Florian Meier

List of Publications by Year
in descending order

26 papers	3,540 citations	361045 20 h-index	552369 26 g-index
39 all docs	39 docs citations	39 times ranked	4439 citing authors

#	Article	IF	Citations
1	Online Parallel Accumulation–Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Molecular and Cellular Proteomics, 2018, 17, 2534-2545.	2.5	602
2	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
3	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. Nature Methods, 2018, 15, 440-448.	9.0	303
4	Parallel Accumulation–Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. Journal of Proteome Research, 2015, 14, 5378-5387.	1.8	281
5	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. Molecular and Cellular Proteomics, 2018, 17, 2284-2296.	2.5	270
6	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	3.2	261
7	Region and cell-type resolved quantitative proteomic map of the human heart. Nature Communications, 2017, 8, 1469.	5.8	213
8	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. Molecular and Cellular Proteomics, 2015, 14, 2014-2029.	2.5	150
9	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. Nature Communications, 2020, 11, 331.	5.8	138
10	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. Molecular and Cellular Proteomics, 2019, 18, 982a-994.	2.5	91
11	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	15.2	91
12	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	9.0	88
13	Trapped Ion Mobility Spectrometry and Parallel Accumulation–Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	2.5	84
14	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	5.8	81
15	Plasma Proteome Profiling Reveals Dynamics of Inflammatory and Lipid Homeostasis Markers after Roux-En-Y Gastric Bypass Surgery. Cell Systems, 2018, 7, 601-612.e3.	2.9	80
16	International Ring Trial of a High Resolution Targeted Metabolomics and Lipidomics Platform for Serum and Plasma Analysis. Analytical Chemistry, 2019, 91, 14407-14416.	3.2	66
17	On the isobaric space of 25-hydroxyvitamin D in human serum: potential for interferences in liquid chromatography/tandem mass spectrometry, systematic errors and accuracy issues. Rapid Communications in Mass Spectrometry, 2015, 29, 1-9.	0.7	43
18	Novel Galvanic Nanostructures of Ag and Pd for Efficient Laser Desorption/Ionization of Low Molecular Weight Compounds. Journal of the American Society for Mass Spectrometry, 2014, 25, 841-851.	1.2	38

#	Article	IF	Citations
19	A simple micro-extraction plate assay for automated LC-MS/MS analysis of human serum 25-hydroxyvitamin D levels. Journal of Mass Spectrometry, 2015, 50, 275-279.	0.7	24
20	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
21	Silver dopants for targeted and untargeted direct analysis of unsaturated lipids via infrared matrixâ€assisted laser desorption electrospray ionization (IRâ€MALDESI). Rapid Communications in Mass Spectrometry, 2014, 28, 2461-2470.	0.7	21
22	TransOmic analysis of forebrain sections in Sp2 conditional knockout embryonic mice using IR-MALDESI imaging of lipids and LC-MS/MS label-free proteomics. Analytical and Bioanalytical Chemistry, 2016, 408, 3453-3474.	1.9	14
23	Tandem Trapped Ion Mobility Spectrometry/Mass Spectrometry (tTIMS/MS) Reveals Sequence-Specific Determinants of Top-Down Protein Fragment Ion Cross Sections. Analytical Chemistry, 2022, 94, 8146-8155.	3.2	11
24	Defining NASH from a Multi-Omics Systems Biology Perspective. Journal of Clinical Medicine, 2021, 10, 4673.	1.0	9
25	High-Throughput Mass Spectrometry-Based Proteomics with dia-PASEF. Methods in Molecular Biology, 2022, , 15-27.	0.4	7
26	Reply to â€œQuality control requirements for the correct annotation of lipidomics dataâ€. Nature Communications, 2021, 12, 4772.	5.8	2