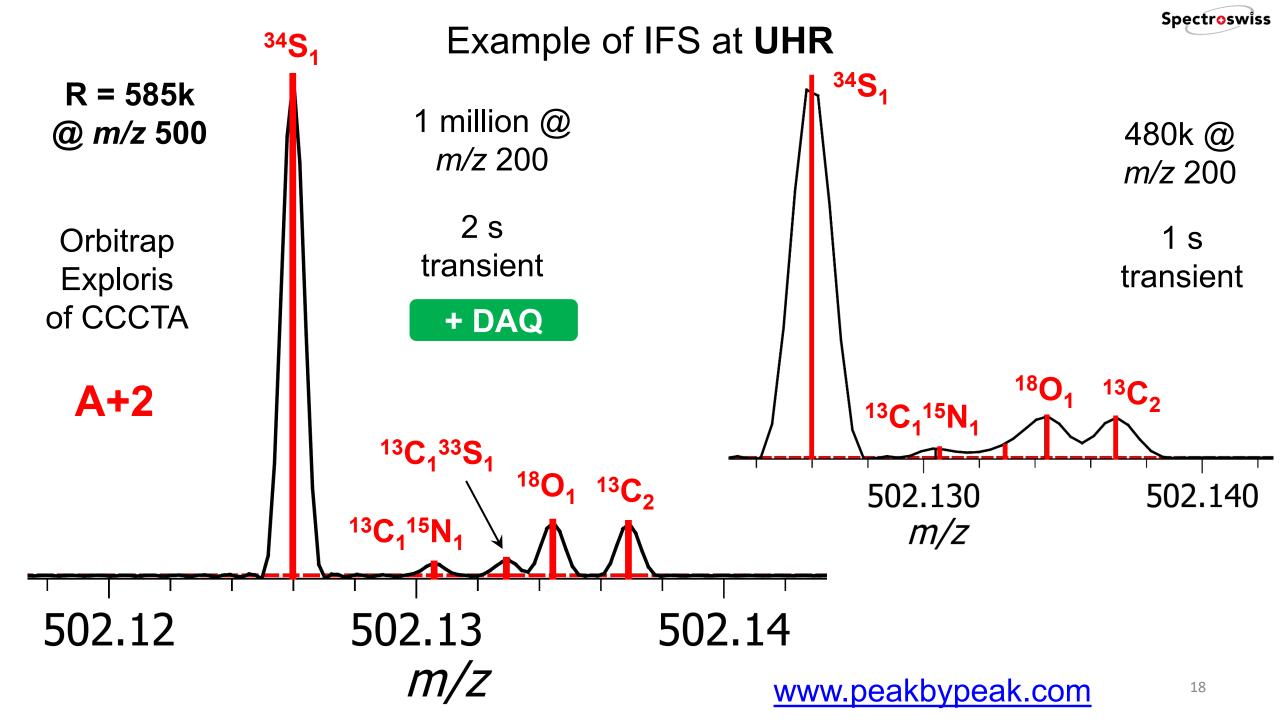




#### In-Browser FTMS Simulator: Craft Your Own UHR MS Data

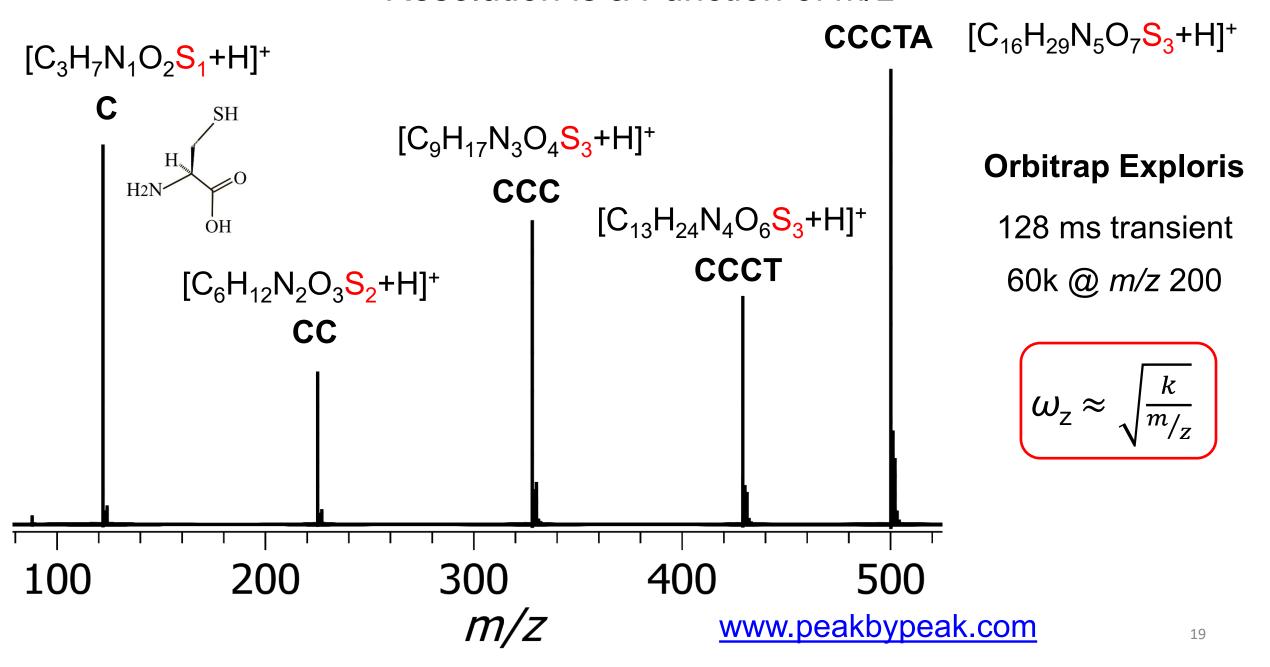






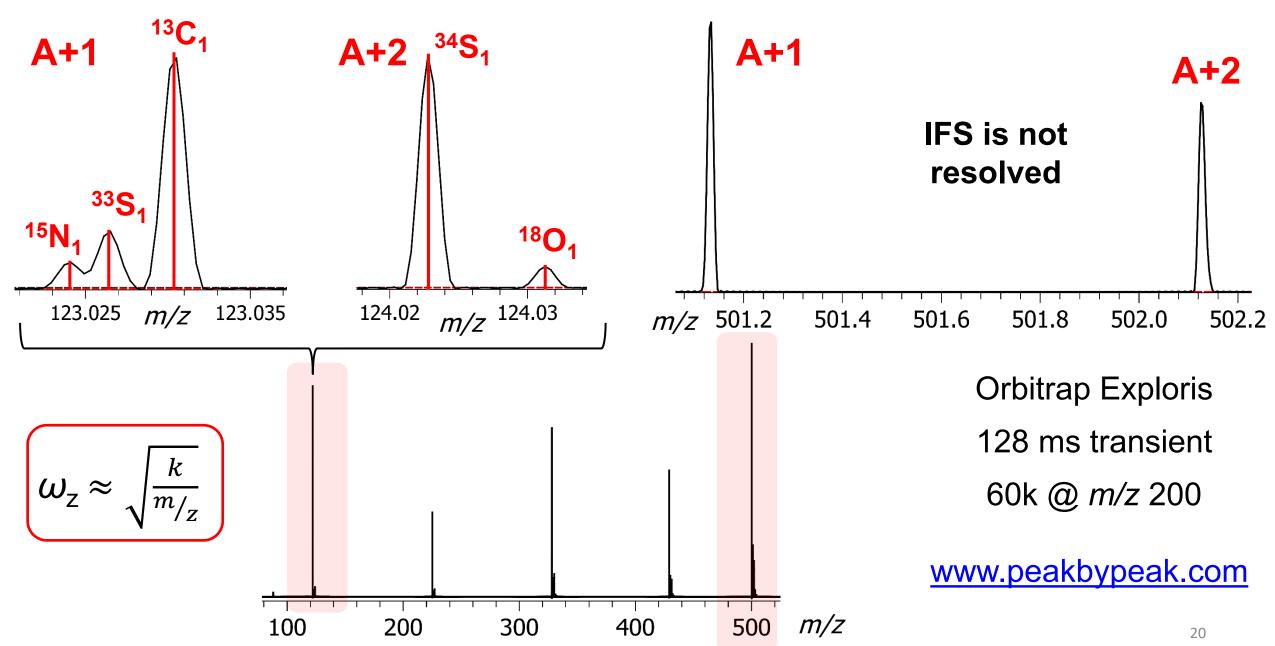
#### Spectroswiss

#### Resolution is a Function of m/z



