Nicolai Bache

List of Publications by Year
in descending order

19	2,118	567281 15	839539 18
papers	citations	h-index	g-index

23	23	23	2651
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Online Parallel Accumulationâ€“Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Molecular and Cellular Proteomics, 2018, 17, 2534-2545.	3.8	602
2	diaPASEF: parallel accumulationâ€“serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	19.0	387
3	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. Molecular and Cellular Proteomics, 2018, 17, 2284-2296.	3.8	270
4	Ultraâ€high sensitivity mass spectrometry quantifies singleâ€cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	7.2	261
5	Dynamin I phosphorylation by GSK3 controls activity-dependent bulk endocytosis of synaptic vesicles. Nature Neuroscience, 2010, 13, 845-851.	14.8	156
6	Evosep One Enables Robust Deep Proteome Coverage Using Tandem Mass Tags while Significantly Reducing Instrument Time. Journal of Proteome Research, 2019, 18, 2346-2353.	3.7	51
7	The in Vivo Phosphorylation Sites of Rat Brain Dynamin I*. Journal of Biological Chemistry, 2007, 282, 14695-14707.	3.4	45
8	Proteomic analysis of dayâ€“night variations in protein levels in the rat pineal gland. Proteomics, 2007, 7, 2009-2018.	2.2	37
9	Collisional Activation by MALDI Tandem Time-of-flight Mass Spectrometry Induces Intramolecular Migration of Amide Hydrogens in Protonated Peptides. Molecular and Cellular Proteomics, 2005, 4, 1910-1919.	3.8	36
10	Gas-Phase Fragmentation of Peptides by MALDI in-Source Decay with Limited Amide Hydrogen (¹H/²H) Scrambling. Analytical Chemistry, 2008, 80, 6431-6435.	6.5	35
11	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. Analytical Chemistry, 2011, 83, 8859-8862.	6.5	35
12	Targeted mass spectrometry analysis of the proteins IGF1, IGF2, IBP2, IBP3 and A2GL by blood protein precipitation. Journal of Proteomics, 2015, 113, 29-37.	2.4	28
13	Hydrogen atom scrambling in selectively labeled anionic peptides upon collisional activation by MALDI tandem time-of-flight mass spectrometry. Journal of the American Society for Mass Spectrometry, 2008, 19, 1719-1725.	2.8	27
14	The in Vivo Phosphorylation Sites in Multiple Isoforms of Amphiphysin I from Rat Brain Nerve Terminals. Molecular and Cellular Proteomics, 2008, 7, 1146-1161.	3.8	25
15	Integrated Solid-Phase Extractionâ€“Capillary Liquid Chromatography (speLC) Interfaced to ESIâ€“MS/MS for Fast Characterization and Quantification of Protein and Proteomes. Journal of Proteome Research, 2014, 13, 6169-6175.	3.7	19
16	Proteomics of the photoneuroendocrine circadian system of the brain. Mass Spectrometry Reviews, 2010, 29, 313-325.	5.4	7
17	Rapid Analyses of Proteomes and Interactomes Using an Integrated Solid-Phase Extractionâ€“Liquid Chromatographyâ€“MS/MS System. Journal of Proteome Research, 2015, 14, 977-985.	3.7	6
18	Development of a Standardized Microflow LC Gradient to Enable Sensitive and Long-Term Detection of Synthetic Anabolic-Androgenic Steroids for High-Throughput Doping Controls. Analytical Chemistry, 2021, 93, 15590-15596.	6.5	5

#	Article	IF	Citations
19	Affinity Proteomics for Interactome and Phosphoproteome Screening in Synaptosomes. Neuromethods, 2018, , 165-191.	0.3	0