

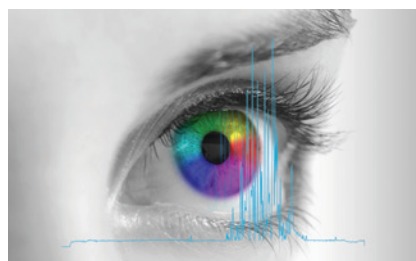


- Increased coverage from limited samples
- High-resolution separation of polar analytes and critical PTMs
- In-depth characterization of proteoforms and protein complexes

The Perfect Accessory for Your Mass Spectrometer

CESI 8000 Plus High Performance Separations - ESI Module and Adapter Kit

CESI is a mass spectrometer accessory for the analysis of biological compounds in every analytical laboratory:



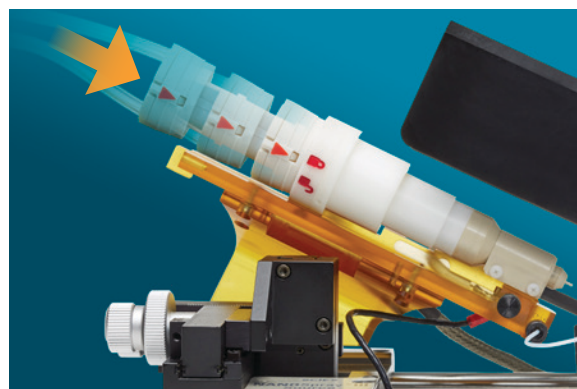
- Consumes minute sample amounts (nL volumes) with extraordinary sensitivity
- Excels at charged & polar metabolites, peptides, and more
- Enables high-resolution separation of proteins and protein-complexes
- Eliminates ion suppression so you can see what you are missing
- Robust and easy-to-use thanks to zero-dead-volume design

CESI-MS “showed better separation efficiency and resolution with 100-fold less sample consumption compared to an LC-based intact protein separation.”

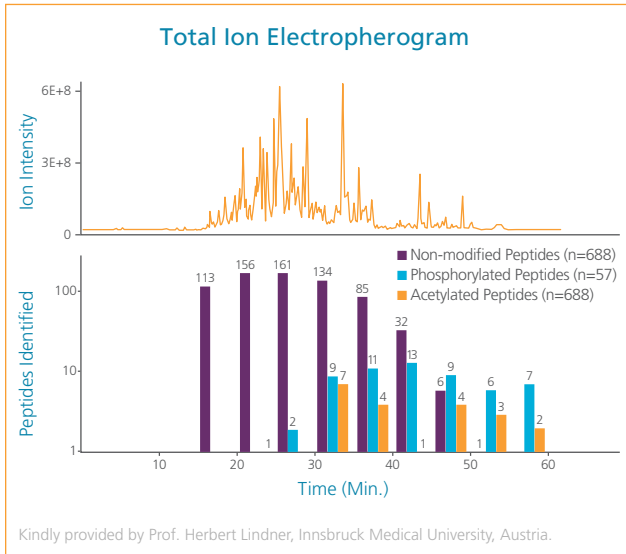
J. Prot. Res. 2014 from the John Yates III research group, The Scripps Research Institute, La Jolla, CA.

CESI-MS “shows a separation efficiency for high-molecular-mass compounds like larger peptides and proteins that is remarkably higher than that seen with any LC method”

