

Van Nguyen Ngoc Tuyet

List of Publications by Year in descending order

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119
papers

3,455
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172207

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121
docs citations

121
times ranked

3986
citing authors

#	ARTICLE	IF	CITATIONS
1	WD40-domain protein GORI is an integrative scaffold that is required for pollen tube growth in rice. <i>Plant Signaling and Behavior</i> , 2023, 18, .	1.2	3
2	Comparative transcriptome analysis of pollen and anther wall reveals novel insights into the regulatory mechanisms underlying anther wall development and its dehiscence in rice. <i>Plant Cell Reports</i> , 2022, 41, 1229-1242.	2.8	2
3	Cytokinin increases vegetative growth period by suppressing florigen expression in rice and maize. <i>Plant Journal</i> , 2022, 110, 1619-1635.	2.8	17
4	Transcriptome Analysis of Triple Mutant for OsMADS62, OsMADS63, and OsMADS68 Reveals the Downstream Regulatory Mechanism for Pollen Germination in Rice (<i>Oryza sativa</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 239.	1.8	15
5	Epitranscriptomics: An Additional Regulatory Layer in Plants' Development and Stress Response. <i>Plants</i> , 2022, 11, 1033.	1.6	7
6	A myosin XI adaptor, TAPE, is essential for pollen tube elongation in rice. <i>Plant Physiology</i> , 2022, 190, 562-575.	2.3	3
7	<i>GOR1</i> , encoding the WD40 domain protein, is required for pollen tube germination and elongation in rice. <i>Plant Journal</i> , 2021, 105, 1645-1664.	2.8	31
8	<i>Arachis hypogaea</i> resveratrol synthase 3 alters the expression pattern of UDP-glycosyltransferase genes in developing rice seeds. <i>PLoS ONE</i> , 2021, 16, e0245446.	1.1	4
9	OsPP2C09 Is a Bifunctional Regulator in Both ABA-Dependent and Independent Abiotic Stress Signaling Pathways. <i>International Journal of Molecular Sciences</i> , 2021, 22, 393.	1.8	19
10	Recurrent mutations promote widespread structural and functional divergence of MULE-derived genes in plants. <i>Nucleic Acids Research</i> , 2021, 49, 11765-11777.	6.5	13
11	Rice PIN Auxin Efflux Carriers Modulate the Nitrogen Response in a Changing Nitrogen Growth Environment. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3243.	1.8	8
12	Global Identification of ANTH Genes Involved in Rice Pollen Germination and Functional Characterization of a Key Member, OsANTH3. <i>Frontiers in Plant Science</i> , 2021, 12, 609473.	1.7	11
13	Interaction of OsRopGEF3 Protein With OsRac3 to Regulate Root Hair Elongation and Reactive Oxygen Species Formation in Rice (<i>Oryza sativa</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 661352.	1.7	6
14	CTP synthase is essential for early endosperm development by regulating nuclei spacing. <i>Plant Biotechnology Journal</i> , 2021, 19, 2177-2191.	4.1	9
15	OsMTD2-mediated reactive oxygen species (ROS) balance is essential for intact pollen tube elongation in rice. <i>Plant Journal</i> , 2021, 107, 1131-1147.	2.8	17
16	Optimization of Protein Isolation and Label-Free Quantitative Proteomic Analysis in Four Different Tissues of Korean Ginseng. <i>Plants</i> , 2021, 10, 1409.	1.6	7
17	A Systemic View of Carbohydrate Metabolism in Rice to Facilitate Productivity. <i>Plants</i> , 2021, 10, 1690.	1.6	5
18	Identification of Genes and MicroRNAs Affecting Pre-harvest Sprouting in Rice (<i>Oryza sativa</i> L.) by Transcriptome and Small RNAome Analyses. <i>Frontiers in Plant Science</i> , 2021, 12, 727302.	1.7	5

