Top 5 reasons to upgrade from a Thermo Scientific™ Hybrid Orbitrap™ to a Thermo Scientific™ Tribrid™ Mass Spectrometer System

Goal

This document is intended to provide conclusive arguments to justify upgrading from an Orbitrap Hybrid MS to an Orbitrap Tribrid mass spectrometer system.

Summary

The Thermo Scientific™ Orbitrap™ Tribrid™ mass spectrometers are an essential tool for high-end life science research. Robustly designed, they come equipped with a quadrupole mass filter as well as an Orbitrap and linear ion trap mass analyzer. This hardware combination (exclusive to Orbitrap based mass spectrometers) provides superior analytical performance that enables multiple complex modes of analysis. This is due to the parallel isolation and detection mechanisms achievable with the Tribrid architecture, which was previously unattainable with Thermo Scientific™ Orbitrap hybrid MS. The most difficult analyses, including multiplexed quantitation of low-abundance peptides in complex matrices, characterization of positional isoforms of intact proteins, protein structure characterization using chemical crosslinking, and the deepest mining of challenging post-translational modifications may be performed on the highly sensitive and versatile Thermo Scientific Orbitrap Fusion family of mass spectrometers. The Tribrid system can perform multiple fragmentation techniques that prove useful in terms of experimental flexibility for applications such as quantitation using isobaric tags, low level PTM analysis, data independent acquisition (DIA), and top-down proteomics. The Tribrid MS provides the highest resolution, heightened sensitivity, rapid acquisition rates, improved ETD fragmentation and exclusive analytical techniques (e.g. multiNotch SPS MS^3) for accurate relative quantitation experiments. These instruments are intended to push the limits of detection, characterization and quantitation and are able to achieve proteome-wide coverage, by combining the versatility of a Tribrid system with the selectivity of Orbitrap technology, and the sensitivity and speed rivaling that of a triple quadrupole instrument.

Introduction

The Thermo Scientific™ Orbitrap™ Fusion™ and Thermo Scientific™ Orbitrap Fusion™ Lumos™ Tribrid™ mass spectrometers are a new class of mass spectrometry instrumentation engineered with a revolutionary Tribrid architecture– combining the best of quadrupole, Orbitrap and linear ion trap mass analyzers. This Tribrid design enables scientists to meet their analytical challenges by offering unprecedented depth of analysis especially for highly complex, low abundance, or difficult-to-analyze biological samples. The Tribrid based mass spectrometers are equipped with well-designed hardware features and a user-friendly software interface allowing for easy method development and instrument operations. The innovations of the Orbitrap Fusion MS and Fusion Lumos MS systems make them the most sensitive, most selective and most versatile mass spectrometers available to date.

Both Orbitrap Fusion MS and Fusion Lumos MS have the following capabilities:

- Sensitivity comparable to a triple quadrupole mass spectrometer is achieved through improved ion transmission with a brighter ion source, advanced quadrupole technology and detection with the most sensitive detector.
- Selectivity of an Orbitrap analyzer allows the lowest detection limit to be achieved due to the highest resolution and highest mass accuracy available.
- Versatility of a Tribrid mass spectrometer provides multiple dissociation techniques (CID, HCD, ETD, EThCD) and full experimental flexibility due to its unique Tribrid architecture.

The Tribrid MS systems are equipped with the following:

- Ultra-high field Orbitrap mass analyzer – Offers resolution exceeding 500,000 resolving power at *m/z* 200 and scan speeds up to 20 Hz at 15,000 FWHM.
- Ion Routing Multipole – Facilitates parallel analysis and performance of HCD at any MS^n stage.
- Dual-Pressure Linear Ion Trap – Performs MS^n and sensitive mass analysis of four fragmentation types (CID, HCD, ETD HD and EThcD HD).

Table 1. Fundamental features and benefits of Tribrid technology.

Features	Benefits
Ultra high resolution	High selectivity, ability to resolve analytes down to a few mDa
Sub ppm mass accuracy	High selectivity and confidence in molecular formula
Dynamic scan management	Intelligent scan scheduling allows for efficient operation at all times
Speed	Sequencing of low abundant components in complex mixture, fast scanning MS^n compatible with UHPLC
Synchronous precursor selection	Ability to carry out highly sensitive and accurate protein quantitation using TMT reagents
Easy to use software	Novel drag-n-drop flexible user interface makes it easy to build complex methods
Experimental flexibility	Use of multiple analyzers and dissociation techniques (HCD, CID, ETD) for any molecule at any MS^n stage

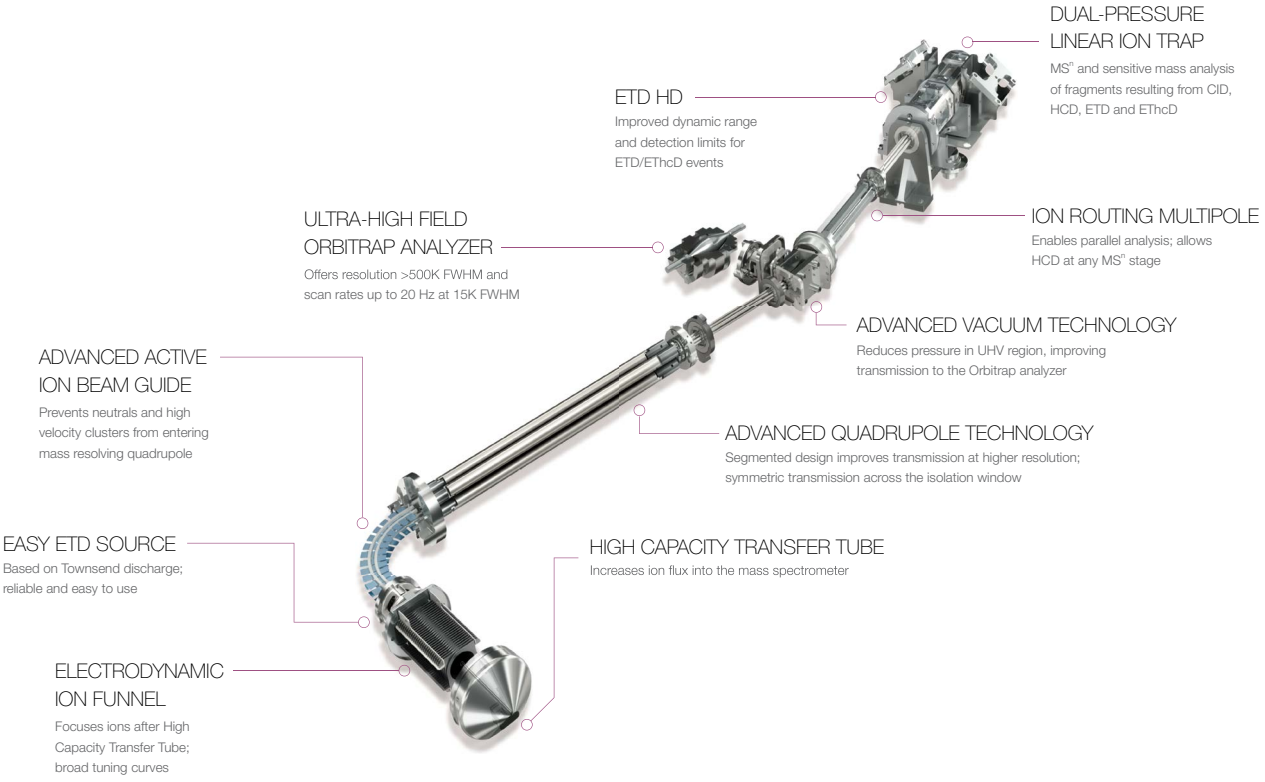


Figure 1. Hardware benefits.

Key improvements have been made to various hardware components on the Orbitrap Fusion Lumos MS to give enhanced analytical performance:

- Brighter ion source increases overall signal by 2–5 times and consists of a High Capacity Transfer Tube (HCTT) and an Electrodynamic Ion Funnel (EDIF) to achieve increased ion flux and lower limits of detection. It also comes optional with an Easy ETD Source (based on Townsend discharge) which provides greater reliability and ease of use due to its ability to produce extremely stable anion flux and retain reagent longevity.
- Advanced Active Ion Beam Guide has been a proven technology that prevents neutrals and high velocity clusters from entering the mass resolving quadrupole, therefore keeping the quadrupole cleaner and reduces background contamination.
- Advanced Quadrupole technology – Segmented design improves transmission efficiency at higher resolution allowing for symmetric transmission across the isolation window.
- Advanced Vacuum Technology reduces pressure in UHV region, improving transmission of high molecular weight species to the Orbitrap analyzer.
- Novel ETD HD gives improved dynamic range and detection limit of ETD analyses, significantly increasing the fragment ion coverage.

Detailed product specifications for the Orbitrap Fusion Tribrid MS and Orbitrap Fusion Lumos Tribrid MS systems can be found on www.thermofisher.com or www.planetorbitrap.com.

Table 2. Specifications.

Feature	Orbitrap Fusion MS and Orbitrap Fusion Lumos MS
Scan rate Orbitrap MS^2	20 Hz
Scan ratelon Trap MS^2	20 Hz
Max resolution	>500,000 at *m/z* 200
Quad isolation	Down to 0.4 amu
Ion trap isolation	Down to 0.2 amu
Mass accuracy	3 ppm (external); 1 ppm (internal)
Dissociation	Source CID, CID, HCD, ETD, EThcD (Orbitrap Fusion MS) Source CID, CID, HCD, ETD HD, ETh-cD HD (Orbitrap Fusion Lumos MS)
MS^n capability	Up to MS^{10} in ion trap or Orbitrap
Analyzers	Quadrupole, Orbitrap, Ion Trap
Detectors	Ion Trap, Orbitrap

Detailed product specifications for the Thermo Scientific Orbitrap Fusion Tribrid Mass Spectrometer.

Detailed product specifications for the Thermo Scientific Orbitrap Fusion Lumos Tribrid Mass Spectrometer.

For sole source specifications, kindly contact your local sales representative or contact us at Grant Central.

Top 5 reasons for upgrading from Hybrid MS to Tribrid MS technology

- Enabling Multiplexing with TMT technology
- Faster scanning MS detectors for increased throughput
- Improved sensitivity for extended coverage of low abundant proteins
- Multiple fragmentation techniques for the elucidation of PTMs
- User-friendly data acquisition software for non-MS experts

Reason 1: Multiplexing with tandem mass tag (TMT) technology

About TMT

TMT reagents (Proteome Sciences®, commercially available from Thermo Fisher Scientific) are isobaric chemical tags consisting of a signature reporter group, a spacer arm, and an amine reactive group. The reagents covalently bind to the *N*-terminus of a peptide or to lysine residues. Upon MS/MS fragmentation, each version of the tag fragments and produces a unique reporter ion. In an experiment that compares several experimental conditions in a single analysis, the protein digest from each experimental condition is labeled with one of the isobaric versions of the TMT reagent. Afterwards, all the samples are pooled together and analyzed with LC-MS/MS. During the first dimension separation (RPLC), the same peptide labeled with different versions of the tag will elute together as they have the same chemical properties. On subsequent MS^1 analysis, these peptides will be detected simultaneously as a single indistinguishable precursor ion peak. Following MS/MS fragmentation of the precursor, the relative levels of each version of the tag used to label the peptide can be quantified by comparing the intensities of the unique reporter ion generated from each tag. Additionally, protein identification is achieved by matching the peptide fragment ions in the MS/MS spectrum to sequences in the appropriate database.

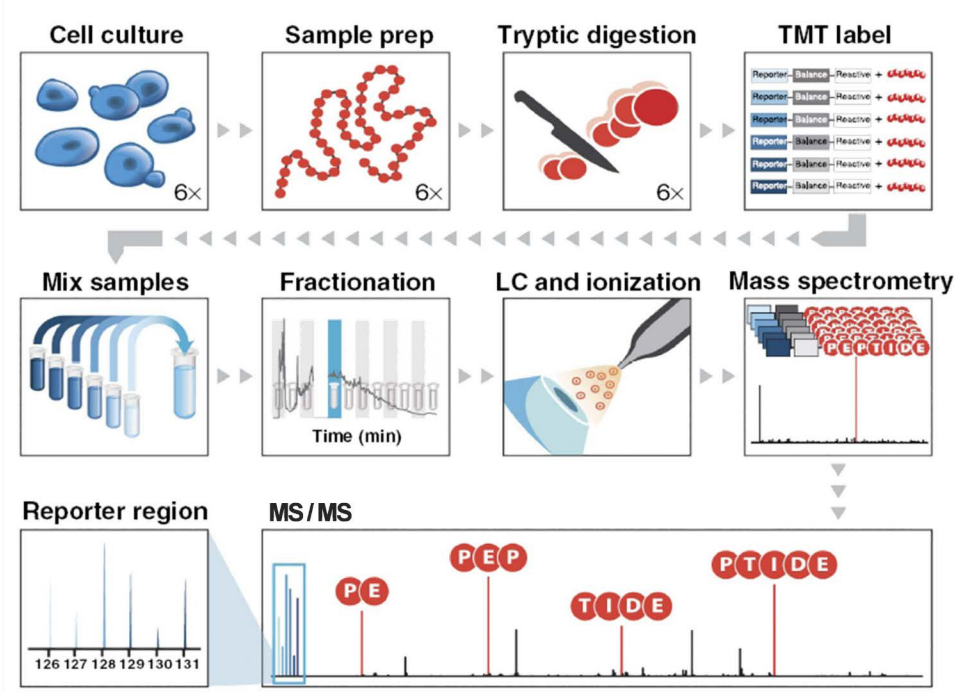


Figure 2. Overview of a tandem mass tag workflow.[1] The Orbitrap Fusion Tribrid mass spectrometers truly differentiates the TMT workflow from Orbitrap hybrid MS and quadrupole time-of-flight mass spectrometers by providing robust multiplexing capabilities and increasing throughput by over 10 folds.

Trying to understand the complexities in biology requires understanding the functional aspects of biology, and that necessitates more sophisticate levels of mass spectrometric performance. The Orbitrap Fusion Lumos MS and Orbitrap Fusion MS are suitable instruments as they combine the analytical capabilities equivalent to three instruments, all within the usability of a single instrument platform.

As proteomics becomes more quantitative, the ability to perform relative quantitation for many samples accurately is absolutely critical. Typical experimental designs require running a separate LC-MS/MS analysis for each individual experiment, which results in the depletion of precious samples, the demand for long instrument analysis times, and introduction of run-to-run variations. Adopting the TMT isobaric tagging approach permits multiple time points, cell lines, or experimental conditions to be analyzed simultaneously (Figure 2). In addition to conserving samples while taking only a fraction of the time to run, a TMT workflow ensures reproducibility by analyzing all experiments under the exact same conditions. A straightforward workflow also allows the inclusion of "technical replicates" by using duplicate labels for the same condition for enhanced confidence and statistical analysis, all accomplished within a single LC-MS/MS analysis.

The Tribrid systems are capable of carrying out accurate quantification of proteins on a massive scale through high-throughput multiplexing. The combination of isobaric labeling technology, tandem mass technology and the novel scan functionality in the Orbitrap Tribrid instruments enable over one hundred thousand protein quantifications in a single day. This performance is heavily driven by the new capabilities in the unique hardware architecture on the Orbitrap Tribrid based MS systems. Parallelization of complex modes of analysis is accomplished by the concurrent isolation of ions with one analyzer and detection with the two other analyzers.

Quantification with higher plexing isobaric tags requires the highest resolution for all reporter ion channels and unexpected interferences in the reporter ion region of the mass spectrum. The multiplexing capabilities of the TMT tags have been extended by simply using a more complex isotopologue design (dependant on the 6.32 mDa mass difference between 13C and 15N) in which the heavy atoms are strategically placed in different positions of the mass reporter to provide 10 different distinct masses to report out each channel (Figure 3). High resolution (at least 50K at *m/z* 200) is absolutely crucial to obtain complete resolution of all 10 mass reporter channels which differ by a very small mass difference.

