

Werner Howad

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,097
citations

361413

20
h-index

477307

29
g-index

33
all docs

33
docs citations

33
times ranked

1492
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Japanese Plum (<i>Prunus salicina</i>) PsMYB10 Alleles Reveals Structural Variation and Polymorphisms Correlating With Fruit Skin Color. <i>Frontiers in Plant Science</i> , 2021, 12, 655267.	3.6	14
2	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	5.7	94
3	Survey of over 4, 500 monumental olive trees preserved on-farm in the northeast Iberian Peninsula, their genotyping and characterization. <i>Scientia Horticulturae</i> , 2018, 231, 253-264.	3.6	34
4	Marker-assisted introgression (MAI) of almond genes into the peach background: a fast method to mine and integrate novel variation from exotic sources in long intergeneration species. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	21
5	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond × peach progenies. <i>Horticulture Research</i> , 2015, 2, 15016.	6.3	35
6	Mapping of a major gene for the slow ripening character in peach: co-location with the maturity date gene and development of a candidate gene-based diagnostic marker for its selection. <i>Euphytica</i> , 2015, 205, 627-636.	1.2	72
7	Combining linkage and association mapping to search for markers linked to the flat fruit character in peach. <i>Euphytica</i> , 2013, 190, 279-288.	1.2	53
8	A first insight into peach [<i>Prunus persica</i> (L.) Batsch] SNP variability. <i>Tree Genetics and Genomes</i> , 2012, 8, 1359-1369.	1.6	39
9	Cell Wall Polysaccharide Chemistry of Peach Genotypes with Contrasted Textures and Other Fruit Traits. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 6594-6605.	5.2	19
10	Molecular Linkage Maps. , 2012, , 76-104.		1
11	Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. <i>Molecular Breeding</i> , 2011, 28, 667-682.	2.1	53
12	Identification of quantitative trait loci associated with self-compatibility in a <i>Prunus</i> species. <i>Tree Genetics and Genomes</i> , 2011, 7, 629-639.	1.6	18
13	Molecular markers for kernel bitterness in almond. <i>Tree Genetics and Genomes</i> , 2010, 6, 237-245.	1.6	49
14	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. <i>BMC Genetics</i> , 2010, 11, 69.	2.7	139
15	Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers. <i>BMC Genomics</i> , 2009, 10, 562.	2.8	61
16	Development of “universal” gene-specific markers from <i>Malus</i> spp. cDNA sequences, their mapping and use in synteny studies within Rosaceae. <i>Tree Genetics and Genomes</i> , 2009, 5, 133-145.	1.6	30
17	A framework physical map for peach, a model Rosaceae species. <i>Tree Genetics and Genomes</i> , 2008, 4, 745-756.	1.6	72
18	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. <i>BMC Genomics</i> , 2008, 9, 543.	2.8	61

#	ARTICLE	IF	CITATIONS
19	Almond. , 2007, , 229-242.		27
20	Mapping major genes and quantitative trait loci controlling agronomic traits in almond. Plant Breeding, 2007, 126, 310-318.	1.9	93
21	Tri-/Hexanucleotide Microsatellite Markers in Peach Derived from Enriched Genomic Libraries and Their Application in Rosaceae. Breeding Science, 2007, 57, 289-296.	1.9	4
22	Development and transportability across Prunus species of 42 polymorphic almond microsatellites. Molecular Ecology Notes, 2005, 5, 531-535.	1.7	84
23	Candidate gene database and transcript map for peach, a model species for fruit trees. Theoretical and Applied Genetics, 2005, 110, 1419-1428.	3.6	71
24	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the Prunus Reference Map. Genetics, 2005, 171, 1305-1309.	2.9	180
25	Simple-sequence repeat (SSR) markers of Japanese plum (Prunus salicina Lindl.) are highly polymorphic and transferable to peach and almond. Molecular Ecology Notes, 2004, 4, 163-166.	1.7	137
26	Microsatellite genetic linkage maps of myrobalan plum and an almond-peach hybrid?location of root-knot nematode resistance genes. Theoretical and Applied Genetics, 2004, 109, 827-838.	3.6	109
27	Comparative mapping and marker-assisted selection in Rosaceae fruit crops. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9891-9896.	7.1	473
28	Nuclear genes from Tx CMS maintainer lines are unable to maintain atp6 RNA editing in any anther cell-type in the Sorghum bicolor A3 cytoplasm. Current Genetics, 1999, 36, 62-68.	1.7	19
29	Mutations at specificatp6codons which cause human mitochondrial diseases also lead to male sterility in a plant. FEBS Letters, 1998, 441, 159-160.	2.8	14
30	Sequence analysis and transcript processing of the mitochondrial nad3-rps12 genes from Sorghum bicolor. Plant Science, 1997, 129, 65-68.	3.6	5
31	Mitochondrial RNA editing is sequence specific and independent of transcript abundance in Sorghum bicolor. Current Genetics, 1996, 30, 186-189.	1.7	10
32	Construction of a collection of introgression lines of "Texas" almond DNA fragments in the "Earlygold" peach genetic background. Horticulture Research, 0, , .	6.3	1