Chaochun Wei

List of Publications by Year
in descending order

44 papers	4,419 citations	394421 19 h-index	289244 40 g-index
45 all docs	45 docs citations	45 times ranked	7586 citing authors

#	Article	IF	Citations
1	Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes. Genome Research, 2022, , .	5.5	21
2	Gene Presence/Absence Variation analysis of coronavirus family displays its pan-genomic diversity. International Journal of Biological Sciences, 2021, 17, 3717-3727.	6.4	5
3	ivTerm—An R package for interactive visualization of functional analysis results of meta€omics data. Journal of Cellular Biochemistry, 2021, 122, 1428-1434.	2.6	0
4	GESLM algorithm for detecting causal SNPs in GWAS with multiple phenotypes. Briefings in Bioinformatics, 2021, 22, .	6.5	4
5	UHRF1 regulates alternative splicing by interacting with splicing factors and U snRNAs in a H3R2me involved manner. Human Molecular Genetics, 2021, 30, 2110-2122.	2.9	4
6	Towards a deeper haplotype mining of complex traits in rice with <scp>RFGB</scp> v2.0. Plant Biotechnology Journal, 2020, 18, 14-16.	8.3	78
7	Genetic Profiles Affect the Biological Effects of Serine on Gastric Cancer Cells. Frontiers in Pharmacology, 2020, 11, 1183.	3.5	4
8	CDKAM: a taxonomic classification tool using discriminative k-mers and approximate matching strategies. BMC Bioinformatics, 2020, 21, 468.	2.6	9
9	Computational Strategies for Eukaryotic Pangenome Analyses. , 2020, , 293-307.		8
10	A powerful HUPAN on a pan-genome study: significance and perspectives. Cancer Biology and Medicine, 2020, 17, 1-5.	3.0	5
11	HUPAN: a pan-genome analysis pipeline for human genomes. Genome Biology, 2019, 20, 149.	8.8	55
12	Discovery and characterization of the evolution, variation and functions of diversity-generating retroelements using thousands of genomes and metagenomes. BMC Genomics, 2019, 20, 595.	2.8	14
13	PaSS: a sequencing simulator for PacBio sequencing. BMC Bioinformatics, 2019, 20, 352.	2.6	19
14	GLAPD: Whole Genome Based LAMP Primer Design for a Set of Target Genomes. Frontiers in Microbiology, 2019, 10, 2860.	3.5	34
15	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. Nature, 2018, 557, 43-49.	27.8	1,091
16	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. Scientific Data, 2018, 5, 180079.	5.3	14
17	Genome-Wide Analysis of the Association of Transposable Elements with Gene Regulation Suggests that Alu Elements Have the Largest Overall Regulatory Impact. Journal of Computational Biology, 2018, 25, 551-562.	1.6	12
18	In silico analysis of endogenous siRNAs associated transposable elements and NATs in Schistosoma japonicum reveals their putative roles during reproductive development. Parasitology Research, 2018, 117, 1549-1558.	1.6	1

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19	Comparative Genomic Analysis and Characterization of Two Salmonella enterica Serovar Enteritidis Isolates From Poultry With Notably Different Survival Abilities in Egg Whites. Frontiers in Microbiology, 2018, 9, 2111.	3.5	11
20	MetaBinG2: a fast and accurate metagenomic sequence classification system for samples with many unknown organisms. Biology Direct, 2018, 13, 15.	4.6	9
21	RPAN: rice pan-genome browser for â˜¼3000 rice genomes. Nucleic Acids Research, 2017, 45, 597-605.	14.5	156
22	EUPAN enables pan-genome studies of a large number of eukaryotic genomes. Bioinformatics, 2017, 33, 2408-2409.	4.1	47
23	Dosage compensation in the process of inactivation/reactivation during both germ cell development and early embryogenesis in mouse. Scientific Reports, 2017, 7, 3729.	3.3	18
24	RNA virus receptor Rig-I monitors gut microbiota and inhibits colitis-associated colorectal cancer. Journal of Experimental and Clinical Cancer Research, 2017, 36, 2.	8.6	42
25	Widespread of horizontal gene transfer in the human genome. BMC Genomics, 2017, 18, 274.	2.8	21
26	Microbe Genomes Associated with Human Body. Evolutionary Studies, 2017, , 285-300.	0.1	0
27	MOST+: A de novo motif finding approach combining genomic sequence and heterogeneous genome-wide signatures. BMC Genomics, 2015, 16, S13.	2.8	6
28	Revealing Missing Human Protein Isoforms Based on Ab Initio Prediction, RNA-seq and Proteomics. Scientific Reports, 2015, 5, 10940.	3.3	51
29	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. Chinese Science Bulletin, 2015, 60, 367-371.	0.7	31
30	LAceP: Lysine Acetylation Site Prediction Using Logistic Regression Classifiers. PLoS ONE, 2014, 9, e89575.	2.5	77
31	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. Genome Research, 2014, 24, 1308-1315.	5.5	235
32	cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets. BMC Systems Biology, 2013, 7, S7.	3.0	13
33	NeSSM: A Next-Generation Sequencing Simulator for Metagenomics. PLoS ONE, 2013, 8, e75448.	2.5	57
34	cGRNexp: a web platform for building combinatorial gene regulation networks based on user-uploaded gene expression datasets. , 2012, , .		0
35	CTF: a CRF-based transcription factor binding sites finding system. BMC Genomics, 2012, 13, S18.	2.8	6
36	iGepros: an integrated gene and protein annotation server for biological nature exploration. BMC Bioinformatics, 2011, 12, S6.	2.6	11

#	ARTICLE	IF	CITATIONS
37	MetaBinG: Using GPUs to Accelerate Metagenomic Sequence Classification. PLoS ONE, 2011, 6, e25353.	2.5	11
38	Analysis of Oral Microbiota in Children with Dental Caries by PCR-DGGE and Barcoded Pyrosequencing. Microbial Ecology, 2010, 60, 677-690.	2.8	240
39	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. ISME Journal, 2010, 4, 232-241.	9.8	845
40	More than 9,000,000 Unique Genes in Human Gut Bacterial Community: Estimating Gene Numbers Inside a Human Body. PLoS ONE, 2009, 4, e6074.	2.5	131
41	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
42	Using ESTs to improve the accuracy of de novo gene prediction. BMC Bioinformatics, 2006, 7, 327.	2.6	47
43	Closing in on the C. elegans ORFeome by cloning TWINSCAN predictions. Genome Research, 2005, 15, 577-582.	5.5	39
44	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812