

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	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
2	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
3	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
4	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
5	GoFDR: A sequence alignment based method for predicting protein functions. <i>Methods</i> , 2016, 93, 3-14.	3.8	57
6	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
7	Explaining the disease phenotype of intergenic SNP through predicted long range regulation. <i>Nucleic Acids Research</i> , 2016, 44, 8641-8654.	14.5	40
8	Regulation of mRNA splicing by MeCP2 via epigenetic modifications in the brain. <i>Scientific Reports</i> , 2017, 7, 42790.	3.3	38
9	LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. <i>Scientific Reports</i> , 2016, 6, 18871.	3.3	37
10	A novel approach to remove the batch effect of single-cell data. <i>Cell Discovery</i> , 2019, 5, 46.	6.7	37
11	The Effect of Multiple Single Nucleotide Polymorphisms in the Folic Acid Pathway Genes on Homocysteine Metabolism. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	28
12	Integration of Cancer Gene Co-expression Network and Metabolic Network To Uncover Potential Cancer Drug Targets. <i>Journal of Proteome Research</i> , 2013, 12, 2354-2364.	3.7	25
13	microRNA expression profiling of heart tissue during fetal development. <i>International Journal of Molecular Medicine</i> , 2014, 33, 1250-1260.	4.0	24
14	qMGR: A new approach for quantifying mitochondrial genome rearrangement. <i>Mitochondrion</i> , 2020, 52, 20-23.	3.4	19
15	GenePANDA—a novel network-based gene prioritizing tool for complex diseases. <i>Scientific Reports</i> , 2017, 7, 43258.	3.3	18
16	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. <i>BMC Health Services Research</i> , 2016, 16, 689.	2.2	17
17	Unsupervised Inference of Developmental Directions for Single Cells Using VECTOR. <i>Cell Reports</i> , 2020, 32, 108069.	6.4	11
18	scMAGIC: accurately annotating single cells using two rounds of reference-based classification. <i>Nucleic Acids Research</i> , 2022, 50, e43-e43.	14.5	11

#	ARTICLE	IF	CITATIONS
19	Whole genome sequencing identifies a novel ALMS1 gene mutation in two Chinese siblings with Alström syndrome. BMC Medical Genetics, 2017, 18, 75.	2.1	10
20	Positive selection on D-lactate dehydrogenases of <i>Lactobacillus delbrueckii</i> subspecies <i>bulgaricus</i> . IET Systems Biology, 2015, 9, 172-179.	1.5	9
21	Prediction of Metabolic Gene Biomarkers for Neurodegenerative Disease by an Integrated Network-Based Approach. BioMed Research International, 2015, 2015, 1-9.	1.9	7
22	Identification of DNA methylation patterns and biomarkers for clear-cell renal cell carcinoma by multi-omics data analysis. PeerJ, 2020, 8, e9654.	2.0	7
23	Prediction of Candidate Drugs for Treating Pancreatic Cancer by Using a Combined Approach. PLoS ONE, 2016, 11, e0149896.	2.5	6
24	Solute Carrier Family 26 Member a2 (slc26a2) Regulates Otic Development and Hair Cell Survival in Zebrafish. PLoS ONE, 2015, 10, e0136832.	2.5	6
25	Evolution and Comprehensive Analysis of DNaseI Hypersensitive Sites in Regulatory Regions of Primate Brain-Related Genes. Frontiers in Genetics, 2019, 10, 152.	2.3	5
26	GSA-Lightning: ultra-fast permutation-based gene set analysis. Bioinformatics, 2016, 32, 3029-3031.	4.1	3
27	CRMarker: A manually curated comprehensive resource of cancer RNA markers. International Journal of Biological Macromolecules, 2021, 174, 263-269.	7.5	3
28	Dynamic Editome of Zebrafish under Aminoglycosides Treatment and Its Potential Involvement in Ototoxicity. Frontiers in Pharmacology, 2017, 8, 854.	3.5	2
29	Single-cell transcriptomics reveals pathogenic dysregulation of previously unrecognised chondral stem/progenitor cells in children with microtia. Clinical and Translational Medicine, 2022, 12, e702.	4.0	1
30	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. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 1579-1580.	2.3	0