Nagarjuna Nagaraj

List of Publications by Year
in descending order

37 papers	19,353 citations	159358 30 h-index	344852 36 g-index
39 all docs	39 docs citations	39 times ranked	33437 citing authors

#	ARTICLE	IF	CITATIONS
1	Universal sample preparation method for proteome analysis. Nature Methods, 2009, 6, 359-362.	9.0	6,678
2	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. Molecular and Cellular Proteomics, 2014, 13, 2513-2526.	2.5	4,178
3	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. Nature Methods, 2014, 11, 319-324.	9.0	1,447
4	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. Cell, 2015, 163, 712-723.	13.5	1,132
5	Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 2011, 7, 548.	3.2	878
6	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. Nature Protocols, 2009, 4, 698-705.	5.5	769
7	Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer. Molecular and Cellular Proteomics, 2011, 10, M111.011015.	2.5	701
8	System-wide Perturbation Analysis with Nearly Complete Coverage of the Yeast Proteome by Single-shot Ultra HPLC Runs on a Bench Top Orbitrap. Molecular and Cellular Proteomics, 2012, 11, M111.013722.	2.5	350
9	The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. Molecular Cell, 2013, 49, 583-590.	4.5	329
10	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. Journal of Proteome Research, 2010, 9, 3280-3289.	1.8	253
11	Global Proteome Turnover Analyses of the Yeasts S.Âcerevisiae and S.Âpombe. Cell Reports, 2014, 9, 1959-1965.	2.9	247
12	Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. Molecular and Cellular Proteomics, 2015, 14, 841-853.	2.5	234
13	Quantitative Analysis of the Intra- and Inter-Individual Variability of the Normal Urinary Proteome. Journal of Proteome Research, 2011, 10, 637-645.	1.8	215
14	Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. Cell Reports, 2017, 19, 2396-2409.	2.9	213
15	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. Molecular and Cellular Proteomics, 2013, 12, 1709-1722.	2.5	204
16	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. Science, 2015, 348, 1253671.	6.0	183
17	Single muscle fiber proteomics reveals unexpected mitochondrial specialization. EMBO Reports, 2015, 16, 387-395.	2.0	163
18	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2010, 9, 6786-6794.	1.8	149

#	Article	IF	Citations
19	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. Cell Metabolism, 2014, 20, 1076-1087.	7.2	143
20	Large-scale phosphosite quantification in tissues by a spike-in SILAC method. Nature Methods, 2011, 8, 655-658.	9.0	141
21	MaxDIA enables library-based and library-free data-independent acquisition proteomics. Nature Biotechnology, 2021, 39, 1563-1573.	9.4	115
22	Phosphorylation of TET Proteins Is Regulated via O-GlcNAcylation by the O-Linked N-Acetylglucosamine Transferase (OGT). Journal of Biological Chemistry, 2015, 290, 4801-4812.	1.6	102
23	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	3.2	100
24	Detergent-Based but Gel-Free Method Allows Identification of Several Hundred Membrane Proteins in Single LC-MS Runs. Journal of Proteome Research, 2008, 7, 5028-5032.	1.8	77
25	Phosphoproteomics analysis of a clinical Mycobacterium tuberculosis Beijing isolate: expanding the mycobacterial phosphoproteome catalog. Frontiers in Microbiology, 2015, 6, 6.	1.5	65
26	Parasite–induced <scp>ER</scp> stress response in hepatocytes facilitates <i>Plasmodium</i> liver stage infection. EMBO Reports, 2015, 16, 955-964.	2.0	46
27	High Performance Computational Analysis of Large-scale Proteome Data Sets to Assess Incremental Contribution to Coverage of the Human Genome. Journal of Proteome Research, 2013, 12, 2858-2868.	1.8	43
28	A proteomic atlas of insulin signalling reveals tissue–specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	3.2	42
29	Identification of signal peptide features for substrate specificity in human Sec62/Sec63–dependent ER protein import. FEBS Journal, 2020, 287, 4612-4640.	2.2	40
30	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF-β. Science Signaling, 2014, 7, rs5.	1.6	39
31	Signatures of muscle disuse in spaceflight and bed rest revealed by single muscle fiber proteomics. , 2022, 1, .		22
32	Tissue-specific modulation of gene expression in response to lowered insulin signalling in Drosophila. ELife, 2021, 10, .	2.8	12
33	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2012, 11, 3506-3508.	1.8	11
34	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	10
35	Calsequestrins in skeletal and cardiac muscle from adult Danio rerio. Journal of Muscle Research and Cell Motility, 2016, 37, 27-39.	0.9	8
36	Loss of the psychiatric risk factor SLC6A15 is associated with increased metabolic functions in primary hippocampal neurons. European Journal of Neuroscience, 2021, 53, 390-401.	1.2	8

#	Article	IF	Citations
37	PEAK1 Y635 phosphorylation regulates cell migration through association with Tensin3 and integrins. Journal of Cell Biology, 2022, 221, .	2.3	5