

Bing Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

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	A SMAD4 -modulated gene profile predicts disease-free survival in stage II and III colorectal cancer. <i>Cancer Reports</i> , 2022, 5, e1423.	1.4	10
2	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	16.8	120
3	NPY1R exerts inhibitory action on estradiol-stimulated growth and predicts endocrine sensitivity and better survival in ER-positive breast cancer. <i>Scientific Reports</i> , 2022, 12, 1972.	3.3	7
4	Abstract PD3-04: Multi-omics characterization of triple-negative breast cancer identifies therapeutic vulnerabilities and epigenetic immune suppression in the mesenchymal subtype. <i>Cancer Research</i> , 2022, 82, PD3-04-PD3-04.	0.9	0
5	Abstract P5-07-01: Proteogenomic analysis of differential chemotherapy responses in patient-derived xenografts of triple-negative breast cancer. <i>Cancer Research</i> , 2022, 82, P5-07-01-P5-07-01.	0.9	0
6	Cancer proteogenomics: current impact and future prospects. <i>Nature Reviews Cancer</i> , 2022, 22, 298-313.	28.4	79
7	Feature Selection Methods for Protein Biomarker Discovery from Proteomics or Multiomics Data. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100083.	3.8	18
8	Spliceosome-targeted therapies trigger an antiviral immune response in triple-negative breast cancer. <i>Cell</i> , 2021, 184, 384-403.e21.	28.9	94
9	Proteogenomics drives therapeutic hypothesis generation for precision oncology. <i>British Journal of Cancer</i> , 2021, 125, 1-3.	6.4	8
10	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.	16.8	189
11	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
12	A novel role of ADGRF1 (GPR110) in promoting cellular quiescence and chemoresistance in human epidermal growth factor receptor 2-positive breast cancer. <i>FASEB Journal</i> , 2021, 35, .	0.5	2
13	A community effort to identify and correct mislabeled samples in proteogenomic studies. <i>Patterns</i> , 2021, 2, 100245.	5.9	6
14	A novel role of ADGRF1 (GPR110) in promoting cellular quiescence and chemoresistance in human epidermal growth factor receptor 2-positive breast cancer. <i>FASEB Journal</i> , 2021, 35, e21719.	0.5	13
15	Abstract 1895: caAtlas: An immunopeptidome atlas of human cancer. , 2021, , .		0
16	Abstract 17: Proteogenomic characterization of pancreatic ductal adenocarcinoma. , 2021, , .		0
17	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
18	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

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19	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
20	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
21	caAtlas: An immunopeptidome atlas of human cancer. <i>IScience</i> , 2021, 24, 103107.	4.1	23
22	A highly annotated database of genes associated with platinum resistance in cancer. <i>Oncogene</i> , 2021, 40, 6395-6405.	5.9	41
23	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100171.	3.8	9
24	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276.	12.8	89
25	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0
26	Multiomic analysis identifies CPT1A as a potential therapeutic target in platinum-refractory, high-grade serous ovarian cancer. <i>Cell Reports Medicine</i> , 2021, 2, 100471.	6.5	26
27	Immune Checkpoint Profiles in Luminal B Breast Cancer (Alliance). <i>Journal of the National Cancer Institute</i> , 2020, 112, 737-746.	6.3	51
28	Using phosphoproteomics data to understand cellular signaling: a comprehensive guide to bioinformatics resources. <i>Clinical Proteomics</i> , 2020, 17, 27.	2.1	35
29	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
30	Computational Proteomics: Focus on Deep Learning. <i>Proteomics</i> , 2020, 20, e2000258.	2.2	2
31	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
32	Deep Learning in Proteomics. <i>Proteomics</i> , 2020, 20, e1900335.	2.2	91
33	DeepRescore: Leveraging Deep Learning to Improve Peptide Identification in Immunopeptidomics. <i>Proteomics</i> , 2020, 20, e1900334.	2.2	42
34	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-omics Data. <i>Proteomics</i> , 2020, 20, e1900409.	2.2	8
35	Neurofibromin Is an Estrogen Receptor- α Transcriptional Co-repressor in Breast Cancer. <i>Cancer Cell</i> , 2020, 37, 387-402.e7.	16.8	59
36	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410