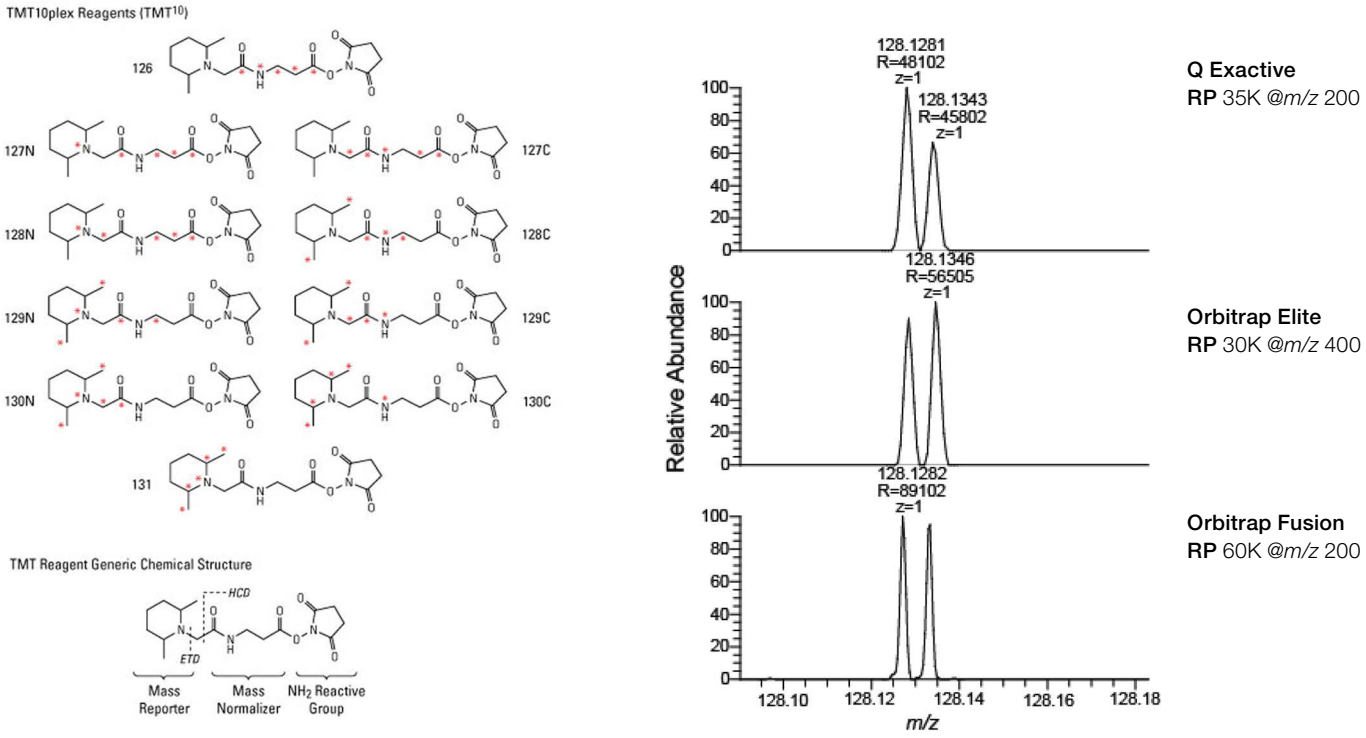


Figure 3. The TMT10-127 (13C and 15N labeled) and TMT10-129 (13C and 15N labeled) reagents differ only by a mass difference of ~6.32 mDa. High resolution Tribrid mass spectrometers have the unique ability to resolve these neighboring isobaric istopologues distinctly.[2]

All Orbitrap instruments are capable of resolving the closely-spaced reporter ions (Figure 3). It is evident, however, that the Tribrid-based MS systems yield the highest resolution in the shortest time due to faster scanning speeds and the ultra-high field Orbitrap analyzer. Although quadrupole time-of-flight mass spectrometers are known for their fast scan rates, they can be limited in achieving high resolution to resolve the tightly-spaced TMT reporter ions with good detection sensitivity. Additionally, improvements of the ion source and ion optics on the Orbitrap Fusion Lumos MS increase the number of quantifiable peptides, which is especially beneficial at lower sample concentrations (Figure 4).

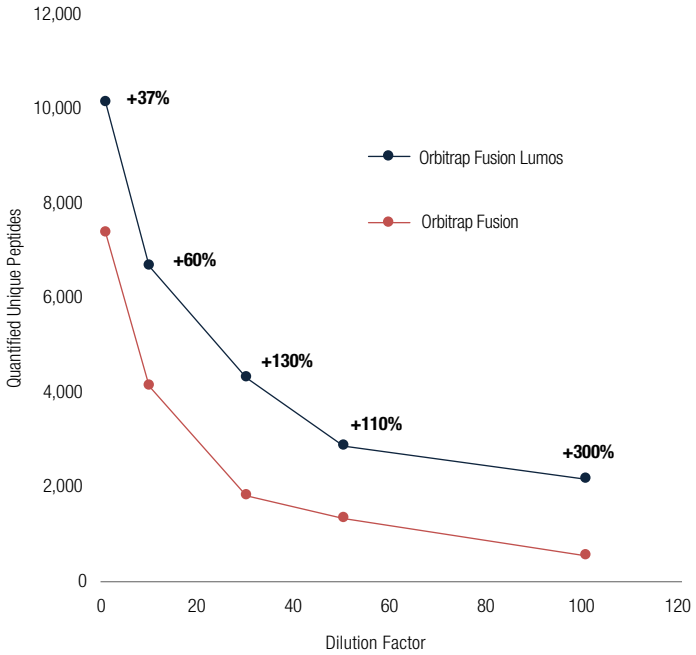


Figure 4: Standard HeLa digest labeled with TMT0 analyzed with an 85 min gradient using SPS MS³ on both Fusion and Fusion Lumos tribrids. The increase in number of quantifiable unique peptides across varying dilution factors becomes apparent at lower concentrations.

Achieving greater accuracy in quantitation using Synchronous Precursor Selection (SPS MS^3) capability

The Orbitrap Fusion MS and Orbitrap Fusion Lumos MS offer the ability to perform "Synchronous precursor Selection (SPS)" for added experimental throughput while providing the depth and coverage needed for a TMT experiment. A common problem affecting the accuracy and precision in TMT quantitation experiments is the co-isolation and co-fragmentation of interfering ions. This causes reporter ion ratio distortions and inaccurate reporting of true fold changes or reporter ion intensities. While the MS^3 method was found to be effective in mitigating the interference issue and restoring accuracy and precision of TMT quantitation[3], an overall drop in sensitivity was observed.

Therefore, the SPS MS^3 method is the ideal solution to address the above-mentioned issues observed from a TMT experiment. This method uses isolation waveforms with multiple frequency notches to co-isolate and co-fragment multiple MS^2 fragment ions (up to 20) (Figure 5), effecting increased number of reporter ions in the MS^3 spectrum over standard MS^3 method.[4] The dynamic range of reporter ion quantitation is better, signal variance decreases and higher quality quantitative measurements are obtained with the SPS MS^3 method. This dramatically increases the signal intensity, improves the ratio accuracy (due to counting statistics) and boosts overall quantitative sensitivity by leveraging on such intense multiplexing capabilities obtainable only with the Tribrid technology mass spectrometers. Sensitivity and interference ion issues are eliminated to bring back accuracy and precision to the TMT experiment. To demonstrate this capability, we performed an SPS MS3 experiment on the Orbitrap Fusion Lumos. Human HeLa cells were spiked with yeast samples labeled with four TMT channels in equal amounts, to simulate interference effects in TMT labeled samples (Figure 6). The true benefits of SPS MS^3 in recovering accurate ratios in TMT experiments are evident from this example. Results from the analysis show that the MS2 acquisition (in blue), even at 0.7 amu isolation width, produced significant reporter ion ratio distortions compared to theoretical ratio values. The implementation of the SPS MS3 method greatly reduced the ratio distortion effect and gave a minimal difference from the expected values. The SPS Multi-notch MS^3 functionality can be implemented only on Tribrid systems and is advantageous over the previous generation top-tier hybrid instruments which can only perform single notch MS^3 methods without the multiple precursor isolation (SPS). This workflow, unique to the Orbitrap Tribrid systems, cannot be achieved with TOF-based analyzers.

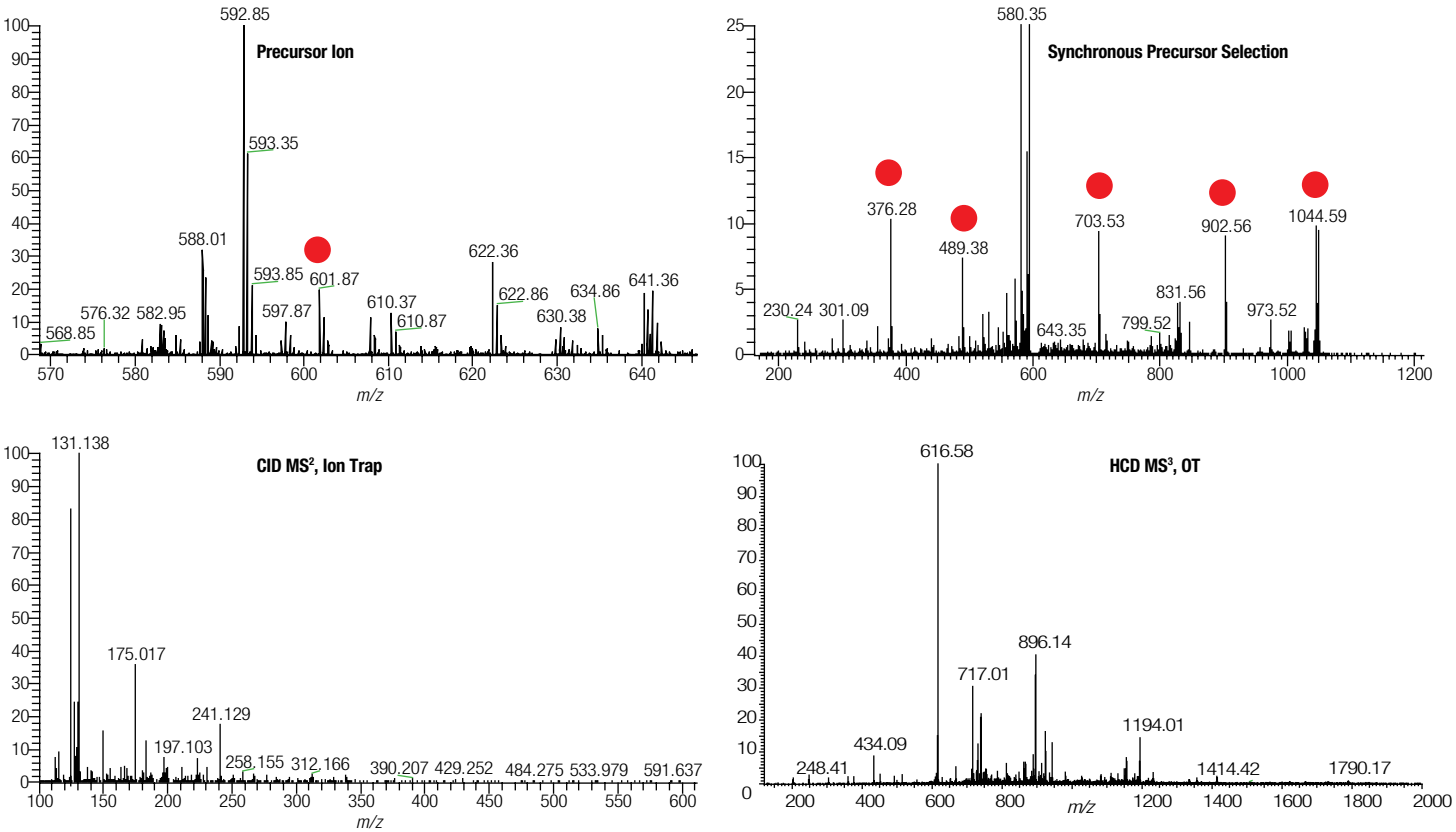


Figure 5. SPS is capable of selecting multiple MS^2 fragments, resulting in increased number of reporter ions in the MS^3 spectrum.

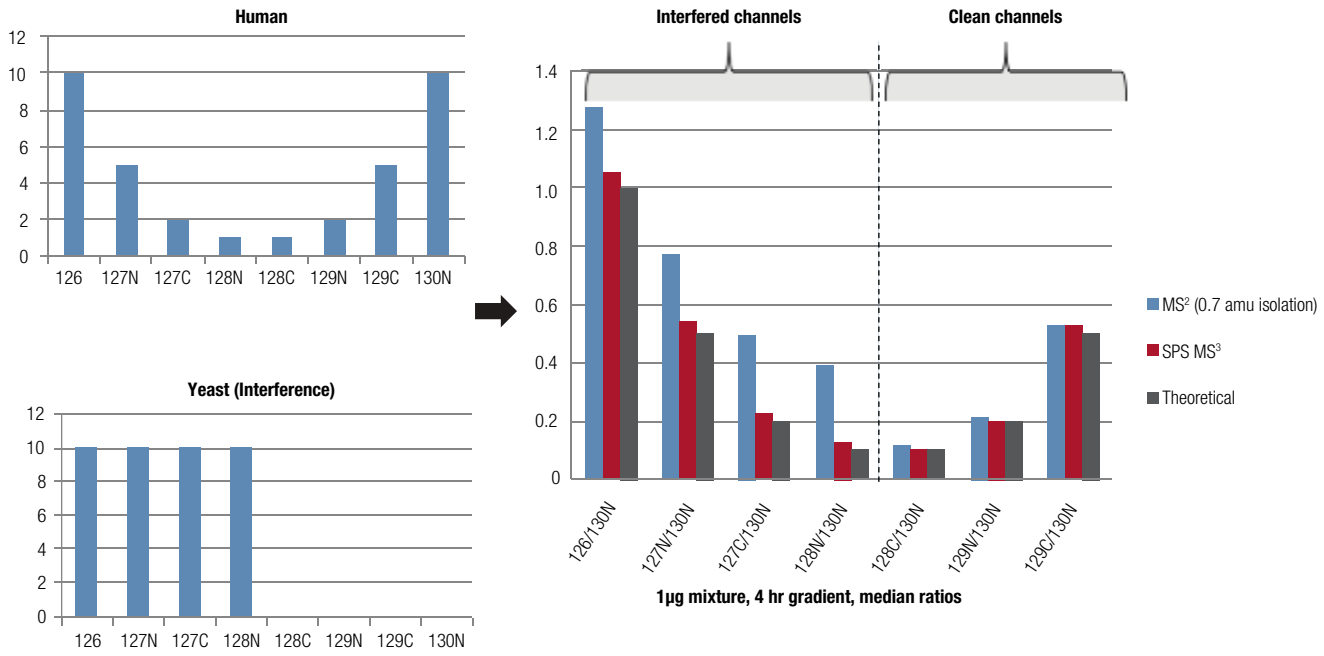


Figure 6. Benefits of the SPS MS³ method on the Orbitrap Fusion Lumos MS are demonstrated to provide accuracy and precision to the TMT quantification experiment and to the resultant observation of true reporter ion intensities. Since the yeast samples only had 4 channels labeled, there is no data for the remaining 4 columns.

Reason 2: Faster scanning speeds give more data points for more accurate relative quantitation

The improvements in speed for Tribrid instrumentation give more data points across the liquid chromatographic (LC) peak. From figures 7 and 8, the Orbitrap Fusion Tribrid MS produces more data scans compared to the Thermo Scientific™ Orbitrap Elite™ Hybrid mass spectrometer. This provides better MS-based quantitation and potentially increases the number of sequencing attempts and identifications. The ultra-high field Orbitrap analyzer is capable of fast acquisition rates of up to 20Hz, thereby fueling the possibilities for various quantitative experiments and greater instrument throughput. The number of protein groups in 1ug of HeLa cell lysate was also determined to be more in the Tribrid MS system. In half the analysis time, the Tribrid-based MS identified more protein groups over the Orbitrap Elite hybrid MS (Figure 9). This brings greater success when it comes to carrying out identification and characterization studies, providing depth in analysis and understanding of the biological significance of the results.

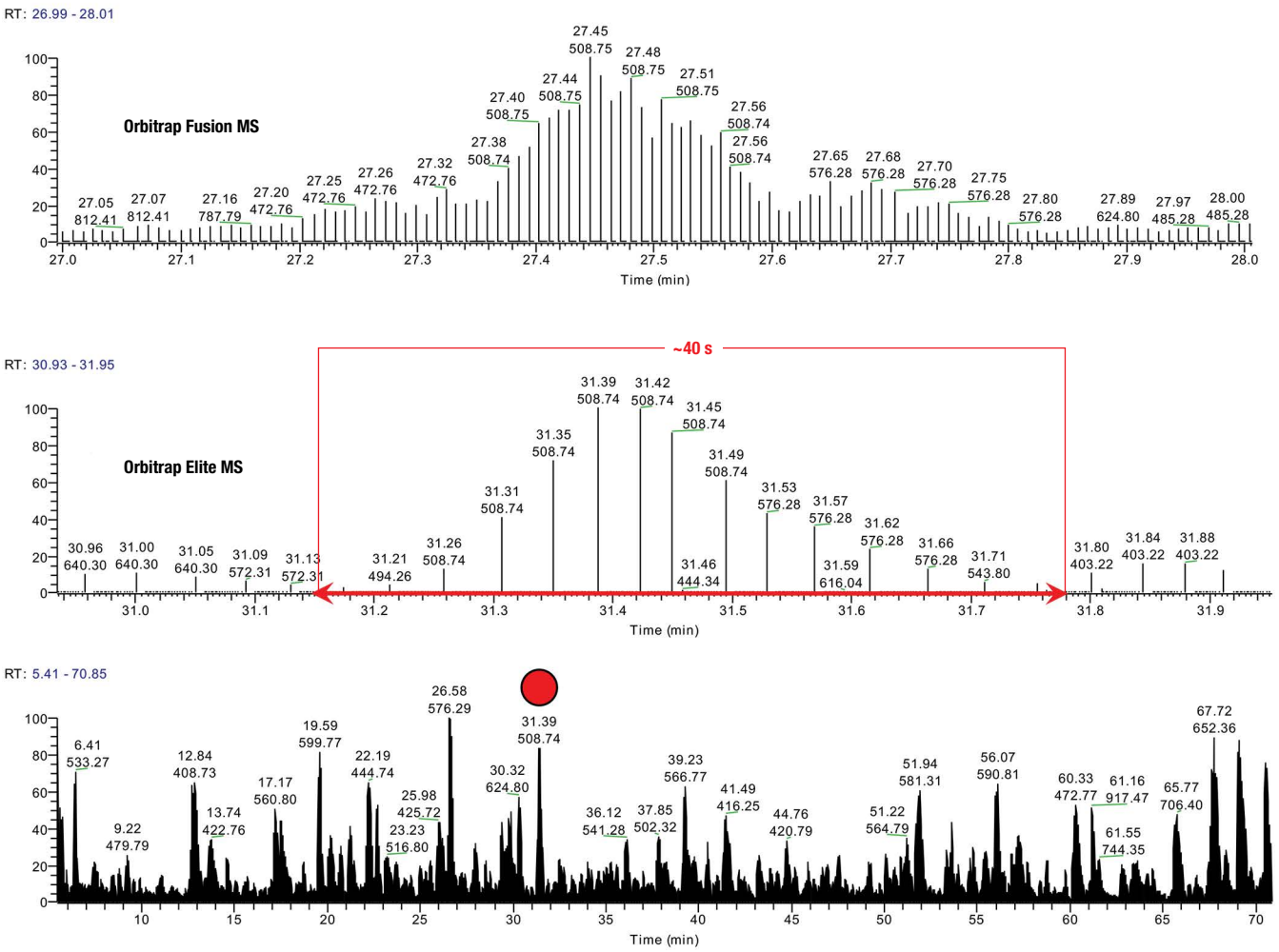


Figure 7. Many more data points are observable across the chromatographic peak for Orbitrap Tribrid MS systems compared to the Orbitrap Hybrid MS systems (1 µg HeLa, 140 min run).

