

Florian Meier

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,540
citations

361296

20
h-index

552653

26
g-index

39
all docs

39
docs citations

39
times ranked

4439
citing authors

#	ARTICLE	IF	CITATIONS
1	Online Parallel Accumulationâ€“Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	2.5	602
2	diaPASEF: parallel accumulationâ€“serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 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. <i>Nature Methods</i> , 2018, 15, 440-448.	9.0	303
4	Parallel Accumulationâ€“Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. <i>Journal of Proteome Research</i> , 2015, 14, 5378-5387.	1.8	281
5	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2284-2296.	2.5	270
6	Ultraâ€“high sensitivity mass spectrometry quantifies singleâ€“cell proteome changes upon perturbation. <i>Molecular Systems Biology</i> , 2022, 18, e10798.	3.2	261
7	Region and cell-type resolved quantitative proteomic map of the human heart. <i>Nature Communications</i> , 2017, 8, 1469.	5.8	213
8	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2014-2029.	2.5	150
9	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020, 11, 331.	5.8	138
10	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 982a-994.	2.5	91
11	Noninvasive proteomic biomarkers for alcohol-related liver disease. <i>Nature Medicine</i> , 2022, 28, 1277-1287.	15.2	91
12	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. <i>Nature Methods</i> , 2018, 15, 527-530.	9.0	88
13	Trapped Ion Mobility Spectrometry and Parallel Accumulationâ€“Serial Fragmentation in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100138.	2.5	84
14	Deep learning the collisional cross sections of the peptide universe from a million experimental values. <i>Nature Communications</i> , 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. <i>Cell Systems</i> , 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. <i>Analytical Chemistry</i> , 2019, 91, 14407-14416.	3.2	66
17	On the isobaric space of 25â€“hydroxyvitamin D in human serum: potential for interferences in liquid chromatography/tandem mass spectrometry, systematic errors and accuracy issues. <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 841-851.	1.2	38

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19	A simple micro-extraction plate assay for automated LC-MS/MS analysis of human serum 25-hydroxyvitamin D levels. <i>Journal of Mass Spectrometry</i> , 2015, 50, 275-279.	0.7	24
20	Dynamic human liver proteome atlas reveals functional insights into disease pathways. <i>Molecular Systems Biology</i> , 2022, 18, e10947.	3.2	22
21	Silver dopants for targeted and untargeted direct analysis of unsaturated lipids via infrared matrix-assisted laser desorption electrospray ionization (IR-MALDESI). <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Analytical and Bioanalytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 2022, 94, 8146-8155.	3.2	11
24	Defining NASH from a Multi-Omics Systems Biology Perspective. <i>Journal of Clinical Medicine</i> , 2021, 10, 4673.	1.0	9
25	High-Throughput Mass Spectrometry-Based Proteomics with dia-PASEF. <i>Methods in Molecular Biology</i> , 2022, , 15-27.	0.4	7
26	Reply to "Quality control requirements for the correct annotation of lipidomics data". <i>Nature Communications</i> , 2021, 12, 4772.	5.8	2