Federico Martinelli

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Advanced methods of plant disease detection. A review. Agronomy for Sustainable Development, 2015, 35, 1-25.	5.3	579
2	Advanced Glycation End Products (AGEs): Biochemistry, Signaling, Analytical Methods, and Epigenetic Effects. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-18.	4.0	213
3	Transcriptome Profiling of Citrus Fruit Response to Huanglongbing Disease. PLoS ONE, 2012, 7, e38039.	2.5	158
4	Soil inoculation with symbiotic microorganisms promotes plant growth and nutrient transporter genes expression in durum wheat. Frontiers in Plant Science, 2015, 6, 815.	3.6	118
5	Gene Regulatory Networks Elucidating Huanglongbing Disease Mechanisms. PLoS ONE, 2013, 8, e74256.	2.5	106
6	Metabolomics Suggests That Soil Inoculation with Arbuscular Mycorrhizal Fungi Decreased Free Amino Acid Content in Roots of Durum Wheat Grown under N-Limited, P-Rich Field Conditions. PLoS ONE, 2015, 10, e0129591.	2.5	69
7	Arbuscular mycorrhizal symbiosis mitigates the negative effects of salinity on durum wheat. PLoS ONE, 2017, 12, e0184158.	2.5	62
8	Epigenetics for Crop Improvement in Times of Global Change. Biology, 2021, 10, 766.	2.8	53
9	Transcriptome and metabolome analysis of Citrus fruit to elucidate puffing disorder. Plant Science, 2014, 217-218, 87-98.	3.6	52
10	lt Is Our Turn to Get Cannabis High: Put Cannabinoids in Food and Health Baskets. Molecules, 2020, 25, 4036.	3.8	52
11	Identification of key genes and its chromosome regions linked to drought responses in leaves across different crops through meta-analysis of RNA-Seq data. BMC Plant Biology, 2019, 19, 194.	3.6	45
12	Stress responses in citrus peel: Comparative analysis of host responses to Huanglongbing disease and puffing disorder. Scientia Horticulturae, 2015, 192, 409-420.	3.6	38
13	Transcriptomic responses to biotic stresses in Malus x domestica: a meta-analysis study. Scientific Reports, 2018, 8, 1970.	3.3	37
14	Deciphering the Epigenetic Alphabet Involved in Transgenerational Stress Memory in Crops. International Journal of Molecular Sciences, 2021, 22, 7118.	4.1	36
15	Plant stress biology in epigenomic era. Plant Science, 2020, 294, 110376.	3.6	34
16	Analysis of Early Host Responses for Asymptomatic Disease Detection and Management of Specialty Crops. Critical Reviews in Immunology, 2010, 30, 277-289.	0.5	34
17	Metabolic Profiling and Post-harvest Behavior of "Dottato―Fig (Ficus carica L.) Fruit Covered With an Edible Coating From O. ficus-indica. Frontiers in Plant Science, 2018, 9, 1321.	3.6	30
18	Detection and identification of Fabavirus species by one-step RT-PCR and multiplex RT-PCR. Journal of Virological Methods, 2014, 197, 77-82.	2.1	28

