



## MSAID announces collaboration with Thermo Fisher Scientific for the development and commercialization of deep learning tools for proteomics

**Garching – (May 26, 2020)** – MSAID, a pioneer in transforming proteomics with deep learning, announces an exclusive license agreement with Thermo Fisher Scientific, the world leader in serving science, to develop and commercialize deep learning tools for proteomics.

“Accurately measuring the proteome is a crucial step in the understanding, diagnosis, and treatment of diseases” said Prof. Bernhard Kuster, a leading expert in proteomics and co-founder of MSAID GmbH. “Harnessing artificial intelligence will enable us to dig deeper into proteomic data and will unlock its true potential.”

Characteristics like chromatographic retention time or fragment ion intensities in tandem mass spectra are crucial for the confident identification of peptides from experimental data. Based on vast amounts of data, artificial intelligence can learn and subsequently predict these characteristics, extrapolating beyond the initial training data. Improving on the published deep learning model Prosit [1], MSAID developed INFERYS, an artificial intelligence, which will be made available to laboratories around the world through the collaboration with Thermo Fisher Scientific.

INFERYS will enable users to predict spectral libraries of entire proteomes for applications like spectral library searching with the click of a button. In addition, it powers INFERYS Rescoring, which automatically calibrates INFERYS to user data and then calculates intensity-based similarity scores for peptide-spectrum-matches, thereby improving the confidence in search results.

“INFERYS is fully compatible with CPUs and end-user hardware and does not require expensive GPUs to run. This marks the beginning of a new era in proteomics, where artificial intelligence is at every researcher’s fingertips,” said Martin Frejno, co-founder and CEO of MSAID GmbH. “INFERYS will dramatically increase the confidence in results of proteomics experiments and help with the analysis of particularly challenging samples commonly encountered for example in Immunopeptidomics experiments.”

MSAID and Thermo Fisher Scientific will present the results of their collaboration at the American Society for Mass Spectrometry (ASMS) Reboot Program, from June 1-12, 2020.

### About MSAID

MSAID GmbH [ɛm ɛs ɛɪd] transforms the way scientists analyze proteomics data. MSAID is a privately-held informatics spin-off from the Technical University of Munich, Germany. The company was founded by an interdisciplinary team of scientists with the vision to provide better computational solutions to the field of proteomics. All founders have an exceptionally strong track record and long-standing expertise in the acquisition, analysis, and interpretation of proteomic data. Our approach is to replace current algorithms for proteomics with powerful, AI-based solutions, thereby paving the way for a smarter, deeper, and more reliable way of interrogating proteomic data. For more details, please visit [www.msaid.de](http://www.msaid.de)

[1] Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning; Gessulat S, Schmidt T et al., Nature Methods 2019.