

Nicolai Bache

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11837701/publications.pdf>

Version: 2024-02-01

19
papers

2,118
citations

567281

15
h-index

839539

18
g-index

23
all docs

23
docs citations

23
times ranked

2651
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation. <i>Molecular Systems Biology</i> , 2022, 18, e10798.	7.2	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. <i>Analytical Chemistry</i> , 2021, 93, 15590-15596.	6.5	5
3	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	19.0	387
4	Evosep One Enables Robust Deep Proteome Coverage Using Tandem Mass Tags while Significantly Reducing Instrument Time. <i>Journal of Proteome Research</i> , 2019, 18, 2346-2353.	3.7	51
5	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	3.8	602
6	Affinity Proteomics for Interactome and Phosphoproteome Screening in Synaptosomes. <i>NeuroMethods</i> , 2018, , 165-191.	0.3	0
7	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.	3.8	270
8	Rapid Analyses of Proteomes and Interactomes Using an Integrated Solid-Phase Extraction-Liquid Chromatography-MS/MS System. <i>Journal of Proteome Research</i> , 2015, 14, 977-985.	3.7	6
9	Targeted mass spectrometry analysis of the proteins IGF1, IGF2, IBP2, IBP3 and A2GL by blood protein precipitation. <i>Journal of Proteomics</i> , 2015, 113, 29-37.	2.4	28
10	Integrated Solid-Phase Extraction-Capillary Liquid Chromatography (speLC) Interfaced to ESI-MS/MS for Fast Characterization and Quantification of Protein and Proteomes. <i>Journal of Proteome Research</i> , 2014, 13, 6169-6175.	3.7	19
11	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. <i>Analytical Chemistry</i> , 2011, 83, 8859-8862.	6.5	35
12	Proteomics of the photoneuroendocrine circadian system of the brain. <i>Mass Spectrometry Reviews</i> , 2010, 29, 313-325.	5.4	7
13	Dynamin I phosphorylation by GSK3 controls activity-dependent bulk endocytosis of synaptic vesicles. <i>Nature Neuroscience</i> , 2010, 13, 845-851.	14.8	156
14	Hydrogen atom scrambling in selectively labeled anionic peptides upon collisional activation by MALDI tandem time-of-flight mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1719-1725.	2.8	27
15	Gas-Phase Fragmentation of Peptides by MALDI In-Source Decay with Limited Amide Hydrogen (¹ H/ ² H) Scrambling. <i>Analytical Chemistry</i> , 2008, 80, 6431-6435.	6.5	35
16	The in Vivo Phosphorylation Sites in Multiple Isoforms of Amphiphysin I from Rat Brain Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1146-1161.	3.8	25
17	The in Vivo Phosphorylation Sites of Rat Brain Dynamin I*. <i>Journal of Biological Chemistry</i> , 2007, 282, 14695-14707.	3.4	45
18	Proteomic analysis of day-night variations in protein levels in the rat pineal gland. <i>Proteomics</i> , 2007, 7, 2009-2018.	2.2	37

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19	Collisional Activation by MALDI Tandem Time-of-flight Mass Spectrometry Induces Intramolecular Migration of Amide Hydrogens in Protonated Peptides. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1910-1919.	3.8	36