

Mass spectrometry

DIA Publications

Featuring Thermo Scientific Orbitrap Exploris 480 Mass Spectrometers

A compact quadrupole-orbitrap mass spectrometer with FAIMS interface improves proteome coverage in short LC gradients

Dorte B. Bekker-Jensen, Ana Martínez-Val, Sophia Steigerwald, Patrick Rütther, Kyle L. Fort, Tabiwang N. Arrey, Alexander Harder, Alexander Makarov, Jesper V. Olsen

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The global phosphorylation landscape of SARS-CoV-2 infection

Mehdi Bouhaddou, Danish Memon, Bjoern Meyer, Kris M. White, Veronica V. Rezelj, Miguel Correa Marrero, Benjamin J. Polacco, James E. Melnyk, Svenja Ulferts, Robyn M. Kaake, Jyoti Batra, Alicia L. Richards, Erica Stevenson, David E. Gordon, Ajda Rojc, Kirsten Obernier, Jacqueline M. Fabius, Margaret Soucheray, Lisa Miorin, Elena Moreno, Cassandra Koh, Quang Dinh Tran, Alexandra Hardy, Remy Robinot, Thomas Vallet, Benjamin E. Nilsson-Payant, Claudia Hernandez-Armenta, Alistair Dunham, Sebastian Weigang, Julian Knerr, Maya Modak, Diego Quintero, Yuan Zhou, Aurelien Dugourd, Alberto Valdeolivas, Trupti Patil, Qiongyu Li, Ruth Huttenhain, Merve Cakir, Monita Muralidharan,

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A simple method for in-depth proteome analysis of mammalian cell culture conditioned media containing fetal bovine serum

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Temporal proteomic and lipidomic profiles of cerulein-induced acute pancreatitis reveal novel insights for metabolic alterations in the disease pathogenesis

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BIRCH: an automated workflow for evaluation, correction, and visualization of batch effect in bottom-up mass spectrometry-based proteomics data

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