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	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
2	ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data. Nucleic Acids Research, 2022, 50, W312-W321.	14.5	6
3	Atg9-centered multi-omics integration reveals new autophagy regulators in<i>Saccharomyces cerevisiae</i>. Autophagy, 2021, 17, 4453-4476.	9.1	6
4	DeepDigest: Prediction of Protein Proteolytic Digestion with Deep Learning. Analytical Chemistry, 2021, 93, 6094-6103.	6.5	23
5	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
6	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
7	A Deep Learning–Based Tumor Classifier Directly Using MS Raw Data. Proteomics, 2020, 20, e1900344.	2.2	13
8	A Comprehensive Evaluation of MS/MS Spectrum Prediction Tools for Shotgun Proteomics. Proteomics, 2020, 20, e1900345.	2.2	16
9	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
10	AP3: An Advanced Proteotypic Peptide Predictor for Targeted Proteomics by Incorporating Peptide Digestibility. Analytical Chemistry, 2019, 91, 8705-8711.	6.5	29
11	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. Theranostics, 2019, 9, 2475-2488.	10.0	76
12	Salmonella Proteomic Profiling during Infection Distinguishes the Intracellular Environment of Host Cells. MSystems, 2019, 4, .	3.8	20
13	PANDA: A comprehensive and flexible tool for quantitative proteomics data analysis. Bioinformatics, 2019, 35, 898-900.	4.1	20
14	KeggExp: a web server for visual integration of KEGG pathways and expression profile data. Bioinformatics, 2019, 35, 1430-1432.	4.1	5
15	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
16	LFAQ: Toward Unbiased Label-Free Absolute Protein Quantification by Predicting Peptide Quantitative Factors. Analytical Chemistry, 2019, 91, 1335-1343.	6.5	8
17	PPICurator: A Tool for Extracting Comprehensive Protein–Protein Interaction Information. Proteomics, 2019, 19, e1800291.	2.2	11
18	PANDA-view: an easy-to-use tool for statistical analysis and visualization of quantitative proteomics data. Bioinformatics, 2018, 34, 3594-3596.	4.1	25

#	Article	IF	Citations
19	Proteomic Delineation of the ArcA Regulon in Salmonella Typhimurium During Anaerobiosis. Molecular and Cellular Proteomics, 2018, 17, 1937-1947.	3.8	17
20	In-depth method assessments of differentially expressed protein detection for shotgun proteomics data with missing values. Scientific Reports, 2017, 7, 3367.	3.3	29
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	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
23	Inflammasome-Derived Exosomes Activate NF-κB Signaling in Macrophages. Journal of Proteome Research, 2017, 16, 170-178.	3.7	72
24	LiverWiki: a wiki-based database for human liver. BMC Bioinformatics, 2017, 18, 452.	2.6	4
25	Human fallopian tube proteome shows high coverage of mesenchymal stem cells associated proteins. Bioscience Reports, 2016, 36, e00297.	2.4	10
26	Quantitative and In-Depth Survey of the Isotopic Abundance Distribution Errors in Shotgun Proteomics. Analytical Chemistry, 2016, 88, 6844-6851.	6.5	7
27	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
28	Statistical Strategies for Selection of Differentially Expressed Proteins Based on Mass Spectrometry Technology. Scientia Sinica Vitae, 2015, 45, 347-358.	0.3	1
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	Systematic research on the pretreatment of peptides for quantitative proteomics using a C$_{18}$ microcolumn. Proteomics, 2013, 13, 2229-2237.	2.2	30

#	Article	IF	Citations
37	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
38	A Fast Workflow for Identification and Quantification of Proteomes. Molecular and Cellular Proteomics, 2013, 12, 2370-2380.	3.8	94
39	A new insight into the impact of different proteases on SILAC quantitative proteome of the mouse liver. Proteomics, 2013, 13, 2238-2242.	2.2	3
40	*N*‐linked glycoproteome profiling of human serum using tandem enrichment and multiple fraction concatenation. Electrophoresis, 2013, 34, 2440-2450.	2.4	24
41	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