Jianzhen Xu

List of Publications by Year
in descending order

29 papers	4,866 citations	516710 16 h-index	477307 29 g-index
29 all docs	29 docs citations	29 times ranked	11750 citing authors

#	Article	IF	Citations
1	Computational Drug Repurposing Based on a Recommendation System and Drug–Drug Functional Pathway Similarity. Molecules, 2022, 27, 1404.	3.8	7
2	TRA2A Binds With LncRNA MALAT1 To Promote Esophageal Cancer Progression By Regulating EZH2/Î²-catenin Pathway. Journal of Cancer, 2021, 12, 4883-4890.	2.5	13
3	Revisiting the Relationship Between Alzheimer's Disease and Cancer With a circRNA Perspective. Frontiers in Cell and Developmental Biology, 2021, 9, 647197.	3.7	6
4	circ-NOL10 regulated by MTDH/CASC3 inhibits breast cancer progression and metastasis via multiple miRNAs and PDCD4. Molecular Therapy - Nucleic Acids, 2021, 26, 773-786.	5.1	12
5	Characterizing the tumor RBP-ncRNA circuits by integrating transcriptomics, interactomics and clinical data. Computational and Structural Biotechnology Journal, 2021, 19, 5235-5245.	4.1	6
6	Circular RNAs: Biogenesis, Mechanism, and Function in Human Cancers. International Journal of Molecular Sciences, 2019, 20, 3926.	4.1	160
7	TGStools: A Bioinformatics Suit to Facilitate Transcriptome Analysis of Long Reads from Third Generation Sequencing Platform. Genes, 2019, 10, 519.	2.4	1
8	OmicsARules: a R package for integration of multi-omics datasets via association rules mining. BMC Bioinformatics, 2019, 20, 554.	2.6	2
9	circRNA expression analysis in lung adenocarcinoma: comparison of paired fresh frozen and formalin-fixed paraffin-embedded specimens. Biochemical and Biophysical Research Communications, 2018, 500, 738-743.	2.1	14
10	RPiRLS: Quantitative Predictions of RNA Interacting with Any Protein of Known Sequence. Molecules, 2018, 23, 540.	3.8	10
11	RBPvsMIR: A Computational Pipeline to Identify Competing miRNAs and RNA-Binding Protein Pairs Regulating the Shared Transcripts. Genes, 2018, 9, 426.	2.4	8
12	LncRNAs and Esophageal Squamous Cell Carcinoma - Implications for Pathogenesis and Drug Development. Journal of Cancer, 2016, 7, 1258-1264.	2.5	33
13	miRNA–mRNA Interaction Network in Non-small Cell Lung Cancer. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 209-219.	3.6	40
14	Current and Emerging Biomarkers of Cell Death in Human Disease. BioMed Research International, 2014, 2014, 1-10.	1.9	20
15	Cell Death in Human Health and Disease. BioMed Research International, 2014, 2014, 1-2.	1.9	5
16	RAID: a comprehensive resource for human RNA-associated (RNA–RNA/RNA–protein) interaction. Rna, 2014, 20, 989-993.	3.5	54
17	Enrichment Analysis of miRNA Targets. Methods in Molecular Biology, 2013, 936, 91-103.	0.9	12
18	Connect the dots. Autophagy, 2013, 9, 436-439.	9.1	46

#	Article	IF	Citations
19	MicroRNAs in autophagy and their emerging roles in crosstalk with apoptosis. Autophagy, 2012, 8, 873-882.	9.1	128
20	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
21	MicroRNA-192 targeting retinoblastoma 1 inhibits cell proliferation and induces cell apoptosis in lung cancer cells. Nucleic Acids Research, 2011, 39, 6669-6678.	14.5	147
22	Chromatinâ€modifying drugs induce miRNAâ€153 expression to suppress Irsâ€2 in glioblastoma cell lines. International Journal of Cancer, 2011, 129, 2527-2531.	5.1	64
23	Downregulations of Bâ€cell lymphoma 2 and myeloid cell leukemia sequence 1 by microRNA 153 induce apoptosis in a glioblastoma cell line DBTRGâ€05MG. International Journal of Cancer, 2010, 126, 1029-1035.	5.1	104
24	Computational approaches for microRNA studies: a review. Mammalian Genome, 2010, 21, 1-12.	2.2	152
25	Decreasing the homodimer interaction: a common mechanism shared by the deltaG91 mutation and deamidation in betaA3-crystallin. Molecular Vision, 2010, 16, 438-44.	1.1	9
26	A computational screen for mouse signaling pathways targeted by microRNA clusters. Rna, 2008, 14, 1276-1283.	3.5	87
27	Effects of replacing the unreliable cDNA microarray measurements on the disease classification based on gene expression profiles and functional modules. Bioinformatics, 2006, 22, 2883-2889.	4.1	36
28	Discovering disease-genes by topological features in human proteinâ€"protein interaction network. Bioinformatics, 2006, 22, 2800-2805.	4.1	422
29	Towards precise classification of cancers based on robust gene functional expression profiles. BMC Bioinformatics, 2005, 6, 58.	2.6	146