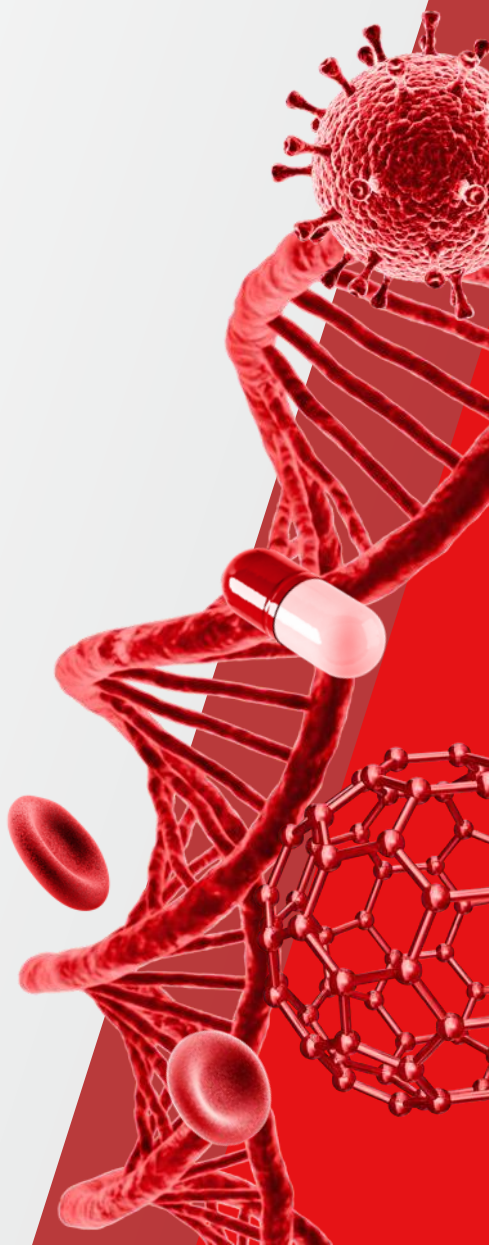
Introduction to common ESI-MS systems and their data. Choosing the Best MS system for your experiment.

Steve Danielson
LCMS Technical Sales Specialist
Feb. 13th, 2024



The world leader in serving science

MS Data Quality

What do you need from your MS Experiment?

- Basic Types of MS Experiments

1. Identify Compounds
   A. Unknowns/Discovery
      I. DDA
      II. DIA
   B. Knowns/Targeted
      I. HRAM (Full Scan, SIM, PRM/Targeted MS2)
      II. Triple Quad (SRM/MRM)

2. Quantify Compounds
   A. Absolute
   B. Relative (LFQ, DIA and TMT)

- Data Quality/Confidence
- How do we know our results are good?
  - Mass Accuracy
  - Resolution (Distinguish Isobaric Compounds)
  - Repeatable (Technical/Sample Replicates) CV, RSD
  - False Discovery Rates
  - Matrix Effects (Contaminants, Ion Suppression)
  - Retention Time Variability
  - Missing Data
  - Internal Standards, Standard Curve

Liquid chromatography (LC) – mass spectrometry (MS)

Fit-for-purpose LC-MS instrumentation with experimental flexibility

Triple Quadrupole

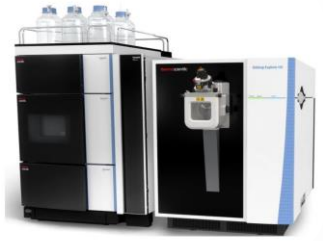
Sensitive Quantitative Performance

- Pharma QA/QC
- BioPharma
- Food Safety
- Clinical
- Environmental

Thermo Scientific™
TSQ+ Triple Quadrupole MS

Quadrupole-Orbitrap Hybrid

Market Leading Qual/Quan HRAM



- Omics
- Pharma/BioPharma
- Food Safety
- Clinical
- Environmental

Thermo Scientific™
Orbitrap™ Exploris MS

Quadrupole-Orbitrap-Ion Trap Tribrid

Ultimate Versatility HRAM

- Omics
- Pharma/BioPharma
- Food Safety
- Clinical
- Environmental

Thermo Scientific™
Orbitrap™ Tribrid™ MS

Profile **Biofluids** **Oligo** **Omics** **SCP** **DIA** **Unknows** **Native** **Ab**

Rethink what is possible with ground-breaking innovation

Thermo Scientific™
Orbitrap™ Astral™
Mass Spectrometer

Thermo Scientific™ Triple
Quadrupole
Mass Spectrometers

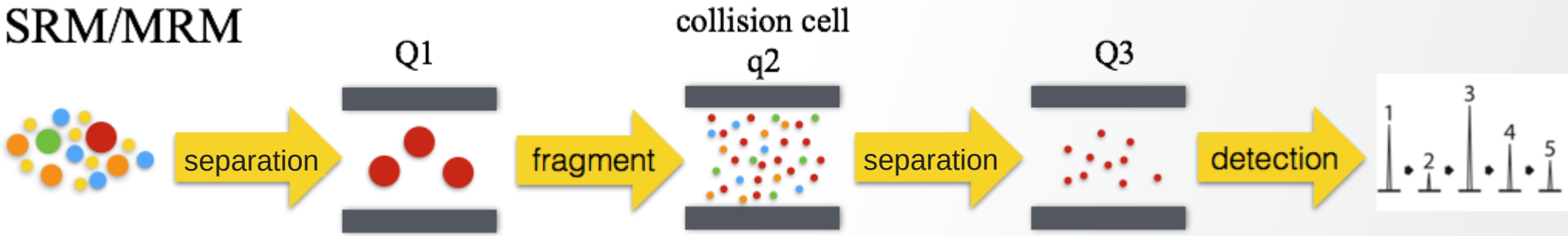
Thermo Scientific™ Hybrid
Orbitrap Mass Spectrometers

Thermo Scientific™ Orbitrap™
Tribrid™ Mass Spectrometers

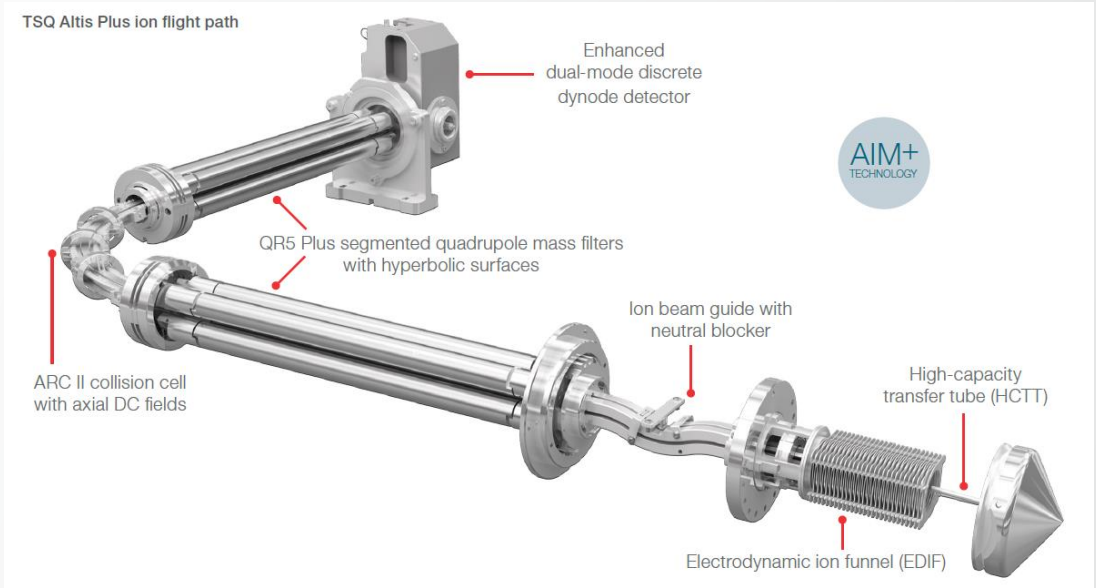
Revolutionary platforms to tackle the unmet needs in mass spectrometry

QqQ Triple Quadrupole

Overview



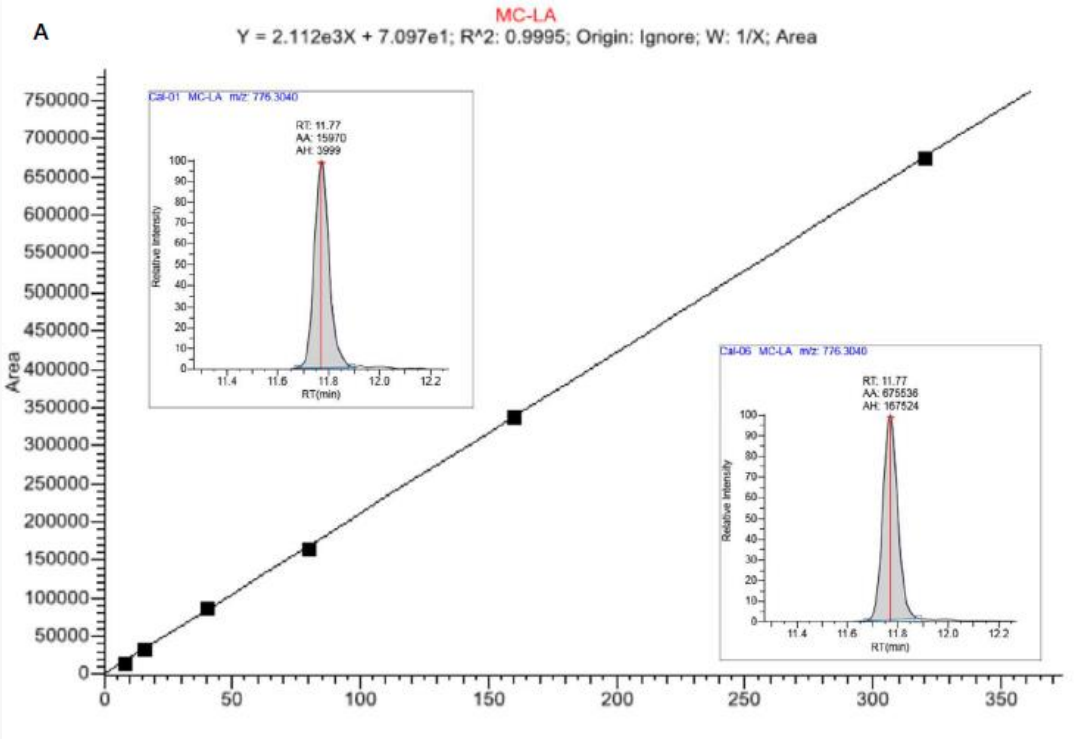
TSQ Altis Plus triple quadrupole mass spectrometer



Ideal Applications for Triple Quadrupole MS

- Targeted Quan
  - ID/Quan specific known targets.
  - Not for Discovery (unknown ID/Quan)
- Benefits of QqQ MS
  - Fast (600 SRM/sec)
  - Sensitive
  - Robust
  - Relative Low Cost
- Keep in Mind
  - Data on targets only, no unknows.
  - Nominal Mass (+/- 0.5 Da Mass Accuracy)
  - Ideally 2 or more SRM/target.
  - 7-15 scans across the peak for good quan.

- Example Applications
  - Pesticides
  - Drugs of Abuse
  - PFAS



Description of sensitivity across triple quadrupole instrumentation can be measured by signal-to-noise (S/N)

TSQ Fortis Plus

Environmental
Food Safety
Clinical Research
Pharma QA/QC

Mass Range m/z 2 – 3000
Max Resolution ***0.4 FWHM***
Polarity Switching 5 msec
Linear Dynamic range >5
Excellent Mass Stability**
150,000:1 S/N*
3 –year factory warranty

TSQ Quantis

Food Safety
Pharma
Clinical Research
Forensic Toxicology

Mass Range m/z 2 – 3000
Max Resolution ***0.4 FWHM***
Polarity Switching 25 msec
Linear Dynamic range 6
Excellent Mass Stability**
150,000:1 S/N*
1 –year factory warranty

TSQ Quantis Plus

Food Safety
Pharma
Clinical Research
Forensic Toxicology

Mass Range m/z 2 – 3000
Max Resolution ***0.4 FWHM***
Polarity Switching 5 msec
Linear Dynamic range >6
Excellent Mass Stability**
500,000:1 S/N*
3 –year factory warranty

TSQ Altis Plus

Pharma/Biopharma
Environmental
Food Safety
Clinical Research
Targeted Omics

Mass Range m/z 2 – 2010
Max Resolution ***0.2 FWHM***
Polarity Switching 5 msec
Linear Dynamic range >6
Excellent Mass Stability**
1,500,000:1 S/N*
3 –year factory warranty

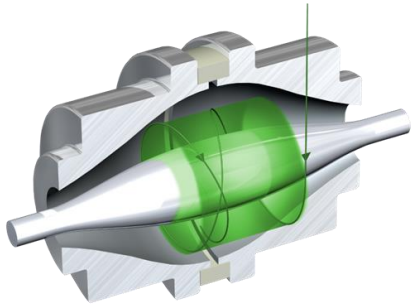
Performance

**The current signal to noise specification highlights the minimum performance specification required at installation*

***For lockout specifications, please contact the Product Management Team*

Orbitrap HRAM-High Resolution Accurate Mass

- Applications for any Orbitrap.
  - Proteomics ID and Quan (DDA and DIA)
  - Intact Proteins
  - Oligonucleotides
  - Metabolomics
  - Lipidomics
  - Small Molecules
  - SCP
  - And more
- Orbitrap Data Quality
  - Mass Accuracy (1-3ppm)
  - Resolution (120,000 up to 1,000,000*)
  - Sensitivity
  - Dynamic Range
  - Ease of Use



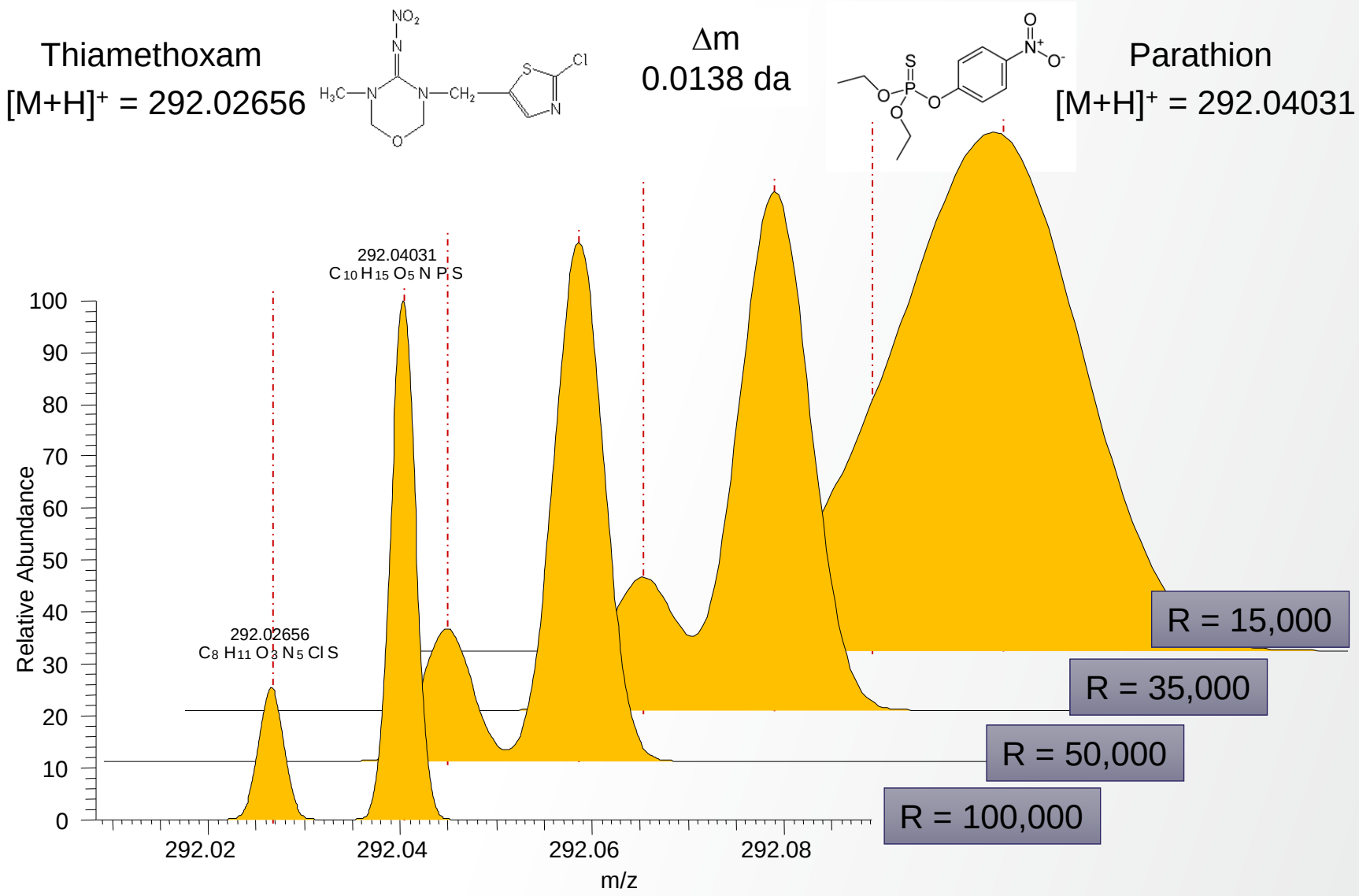
Thermo Scientific™ Hybrid Orbitrap Mass Spectrometers

