Cheng Chang

List of Publications by Year
in descending order

41 papers	909 citations	430874 18 h-index	501196 28 g-index
44 all docs	44 docs citations	44 times ranked	1595 citing authors

#	Article	IF	Citations
1	Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment. Journal of Proteome Research, 2017, 16, 288-297.	3.7	95
2	A Fast Workflow for Identification and Quantification of Proteomes. Molecular and Cellular Proteomics, 2013, 12, 2370-2380.	3.8	94
3	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. Theranostics, 2019, 9, 2475-2488.	10.0	76
4	Inflammasome-Derived Exosomes Activate NF-κB Signaling in Macrophages. Journal of Proteome Research, 2017, 16, 170-178.	3.7	72
5	Systematic Analyses of the Transcriptome, Translatome, and Proteome Provide a Global View and Potential Strategy for the C-HPP. Journal of Proteome Research, 2014, 13, 38-49.	3.7	60
6	Systematic research on the pretreatment of peptides for quantitative proteomics using a C$_{18}$ microcolumn. Proteomics, 2013, 13, 2229-2237.	2.2	30
7	In-depth method assessments of differentially expressed protein detection for shotgun proteomics data with missing values. Scientific Reports, 2017, 7, 3367.	3.3	29
8	AP3: An Advanced Proteotypic Peptide Predictor for Targeted Proteomics by Incorporating Peptide Digestibility. Analytical Chemistry, 2019, 91, 8705-8711.	6.5	29
9	PepDistiller: A quality control tool to improve the sensitivity and accuracy of peptide identifications in shotgun proteomics. Proteomics, 2012, 12, 1720-1725.	2.2	25
10	PANDA-view: an easy-to-use tool for statistical analysis and visualization of quantitative proteomics data. Bioinformatics, 2018, 34, 3594-3596.	4.1	25
11	N-linked glycoproteome profiling of human serum using tandem enrichment and multiple fraction concatenation. Electrophoresis, 2013, 34, 2440-2450.	2.4	24
12	DeepDigest: Prediction of Protein Proteolytic Digestion with Deep Learning. Analytical Chemistry, 2021, 93, 6094-6103.	6.5	23
13	SILVER: an efficient tool for stable isotope labeling LC-MS data quantitative analysis with quality control methods. Bioinformatics, 2014, 30, 586-587.	4.1	22
14	Systematic Analysis of Missing Proteins Provides Clues to Help Define All of the Protein-Coding Genes on Human Chromosome 1. Journal of Proteome Research, 2014, 13, 114-125.	3.7	21
15	First Proteomic Exploration of Protein-Encoding Genes on Chromosome 1 in Human Liver, Stomach, and Colon. Journal of Proteome Research, 2013, 12, 67-80.	3.7	20
16	Salmonella Proteomic Profiling during Infection Distinguishes the Intracellular Environment of Host Cells. MSystems, 2019, 4, .	3.8	20
17	PANDA: A comprehensive and flexible tool for quantitative proteomics data analysis. Bioinformatics, 2019, 35, 898-900.	4.1	20
18	Qualitative and Quantitative Expression Status of the Human Chromosome 20 Genes in Cancer Tissues and the Representative Cell Lines. Journal of Proteome Research, 2013, 12, 151-161.	3.7	19

#	ARTICLE	IF	CITATIONS
19	Mining the human plasma proteome with three-dimensional strategies by high-resolution Quadrupole Orbitrap Mass Spectrometry. Analytica Chimica Acta, 2016, 904, 65-75.	5.4	19
20	Proteomic Delineation of the ArcA Regulon in Salmonella Typhimurium During Anaerobiosis. Molecular and Cellular Proteomics, 2018, 17, 1937-1947.	3.8	17
21	Using the entrapment sequence method as a standard to evaluate key steps of proteomics data analysis process. BMC Genomics, 2017, 18, 143.	2.8	16
22	A Comprehensive Evaluation of MS/MS Spectrum Prediction Tools for Shotgun Proteomics. Proteomics, 2020, 20, e1900345.	2.2	16
23	Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines. Journal of Proteome Research, 2014, 13, 200-211.	3.7	14
24	Proteome Atlas of Human Chromosome 8 and Its Multiple 8p Deficiencies in Tumorigenesis of the Stomach, Colon, and Liver. Journal of Proteome Research, 2013, 12, 81-88.	3.7	13
25	A Deep Learning–Based Tumor Classifier Directly Using MS Raw Data. Proteomics, 2020, 20, e1900344.	2.2	13
26	Chromosome-8-Coded Proteome of Chinese Chromosome Proteome Data Set (CCPD) 2.0 with Partial Immunohistochemical Verifications. Journal of Proteome Research, 2014, 13, 126-136.	3.7	11
27	PPICurator: A Tool for Extracting Comprehensive Protein–Protein Interaction Information. Proteomics, 2019, 19, e1800291.	2.2	11
28	Human fallopian tube proteome shows high coverage of mesenchymal stem cells associated proteins. Bioscience Reports, 2016, 36, e00297.	2.4	10
29	PPIExp: A Web-Based Platform for Integration and Visualization of Protein–Protein Interaction Data and Spatiotemporal Proteomics Data. Journal of Proteome Research, 2019, 18, 633-641.	3.7	8
30	LFAQ: Toward Unbiased Label-Free Absolute Protein Quantification by Predicting Peptide Quantitative Factors. Analytical Chemistry, 2019, 91, 1335-1343.	6.5	8
31	Quantitative and In-Depth Survey of the Isotopic Abundance Distribution Errors in Shotgun Proteomics. Analytical Chemistry, 2016, 88, 6844-6851.	6.5	7
32	Atg9-centered multi-omics integration reveals new autophagy regulators in *Saccharomyces cerevisiae*. Autophagy, 2021, 17, 4453-4476.	9.1	6
33	HPV16 E6-specific T cell response and HLA-A alleles are related to the prognosis of patients with cervical cancer. Infectious Agents and Cancer, 2021, 16, 61.	2.6	6
34	ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data. Nucleic Acids Research, 2022, 50, W312-W321.	14.5	6
35	KeggExp: a web server for visual integration of KEGG pathways and expression profile data. Bioinformatics, 2019, 35, 1430-1432.	4.1	5
36	Phosphoproteomics Reveals Novel Targets and Phosphoprotein Networks in Cell Cycle Mediated by Dsk1 Kinase. Journal of Proteome Research, 2020, 19, 1776-1787.	3.7	5

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37	LiverWiki: a wiki-based database for human liver. BMC Bioinformatics, 2017, 18, 452.	2.6	4
38	A new insight into the impact of different proteases on <scp>SILAC</scp> quantitative proteome of the mouse liver. Proteomics, 2013, 13, 2238-2242.	2.2	3
39	TSMiner: a novel framework for generating time-specific gene regulatory networks from time-series expression profiles. Nucleic Acids Research, 2021, 49, e108-e108.	14.5	3
40	Anaphylactic Rare Saponins Separated from Panax notoginseng Saponin and a Proteomic Approach to Their Anaphylactic Mechanism. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-12.	1.2	2
41	Statistical Strategies for Selection of Differentially Expressed Proteins Based on Mass Spectrometry Technology. Scientia Sinica Vitae, 2015, 45, 347-358.	0.3	1