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19	An Integrated Approach for the Efficient Extraction and Solubilization of Rice Microsomal Membrane Proteins for High-Throughput Proteomics. <i>Frontiers in Plant Science</i> , 2021, 12, 723369.	1.7	6
20	Key Genes in the Melatonin Biosynthesis Pathway with Circadian Rhythm Are Associated with Various Abiotic Stresses. <i>Plants</i> , 2021, 10, 129.	1.6	35
21	Transcriptional Changes in the Developing Rice Seeds Under Salt Stress Suggest Targets for Manipulating Seed Quality. <i>Frontiers in Plant Science</i> , 2021, 12, 748273.	1.7	6
22	Deficiency of rice hexokinase HXK5 impairs synthesis and utilization of starch in pollen grains and causes male sterility. <i>Journal of Experimental Botany</i> , 2020, 71, 116-125.	2.4	28
23	Pathogenesis strategies and regulation of ginsenosides by two species of <i>Ilyonectria</i> in <i>Panax ginseng</i> : power of speciation. <i>Journal of Ginseng Research</i> , 2020, 44, 332-340.	3.0	23
24	Emerging concepts of potassium homeostasis in plants. <i>Journal of Experimental Botany</i> , 2020, 71, 608-619.	2.4	81
25	A modified transient gene expression protocol for subcellular protein localization analysis in rice. <i>Plant Biotechnology Reports</i> , 2020, 14, 131-138.	0.9	3
26	Rice Senescence-Induced Receptor-Like Kinase (OsSRLK) Is Involved in Phytohormone-Mediated Chlorophyll Degradation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 260.	1.8	16
27	Phenylalanine ammonia-lyase family is closely associated with response to phosphate deficiency in rice. <i>Genes and Genomics</i> , 2020, 42, 67-76.	0.5	25
28	CAFRIaRice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	2.8	26
29	Rice Male Gamete Expression Database (RMEDB): A Web Resource for Functional Genomic Studies of Rice Male Organ Development. <i>Journal of Plant Biology</i> , 2020, 63, 421-430.	0.9	14
30	Physiological Importance of Pectin Modifying Genes During Rice Pollen Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4840.	1.8	14
31	Phosphate-Starvation-Inducible S-Like RNase Genes in Rice Are Involved in Phosphate Source Recycling by RNA Decay. <i>Frontiers in Plant Science</i> , 2020, 11, 585561.	1.7	16
32	A Revolution toward Gene-Editing Technology and Its Application to Crop Improvement. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5665.	1.8	62
33	First Steps in the Successful Fertilization of Rice and Arabidopsis: Pollen Longevity, Adhesion and Hydration. <i>Plants</i> , 2020, 9, 956.	1.6	12
34	High-throughput phenotyping platform for analyzing drought tolerance in rice. <i>Planta</i> , 2020, 252, 38.	1.6	50
35	Global Analysis of Cereal microProteins Suggests Diverse Roles in Crop Development and Environmental Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3709-3717.	0.8	7
36	Systematic Analysis of Cold Stress Response and Diurnal Rhythm Using Transcriptome Data in Rice Reveals the Molecular Networks Related to Various Biological Processes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6872.	1.8	8