Thermo Scientific™ Orbitrap™ Tribrid™ Mass Spectrometers

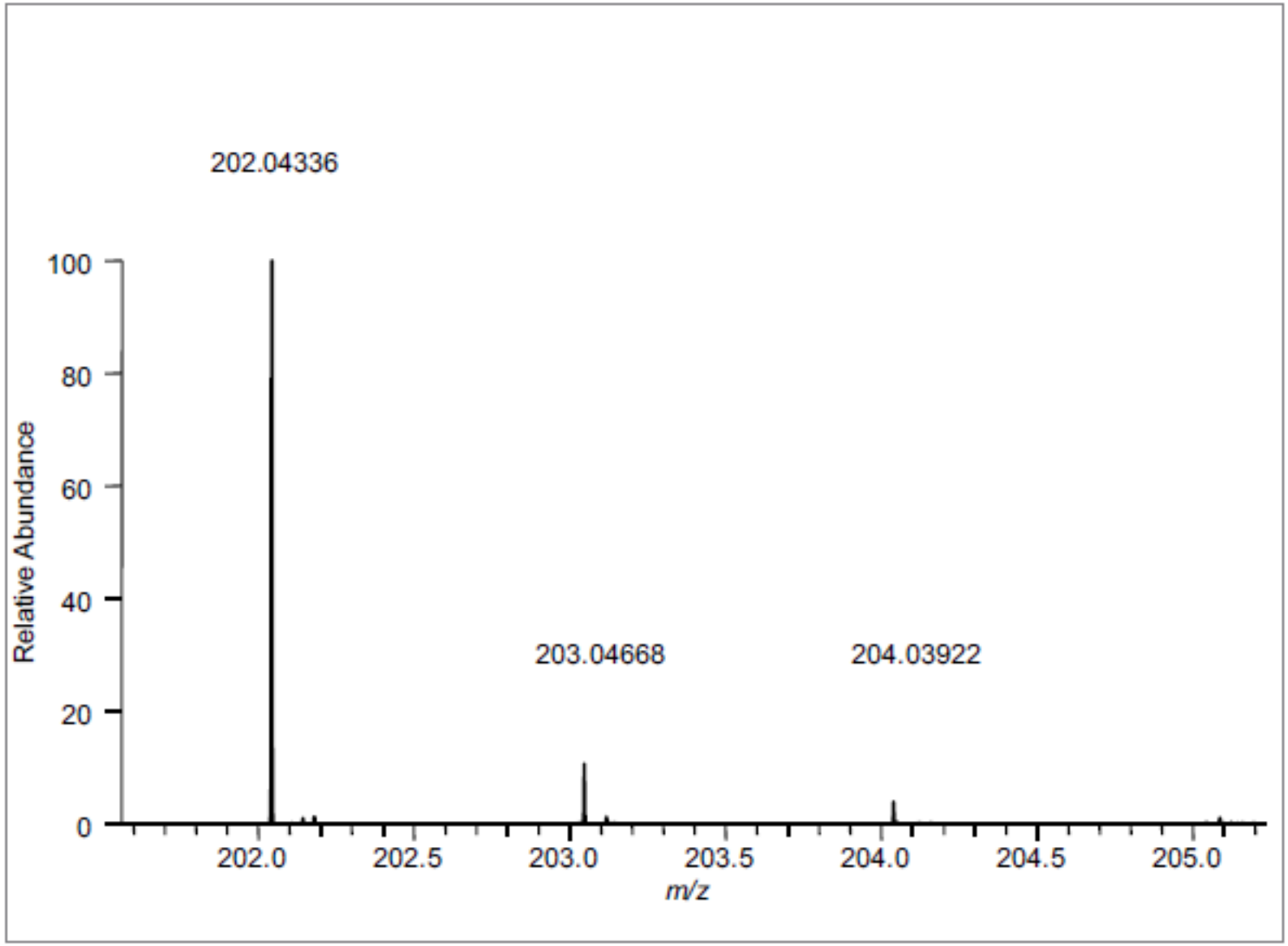
Thermo Scientific™ Orbitrap™ Astral™ Mass Spectrometer

*Optional Equipment

Resolution Ex. Isobaric Pesticides: Mix 1:3 Simulated



Mass Accuracy and Resolution Role in Compound ID



Possible Chemical Formulas

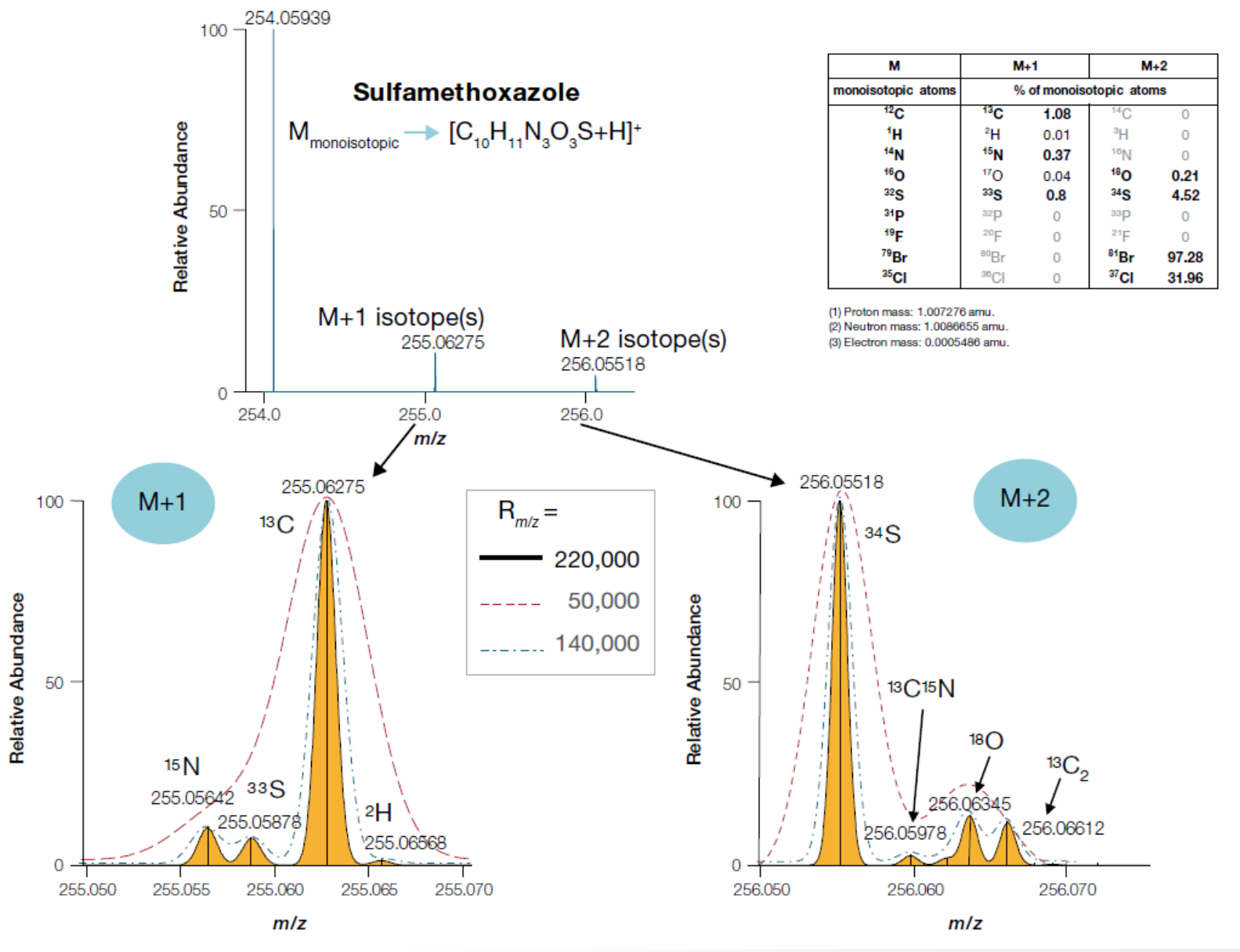
Mass Tolerance Window	± 20 ppm	± 10 ppm	± 5 ppm
Monoisotopic	35	18	9
At least 1 N, 1 S, no Cl, no Br	6	2	1

QE (External) < 5 ppm
QE (Internal) < 3 ppm
Exploris (IC on) sub 1ppm

1) Software Scores Isotope Patterns

2) Software looks for Fine isotope patterns if high enough resolution

Fine Isotope Patterns



M	M+1		M+2	
monoisotopic atoms	% of monoisotopic atoms			
^{12}C	^{13}C	1.08	^{14}C	0
^{1}H	^{2}H	0.01	^{3}H	0
^{14}N	^{15}N	0.37	^{16}N	0
^{16}O	^{17}O	0.04	^{18}O	0.21
^{32}S	^{33}S	0.8	^{34}S	4.52
^{31}P	^{32}P	0	^{33}P	0
^{19}F	^{20}F	0	^{21}F	0
^{79}Br	^{80}Br	0	^{81}Br	97.28
^{35}Cl	^{36}Cl	0	^{37}Cl	31.96

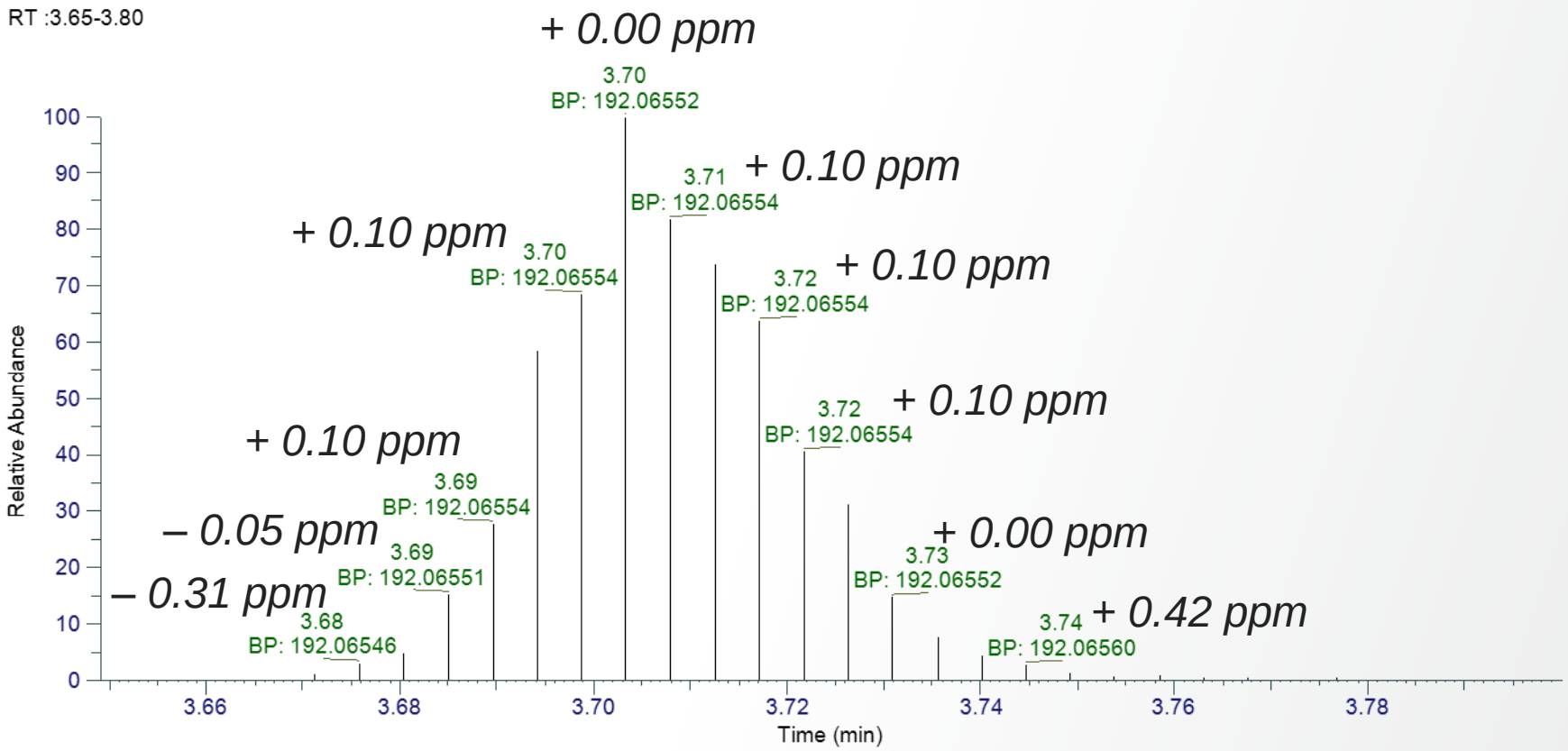
(1) Proton mass: 1.007276 amu.
(2) Neutron mass: 1.0086655 amu.
(3) Electron mass: 0.0005486 amu.

Excellent mass accuracy for every scan

5-HIAA $C_{10}H_9NO_3$

M+H$^+$ *m/z* 192.06552

Orbitrap Exploris 240 MS
mouse plasma QC pool



EASY-IC provides sub-1 ppm mass accuracy for every single mass spectrum across the peak

Note: A single spectrum (MS, MS^2) can provide high quality data – no spectral averaging is needed.

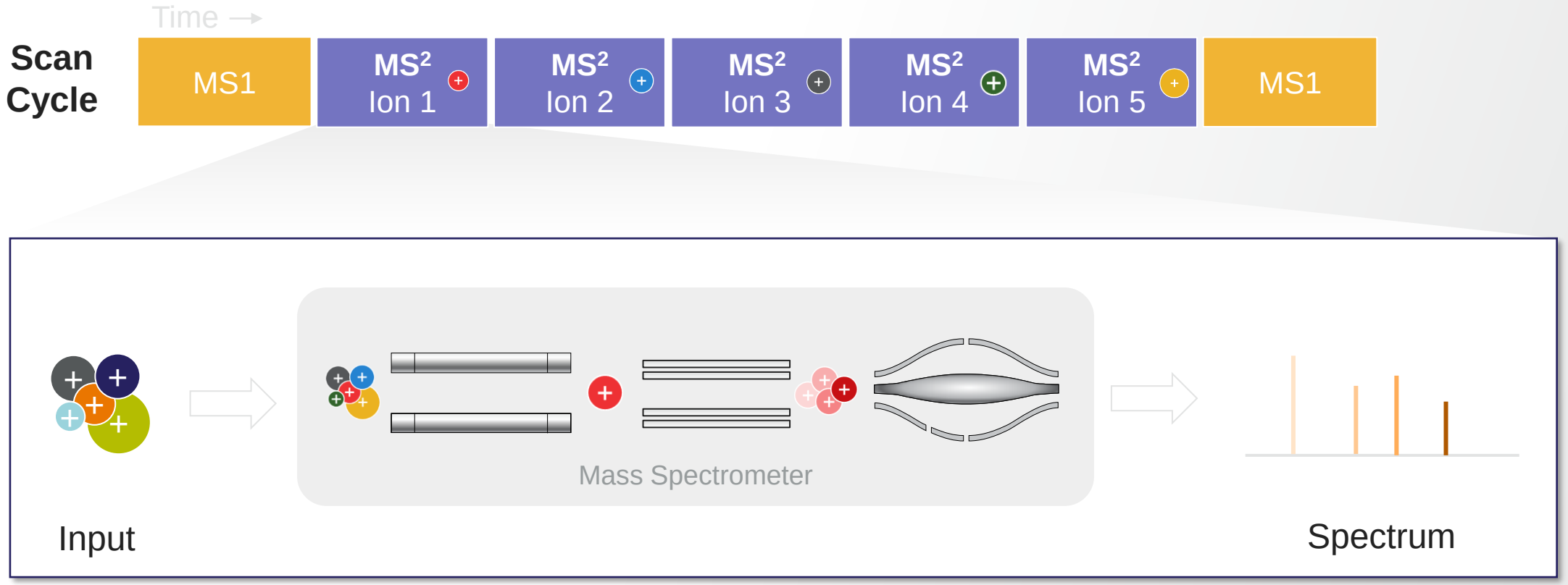
Modes of Instrument Function

- **MS1** MS^1 Only
- **SIM** Targeted MS^1
- **PRM** Targeted MS^2
- **DDA** Data-Dependent MS^2
- **AIF** All Ion Fragmentation
- **DIA** Data-Independent Acquisition

DDA Data-Dependent MS^2

Overview

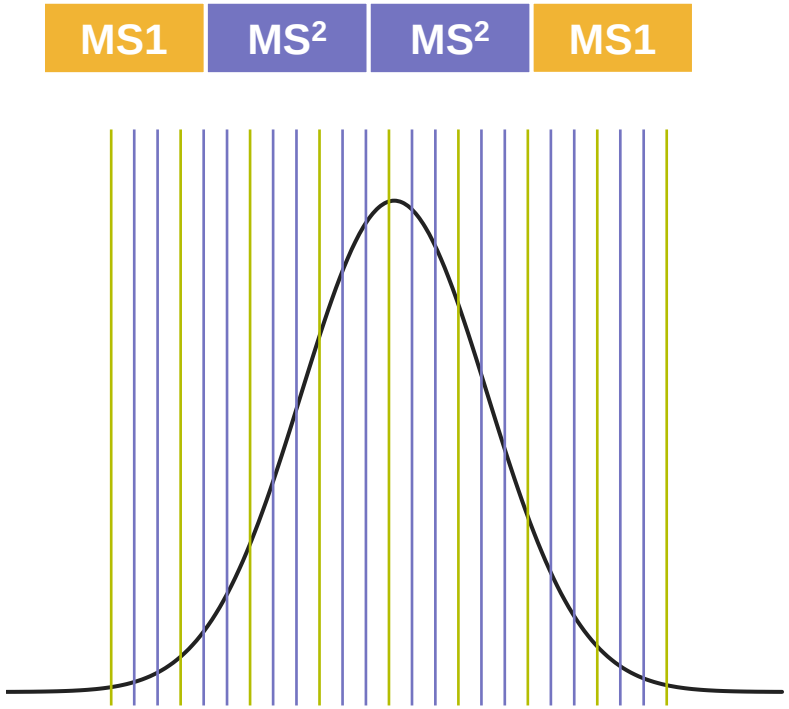
- With Data Dependent MS^2 (DDA), both MS^1 and MS^2 scans are acquired. Data from the MS^1 scans determine which ions are selected for MS^2 fragmentation.



