

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

51
papers

8,198
citations

24
h-index

56
g-index

56
ext. papers

10,657
ext. citations

7.8
avg, IF

5.68
L-index

#	Paper	IF	Citations
51	A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. <i>PLoS ONE</i> , 2011 , 6, e19379	3.7	3791
50	TASSEL-GBS: a high capacity genotyping by sequencing analysis pipeline. <i>PLoS ONE</i> , 2014 , 9, e90346	3.7	994
49	Genetic properties of the maize nested association mapping population. <i>Science</i> , 2009 , 325, 737-40	33.3	775
48	Sorting signals, N-terminal modifications and abundance of the chloroplast proteome. <i>PLoS ONE</i> , 2008 , 3, e1994	3.7	504
47	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015 , 16, 191	18.3	428
46	PPDB, the Plant Proteomics Database at Cornell. <i>Nucleic Acids Research</i> , 2009 , 37, D969-74	20.1	300
45	Comparative analyses of C ₃ and C ₄ photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014 , 32, 1158-65	44.5	160
44	Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , 2018 , 7, 1-12	7.6	127
43	The role of cis regulatory evolution in maize domestication. <i>PLoS Genetics</i> , 2014 , 10, e1004745	6	88
42	MASCP Gator: an aggregation portal for the visualization of Arabidopsis proteomics data. <i>Plant Physiology</i> , 2011 , 155, 259-70	6.6	83
41	Heterozygous Mapping Strategy (HetMappS) for High Resolution Genotyping-By-Sequencing Markers: A Case Study in Grapevine. <i>PLoS ONE</i> , 2015 , 10, e0134880	3.7	83
40	Transcriptomic analyses indicate that maize ligule development recapitulates gene expression patterns that occur during lateral organ initiation. <i>Plant Cell</i> , 2014 , 26, 4718-32	11.6	72
39	Analysis of curated and predicted plastid subproteomes of Arabidopsis. Subcellular compartmentalization leads to distinctive proteome properties. <i>Plant Physiology</i> , 2004 , 135, 723-34	6.6	71
38	A next-generation marker genotyping platform (AmpSeq) in heterozygous crops: a case study for marker-assisted selection in grapevine. <i>Horticulture Research</i> , 2016 , 3, 16002	7.7	57
37	Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C ₄ -related processes. <i>Journal of Experimental Botany</i> , 2014 , 65, 3543-55	7	54
36	White shark genome reveals ancient elasmobranch adaptations associated with wound healing and the maintenance of genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 4446-4455	11.5	51
35	Genetic dissection of powdery mildew resistance in interspecific half-sib grapevine families using SNP-based maps. <i>Molecular Breeding</i> , 2017 , 37, 1	3.4	50

