

Shuilin Jin

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,469
citations

331670

21
h-index

330143

37
g-index

49
all docs

49
docs citations

49
times ranked

1804
citing authors

#	ARTICLE	IF	CITATIONS
1	Meta-Analysis for Epigenome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, 2432, 101-111.	0.9	1
2	The scRNA-seq Expression Profiling of the Receptor ACE2 and the Cellular Protease TMPRSS2 Reveals Human Organs Susceptible to SARS-CoV-2 Infection. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 284.	2.6	82
3	Comprehensive analysis of TCR repertoire in COVID-19 using single cell sequencing. <i>Genomics</i> , 2021, 113, 456-462.	2.9	47
4	SDImpute: A statistical block imputation method based on cell-level and gene-level information for dropouts in single-cell RNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1009118.	3.2	8
5	Circulating Vitamin D Levels and Alzheimer's Disease: A Mendelian Randomization Study in the IGAP and UK Biobank. <i>Journal of Alzheimer's Disease</i> , 2020, 73, 609-618.	2.6	37
6	LAK: Lasso and K-Means Based Single-Cell RNA-Seq Data Clustering Analysis. <i>IEEE Access</i> , 2020, 8, 129679-129688.	4.2	15
7	NDRindex: a method for the quality assessment of single-cell RNA-Seq preprocessing data. <i>BMC Bioinformatics</i> , 2020, 21, 540.	2.6	0
8	Impact of Serum Calcium Levels on Alzheimer's Disease: A Mendelian Randomization Study. <i>Journal of Alzheimer's Disease</i> , 2020, 76, 713-724.	2.6	21
9	A novel estimator of between-study variance in random-effects models. <i>BMC Genomics</i> , 2020, 21, 149.	2.8	1
10	A Method Based on Differential Entropy-Like Function for Detecting Differentially Expressed Genes Across Multiple Conditions in RNA-Seq Studies. <i>Entropy</i> , 2019, 21, 242.	2.2	1
11	Genetic variant rs17185536 regulates <i>SIM1</i> gene expression in human brain hypothalamus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3347-3348.	7.1	33
12	NDRindex: A method for the quality assessment of single-cell RNA-Seq preprocessing data. , 2019, , .		0
13	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. <i>BMC Bioinformatics</i> , 2019, 20, 573.	2.6	13
14	BIN1 rs744373 variant shows different association with Alzheimer's disease in Caucasian and Asian populations. <i>BMC Bioinformatics</i> , 2019, 20, 691.	2.6	10
15	Interleukin-6 Receptor and Inflammatory Bowel Disease: A Mendelian Randomization Study. <i>Gastroenterology</i> , 2019, 156, 823-824.	1.3	22
16	Alzheimer's Disease rs11767557 Variant Regulates EPHA1 Gene Expression Specifically in Human Whole Blood. <i>Journal of Alzheimer's Disease</i> , 2018, 61, 1077-1088.	2.6	55
17	Meta-analysis of association between TCF7L2 polymorphism rs7903146 and type 2 diabetes mellitus. <i>BMC Medical Genetics</i> , 2018, 19, 38.	2.1	50
18	EWAS: epigenome-wide association study software 2.0. <i>Bioinformatics</i> , 2018, 34, 2657-2658.	4.1	23

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19	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization. , 2018, , .		8
20	Parkinsonâ€™s disease and Alzheimerâ€™s disease: a Mendelian randomization study. BMC Medical Genetics, 2018, 19, 215.	2.1	25
21	Disease status affects the association between rs4813620 and the expression of Alzheimerâ€™s disease susceptibility gene <i>TRIB3</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10519-E10520.	7.1	47
22	Circulating vitamin E levels and Alzheimer's disease: a Mendelian randomization study. Neurobiology of Aging, 2018, 72, 189.e1-189.e9.	3.1	53
23	Alzheimerâ€™s Disease Risk Variant rs2373115 Regulates GAB2 and NARS2 Expression in Human Brain Tissues. Journal of Molecular Neuroscience, 2018, 66, 37-43.	2.3	25
24	Relationship Between Alzheimerâ€™s Disease and the Immune System: A Meta-Analysis of Differentially Expressed Genes. Frontiers in Neuroscience, 2018, 12, 1026.	2.8	10
25	Alzheimerâ€™s Disease Variants with the Genome-Wide Significance are Significantly Enriched in Immune Pathways and Active in Immune Cells. Molecular Neurobiology, 2017, 54, 594-600.	4.0	131
26	Genetic variant rs763361 regulates multiple sclerosis <i>CD226</i> gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E906-E907.	7.1	46
27	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	2.8	46
28	GAB2 rs2373115 variant contributes to Alzheimer's disease risk specifically in European population. Journal of the Neurological Sciences, 2017, 375, 18-22.	0.6	43
29	Operational independence and tensor products of C^* -algebras. Journal of Mathematical Physics, 2017, 58, 032303.	1.1	2
30	Autoimmune disease variants regulate <i>GSDMB</i> gene expression in human immune cells and whole blood. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7860-E7862.	7.1	30
31	Rs4878104 contributes to Alzheimerâ€™s disease risk and regulates DAPK1 gene expression. Neurological Sciences, 2017, 38, 1255-1262.	1.9	29
32	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. BMC Bioinformatics, 2017, 18, 270.	2.6	11
33	The Complexity of Promoter Regions Based on a Vector Topological Entropy. Current Bioinformatics, 2017, 12, .	1.5	1
34	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. BioMed Research International, 2016, 2016, 1-8.	1.9	16
35	Transcriptional Regulation of lncRNA Genes by Histone Modification in Alzheimerâ€™s Disease. BioMed Research International, 2016, 2016, 1-4.	1.9	25
36	<i>Cis</i> -eQTLs regulate reduced <i>LST1</i> gene and <i>NCR3</i> gene expression and contribute to increased autoimmune disease risk. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6321-E6322.	7.1	24

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37	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
38	A Reliability-Based Track Fusion Algorithm. PLoS ONE, 2015, 10, e0126227.	2.5	3
39	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
40	A Generalized Topological Entropy for Analyzing the Complexity of DNA Sequences. PLoS ONE, 2014, 9, e88519.	2.5	16
41	Bidirectional-Paralleled Flexible Graphplan. Journal of Computational and Theoretical Nanoscience, 2014, 11, 2190-2193.	0.4	0
42	A track association algorithm based on the weighted association graph for laser triangulation sensors. Optik, 2014, 125, 5973-5977.	2.9	1
43	Joint Spectrum and Joint Distribution. Complex Analysis and Operator Theory, 2013, 7, 1869-1875.	0.6	1
44	Independences of operator algebras and joint spectrum of operators. Linear and Multilinear Algebra, 2013, 61, 565-572.	1.0	1
45	On Curto's open problem. Journal of Mathematical Analysis and Applications, 2013, 405, 342-344.	1.0	0
46	Large Time Behavior of the Vlasov-Poisson-Boltzmann System. Abstract and Applied Analysis, 2013, 2013, 1-9.	0.7	0
47	Predicting human microRNA-disease associations based on support vector machine. International Journal of Data Mining and Bioinformatics, 2013, 8, 282.	0.1	208
48	The Entanglement of Independent Quantum Systems. Advances in Mathematical Physics, 2012, 2012, 1-6.	0.8	6