

# Bo Wen

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

11,176  
citations

81743

39  
h-index

49773

87  
g-index

94  
all docs

94  
docs citations

94  
times ranked

15345  
citing authors

#	ARTICLE	IF	CITATIONS
1	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	13.7	1,966
2	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	5.8	1,029
3	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5135-5140.	3.3	674
4	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 561-577.e22.	13.5	629
5	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875.	5.8	572
6	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
7	metaX: a flexible and comprehensive software for processing metabolomics data. <i>BMC Bioinformatics</i> , 2017, 18, 183.	1.2	489
8	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
9	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
10	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
11	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
12	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
13	IQuant: An automated pipeline for quantitative proteomics based upon isobaric tags. <i>Proteomics</i> , 2014, 14, 2280-2285.	1.3	253
14	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	13.5	236
15	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.	7.7	189
16	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
17	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	6.0	163
18	Lipidomics profiling reveals the role of glycerophospholipid metabolism in psoriasis. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	162

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19	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.	2.8	156
20	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 22525.	1.6	143
21	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
22	Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. <i>Nature Communications</i> , 2020, 11, 1759.	5.8	97
23	Deep Learning in Proteomics. <i>Proteomics</i> , 2020, 20, e1900335.	1.3	91
24	Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. <i>Nature Communications</i> , 2016, 7, 13107.	5.8	88
25	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	5.8	78
26	Detection of Proteome Diversity Resulted from Alternative Splicing is Limited by Trypsin Cleavage Specificity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 422-430.	2.5	75
27	PDV: an integrative proteomics data viewer. <i>Bioinformatics</i> , 2019, 35, 1249-1251.	1.8	71
28	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.	1.1	69
29	PepQuery enables fast, accurate, and convenient proteomic validation of novel genomic alterations. <i>Genome Research</i> , 2019, 29, 485-493.	2.4	68
30	Quantitative Proteomics Reveals the Temperature-Dependent Proteins Encoded by a Series of Cluster Genes in <i>Thermoanaerobacter tengcongensis</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2266-2277.	2.5	58
31	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.	3.8	57
32	High-throughput identification of novel conotoxins from the Chinese tubular cone snail ( <i>Conus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	3.3	52
33	Discrimination of sepsis stage metabolic profiles with an LC/MS-MS-based metabolomics approach. <i>BMJ Open Respiratory Research</i> , 2014, 1, e000056.	1.2	50
34	Lipidomic profiling reveals distinct differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	49
35	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.	1.2	48
36	Tissue-Based Proteogenomics Reveals that Human Testis Endows Plentiful Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3583-3594.	1.8	45

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37	LncRNAs-directed PTEN enzymatic switch governs epithelialâ€“mesenchymal transition. <i>Cell Research</i> , 2019, 29, 286-304.	5.7	43
38	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.	1.6	42
39	DeepRescore: Leveraging Deep Learning to Improve Peptide Identification in Immunopeptidomics. <i>Proteomics</i> , 2020, 20, e1900334.	1.3	42
40	Role of vimentin in modulating immune cell apoptosis and inflammatory responses in sepsis. <i>Scientific Reports</i> , 2019, 9, 5747.	1.6	40
41	Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014, 4, 5288.	1.6	39
42	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.	1.1	38
43	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.	1.8	38
44	An Unexplored O <sub>2</sub> -Involved Pathway for the Decarboxylation of Saturated Carboxylic Acids by TiO <sub>2</sub> Photocatalysis: An Isotopic Probe Study. <i>Chemistry - A European Journal</i> , 2010, 16, 11859-11866.	1.7	37
45	Expansion of the Ion Library for Mining SWATH-MS Data through Fractionation Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 7242-7246.	3.2	36
46	lPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015, 15, 2916-2920.	1.3	33
47	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, 421-430.	1.3	31
48	Peptidomics combined with cDNA library unravel the diversity of centipede venom. <i>Journal of Proteomics</i> , 2015, 114, 28-37.	1.2	31
49	Urinary proteomics analysis for sepsis biomarkers with iTRAQ labeling and two-dimensional liquid chromatographyâ€“tandem mass spectrometry. <i>Journal of Trauma and Acute Care Surgery</i> , 2013, 74, 940-945.	1.1	25
50	sapFinder: an R/Bioconductor package for detection of variant peptides in shotgun proteomics experiments. <i>Bioinformatics</i> , 2014, 30, 3136-3138.	1.8	25
51	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.	4.2	24
52	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, 2022-2033.	1.8	23
53	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	5.8	23
54	caAtlas: An immunopeptidome atlas of human cancer. <i>IScience</i> , 2021, 24, 103107.	1.9	23