34	BrAPI-an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019 , 35, 4147-4155	7.2	49
33	Identification of Photosynthesis-Associated C4 Candidate Genes through Comparative Leaf Gradient Transcriptome in Multiple Lineages of C3 and C4 Species. <i>PLoS ONE</i> , 2015 , 10, e0140629	3.7	36
32	Gene discovery using mutagen-induced polymorphisms and deep sequencing: application to plant disease resistance. <i>Genetics</i> , 2012 , 192, 139-46	4	35
31	The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 5643-5652	11.5	34
30	Transcriptome response of cassava leaves under natural shade. <i>Scientific Reports</i> , 2016 , 6, 31673	4.9	33
29	Workflow for large scale detection and validation of peptide modifications by RPLC-LTQ-Orbitrap: application to the <i>Arabidopsis thaliana</i> leaf proteome and an online modified peptide library. <i>Analytical Chemistry</i> , 2009 , 81, 8015-24	7.8	31
28	Next Generation Mapping of Enological Traits in an F2 Interspecific Grapevine Hybrid Family. <i>PLoS ONE</i> , 2016 , 11, e0149560	3.7	29
27	Haplotyping the <i>Vitis</i> collinear core genome with rhAmpSeq improves marker transferability in a diverse genus. <i>Nature Communications</i> , 2020 , 11, 413	17.4	24
26	Computational Analysis of AmpSeq Data for Targeted, High-Throughput Genotyping of Amplicons. <i>Frontiers in Plant Science</i> , 2019 , 10, 599	6.2	23
25	The Plastid and Mitochondrial Peptidase Network in : A Foundation for Testing Genetic Interactions and Functions in Organellar Proteostasis. <i>Plant Cell</i> , 2017 , 29, 2687-2710	11.6	20
24	Genotyping-by-sequencing of vegetables reveals unique phylogenetic patterns, population structure and domestication footprints. <i>Horticulture Research</i> , 2018 , 5, 38	7.7	20
23	The <i>Arabidopsis</i> Chromatin-Remodeling Factor CHR5 Regulates Plant Immune Responses and Nucleosome Occupancy. <i>Plant and Cell Physiology</i> , 2017 , 58, 2202-2216	4.9	19
22	Developmental and Subcellular Organization of Single-Cell C ₃ Photosynthesis in <i>Bienertia sinuspersici</i> Determined by Large-Scale Proteomics and cDNA Assembly from 454 DNA Sequencing. <i>Journal of Proteome Research</i> , 2015 , 14, 2090-108	5.6	18
21	Lessons from a Phenotyping Center Revealed by the Genome-Guided Mapping of Powdery Mildew Resistance Loci. <i>Phytopathology</i> , 2016 , 106, 1159-1169	3.8	18
20	HOS15 and HDA9 negatively regulate immunity through histone deacetylation of intracellular immune receptor NLR genes in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2020 , 226, 507-522	9.8	18
19	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020 , 16, e1008791	6	17
18	Gene Evolutionary Trajectories and GC Patterns Driven by Recombination in. <i>Frontiers in Plant Science</i> , 2016 , 7, 1433	6.2	11
17	A Role of Cytokinin Transporter in <i>Arabidopsis</i> Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2017 , 30, 325-333	3.6	10

16	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. <i>Plant Cell</i> , 2021 , 33, 3421-3453	11.6	10
15	Multiple independent recombinations led to hermaphroditism in grapevine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	9
14	Cardiac Pathology and Genomics of Sudden Death in Racehorses From New York and Maryland Racetracks. <i>Veterinary Pathology</i> , 2019 , 56, 576-585	2.8	8
13	An integrative AmpSeq platform for highly multiplexed marker-assisted pyramiding of grapevine powdery mildew resistance loci. <i>Molecular Breeding</i> , 2017 , 37, 1	3.4	8
12	Interaction of Arabidopsis Trihelix-Domain Transcription Factors VFP3 and VFP5 with Agrobacterium Virulence Protein VirF. <i>PLoS ONE</i> , 2015 , 10, e0142128	3.7	8
11	Characterization of maize leaf pyruvate orthophosphate dikinase using high throughput sequencing. <i>Journal of Integrative Plant Biology</i> , 2018 , 60, 670-690	8.3	6
10	Natural variations of growth thermo-responsiveness determined by SAUR26/27/28 proteins in Arabidopsis thaliana. <i>New Phytologist</i> , 2019 , 224, 291-305	9.8	4
9	Evolutionary genomic and bacteria GWAS analysis of subsp. and dairy cattle Johne's disease phenotypes. <i>Applied and Environmental Microbiology</i> , 2021 ,	4.8	3
8	Mapping and Cloning of Chemical Induced Mutations by Whole-Genome Sequencing of Bulk Segregants. <i>Methods in Molecular Biology</i> , 2017 , 1578, 285-289	1.4	2
7	The Arabidopsis thaliana PeptideAtlas; harnessing world-wide proteomics data for a comprehensive community proteomics resource		2
6	Mitochondrial genome of an Atlantic white shark (<i>Lamna nasus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 717-719	10.5	2
5	Toward the elucidation of cytoplasmic diversity in North American grape breeding programs. <i>Molecular Breeding</i> , 2016 , 36, 1	3.4	1
4	Mapping Recombination Initiation Sites Using Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2016 , 1429, 177-88	1.4	1
3	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. <i>PLoS Genetics</i> , 2021 , 17, e1009797	6	1
2	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021 , 135, 273	6	0
1	STENCIL: A web templating engine for visualizing and sharing life science datasets. <i>PLoS Computational Biology</i> , 2022 , 18, e1009859	5	