

# Yunpeng Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

2,977  
citations

236925

25  
h-index

182427

51  
g-index

69  
all docs

69  
docs citations

69  
times ranked

3366  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer characterization of immune-related lncRNAs identifies potential oncogenic biomarkers. <i>Nature Communications</i> , 2020, 11, 1000.	12.8	293
2	Molecular characterization and clinical relevance of m6A regulators across 33 cancer types. <i>Molecular Cancer</i> , 2019, 18, 137.	19.2	286
3	Identification of lncRNA-associated competing triplets reveals global patterns and prognostic markers for cancer. <i>Nucleic Acids Research</i> , 2015, 43, 3478-3489.	14.5	219
4	Comprehensive characterization of lncRNA-mRNA related ceRNA network across 12 major cancers. <i>Oncotarget</i> , 2016, 7, 64148-64167.	1.8	171
5	Lnc2Cancer 3.0: an updated resource for experimentally supported lncRNA/circRNA cancer associations and web tools based on RNA-seq and scRNA-seq data. <i>Nucleic Acids Research</i> , 2021, 49, D1251-D1258.	14.5	162
6	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. <i>Nucleic Acids Research</i> , 2018, 46, 1113-1123.	14.5	115
7	miRSponge: a manually curated database for experimentally supported miRNA sponges and ceRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav098.	3.0	112
8	MetSigDis: a manually curated resource for the metabolic signatures of diseases. <i>Briefings in Bioinformatics</i> , 2019, 20, 203-209.	6.5	106
9	LncACTdb 2.0: an updated database of experimentally supported ceRNA interactions curated from low- and high-throughput experiments. <i>Nucleic Acids Research</i> , 2019, 47, D121-D127.	14.5	97
10	Systematic identification of lincRNA-based prognostic biomarkers by integrating lincRNA expression and copy number variation in lung adenocarcinoma. <i>International Journal of Cancer</i> , 2019, 144, 1723-1734.	5.1	85
11	LncTarD: a manually-curated database of experimentally-supported functional lncRNA target regulations in human diseases. <i>Nucleic Acids Research</i> , 2020, 48, D118-D126.	14.5	77
12	The DNA Methylome and Transcriptome of Different Brain Regions in Schizophrenia and Bipolar Disorder. <i>PLoS ONE</i> , 2014, 9, e95875.	2.5	75
13	Dynamic Organization of lncRNA and Circular RNA Regulators Collectively Controlled Cardiac Differentiation in Humans. <i>EBioMedicine</i> , 2017, 24, 137-146.	6.1	73
14	DiseaseEnhancer: a resource of human disease-associated enhancer catalog. <i>Nucleic Acids Research</i> , 2018, 46, D78-D84.	14.5	69
15	FACER: comprehensive molecular and functional characterization of epigenetic chromatin regulators. <i>Nucleic Acids Research</i> , 2018, 46, 10019-10033.	14.5	66
16	LncCeVar: a comprehensive database of genomic variations that disturb ceRNA network regulation. <i>Nucleic Acids Research</i> , 2020, 48, D111-D117.	14.5	59
17	Genome-wide DNA methylome analysis reveals epigenetically dysregulated non-coding RNAs in human breast cancer. <i>Scientific Reports</i> , 2015, 5, 8790.	3.3	54
18	LncACTdb 3.0: an updated database of experimentally supported ceRNA interactions and personalized networks contributing to precision medicine. <i>Nucleic Acids Research</i> , 2022, 50, D183-D189.	14.5	45

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19	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015, 5, 17201.	3.3	43
20	MSDD: a manually curated database of experimentally supported associations among miRNAs, SNPs and human diseases. <i>Nucleic Acids Research</i> , 2018, 46, D181-D185.	14.5	42
21	LnCeCell: a comprehensive database of predicted lncRNA-associated ceRNA networks at single-cell resolution. <i>Nucleic Acids Research</i> , 2021, 49, D125-D133.	14.5	42
22	Gain-of-Function Mutations: An Emerging Advantage for Cancer Biology. <i>Trends in Biochemical Sciences</i> , 2019, 44, 659-674.	7.5	38
23	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015, 6, 39151-39164.	1.8	33
24	RNAactDrug: a comprehensive database of RNAs associated with drug sensitivity from multi-omics data. <i>Briefings in Bioinformatics</i> , 2020, 21, 2167-2174.	6.5	32
25	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015, 5, 13044.	3.3	31
26	A comprehensive overview of oncogenic pathways in human cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 957-969.	6.5	29
27	Inference of patient-specific subpathway activities reveals a functional signature associated with the prognosis of patients with breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 4304-4316.	3.6	28
28	LincSNP 3.0: an updated database for linking functional variants to human long non-coding RNAs, circular RNAs and their regulatory elements. <i>Nucleic Acids Research</i> , 2021, 49, D1244-D1250.	14.5	28
29	Genome-wide DNA methylome reveals the dysfunction of intronic microRNAs in major psychosis. <i>BMC Medical Genomics</i> , 2015, 8, 62.	1.5	27
30	Prioritization of candidate cancer drugs based on a drug functional similarity network constructed by integrating pathway activities and drug activities. <i>Molecular Oncology</i> , 2019, 13, 2259-2277.	4.6	27
31	Comprehensive Characterization of Somatic Mutations Impacting lncRNA Expression for Pan-Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 66-79.	5.1	27
32	Identification of Cancer Dysfunctional Subpathways by Integrating DNA Methylation, Copy Number Variation, and Gene-Expression Data. <i>Frontiers in Genetics</i> , 2019, 10, 441.	2.3	27
33	Identification of miRNA-Mediated Core Gene Module for Glioma Patient Prediction by Integrating High-Throughput miRNA, mRNA Expression and Pathway Structure. <i>PLoS ONE</i> , 2014, 9, e96908.	2.5	26
34	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , 2017, 7, 46566.	3.3	24
35	Prioritizing Candidate Disease Metabolites Based on Global Functional Relationships between Metabolites in the Context of Metabolic Pathways. <i>PLoS ONE</i> , 2014, 9, e104934.	2.5	23
36	Network Analysis Reveals Functional Cross-links between Disease and Inflammation Genes. <i>Scientific Reports</i> , 2013, 3, 3426.	3.3	22

