Qinghua Jiang

List of Publications by Year
in descending order

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37 papers	3,839 citations	430874 18 h-index	377865 34 g-index
37 all docs	37 docs citations	37 times ranked	4435 citing authors

#	Article	IF	Citations
1	miR2Disease: a manually curated database for microRNA deregulation in human disease. Nucleic Acids Research, 2009, 37, D98-D104.	14.5	1,255
2	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. Cell, 2021, 184, 1895-1913.e19.	28.9	512
3	Prioritization of disease microRNAs through a human phenome-microRNAome network. BMC Systems Biology, 2010, 4, S2.	3.0	335
4	LncRNA2Target v2.0: a comprehensive database for target genes of lncRNAs in human and mouse. Nucleic Acids Research, 2019, 47, D140-D144.	14.5	311
5	DincRNA: a comprehensive web-based bioinformatics toolkit for exploring disease associations and ncRNA function. Bioinformatics, 2018, 34, 1953-1956.	4.1	241
6	Predicting human microRNA-disease associations based on support vector machine. International Journal of Data Mining and Bioinformatics, 2013, 8, 282.	0.1	208
7	CircR2Disease: a manually curated database for experimentally supported circular RNAs associated with various diseases. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	166
8	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
9	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
10	PICALM rs3851179 Variant Confers Susceptibility to Alzheimerâ€™s Disease in Chinese Population. Molecular Neurobiology, 2017, 54, 3131-3136.	4.0	66
11	Single-cell transcriptome and TCR profiling reveal activated and expanded T cell populations in Parkinsonâ€™s disease. Cell Discovery, 2021, 7, 52.	6.7	51
12	TF2LncRNA: Identifying Common Transcription Factors for a List of lncRNA Genes from ChIP-Seq Data. BioMed Research International, 2014, 2014, 1-5.	1.9	47
13	Comprehensive analysis of TCR repertoire in COVID-19 using single cell sequencing. Genomics, 2021, 113, 456-462.	2.9	47
14	Genetic variant rs17185536 regulates SIM1 gene expression in human brain hypothalamus. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3347-3348.	7.1	33
15	Single cell RNA and immune repertoire profiling of COVID-19 patients reveal novel neutralizing antibody. Protein and Cell, 2021, 12, 751-755.	11.0	32
16	Alzheimerâ€™s disease CD33 rs3865444 variant does not contribute to cognitive performance. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1589-E1590.	7.1	28
17	Global characterization of B cell receptor repertoire in COVID-19 patients by single-cell V(D)J sequencing. Briefings in Bioinformatics, 2021, 22, .	6.5	28
18	Transcriptional Regulation of lncRNA Genes by Histone Modification in Alzheimerâ€™s Disease. BioMed Research International, 2016, 2016, 1-4.	1.9	25

#	Article	IF	Citations
19	An approach for prioritizing disease-related microRNAs based on genomic data integration. , 2010, , .		20
20	N439K Variant in Spike Protein Alter the Infection Efficiency and Antigenicity of SARS-CoV-2 Based on Molecular Dynamics Simulation. Frontiers in Cell and Developmental Biology, 2021, 9, 697035.	3.7	19
21	Identifying Liver Cancer-Related Enhancer SNPs by Integrating GWAS and Histone Modification ChIP-seq Data. BioMed Research International, 2016, 2016, 1-6.	1.9	17
22	Role of Kruppel homolog 1 (Kr-h1) in methyl farnesoate-mediated vitellogenesis in the swimming crab Portunus trituberculatus. Gene, 2018, 679, 260-265.	2.2	16
23	Impact of mutations in SARS-COV-2 spike on viral infectivity and antigenicity. Briefings in Bioinformatics, 2022, 23, .	6.5	16
24	Alternative splicing associated with cancer stemness in kidney renal clear cell carcinoma. BMC Cancer, 2021, 21, 703.	2.6	15
25	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. BMC Bioinformatics, 2015, 16, 386.	2.6	14
26	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
27	Identification of potential vaccine targets for COVIDâ€19 by combining singleâ€cell and bulk TCR sequencing. Clinical and Translational Medicine, 2021, 11, e430.	4.0	12
28	A pan-cancer analysis of alternative splicing of splicing factors in 6904 patients. Oncogene, 2021, 40, 5441-5450.	5.9	12
29	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. BMC Bioinformatics, 2017, 18, 270.	2.6	11
30	Comprehensive Analysis of Copy Number Variations in Kidney Cancer by Single-Cell Exome Sequencing. Frontiers in Genetics, 2019, 10, 1379.	2.3	9
31	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization. , 2018, , .		8
32	Simultaneous determination of nine major constituents in Agrimonia pilosa Ledeb. by HPLC-DAD-ESI-MS/MS. Analytical Methods, 2014, 6, 4373.	2.7	7
33	Comprehensive analysis of partial methylation domains in colorectal cancer based on single-cell methylation profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	7
34	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. Protein and Peptide Letters, 2020, 27, 295-302.	0.9	6
35	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. Current Bioinformatics, 2020, 15, 574-580.	1.5	6
36	Overview of structural variation calling: Simulation, identification, and visualization. Computers in Biology and Medicine, 2022, 145, 105534.	7.0	4

#	Article	IF	Citations
37	MutCov: A pipeline for evaluating the effect of mutations in spike protein on infectivity and antigenicity of SARS-CoV-2. Computers in Biology and Medicine, 2022, 145, 105509.	7.0	2