Shuilin Jin

List of Publications by Year
in descending order

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	Predicting human microRNA-disease associations based on support vector machine. International Journal of Data Mining and Bioinformatics, 2013, 8, 282.	0.1	208
2	Alzheimer'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
3	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
4	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
5	The scRNA-seq Expression Profiling of the Receptor ACE2 and the Cellular Protease TMPRSS2 Reveals Human Organs Susceptible to SARS-CoV-2 Infection. International Journal of Environmental Research and Public Health, 2021, 18, 284.	2.6	82
6	Alzheimer's Disease rs11767557 Variant Regulates EPHA1 Gene Expression Specifically in Human Whole Blood. Journal of Alzheimer's Disease, 2018, 61, 1077-1088.	2.6	55
7	Circulating vitamin E levels and Alzheimer's disease: a Mendelian randomization study. Neurobiology of Aging, 2018, 72, 189.e1-189.e9.	3.1	53
8	Meta-analysis of association between TCF7L2 polymorphism rs7903146 and type 2 diabetes mellitus. BMC Medical Genetics, 2018, 19, 38.	2.1	50
9	Disease status affects the association between rs4813620 and the expression of Alzheimer's disease susceptibility gene *TRIB3*. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10519-E10520.	7.1	47
10	Comprehensive analysis of TCR repertoire in COVID-19 using single cell sequencing. Genomics, 2021, 113, 456-462.	2.9	47
11	Genetic variant rs763361 regulates multiple sclerosis *CD226* gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E906-E907.	7.1	46
12	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	2.8	46
13	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
14	Circulating Vitamin D Levels and Alzheimer's Disease: A Mendelian Randomization Study in the IGAP and UK Biobank. Journal of Alzheimer's Disease, 2020, 73, 609-618.	2.6	37
15	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
16	Autoimmune disease variants regulate *GSDMB* 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
17	Rs4878104 contributes to Alzheimer's disease risk and regulates DAPK1 gene expression. Neurological Sciences, 2017, 38, 1255-1262.	1.9	29
18	Transcriptional Regulation of lncRNA Genes by Histone Modification in Alzheimer's Disease. BioMed Research International, 2016, 2016, 1-4.	1.9	25

#	ARTICLE	IF	CITATIONS
19	Parkinson's disease and Alzheimer's disease: a Mendelian randomization study. BMC Medical Genetics, 2018, 19, 215.	2.1	25
20	Alzheimer'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
21	*Cis* -eQTLs regulate reduced *LST1* gene and *NCR3* 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
22	EWAS: epigenome-wide association study software 2.0. Bioinformatics, 2018, 34, 2657-2658.	4.1	23
23	Interleukin-6 Receptor and Inflammatory Bowel Disease: AâMendelian Randomization Study. Gastroenterology, 2019, 156, 823-824.	1.3	22
24	Impact of Serum Calcium Levels on Alzheimer's Disease: A Mendelian Randomization Study. Journal of Alzheimer's Disease, 2020, 76, 713-724.	2.6	21
25	A Generalized Topological Entropy for Analyzing the Complexity of DNA Sequences. PLoS ONE, 2014, 9, e88519.	2.5	16
26	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. BioMed Research International, 2016, 2016, 1-8.	1.9	16
27	LAK: Lasso and K-Means Based Single-Cell RNA-Seq Data Clustering Analysis. IEEE Access, 2020, 8, 129679-129688.	4.2	15
28	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. BMC Bioinformatics, 2019, 20, 573.	2.6	13
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	BIN1 rs744373 variant shows different association with Alzheimer's disease in Caucasian and Asian populations. BMC Bioinformatics, 2019, 20, 691.	2.6	10
31	Relationship Between Alzheimer's Disease and the Immune System: A Meta-Analysis of Differentially Expressed Genes. Frontiers in Neuroscience, 2018, 12, 1026.	2.8	10
32	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization. , 2018, , .		8
33	SDImpute: A statistical block imputation method based on cell-level and gene-level information for dropouts in single-cell RNA-seq data. PLoS Computational Biology, 2021, 17, e1009118.	3.2	8
34	The Entanglement of Independent Quantum Systems. Advances in Mathematical Physics, 2012, 2012, 1-6.	0.8	6
35	A Reliability-Based Track Fusion Algorithm. PLoS ONE, 2015, 10, e0126227.	2.5	3
36	Operational independence and tensor products of C*-algebras. Journal of Mathematical Physics, 2017, 58, 032303.	1.1	2

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37	Joint Spectrum and Joint Distribution. Complex Analysis and Operator Theory, 2013, 7, 1869-1875.	0.6	1
38	Independences of operator algebras and joint spectrum of operators. Linear and Multilinear Algebra, 2013, 61, 565-572.	1.0	1
39	A track association algorithm based on the weighted association graph for laser triangulation sensors. Optik, 2014, 125, 5973-5977.	2.9	1
40	A Method Based on Differential Entropy-Like Function for Detecting Differentially Expressed Genes Across Multiple Conditions in RNA-Seq Studies. Entropy, 2019, 21, 242.	2.2	1
41	A novel estimator of between-study variance in random-effects models. BMC Genomics, 2020, 21, 149.	2.8	1
42	The Complexity of Promoter Regions Based on a Vector Topological Entropy. Current Bioinformatics, 2017, 12, .	1.5	1
43	Meta-Analysis for Epigenome-Wide Association Studies. Methods in Molecular Biology, 2022, 2432, 101-111.	0.9	1
44	On Curto's open problem. Journal of Mathematical Analysis and Applications, 2013, 405, 342-344.	1.0	0
45	Large Time Behavior of the Vlasov-Poisson-Boltzmann System. Abstract and Applied Analysis, 2013, 2013, 1-9.	0.7	0
46	Bidirectional-Paralleled Flexible Graphplan. Journal of Computational and Theoretical Nanoscience, 2014, 11, 2190-2193.	0.4	0
47	NDRindex: A method for the quality assessment of single-cell RNA-Seq preprocessing data. , 2019, , .		0
48	NDRindex: a method for the quality assessment of single-cell RNA-Seq preprocessing data. BMC Bioinformatics, 2020, 21, 540.	2.6	0