

Hamid Ashrafi

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

4,675
citations

236833

25
h-index

254106

43
g-index

48
all docs

48
docs citations

48
times ranked

4803
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear DNA contents and ploidy levels of North American <i>Vaccinium</i> species and interspecific hybrids. <i>Scientia Horticulturae</i> , 2022, 297, 110955.	1.7	8
2	Genome sequence of <i>Monilinia vaccinii-corymbosi</i> sheds light on mummy berry disease infection of blueberry and mating type. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
3	Reproductive developmental transcriptome analysis of <i>Tripidium ravennae</i> (Poaceae). <i>BMC Genomics</i> , 2021, 22, 483.	1.2	1
4	An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. <i>Plant Genome</i> , 2021, 14, e20101.	1.6	13
5	High-density linkage map construction and identification of loci regulating fruit quality traits in blueberry. <i>Horticulture Research</i> , 2021, 8, 169.	2.9	10
6	An optimized protocol for stepwise optimization of real-time RT-PCR analysis. <i>Horticulture Research</i> , 2021, 8, 179.	2.9	38
7	Detection of Fruit Meals Within Laboratory-Raised and Field-Trapped Adult <i>Drosophila suzukii</i> (Diptera: Drosophilidae) Guts. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	0
8	Genotype, Environment, Year, and Harvest Effects on Fruit Quality Traits of Five Blueberry (<i>Vaccinium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.3	6
9	Simulated storage causes carbohydrate loss and rooting differences in two poinsettia cultivars. <i>Canadian Journal of Plant Science</i> , 2020, 100, 459-462.	0.3	0
10	A Rosaceae Family-Level Approach To Identify Loci Influencing Soluble Solids Content in Blackberry for DNA-Informed Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3729-3740.	0.8	6
11	Biomass yields, cytogenetics, fertility, and compositional analyses of novel bioenergy grass hybrids () Tj ETQq1 1 0.784314 rgBT /Overlock 2	2.5	14
12	Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. <i>Plant Genome</i> , 2019, 12, 180010.	1.6	65
13	3D point cloud data to quantitatively characterize size and shape of shrub crops. <i>Horticulture Research</i> , 2019, 6, 43.	2.9	29
14	Identification and Mapping of Late Blight Resistance Quantitative Trait Loci in Tomato Accession PI 163245. <i>Plant Genome</i> , 2018, 11, 180007.	1.6	11
15	Breeding Trait Priorities of the Blueberry Industry in the United States and Canada. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 1021-1028.	0.5	56
16	Disease Resistance to Multiple Fungal and Oomycete Pathogens Evaluated Using a Recombinant Inbred Line Population in Pepper. <i>Phytopathology</i> , 2017, 107, 1522-1531.	1.1	5
17	Regions Underlying Population Structure and the Genomics of Organ Size Determination in <i>Capsicum annuum</i> . <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0026.	1.6	41
18	DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. <i>PLoS Genetics</i> , 2016, 12, e1006012.	1.5	27

