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Cerno Bioscience Releases GC/ID V2.0 Software for Highly Confident GC/MS Compound ID

Las Vegas, NV (August 15, 2020) – Cerno Bioscience announced today that it has released version 2.0 of its innovative MassWorks Rx GC/ID software. GC/ID is a fully automated data processing software that enables dramatic improvements for GC/MS qualitative analysis. GC/ID now provides accurate mass formula confirmation through molecular or fragment ions beyond conventional library searches in the NIST, Wiley, or user generated libraries. In addition, GC/ID 2.0 takes advantage of the expanded compound Retention Index (RI) data in the new commercial library collections (NIST20 and Wiley Registry 12) to automatically perform quantitative RI match to provide yet a third metric for compound identification. Together, these 3 metrics - library search, accurate mass formula confirmation, and RI match - can save the analyst hours of tedious review or re-analysis while also increasing the quality and confidence of compound identification.

Molecular and fragment ion formula confirmation is accomplished using Cerno's patented and proven TrueCal™ calibration technology. Using full profile mode data and the GC/MS built-in calibration gas, the MS is automatically calibrated for both accurate mass (easily within +/- 20 mDa) and spectral accuracy (typically >99%). This provides an Effective Mass Accuracy (EMA) on a single quadrupole comparable to high resolution instruments.

Version 2.0 also includes powerful peak deconvolution capability. By using the accurately calibrated profile mode spectral data combined with a novel approach to accurately analyze the actual chromatographic peaks, "false" spectral components are minimized to provide more accurate and confident results. In addition, compound confirmation by RI is now fully comprehensive for all compounds in the new NIST20 libraries thanks to a new computational method using advanced Artificial Intelligence (AI). Combined with the extensive collection of experimental values, NIST20 now provides RI data for every compound in the entire library.

Yongdong Wang, President of Cerno states: "GC/ID may very will be the first breakthrough in GC/MS in decades. While GC/MS library search has been a well-established and effective tool for the ID of organic compounds, advances have been limited to the expansion of spectral libraries and hardware improvements in terms of sensitivity, sample throughput, and ease of use. No significant progress has been made to assist the analyst in determining the correct match from a long list of possible hits, typically requiring tedious and time-consuming manual review or even re-analysis. GC/ID combines reliable mixture deconvolution, accurate mass formula confirmation and RI match capabilities in an easy-to-use, automated, and quantitative manner. This can save the analyst hundreds of hours per year while increasing compound ID confidence and minimizing the number of "unidentified" peaks due to interferences, unresolved peaks, or just ambiguous library search results."

For more information on MassWorks Rx GC/ID, please contact Cerno Bioscience at info@cernobioscience.com, call +1 203-312-1150, or visit www.cernobioscience.com

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About Cerno Bioscience Products
Cerno Bioscience's MassWorks family of software products performs post-acquisition MS calibration, formula determination, and mixture quantitation through either CLIPS at unit mass resolution or sCLIPS at higher resolution and now, fully automated GC/MS qualitative analysis with MassWorks Rx GC/ID. It supports all major MS vendor data formats directly (DirectRead) and works with all MS instruments including GC/MS, LC/MS, TOF, qTOF, and FT MS including Orbitrap. Cerno Bioscience products are used in major R&D or QA/QC labs for pharmaceuticals, food, beverages, flavors, fragrances, natural products, environmental analysis, forensics, chemicals and petrochemicals as well as academic and educational institutions.

About Cerno Bioscience
Cerno is dedicated to the practical application of modern mathematical techniques to Mass Spectrometry for improving the quality, accuracy and reliability of MS analysis. These techniques can be used to dramatically improve the amount of information obtainable from and reduce the amount of time required of many MS experiments. Cerno's technologies are proprietary and protected through numerous patents granted and submitted world-wide. For more information on Cerno MS technologies, applications, or products, please visit our Web site: www.cernobioscience.com.

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