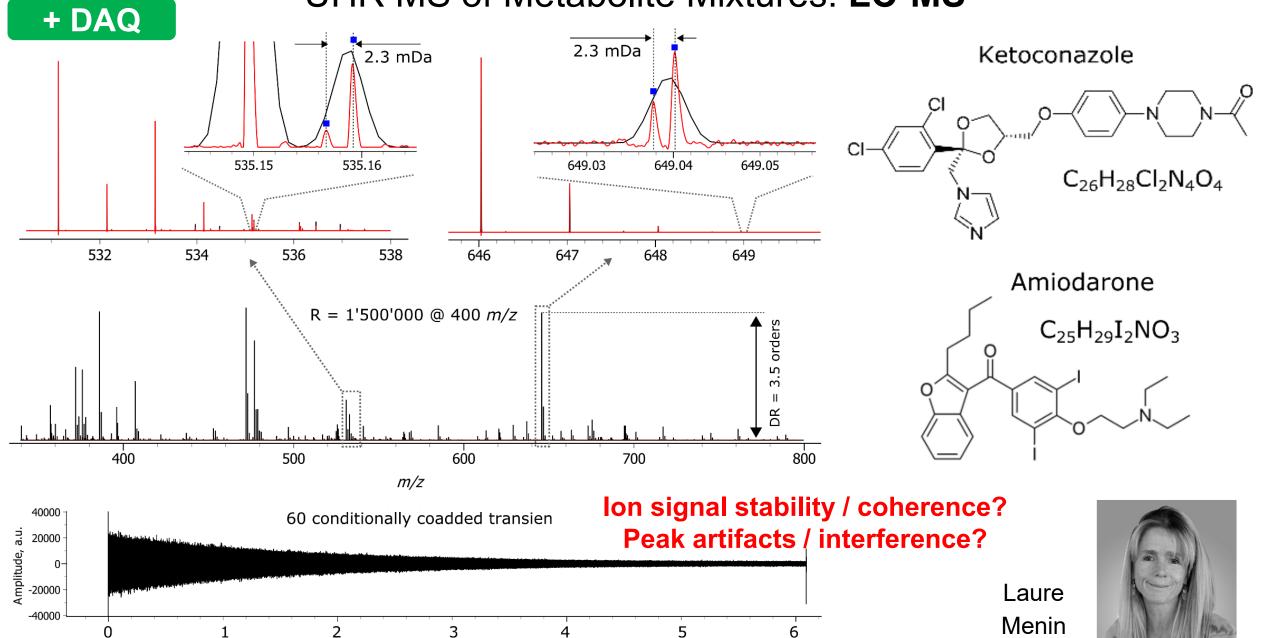
#### Spectroswiss

#### UHR MS: Use with Caution!





#### UHR MS of Metabolite Mixtures: LC-MS

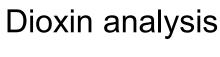


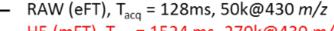
Time, s



