Ge Gao

List of Publications by Year
in descending order

53 papers	19,146 citations	186209 28 h-index	189801 50 g-index
59 all docs	59 docs citations	59 times ranked	24880 citing authors

#	Article	IF	Citations
1	GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. Nucleic Acids Research, 2017, 45, W98-W102.	6.5	7,114
2	GSDS 2.0: an upgraded gene feature visualization server. Bioinformatics, 2015, 31, 1296-1297.	1.8	3,092
3	CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine. Nucleic Acids Research, 2007, 35, W345-W349.	6.5	2,525
4	PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. Nucleic Acids Research, 2017, 45, D1040-D1045.	6.5	1,651
5	CPC2: a fast and accurate coding potential calculator based on sequence intrinsic features. Nucleic Acids Research, 2017, 45, W12-W16.	6.5	970
6	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. Nucleic Acids Research, 2014, 42, D1182-D1187.	6.5	800
7	PlantRegMap: charting functional regulatory maps in plants. Nucleic Acids Research, 2020, 48, D1104-D1113.	6.5	333
8	CasOT: a genome-wide Cas9/gRNA off-target searching tool. Bioinformatics, 2014, 30, 1180-1182.	1.8	312
9	PlantTFDB 2.0: update and improvement of the comprehensive plant transcription factor database. Nucleic Acids Research, 2011, 39, D1114-D1117.	6.5	288
10	PlantTFDB: a comprehensive plant transcription factor database. Nucleic Acids Research, 2007, 36, D966-D969.	6.5	210
11	An *Arabidopsis* Transcriptional Regulatory Map Reveals Distinct Functional and Evolutionary Features of Novel Transcription Factors. Molecular Biology and Evolution, 2015, 32, 1767-1773.	3.5	175
12	Database Resources of the BIG Data Center in 2019. Nucleic Acids Research, 2019, 47, D8-D14.	6.5	157
13	Multi-omics single-cell data integration and regulatory inference with graph-linked embedding. Nature Biotechnology, 2022, 40, 1458-1466.	9.4	153
14	Interactome analysis identifies a new paralogue of XRCC4 in non-homologous end joining DNA repair pathway. Nature Communications, 2015, 6, 6233.	5.8	144
15	DRTF: a database of rice transcription factors. Bioinformatics, 2006, 22, 1286-1287.	1.8	141
16	DPTF: a database of poplar transcription factors. Bioinformatics, 2007, 23, 1307-1308.	1.8	94
17	An expanded landscape of human long noncoding RNA. Nucleic Acids Research, 2019, 47, 7842-7856.	6.5	92
18	Searching large-scale scRNA-seq databases via unbiased cell embedding with Cell BLAST. Nature Communications, 2020, 11, 3458.	5.8	81

