Bing Zhang

List of Publications by Year
in descending order

106 papers	19,534 citations	47006 47 h-index	40979 93 g-index
110 all docs	110 docs citations	110 times ranked	29054 citing authors

#	ARTICLE	IF	CITATIONS
1	WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. Nucleic Acids Research, 2019, 47, W199-W205.	14.5	2,234
2	WebGestalt: an integrated system for exploring gene sets in various biological contexts. Nucleic Acids Research, 2005, 33, W741-W748.	14.5	1,630
3	LinkedOmics: analyzing multi-omics data within and across 32 cancer types. Nucleic Acids Research, 2018, 46, D956-D963.	14.5	1,497
4	WEB-based GEne SeT AnaLysis Toolkit (WebGestalt): update 2013. Nucleic Acids Research, 2013, 41, W77-W83.	14.5	1,458
5	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	27.8	1,384
6	Proteogenomic characterization of human colon and rectal cancer. Nature, 2014, 513, 382-387.	27.8	1,219
7	WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit. Nucleic Acids Research, 2017, 45, W130-W137.	14.5	1,071
8	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
9	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. Cell, 2019, 179, 561-577.e22.	28.9	629
10	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	8.0	580
11	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	28.9	498
12	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
13	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410
14	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
15	Proteomic Parsimony through Bipartite Graph Analysis Improves Accuracy and Transparency. Journal of Proteome Research, 2007, 6, 3549-3557.	3.7	318
16	KRAS-dependent sorting of miRNA to exosomes. ELife, 2015, 4, e07197.	6.0	296
17	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
18	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	28.9	273

#	Article	IF	Citations
19	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236
20	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
21	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
22	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
23	Protein Identification Using Customized Protein Sequence Databases Derived from RNA-Seq Data. Journal of Proteome Research, 2012, 11, 1009-1017.	3.7	156
24	Clinical potential of mass spectrometry-based proteogenomics. Nature Reviews Clinical Oncology, 2019, 16, 256-268.	27.6	149
25	<i>customProDB</i>: an R package to generate customized protein databases from RNA-Seq data for proteomics search. Bioinformatics, 2013, 29, 3235-3237.	4.1	138
26	Methods, Tools and Current Perspectives in Proteogenomics. Molecular and Cellular Proteomics, 2017, 16, 959-981.	3.8	130
27	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	16.8	120
28	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. Molecular and Cellular Proteomics, 2017, 16, 121-134.	3.8	111
29	GLAD4U: deriving and prioritizing gene lists from PubMed literature. BMC Genomics, 2012, 13, S20.	2.8	108
30	Diverse Long RNAs Are Differentially Sorted into Extracellular Vesicles Secreted by Colorectal Cancer Cells. Cell Reports, 2018, 25, 715-725.e4.	6.4	102
31	Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. Nature Communications, 2020, 11, 1759.	12.8	97
32	Nuclear Factor of Activated T-cell Activity Is Associated with Metastatic Capacity in Colon Cancer. Cancer Research, 2014, 74, 6947-6957.	0.9	96
33	Spliceosome-targeted therapies trigger an antiviral immune response in triple-negative breast cancer. Cell, 2021, 184, 384-403.e21.	28.9	94
34	Deep Learning in Proteomics. Proteomics, 2020, 20, e1900335.	2.2	91
35	APOBEC3A is an oral cancer prognostic biomarker in Taiwanese carriers of an APOBEC deletion polymorphism. Nature Communications, 2017, 8, 465.	12.8	89
36	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. Nature Communications, 2021, 12, 6276.	12.8	89

#	Article	IF	Citations
37	EPHB2 carried on small extracellular vesicles induces tumor angiogenesis via activation of ephrin reverse signaling. JCI Insight, 2019, 4, .	5.0	88
38	A Bioinformatics Workflow for Variant Peptide Detection in Shotgun Proteomics. Molecular and Cellular Proteomics, 2011, 10, M110.006536.	3.8	86
39	Cancer proteogenomics: current impact and future prospects. Nature Reviews Cancer, 2022, 22, 298-313.	28.4	79
40	Microscaled proteogenomic methods for precision oncology. Nature Communications, 2020, 11, 532.	12.8	78
41	Detection of Proteome Diversity Resulted from Alternative Splicing is Limited by Trypsin Cleavage Specificity. Molecular and Cellular Proteomics, 2018, 17, 422-430.	3.8	75
42	PDV: an integrative proteomics data viewer. Bioinformatics, 2019, 35, 1249-1251.	4.1	71
43	skittles, a Drosophila Phosphatidylinositol 4-Phosphate 5-Kinase, Is Required for Cell Viability, Germline Development and Bristle Morphology, But Not for Neurotransmitter Release. Genetics, 1998, 150, 1527-1537.	2.9	70
44	PepQuery enables fast, accurate, and convenient proteomic validation of novel genomic alterations. Genome Research, 2019, 29, 485-493.	5.5	68
45	Tumor microenvironment modulation enhances immunologic benefit of chemoradiotherapy. , 2019, 7, 10.		66
46	Neurofibromin Is an Estrogen Receptor-Î± Transcriptional Co-repressor in Breast Cancer. Cancer Cell, 2020, 37, 387-402.e7.	16.8	59
47	Colorectal Cancer Cell Line Proteomes Are Representative of Primary Tumors and Predict Drug Sensitivity. Gastroenterology, 2017, 153, 1082-1095.	1.3	55
48	Revealing Missing Human Protein Isoforms Based on Ab Initio Prediction, RNA-seq and Proteomics. Scientific Reports, 2015, 5, 10940.	3.3	51
49	Immune Checkpoint Profiles in Luminal B Breast Cancer (Alliance). Journal of the National Cancer Institute, 2020, 112, 737-746.	6.3	51
50	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. BMC Bioinformatics, 2016, 17, 244.	2.6	48
51	Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. Nature Medicine, 2018, 24, 505-511.	30.7	47
52	Proteogenomic Analysis Reveals Unanticipated Adaptations of Colorectal Tumor Cells to Deficiencies in DNA Mismatch Repair. Cancer Research, 2014, 74, 387-397.	0.9	46
53	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. Cell Reports Medicine, 2020, 1, 100004.	6.5	46
54	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. Journal of Proteome Research, 2016, 15, 691-706.	3.7	44

