

Bo Wen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85
papers

5,953
citations

32
h-index

77
g-index

94
ext. papers

8,830
ext. citations

12.3
avg, IF

5.04
L-index

#	Paper	IF	Citations
85	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012 , 490, 49-54	30.4	1464
84	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017 , 8, 845	17.4	575
83	Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5135-40	11.5	466
82	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017 , 8, 875	17.4	308
81	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
80	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. <i>Cell</i> , 2019 , 179, 561-577.e22	56.2	232
79	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983.e31	56.2	173
78	metaX: a flexible and comprehensive software for processing metabolomics data. <i>BMC Bioinformatics</i> , 2017 , 18, 183	3.6	168
77	IQuant: an automated pipeline for quantitative proteomics based upon isobaric tags. <i>Proteomics</i> , 2014 , 14, 2280-5	4.8	141
76	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139
75	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
74	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017 , 355,	33.3	101
73	Proteogenomic analysis reveals alternative splicing and translation as part of the abscisic acid response in Arabidopsis seedlings. <i>Plant Journal</i> , 2017 , 91, 518-533	6.9	90
72	Lipidomics profiling reveals the role of glycerophospholipid metabolism in psoriasis. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	90
71	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016 , 6, 22525	4.9	89
70	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	56.2	71
69	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021 , 39, 509-528.e20	43	71

68	Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. <i>Nature Communications</i> , 2016 , 7, 13107	17.4	50
67	Identification of novel biomarkers for sepsis prognosis via urinary proteomic analysis using iTRAQ labeling and 2D-LC-MS/MS. <i>PLoS ONE</i> , 2013 , 8, e54237	3.7	50
66	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021 , 39, 361-379.e16	24.3	50
65	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019 , 3, 679-690	12.3	49
64	Detection of Proteome Diversity Resulted from Alternative Splicing is Limited by Trypsin Cleavage Specificity. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 422-430	7.6	44
63	Tissue-Based Proteogenomics Reveals that Human Testis Endows Plentiful Missing Proteins. <i>Journal of Proteome Research</i> , 2015 , 14, 3583-94	5.6	41
62	Quantitative proteomics reveals the temperature-dependent proteins encoded by a series of cluster genes in thermoanaerobacter tengcongensis. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2266-77 ⁶	7.6	40
61	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. <i>BMC Bioinformatics</i> , 2016 , 17, 244	3.6	39
60	High-throughput identification of novel conotoxins from the Chinese tubular cone snail (<i>Conus betulinus</i>) by multi-transcriptome sequencing. <i>GigaScience</i> , 2016 , 5, 17	7.6	39
59	Discrimination of sepsis stage metabolic profiles with an LC/MS-MS-based metabolomics approach. <i>BMJ Open Respiratory Research</i> , 2014 , 1, e000056	5.6	38
58	PDV: an integrative proteomics data viewer. <i>Bioinformatics</i> , 2019 , 35, 1249-1251	7.2	38
57	Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. <i>Nature Communications</i> , 2020 , 11, 1759	17.4	37
56	Integrated analyses of DNA methylation and hydroxymethylation reveal tumor suppressive roles of ECM1, ATF5, and EOMES in human hepatocellular carcinoma. <i>Genome Biology</i> , 2014 , 15, 533	18.3	37
55	PepQuery enables fast, accurate, and convenient proteomic validation of novel genomic alterations. <i>Genome Research</i> , 2019 , 29, 485-493	9.7	35
54	Stress responsive proteins are actively regulated during rice (<i>Oryza sativa</i>) embryogenesis as indicated by quantitative proteomics analysis. <i>PLoS ONE</i> , 2013 , 8, e74229	3.7	33
53	Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014 , 4, 5288	4.9	32
52	Deep Coverage Proteomics Identifies More Low-Abundance Missing Proteins in Human Testis Tissue with Q-Exactive HF Mass Spectrometer. <i>Journal of Proteome Research</i> , 2016 , 15, 3988-3997	5.6	32
51	An unexplored O ₂ -involved pathway for the decarboxylation of saturated carboxylic acids by TiO ₂ photocatalysis: an isotopic probe study. <i>Chemistry - A European Journal</i> , 2010 , 16, 11859-66	4.8	32

