## Nikolai Slavov

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8155466/publications.pdf

Version: 2024-02-01

45 papers 8,067 citations

201385 27 h-index 264894 42 g-index

72 all docs 72 docs citations

times ranked

72

17474 citing authors

#	Article	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
2	SCoPE-MS: mass spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation. Genome Biology, 2018, 19, 161.	3.8	574
3	Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity using SCoPE2. Genome Biology, 2021, 22, 50.	3.8	298
4	De Novo Reconstruction of Adipose Tissue Transcriptomes Reveals Long Non-coding RNA Regulators of Brown Adipocyte Development. Cell Metabolism, 2015, 21, 764-776.	7.2	201
5	Differential Stoichiometry among Core Ribosomal Proteins. Cell Reports, 2015, 13, 865-873.	2.9	178
6	Post-transcriptional regulation across human tissues. PLoS Computational Biology, 2017, 13, e1005535.	1.5	171
7	Unpicking the proteome in single cells. Science, 2020, 367, 512-513.	6.0	125
8	Coupling among growth rate response, metabolic cycle, and cell division cycle in yeast. Molecular Biology of the Cell, 2011, 22, 1997-2009.	0.9	108
9	Multiplexed single-cell proteomics using SCoPE2. Nature Protocols, 2021, 16, 5398-5425.	5.5	108
10	Transformative Opportunities for Single-Cell Proteomics. Journal of Proteome Research, 2018, 17, 2565-2571.	1.8	107
11	Single-cellÂprotein analysis by mass spectrometry. Current Opinion in Chemical Biology, 2021, 60, 1-9.	2.8	106
12	Increasing the throughput of sensitive proteomics by plexDIA. Nature Biotechnology, 2023, 41, 50-59.	9.4	92
13	Metabolic cycling in single yeast cells from unsynchronized steady-state populations limited on glucose or phosphate. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6946-6951.	3.3	89
14	Global characterization of macrophage polarization mechanisms and identification of M2-type polarization inhibitors. Cell Reports, 2021, 37, 109955.	2.9	89
15	Constant Growth Rate Can Be Supported by Decreasing Energy Flux and Increasing Aerobic Glycolysis. Cell Reports, 2014, 7, 705-714.	2.9	85
16	Metabolic cycling without cell division cycling in respiring yeast. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19090-19095.	3.3	74
17	Single cell protein analysis for systems biology. Essays in Biochemistry, 2018, 62, 595-605.	2.1	73
18	Ribosome Stoichiometry: From Form to Function. Trends in Biochemical Sciences, 2019, 44, 95-109.	3.7	71

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19	Kinase Activities of RIPK1 and RIPK3 Can Direct IFN-Î <sup>2</sup> Synthesis Induced by Lipopolysaccharide. Journal of Immunology, 2017, 198, 4435-4447.	0.4	51
20	DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. Journal of Proteome Research, 2019, 18, 2493-2500.	1.8	51
21	DART-ID increases single-cell proteome coverage. PLoS Computational Biology, 2019, 15, e1007082.	1.5	49
22	A conserved cell growth cycle can account for the environmental stress responses of divergent eukaryotes. Molecular Biology of the Cell, 2012, 23, 1986-1997.	0.9	43
23	Driving Single Cell Proteomics Forward with Innovation. Journal of Proteome Research, 2021, 20, 4915-4918.	1.8	43
24	Correlation signature of the macroscopic states of the gene regulatory network in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4079-4084.	3.3	42
25	Optimizing Accuracy and Depth of Protein Quantification in Experiments Using Isobaric Carriers. Journal of Proteome Research, 2021, 20, 880-887.	1.8	40
26	Decoupling nutrient signaling from growth rate causes aerobic glycolysis and deregulation of cell size and gene expression. Molecular Biology of the Cell, 2013, 24, 157-168.	0.9	37
27	Scaling Up Single-Cell Proteomics. Molecular and Cellular Proteomics, 2022, 21, 100179.	2.5	37
28	Comparative Proteomic Profiling of Divergent Phenotypes for Water Holding Capacity across the Post Mortem Ageing Period in Porcine Muscle Exudate. PLoS ONE, 2016, 11, e0150605.	1.1	34
29	Increasing proteomics throughput. Nature Biotechnology, 2021, 39, 809-810.	9.4	27
30	Calmodulin Transduces Ca <sup>2+</sup> Oscillations into Differential Regulation of Its Target Proteins. ACS Chemical Neuroscience, 2013, 4, 601-612.	1.7	18
31	Quantifying Homologous Proteins and Proteoforms. Molecular and Cellular Proteomics, 2019, 18, 162-168.	2.5	17
32	Learning from natural variation across the proteomes of single cells. PLoS Biology, 2022, 20, e3001512.	2.6	17
33	New Views of Old Proteins: Clarifying the Enigmatic Proteome. Molecular and Cellular Proteomics, 2022, 21, 100254.	2.5	16
34	Counting protein molecules for single-cell proteomics. Cell, 2022, 185, 232-234.	13.5	15
35	Approaches for Studying Ribosome Specialization. Trends in Biochemical Sciences, 2019, 44, 478-479.	3.7	11
36	Analyzing Ribosome Remodeling in Health and Disease. Proteomics, 2020, 20, e2000039.	1.3	10

3

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37	Measuring Protein Shapes in Living Cells. Journal of Proteome Research, 2021, 20, 3017-3017.	1.8	7
38	Multi-Class Biclustering and Classification Based on Modeling of Gene Regulatory Networks. , 0, , .		6
39	Voices in methods development. Nature Methods, 2019, 16, 945-951.	9.0	5
40	Making the most of peer review. ELife, 2015, 4, .	2.8	5
41	Voices of biotech research. Nature Biotechnology, 2021, 39, 281-286.	9.4	3
42	Comprehensive Identification of Regulatory Protein Networks. Journal of Proteome Research, 2021, 20, 4913-4914.	1.8	1
43	Beyond Protein Sequence: Protein Isomerization in Alzheimer's Disease. Journal of Proteome Research, 2022, 21, 299-300.	1.8	1
44	How to Regulate a Gene: To Repress or to Activate?. Molecular Cell, 2012, 46, 551-552.	4.5	0
45	DARTâ€ID Increases Singleâ€Cell Proteome Coverage. FASEB Journal, 2019, 33, 475.2.	0.2	0