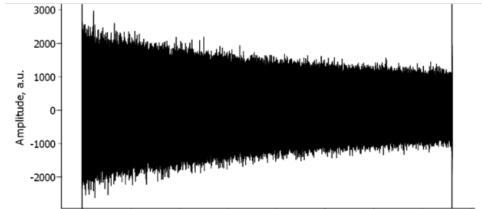
#### + DAQ

#### UHR MS of Volatile Compounds: GC-MS

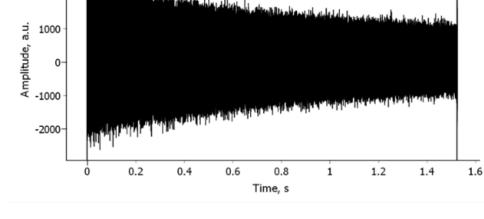


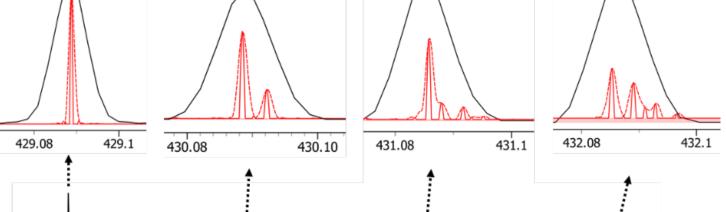


H5 (mFT),  $T_{acq} = 1524$  ms, 270k@430 m/z



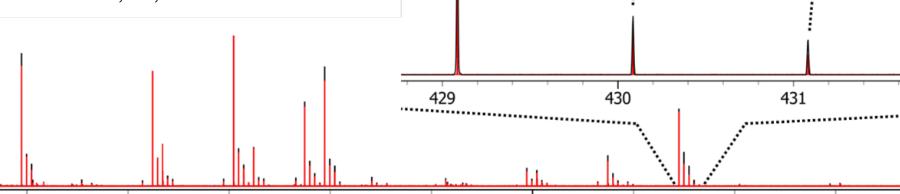






