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List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

7,014
citations

361413

20
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

7676
citing authors

#	ARTICLE	IF	CITATIONS
1	Implementing building-level SARS-CoV-2 wastewater surveillance on a university campus. <i>Science of the Total Environment</i> , 2021, 782, 146749.	8.0	203
2	Performance evaluation of virus concentration methods for implementing SARS-CoV-2 wastewater based epidemiology emphasizing quick data turnaround. <i>Science of the Total Environment</i> , 2021, 801, 149656.	8.0	37
3	Paralog analyses reveal gene duplication events and genes under positive selection in <i>Ixodes scapularis</i> and other ixodid ticks. <i>BMC Genomics</i> , 2016, 17, 241.	2.8	18
4	CONTRAILS: A tool for rapid identification of transgene integration sites in complex, repetitive genomes using low-coverage paired-end sequencing. <i>Genomics Data</i> , 2015, 6, 175-181.	1.3	19
5	Statistical issues associated with modeling of synonymous mutation data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 361-74.	0.6	0
6	The fate of duplicated genes in a polyploid plant genome. <i>Plant Journal</i> , 2013, 73, 143-153.	5.7	243
7	Large-Scale Development of Cost-Effective Single-Nucleotide Polymorphism Marker Assays for Genetic Mapping in Pigeonpea and Comparative Mapping in Legumes. <i>DNA Research</i> , 2012, 19, 449-461.	3.4	99
8	Co-expression of soybean Dicer-like genes in response to stress and development. <i>Functional and Integrative Genomics</i> , 2012, 12, 671-682.	3.5	19
9	Applications of next-generation sequencing in plant biology. <i>American Journal of Botany</i> , 2012, 99, 175-185.	1.7	249
10	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	17.5	788
11	Large-scale development of cost-effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. <i>Plant Biotechnology Journal</i> , 2012, 10, 716-732.	8.3	221
12	Defining the Transcriptome Assembly and Its Use for Genome Dynamics and Transcriptome Profiling Studies in Pigeonpea (<i>Cajanus cajan</i> L.). <i>DNA Research</i> , 2011, 18, 153-164.	3.4	85
13	Comparative Evolution of Photosynthetic Genes in Response to Polyploid and Nonpolyploid Duplication. <i>Plant Physiology</i> , 2011, 155, 2081-2095.	4.8	54
14	Integration of physical and genetic maps of common bean through BAC-derived microsatellite markers. <i>BMC Genomics</i> , 2010, 11, 436.	2.8	59
15	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
16	Retrotransposons within Syntenic Regions between Soybean and <i>Medicago truncatula</i> and Their Contribution to Local Genome Evolution. <i>Plant Genome</i> , 2009, 2, .	2.8	4
17	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.	1.9	70
18	Soybean Genome Structure and Organization. , 2008, , 91-99.		1

#	ARTICLE	IF	CITATIONS
19	<i>Arabidopsis SCAR</i> 's Function Interchangeably to Meet Actin-Related Protein 2/3 Activation Thresholds during Morphogenesis. <i>Plant Cell</i> , 2008, 20, 995-1011.	6.6	73
20	Fractionation of Synteny in a Genomic Region Containing Tandemly Duplicated Genes across <i>Glycine max</i> , <i>Medicago truncatula</i> , and <i>Arabidopsis thaliana</i> . <i>Journal of Heredity</i> , 2008, 99, 390-395.	2.4	32
21	The FAD2 Gene Family of Soybean: Insights into the Structural and Functional Divergence of a Paleopolyploid Genome. <i>Crop Science</i> , 2007, 47, S-14.	1.8	108
22	Gene duplication and paleopolyploidy in soybean and the implications for whole genome sequencing. <i>BMC Genomics</i> , 2007, 8, 330.	2.8	132
23	Paleopolyploidy and gene duplication in soybean and other legumes. <i>Current Opinion in Plant Biology</i> , 2006, 9, 104-109.	7.1	230
24	Sequence Conservation of Homeologous Bacterial Artificial Chromosomes and Transcription of Homeologous Genes in Soybean (<i>Glycine max</i> L. Merr.). <i>Genetics</i> , 2006, 174, 1017-1028.	2.9	45
25	Soybean FGAM synthase promoters direct ectopic nematode feeding site activity. <i>Genome</i> , 2004, 47, 404-413.	2.0	18
26	Mining EST databases to resolve evolutionary events in major crop species. <i>Genome</i> , 2004, 47, 868-876.	2.0	310