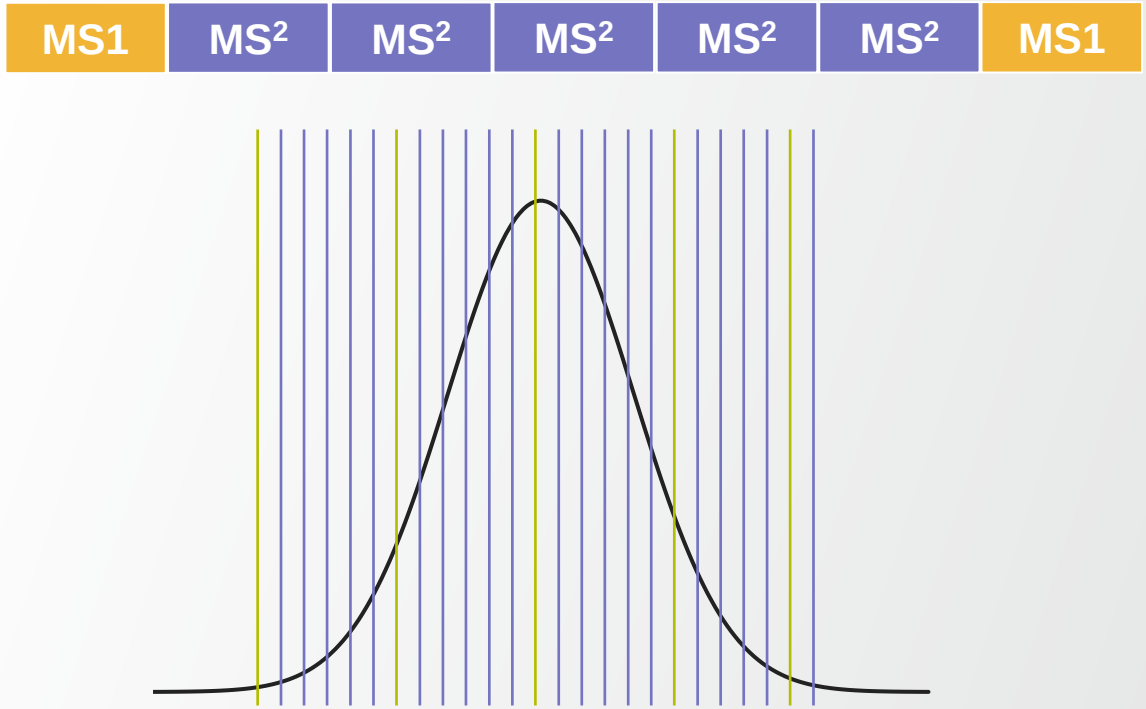
DDA Data-Dependent MS^2

Important Considerations

1. The ‘Top N’ number selected will affect how many MS^1 scans are acquired



<u>9</u> MS^1 Scans Across Peak



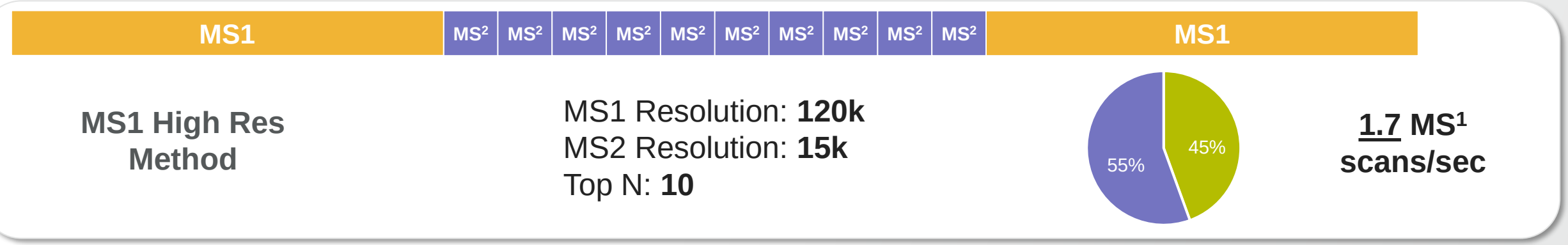
<u>5</u> MS^1 Scans Across Peak

DDA Data-Dependent MS^2

Important Considerations

2. It's important to balance the amount of duty cycle that is used for collecting MS^1 and MS^2 scans

2.1. Orbitrap resolutions also must be carefully considered to allow appropriate cycle times and ensure sufficient MS^2 scans are acquired



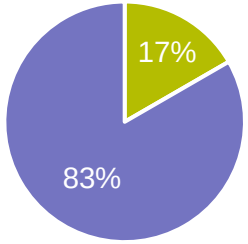
MS1 High Res Method

MS1 Resolution: **120k**
MS2 Resolution: **15k**
Top N: **10**

1.7 MS^1 scans/sec

Identification Focused Method

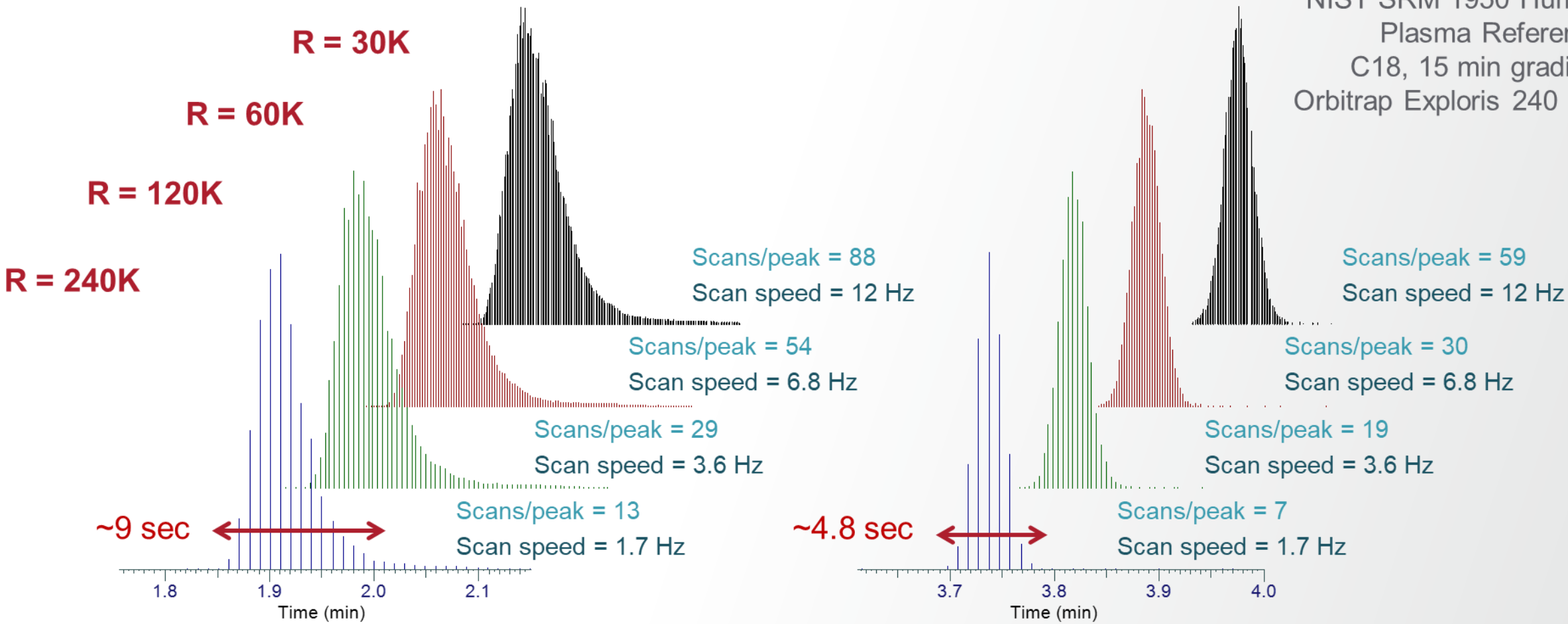
MS1 Resolution: **60k**
MS2 Resolution: **15k**
Top N: **20**



1.3 MS^1 scans/sec

Resolution vs. scan speed

NIST SRM 1950 Human Plasma Reference
C18, 15 min gradient
Orbitrap Exploris 240 MS



Acetylcarnitine
$C_9H_{17}NO_4$, *m/z* 204.1230

5-HIAA
$C_{10}H_9NO_3$, *m/z* 192.0655

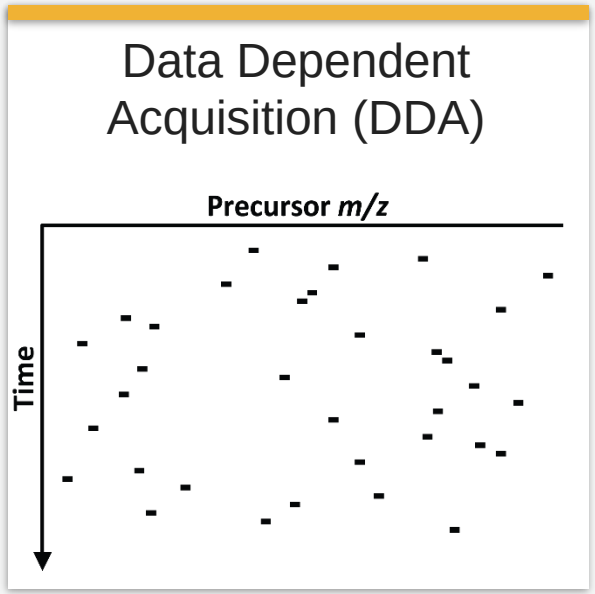
DDA Method Considerations

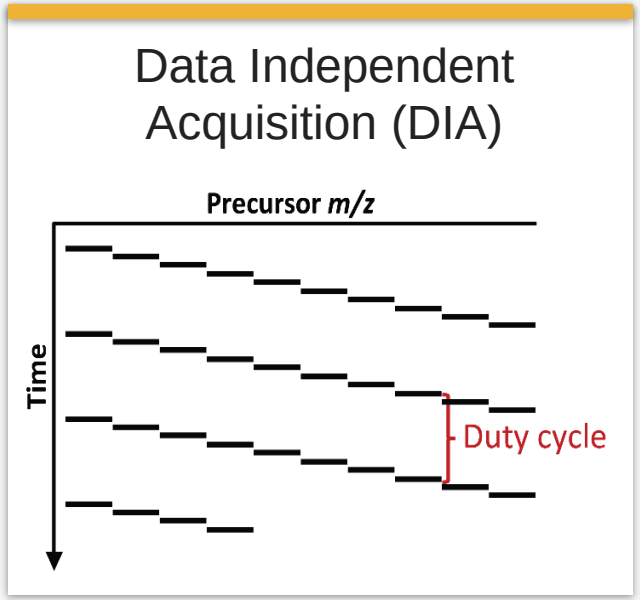
- Throughput/Samples per Day
- Sample Complexity and Coverage
- LC Gradient and Peak Shape
- Ideal TopN experiment
  - MS1 and MS2 Resolution needed
  - # of MS2 per cycle loop/TopN
  - Cycle time
- Match AGC, and Max IT to experiment
- Match Max IT to Resolution used (no wasted time)
- Match Dynamic Exclusion to Peak Shape

Exploris		
Res@ m/z 200	**Transient length (ms)**	**Scan speed (Hz)**
*7,500**	*16*	*40*
15,000	*32*	*22*
30,000	*64*	*12*
45,000	*96*	*10*
60,000	*128*	*7*
120,000	*256*	*3*
*240,000**	*512*	*1.5*
*480,000**	*1024*	*0.7*

*Some Resolution Settings not available on all Exploris Models

DDA vs DIA





Data Dependent Acquisition (DDA)

Data Independent Acquisition (DIA)

Article | Published: 29 September 2004

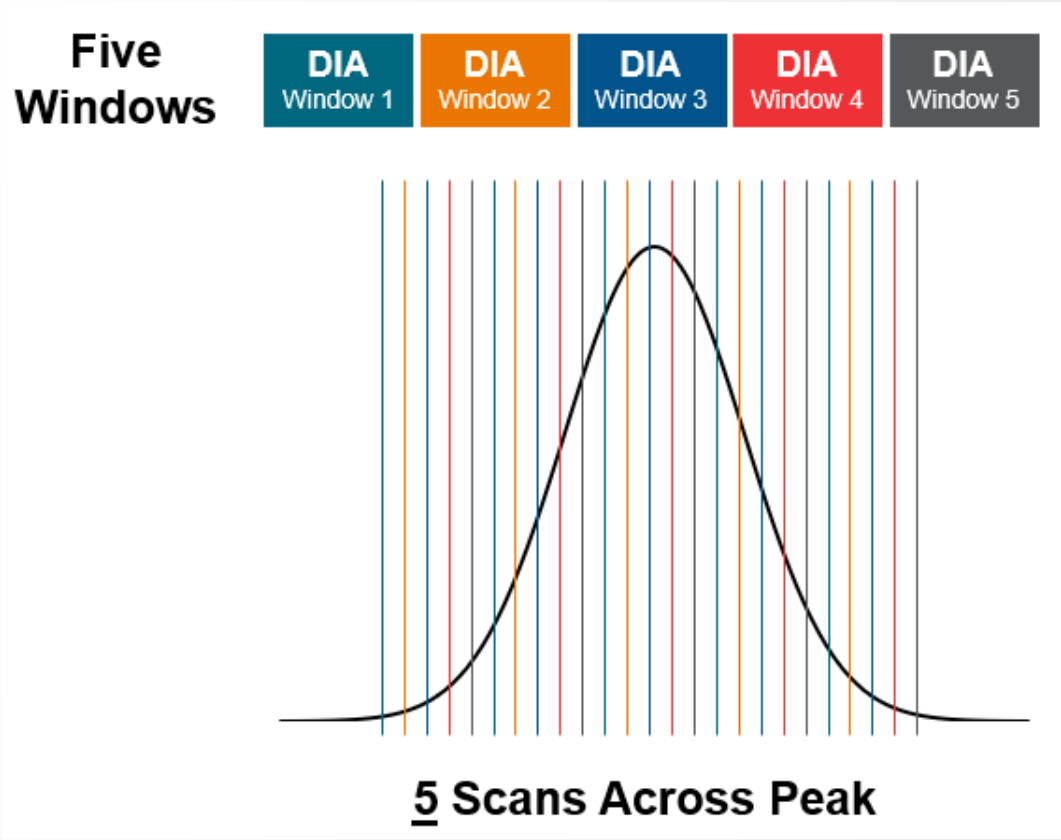
Automated approach for quantitative analysis of complex peptide mixtures from tandem mass spectra

John D Venable, Meng-Qiu Dong, James Wohlschlegel, Andrew Dillin & John R Yates III

Nature Methods **1**, 39–45 (2004) | Cite this article

DIA Considerations

- Throughput/Samples per Day
- Sample Complexity and Coverage
- LC Gradient
- m/z range
- # windows/size of windows
  - Wider Windows → Faster Methods
  - Wider Windows can increase variability
  - Window Overlap
- Scans across the peak depends on scan speed, window size and # of windows.
- Direct DIA vs Library
- PTMs

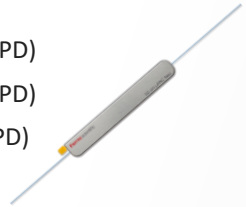


Velocity DIA workflow for quantitative measurements without sacrificing scope

HeLa Protein Digest Standard (P/N 8829), 200 ng/run

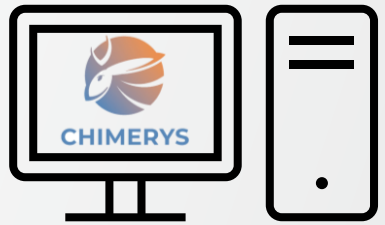
Thermo Scientific™ Vanquish™ NEO UHPLC System

30-minute gradient (36 SPD)
60-minute gradient (20 SPD)
9-minute gradient (80 SPD)



Thermo Scientific™ µPAC™ NEO 50cm HPLC Column

Thermo Scientific™ Orbitrap Exploris™ 480 Mass Spectrometer with Thermo Scientific™ FAIMS Pro™ Interface



DIA processing software, e.g. Proteome Discoverer with Chimerys

Sample preparation → Data acquisition → Data analysis

Software influences ID Numbers

CHIMERYS

Proteome Discoverer software with CHIMERYS intelligent search algorithm

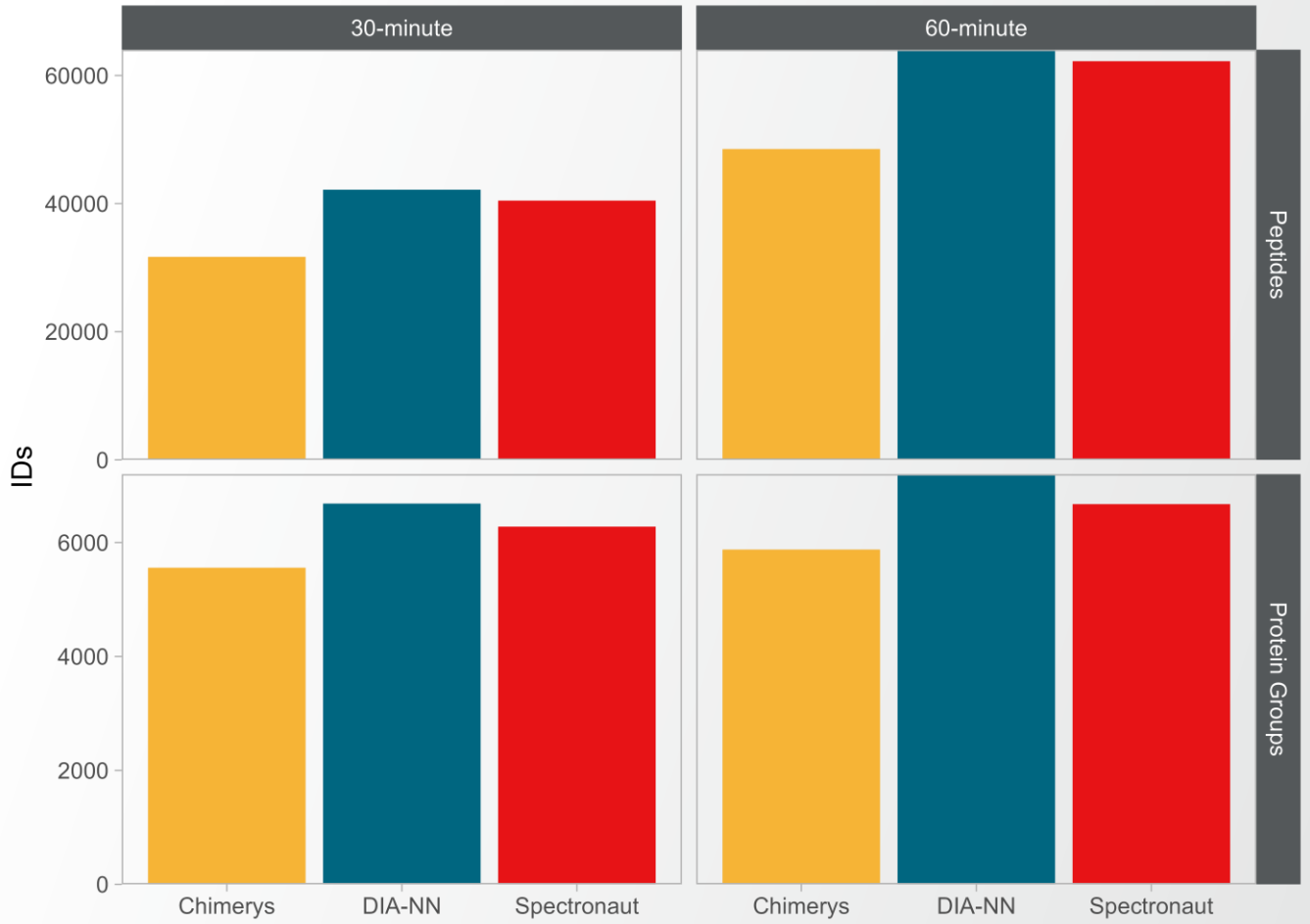
Chimerys DIA: Spectrum-centric search that utilizes predicted combinations of spectra

DIA-NN software

DIA-NN: Peptide-centric library free search

Spectronaut® software

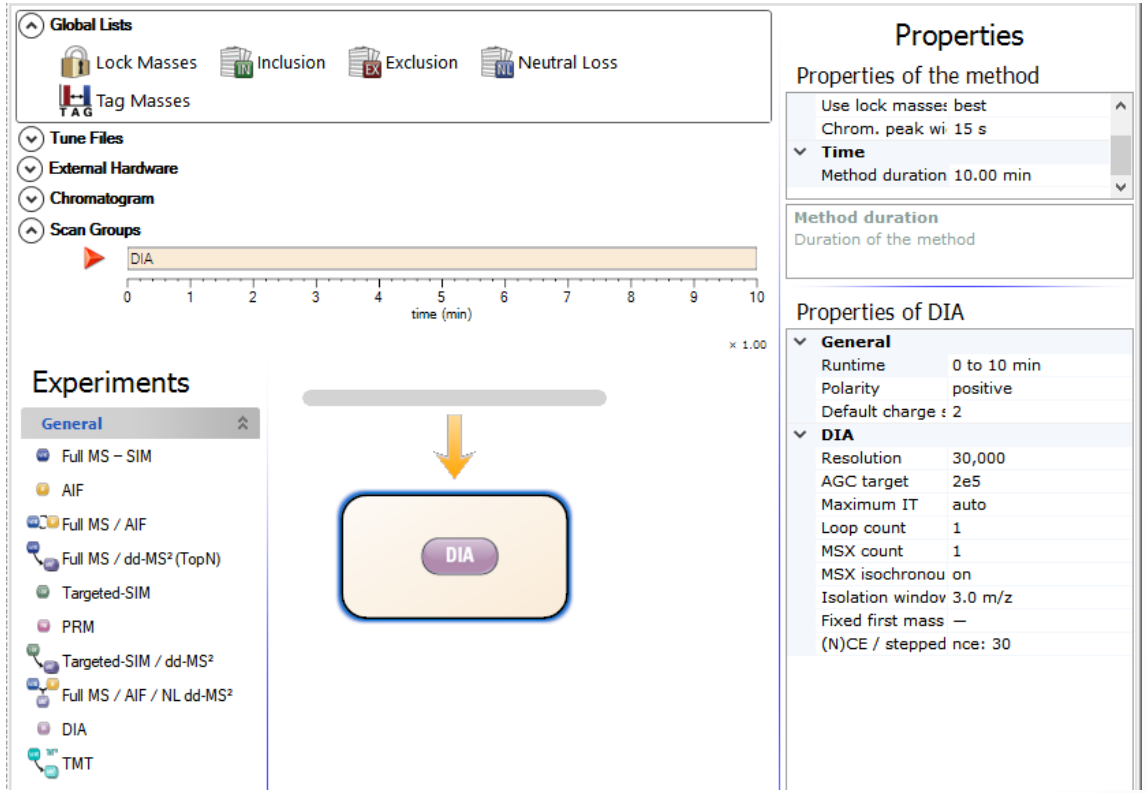
Spectronaut Direct-DIA: Spectrum-centric library free search



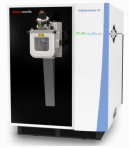
DIA-NN library free search and Spectronaut Direct-DIA search were used. Chimerys results were obtained in Proteome Discoverer software V 3.1 using Inferys 3.0.0 fragmentation model. All results were filtered to 1% FDR at the peptide and protein level.

