Jing Bai

List of Publications by Year in descending order

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43 papers	2,244 citations	331670 21 h-index	265206 42 g-index
45 all docs	45 docs citations	45 times ranked	3450 citing authors

#	Article	IF	Citations
1	CellMarker: a manually curated resource of cell markers in human and mouse. Nucleic Acids Research, 2019, 47, D721-D728.	14.5	856
2	Molecular characterization and clinical relevance of m6A regulators across 33 cancer types. Molecular Cancer, 2019, 18, 137.	19.2	286
3	A comprehensive overview of lncRNA annotation resources. Briefings in Bioinformatics, 2017, 18, bbw015.	6.5	122
4	Co-LncRNA: investigating the lncRNA combinatorial effects in GO annotations and KEGG pathways based on human RNA-Seq data. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	107
5	Systematic identification of lincRNAâ€based prognostic biomarkers by integrating lincRNA expression and copy number variation in lung adenocarcinoma. International Journal of Cancer, 2019, 144, 1723-1734.	5.1	85
6	FACER: comprehensive molecular and functional characterization of epigenetic chromatin regulators. Nucleic Acids Research, 2018, 46, 10019-10033.	14.5	66
7	Novel role for non-homologous end joining in the formation of double minutes in methotrexate-resistant colon cancer cells. Journal of Medical Genetics, 2015, 52, 135-144.	3.2	56
8	Overexpression of RCC2 Enhances Cell Motility and Promotes Tumor Metastasis in Lung Adenocarcinoma by Inducing Epithelialâ€“Mesenchymal Transition. Clinical Cancer Research, 2017, 23, 5598-5610.	7.0	51
9	TRIB1 promotes colorectal cancer cell migration and invasion through activation MMP-2 via FAK/Src and ERK pathways. Oncotarget, 2017, 8, 47931-47942.	1.8	45
10	Survey of miRNA-miRNA cooperative regulation principles across cancer types. Briefings in Bioinformatics, 2019, 20, 1621-1638.	6.5	39
11	DJ-1 may contribute to metastasis of non-small cell lung cancer. Molecular Biology Reports, 2012, 39, 2697-2703.	2.3	38
12	Methylenetetrahydrofolate reductase gene polymorphisms and lung cancer: a meta-analysis. Journal of Human Genetics, 2008, 53, 340-348.	2.3	36
13	Complex impact of DNA methylation on transcriptional dysregulation across 22 human cancer types. Nucleic Acids Research, 2020, 48, 2287-2302.	14.5	35
14	Role of EZH2 in oral squamous cell carcinoma carcinogenesis. Gene, 2014, 537, 197-202.	2.2	32
15	Characterization of Transcriptome Transition Associates Long Noncoding RNAs with Glioma Progression. Molecular Therapy - Nucleic Acids, 2018, 13, 620-632.	5.1	32
16	Identifying Cancer Driver lncRNAs Bridged by Functional Effectors through Integrating Multi-omics Data in Human Cancers. Molecular Therapy - Nucleic Acids, 2019, 17, 362-373.	5.1	30
17	Integrating analysis reveals microRNA-mediated pathway crosstalk among Crohn's disease, ulcerative colitis and colorectal cancer. Molecular BioSystems, 2014, 10, 2317.	2.9	27
18	Construction and analysis of dynamic transcription factor regulatory networks in the progression of glioma. Scientific Reports, 2015, 5, 15953.	3.3	27

