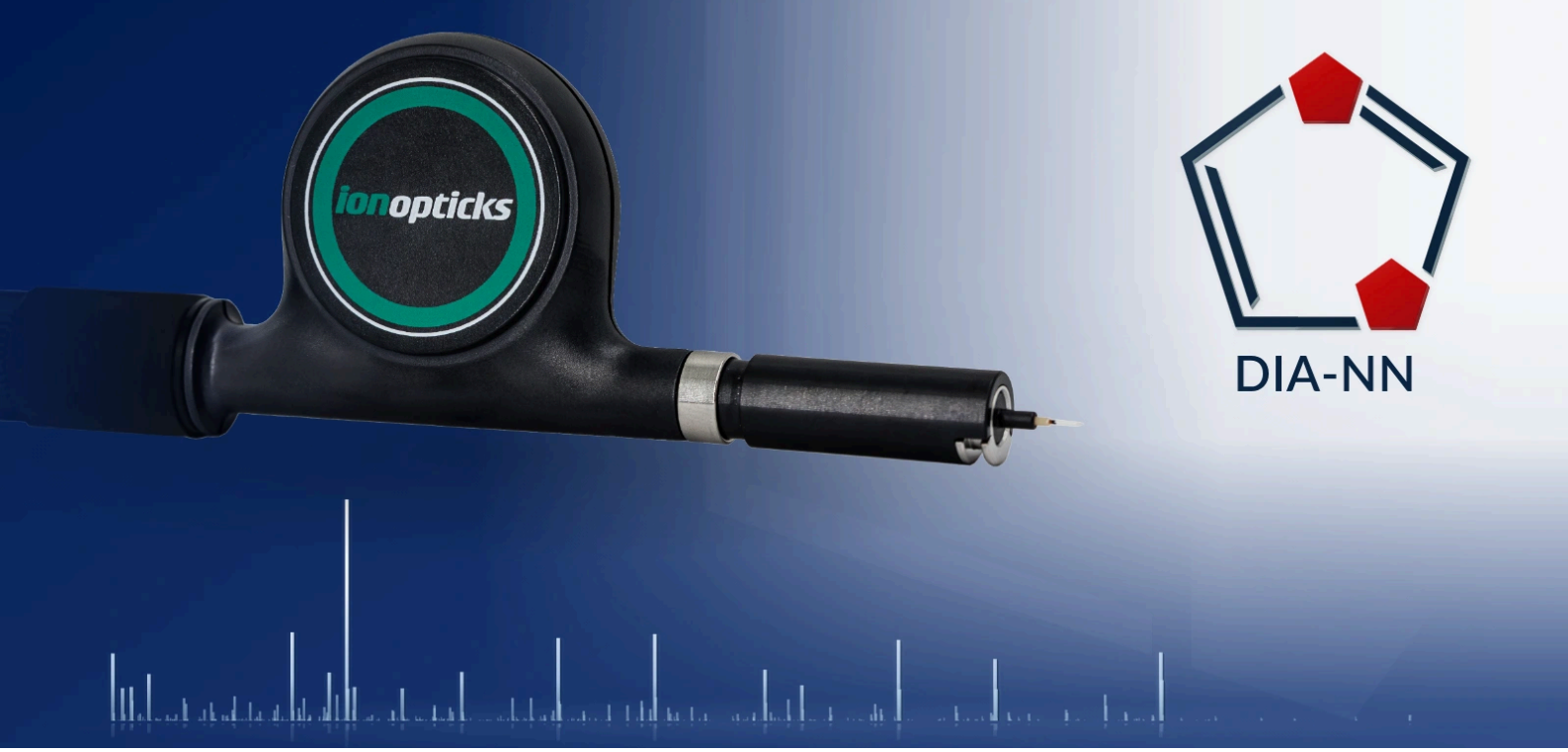

Aptila and IonOpticks announce a collaboration on mass spectrometry data analysis

Aptila supports IonOpticks in deploying DIA-NN Enterprise for chromatography systems and mass spectrometry method development. IonOpticks supplies Aptila with state-of-the-art mass spectrometry data to optimise DIA-NN.

FOR IMMEDIATE RELEASE

Berlin, Germany / Melbourne, Australia, 29 September 2026 — Aptila Biotech, developer of DIA-NN software for proteomics data analysis, and IonOpticks, manufacturer of high-performance chromatography solutions for LC-MS proteomics, today announce a collaboration.

In data-independent acquisition (DIA) proteomics, a mass spectrometer systematically fragments all ions in successive isolation windows rather than selecting individual precursors. The approach produces comprehensive, quantitative datasets but depends on computational methods to disentangle the resulting spectra. Chromatographic separation upstream of the mass spectrometer reduces the complexity of spectra, so the quality of the separation directly shapes what the analysis can recover.

IonOpticks designed the Aurora Series® 5 columns to maintain peak capacity and separation stability across large-scale experiments. Available from September 2026, the Series 5 sustained consistent performance across spans of more than 1,400 injections on different mass spectrometry platforms and with different separation gradients.

Aptila develops DIA-NN for reliable peptide and protein identification and quantification from DIA experiments, with particular emphasis on accuracy under high-throughput conditions. The original paper describing DIA-NN (*Nature Methods*, 2020) has been cited more than 4000 times (Google Scholar).

In a series of 1,380 injections acquired on an Aurora Series 5 column with an 8-minute gradient at 120 samples per day, DIA-NN Enterprise 2.6.1 consistently reported between 9,800 and 10,112 protein identifications.

> "Evaluating our separation methods across fast gradients and varied sample matrices demands computational tools that maximise quantitative depth when analysing complex data. DIA-NN Enterprise delivers the performance we require to characterise our most demanding chromatographic workflows," said Dr Jarrod Sandow, Chief Product Officer at IonOpticks.

> "To ensure DIA-NN remains at the forefront of proteomics data analysis, we optimise our algorithms using the highest-quality chromatography data available. The robustness, sharp peaks, and electrospray stability that IonOpticks columns sustain across long injection series provide exactly the reference data we require," said Justus Grossmann, Founder and Managing Director of Aptila.

About IonOpticks

IonOpticks is a global leader in high-performance chromatography solutions, empowering the research community to push the boundaries of LC-MS and advanced proteomics. By supporting greater sensitivity, reliability, and reproducibility in LC-MS workflows, IonOpticks enables scientists and clinicians to uncover more insights from every sample. These innovations drive discovery across diverse applications, including drug development, phosphoproteomics, shotgun proteomics, and clinical research. Trusted by leading laboratories worldwide, IonOpticks combines advanced technology with a commitment to progressing biological and medical science. For more information about IonOpticks' products and research impact, please visit www.ionopticks.com.

About Aptila

Aptila Biotech, based in Berlin, develops DIA-NN, software for the analysis of mass spectrometry–based proteomics data. By advancing the limits of identification and quantitative accuracy, DIA-NN has been a driving force behind the current adoption of data-independent acquisition proteomics in pharmaceutical, biotechnology, and academic research. DIA-NN Enterprise is the full-functionality edition for industry and academia. A separate edition with limited functionality is available for non-profit academic research. Further information is available at www.aptila.bio.