

Ge Gao

List of Publications by Year in descending order

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Version: 2024-02-01

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	Computational Assessment of the Expression-Modulating Potential for Non-Coding Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 662-673.	3.0	3
2	Quantitative model suggests both intrinsic and contextual features contribute to the transcript coding ability determination in cells. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	0
3	Multi-omics single-cell data integration and regulatory inference with graph-linked embedding. <i>Nature Biotechnology</i> , 2022, 40, 1458-1466.	9.4	153
4	OsAPL controls the nutrient transport systems in the leaf of rice (<i>Oryza sativa</i> L.). <i>Planta</i> , 2022, 256, .	1.6	1
5	Global miRNA dosage control of embryonic germ layer specification. <i>Nature</i> , 2021, 593, 602-606.	13.7	39
6	REVA as A Well-curated Database for Human Expression-modulating Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 590-601.	3.0	0
7	Identifying complex motifs in massive omics data with a variable-convolutional layer in deep neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
8	AnnoLnc: A One-Stop Portal to Systematically Annotate Novel Human Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2021, 2254, 111-131.	0.4	1
9	Expectation pooling: an effective and interpretable pooling method for predicting DNA-protein binding. <i>Bioinformatics</i> , 2020, 36, 1405-1412.	1.8	22
10	PlantRegMap: charting functional regulatory maps in plants. <i>Nucleic Acids Research</i> , 2020, 48, D1104-D1113.	6.5	333
11	Searching large-scale scRNA-seq databases via unbiased cell embedding with Cell BLAST. <i>Nature Communications</i> , 2020, 11, 3458.	5.8	81
12	Genomic and transcriptomic alterations associated with drug vulnerabilities and prognosis in adenocarcinoma at the gastroesophageal junction. <i>Nature Communications</i> , 2020, 11, 6091.	5.8	21
13	AnnoLnc2: the one-stop portal to systematically annotate novel lncRNAs for human and mouse. <i>Nucleic Acids Research</i> , 2020, 48, W230-W238.	6.5	37
14	An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856.	6.5	92
15	The nucleoskeleton protein IFFO1 immobilizes broken DNA and suppresses chromosome translocation during tumorigenesis. <i>Nature Cell Biology</i> , 2019, 21, 1273-1285.	4.6	40
16	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. <i>Genome Research</i> , 2019, 29, 682-696.	2.4	67
17	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	6.5	157
18	Long non-coding RNAs involved in the regulatory network during porcine pre-implantation embryonic development and iPSC induction. <i>Scientific Reports</i> , 2018, 8, 6649.	1.6	29