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37	An Abiotic Stress Responsive U-Box E3 Ubiquitin Ligase Is Involved in OsGI-Mediating Diurnal Rhythm Regulating Mechanism. <i>Plants</i> , 2020, 9, 1071.	1.6	7
38	Overexpression of a novel cytochrome P450 monooxygenase gene, CYP704B1, from <i>Panax ginseng</i> increase biomass of reproductive tissues in transgenic <i>Arabidopsis</i> . <i>Molecular Biology Reports</i> , 2020, 47, 4507-4518.	1.0	5
39	Comparative Transcriptome Analysis Reveals Gene Regulatory Mechanism of UDT1 on Anther Development. <i>Journal of Plant Biology</i> , 2020, 63, 289-296.	0.9	16
40	PERSISTENT TAPETAL CELL2 Is Required for Normal Tapetal Programmed Cell Death and Pollen Wall Patterning. <i>Plant Physiology</i> , 2020, 182, 962-976.	2.3	41
41	Transcriptome analysis of rice leaves in response to <i>Rhizoctonia solani</i> infection and reveals a novel regulatory mechanism. <i>Plant Biotechnology Reports</i> , 2020, 14, 559-573.	0.9	31
42	Genome-wide analysis of RopGEF gene family to identify genes contributing to pollen tube growth in rice (<i>Oryza sativa</i>). <i>BMC Plant Biology</i> , 2020, 20, 95.	1.6	23
43	Rice CaM-binding transcription factor (OsCBT) mediates defense signaling via transcriptional reprogramming. <i>Plant Biotechnology Reports</i> , 2020, 14, 309-321.	0.9	13
44	Comprehensive phylogenomic analysis of ERF genes in sorghum provides clues to the evolution of gene functions and redundancy among gene family members. <i>3 Biotech</i> , 2020, 10, 139.	1.1	16
45	Fast Track to Discover Novel Promoters in Rice. <i>Plants</i> , 2020, 9, 125.	1.6	0
46	OsbHLH073 Negatively Regulates Internode Elongation and Plant Height by Modulating GA Homeostasis in Rice. <i>Plants</i> , 2020, 9, 547.	1.6	12
47	Conventional and Molecular Techniques from Simple Breeding to Speed Breeding in Crop Plants: Recent Advances and Future Outlook. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2590.	1.8	241
48	Homeobox transcription factor OsZHD2 promotes root meristem activity in rice by inducing ethylene biosynthesis. <i>Journal of Experimental Botany</i> , 2020, 71, 5348-5364.	2.4	24
49	Re-Analysis of 16S Amplicon Sequencing Data Reveals Soil Microbial Population Shifts in Rice Fields under Drought Condition. <i>Rice</i> , 2020, 13, 44.	1.7	17
50	A Systematic View Exploring the Role of Chloroplasts in Plant Abiotic Stress Responses. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	14
51	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	1.7	21
52	A web-based tool for the prediction of rice transcription factor function. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
53	Transcriptome analysis of rice-seedling roots under soil "salt stress using RNA-Seq method. <i>Plant Biotechnology Reports</i> , 2019, 13, 567-578.	0.9	37
54	A Multiprotein Complex Regulates Interference-Sensitive Crossover Formation in Rice. <i>Plant Physiology</i> , 2019, 181, 221-235.	2.3	20