Bleiner et al., JASMS 2020, 31, 257-266



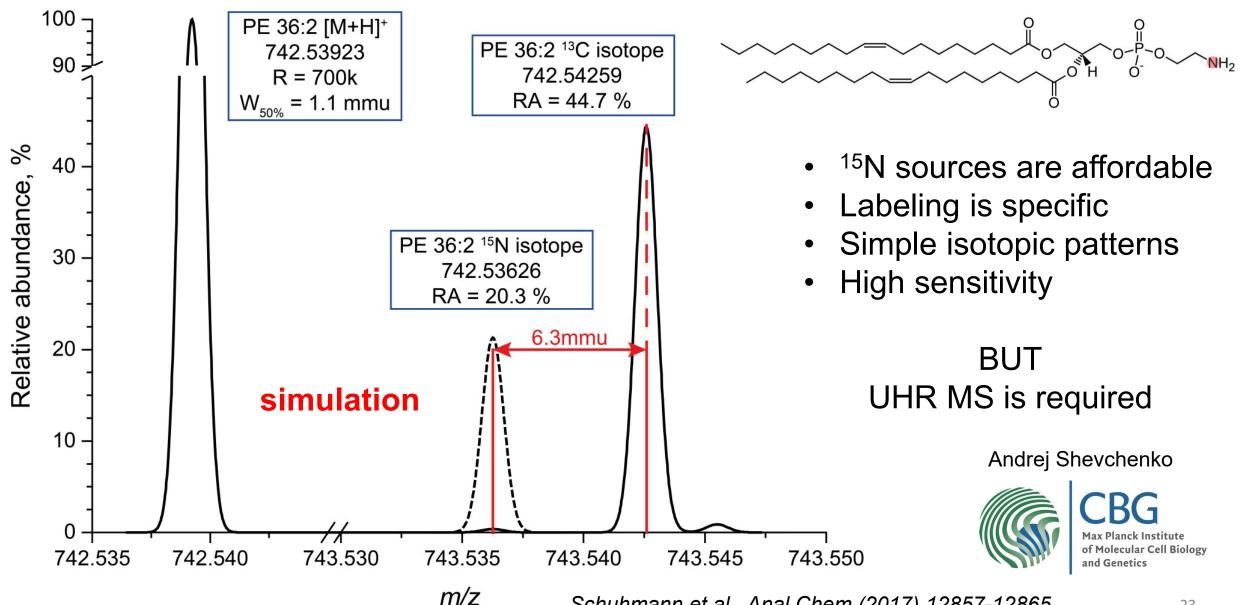


m/z

David Bleiner

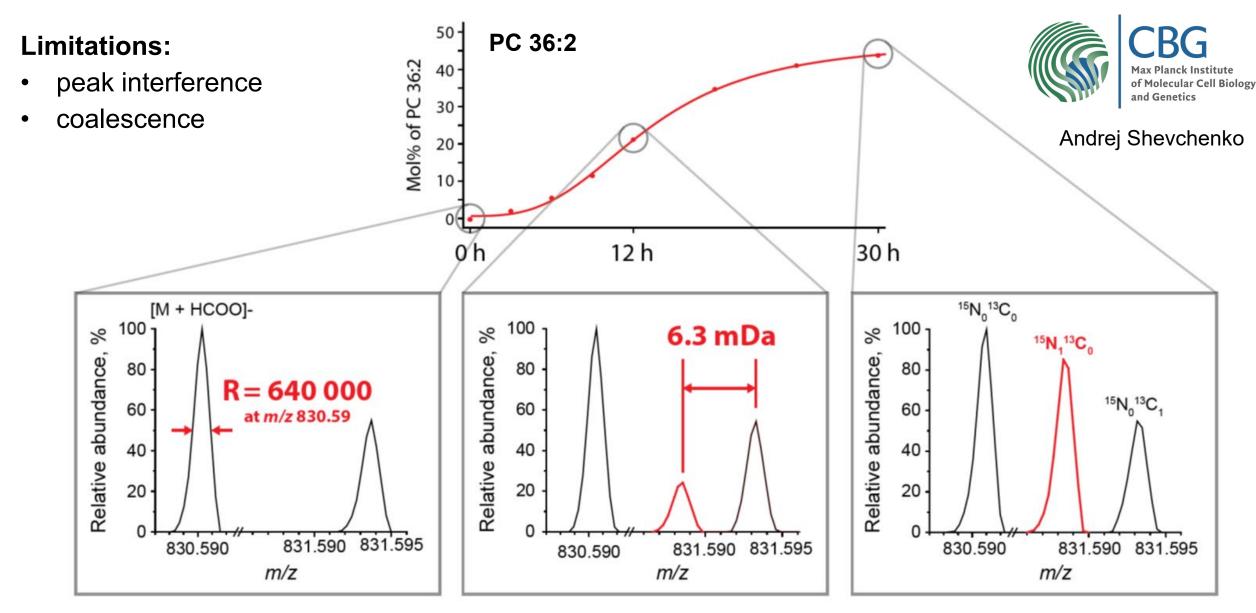


#### UHR MS for **Shotgun Lipidomics**: Multiplexed Quantitation





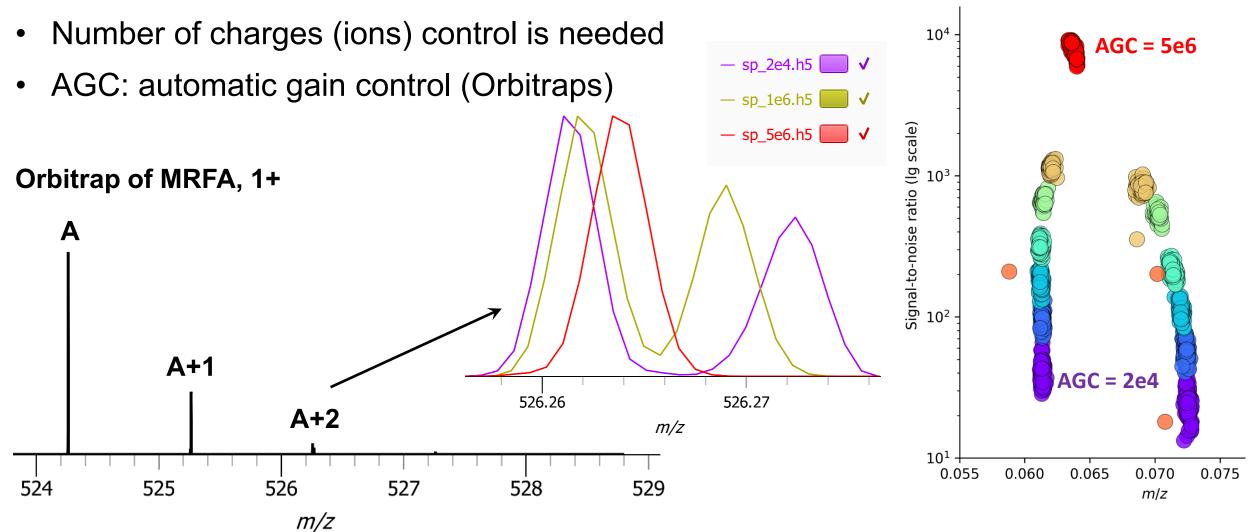