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19	Mitosis-specific MRN complex promotes a mitotic signaling cascade to regulate spindle dynamics and chromosome segregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10079-E10088.	3.3	27
20	CCGD-ESCC: A Comprehensive Database for Genetic Variants Associated with Esophageal Squamous Cell Carcinoma in Chinese Population. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 262-268.	3.0	17
21	Systematic identification and annotation of multiple-variant compound effects at transcription factor binding sites in human genome. <i>Journal of Genetics and Genomics</i> , 2018, 45, 373-379.	1.7	5
22	Painting a specific chromosome with CRISPR/Cas9 for live-cell imaging. <i>Cell Research</i> , 2017, 27, 298-301.	5.7	53
23	GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. <i>Nucleic Acids Research</i> , 2017, 45, W98-W102.	6.5	7,114
24	CPC2: a fast and accurate coding potential calculator based on sequence intrinsic features. <i>Nucleic Acids Research</i> , 2017, 45, W12-W16.	6.5	970
25	Accurately annotate compound effects of genetic variants using a context-sensitive framework. <i>Nucleic Acids Research</i> , 2017, 45, e82-e82.	6.5	9
26	PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. <i>Nucleic Acids Research</i> , 2017, 45, D1040-D1045.	6.5	1,651
27	Expressed Structurally Stable Inverted Duplicates in Mammalian Genomes as Functional Noncoding Elements. <i>Genome Biology and Evolution</i> , 2017, 9, 981-992.	1.1	2
28	AnnoLnc: a web server for systematically annotating novel human lncRNAs. <i>BMC Genomics</i> , 2016, 17, 931.	1.2	51
29	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	3.0	15
30	Ewing Tumor-associated Antigen 1 Interacts with Replication Protein A to Promote Restart of Stalled Replication Forks. <i>Journal of Biological Chemistry</i> , 2016, 291, 21956-21962.	1.6	53
31	LocExpress: a web server for efficiently estimating expression of novel transcripts. <i>BMC Genomics</i> , 2016, 17, 1023.	1.2	6
32	An <i>Arabidopsis</i> Transcriptional Regulatory Map Reveals Distinct Functional and Evolutionary Features of Novel Transcription Factors. <i>Molecular Biology and Evolution</i> , 2015, 32, 1767-1773.	3.5	175
33	GSDS 2.0: an upgraded gene feature visualization server. <i>Bioinformatics</i> , 2015, 31, 1296-1297.	1.8	3,092
34	Interactome analysis identifies a new paralogue of XRCC4 in non-homologous end joining DNA repair pathway. <i>Nature Communications</i> , 2015, 6, 6233.	5.8	144
35	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. <i>BMC Evolutionary Biology</i> , 2015, 15, 66.	3.2	14
36	Postzygotic single-nucleotide mosaicisms in whole-genome sequences of clinically unremarkable individuals. <i>Cell Research</i> , 2014, 24, 1311-1327.	5.7	54

#	ARTICLE	IF	CITATIONS
37	“Bioinformatics: Introduction and Methods,” a Bilingual Massive Open Online Course (MOOC) as a New Example for Global Bioinformatics Education. <i>PLoS Computational Biology</i> , 2014, 10, e1003955.	1.5	14
38	A long-term demasculinization of X-linked intergenic noncoding RNAs in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014, 24, 629-638.	2.4	22
39	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. <i>Nucleic Acids Research</i> , 2014, 42, D1182-D1187.	6.5	800
40	CasOT: a genome-wide Cas9/gRNA off-target searching tool. <i>Bioinformatics</i> , 2014, 30, 1180-1182.	1.8	312
41	Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell. <i>BMC Genomics</i> , 2013, 14, S3.	1.2	9
42	A brief introduction to web-based genome browsers. <i>Briefings in Bioinformatics</i> , 2013, 14, 131-143.	3.2	46
43	ABrowse - a customizable next-generation genome browser framework. <i>BMC Bioinformatics</i> , 2012, 13, 2.	1.2	22
44	Molecular features of secondary vascular tissue regeneration after bark girdling in <i>Populus</i> . <i>New Phytologist</i> , 2011, 192, 869-884.	3.5	43
45	Rice-Map: a new-generation rice genome browser. <i>BMC Genomics</i> , 2011, 12, 165.	1.2	10
46	PlantTFDB 2.0: update and improvement of the comprehensive plant transcription factor database. <i>Nucleic Acids Research</i> , 2011, 39, D1114-D1117.	6.5	288
47	A Non-Random Gait through the Human Genome. , 2009, , .		1
48	WebLab: a data-centric, knowledge-sharing bioinformatic platform. <i>Nucleic Acids Research</i> , 2009, 37, W33-W39.	6.5	27
49	Expression pattern divergence of duplicated genes in rice. <i>BMC Bioinformatics</i> , 2009, 10, S8.	1.2	43
50	PlantTFDB: a comprehensive plant transcription factor database. <i>Nucleic Acids Research</i> , 2007, 36, D966-D969.	6.5	210
51	DPTF: a database of poplar transcription factors. <i>Bioinformatics</i> , 2007, 23, 1307-1308.	1.8	94
52	CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine. <i>Nucleic Acids Research</i> , 2007, 35, W345-W349.	6.5	2,525
53	DRTF: a database of rice transcription factors. <i>Bioinformatics</i> , 2006, 22, 1286-1287.	1.8	141