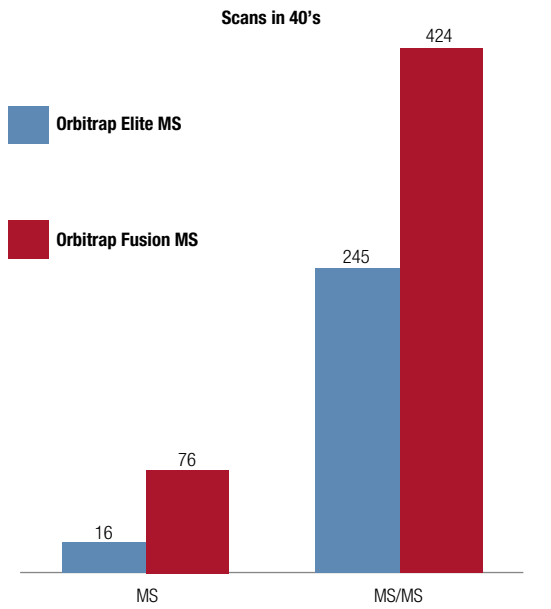


Figure 8. Number of MS and MS/MS scans across the Hybrid and Tribrid platform.

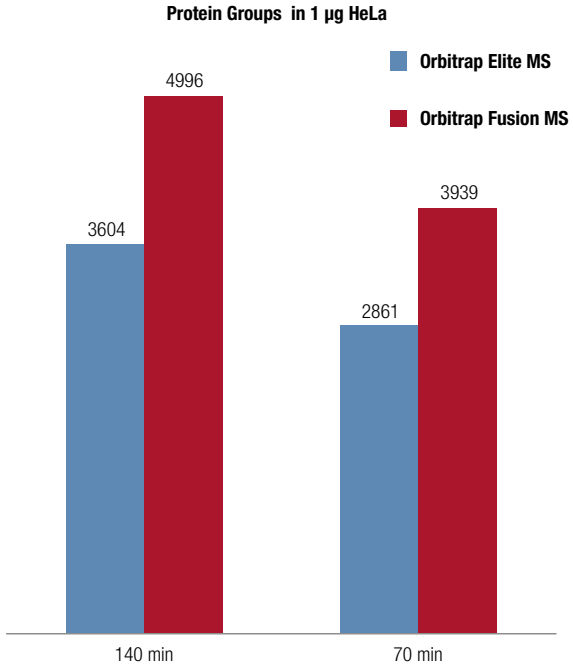


Figure 9. Number of protein groups identified from the Hybrid and Tribrid MS systems at 70 and 140 min gradients.

Reason 3: Most sensitive and fastest performing Orbitrap mass spectrometer guarantees increased productivity and reliable experimental results.

Detection of low abundance proteins is the key to understanding biological systems. Most of the peptides and proteins at low concentration have important biological functions such as protein biomarkers for disease markers, proteins involved in cellular signaling and cancer processes. Therefore it is vital to attain a lower detection limit to identify these significant proteins. Scientific research needs and technological demands have driven the development of more sensitive and faster scanning mass spectrometers to push the limits of performance. The Orbitrap Tribrid mass spectrometers can achieve better low-level detection, particularly for low abundance proteins compared to the Orbitrap Elite and Q Exactive hybrid mass spectrometers (Figure 10, 12). This difference in detection limits is attributed to the revolutionary hardware enhancements that are found only in the Tribrid hardware architecture: increased sensitivity due to brighter ion source design; improved ion optics and segmented quadrupole for better ions transmission; fast acquisition rates and high resolution of the ultra-high field Orbitrap analyzer which gives more detection. The fold change in the number of peptides identified of the Orbitrap Fusion MS versus other Orbitrap hybrid platforms was tremendous and is of great scientific significance when it comes to the identification of important protein biomarkers and transcription factors (Figure 11).

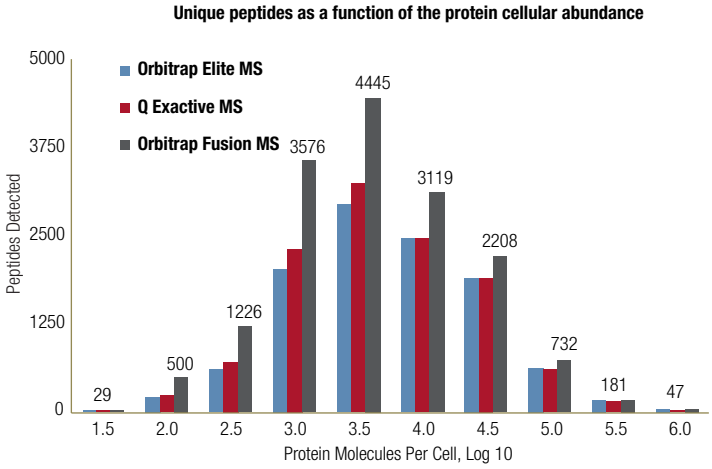


Figure 10. Unique peptides identified across three different Orbitrap-based MS systems.

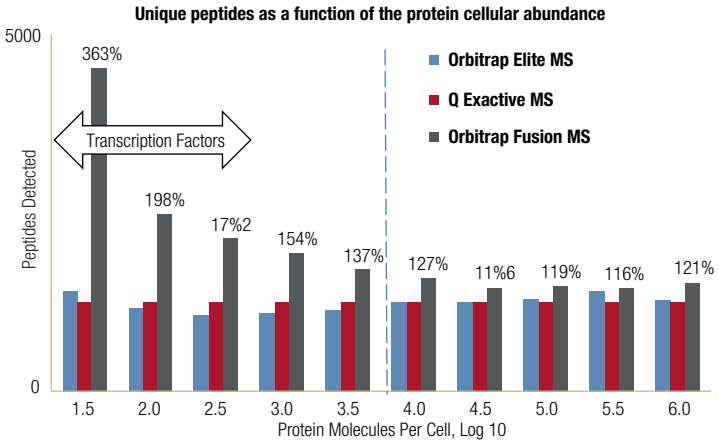


Figure 11. Fold improvement determined for all three Orbitrap-based MS systems.

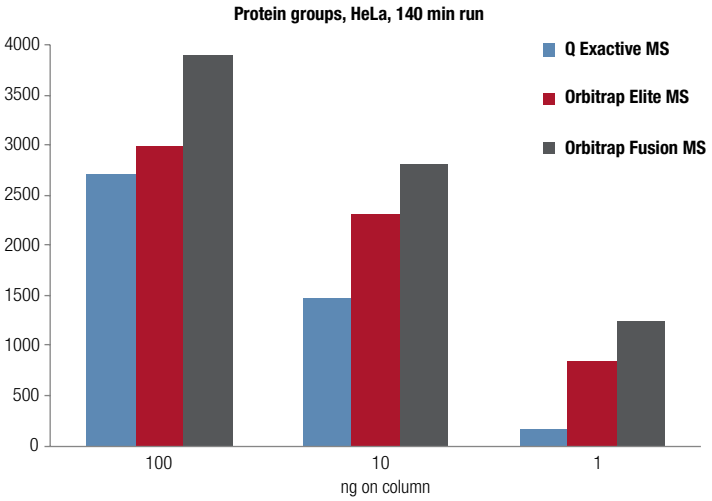


Figure 12. Comparison of number of protein groups identified in HeLa digest across different MS platforms.

A complete yeast proteome analysis is accomplished in half the analysis time for the Orbitrap Fusion Tribrid MS compared to the Q Exactive hybrid mass spectrometer (Figure 13). A comparable number of unique peptides and protein groups identified on the Orbitrap Fusion MS in a 2 hour gradient means faster analysis time, improved experimental efficiency and greater throughput. To further demonstrate the benefits of a Tribrid instrument on whole proteome analysis, high pH fractions of the K562 cell line were analyzed on the Orbitrap Fusion MS and Orbitrap Fusion Lumos MS (Figure 14). Not only did the Orbitrap Fusion Lumos MS identify 20% more protein groups per run, it showed a 2× improvement in experimental throughput. Fewer fractions (2× less) were needed on the Orbitrap Fusion Lumos MS to get the same level of coverage as the Orbitrap Fusion instrument, potentially reducing precious analysis time and providing higher throughput.

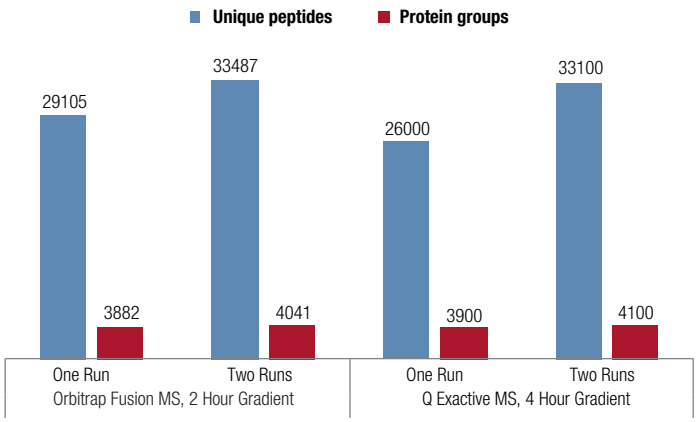


Figure 13. Performance of Orbitrap Fusion Tribrid MS compared to the Q Exactive MS in half the analysis time.

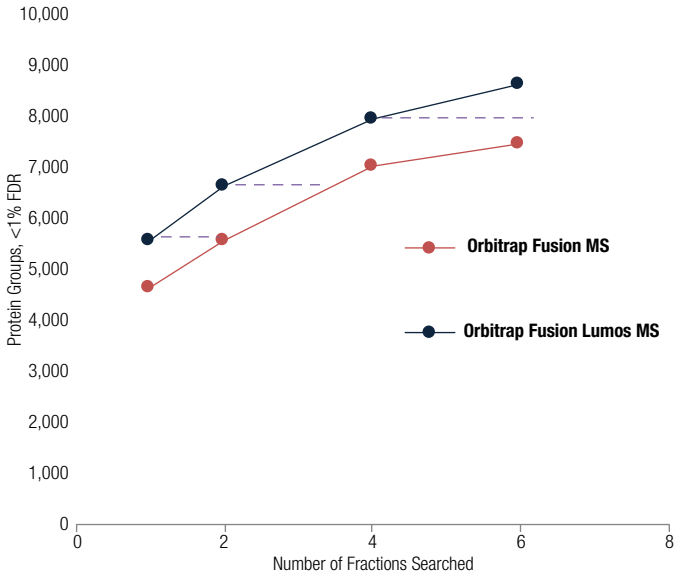


Figure 14. Difference in protein groups identified for Orbitrap Fusion Lumos vs. Orbitrap Fusion.

The Tribrid MS systems come equipped with an ultra-high-field Orbitrap analyzer while the Hybrid platforms use the standard high-field Orbitrap analyzer. This upgraded Orbitrap detector on Fusion-based instruments has faster scanning speeds (20 Hz vs. 4 Hz) and higher resolving power (500,000 vs. 240,000 at *m/z* 200). With these enhanced features based on the innovative Tribrid architecture, more MS^2 scans are obtained on the Tribrid than Hybrids due to faster scan performance and the ability to basically detect more spectral features, therefore giving rise to better identification (Figure 15).

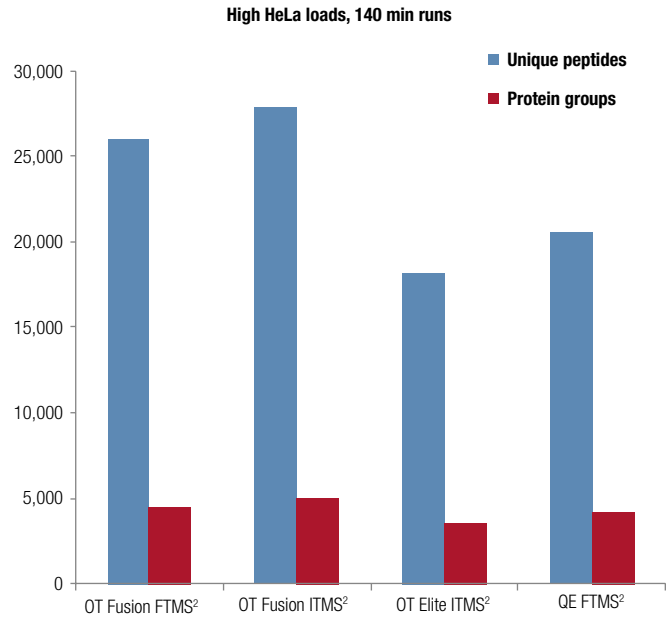


Figure 15. Enhanced hardware improvements gives better analytical performance on the Tribrids vs. Hybrids.

Reason 4: The Orbitrap Tribrid mass spectrometers have multiple fragmentation techniques available (CID, HCD, ETD, EThCD) that provides versatility to explore more experimental possibilities.

As the Orbitrap Fusion Tribrid MS and Orbitrap Fusion Lumos Tribrid MS are equipped with three mass analyzers, these platforms are capable of performing complex parallelization experiments by concurrent isolation of ions in one analyzer and detection in the remaining two analyzers.[5] Another dimension of experimental flexibility is added through multiple fragmentation techniques that are available exclusively on the Tribrid mass spectrometers. These include collision induced dissociation (CID), higher-energy collisional dissociation (HCD) and optional electron transfer dissociation (ETD, ETD HD, EThcD and EThcD HD). Each of these fragmentation techniques can be performed at any stage of MS^n, with detection of the fragment ions in either the dual-pressure linear ion trap or ultra-high-field Orbitrap mass analyzer. These multiple fragmentation capabilities on the Orbitrap Tribrid mass spectrometers unlock new experimental approaches to determine and quantify PTMs, including phosphorylation, acetylation and glycosylation. This capability is uniquely exploited in the Tribrid architecture through product ion dependent scanning functions.

ETD fragmentation is one such example that is especially useful for glycan structure characterization in glycan analysis or for glycoproteomics.[6] The ETD ion source used in Orbitrap Fusion MS is based on Townsend discharge ion source which generates a highly stable reagent ion flux with minimal user input for optimization and tuning as was required on previous ETD sources equipped on the hybrid platforms. Additionally, the Orbitrap Tribrid instruments have been implemented with intelligent, automated precursor ion sorting routines, reagent filtering using the quadrupole mass filter, and charge-state-specific calibration of ETD reaction times that maximize the quality of ETD spectra and increase the number of glycopeptides identified compared to previous generation mass spectrometers. A comparison of Orbitrap Elite MS to Orbitrap Fusion MS for the identification of human serum glycopeptides is shown here (Figure 16). The Orbitrap Elite MS selects precursors based on intensity while Orbitrap Fusion MS can acquire data with intelligent precursor selection giving priority to highest charge precursors which are optimal for ETD fragmentation.

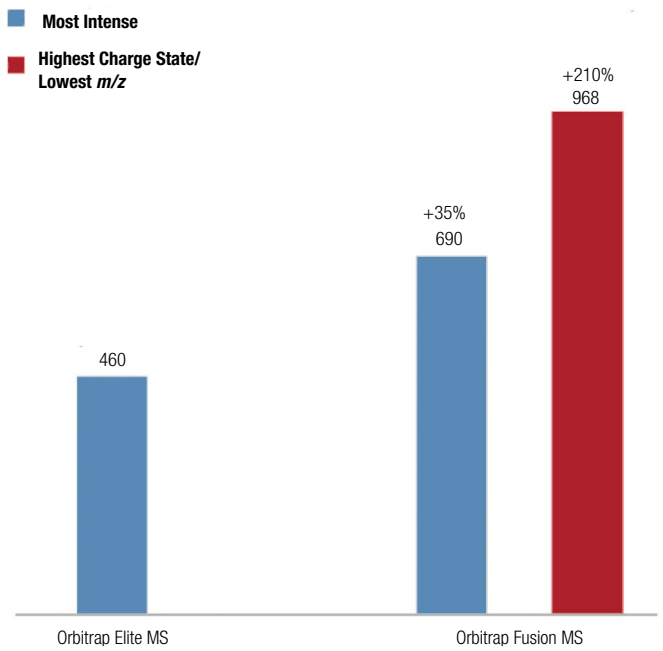


Figure 16. ETD performance on Tribrid mass spectromters outperform Hybrid mass spectrometers due to utilization of intelligent precursor selection feature implemented on Orbitrap Fusion MS and Orbitrap Fusion Lumos MS.

On the Orbitrap Fusion Tribrid MS, an intelligent acquisition strategy termed HCD product-dependent ETD workflow (HCD-pd-ETD) that enables on-the-fly identification of glycopeptides was implemented which improves overall productivity of glycopeptide analyses. In this approach, the Orbitrap Fusion mass spectrometer acquires HRAM HCD spectra in a data-dependent fashion. The instrument identifies glycan oxonium ions on the fly in the HCD spectra and triggers ETD spectra on the glycopeptide precursors only (Figure 17). This results in streamlined data analysis and improvements in dynamic range and duty cycle. The HCD-pd-ETD method is provided within the instrument control software for Orbitrap Tribrid based mass spectrometer. In addition to HCD-pd-ETD, the Tribrid instruments can trigger any fragmentation based on oxonium ion presence including CID and HCD (HCD-pd-CID, HCD-pd-HCD). Triggering CID fragmentation based on the detection of oxonium ions is useful for elucidating glycan composition information as CID tends to produce more detailed glycan backbone fragmentation (Figure 17). This approach is useful as glycans are heterogeneous PTMs; multiple glycans can be present at a single amino acid site and requires complete characterization of all detected compositions.