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55	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.	2.5	22
56	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, 114-125.	1.8	21
57	Quantitative Evaluation of the Mitochondrial Proteomes of <i>Drosophila melanogaster</i> Adapted to Extreme Oxygen Conditions. <i>PLoS ONE</i> , 2013, 8, e74011.	1.1	21
58	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.	1.8	20
59	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, 151-161.	1.8	19
60	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, 2164-2177.	1.8	19
61	Feature Selection Methods for Protein Biomarker Discovery from Proteomics or Multiomics Data. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100083.	2.5	18
62	An LC-MS based untargeted metabolomics study identified novel biomarkers for coronary heart disease. <i>Molecular BioSystems</i> , 2016, 12, 3425-3434.	2.9	17
63	Special Enrichment Strategies Greatly Increase the Efficiency of Missing Proteins Identification from Regular Proteome Samples. <i>Journal of Proteome Research</i> , 2015, 14, 3680-3692.	1.8	15
64	Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines. <i>Journal of Proteome Research</i> , 2014, 13, 200-211.	1.8	14
65	Prediction of Toxin Genes from Chinese Yellow Catfish Based on Transcriptomic and Proteomic Sequencing. <i>International Journal of Molecular Sciences</i> , 2016, 17, 556.	1.8	14
66	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.	1.8	14
67	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, 81-88.	1.8	13
68	The <sc>OMSSAP</sc> ercolator: <sc>A</sc>n automated tool to validate <sc>OMSSA</sc> results. <i>Proteomics</i> , 2014, 14, 1011-1014.	1.3	13
69	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, 126-136.	1.8	11
70	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.	1.5	9
71	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100171.	2.5	9
72	Insights from ENCODE on Missing Proteins: Why $\beta$ -Defensin Expression Is Scarcely Detected. <i>Journal of Proteome Research</i> , 2015, 14, 3635-3644.	1.8	8

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73	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, 286.	1.5	8
74	The serum protein responses to treatment with Xiaohe Pill and Glibenclamide in type 2 diabetes patients. <i>Clinical Proteomics</i> , 2017, 14, 19.	1.1	8
75	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017, 18, 109.	1.2	7
76	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.	1.1	7
77	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.	1.8	7
78	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.	1.1	6
79	The defensive system of tree frog skin identified by peptidomics and RNA sequencing analysis. <i>Amino Acids</i> , 2019, 51, 345-353.	1.2	6
80	A community effort to identify and correct mislabeled samples in proteogenomic studies. <i>Patterns</i> , 2021, 2, 100245.	3.1	6
81	Pathogenicity and Immune Responses in Specific-Pathogen-Free Chickens During Fowl Adenovirus Serotype 4 Infection. <i>Avian Diseases</i> , 2020, 64, 315-323.	0.4	6
82	pClean: An Algorithm To Preprocess High-Resolution Tandem Mass Spectra for Database Searching. <i>Journal of Proteome Research</i> , 2019, 18, 3235-3244.	1.8	3
83	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, 1623.	1.5	3
84	Computational Proteomics: Focus on Deep Learning. <i>Proteomics</i> , 2020, 20, e2000258.	1.3	2
85	Appraisal of the Missing Proteins Based on the mRNAs Bound to Ribosomes. <i>Journal of Proteome Research</i> , 2015, 14, 4976-4984.	1.8	1
86	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, 4967-4975.	1.8	1
87	CHAPTER 10. Modular metaX Pipeline for Processing Untargeted Metabolomics Data. <i>New Developments in Mass Spectrometry</i> , 2020, , 302-314.	0.2	1
88	Abstract 1895: caAtlas: An immunopeptidome atlas of human cancer. , 2021, , .		0