

List of Publications by Year in descending order

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34
papers

1,972
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#	ARTICLE	IF	CITATIONS
1	inGAP-Family: Accurate Detection of Meiotic Recombination Loci and Causal Mutations by Filtering Out Artificial Variants due to Genome Complexities. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 524-535.	6.9	13
2	Histone demethylase IBM1-mediated meiocyte gene expression ensures meiotic chromosome synapsis and recombination. <i>PLoS Genetics</i> , 2022, 18, e1010041.	3.5	1
3	Parental folate deficiency induces birth defects in mice accompanied with increased de novo mutations. <i>Cell Discovery</i> , 2022, 8, 18.	6.7	3
4	The gut microbiome and microbial metabolites in acute myocardial infarction. <i>Journal of Genetics and Genomics</i> , 2022, 49, 569-578.	3.9	11
5	Modulation of evening complex activity enables north-to-south adaptation of soybean. <i>Science China Life Sciences</i> , 2021, 64, 179-195.	4.9	22
6	Comparative Genomic and Transcriptomic Analysis Reveals Specific Features of Gene Regulation in <i>Kluyveromyces marxianus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 598060.	3.5	8
7	Nuclear phylotranscriptomics and phylogenomics support numerous polyploidization events and hypotheses for the evolution of rhizobial nitrogen-fixing symbiosis in Fabaceae. <i>Molecular Plant</i> , 2021, 14, 748-773.	8.3	86
8	Genomic analysis of field pennycress (<i>Thlaspi arvense</i>) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021, 19, 143.	3.8	23
9	Changing Gly311 to an acidic amino acid in the MATE family protein DTX6 enhances Arabidopsis resistance to the dihydropyridine herbicides. <i>Molecular Plant</i> , 2021, 14, 2115-2125.	8.3	22
10	Recurrent genome duplication events likely contributed to both the ancient and recent rise of ferns. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 433-455.	8.5	43
11	Analyses of functional conservation and divergence reveal requirement of bHLH010/089/091 for pollen development at elevated temperature in Arabidopsis. <i>Journal of Genetics and Genomics</i> , 2020, 47, 477-492.	3.9	13
12	Asterid Phylogenomics/Phylotranscriptomics Uncover Morphological Evolutionary Histories and Support Phylogenetic Placement for Numerous Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 3188-3210.	8.9	82
13	Cell free bacterial DNAs in human plasma provide fingerprints for immune-related diseases. <i>Medicine in Microecology</i> , 2020, 5, 100022.	1.6	3
14	PhyloMCL: Accurate clustering of hierarchical orthogroups guided by phylogenetic relationship and inference of polyploidy events. <i>Methods in Ecology and Evolution</i> , 2020, 11, 943-954.	5.2	9
15	H3K4me2 functions as a repressive epigenetic mark in plants. <i>Epigenetics and Chromatin</i> , 2019, 12, 40.	3.9	51
16	Effects of parental genetic divergence on gene expression patterns in interspecific hybrids of <i>Camellia</i> . <i>BMC Genomics</i> , 2019, 20, 828.	2.8	11
17	Amino acid based <i>de Bruijn</i> graph algorithm for identifying complete coding genes from metagenomic and metatranscriptomic short reads. <i>Nucleic Acids Research</i> , 2019, 47, e30-e30.	14.5	7
18	Reply to Zwaenepoel et al.: Meeting the Challenges of Detecting Polyploidy Events from Transcriptomic Data. <i>Molecular Plant</i> , 2019, 12, 137-140.	8.3	5

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19	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. <i>Molecular Plant</i> , 2018, 11, 414-428.	8.3	251
20	Polyphyly in 16S rRNA-based LVTtree Versus Monophyly in Whole-genome-based CVTtree. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 310-319.	6.9	8
21	A well-resolved fern nuclear phylogeny reveals the evolution history of numerous transcription factor families. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 961-977.	2.7	80
22	Evolution of the leucine-rich repeat receptor-like protein kinase gene family: Ancestral copy number and functional divergence of <i>BAM1</i> and <i>BAM2</i> in Brassicaceae. <i>Journal of Systematics and Evolution</i> , 2016, 54, 204-218.	3.1	7
23	Association of the molecular regulation of ear leaf senescence/stress response and photosynthesis/metabolism with heterosis at the reproductive stage in maize. <i>Scientific Reports</i> , 2016, 6, 29843.	3.3	23
24	Multiple Polyploidization Events across Asteraceae with Two Nested Events in the Early History Revealed by Nuclear Phylogenomics. <i>Molecular Biology and Evolution</i> , 2016, 33, 2820-2835.	8.9	149
25	The genome and transcriptome of <i>Trichormus</i> sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. <i>Scientific Reports</i> , 2016, 6, 29404.	3.3	33
26	The <i>DYT</i> interacting proteins <i>HLH010</i> , <i>HLH089</i> and <i>HLH091</i> are redundantly required for <i>A. rabidopsis</i> anther development and transcriptome. <i>Plant Journal</i> , 2015, 83, 976-990.	5.7	136
27	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015, 6, 6986.	12.8	222
28	Alternative splicing during <i>Arabidopsis</i> flower development results in constitutive and stage-regulated isoforms. <i>Frontiers in Genetics</i> , 2014, 5, 25.	2.3	45
29	Detection of genomic variations and DNA polymorphisms and impact on analysis of meiotic recombination and genetic mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10007-10012.	7.1	55
30	RNA-seq analyses of multiple meristems of soybean: novel and alternative transcripts, evolutionary and functional implications. <i>BMC Plant Biology</i> , 2014, 14, 169.	3.6	229
31	Analysis of <i>Arabidopsis</i> genome-wide variations before and after meiosis and meiotic recombination by resequencing Landsberg <i>erecta</i> and all four products of a single meiosis. <i>Genome Research</i> , 2012, 22, 508-518.	5.5	125
32	inGAP-sv: a novel scheme to identify and visualize structural variation from paired end mapping data. <i>Nucleic Acids Research</i> , 2011, 39, W567-W575.	14.5	74
33	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010, 26, 127-129.	4.1	58
34	Characterization of meiotic crossovers and gene conversion by whole-genome sequencing in <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2009, 10, 475.	2.8	62