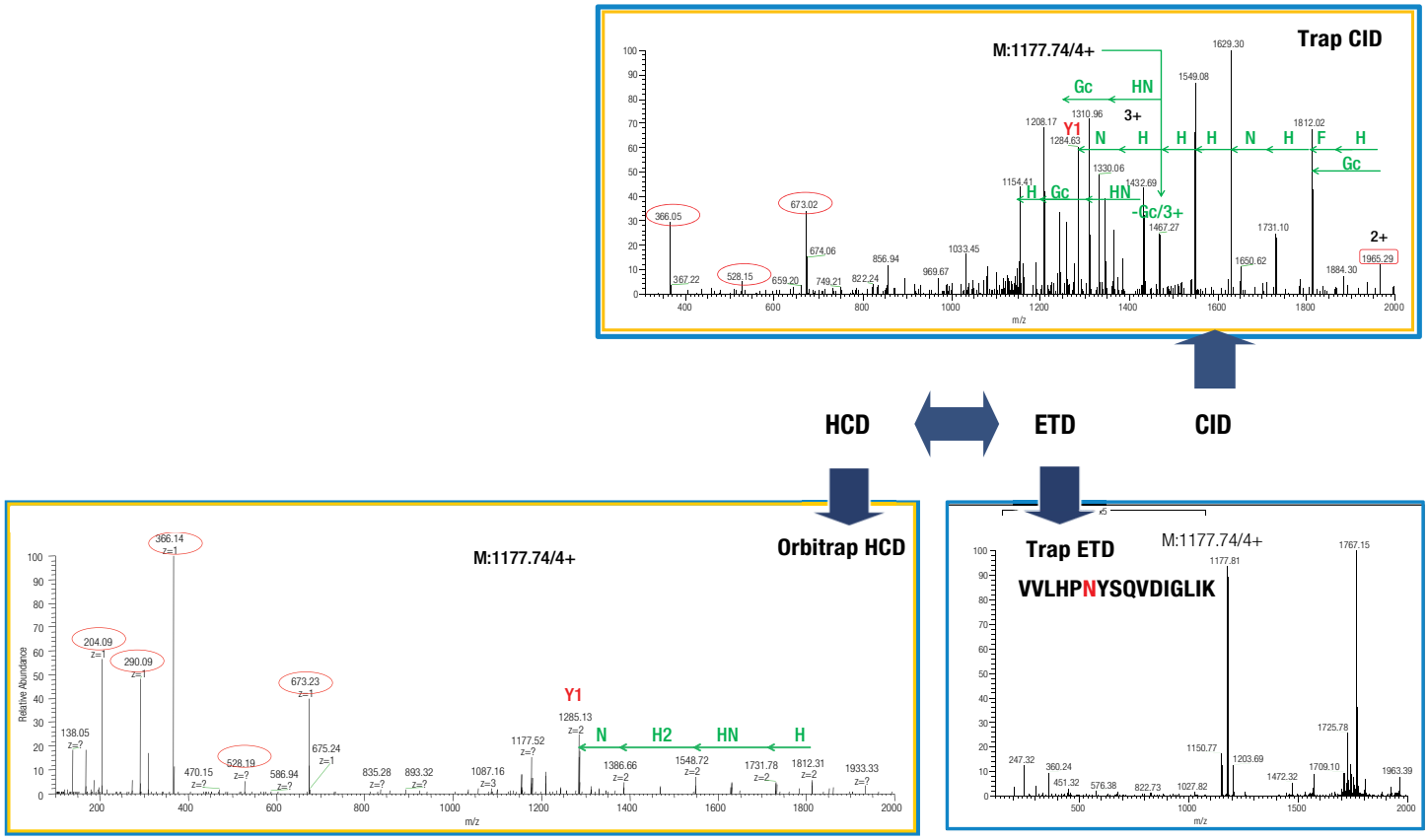


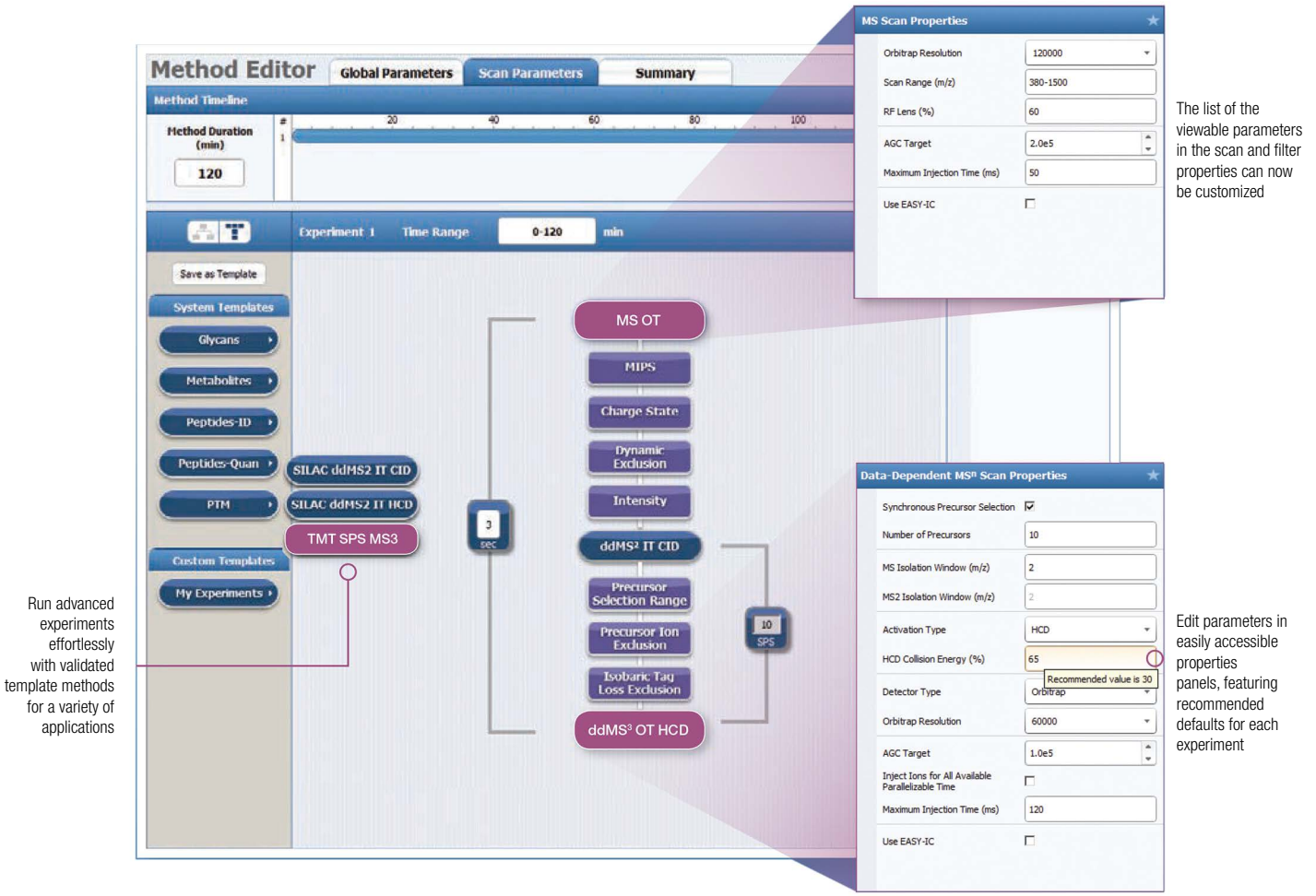
Figure 17. Representation of HCD-pd-ETD and HCD-pd-CID acquisition methods. The HCD spectrum shows diagnostic glycan oxonium ions in the low *m/z* region which are used to trigger ETD and/or CID spectrum. The ETD spectrum gives important information about the peptide and glycosylation site. The CID spectrum provides glycan composition information.

Reason 5: Availability of universal methods – Intelligence built into a new software interface gives non-MS experts access to highly complex technology.

The technological developments in mass spectrometers have grown more powerful and sophisticated, but at the same time more difficult to operate. The Orbitrap Fusion Tribrid mass spectrometer delivers higher-quality information from more sample types, at a rate faster than any mass spectrometer available today. The intelligence built into the Orbitrap Fusion Tribrid instruments and software makes it possible to achieve exemplary results with far less effort than required by previous generations of mass spectrometers. This built-in intelligence provides researchers with greater experimental flexibility, allowing them to focus more on their science instead of intensive method development and instrument operation.

Built-in intelligence features include:

- Dynamic Scan Management schedules scan events to maximize MS efficiency, as well as intelligently prioritizing precursors for data dependent analysis with their optimum fragmentation mode and mass analyzer.
- A library of method templates with application specific defaults is available for common experiments allowing you to run guided methods with less effort. For unique experiments, customized method development is available for maximum flexibility.
- Automated Synchronous Precursor Selection (SPS) for MS^3 significantly increases the number of peptides and proteins identified and quantified by TMT isobaric mass tagging workflows.
- Top-speed (Top S) mode efficiently schedules MS and data-dependent MS^n scans based on user-definable parameters and maximizes the number of high-quality MS^n spectra acquired.
- Simultaneous identification, quantitation, and confirmation are achieved by a combination of high-resolution, accurate-mass, low-detection-limit SIM quantification with the Orbitrap mass analyzer and sensitive full-scan MS/MS confirmation with the ion trap.



Run advanced experiments effortlessly with validated template methods for a variety of applications

The list of the viewable parameters in the scan and filter properties can now be customized

Edit parameters in easily accessible properties panels, featuring recommended defaults for each experiment

Figure 18. Instrument method set-up interface on Orbitrap Fusion based MS instruments, displaying a simple and easy-to-use guided method editor.

Why choose Orbitrap Mass Spectrometry?

Research trends and analytical needs have driven mass spectrometry innovation especially in the past decade. Mass spectrometers of today must be equipped with superior performance features such as high resolution, mass accuracy, dynamic range and fast scanning capabilities in order to fulfil rigorous experimental demands and handle extremely complex samples. In today's research, these same instruments have to provide the flexibility to carry out a variety of analytical techniques including multiplexing, multi-stage fragmentation and multiple dissociation techniques, in addition to being highly robust and giving consistent performance for high throughput analysis. Since its introduction in 2005, the Orbitrap technology has revolutionized mass spectrometry based research to meet these various challenges across multiple application fields of interest. The exceptional value of Orbitrap-based MS systems in delivering uncompromised analytical performance and achieving greater experimental possibilities have been well recognized by the scientific community. Adoption of Orbitrap technology over the years has grown exponentially with the proven increase in numbers of Nature and Science family publications (Figure 19).

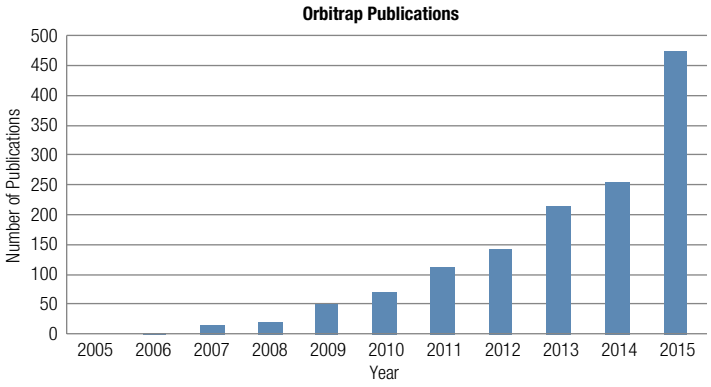


Figure 19. Rising trend in number of Orbitrap MS based research publications in *Nature* and *Science* journals since introduction in 2005.

Which Orbitrap system is right for my research?

Table 3. Orbitrap selection guide.

Instrument Attributes	Q Exactive Focus MS	Q Exactive MS	Q Exactive Plus MS	Q Exactive HF MS	Orbitrap Elite MS	Orbitrap Fusion MS	Orbitrap Fusion Lumos MS
Analyzer	Orbitrap	Orbitrap	Orbitrap	Ultra High Field Orbitrap	Hybrid: Linear ion trap, Orbitrap	Tribrid: Quadrupole with dual pressure linear ion trap, Orbitrap D20	Tribrid: Quadrupole with dual pressure linear ion trap, Orbitrap D20
Mass Range	*m/z* 50–2000	*m/z* 50–6000	*m/z* 50–6000	*m/z* 50–6000	*m/z* 50–2000; *m/z* 200–4000	*m/z* 50–6000	*m/z* 50–6000
Maximum Resolution @ *m/z* 200	70,000	140,000	140,000	240,000	240,000	500,000	500,000
Scan Speed	12 Hz	12 Hz	12 Hz	18 Hz	4 Hz	20 Hz	15 Hz
Top N/MS^n	Top 2 $ddMS^2$	Top 2 $ddMS^2$	Top 2 $ddMS^2$	Top 2 $ddMS^2$	MS^n, n = 1 to 10	MS^n, n = 1 to 10	MS^n, n = 1 to 10
Mass Accuracy - Internal Calibration	< 1ppm	< 1ppm	< 1ppm	< 1ppm	< 1ppm	< 1ppm	< 1ppm
Polarity switching	<1 sec	<1 sec	<1 sec	<1 sec	No	<1 sec	<1 sec
Multiplex	No	Yes, up to 10 precursors	Yes, up to 10 precursors	Yes, up to 10 precursors	No	Yes, up to 10 precursors	Yes, up to 10 precursors
Intact Protein Mode	No	No	Yes	Yes	Yes	Yes	Yes
Enhanced Resolution	No	No	280,000 (Option)	N/A	N/A	N/A	N/A
Collision Energy	CE only	Normalized CE	Normalized CE	Normalized CE			
Dissociation	HCD	HCD	HCD	HCD	CID, ECD	CID, HCD, ETD, EThCD	CID, HCD, ETD HD, EThCD HD
ETD Option	No	No	No	No	Yes, efficiency > 15%	Yes, efficiency > 15%	Yes, efficiency > 15%

Table 4. Which Orbitrap system best suits my experimental requirements?

Performance Features	Q Exactive MS	Q Exactive Plus MS	Q Exactive HF MS	Orbitrap Elite MS	Orbitrap Fusion MS	Orbitrap Fusion Lumos MS
Resolution	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Sensitivity	✓✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Speed	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Dynamic Range	✓✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Mass Accuracy	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Multiplexing	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Fragmentation	✓✓	✓✓	✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
MS^n Capability	–	–	–	✓✓✓	✓✓✓✓	✓✓✓✓✓
ETD	–	–	–	–	✓✓✓✓✓	✓✓✓✓✓
MultiNotch	–	–	–	–	✓✓✓✓✓	✓✓✓✓✓

Table 5. Which Orbitrap system best suits my area of research?

Application	Q Exactive MS	Q Exactive Plus MS	Q Exactive HF MS	Orbitrap Elite MS	Orbitrap Fusion MS	Orbitrap Fusion Lumos MS
Peptide IDs	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
TMT Quantitation	✓✓✓	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
SILAC	✓✓✓	✓✓✓	✓✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Label Free Quantitation	✓✓✓	✓✓✓	✓✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Top Down	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
Intact Analysis	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
PTM Phosphorylation	✓✓✓	✓✓✓	✓✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓
PTM Glycosylation	✓✓	✓✓	✓✓	✓✓✓✓	✓✓✓✓✓	✓✓✓✓✓

References

1. Lee, M.V., *et al, Molecular Systems Biology,* **2011,** 1–12

2. McAlister, G.; Huttlin, E.L.; Haas, W.; Ting, L.; Jedrychowski, M.; Rogers, J.C.; Kuhn, K.; Pike, I.; Grothe, R.A.; Blethrow, J.D.; Gygi, S.P. Increasing the multiplexing capacity of TMT using reporter ion isotopologues with isobaric masses. *Anal. Chem.* **2012,** *84(17),* 7469–7478.

3. Ting, L.; Rad, R.; Gygi, S.P.; Haas, W. MS^3 eliminates ratio distortion in isobaric multiplexed quantitative proteomics *Nature Methods* **2011**, *8,* 937–940.

4. McAlister, G.; Nusinow, D.; Jedrychowski, M.; Wuhr, M.; Huttlin, E.L.; Erickson, B.K.; Rad, R.; Haas, W.; Gygi, S.P. MultiNotch MS^3 enables accurate, sensitive, and multiplexed detection of differential expression across cancer cell line proteomes. *Anal. Chem.* **2014,** *86,* 7150–7158.

5. Eliuk, S.; Makarov, A. Evolution of Orbitrap Mass Spectrometry Instrumentation. *Annu. Rev. Anal. Chem.* **2015, 8,** 61–80.

6. Orbitrap Fusion MS for Glycan and Glycopeptide Analysis. Thermo Scientific White Paper.

Additional References

Orbitrap Fusion Lumos Literature List

Unabridged Analysis of Human Histone H^3 by Differential Top-Down Mass Spectrometry Reveals Hypermethylated Proteoforms from MMSET/NSD2 Overexpression. Yupeng Zheng, Luca Fornelli, Philip D. Compton, Seema Sharma, Jesse Canterbury, Christopher Mullen, Vlad Zabrouskov, Ryan T. Fellers, Paul M. Thomas, Jonathan D. Licht, Michael W. Senko and Neil L. Kelleher. *Mol Cell Proteomics* **2015** *Aug 13.* pii: mcp.M115.053819.