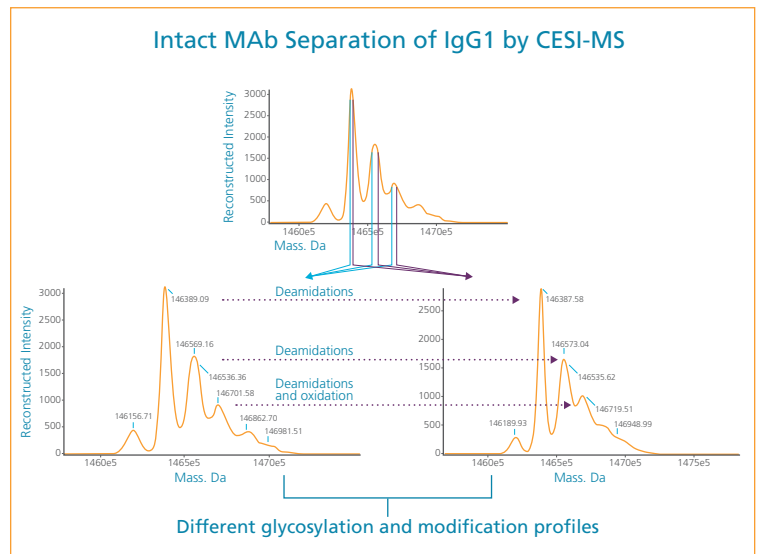
Molecular and Cellular Proteomics 2013 from the Herbert Lindner research group, Innsbruck, Austria



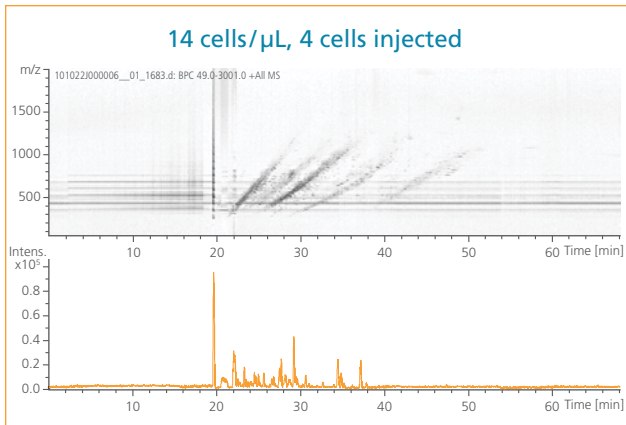
Connecting the CESI 8000 Plus to your mass spectrometer is as easy as plug and spray. Attach the OptiMS Adapter to your mass spectrometer and click the CESI cartridge tip into place.



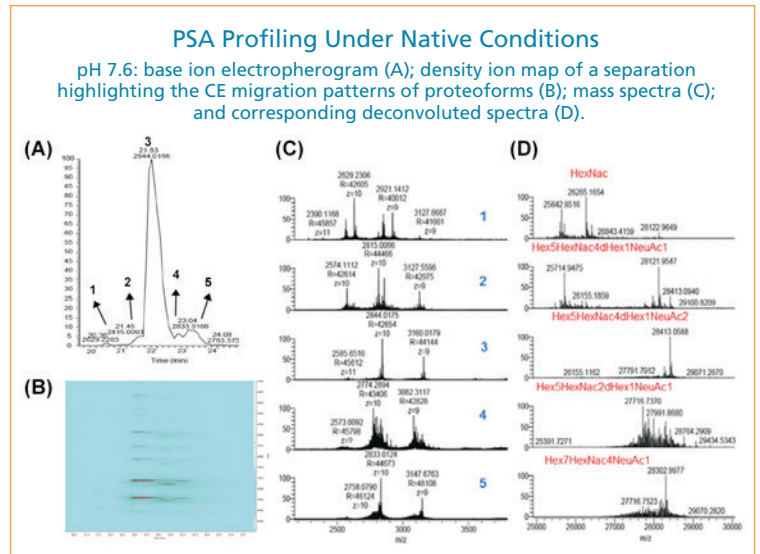
CESI-MS excels at various PTMs revealing important biological functional variations.



For deep characterization of proteoforms, glycoforms, charge states, and PTMs, CESI is the only front-end technology that enables liquid-phase separation of proteins, metal binding, and protein complexes. CESI-MS is an invaluable tool to drive biopharmaceutical development as well as biochemical mechanistic studies.



CESI enables MS signal from minute amounts of sample.



CESI-MS-EMR reveals 236 proteoforms from 2.9 ng of PSA under native conditions.

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