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37	The lncRNA Connectivity Map: Using lncRNA Signatures to Connect Small Molecules, lncRNAs, and Diseases. <i>Scientific Reports</i> , 2017, 7, 6655.	3.3	21
38	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , 2016, 7, 69857-69870.	1.8	18
39	RNA Function Prediction. <i>Methods in Molecular Biology</i> , 2017, 1654, 17-28.	0.9	17
40	Alternative splicing perturbation landscape identifies RNA binding proteins as potential therapeutic targets in cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 792-806.	5.1	15
41	Single-Cell Transcriptomic Analysis Reveals a Tumor-Reactive T Cell Signature Associated With Clinical Outcome and Immunotherapy Response In Melanoma. <i>Frontiers in Immunology</i> , 2021, 12, 758288.	4.8	13
42	MPINet: Metabolite Pathway Identification via Coupling of Global Metabolite Network Structure and Metabolomic Profile. <i>BioMed Research International</i> , 2014, 2014, 1-14.	1.9	12
43	Identification and comprehensive characterization of lncRNAs with copy number variations and their driving transcriptional perturbed subpathways reveal functional significance for cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 2153-2166.	6.5	12
44	Identifying subpathway signatures for individualized anticancer drug response by integrating multi-omics data. <i>Journal of Translational Medicine</i> , 2019, 17, 255.	4.4	11
45	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. <i>Oncogene</i> , 2020, 39, 677-689.	5.9	11
46	Combined homologous recombination repair deficiency and immune activation analysis for predicting intensified responses of anthracycline, cyclophosphamide and taxane chemotherapy in triple-negative breast cancer. <i>BMC Medicine</i> , 2021, 19, 190.	5.5	11
47	Dynamic regulatory networks of T cell trajectory dissect transcriptional control of T cell state transition. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1115-1129.	5.1	11
48	Identification of a lncRNA involved functional module for esophageal cancer subtypes. <i>Molecular BioSystems</i> , 2016, 12, 3312-3323.	2.9	10
49	MiRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , 2016, 7, 55012-55025.	1.8	10
50	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure. <i>Journal of Biomedical Informatics</i> , 2014, 49, 187-197.	4.3	9
51	SEECancer: a resource for somatic events in evolution of cancer genome. <i>Nucleic Acids Research</i> , 2018, 46, D1018-D1026.	14.5	9
52	lncSubpathway: a novel approach for identifying dysfunctional subpathways associated with risk lncRNAs by integrating lncRNA and mRNA expression profiles and pathway topologies. <i>Oncotarget</i> , 2017, 8, 15453-15469.	1.8	9
53	System level characterization of small molecule drugs and their affected long noncoding RNAs. <i>Aging</i> , 2019, 11, 12428-12451.	3.1	8
54	Dissecting dysfunctional crosstalk pathways regulated by miRNAs during glioma progression. <i>Oncotarget</i> , 2016, 7, 25769-25782.	1.8	7

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55	Systematic analysis of enhancer regulatory circuit perturbation driven by copy number variations in malignant glioma. <i>Theranostics</i> , 2021, 11, 3060-3073.	10.0	6
56	Revealing the contribution of somatic gene mutations to shaping tumor immune microenvironment. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	6
57	Identification of Subtype Specific miRNA-mRNA Functional Regulatory Modules in Matched miRNA-mRNA Expression Data: Multiple Myeloma as a Case. <i>BioMed Research International</i> , 2015, 2015, 1-15.	1.9	5
58	BioM2MetDisease: a manually curated database for associations between microRNAs, metabolites, small molecules and metabolic diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	5
59	Identifying and characterizing lincRNA genomic clusters reveals its cooperative functions in human cancer. <i>Journal of Translational Medicine</i> , 2021, 19, 509.	4.4	5
60	Dissecting immune cell stat regulation network reveals biomarkers to predict ICB therapy responders in melanoma. <i>Journal of Translational Medicine</i> , 2021, 19, 296.	4.4	4
61	Shedding light on the hidden human proteome expands immunopeptidome in cancer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
62	Applicability of Anticancer Drugs for the Triple-Negative Breast Cancer Based on Homologous Recombination Repair Deficiency. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 845950.	3.7	4
63	Systematic Identification of Core Transcription Factors Mediating Dysregulated Links Bridging Inflammatory Bowel Diseases and Colorectal Cancer. <i>PLoS ONE</i> , 2013, 8, e83495.	2.5	3
64	Global view of a drug-sensitivity gene network. <i>Oncotarget</i> , 2018, 9, 3254-3266.	1.8	3
65	Integrating gene and lncRNA expression to infer subpathway activity for tumor analyses. <i>Oncotarget</i> , 2017, 8, 111433-111443.	1.8	2
66	Identifying individualized risk subpathways reveals pan-cancer molecular classification based on multi-omics data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 838-849.	4.1	2
67	GABC : A comprehensive resource and Genome Atlas for Breast Cancer. <i>International Journal of Cancer</i> , 2021, 148, 988-994.	5.1	1
68	Genome-Wide Mapping of SNPs in Non-coding RNAs. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1094, 39-48.	1.6	0
69	Computational Inferring of Risk Subpathways Mediated by Dysfunctional Non-coding RNAs. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1094, 87-95.	1.6	0