Enhanced Dissociation of Intact Proteins with High Capacity Electron Transfer Dissociation. Nicholas M. Riley, Christopher Mullen, Chad R. Weisbrod, Seema Sharma, Michael W. Senko, Vlad Zabrouskov, Michael S. Westphall, John E. P. Syka Joshua J. Coon. *J Am Soc Mass Spectrom* **2015** *Nov 20.*

Orbitrap Fusion Literature List

Proteomics, peptide ID

The One Hour Yeast Proteome. Alexander S. Hebert, Alicia L. Richards, Derek J. Bailey, Arne Ulbrich, Emma E. Coughlin, Michael S. Westphall, and Joshua J. Coon. Molecular & Cellular Proteomics **2014** *13,* 339–347, .

Proteomics, neu code

Neutron-encoded Signatures Enable Product Ion Annotation From Tandem Mass Spectra. Alicia L. Richards, Catherine E. Vincent, Adrian Guthals, Christopher M. Rose, Michael S. Westphall, Nuno Bandeira and Joshua J. Coon. *Mol Cell Proteomics* **2013** *12,* 3812–3823.

Proteomics, peptide ID

Novel Parallelized Quadrupole/Linear Ion Trap/Orbitrap Tribrid Mass Spectrometer Improving Proteome Coverage and Peptide Identification Rates. Michael W. Senko, Philip M. Remes, Jesse D. Canterbury, Raman Mathur, Qingyu Song. Shannon M. Eliuk, Chris Mullen, Lee Earley, Mark Hardman, Justin D. Blethrow, Huy Bui, August Specht, Oliver Lange, Eduard Denisov, Alexander Makarov, Stevan Horning, and Vlad Zabrouskov. *Anal. Chem.,* **2013,** *85 (24),* 11710–11714

Glycoproteomics, glycopeptides

A novel LC-MS^2 product dependent parallel data acquisition function and data analysis workflow for sequencing and identification of intact glycopeptides. Sz-Wei Wu, Tsung-Hsien Pu, Rosa Viner, and Kay-Hooi Khoo. *Anal. Chem.*, **2014,** *86 (11),* 5478–5486.

Proteomics, phosphoproteomics, FERTILITY, SPS MS^3 TMT

Structurally Distinct Ca_2^+ Signaling Domains of Sperm Flagella Orchestrate Tyrosine Phosphorylation and Motility. Jean-Ju Chung, Sang-Hee Shim, Robert A. Everley, Steven P. Gygi, Xiaowei Zhuang, and David E. Clapham. *Cell,* **2014,** *157,* 808–822

Proteomics, viral infection, SPS MS^3 TMT

Quantitative Temporal Viromics: An Approach to Investigate Host-Pathogen Interaction. Michael P. Weekes, Peter Tomasec, Edward L. Huttlin, Ceri A. Fielding, David Nusinow, Richard J. Stanton, Eddie C.Y. Wang, Rebecca Aicheler, Isa Murrell, Gavin W.G. Wilkinson, Paul J. Lehner and Steven P. Gygi. *Cell,* **2014,** *157,* 1460–1472.

Glycoproteomics, secretion of protein products, O*-glycosylation*

O-Glycosylation regulates polarized secretion by modulating Tango1 stability. Liping Zhang, Zulfeqhar Ali Syed, Iris van Dijk Härd, Jae-Min Lim, Lance Wells, and Kelly G. Ten Hagen. *PNAS,* **2014,** *111 (20),* 7296–7301.

Glycoproteomics, LDL receptor, O*-glycosylation*

Low-density lipoprotein receptor class A repeats are *O*-glycosylated in linker regions. Nis Borbye Pedersen, Shengjun Wang, Yoshiki Narimatsu, Zhang Yang, Adnan Halim, Katrine Ter-Borch Gram Schjoldager, Thomas Daugbjerg Madsen, Nabil G. Seidah, Eric Paul Bennett, Steven B. Levery, Henrik Clausen. *J. Biol. Chem.,* **2014,** *289,* 17312–17324.

Glycoproteomics, LDL receptor, O*-glycosylation*

In vivo monoubiquitination of anaplerotic phosphoenolpyruvate carboxylase occurs at Lys624 in germinating sorghum seeds. Isabel Ruiz-Ballesta, Ana-Belén Feria, Hong Ni, Yi-Min She, William Charles Plaxton, Cristina Echevarríax. *Journal of Experimental Botany,* **2014,** *65, (2),* 443–451.

Glycomics, food glycomics)

OsMOGS is required for *N*-glycan formation and auxin-mediated root development in rice (*Oryza sativa* L.) . SuiKang Wang, YanXia Xu, ZhiLan Li, SaiNa Zhang, Jae-Min Lim, Kyun Oh Lee, ChuanYou Li, Qian Qian, De An Jiang and YanHua Qi. *Plant J.,* **2014,** *78,* 632–645.

Glycomics
A new high-throughput LC-MS method for the analysis of complex fructan mixtures. Joran Verspreet, Anders Holmgaard Hansen, Emmie Dornez, Christophe M. Courtin and Scott J. Harrison. *Anal Bioanal Chem,* **2014,** *406,* 4785–4788.

Proteomics, neurobiology, peptide ID
Immunoprecipitation and mass spectrometry identify non-cell autonomous Otx2 homeoprotein in the granular and supragranular layers of mouse visual cortex. Namsuk Kim, Dario Acampora, Florent Dingli, Damarys Loew, Antonio Simeone, Alain Prochiantz and Ariel A. Di Nardo. *F1000Research*, **2014,** *3:178.* Last updated 15 Aug **2014**.

Glycomics
B4GAT1 is the Priming Enzyme 1 for the LARGE-dependent Functional Glycosylation of beta-Dystroglycan. Jeremy L. Praissman, David H. Live, Shuo Wang, Annapoorani Ramiah, Zoeisha S. Chinoy, Geert-Jan Boons, Kelley W. Moremen and Lance Wells. *eLife,* **2014,** 3:e03943.

Proteomics, cross-linking, nuclear pore complex
Structural characterization by cross-linking reveals the detailed architecture of a coatomer-related heptameric module from the nuclear pore complex. Yi Shi, Javier Fernandez-Martinez, Elina Tjioe, Riccardo Pellarin, Seung Joong Kim, Rosemary Williams, Dina Schneidman-Duhovny, Andrej Sali, Michael P. Rout and Brian T. Chait. *Mol Cell Proteomics,* **2014,** *13 (11),* 2927–2943.

Proteomics, cross-linking, top down
Reliable Identification of Cross-Linked Products in Protein Interaction Studies by 13C-Labeled *p*-Benzoylphenylalanine. Jens Pettelkau, Christian H. Ihling, Petra Frohberg, Lars van Werven, Olaf Jahn and Andrea Sinz. *J Am Soc Mass Spectrom,* **2014,** *25,* 1628–1641.

Glycomics
Liquid chromatography/mass spectrometry analysis of branched fructans produced in vitro with 13C-labeled substrates. Joran Verspreet, Anders Holmgaard Hansen, Emmie Dornez, Jan A. Delcour, Scott J. Harrison and Christophe M. Courtin. *Rapid Commun. Mass Spectrom.,* **2014,** *28,* 1–10.

Proteomics, peptide ID
Integrated solid phase extraction – capillary liquid chromatography (speLC) interfaced to ESI-MS/MS for fast characterization and quantification of protein and proteomes. Lasse Gaarde Falkenby, Gerard Such-Sanmartín, Martin R. Larsen, Ole Vorm, Nicolai Bache, and Ole Nørregaard Jensen. *J. Proteome Res.,* **2014,** *13(12),* 6169–6175.

Proteomics, peptide ID
Over 10000 Peptide Identifications from the HeLa Proteome by Using Single-Shot Capillary Zone Electrophoresis Combined with Tandem Mass Spectrometry. Liangliang Sun, Alexander S. Hebert, Xiaojing Yan, Yimeng Zhao, Michael S. Westphall, Matthew J. P. Rush, Guijie Zhu, Matthew M. Champion, Joshua J. Coon, and Norman J. Dovichi. Angew. *Chem.,* **2014,** *126,* 1–4.

Proteomics, peptide ID, ubiquitination
Complete and ubiquitinated proteome of the Legionella-containing vacuole within human macrophages. William M. Bruckert and Yousef Abu Kwaik. *J. Proteome Res.,* **2015,** Jan 2;14(1), 236–48.

Proteomics, peptide ID, Cancer
Human Serum Proteins Recognized by CA215 and Cancerous Immunoglobulins and Implications in Cancer Immunology. Gregory Lee, Suefay Liu and Cheng-Yuan Huang. *Cancer and Clinical Oncology,* **2014,** Vol. 3, No. 2.

Proteomics, prion disease, SPSMS^3 TMT
CRISPR-Cas9-Based Knockout of the Prion Protein and Its Effect on the Proteome. Mohadeseh Mehrabian, Dylan Brethour, Sarah MacIsaac, Jin Kyu Kim, C. Geeth Gunawardana, Hansen Wang and Gerold Schmitt-Ulms. PLOS ONE | DOI:10.1371/journal.pone.0114594.

Proteomics, targeted quan, DIA, WiSIM
Quantitative Analysis of Targeted Proteins in Complex Sample Using Novel Data Independent Acquisition. ZHANG Wei, Reiko Kiyonami, JIANG Zheng, CHEN Wei. *Chinese Journal of Analytical Chemistry,* Volume 42, Issue 12, December **2014.**

Proteomics, peptide ID, structural biology
SIRT1 Deacetylates TopBP1 and Modulates Intra-S-Phase Checkpoint and DNA Replication Origin Firing. Rui-Hong Wang, Tyler J. Lahusen, Qiang Chen, Xiaoling Xu, Lisa M. Miller Jenkins, Elisabetta Leo, Haiqing Fu, Mirit Aladjem, Yves Pommier, Ettore Appella, Chu-Xia Deng. *Int J Biol Sci,* **2014,** *10(10),* 1193–1202.

Proteomics, peptide ID, Blau syndrome
Blau Syndrome–Associated Nod2 Mutation Alters Expression of Full-Length NOD2 and Limits Responses to Muramyl Dipeptide in Knock-in Mice. Jae Dugan, Eric Griffiths, Paige Snow, Holly Rosenzweig, Ellen Lee, Brieanna Brown, Daniel W. Carr, Carlos Rose, James Rosenbaum, Michael P. Davey. *J Immunol,* **2015,** *194,* 349–357.

Proteomics, tuberous sclerosis complex, TMT SPSMS³
Cortical Tubers: Windows into Dysregulation of Epilepsy Risk and Synaptic Signaling Genes by MicroRNAs. Alan A. Dombkowski, Carlos E. Batista, Daniela Cukovic,Nicholas J. Carruthers, Ramya Ranganathan, Upasana Shukla, Paul M. Stemmer, Harry T. Chugani and Diane C. Chugani. *Cerebral Cortex,* **2014,** 1–13.

Proteomics, phosphoroteomics, TMT SPSMS³
Evaluating multiplexed quantitative phosphopeptide analysis on a hybrid quadrupole mass filter/linear ion trap/Orbitrap mass spectrometer. Brian K Erickson, Mark P Jedrychowski, Graeme C. McAlister, Robert A. Everley, Ryan C Kunz, and Steven P. Gygi. *Anal. Chem.,* **2015,** *87 (2),* 1241–1249.

Glycoproteomics
Versatile characterization of glycosylation modification in CTLA4-Ig fusion proteins by liquid chromatography mass spectrometry. Lei Zhu, Qingcheng Guo, Huaizu Guo, Tao Liu, Yingxin Zheng, Peiming Gu, Xi Chen, Hao Wang, Sheng Hou and Yajun Guo. *mAbs,* **2014,** *6 (6),* 1474–1485.

Glycomics
LC-MS analysis reveals the presence of graminan- and neo-type fructans 1 in wheat grains. Joran Verspreet, Anders Holmgaard Hansen, Emmie Dornez, Jan A. Delcour, Wim Van den Ende, Scott J. Harrison and Christophe M. Courtin. *Journal of Cereal Science,* online, **2014.**

Proteomics, structural biology, TMT SPSMS³
Lysine Demethylase KDM4A Associates with Translation Machinery and Regulates Protein Synthesis. Capucine Van Rechem, Joshua C. Black, Myriam Boukhali, Martin J. Aryee, Susanne Gräslund, Wilhelm Haas, Cyril H. Benes and Johnathan R. Whetstine. *Cancer Discovery,* **2015.**

Proteomics, peptide IDs, histones
Drawbacks in the use of unconventional hydrophobic anhydrides for histone derivatization in bottom-up proteomics PTM analysis. Simone Sidoli, Zuo-Fei Yuan, Shu Lin, Kelly Karch, Xiaoshi Wang, Natarajan Bhanu, Anna M. Arnaudo, Laura-Mae Britton, Xing-Jun Cao, Michelle Gonzales-Cope, Yumiao Han, Shichong Liu, Rosalynn C. Molden, SamuelWein, Leila Afjehi-Sadat and Benjamin A. Garcia. *Proteomics,* **2015.**

Glycomics
Hyaluronan synthase assembles chitin oligomers with -GlcNAc(α1)UDP at the reducing end. Paul H. Weigel, Christopher M. West, Peng Zhao, Lance Wells, Bruce A. Baggenstoss and Jennifer L. Washburn. *Glycobiology,* **2015.**

Proteomics, DIA neucode
Multiplexed quantification for data-independent acquisition. Catherine E. Minogue, Alexander S. Hebert, Jarred W. Rensvold, Michael S. Westphall, David J. Pagliarini, and Joshua J. Coon. *Anal. Chem.,* **2015,** *87 (5),* 2570–2575.

Proteomics, cross-linking
Dissociation behavior of a bifunctional tempoactive ester reagent for peptide structure analysis by free radical initiated peptide sequencing (FRIPS) mass spectrometry. Christian Ihling, Francesco Falvo, Isabel Kratochvil, Andrea Sinz and Mathias Schäfer. *J. Mass Spectrom.,* **2015,** *50,* 396–406.

Proteomics, peptide ID, herpes virus
Regulation and Function of Phosphorylation on VP8, the Major Tegument Protein of 2 Bovine Herpesvirus-1. Kuan Zhang , Sharmin Afroz , Robert Brownlie, Marlene Snider , Sylvia van Drunen Littel-van den Hurk. *Journal of Virology,* **2015.**

Proteomics, cross-linking
Extending the Cross-Linking/Mass Spectrometry Strategy: Facile Incorporation of Photo-Activatable Amino Acids into the Model Protein Calmodulin in *Escherichia coli* Cells. Christine Piotrowski, Christian H. Ihling, and Andrea Sinz. *Methods,* **2015,** Nov 1;89, 121–7.

Proteomics, middle-down, PTM
Bottom-up and middle-down proteomics have comparable accuracies in defining histone PTM relative abundance and stoichiometry. Simone Sidoli, Shu Lin, Kelly Rose Karch, and Benjamin Aaron Garcia. *Anal. Chem.,* **2015,** Mar 17;87(6, 3129–33.

Proteomics, peptide ID, neurobiology
Phosphorylation of Synaptic GTPase-activating Protein (synGAP) by Ca_2^+/Calmodulin-dependent Protein Kinase II (CaMKII) and Cyclin-dependent Kinase 5 (CDK5) Alters the Ratio of Its GAP Activity toward Ras and Rap GTPases. Ward G. Walkup IV, Lorraine Washburn , Michael J. Sweredoski , Holly J. Carlisle, Robert L. Graham, Sonja Hess, and Mary B. Kennedy. *Journal of Biological Chemistry,* vol. 290, no. 8, 4908–4927.

Proteomics, peptide ID, marine
"You produce while I clean up", a strategy revealed by exoproteomics during Synechococcus-Roseobacter interactions. Joseph A. Christie-Oleza, David J. Scanlan, Jean Armengaud. *Proteomics,* **2015,** Volume 15, Issue 20 October 2015, 3454–3462.

Proteomics, TMT(not SPSMS^3) personalized medicine
Maximal Oxidative Capacity during Exercise Is Associated with Skeletal Muscle Fuel Selection and Dynamic Changes in Mitochondrial Protein Acetylation. Katherine A. Overmyer, Charles R. Evans, Nathan R. Qi, Catherine E. Minogue, Joshua J. Carson, Christopher J. Chermside-Scabbo, Lauren G. Koch, Steven L. Britton, David J. Pagliarini, Joshua J. Coon, Charles F. Burant. *Cell Metabolism,* **2015,** *21,* 468–478.

Proteomics, cancer, cross-linking
Structure of Full-Length p53 Tumor Suppressor Probed by Chemical Cross-Linking and Mass Spectrometry. Christian Arlt, Christian H. Ihling, and Andrea Sinz. *Proteomics,* **2015,** *15,* 2746–2755.

Proteomics, peptide ID, venom proteomics
Venomics, lethality and Neutralization of Naja kaouthia (monocled cobra) venoms from three different geographical regions of Southeast Asia. Kae Yi Tan , Choo Hock Tan, Shin Yee Fung, Nget Hong Tan. *Journal of Proteomics,* **2015.**

Proteomics, di-methyl labeling, human fungal pathogen
Analysis of the Candida albicans phosphoproteome. Willger SD , Liu Z , Olarte RA , Adamo ME , Stajich JE , Myers LC , Kettenbach AN , Hogan DA. *Eukaryot Cell,* **2015.**

Proteomics, peptide ID, translocon associations
Cotranslational Stabilization of Sec62/63 within the ER Sec61 Translocon Is Controlled by Distinct Substrate-Driven Translocation Events. Brian J. Conti, Prasanna K. Devaraneni, Zhongying Yang, Larry L. David and William R. Skach. *Molecular Cell,* **2015,** *58,* 1–15.

