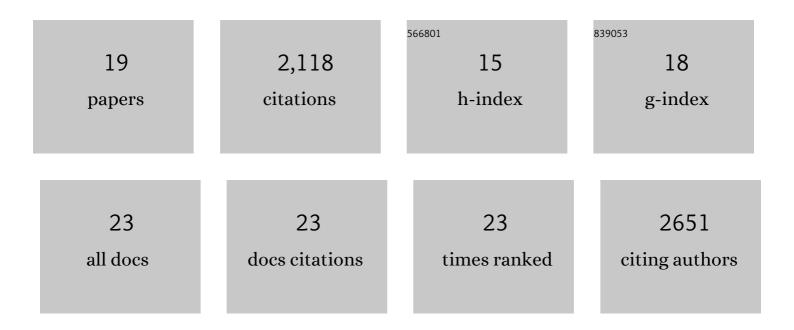
## Nicolai Bache

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11837701/publications.pdf Version: 2024-02-01



#	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	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.	3.2	5
3	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
4	Evosep One Enables Robust Deep Proteome Coverage Using Tandem Mass Tags while Significantly Reducing Instrument Time. Journal of Proteome Research, 2019, 18, 2346-2353.	1.8	51
5	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
6	Affinity Proteomics for Interactome and Phosphoproteome Screening in Synaptosomes. Neuromethods, 2018, , 165-191.	0.2	0
7	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
8	Rapid Analyses of Proteomes and Interactomes Using an Integrated Solid-Phase Extraction–Liquid Chromatography–MS/MS System. Journal of Proteome Research, 2015, 14, 977-985.	1.8	6
9	Targeted mass spectrometry analysis of the proteins IGF1, IGF2, IBP2, IBP3 and A2GL by blood protein precipitation. Journal of Proteomics, 2015, 113, 29-37.	1.2	28
10	Integrated Solid-Phase Extraction–Capillary Liquid Chromatography (speLC) Interfaced to ESI–MS/MS for Fast Characterization and Quantification of Protein and Proteomes. Journal of Proteome Research, 2014, 13, 6169-6175.	1.8	19
11	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. Analytical Chemistry, 2011, 83, 8859-8862.	3.2	35
12	Proteomics of the photoneuroendocrine circadian system of the brain. Mass Spectrometry Reviews, 2010, 29, 313-325.	2.8	7
13	Dynamin I phosphorylation by GSK3 controls activity-dependent bulk endocytosis of synaptic vesicles. Nature Neuroscience, 2010, 13, 845-851.	7.1	156
14	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.	1.2	27
15	Gas-Phase Fragmentation of Peptides by MALDI in-Source Decay with Limited Amide Hydrogen ( <sup>1</sup> H/ <sup>2</sup> H) Scrambling. Analytical Chemistry, 2008, 80, 6431-6435.	3.2	35
16	The in Vivo Phosphorylation Sites in Multiple Isoforms of Amphiphysin I from Rat Brain Nerve Terminals. Molecular and Cellular Proteomics, 2008, 7, 1146-1161.	2.5	25
17	The in Vivo Phosphorylation Sites of Rat Brain Dynamin I*. Journal of Biological Chemistry, 2007, 282, 14695-14707.	1.6	45
18	Proteomic analysis of day–night variations in protein levels in the rat pineal gland. Proteomics, 2007, 7, 2009-2018.	1.3	37

#	Article	IF	CITATIONS
19	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.	2.5	36