Christopher Toomajian

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5632259/publications.pdf

Version: 2024-02-01

28 papers 6,305 citations

20 h-index 28 g-index

30 all docs 30 docs citations

30 times ranked

8075 citing authors

#	Article	IF	CITATIONS
1	The Pattern of Polymorphism in Arabidopsis thaliana. PLoS Biology, 2005, 3, e196.	5.6	895
2	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . Science, 2007, 317, 338-342.	12.6	689
3	Adaptation to Climate Across the <i>Arabidopsis thaliana</i> Genome. Science, 2011, 334, 83-86.	12.6	636
4	An Arabidopsis Example of Association Mapping in Structured Samples. PLoS Genetics, 2007, 3, e4.	3.5	625
5	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. Nature, 2011, 477, 419-423.	27.8	593
6	Recombination and linkage disequilibrium in Arabidopsis thaliana. Nature Genetics, 2007, 39, 1151-1155.	21.4	497
7	Genome-wide patterns of genetic variation in worldwide Arabidopsis thaliana accessions from the RegMap panel. Nature Genetics, 2012, 44, 212-216.	21.4	476
8	Genome-Wide Association Mapping in Arabidopsis Identifies Previously Known Flowering Time and Pathogen Resistance Genes. PLoS Genetics, 2005, 1, e60.	3.5	378
9	A Genome-Wide Survey of R Gene Polymorphisms in Arabidopsis. Plant Cell, 2006, 18, 1803-1818.	6.6	309
10	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. Genome Biology, 2015, 16, 48.	8.8	216
11	The Evolution of Selfing in <i>Arabidopsis thaliana</i> . Science, 2007, 317, 1070-1072.	12.6	160
12	Heterogeneity of Microsatellite Mutations Within and Between Loci, and Implications for Human Demographic Histories. Genetics, 1998, 148, 1269-1284.	2.9	154
13	A Nonparametric Test Reveals Selection for Rapid Flowering in the Arabidopsis Genome. PLoS Biology, 2006, 4, e137.	5.6	118
14	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> Includes the <i>Fusarium solani</i> Species Complex. Phytopathology, 2021, 111, 1064-1079.	2.2	107
15	Distribution of genetic variation within and among local populations of Arabidopsis thaliana over its species range. Molecular Ecology, 2006, 15, 1405-1418.	3.9	89
16	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . Plant Journal, 2016, 88, 159-178.	5.7	81
17	A Method for Detecting Recent Selection in the Human Genome From Allele Age Estimates. Genetics, 2003, 165, 287-297.	2.9	60
18	Low Levels of Polymorphism in Genes That Control the Activation of Defense Response in <i>Arabidopsis thaliana</i>	2.9	57

#	Article	IF	CITATIONS
19	Sequence Variation and Haplotype Structure at the HumanHFELocus. Genetics, 2002, 161, 1609-1623.	2.9	46
20	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> Cenome Biology and Evolution, 2015, 7, 3062-3069.	2.5	36
21	Unbiased K-mer Analysis Reveals Changes in Copy Number of Highly Repetitive Sequences During Maize Domestication and Improvement. Scientific Reports, 2017, 7, 42444.	3.3	16
22	Segregation of secondary metabolite biosynthesis in hybrids of Fusarium fujikuroi and Fusarium proliferatum. Fungal Genetics and Biology, 2012, 49, 567-577.	2.1	14
23	Fumonisin and Beauvericin Chemotypes and Genotypes of the Sister Species <i>Fusarium subglutinans</i> and <i>Fusarium temperatum</i> . Applied and Environmental Microbiology, 2020, 86, .	3.1	14
24	Climate change and plant health: designing research spillover from plant genomics for understanding the role of microbial communities. Canadian Journal of Plant Pathology, 2012, 34, 349-361.	1.4	11
25	Parental genetic distance and patterns in nonrandom mating and seed yield in predominately selfing Arabidopsis thaliana. Plant Reproduction, 2013, 26, 317-328.	2.2	11
26	Plant organ evolution revealed by phylotranscriptomics in Arabidopsis thaliana. Scientific Reports, 2017, 7, 7567.	3.3	11
27	Divergence and Gene Flow Between Fusarium subglutinans and F. temperatum Isolated from Maize in Argentina. Phytopathology, 2021, 111, 170-183.	2.2	3
28	Genome-wide association mapping in Arabidopsis thaliana identifies previously known genes responsible for variation in flowering time and pathogen resistance. PLoS Genetics, 2005, preprint, e60.	3.5	3