Proteomics, topdown
Benchmarking multiple fragmentation methods on an Orbitrap Fusion for top-down phospho-proteoform characterization. Andrea M. Brunner, Philip Lossl, Fan Liu, Romain Huguet, Christopher Mullen, Masam, Yamashita, Vlad Zabrouskov, Alexander Makarov, A. F. Maarten Altelaar, and Albert J.R. Heck. *Anal. Chem.,* **2015** Apr 21;87(8), 4152–8.

Proteomics, peptide ID, phosphorylation
Two-dimensional phos-tag zymograms for tracing phosphoproteins by activity in-gel staining. Claudia-Nicole Meisrimler, Alexandra Schwendke and Sabine Lüthje. *Front Plant Sci.,* **2015,** Apr 14, 6, 230.

Proteomics, peptide ID, immunoprecipitation evaluation
Enrichment of Low-Abundant Protein Targets by Immunoprecipitation Upstream of Mass Spectrometry. Barbara Kaboord , Suzanne Smith , Bhavin Patel , and Scott Meier. *Methods Mol Biol.,* **2015,** *1295,* 135–151.

Proteomics, TMT (not SPSMS^3), neural disease study-bimarker research
Deterministic HOX Patterning in Human Pluripotent Stem Cell-Derived Neuroectoderm. Ethan S. Lippmann, Clay E. Williams, David A. Ruhl, Maria C. Estevez-Silva, Edwin R. Chapman, Joshua J. Coon and Randolph S. Ashton. *Stem Cell Reports,* **2015,** *4,* 1–13.

Proteomics, TMT (not SPSMS^3)
SIRT3 Mediates Multi-Tissue Coupling for Metabolic Fuel Switching. Kristin E. Dittenhafer-Reed, Alicia L. Richards, Jing Fan, Michael J. Smallegan, Alireza Fotuhi Siahpirani, Zachary A. Kemmerer, Tomas A. Prolla, Sushmita Roy, Joshua J. Coon and John M. Denu. *Cell Metabolism*, **2015,** *21,* 637–646.

Proteomics, peptide ID
One-hour proteome analysis in yeast. Alicia L Richards, Alexander S Hebert, Arne Ulbrich, Derek J Bailey, Emma E Coughlin, Michael S Westphall and Joshua J Coon. *Nature Protocols,* **2015,** *10,* 701–714.

Proteomics, peptide ID, malaria disease study- bimarker research
The Plasmodium falciparum exportome contains non-canonical PEXEL/HT proteins. Jana Schulze, Marcel Kwiatkowski, Janus Borner, Hartmut Schlüter, Iris Bruchhaus, Thorsten Burmester, Tobias Spielmann, Christian Pick. *Mol Microbiol.* **2015,** Jul;97(2), 301–14.

Proteomics, peptide ID, plant proteomics
Identification of regulatory and cargo proteins of endosomal and secretory pathways in *Arabidopsis thaliana* by proteomic dissection. William Heard, Jan Sklenar, Daniel F. A. Tome, Silke Robatzek, and Alexandra M. E. Jones. *Mol Cell Proteomics,* **2015,** Jul;14(7), 1796–813.

Proteomics, peptide ID, plant proteomics
Deforestation fosters bacterial diversity and the cyanobacterial community responsible for carbon fixation processes under semiarid climate: a metaproteomics study. Felipe Bastida, Carlos García, Martin von Bergen, José L. Moreno, Hans H. Richnow, Nico Jehmlich. *Applied Soil Ecology,* **2015,** *93,* 65–67.

Proteomics, peptide ID
Enzymatic characterization of recombinant nitrate reductase expressed 5 and purified from *Neurospora crassa.* Phillip Ringel, Corinna Probst, Thorben Dammeyer, Sabine Buchmeier, Lothar Jänsch, Josef Wissing, Philip Tinnefeld, Ralf R. Mendel, Brigitte M. Jockusch, Tobias *Kruse. Fungal Genet Biol.,* **2015**, Jul;80, 10–8

Proteomics, TMT (no SPSMS^3), phosphoproteomics
Low pH Solid Phase Amino-Labelling of Complex Peptide Digests with TMTs Improves Peptide Identification Rates for Multiplexed Global Phosphopeptide Analysis. Gitte Böhm, Petra Prefot, Stephan Jung, Stefan Selzer, Vikram Mitra, David Britton, Karsten Kuhn, Ian Pike, and Andrew Hugin Thompson. *J. Proteome Res.,* **2015,** Jun 5;14(6, 2500–10.

Proteomics, peptide ID metabolimcs done Orbi XL
N-lactoyl-amino acids are ubiquitous metabolites that originate from CNDP2-mediated reverse proteolysis of lactate and amino acids. Robert S. Jansen , Ruben Addie , Remco Merk , Alexander Fish, Sunny Mahakena, Onno B. Bleijerveld, Maarten Altelaar, Lodewijk IJlste, Ronald J. Wanderse, P. Borst, and Koen van de Wetering. *Proc Natl Acad Sci U S A.,* **2015,** May 26;112(21), 6601–6.

Proteomics, top down proteomics, histone
Multi-faceted quantitative proteomics analysis of histone H2B isoforms and their modifications. Rosalynn C Molden, Natarajan V Bhanu, Gary LeRoy, Anna M Arnaudo and Benjamin A Garcia, Molden *et al. Epigenetics & Chromatin,* **2015,** 8:15.

Proteomics, peptide ID
SuperQuant: a Data Processing Approach to Increase Quantitative Proteome Coverage. Vladimir Gorshkov, Thiago Verano-Braga, and Frank Kjeldsen. *Anal. Chem.,* **2015,** Jun 16;87(12), 6319–27.

Proteomics, cross-linking
Subunit Interactions within the Carbon–Phosphorus Lyase Complex from *Escherichia coli.* Zhongjie Ren, Soumya Ranganathan, Nathanael F. Zinnel, William K. Russell, David H. Russell and Frank M. Raushel. *Biochemistry,* **2015,** Jun 2;54(21), 3400–11.

Proteomics, phosphorylation, cell signaling
Identification of peptidic substrates for the human kinase Myt1 using peptide microarrays. Alexander Rohe, Charlott Platzer, Antonia Masch, Sandra Greiner, Claudia Henze, Christian Ihling, Frank Erdmann, Mike Schutkowski, Wolfgang Sippl, Matthias Schmidt. *Bioorganic & Medicinal Chemistry,* **2015,** Aug 1;23(15), 4936–42.

Proteomics, peptide ID, cardiovascular disease
Redox Control of Protein Arginine Methyltransferase 1 (PRMT1) Activity. Yalemi Morales, Damon V. Nitzel, Owen M. Price, Shanying Gui, Jun Li, Jun Qu, Joan M. Hevel. *Journal of Biological Chemistry,* **2015,** *290,* 14915–14926.

Proteomics, PTM methylation, parasites
Arginine methylation of DRBD18 differentially impacts its opposing effects on the trypanosome transcriptome. Kaylen Lott, Shreya Mukhopadhyay, Jun Li, Jie Wang, Jin Yao, Yijun Sun, Jun Qu and Laurie K. Read. *Nucl. Acids Res.,* **2015,** Jun 23;43(11), 5501–23.

Proteomics, peptide ID, interactomic screening
Rapid, optimized interactomic screening. Zhanna Hakhverdyan, Michal Domanski, Loren E Hough, Asha A Oroskar, Anil R Oroskar, Sarah Keegan, David J Dilworth, Kelly R Molloy, Vadim Sherman, John D Aitchison, David Fenyö, Brian T Chait, Torben Heick Jensen, Michael P Rout and John LaCava. *Nature Methods,* **2015,** *12,* 553–560.

(Proteomics, peptide ID, microalgae
Identification of regulatory network hubs that control lipid metabolism in *Chlamydomonas reinhardtii*. Mahmoud Gargouri, Jeong-Jin Park, F. Omar Holguin, Min-Jeong Kim, Hongxia Wang, Rahul R. Deshpande, Yair Shachar-Hill, Leslie M. Hicks and David R. Gang. *Exp. Bot.,* **2015,** *66 (15),* 4551–4566.

Proteomics, histone, peptide ID
An Improvement on MS-based Epigenetic Analysis of Large Histone-derived Peptides by Using the IVU Interface. Tetsuya Fukuda, Hiroshi Hike, Fumihiko Usui, Yasuhiko Bando, Toshihide Nishimura, Tatsuhiko Kodama, and Takeshi Kawamura. *Anal Biochem.,* **2015,** Oct 1;486:14-6.

Proteomics, venomics, peptide ID
Venomics of the beaked sea snake, *Hydrophis schistosus*: a minimalist toxin arsenal and its cross-neutralization by heterologous antivenoms. Choo Hock Tan, Kae Yi Tan, Sin Ee Lim, Nget Hong Tan. *Journal of Proteomics,* **2015,** Aug 3;126, 121–30.

Proteomics, peptide ID, parkinson's
Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. Alban Ordureau, Jin-Mi Heo, David M. Duda, Joao A. Paulo, Jennifer L. Olszewski, David Yanishevski, Jesse Rinehart, Brenda A. Schulman and J. Wade Harper. *PNAS,* **2005,** *112,* 6637–6642.

Proteomics, top down, biotherapeutics primary sequence
Confirmation of a Protein Therapeutic using Top Down MS/MS and MS^3. Michaella J. Levy, Ashley C. Gucinski, and Michael T. Boyne. *Anal. Chem.,* **2015,** Jul 21;87(14), 6995–9.

Proteomics, phosphoproteomics, signalling
An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. Piero Giansanti, Thin Thin Aye, Henk van den Toorn, Mao Peng, Bas van Breukelen, Albert J.R. Heck. *Cell Reports,* **2015** June 23, *11,* 1–10.

Proteomics, TMT (no $SPSMS^3$), phosphoproteomics
Low-pH Solid-Phase Amino Labeling of Complex Peptide Digests with TMTs Improves Peptide Identification Rates for Multiplexed Global Phosphopeptide Analysis. Gitte Böhm, Petra Prefot, Stephan Jung, Stefan Selzer, Vikram Mitra, David Britton, Karsten Kuhn, Ian Pike and Andrew H. Thompson. *J. Proteome Res.,* **2015,** *14 (6),* 2500–2510.

Proteomics, TMT $SPSMS^3$, yeast micobiology
Comprehensive temporal protein dynamics during the diauxic shift in *Saccharomyces cerevisiae*. J. Patrick Murphy , Ekaterina Stepanova , Robert A. Everley, Joao A. Paulo and Steven P. Gygi. *Mol Cell Proteomics,* **2015,** Sep;14(9), 2454–65.

Proteomics, marine bacterium, peptide IDs
Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylotroph. Carolina Grob, Martin Taubert, Alexandra M. Howat , Oliver J. Burns , Joanna L. Dixon , Hans H. Richnow, Nico Jehmlich , Martin von Bergen, Yin Chen and J. Colin Murrell. *Environmental Microbiology,* **2015,** Oct;17(10), 4007–18.

Proteomics, O-GlcNAcylation, histone
Undetectable Histone O-GlcNAcylation in Mammalian Cells. Jessica Gagnon, Salima Daou, Natalia Zamorano, Nicholas V G Ianantuono, Ian HammondMartel, Nazar Mashtalir, Eric Bonneil, Hugo Wurtele, Pierre Thibault, and El Bachir Affar. *Epigenetics,* **2015,** 10(8), 677–91.

Proteomics, HDX, biotherapeutics
Fast Comparative Structural Characterization of Intact Therapeutic Antibodies Using Hydrogen–Deuterium Exchange and Electron Transfer Dissociation. Jingxi Pan, Suping Zhang, Albert Chou, Darryl B. Hardie and Christoph H. Borchers. *Anal. Chem.,* **2015,** *87 (12),* 5884–5890.

Proteomics, histone PTMs
Characterization of histone post-translational modifications during virus infection using mass spectrometry-based proteomics. Katarzyna Kulej, Daphne C. Avgousti, Matthew D. Weitzman and Benjamin A. Garcia. *Methods,* **2015,** Nov 15;90, 8–20.

Proteomics, middle-down histones
Middle-down electron capture dissociation and electron transfer dissociation for histone analysis. Annie Moradian, Catarina Franco, Michael J. Sweredoski and Sonja Hess. *Journal of Analytical Science and Technology,* **2015,** 6:21

Proteomics, peptide ID, cancer
Filamin A phosphorylation by Akt promotes cell migration in response to arsenic. Lingzhi Li, Yongju Lu, Paul M. Stemmer and Fei Chen. *Oncotarget,* **2015,** *6,* 12009–12019.

Proteomics, peptide ID, anaerobic biotransformation
Reductive dehalogenation of oligocyclic phenolic bromoaromatics by *Dehalococcoides mccarty*i strain CBDB1. Chao Yang, Anja Kublik, Cindy Weidauer, Bettina Seiwert, and Lorenz Adrian. *Environ. Sci. Technol.,* **2015,** Jul 21;49.

Proteomics, peptide IDs, plant proteomics
Two serine residues in *Pseudomonas syringae* effector HopZ1a are required for acetyltransferase activity and association with the host co-factor. Ka-Wai Ma, Shushu Jiang, Eva Hawara, DongHyuk Lee, Songqin Pan, Gitta Coaker, Jikui Song and Wenbo Ma. *New Phytologist,* **2015,** Dec;208(4), 1157–68.

Proteomics, SPSMS^3 TMT, gene expression
A comprehensive Xist interactome reveals cohesin repulsion and an RNA-directed chromosome conformation. Anand Minajigi, John E. Froberg, Chunyao Wei, Hongjae Sunwoo, Barry Kesner, David Colognori, Derek Lessing, Bernhard Payer, Myriam Boukhali, Wilhelm Haas Jeannie T. Lee. *Science,* **2015,** Jul 17;349(6245). pii: aab2276

Proteomics, peptide ID
A Calibration Routine for Efficient ETD in Large-Scale Proteomics. Christopher M. Rose, Matthew J. P. Rush, Nicholas M. Riley, Anna E. Merrill, Nicholas W. Kwiecien, Dustin D. Holden, Christopher Mullen, Michael S. Westphall and Joshua J. Coon. *J. Am. Soc. Mass Spectrom.,* **2015,** Nov;26(11), 1848–57.

Proteomics, HDX
Determination of Histidine pKa Values in the Propeptides of Furin and Proprotein Convertase 1/3 Using Histidine Hydrogen-Deuterium Exchange Mass Spectrometry. Johannes Elferich, Danielle M Williamson, Larry L. David, and Ujwal P Shinde. *Anal. Chem.,* **2015,** Aug 4;87(15), 7909–17.

Glycomics
Purification of wheat grain fructans from wheat bran. Joran Verspreet, Emmie Dornez, Jan A. Delcour, Scott J. Harrison, Christophe M. Courtin. *Journal of Cereal Science,* **2015,** September, *65,* 57–59.

Proteomics, TMT SPS MS^3, disease biomarker
Lenalidomide induces ubiquitination and degradation of CK1a in del(5q) MDS. Jan Kronke, Emma C. Fink, Paul W. Hollenbach, Kyle J. MacBeth, Slater N. Hurst, Namrata D. Udeshi, Philip P. Chamberlain, D. R. Mani, Hon Wah Man, Anita K. Gandhi, Tanya Svinkina, Rebekka K. Schneider, Marie McConkey, Marcus Jaras, Elizabeth Griffiths, Meir Wetzler, Lars Bullinger, Brian E. Cathers, Steven A. Carr, Rajesh Chopra & Benjamin L. Ebert. *Nature,* **2015,** Jul 9;523(7559), 183–8.

Proteomics, PRM
CRL2 aids elimination of truncated selenoproteins produced by failed UGA/Sec decoding. Hsiu-Chuan Lin, Szu-Chi Ho, Yi-Yun Chen, Kay-Hooi Khoo, Pang-Hung Hsu, Hsueh-Chi S. Yen. *Science,* **2015,** *349,* 91–95.

Proteomics, cross-linking, HDX
Differences in solution dynamics between lens β-crystallin homodimers and heterodimers probed by hydrogen-deuterium exchange and deamidation. Kirsten J. Lampi, Matthew R. Murray, Matthew P. Peterson, Bryce S. Eng, Eileen Yue, Alice R. Clark, Elisar Barbar, Larry L. David. *Biochim Biophys Acta,* **2016,** Jan;1860(1 Pt B), 304–14.

Proteomics, PRM, middle down, histones
High Resolution Parallel Reaction Monitoring with Electron Transfer Dissociation for Middle-Down Proteomics. Michael J. Sweredoski, Annie Moradian, Matthias Raedle, Catarina Franco and Sonja Hess. *Anal. Chem.,* **2015,** *87 (16),* 8360–8366.

Proteomics, peptideID, method development
A High-Efficiency Cellular Extraction System for Biological Proteomics. Avantika Dhabaria, Paolo Cifani, Casie Reed, Hanno Steen and Alex Kentsis. *J. Proteome Res.,* **2015,** 1*4 (8),* 3403–3408.

Proteomics, cross-linking
Acidosis-Induced Changes in Proteome Patterns of the Prostate Cancer-Derived Tumor Cell Line AT-1. Angelika Ihling, Christian H. Ihling, Andrea Sinz, and Michael Gekle. *J. Proteome Res.,* **2015,** Sep 4;14(9), 3996–4004.

