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List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

4,383
citations

236925

25
h-index

197818

49
g-index

53
all docs

53
docs citations

53
times ranked

5631
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitogen-activated protein kinase cascades in plants: a new nomenclature. <i>Trends in Plant Science</i> , 2002, 7, 301-308.	8.8	1,080
2	The AP2/ERF Domain Transcription Factor ORA59 Integrates Jasmonic Acid and Ethylene Signals in Plant Defense. <i>Plant Physiology</i> , 2008, 147, 1347-1357.	4.8	609
3	A novel jasmonate- and elicitor-responsive element in the periwinkle secondary metabolite biosynthetic gene <i>Str</i> interacts with a jasmonate- and elicitor-inducible AP2-domain transcription factor, ORCA2. <i>EMBO Journal</i> , 1999, 18, 4455-4463.	7.8	406
4	Two GCC boxes and AP2/ERF-domain transcription factor ORA59 in jasmonate/ethylene-mediated activation of the PDF1.2 promoter in Arabidopsis. <i>Plant Molecular Biology</i> , 2011, 75, 321-331.	3.9	233
5	Regulatory Mechanisms Underlying Oil Palm Fruit Mesocarp Maturation, Ripening, and Functional Specialization in Lipid and Carotenoid Metabolism. <i>Plant Physiology</i> , 2011, 156, 564-584.	4.8	190
6	Colonization of Rice Leaf Blades by an African Strain of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Depends on a New TAL Effector That Induces the Rice Nodulin-3 <i>Os11N3</i> Gene. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1102-1113.	2.6	179
7	Zinc Finger Proteins Act as Transcriptional Repressors of Alkaloid Biosynthesis Genes in <i>Catharanthus roseus</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 52940-52948.	3.4	167
8	Expression Profiling of the Whole Arabidopsis Shaggy-Like Kinase Multigene Family by Real-Time Reverse Transcriptase-Polymerase Chain Reaction. <i>Plant Physiology</i> , 2002, 130, 577-590.	4.8	166
9	A fluorescent hormone biosensor reveals the dynamics of jasmonate signalling in plants. <i>Nature Communications</i> , 2015, 6, 6043.	12.8	130
10	Arabidopsis kinome: after the casting. <i>Functional and Integrative Genomics</i> , 2004, 4, 163-87.	3.5	113
11	The <i>Casuarina</i> <i>NIN</i> gene is transcriptionally activated throughout <i>Frankia</i> root infection as well as in response to bacterial diffusible signals. <i>New Phytologist</i> , 2015, 208, 887-903.	7.3	87
12	Agrobacterium-mediated genetic transformation of <i>Coffea arabica</i> (L.) is greatly enhanced by using established embryogenic callus cultures. <i>BMC Plant Biology</i> , 2011, 11, 92.	3.6	77
13	Heart of Endosymbioses: Transcriptomics Reveals a Conserved Genetic Program among Arbuscular Mycorrhizal, Actinorhizal and Legume-Rhizobial Symbioses. <i>PLoS ONE</i> , 2012, 7, e44742.	2.5	77
14	Identification of the <i>Hevea brasiliensis</i> AP2/ERF superfamily by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 30.	2.8	73
15	Reassessing the MAP3K and MAP4K relationships. <i>Trends in Plant Science</i> , 2004, 9, 123-129.	8.8	70
16	Genomic, transcriptomic, and proteomic approaches towards understanding the molecular mechanisms of salt tolerance in <i>Frankia</i> strains isolated from <i>Casuarina</i> trees. <i>BMC Genomics</i> , 2017, 18, 633.	2.8	46
17	Actinorhizal Signaling Molecules: <i>Frankia</i> Root Hair Deforming Factor Shares Properties With <i>NIN</i> Inducing Factor. <i>Frontiers in Plant Science</i> , 2018, 9, 1494.	3.6	46
18	The 9-lipoxygenase <i>GhLOX1</i> gene is associated with the hypersensitive reaction of cotton <i>Gossypium hirsutum</i> to <i>Xanthomonas campestris</i> pv. <i>malvacearum</i> . <i>Plant Physiology and Biochemistry</i> , 2007, 45, 596-606.	5.8	44

