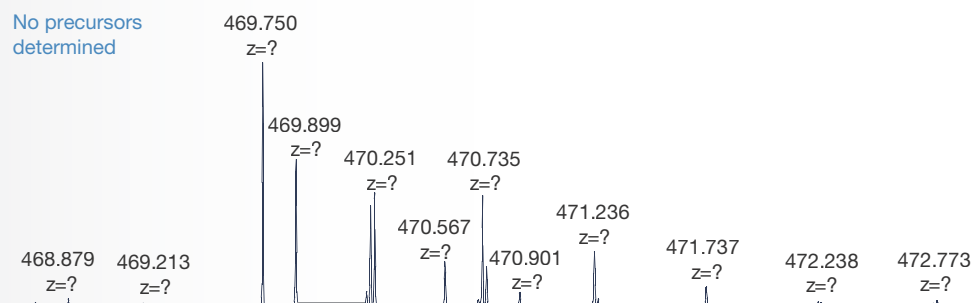


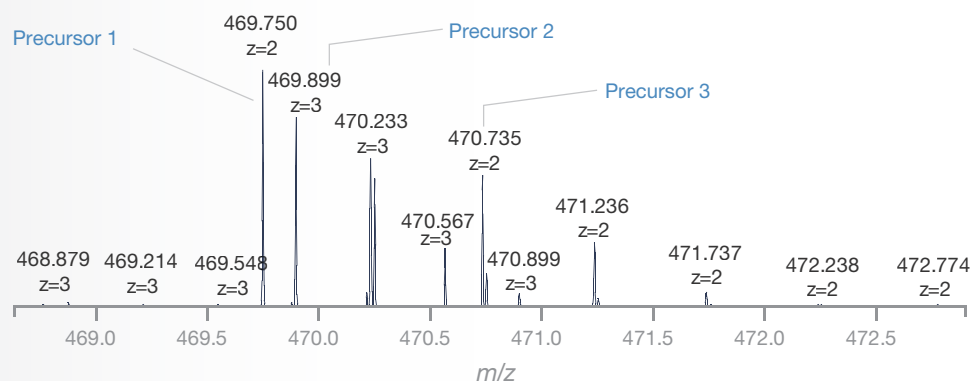
Reading Between the Lines with Advanced Peak Determination

High performance mass spectrometers with extreme sensitivity and resolution have illuminated a need for improved on-the-fly spectral analysis and peak assignment. The Advanced Peak Determination (APD) algorithm fills this need by identifying the charge states and monoisotopic m/z values of isotopic envelopes at greatly improved peak depths. This algorithm dramatically increases the population of precursors available for data-dependent analysis, which in turn results in more MS² spectra, PSMs, and unique peptide identifications.

STANDARD PEAK DETERMINATION

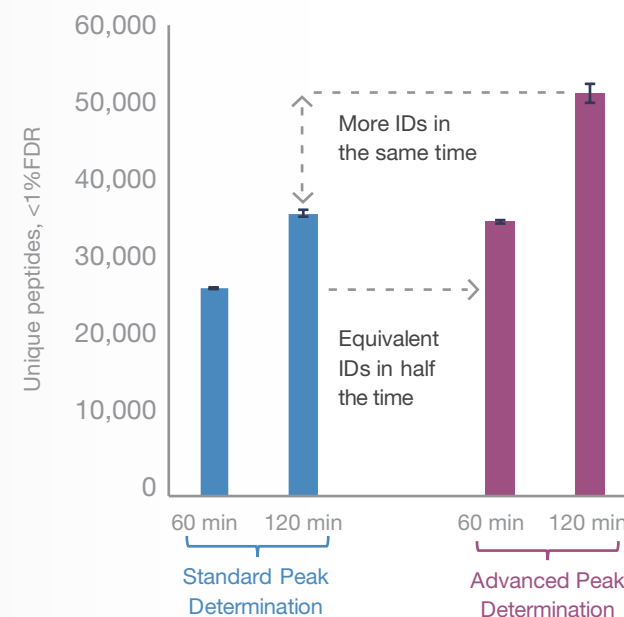


ADVANCED PEAK DETERMINATION

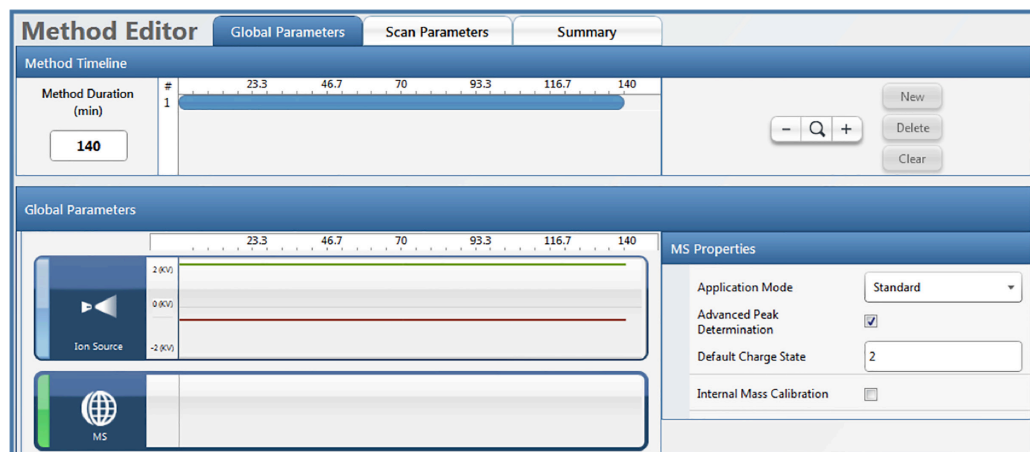


Advanced Peak Determination allows for real-time assignment of a significantly larger number of charge states and monoisotopic peaks in complex MS spectra in comparison with Standard Peak Determination. This results in a corresponding increase in MS/MS data-dependent events, PSMs, unique peptide and protein identifications.

NEW DEPTHS OF ANALYSIS OF COMPLEX PROTEOMICS SAMPLES



The Thermo Scientific™ Orbitrap Fusion™ Lumos™ Tribrid™ MS with Advanced Peak Determination, in conjunction with LC-MS/MS methods that leverage the low detection limits of the MS and incredibly high ion trap MS/MS scan rates, significantly boosts the rate of unique peptide identifications, shown here with a 1 μ g HeLa digest analyzed using 1 h and 2 h gradients (n=3).



Advanced Peak Determination is an optional Global MS property of the Method Editor.

“The new APD algorithm provides new peptide precursors to go after and amounts to a 25–35% identification bonus. I have no doubt this will be a key technology in achieving deeper coverage and higher throughput for proteome analyses.”

—Josh Coon, Professor, The University of Wisconsin-Madison

www.planetorbitrap.com/orbitrap-fusion-lumos



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