Glycomics
Engineered CHO cells for production of diverse, homogeneous glycoproteins. Zhang Yang, Shengjun Wang, Adnan Halim, Morten Alder Schulz, Morten Frodin, Shamim H Rahman, Malene B Vester-Christensen, Carsten Behrens, Claus Kristensen, Sergey Y Vakhrushev, Eric Paul Bennett, Hans H Wandall & Henrik Clausen. *Nature Biotechnology,* **2015,** Aug;33(8), 842–4.

Proteomics, peptide ID, microbiology
Cyanate as an energy source for nitrifiers. Marton Palatinszky, Craig Herbold, Nico Jehmlich, Mario Pogoda, Ping Han, Martin von Bergen, Ilias Lagkouvardos, Søren M. Karst, Alexander Galushko, Hanna Koch, David Berry, Holger Daims and Michael Wagner. *Nature,* **2015,** Aug 6;524(7563), 105–8.

Proteomics, TMT SPS MS^3, cancer
Transcriptional control of autophagy–lysosome function drives pancreatic cancer metabolism. Rushika M. Perera, Svetlana Stoykova, Brandon N. Nicolay, Kenneth N. Ross, Julien Fitamant, Myriam Boukhali, Justine Lengrand, Vikram Deshpande, Martin K. Selig, Cristina R. Ferrone, Jeff Settleman, Gregory Stephanopoulos, Nicholas J. Dyson, Roberto Zoncu, Sridhar Ramaswamy, Wilhelm Haas & Nabeel Bardeesy. *Nature,* **2015,** Aug 20;524(7565), 361–5.

Proteomics, TMT SPS MS^3, leukemia
Coordinate regulation of residual bone marrow function by paracrine trafficking of AML exosomes. J Huan, NI Hornick, NA Goloviznina, AN Kamimae- Lanning, LL David , PA Wilmarth , T Mori , JR Chevillet , A Narla , CT Roberts Jr, MM Loriaux, BH Chang and P Kurre. *Leukemia,* **2015,** Dec;29(12), 2285–95.

Proteomics, peptide ID, microbial communities
The ecological and physiological responses of the microbial community from a semiarid soil to hydrocarbon contamination and its bioremediation using compost amendment. F. Bastida, N. Jehmlich, K. Lima, B.E.L. Morris, H.H. Richnow, T. Hernandez, M. von Bergen, C. Garcıa. *Journal of Proteomics,* **2016,** Mar 1;135, 162–9.

Proteomics, peptide ID, microbiology
Selenocysteine-independent suppression of UGA codons in the archaeon *Methanococcus maripaludis.* Deniz Seyhan, Nico Jehmlich, Martin von Bergen, Julia Fersch, Michael Rother. *Biochim Biophys Acta.,* **2015,** Nov;1850(11), 2385–92.

Proteomics, peptide IDs, goat milk proteome
Zeus, Aesculapius, Amalthea and the proteome of goat milk. Vincenzo Cunsolo, Elisa Fasoli, Rosaria Saletti, Vera Muccilli, Serafina Gallina, Pier Giorgio Righetti, Salvatore Foti. *Journal of Proteomics,* **2015,** *128,* 69–82.

Proteomics, DIA, middle down, histones
High resolution data-independent acquisition with electron transfer dissociation mass spectrometry: Multiplexed analysis of post-translationally modified proteins. Michael J. Sweredoski, Tonya Pekar Second, Jenny Broeker, Annie Moradian, Sonja Hess. *International Journal of Mass Spectrometry,* Volume 390, 15 November **2015,** 155–162.

Proteomics, food proteomics, peptide IDs
Recognition pattern of kiwi seed storage proteins in kiwifruit allergic children. Caroline Nilsson, Peter Brostedt , Johanna Hidman , Jenny van Odijk , Magnus P Borres, Sigrid Sjölander , Hillevi Englund. *Pediatr Allergy Immunol.,* **2015,** Dec;26(8), 817–20.

Proteomics, TMT SPS MS^3, phosphoproteomics, pancreatic cancer
Global analysis of protein expression and phosphorylation levels in nicotine-treated pancreatic stellate cells. Joao A. Paulo, Aleksandr Gaun, and Steven P. Gygi. *J. Proteome Res.,* **2015,** Oct 2;14(10), 4246–56.

Proteomics, peptide IDs, cell signaling
Development of Selective Covalent JAK3 Inhibitors. Li Tan, Koshi Akahane, Randall McNally, Kathleen M.S.E Reyskens, Scott B Ficarro, Suhu Liu, Grit S. HerterSprie, Shohei Koyama, Michael J. Pattison, Katherine M. Labella, Liv Johannessen, Esra A Akbay, Kwok-Kin Wong, David A. Frank, Jarrod A. Marto, A Thomas Look, Simon Arthur, Michael J. Eck, and Nathanael S Gray. *J. Med. Chem.,* **2015,** Aug 27;58(16), 6589–606.

Proteomics, TMT SPSMS³, drug mechanism study
Phthalimide conjugation as a strategy for in vivo target protein degradation. Georg E. Winter, Dennis L. Buckley, Joshiawa Paulk, Justin M. Roberts, Amanda Souza, Sirano Dhe-Paganon, James E. Bradner. *Science,* **2015,** Jun 19;348(6241), 1376–81.

Proteomics, TMT SPSMS³, drug mechanism study
CC-122, a pleiotropic pathway modifier, mimics an interferon response and has antitumor activity in DLBCL. Patrick R. Hagner, Hon-Wah Man, Celia Fontanillo, Maria Wang, Suzana Couto, Mike Breider, Chad Bjorklund, Courtney G. Havens, Gang Lu, Emily Rychak, Heather Raymon, Rama Krishna Narla, Leo Barnes, Gody Khambatta, Hsiling Chiu, Jolanta Kosek, Jian Kang, Michael D. Amantangelo, Michelle Waldman, Antonia Lopez-Girona, Ti Cai, Michael Pourdehnad, Matthew Trotter, Thomas O. Daniel, Peter H. Schafer, Anke Klippel, Anjan Thakurta, Rajesh Chopra, and Anita K. Gandhi. *Blood,* **2015,** Aug 6;126(6):779-89. doi: 10.1182/blood-2015-02-628669. Epub 2015 May 22.

Proteomics, TMT SPSMS³, cell signaling
Separating myoblast differentiation from muscle cell fusion using IGF-I and the 5 p38 MAP kinase inhibitor SB202190. Samantha Gardner, Sean M. Gross, Larry L. David, John E. Klimek and Peter Rotwein. *Am J Physiol Cell Physiol.,* **2015,** Oct 1;309(7):C491-500.

Proteomics, TMT SPSMS³, neurodegenerative diseases
The human tau interactome: binding to the ribonucleoproteome, and impaired binding of the P301L mutant to chaperones and the proteasome. C. Geeth Gunawardana , Mohadeseh Mehrabian, Xinzhu Wang, Iris Mueller , Isabela B. Lubambo , James E. N. Jonkman , Hansen Wang , Gerold Schmitt-Ulms. *Molecular & Cellular Proteomics,* **2015,** Nov;14(11), 3000–14.

Glycoproteomics
Extended O-GlcNAc on HLA Class-I-Bound Peptides. Fabio Marino, Marshall Bern, Geert P. M. Mommen, Aneika C. Leney, Jacqueline A. M. van Gaans-van den Brink, Alexandre M. J. J. Bonvin, Christopher Becker, Cécile A. C. M. van Els, and Albert J. R. Heck. *J Am Chem Soc.,* **2015,** Sep 2;137(34), 10922–5.

Proteomics
Proteomics of the organohaliderespiring Epsilonproteobacterium *Sulfurospirillum multivorans* adapted to tetrachloroethene and other energy substrates. Tobias Goris, Christian L. Schiffmann, Jennifer Gadkari, Torsten Schubert, Jana Seifert, Nico Jehmlich, Martin von Bergen and Gabriele Diekert. *Sci Rep.,* **2015,** Sep 21;5:13794. doi: 10.1038/srep13794.

Glycoproteomics
Secreted and O-GlcNAcylated MIF binds to the human EGF receptor and inhibits its activation. Yanhua Zheng , Xinjian Li, Xu Qian1, Yugang Wang, Jong-Ho Lee, Yan Xia, David H. Hawke, Gang Zhang, Jianxin Lyu and Zhimin Lu. Nature *Cell Biology,* **2015,** *17,* 1348–1355.

Proteomics
Transcriptional control of autophagy–lysosome function drives pancreatic cancer metabolism. Rushika M. Perera, Svetlana Stoykova, Brandon N. Nicolay, Kenneth N. Ross, Julien Fitamant, Myriam Boukhali , Justine Lengrand, Vikram Deshpande, Martin K. Selig , Cristina R. Ferrone, Jeff Settleman, Gregory Stephanopoulos , Nicholas J. Dyson, Roberto Zoncu , Sridhar Ramaswamy, Wilhelm Haas & Nabeel Bardeesy. *Nature,* **2015,** *524,* 361–365.

Proteomics
A strategy for dissecting the architectures of native macromolecular assemblies. Yi Shi, Riccardo Pellarin, Peter C Fridy, Javier Fernandez-Martinez, Mary K Thompson, Yinyin Li, Qing Jun Wang, Andrej Sali, Michael P Rout & Brian T Chait. *Nature Methods*, **2015,** Dec;12(12), 1135–8.

Proteomics
Characterization of the cardiac succinylome and its role in ischemia–reperfusion injury. Jennifer A. Boylston, Junhui Sun, Yong Chen, Marjan Gucek, Michael N. Sack, Elizabeth Murphy. *Journal of Molecular and Cellular Cardiology,* **2015,** *88,* 73–81.

Proteomics
Cell Surface Proteomic Map of HIV Infection Reveals Antagonism of Amino Acid Metabolism by Vpu and Nef. Nicholas J. Matheson, Jonathan Sumner, Kim Wals, Radu Rapiteanu, Michael P. Weekes, Raphael Vigan, Julia Weinelt, Michael Schindler, Robin Antrobus, Ana S.H. Costa, Christian Frezza, Clary B. Clish, Stuart J.D. Neil, and Paul J. Lehner. *Cell Host & Microbe* 18, 1–15, October 14, **2015**.

Proteomics
Bacterial Rotary Export ATPases Are Allosterically Regulated by the Nucleotide Second Messenger Cyclic-di-GMP. Eleftheria Trampari, Clare E. M. Stevenson, Richard H. Little, Thomas Wilhelm, David M. Lawson and Jacob G. Malone. *Journal of Biological Chemistry,* **2015,** *290 (40),* 24470–24483.

Proteomics
Mechanism-Based Post-Translational Modification and Inactivation in Terpene Synthases. Roland D. Kersten, Jolene K. Diedrich, John R. Yates, III, and Joseph P. Noel. *ACS Chem. Biol.,* **2015,** Nov 20;10(11), 2501–11.

Proteomics
Fragment Ion Patchwork Quantification for Measuring Site-Specific Acetylation Degrees. Rasha ElBashir, Jens T. Vanselow, Amelie Kraus, Christian J. Janzen, Nicolai Siegel and Andreas Schlosser. *Anal. Chem.,* **2015,** *87 (19),* 9939–9945.

Proteomics
Generation of Multiple Reporter Ions from a Single Isobaric Reagent Increases Multiplexing Capacity for Quantitative Proteomics. Craig R. Braun, Gregory H. Bird, Martin Wühr, Brian K. Erickson, Ramin Rad, Loren D. Walensky, Steven P. Gygi and Wilhelm Haas. *Anal. Chem.,* **2015,** *87 (19),* 9855–9863.

Proteomics
Targeting Drug Resistance in EGFR with Covalent Inhibitors: A Structure-Based Design Approach. Julian Engel, AndréRichters, Matthaus Getlik, Stefano Tomassi, Marina Keul, Martin Termathe, Jonas Lategahn, Christian Becker, Svenja Mayer-Wrangowski, Christian Grütter, Niklas Uhlenbrock, Jasmin Krüll, Niklas Schaumann, Simone Eppmann, Patrick Kibies, Franziska Hoffgaard, Jochen Heil, Sascha Menninger, Sandra Ortiz-Cuaran, Johannes M. Heuckmann, Verena Tinnefeld, RenéP. Zahedi, Martin L. Sos, Carsten Schultz-Fademrecht, Roman K. Thomas, Stefan M. Kast and Daniel Rauh. *J. Med. Chem.,* **2015,** *58 (17),* 6844–6863.

Proteomics
Identification of the S-layer glycoproteins and their covalently linked glycans in the halophilic archaeon *Haloarcula hispanica.* Hua Lu, Yang Lü, Jinwei Ren, Zhongfu Wang, Qian Wang, Yuanming Luo, Jing Han, Hua Xiang, Yuguo Du, and Cheng Jin. *Glycobiology,* **2015,** *25 (11),* 1150–1162.

Glycoproteomics
Automated *N*-glycan profiling of a mutant Trypanosoma rangeli sialidase expressed in Pichia pastoris, using tandem mass spectrometry and bioinformatics. Haiying Li, Morten I. Rasmussen, Martin R. Larsen, Yao Guo, Carsten Jers, Giuseppe Palmisano, Jørn D. Mikkelsen and Finn Kirpekar. *Glycobiology,* **2015,** doi: 10.1093/glycob/cwv063

Proteomics
Top-down and middle-down protein analysis reveals that intact and clipped human histones differ in post-translational modification patterns. Andrey Tvardovskiy, Krzysztof Wrzesinski, Simone Sidoli, Stephen J. Fey , Adelina Rogowska-Wrzesinska, Ole N. Jensen. *Mol Cell Proteomics,* **2015,** Dec;14(12), 3142–53.

Proteomics
The PINK1-PARKIN Mitochondrial Ubiquitylation Pathway Drives a Program of OPTN/NDP52 Recruitment and TBK1 Activation to Promote Mitophagy. Jin-Mi Heo, Alban Ordureau, Joao A. Paulo, Jesse Rinehart, and J. Wade Harper. *Molecular Cell* 60, 7–20, October 1, **2015**.

Proteomics
The Prion Protein Controls Polysialylation of Neural Cell Adhesion Molecule 1 during Cellular Morphogenesis. Mohadeseh Mehrabian, Dylan Brethour, Hansen Wang, Zhengrui Xi, Ekaterina Rogaeva, Gerold Schmitt-Ulms. *PLOS ONE,* **2015** Aug 19;10(8):e0133741.

Proteomics
Quantitative phosphoproteomics reveals new roles for the protein phosphatase PP6 in mitotic cells. Scott F. Rusin,1 Kate A. Schlosser,2 Mark E. Adamo,2 Arminja N. Kettenbach1,2*. *Sci Signal.,* **2015** Oct 13;8(398):rs12.

Proteomics
Multiplexed, Proteome-wide Protein Expression Profiling: Yeast Deubiquitylating Enzyme Knockout Strains. Marta Isasa, Christopher M. Rose, Suzanne Elsasser, José Navarrete-Perea, Joao A. Paulo, Daniel J. Finley and Steven P. Gygi. *Journal of Proteome Research,* **2015,** Dec 4;14(12), 5306–17.

Glycoproteomics
Glycosylation of Human Plasma Clusterin Yields a Novel Candidate Biomarker of Alzheimer's Disease. Hui-Chung Liang, Claire Russell, Vikram Mitra, Raymond Chung, Abdul Hye , Chantal Bazenet, Simon Lovestone, Ian Pike, and Malcolm Ward. *J. Proteome Res.*, **2015,** Dec 4;14(12), 5063–76.

Proteomics
Rapid High-pH Reverse Phase StageTip for Sensitive Small-Scale Membrane Proteomic Profiling. Baby Rorielyn T. Dimayacyac-Esleta, Chia-Feng Tsai, Reta Birhanu Kitata, Pei-Yi Lin, Wai-Kok Choong, Tai-Du Lin, Yi-Ting Wang, Shao-Hsing Weng, Pan-Chyr Yang, Susan D. Arco, Ting-Yi Sung, and Yu-Ju Chen. *Anal. Chem.*, **2015,** *87,* 12016–12023.

Proteomics
The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF-kB signalling. Theo Klein, Shan-Yu Fung, Florian Renner, Michael A. Blank, Antoine Dufour, Sohyeong Kang, Madison Bolger-Munro, Joshua M. Scurll, John J. Priatel, Patrick Schweigler, Samu Melkko, Michael R. Gold, Rosa I. Viner, Catherine H. Regnier, Stuart E. Turvey and Christopher M. Overall. *Nature Communications,* **2015,** Nov 3;6:8777.

Proteomics
Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. Paulo C Carvalho, Diogo B Lima, Felipe V Leprevost, Marlon D M Santos, Juliana S G Fischer, Priscila F Aquino, James J Moresco, John R Yates III and Valmir C Barbosa. *Nature Protocols,* **2016,** *11,* 102–117.

Glycoproteomics
An innate antiviral pathway acting before interferons at epithelial surfaces. Marie B Iversen, Line S Reinert, Martin K Thomsen, Ieva Bagdonaite, Ramya Nandakumar, Natalia Cheshenko, Thaneas Prabakaran, Sergey Y Vakhrushev, Malgosha Krzyzowska, Sine K Kratholm, Fernando Ruiz-Perez, Steen V Petersen, Stanislas Goriely, Bo Martin Bibby, Kristina Eriksson, Jürgen Ruland, Allan R Thomsen, Betsy C Herold, Hans H Wandall, Sebastian Frische, Christian K Holm and Søren R Paludan. *Nature Immunology,* **2016,** Feb;17(2), 150–8.

N-*Glycoproteomics*
Terminal galactosylation and sialylation switching on membrane glycoproteins upon TNF-alpha-induced insulin resistance in adipocytes. Benjamin L. Parker, Morten Thaysen-Andersen, Daniel J. Fazakerley, Mira Holliday, Nicolle H. Packer, David E. James. *Mol Cell Proteomics,* **2016,** Jan;15(1), 141–53.

