

EVOSEP

SPRING WEBINAR SERIES

Unleashing the power of DIA combined with short gradients using the Evosep One

May 27, 2021 | 4:00 PM CET / 10:00 AM EDT / 7:00 AM PDT

In this webinar, we will discuss the practical features of DIA to generate record high IDs per minute with the Evosep One.

PROGRAM

A practical guide to high-throughput data-independent acquisition

Talk by Florian Meier, Junior Professor at Friedrich Schiller University Jena



Data-independent acquisition (DIA) is an increasingly attractive strategy for high-throughput mass spectrometry-based proteomics. Florian will give an introduction to state-of-the-art acquisition methods such as very fast Orbitrap mass analysis and diaPASEF. Key method parameters will be highlighted and their optimization for short gradients illustrated.

Beyond 5000 proteins in 4.8 minutes from low sample amounts

Talk by Vadim Demichev, Post Doc at the Francis Crick Institute



There is an increasing need for fast methods in proteomics. With the introduction of DIA-NN, a neural network-based software suite capable of processing complex DIA proteomic data, Vadim demonstrates the quantification of more than 5000 proteins from just 200ng of a HeLa sample analysed with the 200 samples/day method on an Evosep One coupled to a timsTOF Pro.

To learn more about Evosep One and register for the webinar, follow the link



www.evosep.com/webinars