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19	New Insights on Eggplant/Tomato/Pepper Synteny and Identification of Eggplant and Pepper Orthologous QTL. <i>Frontiers in Plant Science</i> , 2016, 7, 1031.	1.7	28
20	A HapMap leads to a <i>Capsicum annuum</i> SNP Infinium array: a new tool for pepper breeding. <i>Horticulture Research</i> , 2016, 3, 16036.	2.9	47
21	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. <i>Nature Genetics</i> , 2016, 48, 657-666.	9.4	432
22	Ultra-High Density, Transcript-Based Genetic Maps of Pepper Define Recombination in the Genome and Synteny Among Related Species. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2341-2355.	0.8	23
23	A Long-Read Transcriptome Assembly of Cotton (<i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	1.6	12
24	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton (<i>Gossypium</i>) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1095-1105.	0.8	20
25	Detached-Leaflet Evaluation of Tomato Germplasm for Late Blight Resistance and Its Correspondence to Field and Greenhouse Screenings. <i>Plant Disease</i> , 2015, 99, 718-722.	0.7	28
26	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209.	0.8	226
27	Development and bin mapping of gene-associated interspecific SNPs for cotton (<i>Gossypium hirsutum</i> L.) introgression breeding efforts. <i>BMC Genomics</i> , 2014, 15, 945.	1.2	25
28	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	9.4	867
29	QTL Mapping of Fruit Rot Resistance to the Plant Pathogen <i>Phytophthora capsici</i> in a Recombinant Inbred Line <i>Capsicum annuum</i> Population. <i>Phytopathology</i> , 2014, 104, 479-483.	1.1	35
30	<i>CaDMR1</i> cosegregates with QTL <i>Pc5.1</i> for Resistance to <i>Phytophthora capsici</i> in Pepper (<i>Capsicum annuum</i>). <i>Plant Genome</i> , 2014, 7, plantgenome2014.03.0011.	1.6	46
31	Identification of QTLs for capsaicinoids, fruit quality, and plant architecture-related traits in an interspecific <i>Capsicum</i> RIL population. <i>Genome</i> , 2013, 56, 61-74.	0.9	69
32	Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1809-1818.	0.8	73
33	An Ultra-High-Density, Transcript-Based, Genetic Map of Lettuce. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 617-631.	0.8	91
34	Characterization of <i>Capsicum annuum</i> Genetic Diversity and Population Structure Based on Parallel Polymorphism Discovery with a 30K Unigene Pepper GeneChip. <i>PLoS ONE</i> , 2013, 8, e56200.	1.1	99
35	Selective genotyping to identify late blight resistance genes in an accession of the tomato wild species <i>Solanum pimpinellifolium</i> . <i>Euphytica</i> , 2012, 187, 63-75.	0.6	49
36	Development and application of a 6.5 million feature Affymetrix Genechip® for massively parallel discovery of single position polymorphisms in lettuce (<i>Lactuca</i> spp.). <i>BMC Genomics</i> , 2012, 13, 185.	1.2	36

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37	De novo assembly of the pepper transcriptome (<i>Capsicum annuum</i>): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. <i>BMC Genomics</i> , 2012, 13, 571.	1.2	109
38	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	13.7	1,204
39	<i>Uniform ripening</i> Encodes a <i>Golden 2-like</i> Transcription Factor Regulating Tomato Fruit Chloroplast Development. <i>Science</i> , 2012, 336, 1711-1715.	6.0	384
40	Identification of novel quantitative trait loci for increased lycopene content and other fruit quality traits in a tomato recombinant inbred line population. <i>Molecular Breeding</i> , 2012, 30, 549-567.	1.0	35
41	De novo assembly and characterization of the carrot transcriptome reveals novel genes, new markers, and genetic diversity. <i>BMC Genomics</i> , 2011, 12, 389.	1.2	178
42	A new genetic linkage map of tomato based on a <i>Solanum lycopersicum</i> × <i>S. pimpinellifolium</i> RIL population displaying locations of candidate pathogen response genes. <i>Genome</i> , 2009, 52, 935-956.	0.9	48
43	Genetics, Genomics and Breeding of Late Blight and Early Blight Resistance in Tomato. <i>Critical Reviews in Plant Sciences</i> , 2008, 27, 75-107.	2.7	141
44	A <i>Solanum lycopersicum</i> × <i>Solanum pimpinellifolium</i> Linkage Map of Tomato Displaying Genomic Locations of R-Genes, RGAs, and Candidate Resistance/Defense-Response ESTs. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-18.	2.2	24
45	Characterization of early blight resistance in a recombinant inbred line population of tomato: I. Heritability and trait correlations. <i>Advanced Studies in Biology</i> , 0, 7, 131-148.	0.2	5
46	Characterization of early blight resistance in a recombinant inbred line population of tomato: II. Identification of QTLs and their co-localization with candidate resistance genes. <i>Advanced Studies in Biology</i> , 0, 7, 149-168.	0.2	16