

Innovative Approach Redefines Data Analysis in Proteomics Research **Thermo Fisher Scientific and MSAID continue their collaboration to deliver transformative deep learning tools for proteomics data analysis**

PHILADELPHIA, Nov. 1, 2021 /PRNewswire/ -- **ASMS 2021** - Thermo Fisher Scientific, the world leader in serving science, and MSAID, the leader in proteomics artificial intelligence, have collaborated to provide proteomics researchers with advanced mass spectrometry software that generates market-leading biological insight from acquired data by substantially increasing peptide identification and quantitation capabilities using artificial intelligence (AI) and deep learning.

[Thermo Scientific Proteome Discoverer 3.0 software](#) with [CHIMERYYS by MSAID](#) leverages artificial intelligence (AI) to substantially enhance the identification rate and number of unique peptide identifications in proteomics data. CHIMERYYS identifies a minimal set of peptides that can explain the acquired tandem mass spectrum, in comparison to existing methodologies, which typically assume all peaks in a tandem mass spectrum are derived from a single peptide. This innovative approach provides a 1.8-fold increase in the number of unique peptide identifications and a 1.5-fold increase in the number of protein identifications for typical proteomics data sets when compared to existing tools. In addition to improved protein coverage and quantitation capabilities, Proteome Discoverer 3.0 software paired with CHIMERYYS also facilitates faster data acquisition for increased sample throughput.

Thermo Fisher Scientific and MSAID are showcasing their new software solution during the 69th American Society for Mass Spectrometry (ASMS) Conference on Mass Spectrometry and Allied Topics, being held October 31-November 4, in the Pennsylvania Convention Center, Philadelphia, Pennsylvania.

"Previous technologies have been unable to fully interpret data generated using mass spectrometry, as mass spectra can contain fragments from multiple co-isolated peptides that cannot be identified using current algorithms," said August Specht, vice president, research and development, chromatography and mass spectrometry, Thermo Fisher Scientific. "By using Proteome Discoverer 3.0 software and CHIMERYYS, scientists can now leverage AI for deeper mining of proteomic data. This not only improves proteomic coverage, but also expands the ways in which proteomics scientists can acquire and apply their data."

Martin Frejno, chief executive officer, MSAID said: "Chimeric spectra were a long-standing problem in mass spectrometry-based proteomics. With CHIMERYYS, we reimaged the analysis of tandem mass spectra from the ground up using AI to solve it."

The Proteome Discoverer 3.0 software release also includes an updated INFERYYS prediction model, extending support to tandem mass tagging (TMT), collisionally induced dissociation (CID), and providing improved results for immunopeptidomics. By pairing intelligent data analysis through Proteome Discoverer 3.0 software and CHIMERYYS with leading hardware technology in the [Thermo Scientific Vanquish Neo Ultra-High Performance Liquid Chromatography \(UHPLC\) system](#) and [Thermo Scientific Orbitrap mass spectrometry platforms](#), researchers will be empowered to continue pushing the boundaries of proteomics research.

For more information on Thermo Scientific Proteome Discoverer 3.0 software and CHIMERYYS by MSAID, please visit www.thermofisher.com/proteomediscoverer, or join us at ASMS 2021 from October 31-November 4, 2021.

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