#### Metabolic <sup>15</sup>N labeling: Quantitative Shotgun Lipidomics





#### Space Charge Effects: Peak Artifacts

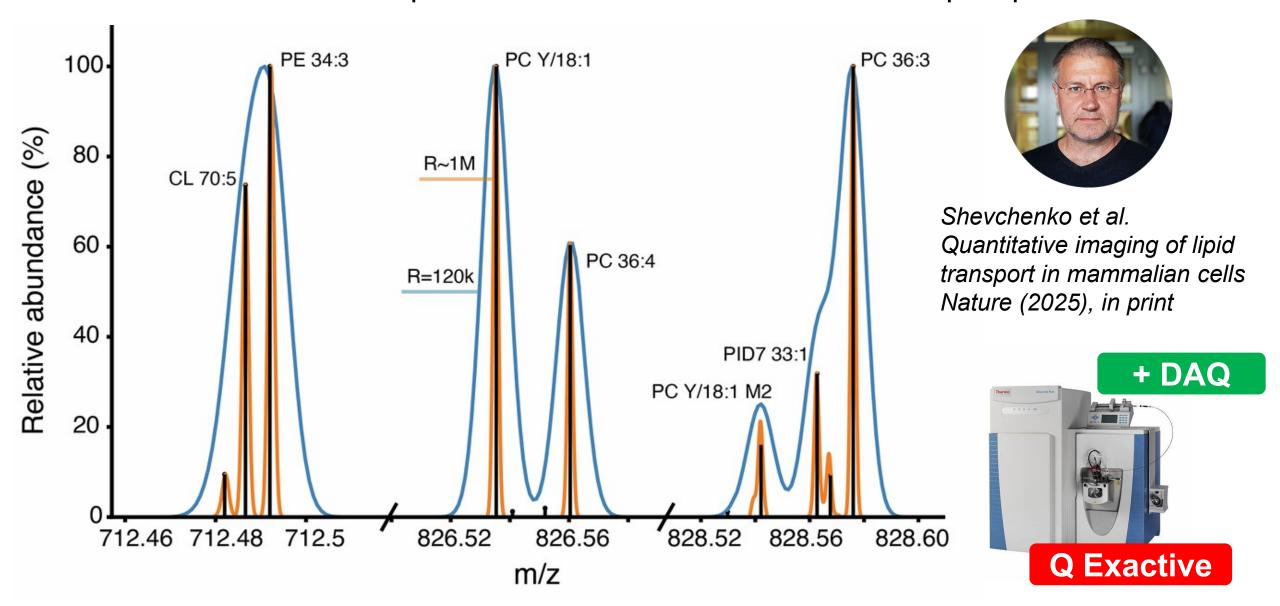
Too many charges (ions): peak artifacts (m/z, abundance errors), coalescence