50	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020 , 11, 532	17.4	31
49	Expansion of the ion library for mining SWATH-MS data through fractionation proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 7242-6	7.8	29
48	Lipidomic profiling reveals distinct differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	28
47	A Targeted Metabolomics MRM-MS Study on Identifying Potential Hypertension Biomarkers in Human Plasma and Evaluating Acupuncture Effects. <i>Scientific Reports</i> , 2016 , 6, 25871	4.9	28
46	Deep Learning in Proteomics. <i>Proteomics</i> , 2020 , 20, e1900335	4.8	27
45	Role of vimentin in modulating immune cell apoptosis and inflammatory responses in sepsis. <i>Scientific Reports</i> , 2019 , 9, 5747	4.9	26
44	IPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015 , 15, 2916-20	4.8	26
43	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021 , 184, 5031-5052.e26	56.2	26
42	Integrated detection of both 5-mC and 5-hmC by high-throughput tag sequencing technology highlights methylation reprogramming of bivalent genes during cellular differentiation. <i>Epigenetics</i> , 2013 , 8, 421-30	5.7	25
41	LncRNAs-directed PTEN enzymatic switch governs epithelial-mesenchymal transition. <i>Cell Research</i> , 2019 , 29, 286-304	24.7	25
40	Peptidomics combined with cDNA library unravel the diversity of centipede venom. <i>Journal of Proteomics</i> , 2015 , 114, 28-37	3.9	22
39	Urinary proteomics analysis for sepsis biomarkers with iTRAQ labeling and two-dimensional liquid chromatography-tandem mass spectrometry. <i>Journal of Trauma and Acute Care Surgery</i> , 2013 , 74, 940-5	3.3	22
38	sapFinder: an R/Bioconductor package for detection of variant peptides in shotgun proteomics experiments. <i>Bioinformatics</i> , 2014 , 30, 3136-8	7.2	21
37	Systematic analysis of missing proteins provides clues to help define all of the protein-coding genes on human chromosome 1. <i>Journal of Proteome Research</i> , 2014 , 13, 114-25	5.6	21
36	First proteomic exploration of protein-encoding genes on chromosome 1 in human liver, stomach, and colon. <i>Journal of Proteome Research</i> , 2013 , 12, 67-80	5.6	20
35	Qualitative and quantitative expression status of the human chromosome 20 genes in cancer tissues and the representative cell lines. <i>Journal of Proteome Research</i> , 2013 , 12, 151-61	5.6	19
34	Quantitative analysis of the human AKR family members in cancer cell lines using the mTRAQ/MRM approach. <i>Journal of Proteome Research</i> , 2013 , 12, 2022-33	5.6	18
33	Quantitative evaluation of the mitochondrial proteomes of <i>Drosophila melanogaster</i> adapted to extreme oxygen conditions. <i>PLoS ONE</i> , 2013 , 8, e74011	3.7	17

32	Supported noble metal nanoparticles as photo/sono-catalysts for synthesis of chemicals and degradation of pollutants. <i>Science China Chemistry</i> , 2011 , 54, 887-897	7.9	16
31	DeepRescore: Leveraging Deep Learning to Improve Peptide Identification in Immunopeptidomics. <i>Proteomics</i> , 2020 , 20, e1900334	4.8	15
30	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15
29	Special Enrichment Strategies Greatly Increase the Efficiency of Missing Proteins Identification from Regular Proteome Samples. <i>Journal of Proteome Research</i> , 2015 , 14, 3680-92	5.6	14
28	Omics evidence: single nucleotide variants transmissions on chromosome 20 in liver cancer cell lines. <i>Journal of Proteome Research</i> , 2014 , 13, 200-11	5.6	14
27	Improvements to the Rice Genome Annotation Through Large-Scale Analysis of RNA-Seq and Proteomics Data Sets. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 86-98	7.6	14
26	Drug Resistance in Colorectal Cancer Cell Lines is Partially Associated with Aneuploidy Status in Light of Profiling Gene Expression. <i>Journal of Proteome Research</i> , 2016 , 15, 4047-4059	5.6	13
25	Integrated omics in Drosophila uncover a circadian kinome. <i>Nature Communications</i> , 2020 , 11, 2710	17.4	12
24	The OMSSAPercolator: an automated tool to validate OMSSA results. <i>Proteomics</i> , 2014 , 14, 1011-4	4.8	12
23	A Comprehensive Investigation toward the Indicative Proteins of Bladder Cancer in Urine: From Surveying Cell Secretomes to Verifying Urine Proteins. <i>Journal of Proteome Research</i> , 2016 , 15, 2164-77	5.6	11
22	Chromosome-8-coded proteome of Chinese Chromosome Proteome Data set (CCPD) 2.0 with partial immunohistochemical verifications. <i>Journal of Proteome Research</i> , 2014 , 13, 126-36	5.6	11
21	Proteome atlas of human chromosome 8 and its multiple 8p deficiencies in tumorigenesis of the stomach, colon, and liver. <i>Journal of Proteome Research</i> , 2013 , 12, 81-8	5.6	11
20	Prediction of Toxin Genes from Chinese Yellow Catfish Based on Transcriptomic and Proteomic Sequencing. <i>International Journal of Molecular Sciences</i> , 2016 , 17, 556	6.3	11
19	An LC-MS based untargeted metabolomics study identified novel biomarkers for coronary heart disease. <i>Molecular BioSystems</i> , 2016 , 12, 3425-3434		9
18	Feature Selection Methods for Protein Biomarker Discovery from Proteomics or Multiomics Data. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100083	7.6	7
17	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017 , 18, 109	3.6	6
16	A Combinational Strategy upon RNA Sequencing and Peptidomics Unravels a Set of Novel Toxin Peptides in Scorpion <i>Mesobuthus martensii</i> . <i>Toxins</i> , 2016 , 8,	4.9	6
15	The serum protein responses to treatment with Xiaoke Pill and Glibenclamide in type 2 diabetes patients. <i>Clinical Proteomics</i> , 2017 , 14, 19	5	5

