

MarÃ-a MuÃ±oz-AmatriaÃ-n

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,995
citations

218677

26
h-index

289244

40
g-index

53
all docs

53
docs citations

53
times ranked

4437
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
2	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
3	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
4	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
5	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. <i>PLoS ONE</i> , 2014, 9, e94688.	2.5	188
6	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011, 4, 238-249.	2.8	150
7	A multi-parent advanced generation inter-cross (<sc>MAGIC</sc>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). <i>Plant Journal</i> , 2018, 93, 1129-1142.	5.7	132
8	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
9	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	8.8	125
10	Identification of QTL controlling domestication-related traits in cowpea (<i>Vigna unguiculata</i> L. Walp). <i>Scientific Reports</i> , 2018, 8, 6261.	3.3	105
11	A receptor-like protein mediates plant immune responses to herbivore-associated molecular patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31510-31518.	7.1	86
12	Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032.	2.8	75
13	Genomic regions, cellular components and gene regulatory basis underlying pod length variations in cowpea (<i>V. unguiculata</i> L. Walp). <i>Plant Biotechnology Journal</i> , 2017, 15, 547-557.	8.3	68
14	Identification of Candidate Genes Controlling Black Seed Coat and Pod Tip Color in Cowpea (<i>Vigna</i> Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	56
15	The detection of QTLs in barley associated with endosperm hardness, grain density, grain size and malting quality using rapid phenotyping tools. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2533-2551.	3.6	53
16	Genetic diversity and structure of Iberian Peninsula cowpeas compared to world-wide cowpea accessions using high density SNP markers. <i>BMC Genomics</i> , 2017, 18, 891.	2.8	50
17	A genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [<i>Vigna unguiculata</i> (L.) Walp]. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3079-3087.	3.6	42
18	Transcriptome analysis of barley anthers: effect of mannitol treatment on microspore embryogenesis. <i>Physiologia Plantarum</i> , 2006, 127, 551-560.	5.2	37

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19	Microspore embryogenesis: assignment of genes to embryo formation and green vs. albino plant production. <i>Functional and Integrative Genomics</i> , 2009, 9, 311-323.	3.5	37
20	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
21	Seed Coat Pattern QTL and Development in Cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Frontiers in Plant Science</i> , 2019, 10, 1346.	3.6	36
22	Genetic, textual, and archeological evidence of the historical global spread of cowpea (<i>Vigna</i>). <i>Overlock 10 T</i>		34
23	Genetic markers for doubled haploid response in barley. <i>Euphytica</i> , 2007, 158, 287-294.	1.2	33
24	Single Nucleotide Polymorphism Mapping and Alignment of Recombinant Chromosome Substitution Lines in Barley. <i>Plant and Cell Physiology</i> , 2011, 52, 728-737.	3.1	32
25	Identification and validation of QTLs for green plant percentage in barley (<i>Hordeum vulgare</i> L.) anther culture. <i>Molecular Breeding</i> , 2008, 22, 119-129.	2.1	31
26	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
27	Transcriptome analysis of a barley breeding program examines gene expression diversity and reveals target genes for malting quality improvement. <i>BMC Genomics</i> , 2010, 11, 653.	2.8	29
28	Barley genetic variation: implications for crop improvement. <i>Briefings in Functional Genomics</i> , 2014, 13, 341-350.	2.7	29
29	The Relationships between Development and Low Temperature Tolerance in Barley Near Isogenic Lines Differing for Flowering Behavior. <i>Plant and Cell Physiology</i> , 2015, 56, 2312-2324.	3.1	27
30	The UCR Minicore: a resource for cowpea research and breeding. , 2021, 3, e95.		26
31	Fine mapping of barley locus Rps6 conferring resistance to wheat stripe rust. <i>Theoretical and Applied Genetics</i> , 2016, 129, 845-859.	3.6	21
32	Perspectives on Low Temperature Tolerance and Vernalization Sensitivity in Barley: Prospects for Facultative Growth Habit. <i>Frontiers in Plant Science</i> , 2020, 11, 585927.	3.6	19
33	Genome-Wide Association Study Reveals Candidate Genes for Flowering Time in Cowpea (<i>Vigna</i>). <i>Overlock 10 T</i>	1.0784314	19
34	BAC- and oligo-FISH mapping reveals chromosome evolution among <i>Vigna angularis</i> , <i>V. unguiculata</i> , and <i>Phaseolus vulgaris</i> . <i>Chromosoma</i> , 2021, 130, 133-147.	2.2	17
35	Orphan genes are involved in drought adaptations and ecoclimatic-oriented selections in domesticated cowpea. <i>Journal of Experimental Botany</i> , 2019, 70, 3101-3110.	4.8	15
36	Population Structure and Genetic Diversity in Korean Cowpea Germplasm Based on SNP Markers. <i>Plants</i> , 2020, 9, 1190.	3.5	15

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37	Structural and functional characterization of a winter malting barley. Theoretical and Applied Genetics, 2010, 120, 971-984.	3.6	14
38	Identification of QTL for perenniality and floral scent in cowpea (<i>Vigna unguiculata</i> [L.] Walp.). PLoS ONE, 2020, 15, e0229167.	2.5	13
39	Genetic, anatomical, and environmental patterns related to pod shattering resistance in domesticated cowpea [<i>Vigna unguiculata</i> (L.) Walp]. Journal of Experimental Botany, 2021, 72, 6219-6229.	4.8	12
40	A Novel Root-Knot Nematode Resistance QTL on Chromosome Vu01 in Cowpea. G3: Genes, Genomes, Genetics, 2019, 9, 1199-1209.	1.8	10
41	Breaks of macrosynteny and collinearity among moth bean (<i>Vigna aconitifolia</i>), cowpea (<i>V.</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	2.2	10
42	Sequence Diversity and Structural Variation. Compendium of Plant Genomes, 2018, , 109-122.	0.5	9
43	Genetic basis of barley contributions to beer flavor. Journal of Cereal Science, 2022, 104, 103430.	3.7	9