

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	Genetic basis of barley contributions to beer flavor. <i>Journal of Cereal Science</i> , 2022, 104, 103430.	3.7	9
2	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
3	The UCR Minicore: a resource for cowpea research and breeding. , 2021, 3, e95.		26
4	Genome-Wide Association Study Reveals Candidate Genes for Flowering Time in Cowpea (<i>Vigna</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	2.3	19
5	Genetic, anatomical, and environmental patterns related to pod shattering resistance in domesticated cowpea [<i>Vigna unguiculata</i> (L.) Walp]. <i>Journal of Experimental Botany</i> , 2021, 72, 6219-6229.	4.8	12
6	Breaks of macrosynteny and collinearity among moth bean (<i>Vigna aconitifolia</i>), cowpea (<i>V.</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	2.2	10
7	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
8	Genetic, textual, and archeological evidence of the historical global spread of cowpea (<sc><i>Vigna) Tj ETQq0 0 0 rgBT /Overlock 10 T		34
9	Population Structure and Genetic Diversity in Korean Cowpea Germplasm Based on SNP Markers. <i>Plants</i> , 2020, 9, 1190.	3.5	15
10	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
11	Identification of QTL for perenniality and floral scent in cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>PLoS ONE</i> , 2020, 15, e0229167.	2.5	13
12	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
13	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
14	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
15	A Novel Root-Knot Nematode Resistance QTL on Chromosome Vu01 in Cowpea. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1199-1209.	1.8	10
16	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
17	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
18	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

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19	A multi-parent advanced generation intercross (<sc>MAGIC</sc>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). Plant Journal, 2018, 93, 1129-1142.	5.7	132
20	Identification of Candidate Genes Controlling Black Seed Coat and Pod Tip Color in Cowpea (<i>Vigna unguiculata</i> L. Walp.). Plant Journal, 2018, 93, 1143-1156.	1.8	56
21	Sequence Diversity and Structural Variation. Compendium of Plant Genomes, 2018, , 109-122.	0.5	9
22	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
23	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. Scientific Data, 2017, 4, 170044.	5.3	130
24	Genome resources for climate-resilient cowpea, an essential crop for food security. Plant Journal, 2017, 89, 1042-1054.	5.7	199
25	Genomic regions, cellular components and gene regulatory basis underlying pod length variations in cowpea (<i>V. unguiculata</i> L. Walp). Plant Biotechnology Journal, 2017, 15, 547-557.	8.3	68
26	Genetic diversity and structure of Iberian Peninsula cowpeas compared to world-wide cowpea accessions using high density SNP markers. BMC Genomics, 2017, 18, 891.	2.8	50
27	Fine mapping of barley locus Rps6 conferring resistance to wheat stripe rust. Theoretical and Applied Genetics, 2016, 129, 845-859.	3.6	21
28	The Relationships between Development and Low Temperature Tolerance in Barley Near Isogenic Lines Differing for Flowering Behavior. Plant and Cell Physiology, 2015, 56, 2312-2324.	3.1	27
29	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
30	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. PLoS ONE, 2014, 9, e94688.	2.5	188
31	Barley genetic variation: implications for crop improvement. Briefings in Functional Genomics, 2014, 13, 341-350.	2.7	29
32	Genetics of Tillering in Rice and Barley. Plant Genome, 2014, 7, plantgenome2013.10.0032.	2.8	75
33	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. Genome Biology, 2013, 14, R58.	8.8	125
34	The detection of QTLs in barley associated with endosperm hardness, grain density, grain size and malting quality using rapid phenotyping tools. Theoretical and Applied Genetics, 2013, 126, 2533-2551.	3.6	53
35	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). Plant Journal, 2013, 76, 718-727.	5.7	264
36	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. Plant Genome, 2011, 4, 238-249.	2.8	150

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37	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
38	Structural and functional characterization of a winter malting barley. <i>Theoretical and Applied Genetics</i> , 2010, 120, 971-984.	3.6	14
39	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
40	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
41	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
42	Genetic markers for doubled haploid response in barley. <i>Euphytica</i> , 2007, 158, 287-294.	1.2	33
43	Transcriptome analysis of barley anthers: effect of mannitol treatment on microspore embryogenesis. <i>Physiologia Plantarum</i> , 2006, 127, 551-560.	5.2	37