DIA Data Independent Acquisition

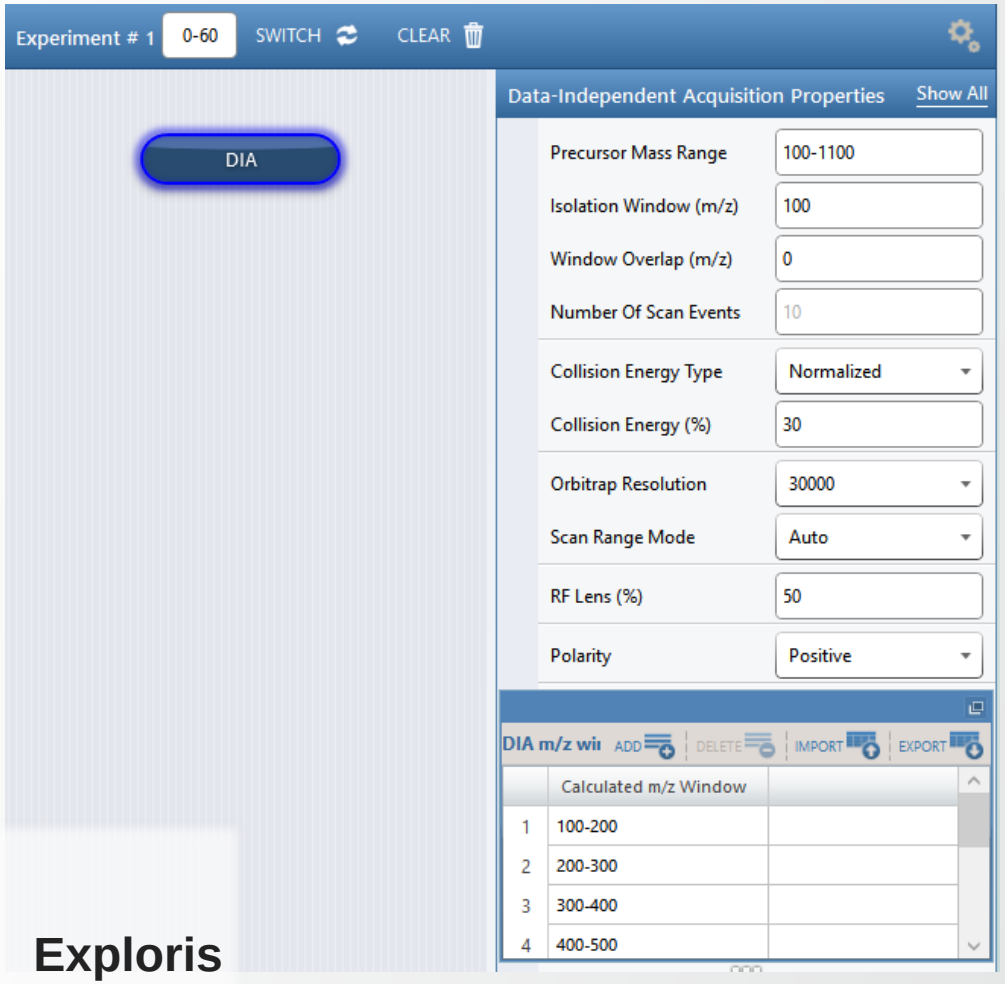
Method



Q Exactive



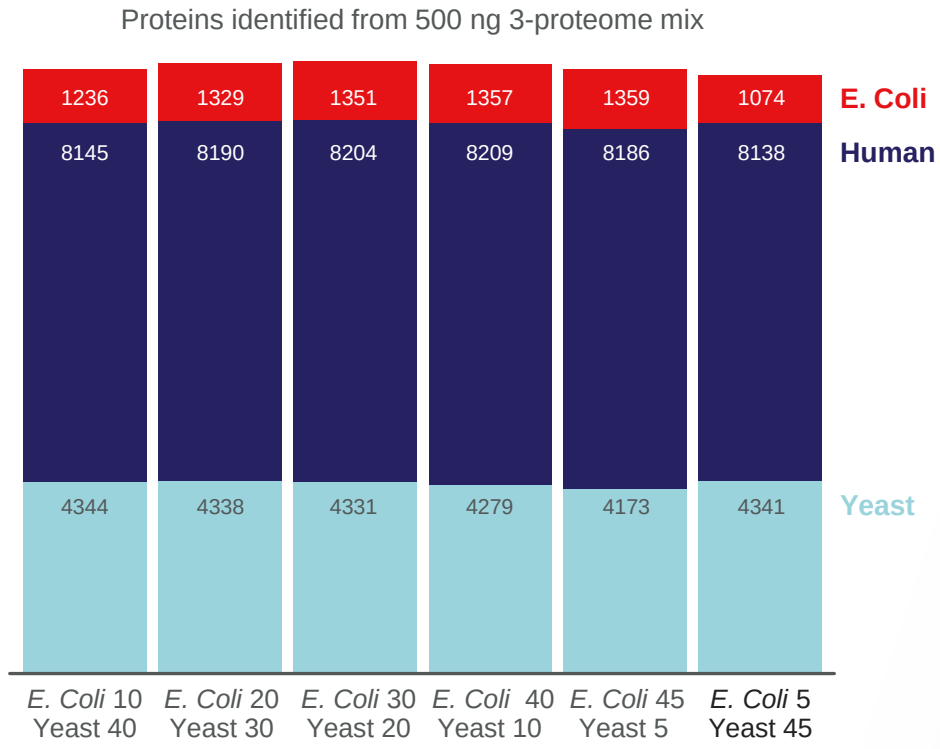
Exploris

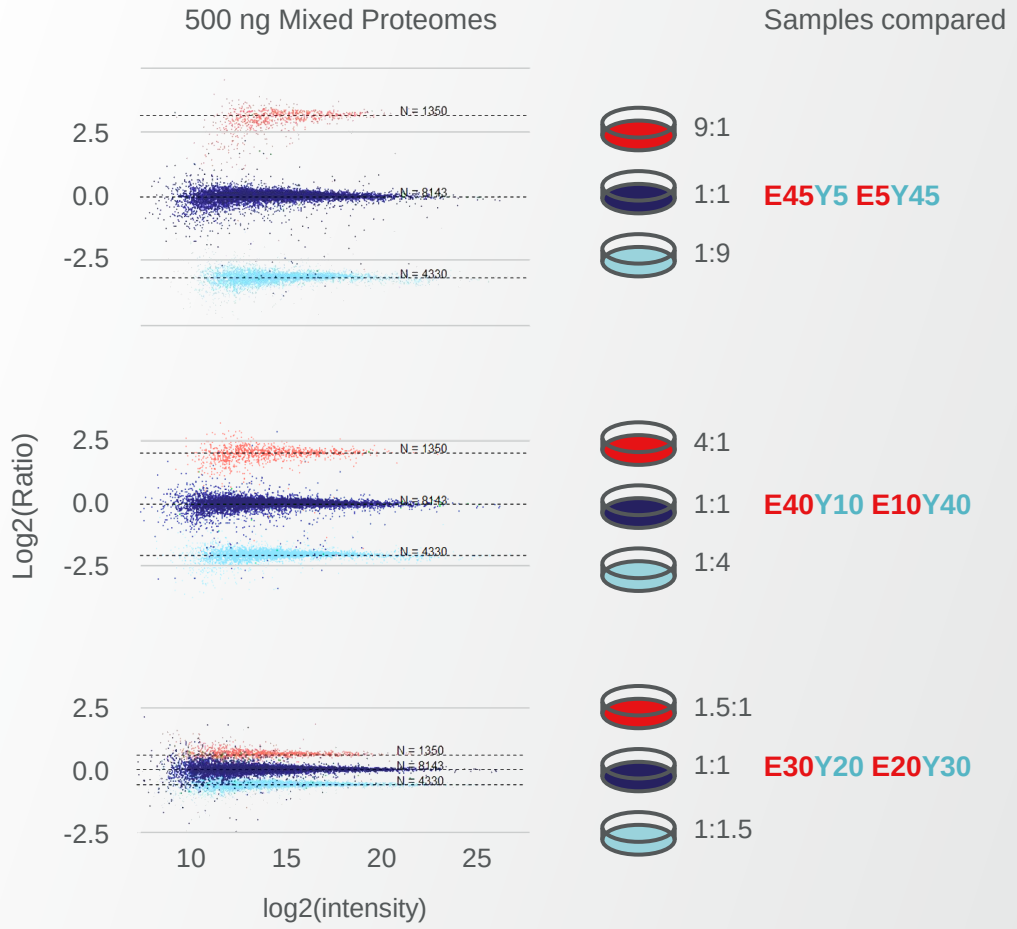


Accurate and Precise Quantitation

Discover more biomarkers with a larger dynamic range

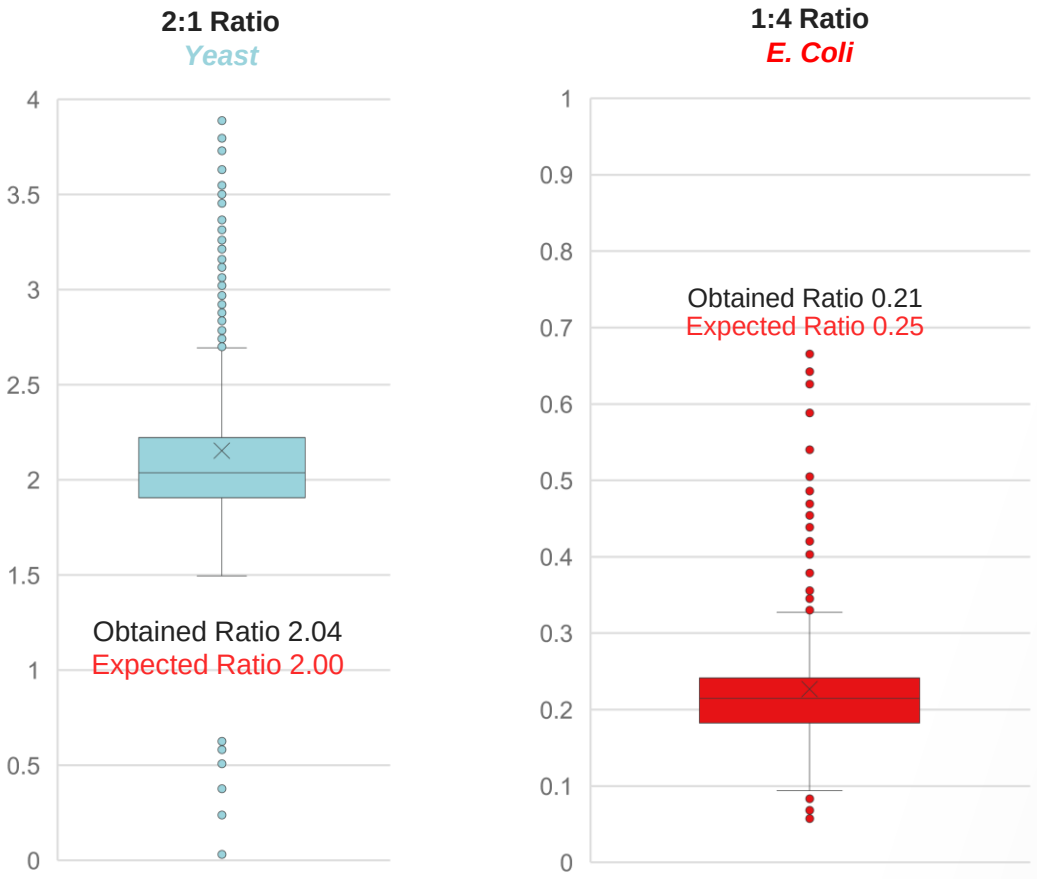
Accurate and precise label-free quantitation with data-independent acquisition for greater statistical power

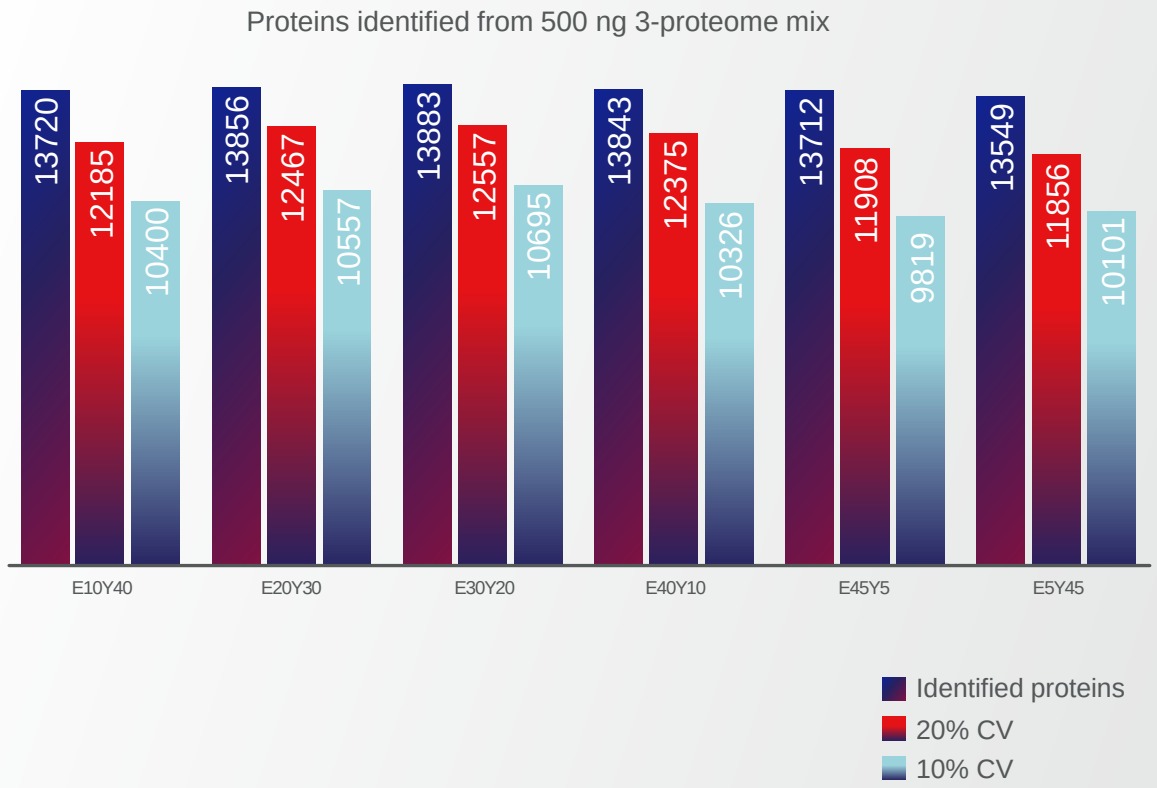




Accurate and precise label-free quantitation

Correct mixing ratios with highly reproducible measurements



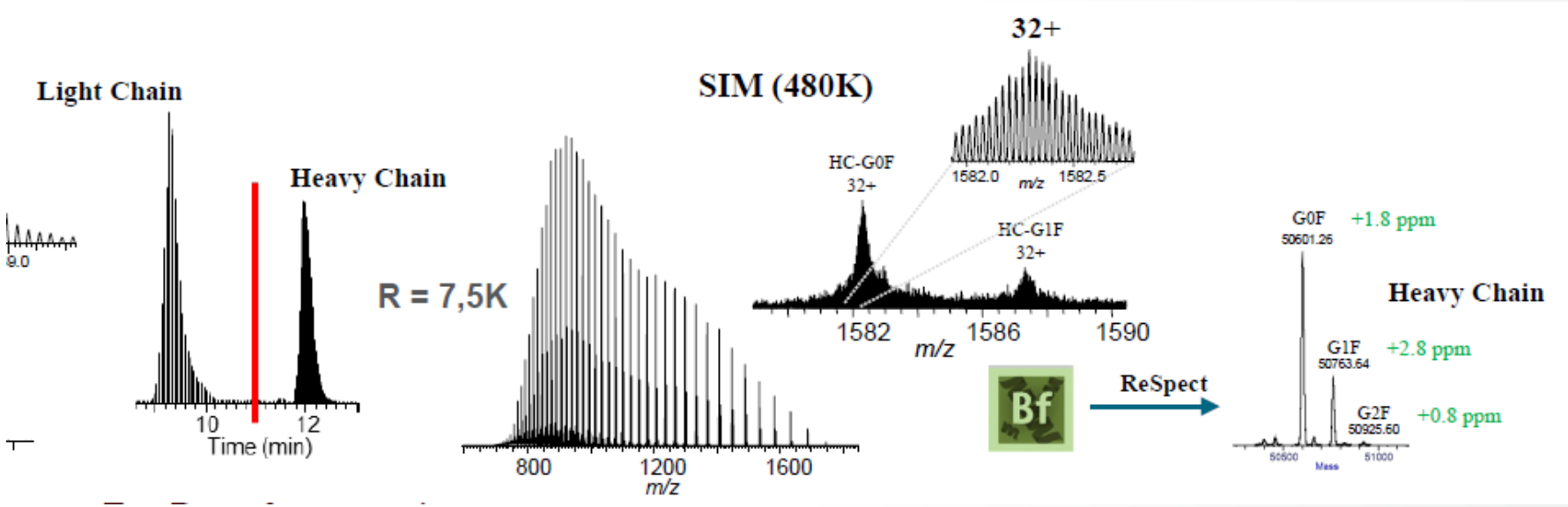


Intact Protein, mAb/ADC Analysis

- **Therapeutic Protein Challenges**
  - Sample Heterogeneity/Complexity
  - Size >150kD

- **High Resolution Accurate Mass Orbitrap**
  - Superior Resolution and accurate mass can separate contaminants and variability in complex samples.
  - Provides confident mAb/ADC characterization.

