Jiebiao Wang

List of Publications by Year
in descending order

26 papers	2,197 citations	687363 13 h-index	610901 24 g-index
41 all docs	41 docs citations	41 times ranked	4991 citing authors

#	Article	IF	Citations
1	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. Bioinformatics, 2022, 38, 3004-3010.	4.1	10
2	ESCO: single cell expression simulation incorporating gene co-expression. Bioinformatics, 2021, 37, 2374-2381.	4.1	21
3	CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. Bioinformatics, 2021, 37, 2513-2520.	4.1	4
4	Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. Translational Psychiatry, 2021, 11, 171.	4.8	13
5	Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. Bioinformatics, 2021, 37, 3228-3234.	4.1	9
6	Bayesian estimation of cell type–specific gene expression with prior derived from single-cell data. Genome Research, 2021, 31, 1807-1818.	5.5	40
7	Prospective Development and Validation of the Computerized Adaptive Screen for Suicidal Youth. JAMA Psychiatry, 2021, 78, 540.	11.0	30
8	MAD1L1 Harbors Schizophrenia-Associated Differential Methylation and Methylation/Transcription Quantitative Trait Loci that Colocalize With Genetic Risk for Schizophrenia. Biological Psychiatry, 2021, 89, S153.	1.3	0
9	Transcriptional Alterations in Dorsolateral Prefrontal Cortex and Nucleus Accumbens Implicate Neuroinflammation and Synaptic Remodeling in Opioid Use Disorder. Biological Psychiatry, 2021, 90, 550-562.	1.3	76
10	Small nucleolar RNAs in plasma extracellular vesicles and their discriminatory power as diagnostic biomarkers of Alzheimer's disease. Neurobiology of Disease, 2021, 159, 105481.	4.4	17
11	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. Bioinformatics, 2020, 36, 782-788.	4.1	28
12	De novo missense variants disrupting protein–protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. Molecular Autism, 2020, 11, 76.	4.9	19
13	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	5.3	75
14	Gene Expression Deconvolution Implicates Cell-Type-Specific Gene Expression and Co-Expression in Autism. Biological Psychiatry, 2020, 87, S60-S61.	1.3	1
15	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
16	Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. Biostatistics, 2019, 20, 648-665.	1.5	3
17	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.	14.8	63
18	A meta-analysis approach with filtering for identifying gene-level gene–environment interactions. Genetic Epidemiology, 2018, 42, 434-446.	1.3	5

#	Article	IF	Citations
19	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nature Communications, 2018, 9, 4181.	12.8	77
20	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	21.4	64
21	Identifying *cis*-mediators for *trans*-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
22	A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. Annals of Applied Statistics, 2017, 11, 114-138.	1.1	9
23	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
24	Abstract 4494: Whole genome sequencing reveals different patterns of mutational mechanisms in breast tumors between women of African and European descent. , 2016, , .		0
25	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. SSRN Electronic Journal, 0, , .	0.4	12
26	Medications and Suicide: High Dimensional Empirical Bayes Screening (iDEAS). , 0, , .		7