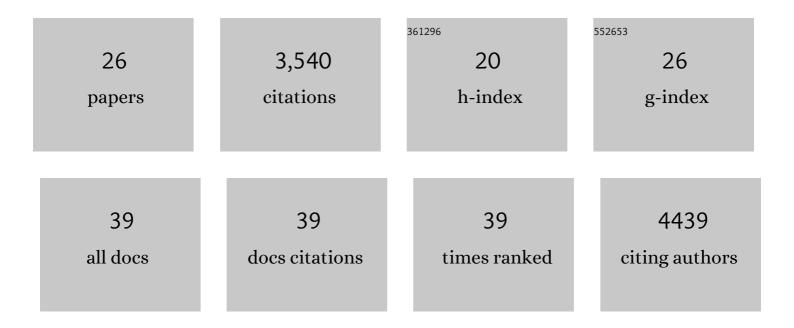
Florian Meier

List of Publications by Year in descending order

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FLODIAN MELED

#	Article	IF	CITATIONS
1	Ultraâ€high sensitivity mass spectrometry quantifies singleâ€cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	3.2	261
2	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
3	High-Throughput Mass Spectrometry-Based Proteomics with dia-PASEF. Methods in Molecular Biology, 2022, , 15-27.	0.4	7
4	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
5	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	15.2	91
6	Trapped Ion Mobility Spectrometry and Parallel Accumulation–Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	2.5	84
7	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	5.8	81
8	Reply to $\hat{a} \in \mathfrak{A}$ Quality control requirements for the correct annotation of lipidomics data $\hat{a} \in \mathfrak{A}$ Nature Communications, 2021, 12, 4772.	5.8	2
9	Defining NASH from a Multi-Omics Systems Biology Perspective. Journal of Clinical Medicine, 2021, 10, 4673.	1.0	9
10	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
11	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. Nature Communications, 2020, 11, 331.	5.8	138
12	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
13	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. Molecular and Cellular Proteomics, 2019, 18, 982a-994.	2.5	91
14	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
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	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
17	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
18	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	9.0	88

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#	Article	IF	CITATIONS
19	Region and cell-type resolved quantitative proteomic map of the human heart. Nature Communications, 2017, 8, 1469.	5.8	213
20	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
21	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
22	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
23	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
24	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. Rapid Communications in Mass Spectrometry, 2015, 29, 1-9.	0.7	43
25	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
26	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