- High Resolution Thermo Scientific Orbitrap Exploris 480 Herceptin Heavy Chain



- Orbitrap isotopically resolved HC peaks.
- G0F identified with 2 ppm Mass Accuracy for Herceptin HC.

High Quality Orbitrap Data for Intact ADC

analytical chemistry

Article

pubs.acs.org/ac

High-Resolution Accurate-Mass Mass Spectrometry Enabling In-Depth Characterization of *in Vivo* Biotransformations for Intact Antibody-Drug Conjugates

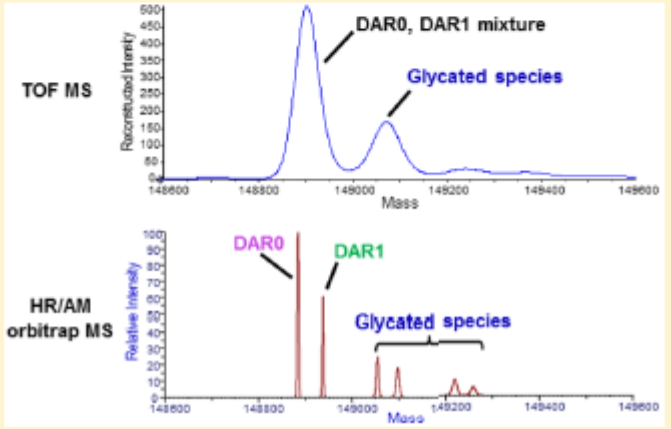
Jintang He,*[,†] Dian Su,[†] Carl Ng,[†] Luna Liu,[†] Shang-Fan Yu,[†] Thomas H. Pillow,[†] Geoffrey Del Rosario,[†] Martine Darwish,[†] Byoung-Chul Lee,[†] Rachana Ohri,[†] Hongxiang Zhou,[‡] Xueji Wang,[‡] Jiawei Lu,[‡] Surinder Kaur,[†] and Keyang Xu*[,†]

[†]Genentech Inc., 1 DNA Way, South San Francisco, California 94080, United States

[‡]Wuxi Apptec, 288 Fute Zhong Road, Waigaoqiao Free Trade Zone, Shanghai, 200131, China

Supporting Information

ABSTRACT: Antibody-drug conjugates (ADCs) represent a promising class of therapeutics for the targeted delivery of highly potent cytotoxic drugs to tumor cells to improve bioactivity while minimizing side effects. ADCs are composed of both small and large molecules and therefore have complex molecular structures. *In vivo* biotransformations may further increase the complexity of ADCs, representing a unique challenge for bioanalytical assays. Quadrupole-time-of-flight mass spectrometry (Q-TOF MS) with electrospray ionization has been widely used for characterization of intact ADCs. However, interpretation of ADC biotransformations with small mass changes, for the intact molecule, remains a limitation due to the insufficient mass resolution and accuracy of Q-TOF MS. Here, we have investigated *in vivo* biotransformations of multiple site-specific THIOMAB antibody-drug conjugates (TDCs), in the intact form,



Orbitrap HRAM-High Resolution Accurate Mass

Thermo Scientific™ Hybrid Orbitrap Mass Spectrometers

- Exploris 240 and 480
  - Proteomics (DDA and DIA)
  - Intact Proteins, Protein Complexes
  - Top Down
  - SCP
  - Oligonucleotides
  - Metabolomics
  - Lipidomics
  - Small Molecules

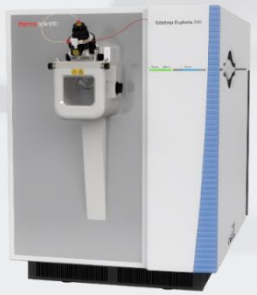
Thermo Scientific™ Orbitrap™ Tribrid™ Mass Spectrometers

- Orbitrap Ascend (Tribrid)
  - All applications for Exploris +
  - TMT (SPS)
  - MSn
  - Multiple Fragmentation (HCD, CID, ETD, EThcD, UVPD, PTCR)
  - Real Time Search (TMT, Lipid, Met ID)

Thermo Scientific™ Orbitrap™ Astral™ Mass Spectrometer

- Orbitrap Astral
  - All Application for Exploris +
  - Higher Throughput
  - Deeper Coverage
  - Higher Sensitivity

Differences across Orbitrap Exploris 240 and Orbitrap Exploris 480 are demonstrated by increases in sensitivity and mass resolution capability



Orbitrap Exploris 240 MS

- S-Lens
- Segmented quadrupole with configuration switching
- FS-MS, t-MS^2, DDA Scan Rate: 22 Hz
- Mass Range *m/z* 40-6,000 (opt. 8,000)
- Max. Mass Resolution 240,000

Orbitrap Exploris 480 MS

- High Capacity Transfer Tube (HCTT)
- Electrodynamic Ion Funnel (EDIF)
- Segmented quadrupole with configuration switching
- FS-MS, t-MS^2, DDA Scan Rate: 40 Hz
- Mass Range *m/z* 40-6,000 (opt. 8,000)
- Max. Mass Resolution 480,000

Options: Intact Protein (Thermo Scientific™ BioPharma option), Thermo Scientific™ FAIMS Pro™ interface

New Orbitrap Ascend Tribrid MS system

PARAMETER	CHARACTERISTICS
Acquisition rate OTMS^2	45 Hz
Acquisition rate ITMS^2	50 Hz
Maximum resolution	480K FWHM at m/z 200
Quadrupole minimum isolation width	0.4 m/z
Mass range	m/z 50-6,000, up to m/z 16,000 with HMR^n+
Mass Accuracy	3 ppm external, 1 ppm internal
Dissociation / Ion Activation	CID, HCD, ETD, EThcD, ETciD, UVPD, PTCR
MS^n	Up to MS^{10} with the ion trap or Orbitrap mass analyzer
Analyzers	Q, OTMS, ITMS
Detectors	Ion Trap, Orbitrap mass analyzer
Size	1270 × 805 × 703 mm (w, d, h)

Unmatched Analytical Performance and Versatility

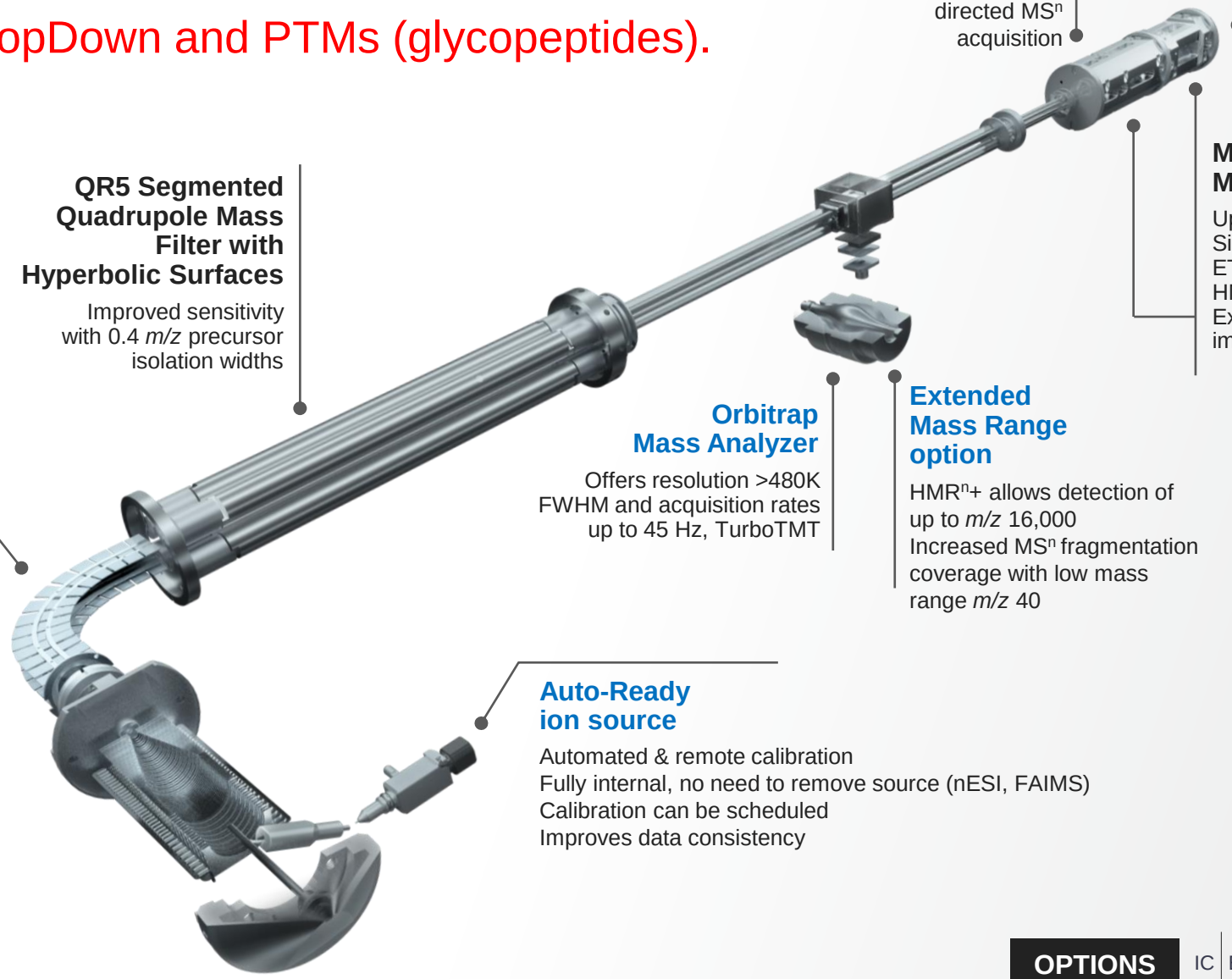
- **Improved ion introduction and transfer** for greater sensitivity and acquisition rates
- **QR5 Segmented Quadrupole Mass Filter** for outstanding precursor selectivity and sensitivity
- **Real-Time Database/Library Search** for exceptional depth and accuracy for TMT analysis
- **Higher Mass Range MS^n (HMR^n+) option** for structural analysis of native protein complexes
- **Proton Transfer Charge Reduction (PTCR) option** for simplification of complex spectra and improved top-down data interpretation
- **The fully integrated Auto-Ready ion source** for complete, unattended system calibration, without the need for manual hardware reconfiguration
- **Full Customization** with a range of optional capabilities:

  EASY-IC | ETD | UVPD | HMR^n +| PTCR | FAIMS Pro interface

- **Common interface** with Orbitrap Exploris 480 MS and TSQ Triple Quadrupole MS

Orbitrap Ascend Tribrid MS

- Orbitrap Tribrids have multiple fragmentation options.
- Critical for TopDown and PTMs (glycopeptides).



Real-Time Database/Library Search

Database Search/ Spectral library directed MS^n acquisition

UVPD option

Unique fragmentation mode for analyte structure elucidation

Modified Linear Ion Trap Mass Analyzer

Up to 50 Hz MS^n and sensitive mass analysis
Six fragmentation types: CID, HCD, ETD/EThcD/ETciD and UVPD;
HMR^n+ of up to *m/z* 8000
Extended front section of the high-pressure cell for improved control over ETD and PTCR reactions

QR5 Segmented Quadrupole Mass Filter with Hyperbolic Surfaces

Improved sensitivity with 0.4 *m/z* precursor isolation widths

Advanced Active Ion Beam Guide

Prevents neutrals and high velocity clusters from entering mass resolving quadrupole

Orbitrap Mass Analyzer

Offers resolution >480K FWHM and acquisition rates up to 45 Hz, TurboTMT

Extended Mass Range option

HMR^n+ allows detection of up to *m/z* 16,000
Increased MS^n fragmentation coverage with low mass range *m/z* 40

Auto-Ready ion source

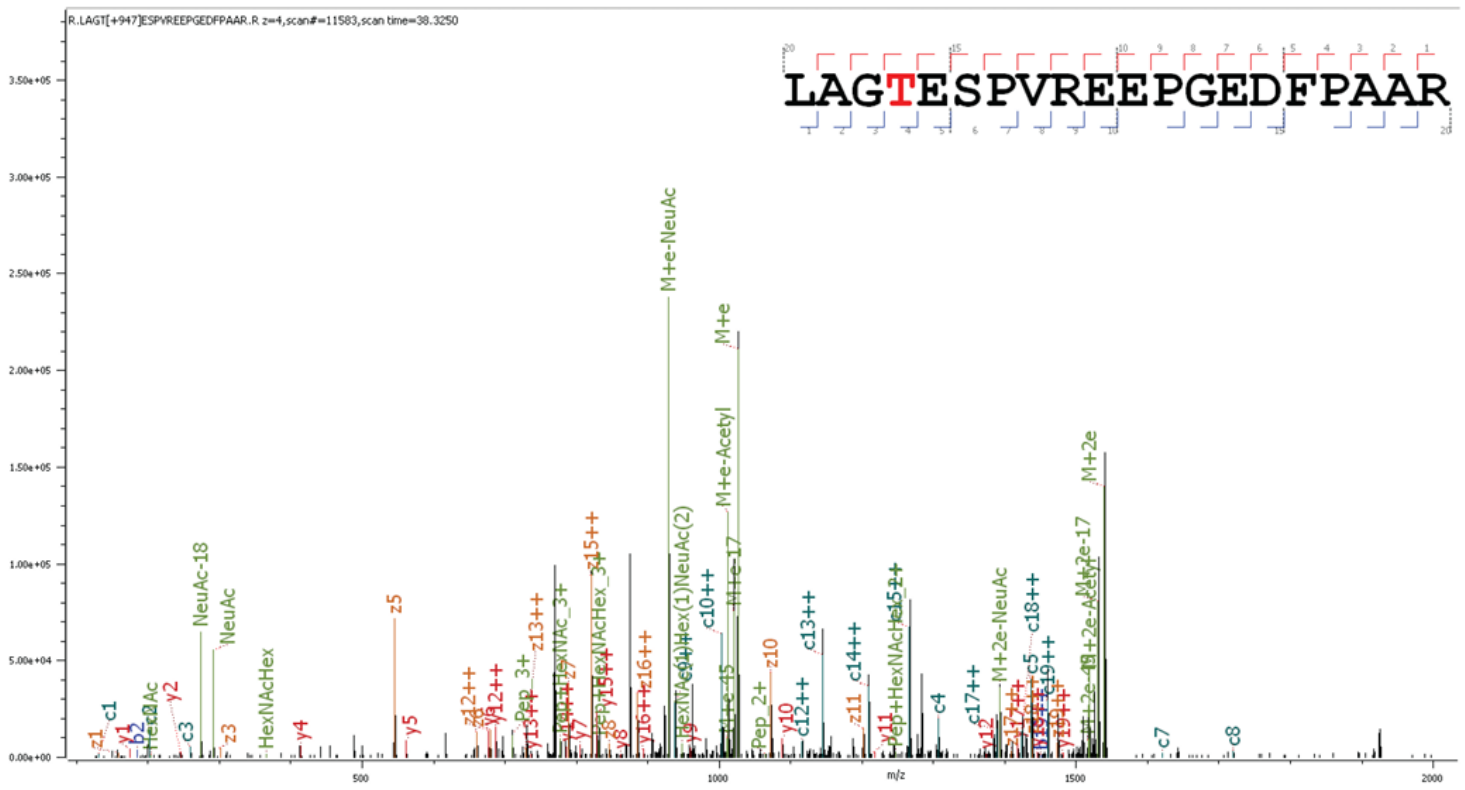
Automated & remote calibration
Fully internal, no need to remove source (nESI, FAIMS)
Calibration can be scheduled
Improves data consistency

OPTIONS | IC | ETD | PTCR | HMR^n+ | UVPD | FAIMS Pro Duo interface

Advantages of Multiple Fragmentation Options

mAb Glycopeptide Analysis with EThcD*

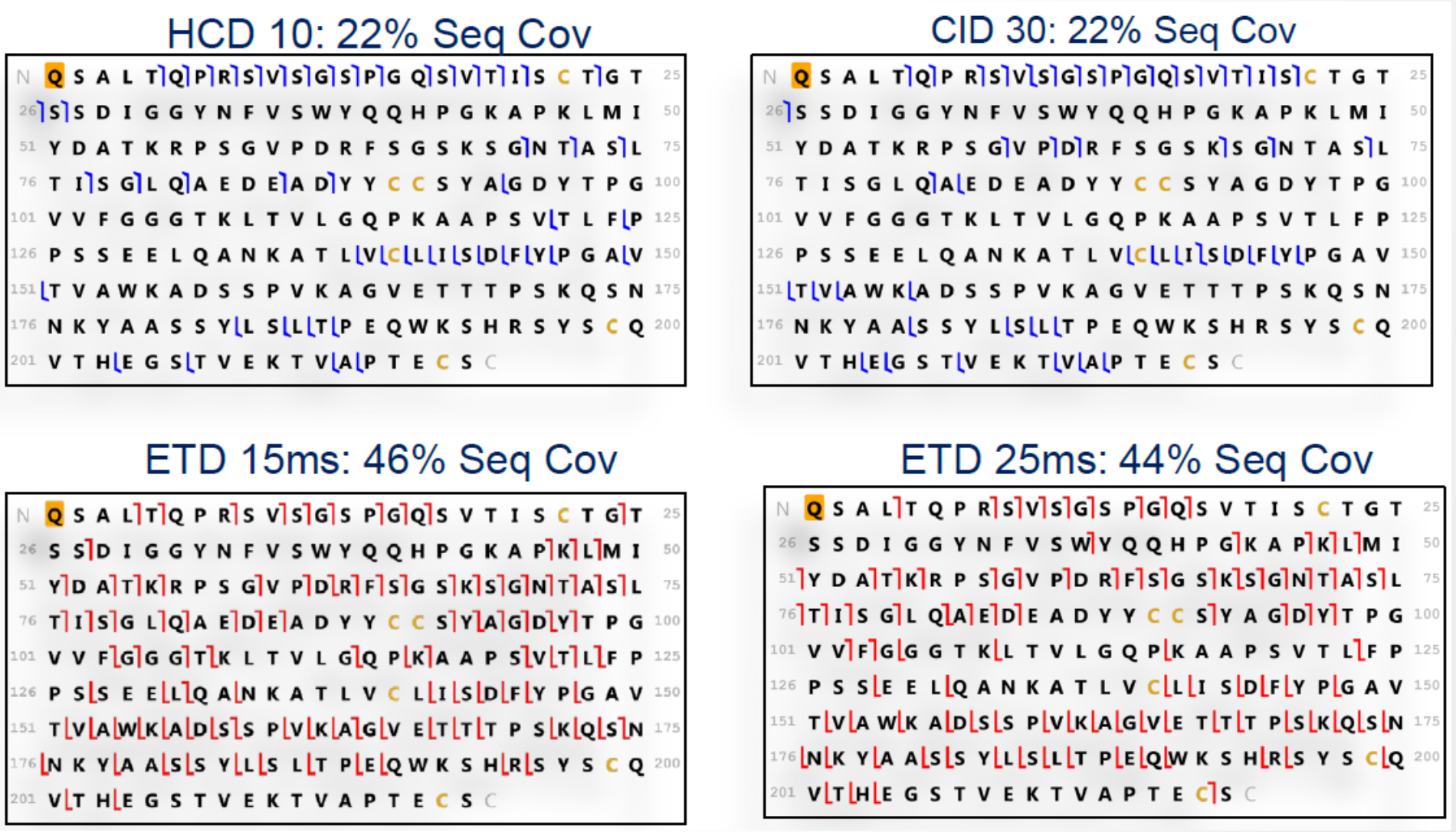
Figure 8. EThcD FT-MS/MS spectrum of *O*-linked glycopeptide



- Sugar-Peptide Linkage often weakest bond and preferentially cleaved during MS/MS fragmentation.
- Fragmenting with EThcD (combination of ETD and HCD) preserves sugar-peptide bond, allowing PTM site localization as well as peptide backbone fragmentation for sequencing.