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19	Genome-wide DNA methylome reveals the dysfunction of intronic microRNAs in major psychosis. BMC Medical Genomics, 2015, 8, 62.	1.5	27
20	RPL13A as a reference gene for normalizing mRNA transcription of ovarian cancer cells with paclitaxel and 10-hydroxycamptothecin treatments. Molecular Medicine Reports, 2015, 11, 3188-3194.	2.4	24
21	Ribosomal L22-like1 (RPL22L1) Promotes Ovarian Cancer Metastasis by Inducing Epithelial-to-Mesenchymal Transition. PLoS ONE, 2015, 10, e0143659.	2.5	23
22	Computational identification of epigenetically regulated lncRNAs and their associated genes based on integrating genomic data. FEBS Letters, 2015, 589, 521-531.	2.8	23
23	Predicting the Functions of Long Noncoding RNAs Using RNA-Seq Based on Bayesian Network. BioMed Research International, 2015, 2015, 1-14.	1.9	22
24	Gene Perturbation Atlas (GPA): a single-gene perturbation repository for characterizing functional mechanisms of coding and non-coding genes. Scientific Reports, 2015, 5, 10889.	3.3	21
25	ImmReg: the regulon atlas of immune-related pathways across cancer types. Nucleic Acids Research, 2021, 49, 12106-12118.	14.5	14
26	Decreased TOB1 expression and increased phosphorylation of nuclear TOB1 promotes gastric cancer. Oncotarget, 2017, 8, 75243-75253.	1.8	13
27	<scp>NUBPL</scp>, a novel metastasisâ€related gene, promotes colorectal carcinoma cell motility by inducing epithelialâ€“mesenchymal transition. Cancer Science, 2017, 108, 1169-1176.	3.9	12
28	SEI1 induces genomic instability by inhibiting DNA damage response in ovarian cancer. Cancer Letters, 2017, 385, 271-279.	7.2	11
29	Landscape of Enhancer-Enhancer Cooperative Regulation during Human Cardiac Commitment. Molecular Therapy - Nucleic Acids, 2019, 17, 840-851.	5.1	11
30	Met promotes the formation of double minute chromosomes induced by Sei-1 in NIH-3T3 murine fibroblasts. Oncotarget, 2016, 7, 56664-56675.	1.8	11
31	MeImmS: Predict Clinical Benefit of Anti-PD-1/PD-L1 Treatments Based on DNA Methylation in Non-small Cell Lung Cancer. Frontiers in Genetics, 2021, 12, 676449.	2.3	10
32	Molecular structure and evolution mechanism of two populations of double minutes in human colorectal cancer cells. Journal of Cellular and Molecular Medicine, 2020, 24, 14205-14216.	3.6	9
33	Evaluation of a Novel Missense Mutation inABCB4Gene Causing Progressive Familial Intrahepatic Cholestasis Type 3. Disease Markers, 2020, 2020, 1-10.	1.3	9
34	A heterozygous duplication variant of the HOXD13 gene caused synpolydactyly type 1 with variable expressivity in a Chinese family. BMC Medical Genetics, 2019, 20, 203.	2.1	8
35	Association between sister chromatid exchange and double minute chromosomes in human tumor cells. Molecular Cytogenetics, 2015, 8, 91.	0.9	5
36	Polymorphisms in cytokine genes as prognostic markers in diffuse large B cell lymphoma patients treated with (R)-CHOP. Annals of Hematology, 2017, 96, 227-235.	1.8	5

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37	Computationally Modeling ncRNA-ncRNA Crosstalk. Advances in Experimental Medicine and Biology, 2018, 1094, 77-86.	1.6	4
38	Identification of a pathogenic mutation in a Chinese pedigree with polycystic kidney disease. Molecular Medicine Reports, 2019, 19, 2671-2679.	2.4	4
39	Disease causing property analyzation of variants in 12 Chinese families with polycystic kidney disease. Molecular Genetics & Genomic Medicine, 2020, 8, e1467.	1.2	2
40	Population Genetic Polymorphism of Skeletal Muscle Strength Related Genes in Five Ethnic Minorities in North China. Frontiers in Genetics, 2021, 12, 756802.	2.3	2
41	Genetic Polymorphism of Drug Metabolic Gene CYPs, VKORC1, NAT2, DPYD and CHST3 of Five Ethnic Minorities in Heilongjiang Province, Northeast China. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 1537-1547.	0.7	1
42	Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes. Frontiers in Cell and Developmental Biology, 2021, 9, 768981.	3.7	1
43	A novel variant of GLI3 , p. <scp>Asp1514Thrfs</scp> *5, is identified in a Chinese family affected by polydactyly. Molecular Genetics & Genomic Medicine, 2022, , e1968.	1.2	1