

Ron Ophir

List of Publications by Year in descending order

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52
papers

4,768
citations

147566

31
h-index

182168

51
g-index

54
all docs

54
docs citations

54
times ranked

7906
citing authors

#	ARTICLE	IF	CITATIONS
1	Drivers of genetic differentiation and recent evolutionary history of an Eurasian wild pea. <i>Journal of Biogeography</i> , 2022, 49, 794-808.	1.4	7
2	Phylogeny and disparate selection signatures suggest two genetically independent domestication events in pea (<i>Pisum</i> L.). <i>Plant Journal</i> , 2022, 110, 419-439.	2.8	9
3	The Pomegranate Deciduous Trait Is Genetically Controlled by a PgPolyQ-MADS Gene. <i>Frontiers in Plant Science</i> , 2022, 13, 870207.	1.7	1
4	Fine Mapping of the "black" Peel Color in Pomegranate (<i>Punica granatum</i> L.) Strongly Suggests That a Mutation in the Anthocyanidin Reductase (ANR) Gene Is Responsible for the Trait. <i>Frontiers in Plant Science</i> , 2021, 12, 642019.	1.7	17
5	The "Tommy Atkins" mango genome reveals candidate genes for fruit quality. <i>BMC Plant Biology</i> , 2021, 21, 108.	1.6	28
6	Prospects for the natural distribution of crop wild-relatives with limited adaptability: The case of the wild pea <i>Pisum fulvum</i> . <i>Plant Science</i> , 2021, 310, 110957.	1.7	10
7	Identification of potential post-ethylene events in the signaling cascade induced by stimuli of bud dormancy release in grapevine. <i>Plant Journal</i> , 2020, 104, 1251-1268.	2.8	11
8	Limited divergent adaptation despite a substantial environmental cline in wild pea. <i>Molecular Ecology</i> , 2020, 29, 4322-4336.	2.0	7
9	Environmental and genetic determinants of amphicarpy in <i>Pisum fulvum</i> , a wild relative of domesticated pea. <i>Plant Science</i> , 2020, 298, 110566.	1.7	3
10	Genetic diversity of avocado (<i>Persea americana</i> Mill.) germplasm using pooled sequencing. <i>BMC Genomics</i> , 2019, 20, 379.	1.2	39
11	Gene expression and metabolite profiling analyses of developing pomegranate fruit peel reveal interactions between anthocyanin and punicalagin production. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	12
12	Distinct gibberellin functions during and after grapevine bud dormancy release. <i>Journal of Experimental Botany</i> , 2018, 69, 1635-1648.	2.4	64
13	Differential expression of cucumber RNA-dependent RNA polymerase 1 genes during antiviral defence and resistance. <i>Molecular Plant Pathology</i> , 2018, 19, 300-312.	2.0	42
14	Transient induction of a subset of ethylene biosynthesis genes is potentially involved in regulation of grapevine bud dormancy release. <i>Plant Molecular Biology</i> , 2018, 98, 507-523.	2.0	18
15	Abscisic acid catabolism enhances dormancy release of grapevine buds. <i>Plant, Cell and Environment</i> , 2018, 41, 2490-2503.	2.8	52
16	ctsGE clustering subgroups of expression data. <i>Bioinformatics</i> , 2017, 33, 2053-2055.	1.8	2
17	Variation in cucumber (<i>Cucumis sativus</i> L.) fruit size and shape results from multiple components acting pre-anthesis and post-pollination. <i>Planta</i> , 2017, 246, 641-658.	1.6	53
18	Genetic Map of Mango: A Tool for Mango Breeding. <i>Frontiers in Plant Science</i> , 2017, 8, 577.	1.7	51