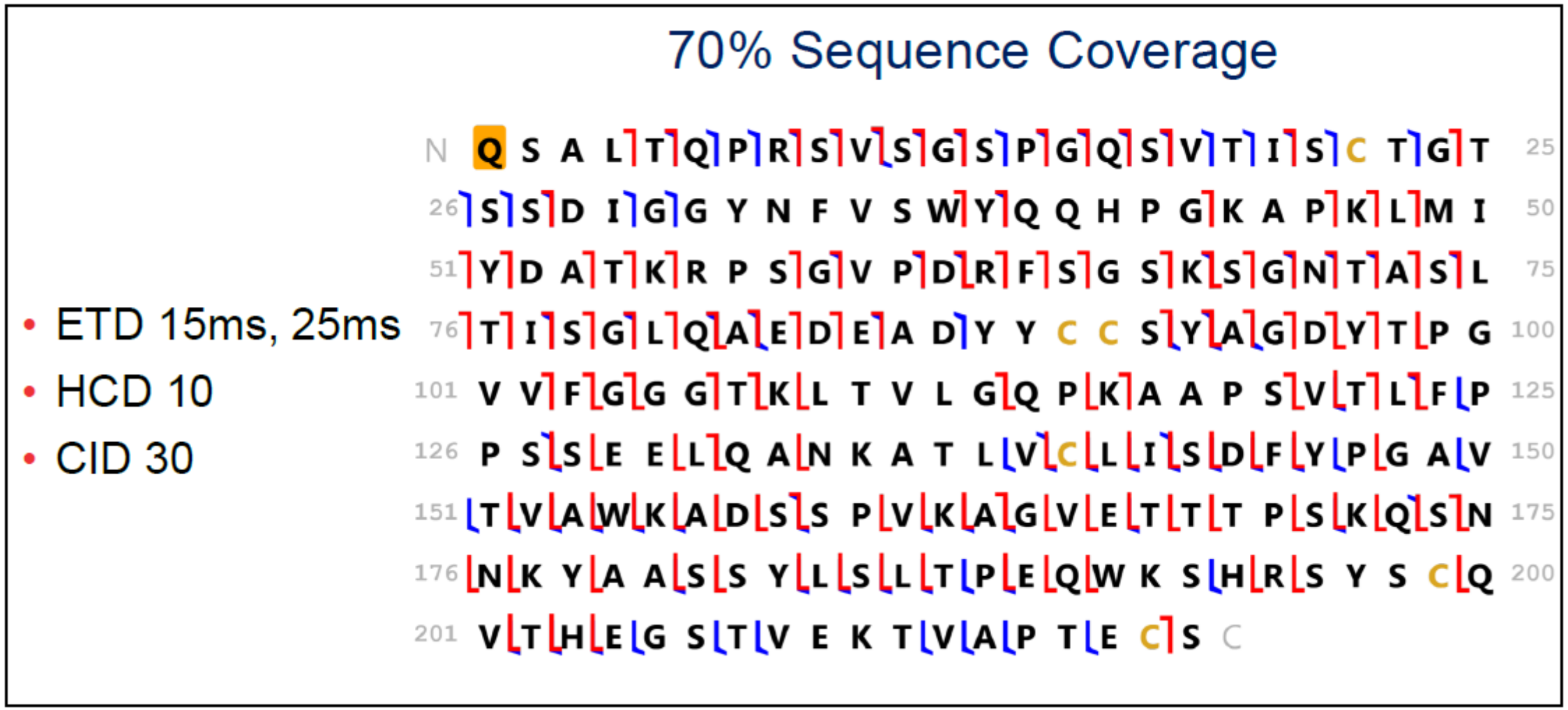
- *EThcD only possible in Thermo Scientific Tribrid Orbitraps: Ascend, Eclipse and Lumos.

Combination of Multiple Fragmentation Options Provide best TopDown Sequence Coverage (mAb LC)

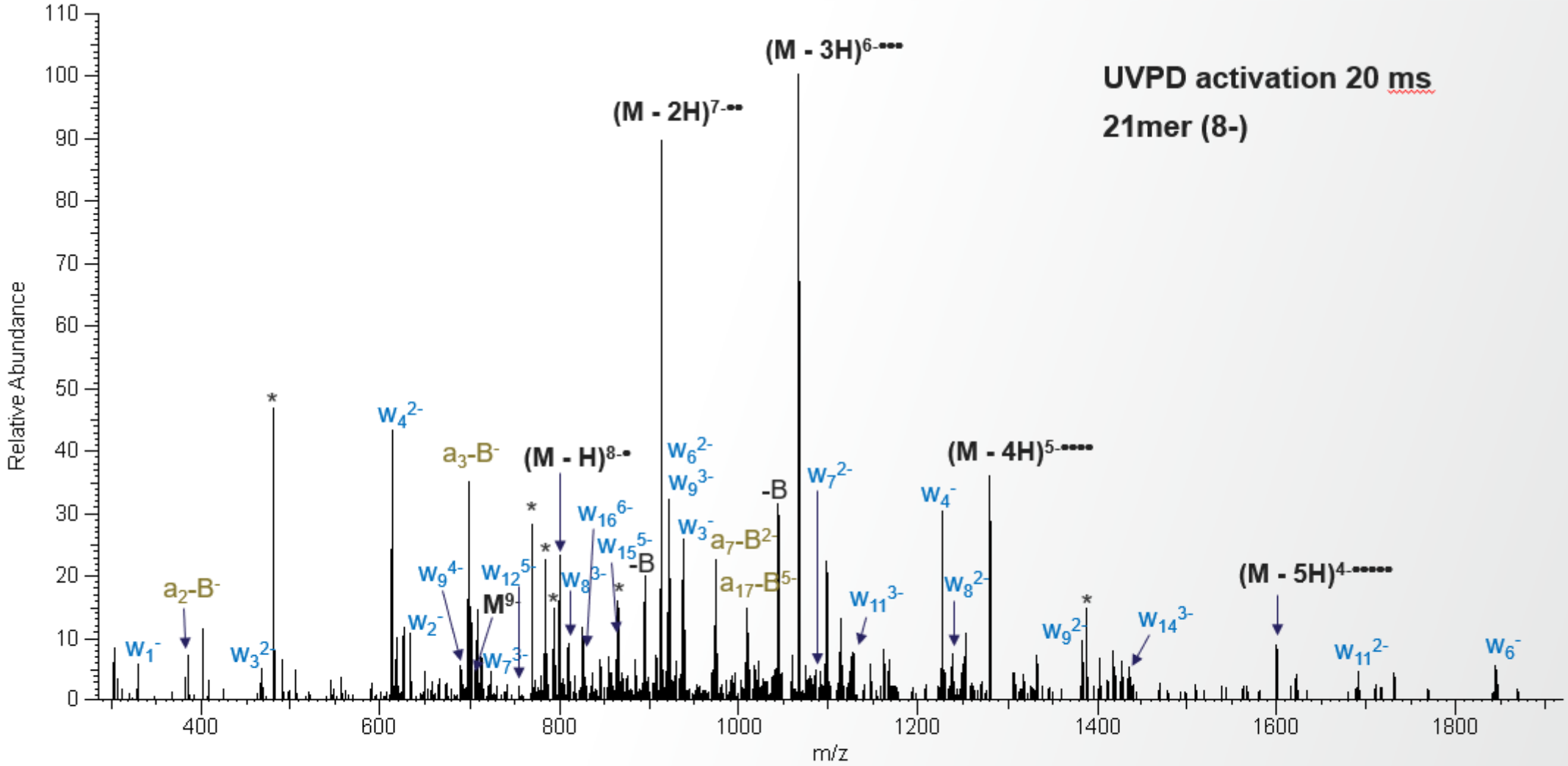


mAb LC Combined Sequence Coverage ETD, HCD, CID

- ETD 15ms, 25ms
- HCD 10
- CID 30



UVPD fragmentation of oligonucleotides



UVPD of 21mer leads to abundant charge reduced species and a series of w and a-B ions for sequencing

* = *internal fragments. Not all UVPD fragments are annotated in the spectrum above.*

Characterizing lipids using HCD/UVPD and MS3 scans

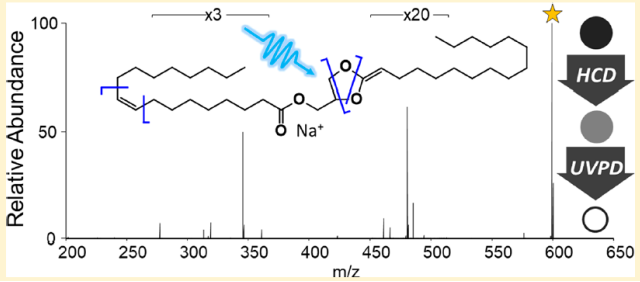
JACS
JOURNAL OF THE AMERICAN CHEMICAL SOCIETY
Article
Cite This: J. Am. Chem. Soc. 2017, 139, 15681-15690
pubs.acs.org/JACS

Pinpointing Double Bond and *sn*-Positions in Glycerophospholipids via Hybrid 193 nm Ultraviolet Photodissociation (UVPD) Mass Spectrometry

Peggy E. Williams, Dustin R. Klein, Sylvester M. Greer, and Jennifer S. Brodbelt*

Department of Chemistry, University of Texas at Austin, Austin, Texas 78712, United States

Supporting Information



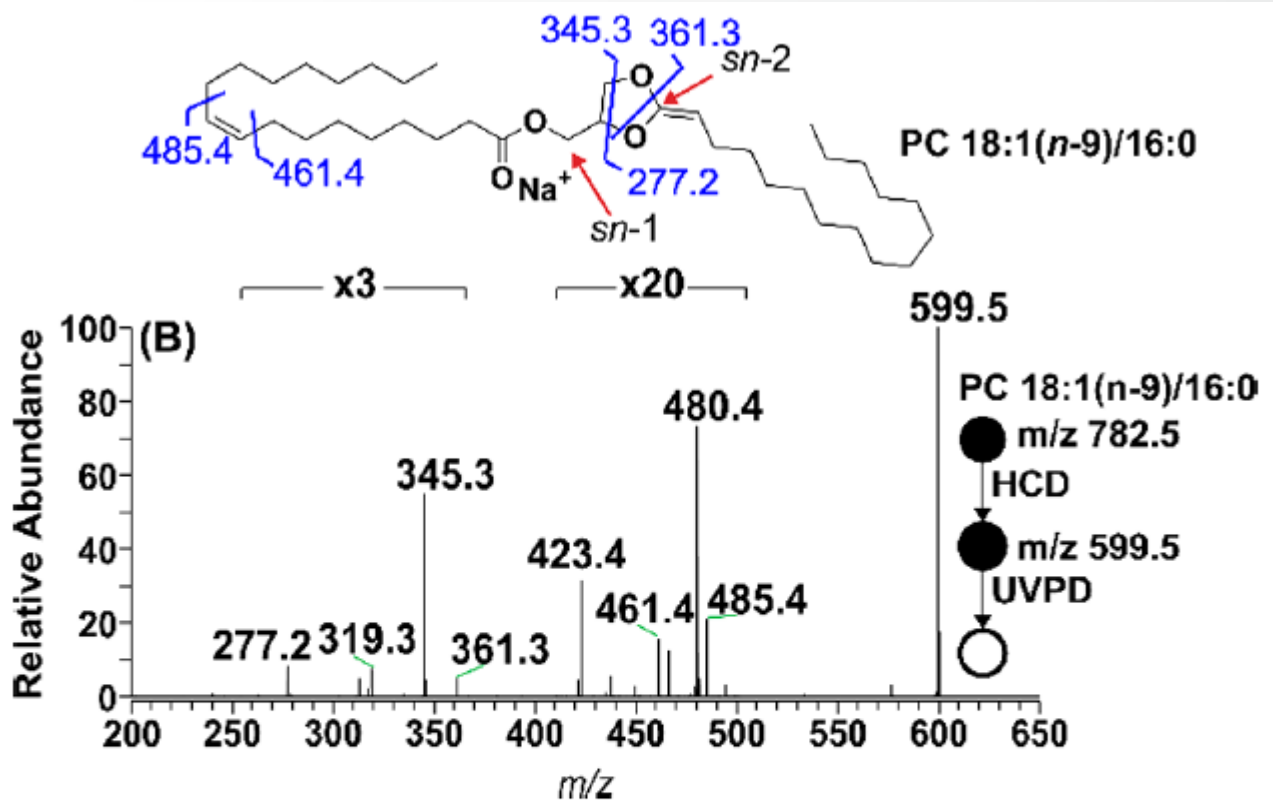


Figure 1. HCD/UVPD spectra of two sodium-cationized *sn*-regioisomeric PCs (A) PC 16:0/18:1(*n*-9) and (B) PC 18:1(*n*-9)/16:0. These spectra were obtained by isolating the headgroup loss ions (*m*/*z* 599.5) generated by HCD and subjecting them to 10 laser pulses (193 nm) with 4 mJ per pulse.

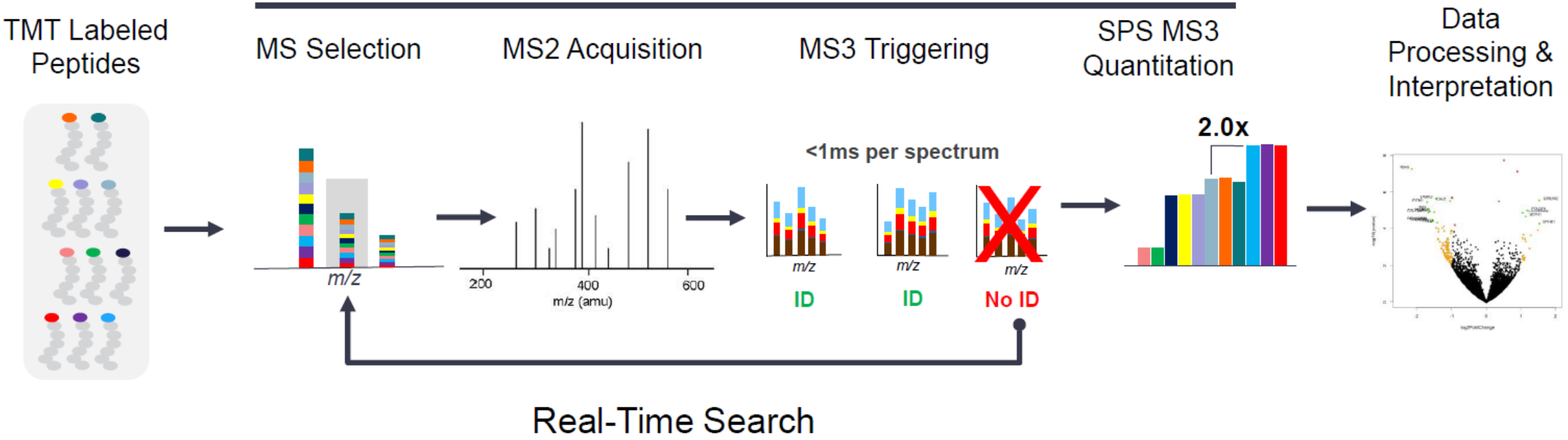
Real-time Search and Intelligent MS^3 data acquisition aid Quan and Identification