DOI: abs/10.1002/rcm.6289; DOI: 10.1021/acs.analchem.7b03437

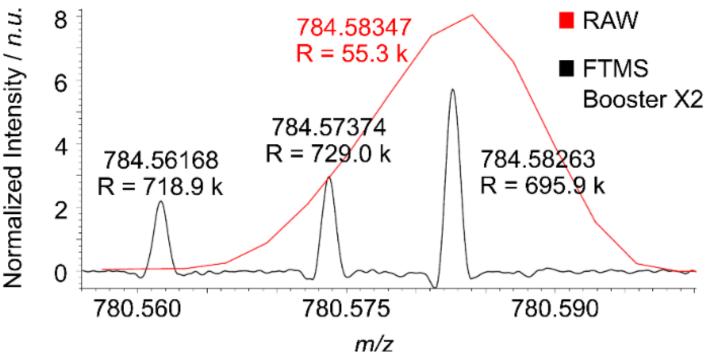


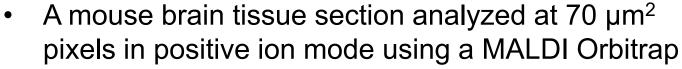
Shotgun UHR MS resolves lipid peaks spaced by a few mDa, matches bifunctional precursors & their metabolites in multiple lipid classes





#### UHR MS Imaging of Lipids





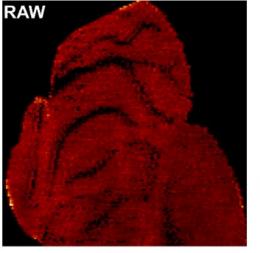
Resolution from 256 ms & 7 s (Booster) transients