14	Insights from ENCODE on Missing Proteins: Why β -Defensin Expression Is Scarcely Detected. <i>Journal of Proteome Research</i> , 2015 , 14, 3635-44	5.6	5
13	Interactions Among Expressed MicroRNAs and mRNAs in the Early Stages of Fowl Adenovirus Aerotype 4-Infected Leghorn Male Hepatocellular Cells. <i>Frontiers in Microbiology</i> , 2020 , 11, 831	5.7	5
12	Fusion-related host proteins are actively regulated by NA during influenza infection as revealed by quantitative proteomics analysis. <i>PLoS ONE</i> , 2014 , 9, e105947	3.7	5
11	High-throughput identification of heavy metal binding proteins from the byssus of chinese green mussel (<i>Perna viridis</i>) by combination of transcriptome and proteome sequencing. <i>PLoS ONE</i> , 2019 , 14, e0216605	3.7	4
10	The defensive system of tree frog skin identified by peptidomics and RNA sequencing analysis. <i>Amino Acids</i> , 2019 , 51, 345-353	3.5	4
9	pClean: An Algorithm To Preprocess High-Resolution Tandem Mass Spectra for Database Searching. <i>Journal of Proteome Research</i> , 2019 , 18, 3235-3244	5.6	3
8	Pathogenicity and Immune Responses in Specific-Pathogen-Free Chickens During Fowl Adenovirus Serotype 4 Infection. <i>Avian Diseases</i> , 2020 , 64, 315-323	1.6	3
7	caAtlas: An immunopeptidome atlas of human cancer. <i>iScience</i> , 2021 , 24, 103107	6.1	3
6	A community effort to identify and correct mislabeled samples in proteogenomic studies. <i>Patterns</i> , 2021 , 2, 100245	5.1	2
5	Appraisal of the Missing Proteins Based on the mRNAs Bound to Ribosomes. <i>Journal of Proteome Research</i> , 2015 , 14, 4976-84	5.6	1
4	Assessing Transcription Regulatory Elements To Evaluate the Expression Status of Missing Protein Genes on Chromosomes 11 and 19. <i>Journal of Proteome Research</i> , 2015 , 14, 4967-75	5.6	1
3	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100171	7.6	1
2	Quantitative Proteomics Reveals a Novel Role of the E3 Ubiquitin-Protein Ligase FANCL in the Activation of the Innate Immune Response through Regulation of TBK1 Phosphorylation during Peste des Petits Ruminants Virus Infection. <i>Journal of Proteome Research</i> , 2021 , 20, 4113-4130	5.6	1
1	Transcriptome Analysis Reveals the Potential Role of Long Noncoding RNAs in Regulating Fowl Adenovirus Serotype 4-Induced Apoptosis in Leghorn Male Hepatocellular Cells. <i>Viruses</i> , 2021 , 13,	6.2	1