Increasing Accuracy and Depth for TMT SP3

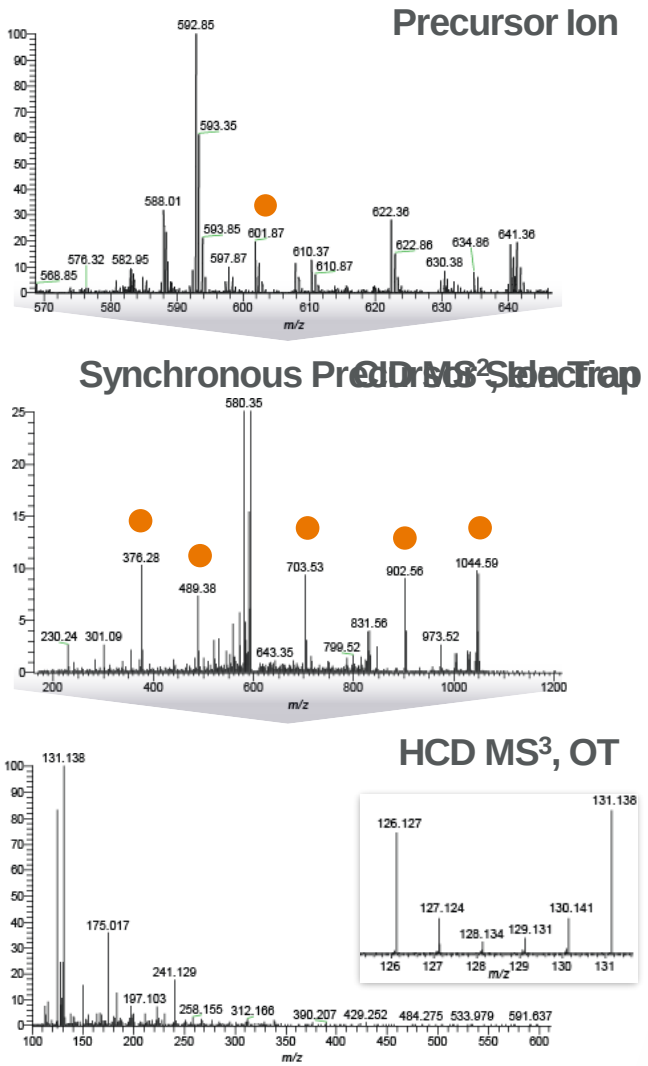
TMTpro 18plex reagents

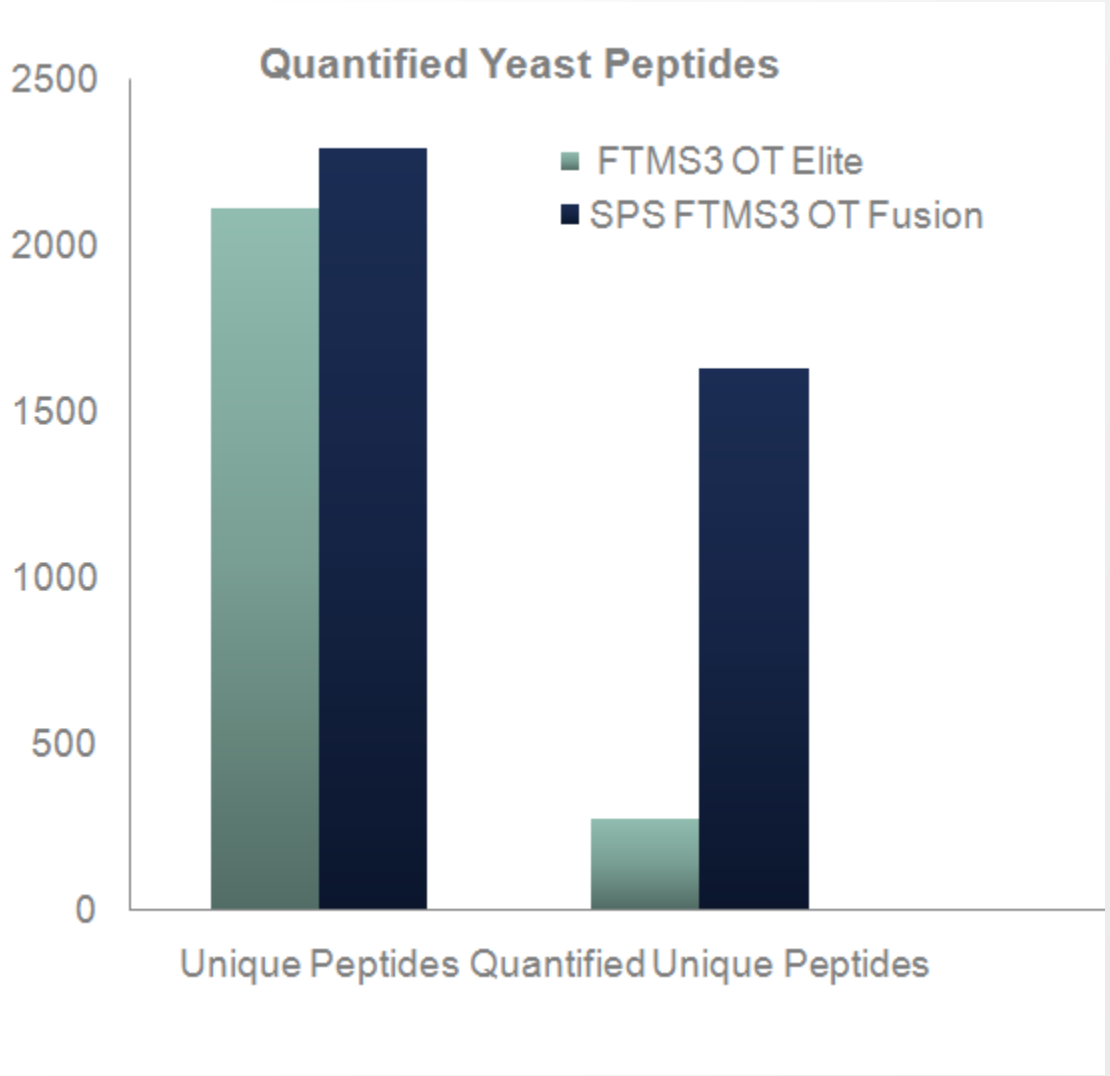
Thermo Scientific™ Orbitrap Eclipse™ Tribrid™ Mass Spectrometer

Proteome Discoverer Software 3.0



Synchronous Precursor Selection - Accurate and Sensitive TMT Quantitation



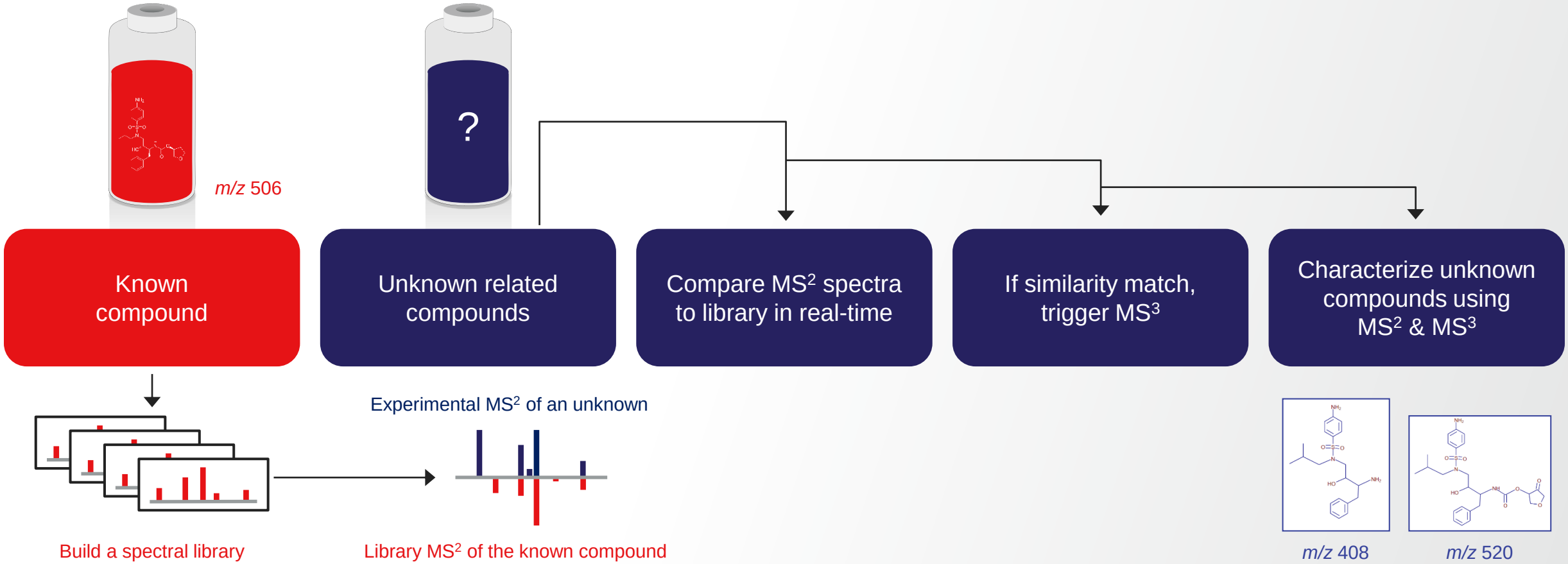


Source: Data courtesy Graeme McAllister

MET-IQ: Intelligent mass spectrometry for small molecules

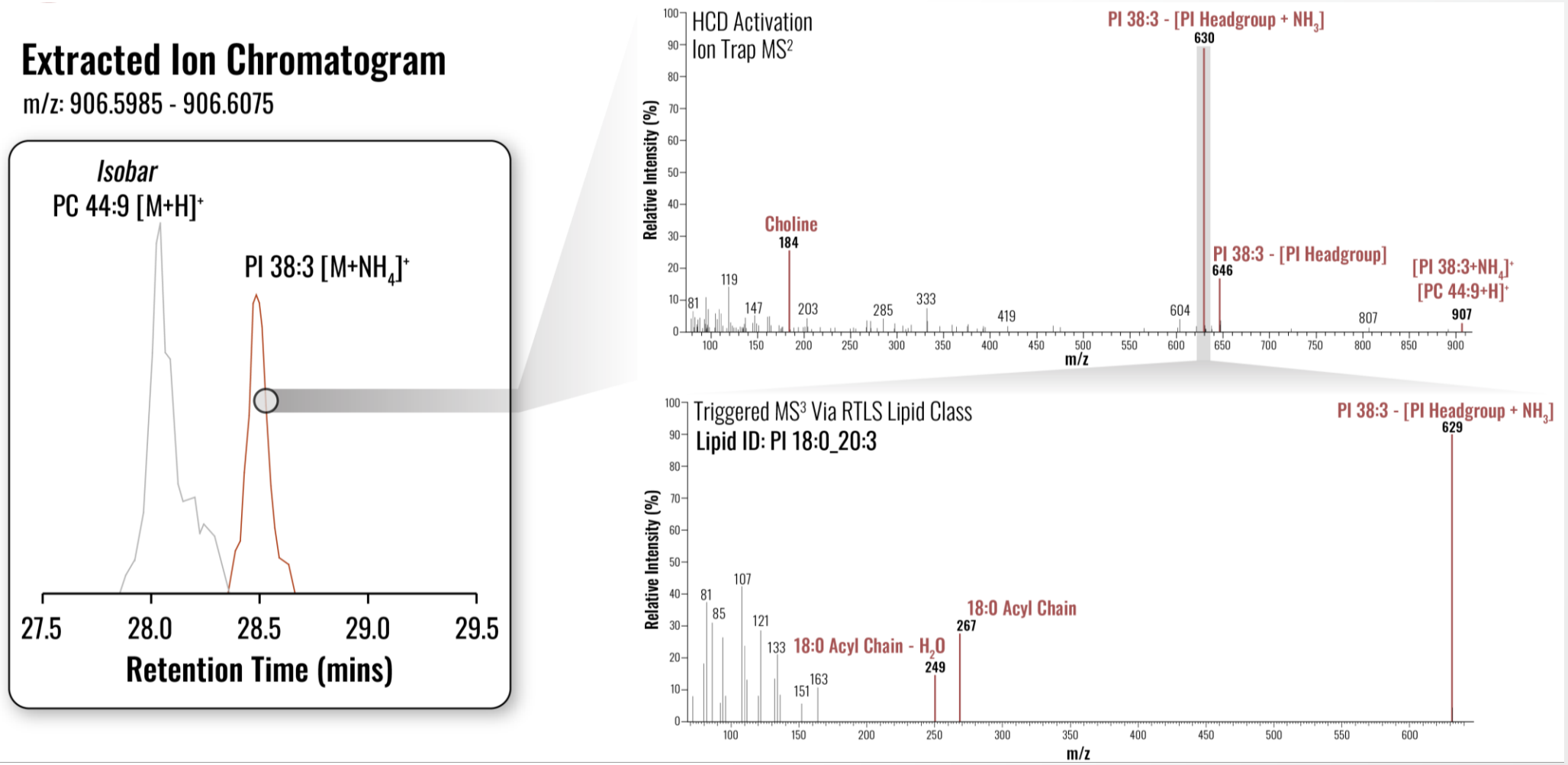
Challenge: Identification of unknown metabolites, degradants, or transformation products

Solution: Intelligent MS^3 data acquisition enables annotation and characterization of unknown compounds



Designed to unravel complex chemical structures: www.thermofisher.com/OrbitrapIQ-X

Real-Time Library Search triggered MS^3 reveals Phosphatidylinositol (PI) Acyl chain composition

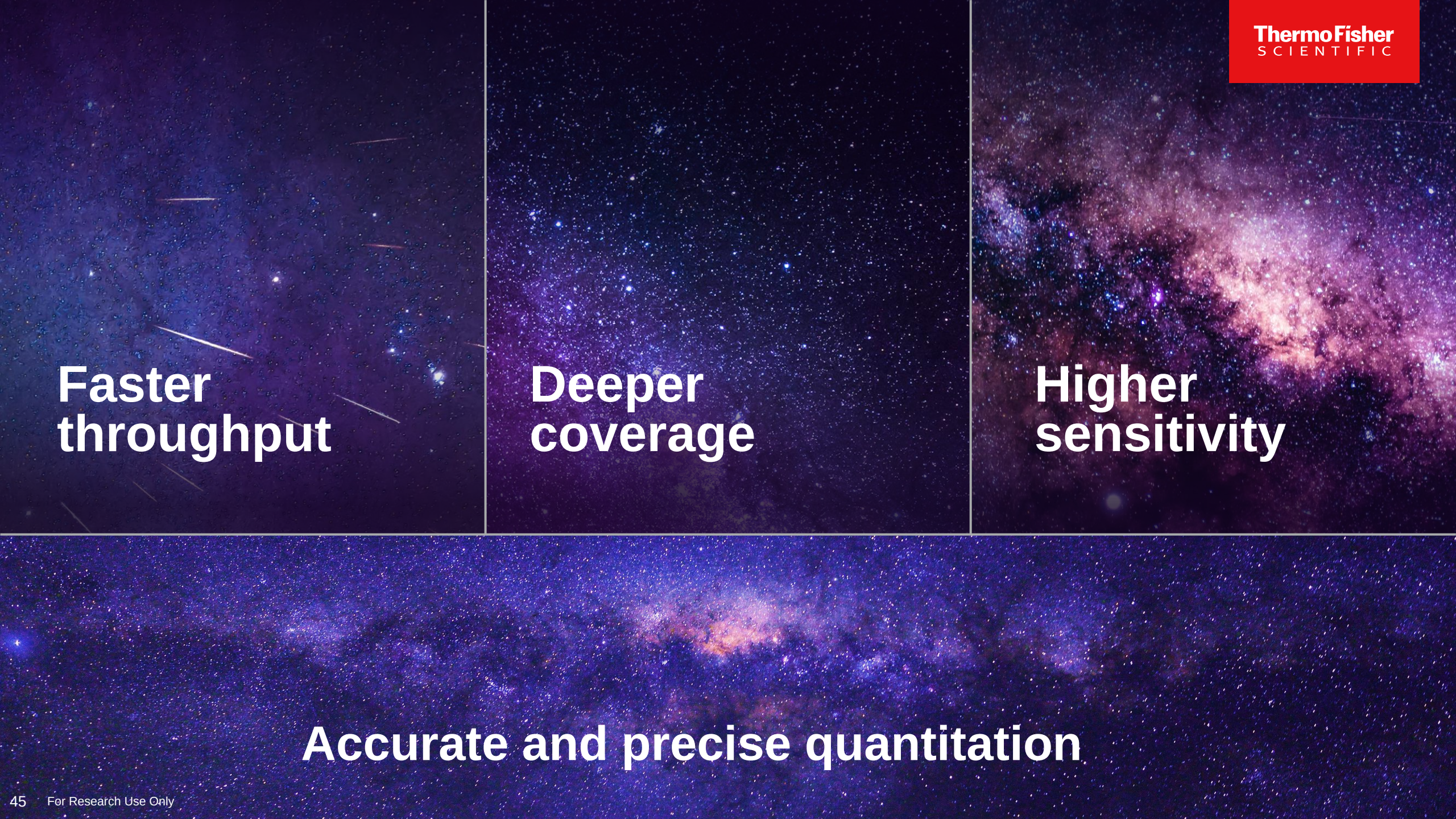


Data courtesy of Dr. Joshua Coon,
University of Wisconsin-Madison

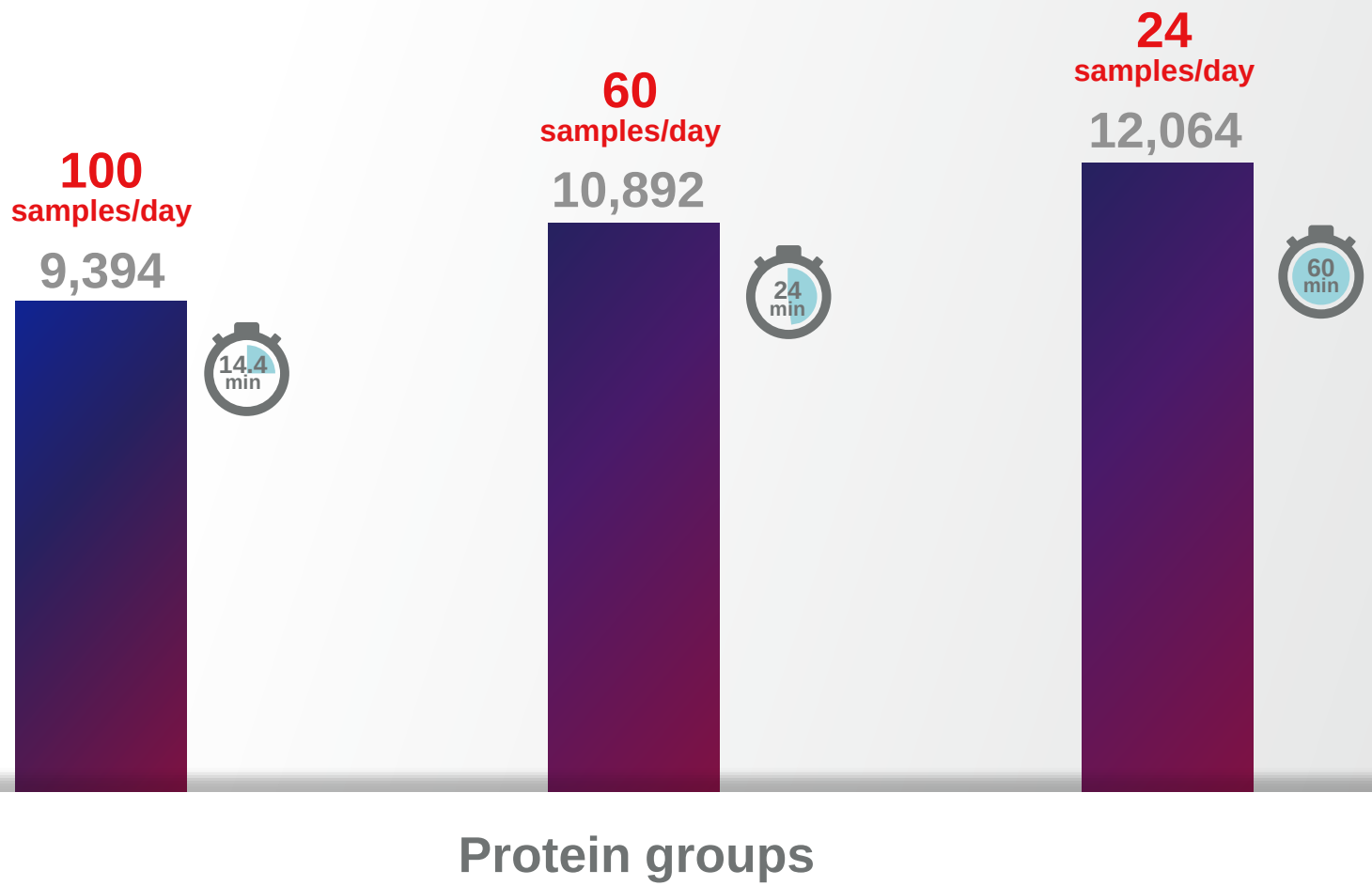
Introducing the

Thermo Scientific™ Orbitrap™ Astral™

MASS SPECTROMETER


Faster throughput
Deeper coverage
Higher sensitivity
Accurate and precise quantitation