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55	Rice Genome-Scale Network Integration Reveals Transcriptional Regulators of Grass Cell Wall Synthesis. <i>Frontiers in Plant Science</i> , 2019, 10, 1275.	1.7	14
56	Molecular Basis of Pollen Germination in Cereals. <i>Trends in Plant Science</i> , 2019, 24, 1126-1136.	4.3	34
57	Mutations in the microRNA172 binding site of SUPERNUMERARY BRACKET (SNB) suppress internode elongation in rice. <i>Rice</i> , 2019, 12, 62.	1.7	19
58	Identification of a module of HAP transcription factors for seed development in rice. <i>Plant Biotechnology Reports</i> , 2019, 13, 389-397.	0.9	0
59	Genome-wide Analysis of Root Hair Preferred RBOH Genes Suggests that Three RBOH Genes are Associated with Auxin-mediated Root Hair Development in Rice. <i>Journal of Plant Biology</i> , 2019, 62, 229-238.	0.9	29
60	Triterpenoid-biosynthetic UDP-glycosyltransferases from plants. <i>Biotechnology Advances</i> , 2019, 37, 107394.	6.0	114
61	Rice RHC Encoding a Putative Cellulase is Essential for Normal Root Hair Elongation. <i>Journal of Plant Biology</i> , 2019, 62, 82-91.	0.9	35
62	Genome-Wide Transcriptome Analysis of Rice Seedlings after Seed Dressing with <i>Paenibacillus yonginensis</i> DCY84T and Silicon. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5883.	1.8	15
63	Comparative Expression Analyses of Rice and Arabidopsis Phosphate Transporter Families Revealed Their Conserved Roles for the Phosphate Starvation Response. <i>Plant Breeding and Biotechnology</i> , 2019, 7, 42-49.	0.3	12
64	Defense Response to Pathogens Through Epigenetic Regulation in Rice. <i>Journal of Plant Biology</i> , 2018, 61, 1-10.	0.9	9
65	The transcriptomic changes of Huipizhi Heidou (<i>Glycine max</i>), a nematode-resistant black soybean during <i>Heterodera glycines</i> race 3 infection. <i>Journal of Plant Physiology</i> , 2018, 220, 96-104.	1.6	16
66	Comparative Analysis of Flanking Sequence Tags of T-DNA/Transposon Insertional Mutants and Genetic Variations of Fast-neutron Treated Mutants in Rice. <i>Journal of Plant Biology</i> , 2018, 61, 80-84.	0.9	8
67	Circadian rhythm gene expression and daily melatonin levels vary in athletes and sedentary males. <i>Biological Rhythm Research</i> , 2018, 49, 237-245.	0.4	6
68	Meta-expression analysis of unannotated genes in rice and approaches for network construction to suggest the probable roles. <i>Plant Molecular Biology</i> , 2018, 96, 17-34.	2.0	4
69	Integrated omics analysis of root-preferred genes across diverse rice varieties including Japonica and indica cultivars. <i>Journal of Plant Physiology</i> , 2018, 220, 11-23.	1.6	6
70	Lack of a Cytoplasmic RLK, Required for ROS Homeostasis, Induces Strong Resistance to Bacterial Leaf Blight in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 577.	1.7	13
71	Genome-wide analyses of late pollen-preferred genes conserved in various rice cultivars and functional identification of a gene involved in the key processes of late pollen development. <i>Rice</i> , 2018, 11, 28.	1.7	32
72	OsABCG9 Is an Important ABC Transporter of Cuticular Wax Deposition in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 960.	1.7	26

