MSAID Launches CHIMERYS 2.0: The Intelligent Search Algorithm for Proteomics with Support for All Major Acquisition Methods

Munich – (September 28, 2023) – MSAID GmbH, the leader in artificial intelligence for proteomics, announces the launch of CHIMERYS 2.0, the next generation of its intelligent search algorithm for proteomics. The standout features of this release are the addition of support for phosphorylated peptides, as well as Data-Independent Acquisition (DIA) and Parallel Reaction Monitoring (PRM) data.

With these new additions, CHIMERYS 2.0 now supports Data-Dependent Acquisition (DDA), Wide Window Acquisition (WWA), Data-Independent Acquisition (DIA) and Parallel Reaction Monitoring (PRM) data from unmodified and phosphorylated peptides in the same software, turning it into a unifying solution for the analysis of bottom-up proteomics measurements. For the first time, this enables researchers to perform unbiased, head-to-head comparisons of different acquisition methods.

"We are thrilled to introduce CHIMERYS 2.0, the next generation of our intelligent search algorithm for proteomics," said Martin Frejno, CEO of MSAID. "Unifying the analysis of bottom-up proteomics data is a major milestone for us and will help researchers to make breakthrough discoveries in their field. This release sets a new standard for simplifying proteomics."

CHIMERYS 2.0 also offers an improved user experience, with a redesigned interface and increased scalability in the cloud. It's powerful algorithms and innovative tools make it easier for researchers to uncover new insights into the functions and interactions of proteins.

MSAID showcased their new software solution during the 22nd Human Proteome Organization (HUPO) World Congress from September 17-21, 2023 in Busan, South Korea.

About MSAID

MSAID - the leader in artificial intelligence for proteomics - transforms the way scientists analyze proteomic data. The company was founded by an interdisciplinary team of scientists with the vision to provide better computational solutions to the field of proteomics. Our approach is to replace current algorithms with powerful, artificial intelligence-fueled software solutions, thereby paving the way for a smarter, deeper and more reliable way of interrogating proteomics data. For more information, please visit www.msaid.de.

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