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19	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. Genome Research, 2019, 29, 682-696.	2.4	67
20	Postzygotic single-nucleotide mosaicisms in whole-genome sequences of clinically unremarkable individuals. Cell Research, 2014, 24, 1311-1327.	5.7	54
21	Ewing Tumor-associated Antigen 1 Interacts with Replication Protein A to Promote Restart of Stalled Replication Forks. Journal of Biological Chemistry, 2016, 291, 21956-21962.	1.6	53
22	Painting a specific chromosome with CRISPR/Cas9 for live-cell imaging. Cell Research, 2017, 27, 298-301.	5.7	53
23	AnnoLnc: a web server for systematically annotating novel human lncRNAs. BMC Genomics, 2016, 17, 931.	1.2	51
24	A brief introduction to web-based genome browsers. Briefings in Bioinformatics, 2013, 14, 131-143.	3.2	46
25	Expression pattern divergence of duplicated genes in rice. BMC Bioinformatics, 2009, 10, S8.	1.2	43
26	Molecular features of secondary vascular tissue regeneration after bark girdling in <i>Populus</i>. New Phytologist, 2011, 192, 869-884.	3.5	43
27	The nucleoskeleton protein IFFO1 immobilizes broken DNA and suppresses chromosome translocation during tumorigenesis. Nature Cell Biology, 2019, 21, 1273-1285.	4.6	40
28	Global miRNA dosage control of embryonic germ layer specification. Nature, 2021, 593, 602-606.	13.7	39
29	AnnoLnc2: the one-stop portal to systematically annotate novel lncRNAs for human and mouse. Nucleic Acids Research, 2020, 48, W230-W238.	6.5	37
30	Long non-coding RNAs involved in the regulatory network during porcine pre-implantation embryonic development and iPSC induction. Scientific Reports, 2018, 8, 6649.	1.6	29
31	WebLab: a data-centric, knowledge-sharing bioinformatic platform. Nucleic Acids Research, 2009, 37, W33-W39.	6.5	27
32	Mitosis-specific MRN complex promotes a mitotic signaling cascade to regulate spindle dynamics and chromosome segregation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10079-E10088.	3.3	27
33	ABrowse - a customizable next-generation genome browser framework. BMC Bioinformatics, 2012, 13, 2.	1.2	22
34	A long-term demasculinization of X-linked intergenic noncoding RNAs in Drosophila melanogaster. Genome Research, 2014, 24, 629-638.	2.4	22
35	Expectation pooling: an effective and interpretable pooling method for predicting DNA–protein binding. Bioinformatics, 2020, 36, 1405-1412.	1.8	22
36	Genomic and transcriptomic alterations associated with drug vulnerabilities and prognosis in adenocarcinoma at the gastroesophageal junction. Nature Communications, 2020, 11, 6091.	5.8	21

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37	CCGD-ESCC: A Comprehensive Database for Genetic Variants Associated with Esophageal Squamous Cell Carcinoma in Chinese Population. Genomics, Proteomics and Bioinformatics, 2018, 16, 262-268.	3.0	17
38	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	3.0	15
39	â€œBioinformatics: Introduction and Methods,â€•a Bilingual Massive Open Online Course (MOOC) as a New Example for Global Bioinformatics Education. PLoS Computational Biology, 2014, 10, e1003955.	1.5	14
40	Identification and analysis of unitary loss of long-established protein-coding genes in Poaceae shows evidences for biased gene loss and putatively functional transcription of relics. BMC Evolutionary Biology, 2015, 15, 66.	3.2	14
41	Rice-Map: a new-generation rice genome browser. BMC Genomics, 2011, 12, 165.	1.2	10
42	Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell. BMC Genomics, 2013, 14, S3.	1.2	9
43	Accurately annotate compound effects of genetic variants using a context-sensitive framework. Nucleic Acids Research, 2017, 45, e82-e82.	6.5	9
44	LocExpress: a web server for efficiently estimating expression of novel transcripts. BMC Genomics, 2016, 17, 1023.	1.2	6
45	Systematic identification and annotation of multiple-variant compound effects at transcription factor binding sites in human genome. Journal of Genetics and Genomics, 2018, 45, 373-379.	1.7	5
46	Identifying complex motifs in massive omics data with a variable-convolutional layer in deep neural network. Briefings in Bioinformatics, 2021, 22, .	3.2	4
47	Computational Assessment of the Expression-Modulating Potential for Non-Coding Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 662-673.	3.0	3
48	Expressed Structurally Stable Inverted Duplicates in Mammalian Genomes as Functional Noncoding Elements. Genome Biology and Evolution, 2017, 9, 981-992.	1.1	2
49	A Non-Random Gait through the Human Genome. , 2009, , .		1
50	AnnoLnc: A One-Stop Portal to Systematically Annotate Novel Human Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 111-131.	0.4	1
51	OsAPL controls the nutrient transport systems in the leaf of rice (Oryza sativa L.). Planta, 2022, 256, .	1.6	1
52	REVA as A Well-curated Database for Human Expression-modulating Variants. Genomics, Proteomics and Bioinformatics, 2021, 19, 590-601.	3.0	0
53	Quantitative model suggests both intrinsic and contextual features contribute to the transcript coding ability determination in cells. Briefings in Bioinformatics, 2022, 23, .	3.2	0