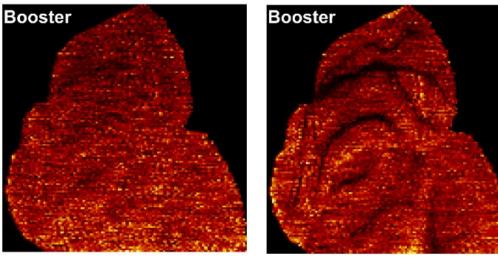
Anal. Chem. 2024, 96, 2, 794–801

+ DAQ





784.58347 [PC 34:0 + Na]+  $\Delta m_i = 1.01 \text{ ppm}$ 



**Booster** 

784.57374 [13C2][PC 34:1 + Na]+  $\Delta m_i = 20.4 \text{ ppb}$ 

 $\Delta m_i = -56.1 \text{ ppb}$ 700 µm **├** 

784.58263

[PC 34:0 + Na]+

784.56168

[PC O-34:1 + K]<sup>+</sup>

 $\Delta m_i$ = -24.2 ppb

0%1

100%

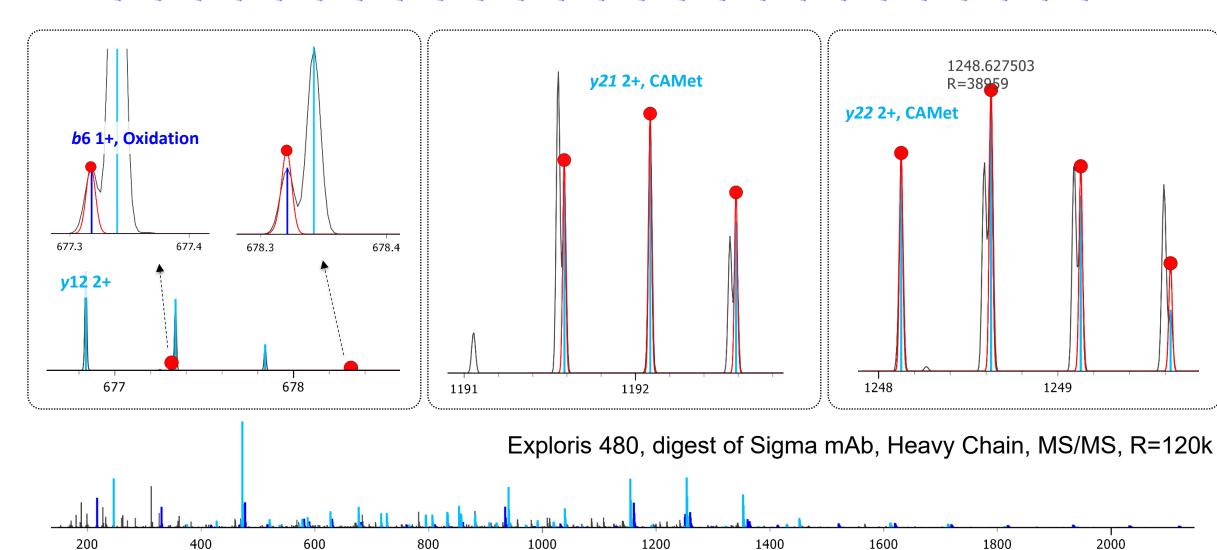
Heeren et al.,



28

#### UHR Bottom-Up Proteomics (Peptide MS/MS)

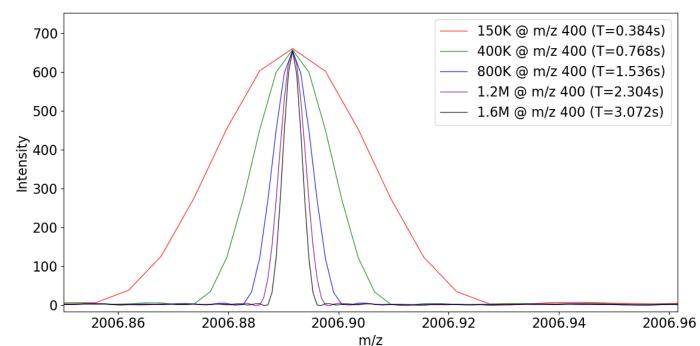
#### N [D[T]LMI]S]R]T]P]E[V]T[C]V]V]V]D]V]S]H]E]D]P]E]V]K]C



m/z



#### UHR Top-Down Proteomics (Protein MS/MS): High Mass Ions



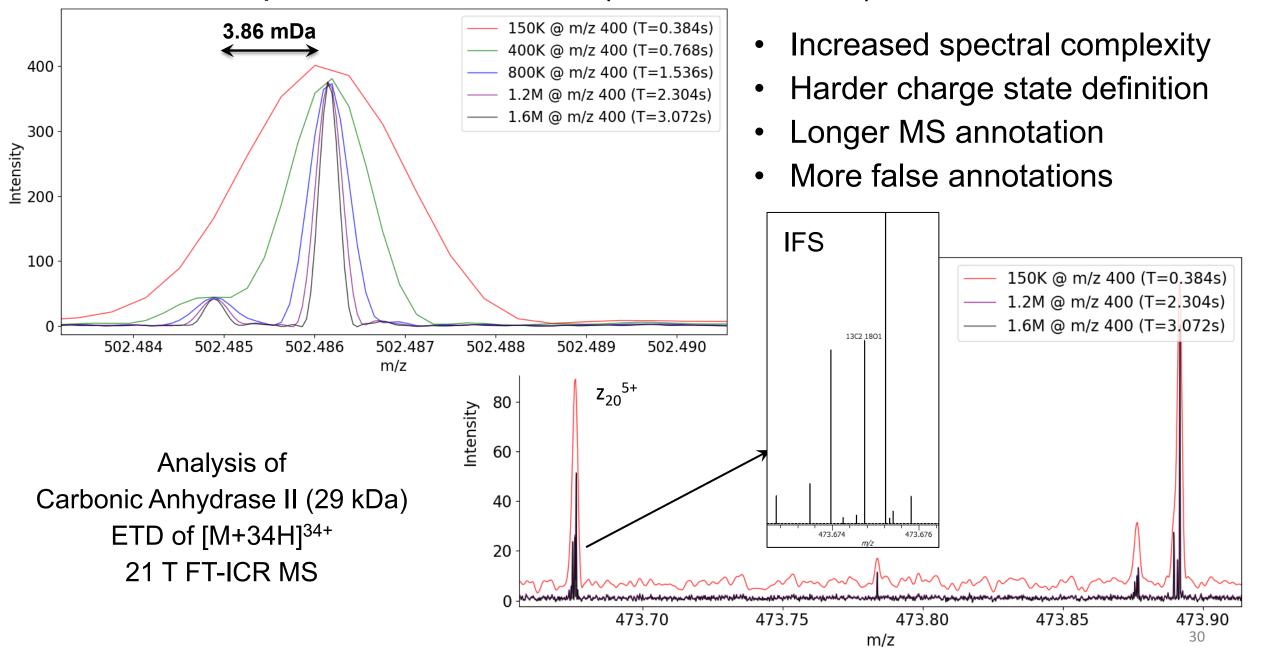
 better detection of the overlapping product ion distributions