#	Article	IF	Citations
55	LncRNAs-directed PTEN enzymatic switch governs epithelial–mesenchymal transition. Cell Research, 2019, 29, 286-304.	12.0	43
56	DeepRescore: Leveraging Deep Learning to Improve Peptide Identification in Immunopeptidomics. Proteomics, 2020, 20, e1900334.	2.2	42
57	A highly annotated database of genes associated with platinum resistance in cancer. Oncogene, 2021, 40, 6395-6405.	5.9	41
58	A CTC-Cluster-Specific Signature Derived from OMICS Analysis of Patient-Derived Xenograft Tumors Predicts Outcomes in Basal-Like Breast Cancer. Journal of Clinical Medicine, 2019, 8, 1772.	2.4	36
59	Using phosphoproteomics data to understand cellular signaling: a comprehensive guide to bioinformatics resources. Clinical Proteomics, 2020, 17, 27.	2.1	35
60	Relating protein adduction to gene expression changes: a systems approach. Molecular BioSystems, 2011, 7, 2118.	2.9	28
61	Blockade of the 5-HT transporter contributes to the behavioural, neuronal and molecular effects of cocaine. British Journal of Pharmacology, 2017, 174, 2716-2738.	5.4	28
62	Proteomics Is Not an Island: Multi-omics Integration Is the Key to Understanding Biological Systems. Molecular and Cellular Proteomics, 2019, 18, S1-S4.	3.8	27
63	Multiomic analysis identifies CPT1A as a potential therapeutic target in platinum-refractory, high-grade serous ovarian cancer. Cell Reports Medicine, 2021, 2, 100471.	6.5	26
64	proBAMsuite, a Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data. Molecular and Cellular Proteomics, 2016, 15, 1164-1175.	3.8	25
65	caAtlas: An immunopeptidome atlas of human cancer. IScience, 2021, 24, 103107.	4.1	23
66	Proteomic analysis of colon and rectal carcinoma using standard and customized databases. Scientific Data, 2015, 2, 150022.	5.3	22
67	FGFR1-Activated Translation of WNT Pathway Components with Structured 5′ UTRs Is Vulnerable to Inhibition of EIF4A-Dependent Translation Initiation. Cancer Research, 2018, 78, 4229-4240.	0.9	22
68	Anti-tumor immunity induced by ectopic expression of viral antigens is transient and limited by immune escape. OncoImmunology, 2019, 8, e1568809.	4.6	22
69	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. Genome Biology, 2018, 19, 12.	8.8	21
70	Feature Selection Methods for Protein Biomarker Discovery from Proteomics or Multiomics Data. Molecular and Cellular Proteomics, 2021, 20, 100083.	3.8	18
71	Chromosome 12p Amplification in Triple-Negative/*BRCA1-*Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. Cancer Research, 2019, 79, 4258-4270.	0.9	17
72	Graph Algorithms for Condensing and Consolidating Gene Set Analysis Results. Molecular and Cellular Proteomics, 2019, 18, S141-S152.	3.8	17

