

Weidong Tian

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,195
citations

567281

15
h-index

477307

29
g-index

30
all docs

30
docs citations

30
times ranked

1879
citing authors

#	ARTICLE	IF	CITATIONS
1	scMAGIC: accurately annotating single cells using two rounds of reference-based classification. <i>Nucleic Acids Research</i> , 2022, 50, e43-e43.	14.5	11
2	Single-cell transcriptomics reveals pathogenic dysregulation of previously unrecognised chondral stem/progenitor cells in children with microtia. <i>Clinical and Translational Medicine</i> , 2022, 12, e702.	4.0	1
3	CRMarker: A manually curated comprehensive resource of cancer RNA markers. <i>International Journal of Biological Macromolecules</i> , 2021, 174, 263-269.	7.5	3
4	Unsupervised Inference of Developmental Directions for Single Cells Using VECTOR. <i>Cell Reports</i> , 2020, 32, 108069.	6.4	11
5	Authors' reply re: Association between preconception paternal smoking and birth defects in offspring: evidence from the database of the National Free Preconception Health Examination Project in China. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020, 127, 1579-1580.	2.3	0
6	qMGR: A new approach for quantifying mitochondrial genome rearrangement. <i>Mitochondrion</i> , 2020, 52, 20-23.	3.4	19
7	Identification of DNA methylation patterns and biomarkers for clear-cell renal cell carcinoma by multi-omics data analysis. <i>PeerJ</i> , 2020, 8, e9654.	2.0	7
8	Single-Cell Transcriptomics in Medulloblastoma Reveals Tumor-Initiating Progenitors and Oncogenic Cascades during Tumorigenesis and Relapse. <i>Cancer Cell</i> , 2019, 36, 302-318.e7.	16.8	96
9	A novel approach to remove the batch effect of single-cell data. <i>Cell Discovery</i> , 2019, 5, 46.	6.7	37
10	Evolution and Comprehensive Analysis of DNaseI Hypersensitive Sites in Regulatory Regions of Primate Brain-Related Genes. <i>Frontiers in Genetics</i> , 2019, 10, 152.	2.3	5
11	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
12	Regulation of mRNA splicing by MeCP2 via epigenetic modifications in the brain. <i>Scientific Reports</i> , 2017, 7, 42790.	3.3	38
13	GenePANDA—a novel network-based gene prioritizing tool for complex diseases. <i>Scientific Reports</i> , 2017, 7, 43258.	3.3	18
14	Dynamic Editome of Zebrafish under Aminoglycosides Treatment and Its Potential Involvement in Ototoxicity. <i>Frontiers in Pharmacology</i> , 2017, 8, 854.	3.5	2
15	Whole genome sequencing identifies a novel ALMS1 gene mutation in two Chinese siblings with Alström syndrome. <i>BMC Medical Genetics</i> , 2017, 18, 75.	2.1	10
16	Prediction of Candidate Drugs for Treating Pancreatic Cancer by Using a Combined Approach. <i>PLoS ONE</i> , 2016, 11, e0149896.	2.5	6
17	Cellulose synthesis genes <i>CESA6</i> and <i>CS11</i> are important for salt stress tolerance in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2016, 58, 623-626.	8.5	45
18	Genome-Wide Identification of Regulatory Sequences Undergoing Accelerated Evolution in the Human Genome. <i>Molecular Biology and Evolution</i> , 2016, 33, 2565-2575.	8.9	64

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19	China's community-based strategy of universal preconception care in rural areas at a population level using a novel risk classification system for stratifying couples' preconception health status. BMC Health Services Research, 2016, 16, 689.	2.2	17
20	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
21	LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. Scientific Reports, 2016, 6, 18871.	3.3	37
22	Explaining the disease phenotype of intergenic SNP through predicted long range regulation. Nucleic Acids Research, 2016, 44, 8641-8654.	14.5	40
23	GSA-Lightning: ultra-fast permutation-based gene set analysis. Bioinformatics, 2016, 32, 3029-3031.	4.1	3
24	GoFDR: A sequence alignment based method for predicting protein functions. Methods, 2016, 93, 3-14.	3.8	57
25	Positive selection on <i>Lactate dehydrogenases of Lactobacillus delbrueckii subspecies bulgaricus</i> . IET Systems Biology, 2015, 9, 172-179.	1.5	9
26	Prediction of Metabolic Gene Biomarkers for Neurodegenerative Disease by an Integrated Network-Based Approach. BioMed Research International, 2015, 2015, 1-9.	1.9	7
27	Solute Carrier Family 26 Member a2 (slc26a2) Regulates Otic Development and Hair Cell Survival in Zebrafish. PLoS ONE, 2015, 10, e0136832.	2.5	6
28	The Effect of Multiple Single Nucleotide Polymorphisms in the Folic Acid Pathway Genes on Homocysteine Metabolism. BioMed Research International, 2014, 2014, 1-9.	1.9	28
29	microRNA expression profiling of heart tissue during fetal development. International Journal of Molecular Medicine, 2014, 33, 1250-1260.	4.0	24
30	Integration of Cancer Gene Co-expression Network and Metabolic Network To Uncover Potential Cancer Drug Targets. Journal of Proteome Research, 2013, 12, 2354-2364.	3.7	25