

# Yuji Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

1,595  
citations

361413

20  
h-index

345221

36  
g-index

66  
all docs

66  
docs citations

66  
times ranked

3416  
citing authors

#	ARTICLE	IF	CITATIONS
1	Morphological Phenotyping of Organotropic Brain- and Bone-Seeking Triple Negative Metastatic Breast Tumor Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 790410.	3.7	2
2	Polygenic risk scores for CARDINAL study. <i>Nature Genetics</i> , 2022, 54, 527-530.	21.4	5
3	Transcriptome profiling reveals that VNPP433-3 <sup>12</sup> , the lead next-generation galeterone analog inhibits prostate cancer stem cells by downregulating epithelial-mesenchymal transition and stem cell markers. <i>Molecular Carcinogenesis</i> , 2022, 61, 643-654.	2.7	25
4	C5a Activates a Pro-Inflammatory Gene Expression Profile in Human Gaucher iPSC-Derived Macrophages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9912.	4.1	14
5	MYC DNA Methylation in Prostate Tumor Tissue is Associated with Gleason Score. <i>Genes</i> , 2021, 12, 12.	2.4	6
6	Laminar Flow on Endothelial Cells Suppresses eNOS O-GlcNAcylation to Promote eNOS Activity. <i>Circulation Research</i> , 2021, 129, 1054-1066.	4.5	11
7	Photodynamic Priming Improves the Anti-Migratory Activity of Prostaglandin E Receptor 4 Antagonist in Cancer Cells In Vitro. <i>Cancers</i> , 2021, 13, 5259.	3.7	4
8	Inhibition of mTOR or MAPK ameliorates vmhcl/myh7 cardiomyopathy in zebrafish. <i>JCI Insight</i> , 2021, 6, .	5.0	10
9	Alcohol consumption and serum metabolite concentrations in young women. <i>Cancer Causes and Control</i> , 2020, 31, 113-126.	1.8	8
10	Photodynamic Priming Modulates Endothelial Cell Cell Junction Phenotype for Light-activated Remote Control of Drug Delivery. <i>IEEE Journal of Selected Topics in Quantum Electronics</i> , 2020, 27, 1-1.	2.9	23
11	Induction of IRAK-M in melanoma induces caspase-3 dependent apoptosis by reducing TRAF6 and calpastatin levels. <i>Communications Biology</i> , 2020, 3, 306.	4.4	5
12	Integrated urine proteomics and renal single-cell genomics identify an IFN- $\beta$ response gradient in lupus nephritis. <i>JCI Insight</i> , 2020, 5, .	5.0	57
13	RIP sequencing in mantle cell lymphoma identifies functional long non-coding RNAs associated with translation machinery. <i>Blood Cancer Journal</i> , 2019, 9, 55.	6.2	4
14	Galeterone and The Next Generation Galeterone Analogs, VNPP414 and VNPP433-3 <sup>12</sup> Exert Potent Therapeutic Effects in Castration-/Drug-Resistant Prostate Cancer Preclinical Models In Vitro and In Vivo. <i>Cancers</i> , 2019, 11, 1637.	3.7	20
15	A statistical analysis of vaccine-adverse event data. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 101.	3.0	16
16	The Novel Mnk1/2 Degradar and Apoptosis Inducer VNLG-152 Potently Inhibits TNBC Tumor Growth and Metastasis. <i>Cancers</i> , 2019, 11, 299.	3.7	18
17	Intratumor genetic heterogeneity in squamous cell carcinoma of the oral cavity. <i>Head and Neck</i> , 2019, 41, 2514-2524.	2.0	22
18	Haploinsufficiency of mechanistic target of rapamycin ameliorates bag3 cardiomyopathy in adult zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	2.4	17

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19	Exploring the effect of library preparation on RNA sequencing experiments. <i>Genomics</i> , 2019, 111, 1752-1759.	2.9	3
20	Association between changes in gene signatures expression and disease activity among patients with systemic lupus erythematosus. <i>BMC Medical Genomics</i> , 2019, 12, 4.	1.5	55
21	Gene Expression Signatures Characterized by Longitudinal Stability and Interindividual Variability Delineate Baseline Phenotypic Groups with Distinct Responses to Immune Stimulation. <i>Journal of Immunology</i> , 2018, 200, j1701099.	0.8	5
22	Adverse event detection by integrating twitter data and VAERS. <i>Journal of Biomedical Semantics</i> , 2018, 9, 19.	1.6	16
23	Integrative Genome-Wide Analysis of Long Noncoding RNAs in Diverse Immune Cell Types of Melanoma Patients. <i>Cancer Research</i> , 2018, 78, 4411-4423.	0.9	39
24	Systematic identification of latent disease-gene associations from PubMed articles. <i>PLoS ONE</i> , 2018, 13, e0191568.	2.5	15
25	Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. <i>Scientific Reports</i> , 2017, 7, 1250.	3.3	12
26	A Synthetic CD8 $\alpha$ :MyD88 Coreceptor Enhances CD8+ T-cell Responses to Weakly Immunogenic and Lowly Expressed Tumor Antigens. <i>Cancer Research</i> , 2017, 77, 7049-7058.	0.9	10
27	Pathophysiological mechanisms underlying phenotypic differences in pulmonary radioresponse. <i>Scientific Reports</i> , 2016, 6, 36579.	3.3	18
28	microRNA expression profiling and functional annotation analysis of their targets modulated by oxidative stress during embryonic heart development in diabetic mice. <i>Reproductive Toxicology</i> , 2016, 65, 365-374.	2.9	29
29	Retinoblastoma Binding Protein 4 Modulates Temozolomide Sensitivity in Glioblastoma by Regulating DNA Repair Proteins. <i>Cell Reports</i> , 2016, 14, 2587-2598.	6.4	58
30	Next generation informatics for big data in precision medicine era. <i>BioData Mining</i> , 2015, 8, 34.	4.0	8
31	Identification of sex-associated network patterns in Vaccine-Adverse Event Association Network in VAERS. <i>Journal of Biomedical Semantics</i> , 2015, 6, 33.	1.6	5
32	Cardiac Transcriptome and Dilated Cardiomyopathy Genes in Zebrafish. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 261-269.	5.1	98
33	Network analysis reveals stage-specific changes in zebrafish embryo development using time course whole transcriptome profiling and prior biological knowledge. <i>BioData Mining</i> , 2015, 8, 26.	4.0	1
34	Gene expression patterns in CD4+ peripheral blood cells in healthy subjects and stage IV melanoma patients. <i>Cancer Immunology, Immunotherapy</i> , 2015, 64, 1437-1447.	4.2	4
35	Linked vaccine adverse event data from VAERS for biomedical data analysis and longitudinal studies. <i>BioData Mining</i> , 2014, 7, 36.	4.0	3
36	Network-based analysis of time series RNA-seq gene expression data by integrating the interactome and gene ontology information. , 2014, , .		0