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19	Drought Response and Genetic Diversity in <i>Pisum fulvum</i> , a Wild Relative of Domesticated Pea. <i>Crop Science</i> , 2017, 57, 1145-1159.	0.8	26
20	Mango (<i>Mangifera indica</i> L.) germplasm diversity based on single nucleotide polymorphisms derived from the transcriptome. <i>BMC Plant Biology</i> , 2015, 15, 277.	1.6	41
21	A novel genetic map of pomegranate based on transcript markers enriched with QTLs for fruit quality traits. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	38
22	QTL mapping in multiple populations and development stages reveals dynamic quantitative trait loci for fruit size in cucumbers of different market classes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1747-1763.	1.8	128
23	Ultrahigh-Density Linkage Map for Cultivated Cucumber (<i>Cucumis sativus</i> L.) Using a Single-Nucleotide Polymorphism Genotyping Array. <i>PLoS ONE</i> , 2015, 10, e0124101.	1.1	29
24	Analysis of Microtubule-Associated-Proteins during IBA-Mediated Adventitious Root Induction Reveals KATANIN Dependent and Independent Alterations of Expression Patterns. <i>PLoS ONE</i> , 2015, 10, e0143828.	1.1	29
25	The PH gene determines fruit acidity and contributes to the evolution of sweet melons. <i>Nature Communications</i> , 2014, 5, 4026.	5.8	100
26	Single-Nucleotide Polymorphism Markers from De-Novo Assembly of the Pomegranate Transcriptome Reveal Germplasm Genetic Diversity. <i>PLoS ONE</i> , 2014, 9, e88998.	1.1	70
27	Effects of gibberellin treatment during flowering induction period on global gene expression and the transcription of flowering-control genes in Citrus buds. <i>Plant Science</i> , 2013, 198, 46-57.	1.7	91
28	Combining bulk segregation analysis and microarrays for mapping of the pH trait in melon. <i>Theoretical and Applied Genetics</i> , 2013, 126, 349-358.	1.8	8
29	The molecular and enzymatic basis of bitter/non-bitter flavor of citrus fruit: evolution of branch-forming rhamnosyltransferases under domestication. <i>Plant Journal</i> , 2013, 73, 166-178.	2.8	92
30	Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen <i>Fusarium fujikuroi</i> Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. <i>PLoS Pathogens</i> , 2013, 9, e1003475.	2.1	406
31	Self-Custom-Made SFP Arrays for Nonmodel Organisms. <i>Methods in Molecular Biology</i> , 2012, 815, 39-47.	0.4	0
32	Microarray analysis revealed upregulation of nitrate reductase in juvenile cuttings of <i>Eucalyptus grandis</i> , which correlated with increased nitric oxide production and adventitious root formation. <i>Plant Journal</i> , 2012, 71, 787-799.	2.8	76
33	Metabolism of soluble sugars in developing melon fruit: a global transcriptional view of the metabolic transition to sucrose accumulation. <i>Plant Molecular Biology</i> , 2011, 76, 1-18.	2.0	101
34	Identification of defense-related genes newly-associated with tomato flower abscission. <i>Plant Signaling and Behavior</i> , 2011, 6, 590-593.	1.2	20
35	High-throughput marker discovery in melon using a self-designed oligo microarray. <i>BMC Genomics</i> , 2010, 11, 269.	1.2	13
36	Microarray Analysis of the Abscission-Related Transcriptome in the Tomato Flower Abscission Zone in Response to Auxin Depletion. <i>Plant Physiology</i> , 2010, 154, 1929-1956.	2.3	202

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37	Transcriptomic profiling of heat-stress response in potato periderm. <i>Journal of Experimental Botany</i> , 2009, 60, 4411-4421.	2.4	80
38	Transcriptional profiling of maturing tomato (<i>Solanum lycopersicum</i> L.) microspores reveals the involvement of heat shock proteins, ROS scavengers, hormones, and sugars in the heat stress response. <i>Journal of Experimental Botany</i> , 2009, 60, 3891-3908.	2.4	289
39	Gene-expression profiling of grape bud response to two alternative dormancy-release stimuli expose possible links between impaired mitochondrial activity, hypoxia, ethylene-ABA interplay and cell enlargement. <i>Plant Molecular Biology</i> , 2009, 71, 403-423.	2.0	131
40	Differential pathogenicity and genetic diversity among <i>Pectobacterium carotovorum</i> ssp. <i>carotovorum</i> isolates from monocot and dicot hosts support early genomic divergence within this taxon. <i>Environmental Microbiology</i> , 2008, 10, 2746-2759.	1.8	43
41	Digital expression profiling of a grape-bud EST collection leads to new insight into molecular events during grape-bud dormancy release. <i>Plant Science</i> , 2007, 173, 446-457.	1.7	44
42	Widespread ectopic expression of olfactory receptor genes. <i>BMC Genomics</i> , 2006, 7, 121.	1.2	216
43	Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. <i>Bioinformatics</i> , 2005, 21, 650-659.	1.8	971
44	Incongruent Expression Profiles between Human and Mouse Orthologous Genes Suggest Widespread Neutral Evolution of Transcription Control. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 15-24.	1.0	124
45	Plant Respiratory Burst Oxidase Homologs Impinge on Wound Responsiveness and Development in <i>Lycopersicon esculentum</i> [W]. <i>Plant Cell</i> , 2004, 16, 616-628.	3.1	248
46	Intron retention is a major phenomenon in alternative splicing in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2004, 39, 877-885.	2.8	297
47	Prediction of high risk Ewing's sarcoma by gene expression profiling. <i>Oncogene</i> , 2004, 23, 8997-9006.	2.6	92
48	GeneNote: whole genome expression profiles in normal human tissues. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1067-1072.	0.1	153
49	GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. <i>Briefings in Bioinformatics</i> , 2003, 4, 349-360.	3.2	17
50	Constructing Phylogenies from Quartets: Elucidation of Eutherian Superordinal Relationships. <i>Journal of Computational Biology</i> , 1998, 5, 377-390.	0.8	34
51	Patterns and rates of indel evolution in processed pseudogenes from humans and murids. <i>Gene</i> , 1997, 205, 191-202.	1.0	124
52	Biased random mutagenesis of peptides: determination of mutation frequency by computer simulation. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 143-146.	1.0	8