Incredible flexibility to deliver high coverage at high throughput or unprecedented depth in 1 hour



Now identify over

15,000

proteins

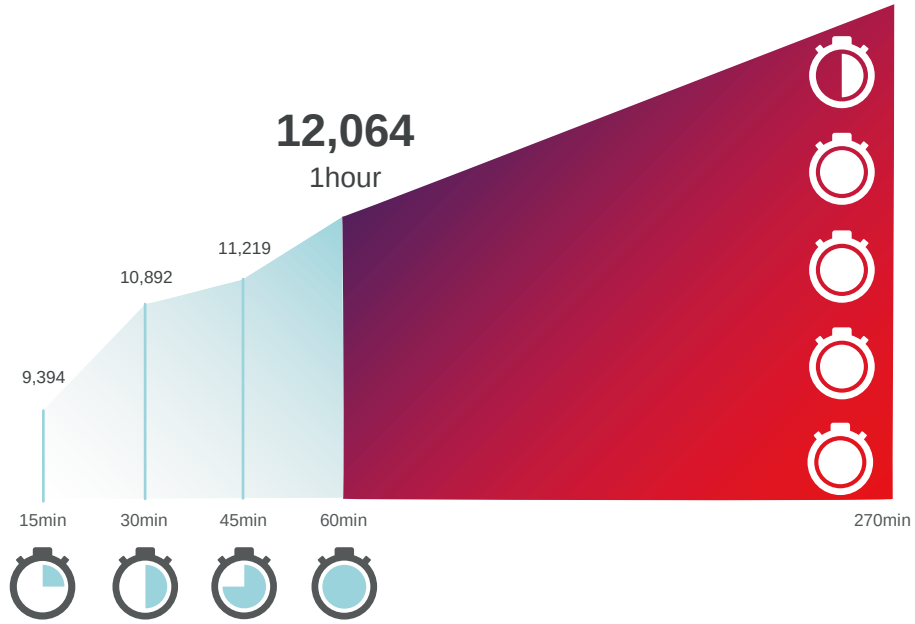
See more in less time

or

Spend more time and go even deeper

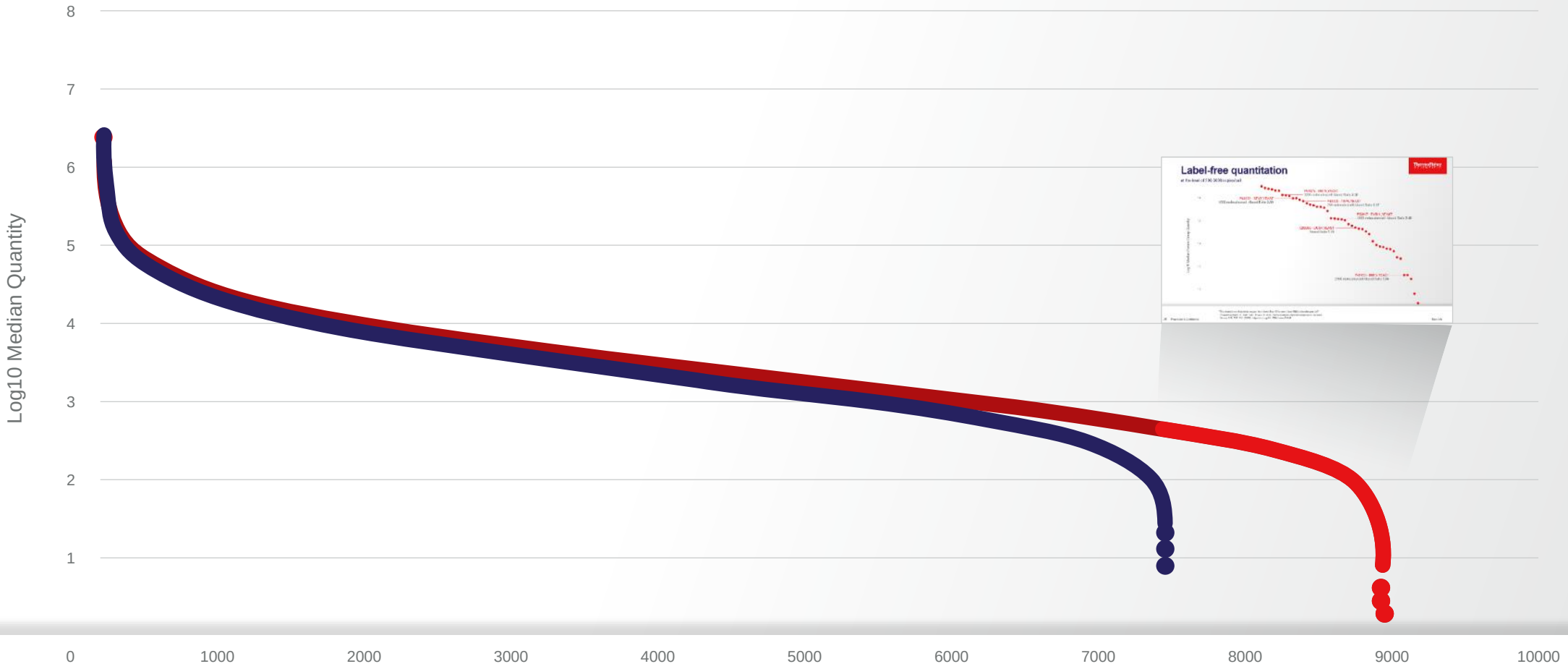
15,147

In 4.5 hours



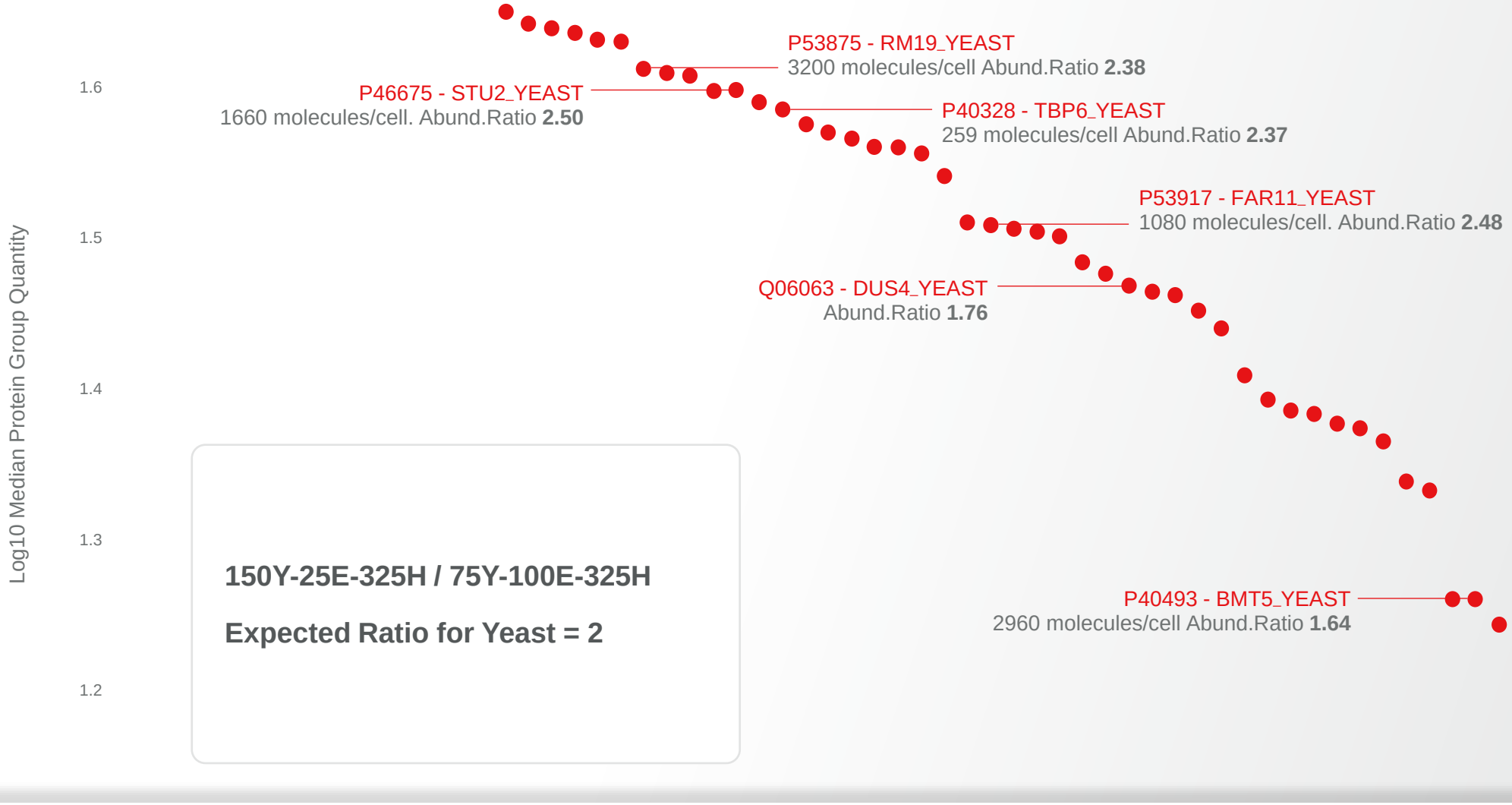
Discover more biomarkers with a larger dynamic range

Comparison of LFQ DIA performance between state-of-the-art Orbitrap MS and Orbitrap Astral MS



High sensitivity label-free quantitation

Accurate and precise quantitation at the level of 200-3000 copies/cell



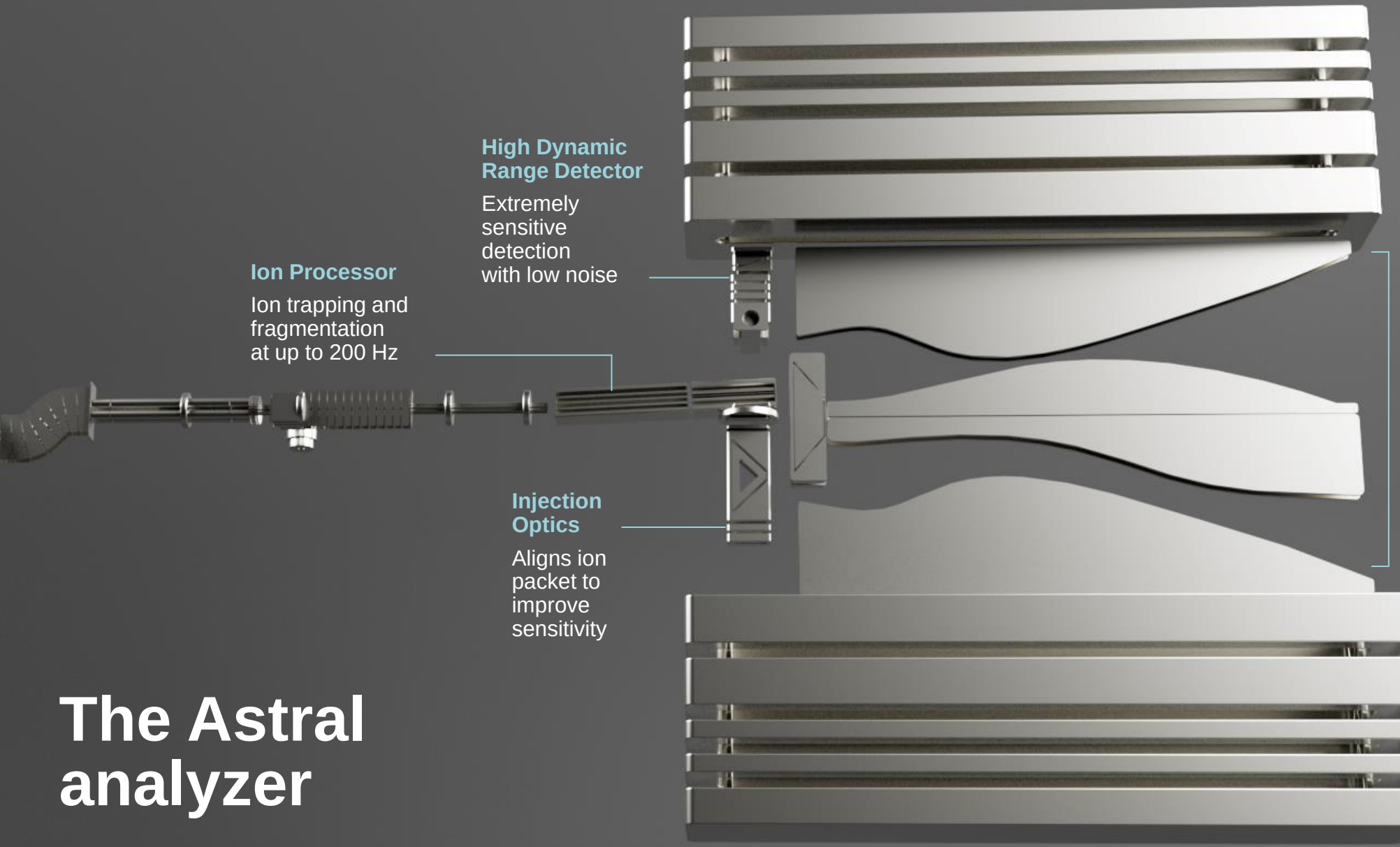
"The abundance of proteins ranges from fewer than 50 to more than 10(6) molecules per cell"

Ghaemmaghami, S., Huh, WK., Bower, K. et al. Global analysis of protein expression in yeast. Nature 425, 737–741 (2003). https://doi.org/10.1038/nature02046

• Orbitrap Astral MS

More info

The Astral analyzer



High Dynamic Range Detector

Extremely sensitive detection with low noise

Ion Processor

Ion trapping and fragmentation at up to 200 Hz

Injection Optics

Aligns ion packet to improve sensitivity

Ion Foil

Shapes and focuses ions onto asymmetric track with minimal loss

Asymmetric Ion Mirrors

Elongated ion track for up to 80,000 resolution

Q Exactive™ UHMR

Instrumentation for native MS

1. Ultra-High Mass Range,

   m/z 350-80,000

2. High Mass Quadrupole

   Isolation up to *m/z* 25,000

3. Desolvation and Dissociation

   In-source trapping or CID, and HCD

4. Direct Mass Technology

   Enabling Charge Detection MS0

Thermo Scientific™ Q Exactive™ UHMR Hybrid Quadrupole-Orbitrap™ Mass Spectrometer

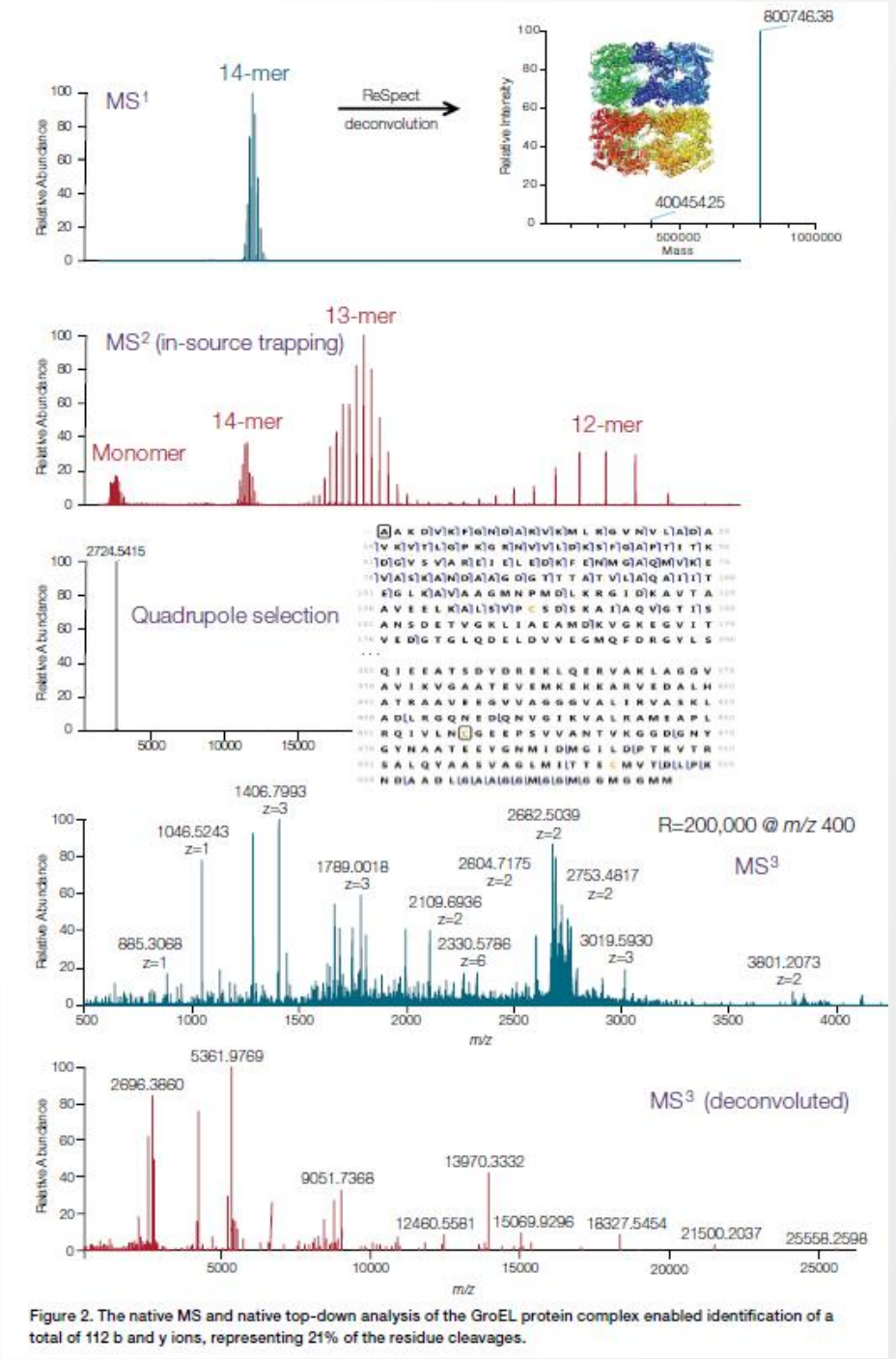


Figure 2. The native MS and native top-down analysis of the GroEL protein complex enabled identification of a total of 112 b and y ions, representing 21% of the residue cleavages.

Learn more at www.thermofisher.com/massspec

Contact Information
For HPLC, GC, IC and LCMS products
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navette.shirakawa@thermofisher.com

Thank you