#	Article	IF	Citations
73	Identification of HPV Integration and Gene Mutation in HeLa Cell Line by Integrated Analysis of RNA-Seq and MS/MS Data. Journal of Proteome Research, 2015, 14, 1678-1686.	3.7	16
74	Right data for right patientâ€"a precisionFDA NCIâ€"CPTAC Multi-omics Mislabeling Challenge. Nature Medicine, 2018, 24, 1301-1302.	30.7	14
75	A novel role of ADGRF1 (GPR110) in promoting cellular quiescence and chemoresistance in human epidermal growth factor receptor 2â€positive breast cancer. FASEB Journal, 2021, 35, e21719.	0.5	13
76	Integrative Omics Analysis Reveals Post-Transcriptionally Enhanced Protective Host Response in Colorectal Cancers with Microsatellite Instability. Journal of Proteome Research, 2016, 15, 766-776.	3.7	10
77	A <scp>SMAD4</scp>â€modulated gene profile predicts diseaseâ€free survival in stage <scp>II</scp> and <scp>III</scp> colorectal cancer. Cancer Reports, 2022, 5, e1423.	1.4	10
78	Linking patient outcome to high throughput protein expression data identifies novel regulators of colorectal adenocarcinoma aggressiveness. F1000Research, 2015, 4, 99.	1.6	9
79	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. Molecular and Cellular Proteomics, 2021, 20, 100171.	3.8	9
80	An open-source analytical platform for analysis of C. elegans swimming-induced paralysis. Journal of Neuroscience Methods, 2014, 232, 58-62.	2.5	8
81	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multiâ€Omics Data. Proteomics, 2020, 20, e1900409.	2.2	8
82	Proteogenomics drives therapeutic hypothesis generation for precision oncology. British Journal of Cancer, 2021, 125, 1-3.	6.4	8
83	Interactions between calcium intake and polymorphisms in genes essential for calcium reabsorption and risk of colorectal neoplasia in a twoâ€phase study. Molecular Carcinogenesis, 2017, 56, 2258-2266.	2.7	7
84	Effects of a social stimulus on gene expression in a mouse model of fragile X syndrome. Molecular Autism, 2017, 8, 30.	4.9	7
85	A social encounter drives gene expression changes linked to neuronal function, brain development, and related disorders in mice expressing the serotonin transporter Ala56 variant. Neuroscience Letters, 2020, 730, 135027.	2.1	7
86	NPY1R exerts inhibitory action on estradiol-stimulated growth and predicts endocrine sensitivity and better survival in ER-positive breast cancer. Scientific Reports, 2022, 12, 1972.	3.3	7
87	Integrating mRNA and Protein Sequencing Enables the Detection and Quantitative Profiling of Natural Protein Sequence Variants of <i>Populus trichocarpa</i>. Journal of Proteome Research, 2015, 14, 5318-5326.	3.7	6
88	A community effort to identify and correct mislabeled samples in proteogenomic studies. Patterns, 2021, 2, 100245.	5.9	6
89	Comprehensive and sensitive proteogenomics data analysis strategy based on complementary multi-stage database search. International Journal of Mass Spectrometry, 2018, 427, 11-19.	1.5	4
90	DLAD4U: deriving and prioritizing disease lists from PubMed literature. BMC Bioinformatics, 2018, 19, 495.	2.6	2

#	Article	IF	Citations
91	Computational Proteomics: Focus on Deep Learning. Proteomics, 2020, 20, e2000258.	2.2	2
92	A novel role of ADGRF1 (GPR110) in promoting cellular quiescence and chemoresistance in human epidermal growth factor receptor 2â€positive breast cancer. FASEB Journal, 2021, 35, .	0.5	2
93	Predicting colorectal cancer recurrence by utilizing multiple-view multiple-learner supervised learning.. Journal of Clinical Oncology, 2017, 35, 635-635.	1.6	2
94	Integrative Genomics and Computational Systems Medicine. BioMed Research International, 2014, 2014, 1-3.	1.9	1
95	Network Approaches for Shotgun Proteomics Data Analysis. , 2009, , .		0
96	Abstract 1895: caAtlas: An immunopeptidome atlas of human cancer. , 2021, , .		0
97	Abstract 17: Proteogenomic characterization of pancreatic ductal adenocarcinoma. , 2021, , .		0
98	Abstract 1426: Multiomic analysis identifies CPT1A and fatty acid oxidation as a potential therapeutic target in platinum-refractory high grade serous ovarian cancer. , 2021, , .		0
99	Abstract 2992: Proteogenomic characterization of triple-negative breast cancer patient-derived xenografts reveals molecular correlates of differential chemotherapy response and potential therapeutic targets to overcome resistance. , 2021, , .		0
100	Modules in Biological Networks. , 2011, , 248-274.		0
101	Colorectal cancer gene expression profiling using nanostring nCounter analysis.. Journal of Clinical Oncology, 2013, 31, 3555-3555.	1.6	0
102	Modules in Biological Networks. , 0, , 637-663.		0
103	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0
104	Abstract PD3-04: Multi-omics characterization of triple-negative breast cancer identifies therapeutic vulnerabilities and epigenetic immune suppression in the mesenchymal subtype. Cancer Research, 2022, 82, PD3-04-PD3-04.	0.9	0
105	Abstract P5-07-01: Proteogenomic analysis of differential chemotherapy responses in patient-derived xenografts of triple-negative breast cancer. Cancer Research, 2022, 82, P5-07-01-P5-07-01.	0.9	0
106	Computational methods for omics data. International Journal of Computational Biology and Drug Design, 2014, 7, 97-101.	0.3	0