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19	Identification and characterization of durum wheat microRNAs in leaf and root tissues. Functional and Integrative Genomics, 2017, 17, 583-598.	3.5	28
20	Gaining Insight into Exclusive and Common Transcriptomic Features Linked with Biotic Stress Responses in Malus. Frontiers in Plant Science, 2017, 8, 1569.	3.6	28
21	Identifying Host Molecular Features Strongly Linked With Responses to Huanglongbing Disease in Citrus Leaves. Frontiers in Plant Science, 2018, 9, 277.	3.6	25
22	Botanical, Phytochemical, Anti-Microbial and Pharmaceutical Characteristics of Hawthorn (Crataegus monogyna Jacq.), Rosaceae. Molecules, 2021, 26, 7266.	3.8	25
23	Light induces expression of a dehydrin-encoding gene during seedling de-etiolation in sunflower (Helianthus annuus L.). Journal of Plant Physiology, 2007, 164, 263-273.	3.5	23
24	Transcriptome analysis of Phoenix canariensis Chabaud in response to Rhynchophorus ferrugineus Olivier attacks. Frontiers in Plant Science, 2015, 6, 817.	3.6	18
25	A microarray analysis highlights the role of tetrapyrrole pathways in grapevine responses to "stolbur―phytoplasma, phloem virus infections and recovered status. Physiological and Molecular Plant Pathology, 2016, 93, 129-137.	2.5	17
26	<i>Rhynchophorus ferrugineus</i> attack affects a group of compounds rather than rearranging <i>Phoenix canariensis</i> metabolic pathways. Journal of Integrative Plant Biology, 2016, 58, 388-396.	8.5	15
27	A Comparative Transcriptomic Meta-Analysis Revealed Conserved Key Genes and Regulatory Networks Involved in Drought Tolerance in Cereal Crops. International Journal of Molecular Sciences, 2021, 22, 13062.	4.1	15
28	An Epigenetic Alphabet of Crop Adaptation to Climate Change. Frontiers in Genetics, 2022, 13, 818727.	2.3	15
29	RNA uridylation and decay in plants. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20180163.	4.0	14
30	A robust workflow for indirect somatic embryogenesis and cormlet production in saffron (Crocus) Tj ETQq0 0 0	rgBT /Ovei 3.2	rlock 10 Tf 50
31	Identification of miRNAs linked with the drought response of tef [Eragrostis tef (Zucc.) Trotter]. Journal of Plant Physiology, 2018, 224-225, 163-172.	3.5	13
32	Water Deficit Affects the Growth and Leaf Metabolite Composition of Young Loquat Plants. Plants, 2020, 9, 274.	3.5	12
33	The priming fingerprint on the plant transcriptome investigated through meta-analysis of RNA-Seq data. European Journal of Plant Pathology, 2020, 156, 779-797.	1.7	12
34	Computational screening of miRNAs and their targets in saffron (Crocus sativus L.) by transcriptome mining. Planta, 2021, 254, 117.	3.2	12
35	Identification of microRNAS differentially regulated by water deficit in relation to mycorrhizal treatment in wheat. Molecular Biology Reports, 2019, 46, 5163-5174.	2.3	11
36	Short-Term Responses of Apple Fruit to Partial Reoxygenation during Extreme Hypoxic Storage Conditions. Journal of Agricultural and Food Chemistry, 2019, 67, 4754-4763.	5.2	11

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37	Identification of conserved genes linked to responses to abiotic stresses in leaves among different plant species. Functional Plant Biology, 2021, 48, 54.	2.1	10
38	In-Field and Early Detection of Xylella fastidiosa Infections in Olive Using a Portable Instrument. Frontiers in Plant Science, 2018, 9, 2007.	3.6	9
39	Transcriptome Analysis of Pistacia vera Inflorescence Buds in Bearing and Non-Bearing Shoots Reveals the Molecular Mechanism Causing Premature Flower Bud Abscission. Genes, 2020, 11, 851.	2.4	9
40	Gaining Insight into Exclusive and Common Transcriptomic Features Linked to Drought and Salinity Responses across Fruit Tree Crops. Plants, 2020, 9, 1059.	3.5	9
41	Application of a portable instrument for rapid and reliable detection of SARS oVâ€2 infection in any environment. Immunological Reviews, 2020, 295, 4-10.	6.0	9
42	Molecular Responses to Small Regulating Molecules against Huanglongbing Disease. PLoS ONE, 2016, 11, e0159610.	2.5	7
43	Agronomic, metabolomic and lipidomic characterisation of Sicilian Origanum vulgare (L.) ecotypes. Natural Product Research, 2016, 30, 1103-1107.	1.8	6
44	Proposed Research for Innovative Solutions for Chickpeas and Beans in a Climate Change Scenario: The Mediterranean Basin. Sustainability, 2020, 12, 1315.	3.2	5
45	LEGU-MED: Developing Biodiversity-Based Agriculture with Legume Cropping Systems in the Mediterranean Basin. Agronomy, 2022, 12, 132.	3.0	4
46	Transcriptomic Analysis of the Pistacia vera (L.) Fruits Enable the Identification of Genes and Hormone-Related Gene Linked to Inflorescence Bud Abscission. Genes, 2022, 13, 60.	2.4	4
47	Identifying conserved genes involved in crop tolerance to cold stress. Functional Plant Biology, 2022, 49, 861-873.	2.1	4
48	Deciphering transcriptional regulation mechanisms underlining fruit development and ripening in Vitis vinifera. Journal of Berry Research, 2019, 9, 641-664.	1.4	2
49	Transcriptome Response of Metallicolous and a Non-Metallicolous Ecotypes of Noccaea goesingensis to Nickel Excess. Plants, 2020, 9, 951.	3.5	2
50	Meta-analysis of transcriptomic responses to cold stress in plants. Functional Plant Biology, 2022, 49, 704-724.	2.1	2
51	Members of the WRKY gene family are upregulated in Canary palms attacked by Red Palm Weevil. Arthropod-Plant Interactions, 2019, 13, 109-116.	1.1	1