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19	Molecular diversity and gene expression of cotton ERF transcription factors reveal that group IXa members are responsive to jasmonate, ethylene and <i>Xanthomonas</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 471-485.	4.2	44
20	Symbiotic Performance of Diverse Frankia Strains on Salt-Stressed <i>Casuarina glauca</i> and <i>Casuarina equisetifolia</i> Plants. <i>Frontiers in Plant Science</i> , 2016, 7, 1331.	3.6	43
21	Tolerance to environmental stress by the nitrogen-fixing actinobacterium Frankia and its role in actinorhizal plants adaptation. <i>Symbiosis</i> , 2016, 70, 17-29.	2.3	42
22	Jasmonates—the Master Regulator of Rice Development, Adaptation and Defense. <i>Plants</i> , 2019, 8, 339.	3.5	37
23	The protein kinases AtMAP3K1 and BnMAP3K1 are functional homologues of <i>S. pombe</i> cdc7p and may be involved in cell division. <i>Plant Journal</i> , 2001, 26, 637-649.	5.7	35
24	Identification of potential transcriptional regulators of actinorhizal symbioses in <i>Casuarina glauca</i> and <i>Alnus glutinosa</i> . <i>BMC Plant Biology</i> , 2014, 14, 342.	3.6	34
25	Unraveling the Genetic Elements Involved in Shoot and Root Growth Regulation by Jasmonate in Rice Using a Genome-Wide Association Study. <i>Rice</i> , 2019, 12, 69.	4.0	31
26	Field Trials Reveal Ecotype-Specific Responses to Mycorrhizal Inoculation in Rice. <i>PLoS ONE</i> , 2016, 11, e0167014.	2.5	28
27	NaCl Effects on <i>In Vitro</i> Germination and Growth of Some Senegalese Cowpea (<i>Vigna</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.9	26
28	Inhibition of Auxin Signaling in <i>Frankia</i> Species-Infected Cells in <i>Casuarina glauca</i> Nodules Leads to Increased Nodulation. <i>Plant Physiology</i> , 2015, 167, 1149-1157.	4.8	25
29	Permanent Draft Genome Sequence for <i>Frankia</i> sp. Strain CeD, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of <i>Casuarina equisetifolia</i> Grown in Senegal. <i>Genome Announcements</i> , 2016, 4, .	0.8	22
30	Rhizobial root hair infection requires auxin signaling. <i>Trends in Plant Science</i> , 2015, 20, 332-334.	8.8	20
31	Role of auxin during intercellular infection of <i>Discaria trinervis</i> by Frankia. <i>Frontiers in Plant Science</i> , 2014, 5, 399.	3.6	19
32	Selection of arbuscular mycorrhizal fungal strains to improve <i>Casuarina equisetifolia</i> L. and <i>Casuarina glauca</i> Sieb. tolerance to salinity. <i>Annals of Forest Science</i> , 2018, 75, 1.	2.0	17
33	AtSGP1, AtSGP2 and MAP4K1± are nucleolar plant proteins that can complement fission yeast mutants lacking a functional SIN pathway. <i>Journal of Cell Science</i> , 2004, 117, 4265-4275.	2.0	16
34	GhERF3 regulates the accumulation of jasmonate and leads to enhanced cotton resistance to blight disease. <i>Molecular Plant Pathology</i> , 2017, 18, 825-836.	4.2	16
35	Plants, MEN and SIN. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 1-10.	5.8	14
36	Association of Lipoxygenase Response with Resistance of Various Cotton Genotypes to the Bacterial Blight Disease. <i>Journal of Phytopathology</i> , 2008, 156, 542-549.	1.0	14

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37	CRISPR/Cas9-Mediated Gene Editing of the Jasmonate Biosynthesis OsAOC Gene in Rice. <i>Methods in Molecular Biology</i> , 2020, 2085, 199-209.	0.9	14
38	Inference of the gene regulatory network acting downstream of <i>CROWN ROOTLESS1</i> in rice reveals a regulatory cascade linking genes involved in auxin signaling, crown root initiation, and root meristem specification and maintenance. <i>Plant Journal</i> , 2019, 100, 954-968.	5.7	13
39	Physiological and genetic control of transpiration efficiency in African rice, <i>Oryza glaberrima</i> Steud. <i>Journal of Experimental Botany</i> , 2022, 73, 5279-5293.	4.8	12
40	Permanent Draft Genome Sequence of <i>Frankia</i> sp. Strain Allo2, a Salt-Tolerant Nitrogen-Fixing Actinobacterium Isolated from the Root Nodules of <i>Allocastrucaria</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	11
41	Symbiotic ability of diverse <i>Frankia</i> strains on <i>Casuarina glauca</i> plants in hydroponic conditions. <i>Symbiosis</i> , 2016, 70, 79-86.	2.3	11
42	Effect of <i>Casuarina</i> Plantations Inoculated with Arbuscular Mycorrhizal Fungi and <i>Frankia</i> on the Diversity of Herbaceous Vegetation in Saline Environments in Senegal. <i>Diversity</i> , 2020, 12, 293.	1.7	11
43	PUCHI represses early meristem formation in developing lateral roots of <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 3496-3510.	4.8	11
44	Transcriptome profiling of laser-captured crown root primordia reveals new pathways activated during early stages of crown root formation in rice. <i>PLoS ONE</i> , 2020, 15, e0238736.	2.5	7
45	<i>CROWN ROOTLESS1</i> binds <i>DNA</i> with a relaxed specificity and activates <i>OsROP</i> and <i>OsbHLH044</i> genes involved in crown root formation in rice. <i>Plant Journal</i> , 2022, 111, 546-566.	5.7	7
46	A model for the evolution and genesis of the pseudotetraploid <i>Arabidopsis thaliana</i> genome. <i>Advances in Botanical Research</i> , 2002, 38, 235-249.	1.1	3
47	Advances in <i>Frankia</i> genome studies and molecular aspects of tolerance to environmental stresses. , 2020, , 381-389.		3
48	Establishment of Actinorhizal Symbioses. <i>Soil Biology</i> , 2013, , 89-101.	0.8	2
49	Establishment of Actinorhizal Symbiosis in Response to Ethylene, Salicylic Acid, and Jasmonate. <i>Methods in Molecular Biology</i> , 2020, 2085, 117-130.	0.9	1
50	Use of Fluorescent Reporters to Analyse Dynamic and Spatial Responses to Mechanical Wounding. <i>Methods in Molecular Biology</i> , 2020, 2085, 161-168.	0.9	0