Proteomics
An Optimization of LC-MS/MS Workflow for Deep Proteome Profiling on Orbitrap Fusion. Litong Nie, Mingrui Zhu, Shengnan Sun, Linhui Zhai, Zhixiang Wu, Lili Qiana and Minjia Tan. *Anal. Methods,* **2016,** *8,* 425–434.

Glycoproteomics
Neisseria meningitidis Type IV Pili Composed of Sequence Invariable Pilins Are Masked by Multisite Glycosylation. Joseph Gault, Mathias Ferber, Silke Machata, Anne-Flore Imhaus, Christian Malosse, Arthur Charles-Orszag, Corinne Millien, Guillaume Bouvier, Benjamin Bardiaux, Gérard Péhau-Arnaudet, Kelly Klinge, Isabelle Podglajen, Marie Cécile Ploy, H. Steven Seifert, Michael Nilges, Julia Chamot-Rooke, Guillaume Duménil. *PLoS Pathog,.* **2015,** Sep 14;11(9):e1005162. doi: 10.1371/journal.ppat.1005162. eCollection 2015.

Proteomics
Proteomic Analysis Identifies Ribosome Reduction as an Effective Proteotoxic Stress Response. Angel Guerra-Moreno, Marta Isasa, Meera K. Bhanu, David P. Waterman, Vinay V. Eapen, Steven P. Gygi, and John Hanna. *J Biol Chem.,* **2015,** Dec 11;290(50), 29695–706.

Proteomics
Protein species-specific characterization of conformational change induced by multisite phosphorylation. Jingxi Pan, Suping Zhang, Christoph H. Borchers. *Journal of Proteomics,* **2016,** Feb 16;134, 138–43.

Proteomics
Data detailing the platelet acetyl-lysine proteome. Joseph E. Aslan, Larry L. David, Owen J.T. McCarty. *Data Brief.,* **2015,** Oct 9;5, 368–71.

Proteomics
Metabolic Interplay between the Asian Citrus Psyllid and Its Profftella Symbiont: An Achilles' Heel of the Citrus Greening Insect Vector. John S. Ramsey, Richard S. Johnson, Jason S. Hoki, Angela Kruse, Jaclyn Mahoney, Mark E. Hilf , Wayne B. Hunter, David G. Hall , Frank C. Schroeder, Michael J. MacCoss , Michelle Cilia. *Plos One,* **2015,** Nov 18;10(11):e0140826

Proteomics
Evolution of Helicobacter: Acquisition by Gastric Species of Two Histidine-Rich Proteins Essential for Colonization. Daniel Vinella, Frédéric Fischer, Egor Vorontsov , Julien Gallaud, Christian Malosse , Valérie Michel , Christine Cavazza , Marie Robbe-Saule , Pierre Richaud , Julia Chamot-Rooke , Céline Brochier-Armanet , Hilde De Reuse. *PLOS Pathog.,* **2015,** Dec 7;11(12):e1005312.

Glycomics
Schistosoma mansoni α1,3-fucosyltransferase-F generates the Lewis X antigen. Megan L Mickum, Teerapat Rojsajjakul, Ying Yu and Richard D Cummings. *Glycobiology*, **2016,** Mar;26(3), 270–85.

Proteomics
Functional dichotomy in the 16S rRNA (m1A1408) methyltransferase family and control of catalytic activity via a novel tryptophan mediated loop reorganization. Marta A. Witek and Graeme L. Conn. *Nucleic Acids Res.,* **2016,** Jan 8;44(1), 342–53.

Proteomics
The use of matrix coating assisted by an electric field (MCAEF) to enhance mass spectrometric imaging of human prostate cancer biomarkers. Xiaodong Wang, Jun Han, Darryl B. Hardie, Juncong Yang and Christoph H. Borchers. J*ournal of Mass Spectrometry, 51 (1),* 86–95, January **2016.**

Glycoproteomics
Distinctive MS/MS Fragmentation Pathways of Glycopeptide-Generated Oxonium Ions Provide Evidence of the Glycan Structure. Jin Yu, Manuel Schorlemer, Alejandro Gomez Toledo, Christian Pett, Dr. Carina Sihlbom, Prof. Göran Larson, Dr. Ulrika Westerlind, Dr. Jonas Nilsson. *Chemistry,* **2016,** Jan 18;22(3), 1114–24.

Proteomics
Myc coordinates transcription and translation to enhance transformation and suppress invasiveness. Ran Elkon, Fabricio Loayza-Puch, Gozde Korkmaz, Rui Lopes, Pieter C van Breugel, Onno B Bleijerveld, AF Maarten Altelaar, Elmar Wolf, Francesca Lorenzin, Martin Eilers and Reuven Agami. *EMBO reports,* 16 (2) 1723–1736, December **2015.**

Glycoproteomics
Glycomic analysis of gastric carcinoma cells discloses glycans as modulators of RON receptor tyrosine kinase activation in cancer. Stefan Mereiter, Ana Magalhães, Barbara Adamczyk, Chunsheng Jin, Andreia Almeida, Lylia Drici, Maria Ibáñez-Vea, Catarina Gomes, José A. Ferreira, Luis P. Afonso, Lúcio L. Santos, Martin R. Larsen, Daniel Kolarich, Niclas G. Karlsson, Celso A. Reis. *Biochimica et Biophysica Acta (BBA),* **2016,** Aug;1860(8), 1795–808.

Proteomics
AKT Inhibition Promotes Nonautonomous Cancer Cell Survival. Salony, Xavier Sole, Cleidson P. Alves, Ipsita Dey-Guha, Laila Ritsma, Myriam Boukhali, Ju H. Lee, Joeeta Chowdhury, Kenneth N. Ross, Wilhelm Haas, Shobha Vasudevan and Sridhar Ramaswamy. *Mol Cancer Ther.,* **2016,** Jan;15(1), 142–53.

Proteomics
Proteomic analysis of pRb loss highlights a signature of decreased mitochondrial oxidative phosphorylation. Brandon N. Nicolay, Paul S. Danielian, Filippos Kottakis, John D. Lapek Jr, Ioannis Sanidas, Wayne O. Miles, Mantre Dehnad, Katrin Tschöp, Jessica J. Gierut, Amity L. Manning, Robert Morris, Kevin Haigis, Nabeel Bardeesy, Jacqueline A. Lees, Wilhelm Haas and Nicholas J. Dyson. *Genes Dev.,* **2015,** Sep 1;29(17), 1875–89.

Proteomics
A draft map of the mouse pluripotent stem cell spatial proteome. Andy Christoforou, Claire M. Mulvey, Lisa M. Breckels, Aikaterini Geladaki, Tracey Hurrell, Penelope C. Hayward, Thomas Naake, Laurent Gatto, Rosa Viner, Alfonso Martinez Arias & Kathryn S. Lilley. *Nat Commun.,* **2016,** Jan 12;7:9992. doi: 10.1038/ncomms9992

Proteomics
Quantitative proteomics identify DAB2 as a cardiac developmental regulator that inhibits WNT/β-catenin signaling. Peter Hofsteen, Aaron M. Robitaille, Daniel Patrick Chapman, Randall T. Moon and Charles E. Murry. *Proc Natl Acad Sci U S A.,* **2016,** Jan 26;113(4), 1002–7.

Proteomics
Functional Genomic Screening Reveals Splicing of the EWS-FLI1 Fusion Transcript as a Vulnerability in Ewing Sarcoma. Patrick J. Grohar, Suntae Kim, Guillermo O. Rangel Rivera, Nirmalya Sen, Sara Haddock, Matt L. Harlow, Nichole K. Maloney, Jack Zhu, Maura O'Neill, Tamara L. Jones, Konrad Huppi, Magdalena Grandin, Kristen Gehlhaus, Carleen A. Klumpp-Thomas, Eugen Buehler, Lee J. Helman, Scott E. Martin and Natasha J. *Caplen. Cell Reports,* **2016,** Jan 26;14(3), 598–610.

Proteomics
Homogenization of tissues via picosecond-infrared laser (PIRL) ablation: Giving a closer view on the in-vivo composition of protein species as compared to mechanical homogenization. M. Kwiatkowski, M. Wurlitzer, A. Krutilin, P. Kiani, R. Nimer, M. Omidi, A. Mannaa, T. Bussmann, K. Bartkowiak, S. Kruber, S. Uschold, P. Steffen, J. Lübberstedt, N. Küpker, H. Petersen , R. Knecht, N.O. Hansen, A. Zarrine-Afsar, W.D. Robertson, R.J.D. Miller, H. Schlüter. *Journal of Proteomics,* **2016,** Feb 16;134, 193–202.

Proteomics
Identifying Family-Member-Specific Targets of Mono-ARTDs by Using a Chemical Genetics Approach. Ian Carter-O'Connell, Haihong Jin, Rory K. Morgan, Roko Zaja, Larry L. David, Ivan Ahel and Michael S. Cohen. *Cell Reports,* **2016,** Jan 26;14(3), 621–31.

Proteomics
Cold Temperature Induces the Reprogramming of Proteolytic Pathways in Yeast

Marta Isasa, Clara Suner, Miguel Díaz, Pilar Puig-Sarries, Alice Zuin, Anne Bichman, Steven P. Gygi, Elena Rebollo and Bernat Crosas. *Journal of Biological Chemistry, 291 (4*) 1664 –1675, January 22, 2016.

Proteomics
Selective Exo-Enzymatic Labeling Detects Increased Cell Surface Sialoglycoprotein Expression Upon Megakaryocytic Differentiation. Seok-Ho Yu, Peng Zhao , Tiantian Sun, Zhongwei Gao, Kelley W. Moremen, Geert-Jan Boons, Lance Wells, Richard Steet. *J Biol Chem.,* **2016**, Feb 19;291(8), 3982–9.

Proteomics
Stress granules and RNA processing bodies are novel autoantibody targets in systemic sclerosis. Michael E. Johnson, Andrew V. Grassetti, Jaclyn N. Taroni, Shawn M. Lyons, Devin Schweppe, Jessica K. Gordon, Robert F. Spiera, Robert Lafyatis , Paul J. Anderson , Scott A. Gerber and Michael L. Whitfield. *Arthritis Research & Therapy,* **2016,** Jan 22;18:27.

Proteomics
An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. Matthew M. Makowski, Esther Willems, Jun Fang, Jiyeon Choi, Tongwu Zhang, Pascal W. T. C. Jansen, Kevin M. Brown and Michiel Vermeulen. *Proteomics,* **2016,** Feb;16(3), 417–26.

Top-down proteomics
The use of matrix coating assisted by an electric field (MCAEF) to enhance mass spectrometric imaging of human prostate cancer biomarkers. Xiaodong Wang,a Jun Han,a Darryl B. Hardie,a Juncong Yanga and Christoph H. Borchers. *J. Mass Spectrom.,* **2016,** *51,* 86–95.

Proteomics
Site-Specific Identification of Lysine Acetylation Stoichiometries in Mammalian Cells. Tong Zhou,† Ying-hua Chung,† Jianji Chen, and Yue Chen. *J. Proteome Res.,* **2016,** Mar 4;15(3), 1103–13.

Proteomics
Effect of Fc-Glycan Structure on the Conformational Stability of IgG Revealed by Hydrogen/Deuterium Exchange and Limited Proteolysis. Jing Fang, Jason Richardson, Zhimei Du and Zhongqi Zhang. *Biochemistry,* **2016,** Feb 16;55(6), 860–8.

Glycoproteomics
Comparative Assessment of Glycosylation of a Recombinant Human FSH and a Highly Purified FSH Extracted from Human Urine. Hong Wang, Chen,‡ Xiaoxi Zhang, Wei Zhang, Yan Li, Hongrui Yin, Hong Shao and Gang Chen. *J. Proteome Res.,* **2016,** Mar 4;15(3), 923–32.

Proteomics
Mechanisms of ribosome stalling by SecM at multiple elongation steps. Jun Zhang, Xijiang Pan, Kaige Yan, Shan Sun, Ning Gao, Sen-Fang Sui. *Elife.,* **2015,** Dec 14;4. pii: e09684.

Proteomics
An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. Makowski MM, Willems E, Fang J, Choi J, Zhang T, Jansen PW, Brown KM, Vermeulen M. Proteomics. 2016 Feb;16(3):417-26

Proteomics
Structural basis of lenalidomide-induced CK1α degradation by the CRL4(CRBN) ubiquitin ligase. Georg Petzold, Eric S. Fischer and Nicolas H. Thomä. *Nature,* **2016,** Apr 7;532(7597), 127–30.

Glycoproteomics
Genome analysis of three Pneumocystis species reveals adaptation mechanisms to life exclusively in mammalian hosts. Liang Ma, Zehua Chen, Da Wei Huang, Geetha Kutty, Mayumi Ishihara, Honghui Wang, Amr Abouelleil, Lisa Bishop, Emma Davey, Rebecca Deng, Xilong Deng, Lin Fan, Giovanna Fantoni, Michael Fitzgerald, Emile Gogineni, Jonathan M. Goldberg, Grace Handley, Xiaojun Hu, Charles Huber, Xiaoli Jiao, Kristine Jones, Joshua Z. Levin, Yueqin Liu, Pendexter Macdonald, Alexandre Melnikov, Castle Raley, Monica Sassi, Brad T. Sherman, Xiaohong Song, Sean Sykes, Bao Tran, Laura Walsh, Yun Xia, Jun Yang, Sarah Young, Qiandong Zeng, Xin Zheng, Robert Stephens, Chad Nusbaum, Bruce W. Birren, Parastoo Azadi, Richard A. Lempicki, Christina A. Cuomo and Joseph A. Kovacs. *Nat Commun.,* **2016,** Feb 22;7, 10740.

Proteomics
The HIV-1 protein Vpr impairs phagosome maturation by controlling microtubule-dependent trafficking. Audrey Dumas, Gabrielle Lê-Bury, Florence Marie-Anaïs, Floriane Herit, Julie Mazzolini, Thomas Guilbert, Pierre Bourdoncle, David G. Russell, Serge Benichou, Ahmed Zahraoui and Florence Niedergang. *J. Cell Biol., 211 (20)* 359–372.

Proteomics
γ-crystallins of the chicken lens: remnants of an ancient vertebrate gene family in birds. Yingwei Chen, Vatsala Sagar, Hoay-Shuen Len, Katherine Peterson, Jianguo Fan, Sanghamitra Mishra, John McMurtry, Phillip A. Wilmarth, Larry L. David, Graeme Wistow. *FEBS Journal.,* **2016,** Apr;283(8), 1516–30.

Proteomics
Identifying Predictors of Taxane-Induced Peripheral Neuropathy Using Mass Spectrometry-Based Proteomics Technology. Emily I. Chen, Katherine D. Crew, Meghna Trivedi, Danielle Awad, Mathew Maurer Kevin Kalinsky, Antonius Koller, Purvi Patel, Jenny Kim Kim, Dawn L. Hershman. *PLOS ONE.,* **2015,** Dec 28;10(12):e0145816

Proteomics
Quantitative Profiling of Long-Chain Bases by Mass Tagging and Parallel Reaction Monitoring. Christer S. Ejsing , Mesut Bilgin, Andreu Fabregat. *PLOS ONE.*, **2015,** Dec 11;10(12):e0144817

Proteomics
Proteomic comparison defines novel markers to characterize heterogeneous populations of extracellular vesicle subtypes. Joanna Kowal, Guillaume Arras, Marina Colombo, Mabel Jouve, Jakob Paul Morath, Bjarke Primdal-Bengtson, Florent Dingli, Damarys Loew, Mercedes Tkach and Clotilde Théry. *Proc Natl Acad Sci U S A.,* **2016,** Feb 23;113(8):E968-77

Proteomics
Protein carbamylation is a hallmark of aging. Laëtitia Gorisse, Christine Pietrement, Vincent Vuiblet, Christian E. H. Schmelzer, Martin Köhler, Laurent Duca, Laurent Debelle, Paul Fornè, Stéphane Jaisson and Philippe Gillery. *Proc Natl Acad Sci U S A.,* **2016,** Feb 2;113(5), 1191–6.

Proteomics
Pseudomonas aeruginosa EftM Is a Thermoregulated Methyltransferase. Joshua P. Owings, Emily G. Kuiper, Samantha M. Prezioso, Jeffrey Meisner, John J. Varga, Natalia Zelinskaya, Eric B. Dammer, Duc M. Duong, Nicholas T. Seyfried, Sebastian Albertí, Graeme L. Conn and Joanna B. Goldberg. *Journal of Biological Chemistry,* **2016,** Feb 12;291(7), 3280–90.

Cross-linking
Nanobodies: site-specific labeling for super-resolution imaging, rapid epitopemapping and native protein complex isolation. Tino Pleiner, Mark Bates, Sergei Trakhanov, Chung-Tien Lee, Jan Erik Schliep, Hema Chug, Marc Bo hning, Holger Stark, Henning Urlaub, Dirk Gorlich. *Elife,* **2015,** Dec 3;4. pii: e11349. doi: 10.7554/eLife.11349.

thermo scientific

Proteomics
Global Analysis of Cellular Protein Flux Quantifies the Selectivity of Basal Autophagy. Tian Zhang, Shichen Shen, Jun Qu and Sina Ghaemmaghami. *Cell Reports,* 14, 1–14, March 15, **2016.**

Proteomics, antibody, intact profiling
De novo sequencing and resurrection of a human astrovirus-neutralizing antibody.Walter A. Bogdanoff, David Morgenstern, Marshall Bern, Beatrix M. Ueberheide, Alicia Sanchez-Fauquier, and Rebecca M. DuBois. *ACS Infect. Dis.,* **2016,** May 13;2(5), 313–321.

Find out more at **www.thermofisher.com/grantcentral**

ThermoFisher SCIENTIFIC

WP64906-EN 0217S