Analysis of
Carbonic Anhydrase II (29 kDa)
ETD of [M+34H]<sup>34+</sup>
21 T FT-ICR MS

Nina Khristenko



#### UHR Top-Down Proteomics (Protein MS/MS): Low Mass Ions





#### nature methods

**Article** 

https://doi.org/10.1038/s41592-024-02207-8

## Ultralong transients enhance sensitivity and resolution in Orbitrap-based single-ion mass

spectrometry



150 kDa mAbs

1-10 MDa AAVs



Accepted: 7 February 2024

Published online: 05 March 2024

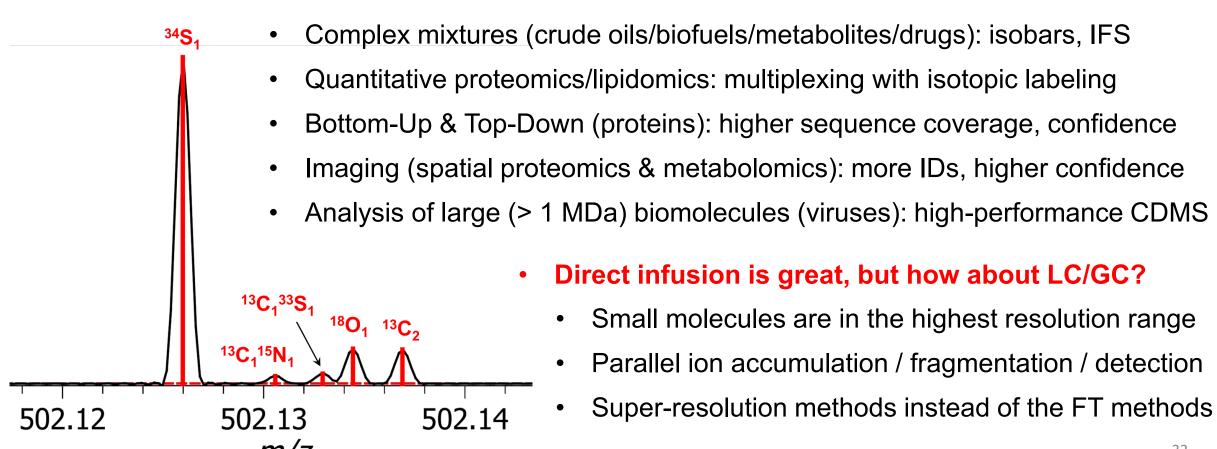


Evolène Deslignière **1**, Victor C. Yin **1**, Eduard H. T. M. Ebberink<sup>1</sup>, Amber D. Rolland **1**, Arjan Barendregt<sup>1</sup>, Tobias P. Wörner<sup>2</sup>, Konstantin O. Nagornov<sup>3</sup>, Anton N. Kozhinov<sup>3</sup>, Kyle L. Fort<sup>2</sup>, Yury O. Tsybin **1**, Alexander A. Makarov **1**, & Albert J. R. Heck **1** 



#### The UHR MS **Blessing**: Sharper Vision, Analytical Clarity

- Ultra-high-resolution is needed to separate isobaric compounds
- Improved confidence in annotation and identification of unknowns
- Exploring previously inaccessible chemical space (novel metabolites, toxins)





#### The UHR MS Curse: Bigger Burden

#### Longer experiment optimization:

Space charge – control of ion (charge) number, fine tuning of all parameters.

#### Instrumental cost & complexity:

Long transient acquisition times, maintenance, accessibility limited to few labs.

#### Sensitivity trade-offs:

Sometimes resolution is gained at the expense of duty cycle or sensitivity.

#### Interpretation bottleneck:

Higher resolution doesn't always mean better biological insight

#### Overfitting danger:

Assigning meaning to noise/artifacts, spurious peak picking.

High level of expertise is required to overcome these limitations



#### The UHR MS Data Overload: New Skills & Tools Needed

#### •Explosion of peak lists:

One LC-MS run generates millions and billions of datapoints.

#### Challenges in (toxicology) workflows:

- Database matching becomes slow and error-prone.
- False positives increase if not carefully controlled.

#### •Need for computational solutions:

- Peak filtering, data reduction, machine learning.
- Examples: Kendrick mass defect analysis, network visualization, Al annotation.

#### •Future perspective:

 Move toward "smart resolution" - adaptive acquisition, cloud computing, collaborative databases.

When does UHR MS change the scientific answer - and when doesn't it?