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37	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
38	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	12.8	78
39	Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. <i>Nature Communications</i> , 2020, 11, 1759.	12.8	97
40	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	6.5	46
41	A social encounter drives gene expression changes linked to neuronal function, brain development, and related disorders in mice expressing the serotonin transporter Ala56 variant. <i>Neuroscience Letters</i> , 2020, 730, 135027.	2.1	7
42	Proteomics Is Not an Island: Multi-omics Integration Is the Key to Understanding Biological Systems. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S1-S4.	3.8	27
43	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
44	A CTC-Cluster-Specific Signature Derived from OMICS Analysis of Patient-Derived Xenograft Tumors Predicts Outcomes in Basal-Like Breast Cancer. <i>Journal of Clinical Medicine</i> , 2019, 8, 1772.	2.4	36
45	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 561-577.e22.	28.9	629
46	Chromosome 12p Amplification in Triple-Negative/ <i>BRCA1</i> -Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. <i>Cancer Research</i> , 2019, 79, 4258-4270.	0.9	17
47	Graph Algorithms for Condensing and Consolidating Gene Set Analysis Results. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S141-S152.	3.8	17
48	WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. <i>Nucleic Acids Research</i> , 2019, 47, W199-W205.	14.5	2,234
49	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
50	Anti-tumor immunity induced by ectopic expression of viral antigens is transient and limited by immune escape. <i>Oncolmmunology</i> , 2019, 8, e1568809.	4.6	22
51	PDV: an integrative proteomics data viewer. <i>Bioinformatics</i> , 2019, 35, 1249-1251.	4.1	71
52	PepQuery enables fast, accurate, and convenient proteomic validation of novel genomic alterations. <i>Genome Research</i> , 2019, 29, 485-493.	5.5	68
53	Clinical potential of mass spectrometry-based proteogenomics. <i>Nature Reviews Clinical Oncology</i> , 2019, 16, 256-268.	27.6	149
54	Tumor microenvironment modulation enhances immunologic benefit of chemoradiotherapy. , 2019, 7, 10.		66

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55	LncRNAs-directed PTEN enzymatic switch governs epithelialâ€“mesenchymal transition. <i>Cell Research</i> , 2019, 29, 286-304.	12.0	43
56	EPHB2 carried on small extracellular vesicles induces tumor angiogenesis via activation of ephrin reverse signaling. <i>JCI Insight</i> , 2019, 4, .	5.0	88
57	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
58	Detection of Proteome Diversity Resulted from Alternative Splicing is Limited by Trypsin Cleavage Specificity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 422-430.	3.8	75
59	LinkedOmics: analyzing multi-omics data within and across 32 cancer types. <i>Nucleic Acids Research</i> , 2018, 46, D956-D963.	14.5	1,497
60	Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. <i>Nature Medicine</i> , 2018, 24, 505-511.	30.7	47
61	Comprehensive and sensitive proteogenomics data analysis strategy based on complementary multi-stage database search. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 11-19.	1.5	4
62	DLAD4U: deriving and prioritizing disease lists from PubMed literature. <i>BMC Bioinformatics</i> , 2018, 19, 495.	2.6	2
63	Diverse Long RNAs Are Differentially Sorted into Extracellular Vesicles Secreted by Colorectal Cancer Cells. <i>Cell Reports</i> , 2018, 25, 715-725.e4.	6.4	102
64	Right data for right patientâ€“a precisionFDA NCIâ€“CPTAC Multi-omics Mislabeling Challenge. <i>Nature Medicine</i> , 2018, 24, 1301-1302.	30.7	14
65	FGFR1-Activated Translation of WNT Pathway Components with Structured 5â€“UTRs Is Vulnerable to Inhibition of EIF4A-Dependent Translation Initiation. <i>Cancer Research</i> , 2018, 78, 4229-4240.	0.9	22
66	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018, 19, 12.	8.8	21
67	WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit. <i>Nucleic Acids Research</i> , 2017, 45, W130-W137.	14.5	1,071
68	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	3.8	130
69	Colorectal Cancer Cell Line Proteomes Are Representative of Primary Tumors and Predict Drug Sensitivity. <i>Gastroenterology</i> , 2017, 153, 1082-1095.	1.3	55
70	Blockade of the 5â€“HT transporter contributes to the behavioural, neuronal and molecular effects of cocaine. <i>British Journal of Pharmacology</i> , 2017, 174, 2716-2738.	5.4	28
71	Interactions between calcium intake and polymorphisms in genes essential for calcium reabsorption and risk of colorectal neoplasia in a twoâ€“phase study. <i>Molecular Carcinogenesis</i> , 2017, 56, 2258-2266.	2.7	7
72	APOBEC3A is an oral cancer prognostic biomarker in Taiwanese carriers of an APOBEC deletion polymorphism. <i>Nature Communications</i> , 2017, 8, 465.	12.8	89