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37	MACE: model based analysis of ChIP-exo. <i>Nucleic Acids Research</i> , 2014, 42, e156-e156.	14.5	84
38	Evidence based computational drug repositioning candidate screening pipeline design: Case Study. , 2014, , .		0
39	Detection of 1 $\alpha$ ,25-Dihydroxyvitamin D-Regulated miRNAs in Zebrafish by Whole Transcriptome Sequencing. <i>Zebrafish</i> , 2014, 11, 207-218.	1.1	14
40	Network-based analysis reveals distinct association patterns in a semantic MEDLINE-based drug-disease-gene network. <i>Journal of Biomedical Semantics</i> , 2014, 5, 33.	1.6	24
41	Network Analysis of Cancer-focused Association Network Reveals Distinct Network Association Patterns. <i>Cancer Informatics</i> , 2014, 13s3, CIN.S14033.	1.9	5
42	Linked Vaccine Adverse Event Data Representation from VAERS for Biomedical Informatics Research. <i>Lecture Notes in Computer Science</i> , 2014, , 652-661.	1.3	2
43	Network-based analysis of vaccine-related associations reveals consistent knowledge with the vaccine ontology. <i>Journal of Biomedical Semantics</i> , 2013, 4, 33.	1.6	21
44	APOBEC3B Upregulation and Genomic Mutation Patterns in Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2013, 73, 7222-7231.	0.9	153
45	Module-based breast cancer classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 284.	0.1	16
46	An integrative computational approach to identify disease-specific networks from PubMed literature information. , 2013, , .		9
47	Calculating Sample Size Estimates for RNA Sequencing Data. <i>Journal of Computational Biology</i> , 2013, 20, 970-978.	1.6	238
48	Induction of an Inflammatory Loop by Interleukin-1 $\beta$ and Tumor Necrosis Factor- $\alpha$ Involves NF- $\kappa$ B and STAT-1 in Differentiated Human Neuroprogenitor Cells. <i>PLoS ONE</i> , 2013, 8, e69585.	2.5	66
49	Impact of Library Preparation on Downstream Analysis and Interpretation of RNA-Seq Data: Comparison between Illumina PolyA and NuGEN Ovation Protocol. <i>PLoS ONE</i> , 2013, 8, e71745.	2.5	19
50	Research Resource: Whole Transcriptome RNA Sequencing Detects Multiple 1 $\alpha$ ,25-Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Developing Zebrafish. <i>Molecular Endocrinology</i> , 2012, 26, 1630-1642.	3.7	41
51	TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. <i>Bioinformatics</i> , 2012, 28, 277-278.	4.1	59
52	Optimizing semantic MEDLINE for translational science studies using semantic web technologies. , 2012, , .		8
53	SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , 2012, 28, 2180-2181.	4.1	49
54	Identification of aberrant pathways and network activities from high-throughput data. <i>Briefings in Bioinformatics</i> , 2012, 13, 406-419.	6.5	23

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55	Module-based biomarker discovery in breast cancer. , 2010, , .		2
56	Reconstruction of Gene Regulatory Modules in Cancer Cell Cycle by Multi-Source Data Integration. PLoS ONE, 2010, 5, e10268.	2.5	13
57	Reverse engineering module networks by PSO-RNN hybrid modeling. BMC Genomics, 2009, 10, S15.	2.8	34
58	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. BMC Bioinformatics, 2008, 9, 203.	2.6	35
59	Network motif-based identification of breast cancer susceptibility genes. , 2008, 2008, 5696-9.		26
60	Integrating multi-source biological data for transcriptional regulatory module discovery. , 2007, , .		0
61	Inferring Network Interactions Using Recurrent Neural Networks and Swarm Intelligence. , 2006, 2006, 4241-4.		6