Jianzhen Xu

List of Publications by Year in descending order

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516561 477173 4,866 29 16 29 citations g-index h-index papers 29 29 29 11750 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	4.3	3,122
2	Discovering disease-genes by topological features in human protein–protein interaction network. Bioinformatics, 2006, 22, 2800-2805.	1.8	422
3	Circular RNAs: Biogenesis, Mechanism, and Function in Human Cancers. International Journal of Molecular Sciences, 2019, 20, 3926.	1.8	160
4	Computational approaches for microRNA studies: a review. Mammalian Genome, 2010, 21, 1-12.	1.0	152
5	MicroRNA-192 targeting retinoblastoma 1 inhibits cell proliferation and induces cell apoptosis in lung cancer cells. Nucleic Acids Research, 2011, 39, 6669-6678.	6.5	147
6	Towards precise classification of cancers based on robust gene functional expression profiles. BMC Bioinformatics, 2005, 6, 58.	1,2	146
7	MicroRNAs in autophagy and their emerging roles in crosstalk with apoptosis. Autophagy, 2012, 8, 873-882.	4.3	128
8	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.	2.3	104
9	A computational screen for mouse signaling pathways targeted by microRNA clusters. Rna, 2008, 14, 1276-1283.	1.6	87
10	Chromatinâ€modifying drugs induce miRNAâ€153 expression to suppress Irsâ€2 in glioblastoma cell lines. International Journal of Cancer, 2011, 129, 2527-2531.	2.3	64
11	RAID: a comprehensive resource for human RNA-associated (RNA–RNA/RNA–protein) interaction. Rna, 2014, 20, 989-993.	1.6	54
12	Connect the dots. Autophagy, 2013, 9, 436-439.	4.3	46
13	miRNA–mRNA Interaction Network in Non-small Cell Lung Cancer. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 209-219.	2.2	40
14	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.	1.8	36
15	LncRNAs and Esophageal Squamous Cell Carcinoma - Implications for Pathogenesis and Drug Development. Journal of Cancer, 2016, 7, 1258-1264.	1.2	33
16	Current and Emerging Biomarkers of Cell Death in Human Disease. BioMed Research International, 2014, 2014, 1-10.	0.9	20
17	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.	1.0	14
18	TRA2A Binds With LncRNA MALAT1 To Promote Esophageal Cancer Progression By Regulating EZH2/ \hat{l}^2 -catenin Pathway. Journal of Cancer, 2021, 12, 4883-4890.	1,2	13

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19	Enrichment Analysis of miRNA Targets. Methods in Molecular Biology, 2013, 936, 91-103.	0.4	12
20	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.	2.3	12
21	RPiRLS: Quantitative Predictions of RNA Interacting with Any Protein of Known Sequence. Molecules, 2018, 23, 540.	1.7	10
22	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
23	RBPvsMIR: A Computational Pipeline to Identify Competing miRNAs and RNA-Binding Protein Pairs Regulating the Shared Transcripts. Genes, 2018, 9, 426.	1.0	8
24	Computational Drug Repurposing Based on a Recommendation System and Drug–Drug Functional Pathway Similarity. Molecules, 2022, 27, 1404.	1.7	7
25	Revisiting the Relationship Between Alzheimer's Disease and Cancer With a circRNA Perspective. Frontiers in Cell and Developmental Biology, 2021, 9, 647197.	1.8	6
26	Characterizing the tumor RBP-ncRNA circuits by integrating transcriptomics, interactomics and clinical data. Computational and Structural Biotechnology Journal, 2021, 19, 5235-5245.	1.9	6
27	Cell Death in Human Health and Disease. BioMed Research International, 2014, 2014, 1-2.	0.9	5
28	OmicsARules: a R package for integration of multi-omics datasets via association rules mining. BMC Bioinformatics, 2019, 20, 554.	1,2	2
29	TGStools: A Bioinformatics Suit to Facilitate Transcriptome Analysis of Long Reads from Third Generation Sequencing Platform. Genes, 2019, 10, 519.	1.0	1