

Yue Chen

List of Publications by Year in descending order

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41
papers

7,075
citations

331670

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docs citations

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times ranked

7822
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative Proteome and Transcriptome Dynamics Analysis Reveals Iron Deficiency Response Networks and Signature in Neuronal Cells. <i>Molecules</i> , 2022, 27, 484.	3.8	2
2	UbE3-APA: a bioinformatic strategy to elucidate ubiquitin E3 ligase activities in quantitative proteomics study. <i>Bioinformatics</i> , 2022, 38, 2211-2218.	4.1	1
3	Iron Deficiency Reprograms Phosphorylation Signaling and Reduces O-GlcNAc Pathways in Neuronal Cells. <i>Nutrients</i> , 2021, 13, 179.	4.1	9
4	Label-Free Interactome Analysis Revealed an Essential Role of CUL3-KEAP1 Complex in Mediating the Ubiquitination and Degradation of PHD2. <i>Journal of Proteome Research</i> , 2020, 19, 260-268.	3.7	4
5	Proteome dynamics analysis identifies functional roles of SDE2 and hypoxia in DNA damage response in prostate cancer cells. <i>NAR Cancer</i> , 2020, 2, zcaa010.	3.1	7
6	HDAC6 Regulates Radiosensitivity of Non-Small Cell Lung Cancer by Promoting Degradation of Chk1. <i>Cells</i> , 2020, 9, 2237.	4.1	12
7	Histone Carbonylation Is a Redox-Regulated Epigenomic Mark That Accumulates with Obesity and Aging. <i>Antioxidants</i> , 2020, 9, 1210.	5.1	14
8	Fluorescent Detection of <i>O</i> -GlcNAc via Tandem Glycan Labeling. <i>Bioconjugate Chemistry</i> , 2020, 31, 2098-2102.	3.6	7
9	Inhalation exposure to cigarette smoke and inflammatory agents induces epigenetic changes in the lung. <i>Scientific Reports</i> , 2020, 10, 11290.	3.3	19
10	Herpes simplex virus blocks host transcription termination via the bimodal activities of ICP27. <i>Nature Communications</i> , 2020, 11, 293.	12.8	58
11	Site-specific determination of lysine acetylation stoichiometries on the proteome-scale. <i>Methods in Enzymology</i> , 2019, 626, 115-132.	1.0	2
12	mTOR-regulated U2af1 tandem exon splicing specifies transcriptome features for translational control. <i>Nucleic Acids Research</i> , 2019, 47, 10373-10387.	14.5	13
13	Targeted and Interactome Proteomics Revealed the Role of PHD2 in Regulating BRD4 Proline Hydroxylation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1772-1781.	3.8	18
14	A Quantitative Chemical Proteomics Approach for Site-specific Stoichiometry Analysis of Ubiquitination. <i>Angewandte Chemie</i> , 2019, 131, 547-551.	2.0	4
15	A Quantitative Chemical Proteomics Approach for Site-specific Stoichiometry Analysis of Ubiquitination. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 537-541.	13.8	17
16	Quantifying Ubiquitination Signaling with a Chemical Proteomics Strategy. <i>FASEB Journal</i> , 2019, 33, lb245.	0.5	0
17	Mitochondrial Oxidative Stress And Adipocyte Protein Carbonylation. <i>FASEB Journal</i> , 2019, 33, 651.9.	0.5	0
18	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	28.9	123

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19	Characterization and metabolic synthetic lethal testing in a new model of SDH-loss familial pheochromocytoma and paraganglioma. <i>Oncotarget</i> , 2018, 9, 6109-6127.	1.8	13
20	Chromatin Succinylation Correlates with Active Gene Expression and Is Perturbed by Defective TCA Cycle Metabolism. <i>IScience</i> , 2018, 2, 63-75.	4.1	98
21	Obesity-induced protein carbonylation in murine adipose tissue regulates the DNA-binding domain of nuclear zinc finger proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 13464-13476.	3.4	15
22	NRF2 Is a Major Target of ARF in p53-Independent Tumor Suppression. <i>Molecular Cell</i> , 2017, 68, 224-232.e4.	9.7	219
23	The histone H3.3K36M mutation reprograms the epigenome of chondroblastomas. <i>Science</i> , 2016, 352, 1344-1348.	12.6	211
24	Site-Specific Identification of Lysine Acetylation Stoichiometries in Mammalian Cells. <i>Journal of Proteome Research</i> , 2016, 15, 1103-1113.	3.7	41
25	Quantitative Analysis of the Sirt5-Regulated Lysine Succinylation Proteome in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2016, 1410, 23-37.	0.9	12
26	Proteomic analysis reveals diverse proline hydroxylation-mediated oxygen-sensing cellular pathways in cancer cells. <i>Oncotarget</i> , 2016, 7, 79154-79169.	1.8	26
27	Lysine Glutarylation Is a Protein Posttranslational Modification Regulated by SIRT5. <i>Cell Metabolism</i> , 2014, 19, 605-617.	16.2	647
28	Lysine 2-hydroxyisobutyrylation is a widely distributed active histone mark. <i>Nature Chemical Biology</i> , 2014, 10, 365-370.	8.0	368
29	Identification of Lysine Succinylation Substrates and the Succinylation Regulatory Enzyme CobB in <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3509-3520.	3.8	236
30	SIRT5-Mediated Lysine Desuccinylation Impacts Diverse Metabolic Pathways. <i>Molecular Cell</i> , 2013, 50, 919-930.	9.7	786
31	Quantitative Acetylome Analysis Reveals the Roles of SIRT1 in Regulating Diverse Substrates and Cellular Pathways. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1048-1062.	3.8	188
32	The First Identification of Lysine Malonylation Substrates and Its Regulatory Enzyme. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012658.	3.8	598
33	Identification of lysine succinylation as a new post-translational modification. <i>Nature Chemical Biology</i> , 2011, 7, 58-63.	8.0	698
34	PTMap—A sequence alignment software for unrestricted, accurate, and full-spectrum identification of post-translational modification sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 761-766.	7.1	94
35	Identification and Verification of Lysine Propionylation and Butyrylation in Yeast Core Histones Using PTMap Software. <i>Journal of Proteome Research</i> , 2009, 8, 900-906.	3.7	141
36	Mascot-Derived False Positive Peptide Identifications Revealed by Manual Analysis of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 3141-3147.	3.7	51

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37	Lysine Propionylation and Butyrylation Are Novel Post-translational Modifications in Histones. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 812-819.	3.8	639
38	Substrate and Functional Diversity of Lysine Acetylation Revealed by a Proteomics Survey. <i>Molecular Cell</i> , 2006, 23, 607-618.	9.7	1,372
39	High-Throughput Identification of In-Gel Digested Proteins by Rapid, Isocratic HPLC/MS/MS. <i>Analytical Chemistry</i> , 2005, 77, 8179-8184.	6.5	9
40	Tagging-via-Substrate Strategy for Probing O-GlcNAc Modified Proteins. <i>Journal of Proteome Research</i> , 2005, 4, 950-957.	3.7	133
41	Integrated Approach for Manual Evaluation of Peptides Identified by Searching Protein Sequence Databases with Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2005, 4, 998-1005.	3.7	168