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73	Effects of a social stimulus on gene expression in a mouse model of fragile X syndrome. <i>Molecular Autism</i> , 2017, 8, 30.	4.9	7
74	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	3.8	111
75	Predicting colorectal cancer recurrence by utilizing multiple-view multiple-learner supervised learning.. <i>Journal of Clinical Oncology</i> , 2017, 35, 635-635.	1.6	2
76	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	27.8	1,384
77	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.	2.6	48
78	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
79	Integrative Omics Analysis Reveals Post-Transcriptionally Enhanced Protective Host Response in Colorectal Cancers with Microsatellite Instability. <i>Journal of Proteome Research</i> , 2016, 15, 766-776.	3.7	10
80	proBAMsuite, a Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1164-1175.	3.8	25
81	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
82	Proteomic analysis of colon and rectal carcinoma using standard and customized databases. <i>Scientific Data</i> , 2015, 2, 150022.	5.3	22
83	KRAS-dependent sorting of miRNA to exosomes. <i>ELife</i> , 2015, 4, e07197.	6.0	296
84	Identification of HPV Integration and Gene Mutation in HeLa Cell Line by Integrated Analysis of RNA-Seq and MS/MS Data. <i>Journal of Proteome Research</i> , 2015, 14, 1678-1686.	3.7	16
85	Revealing Missing Human Protein Isoforms Based on Ab Initio Prediction, RNA-seq and Proteomics. <i>Scientific Reports</i> , 2015, 5, 10940.	3.3	51
86	Integrating mRNA and Protein Sequencing Enables the Detection and Quantitative Profiling of Natural Protein Sequence Variants of <i>Populus trichocarpa</i> . <i>Journal of Proteome Research</i> , 2015, 14, 5318-5326.	3.7	6
87	Linking patient outcome to high throughput protein expression data identifies novel regulators of colorectal adenocarcinoma aggressiveness. <i>F1000Research</i> , 2015, 4, 99.	1.6	9
88	Integrative Genomics and Computational Systems Medicine. <i>BioMed Research International</i> , 2014, 2014, 1-3.	1.9	1
89	Proteogenomic Analysis Reveals Unanticipated Adaptations of Colorectal Tumor Cells to Deficiencies in DNA Mismatch Repair. <i>Cancer Research</i> , 2014, 74, 387-397.	0.9	46
90	Nuclear Factor of Activated T-cell Activity Is Associated with Metastatic Capacity in Colon Cancer. <i>Cancer Research</i> , 2014, 74, 6947-6957.	0.9	96

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91	An open-source analytical platform for analysis of <i>C. elegans</i> swimming-induced paralysis. <i>Journal of Neuroscience Methods</i> , 2014, 232, 58-62.	2.5	8
92	Proteogenomic characterization of human colon and rectal cancer. <i>Nature</i> , 2014, 513, 382-387.	27.8	1,219
93	Computational methods for omics data. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 97-101.	0.3	0
94	<i>customProDB</i> : an R package to generate customized protein databases from RNA-Seq data for proteomics search. <i>Bioinformatics</i> , 2013, 29, 3235-3237.	4.1	138
95	WEB-based GENE SeT Analysis Toolkit (WebGestalt): update 2013. <i>Nucleic Acids Research</i> , 2013, 41, W77-W83.	14.5	1,458
96	Colorectal cancer gene expression profiling using nanostring nCounter analysis. <i>Journal of Clinical Oncology</i> , 2013, 31, 3555-3555.	1.6	0
97	Protein Identification Using Customized Protein Sequence Databases Derived from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2012, 11, 1009-1017.	3.7	156
98	GLAD4U: deriving and prioritizing gene lists from PubMed literature. <i>BMC Genomics</i> , 2012, 13, S20.	2.8	108
99	Relating protein adduction to gene expression changes: a systems approach. <i>Molecular BioSystems</i> , 2011, 7, 2118.	2.9	28
100	A Bioinformatics Workflow for Variant Peptide Detection in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006536.	3.8	86
101	Modules in Biological Networks. , 2011, , 248-274.		0
102	Network Approaches for Shotgun Proteomics Data Analysis. , 2009, , .		0
103	Proteomic Parsimony through Bipartite Graph Analysis Improves Accuracy and Transparency. <i>Journal of Proteome Research</i> , 2007, 6, 3549-3557.	3.7	318
104	WebGestalt: an integrated system for exploring gene sets in various biological contexts. <i>Nucleic Acids Research</i> , 2005, 33, W741-W748.	14.5	1,630
105	skittles, a <i>Drosophila</i> Phosphatidylinositol 4-Phosphate 5-Kinase, Is Required for Cell Viability, Germline Development and Bristle Morphology, But Not for Neurotransmitter Release. <i>Genetics</i> , 1998, 150, 1527-1537.	2.9	70
106	Modules in Biological Networks. , 0, , 637-663.		0