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73	S-nitrosocysteine-responsive genes modulate diverse regulatory pathways in <i>Oryza sativa</i> : a transcriptome profiling study. <i>Functional Plant Biology</i> , 2018, 45, 630.	1.1	14
74	A systemic view of phosphate starvation-responsive genes in rice roots to enhance phosphate use efficiency in rice. <i>Plant Biotechnology Reports</i> , 2018, 12, 249-264.	0.9	25
75	A secreted chitinase-like protein (<scp>OsCLP</scp>) supports root growth through calcium signaling in <i>Oryza sativa</i>. <i>Physiologia Plantarum</i> , 2017, 161, 273-284.	2.6	16
76	Genome-wide identification and extensive analysis of rice-endosperm preferred genes using reference expression database. <i>Journal of Plant Biology</i> , 2017, 60, 249-258.	0.9	15
77	The protein phosphatase 2C clade A protein OsPP2C51 positively regulates seed germination by directly inactivating OsbZIP10. <i>Plant Molecular Biology</i> , 2017, 93, 389-401.	2.0	56
78	Profile and Time-Scale Dynamics of Differentially Expressed Genes in Transcriptome of <i>Populus davidiana</i> Under Drought Stress. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 647-660.	1.0	6
79	Crosstalk between diurnal rhythm and water stress reveals an altered primary carbon flux into soluble sugars in drought-treated rice leaves. <i>Scientific Reports</i> , 2017, 7, 8214.	1.6	15
80	Construction and application of functional gene modules to regulatory pathways in rice. <i>Journal of Plant Biology</i> , 2017, 60, 358-379.	0.9	2
81	Comparative Expression Analysis of Rice and Arabidopsis Peroxiredoxin Genes Suggests Conserved or Diversified Roles Between the Two Species and Leads to the Identification of Tandemly Duplicated Rice Peroxiredoxin Genes Differentially Expressed in Seeds. <i>Rice</i> , 2017, 10, 30.	1.7	20
82	Global analysis of differentially expressed genes between japonica and indica rice roots reveals the molecular basis for enhanced cold tolerance in japonica rice. <i>Plant Biotechnology Reports</i> , 2017, 11, 461-473.	0.9	4
83	OsPhyB-Mediating Novel Regulatory Pathway for Drought Tolerance in Rice Root Identified by a Global RNA-Seq Transcriptome Analysis of Rice Genes in Response to Water Deficiencies. <i>Frontiers in Plant Science</i> , 2017, 8, 580.	1.7	56
84	A Systematic View of the MLO Family in Rice Suggests Their Novel Roles in Morphological Development, Diurnal Responses, the Light-Signaling Pathway, and Various Stress Responses. <i>Frontiers in Plant Science</i> , 2016, 7, 1413.	1.7	36
85	Genome-wide identification and analysis of rice genes preferentially expressed in pollen at an early developmental stage. <i>Plant Molecular Biology</i> , 2016, 92, 71-88.	2.0	32
86	Comparative phylogenomic analysis provides insights into TCP gene functions in Sorghum. <i>Scientific Reports</i> , 2016, 6, 38488.	1.6	48
87	Genome-wide identification and analysis of rice genes to elucidate morphological agronomic traits. <i>Journal of Plant Biology</i> , 2016, 59, 639-647.	0.9	5
88	Updated Rice Kinase Database RKD 2.0: enabling transcriptome and functional analysis of rice kinase genes. <i>Rice</i> , 2016, 9, 40.	1.7	20
89	Genome-wide transcriptome analysis of expression in rice seedling roots in response to supplemental nitrogen. <i>Journal of Plant Physiology</i> , 2016, 200, 62-75.	1.6	33
90	Functional classification of rice flanking sequence tagged genes using MapMan terms and global understanding on metabolic and regulatory pathways affected by dxr mutant having defects in light response. <i>Rice</i> , 2016, 9, 17.	1.7	17

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91	Development of functional modules based on co-expression patterns for cell-wall biosynthesis related genes in rice. <i>Journal of Plant Biology</i> , 2016, 59, 1-15.	0.9	18
92	Genome-Wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2015, 8, 276-289.	3.9	16
93	Phylogenomics databases for facilitating functional genomics in rice. <i>Rice</i> , 2015, 8, 60.	1.7	12
94	Integrating omics analysis of salt stress-responsive genes in rice. <i>Genes and Genomics</i> , 2015, 37, 645-655.	0.5	6
95	Genome-wide identification and analysis of genes associated with lysigenous aerenchyma formation in rice roots. <i>Journal of Plant Biology</i> , 2015, 58, 117-127.	0.9	22
96	Rice tissue-specific promoters and condition-dependent promoters for effective translational application. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 913-924.	4.1	35
97	Genome-wide transcriptome comparison of flag leaves among japonica and indica varieties. <i>Journal of Plant Biology</i> , 2015, 58, 333-343.	0.9	2
98	Molecular insights into the function of ankyrin proteins in plants. <i>Journal of Plant Biology</i> , 2015, 58, 271-284.	0.9	34
99	A systematic view of the rice calcineurin B-like protein interacting protein kinase family. <i>Genes and Genomics</i> , 2015, 37, 55-68.	0.5	7
100	Genome-wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2014, , .	3.9	0
101	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	0.9	34
102	A rice ABC transporter, OsABCC1, reduces arsenic accumulation in the grain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15699-15704.	3.3	406
103	Genome-wide expression analysis of rice ABC transporter family across spatio-temporal samples and in response to abiotic stresses. <i>Journal of Plant Physiology</i> , 2014, 171, 1276-1288.	1.6	95
104	Cross-Family Translational Genomics of Abiotic Stress-Responsive Genes between Arabidopsis and <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2014, 9, e91721.	1.1	19
105	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014, 30, 343-354.	0.7	40
106	Transcriptomic analysis of UV-treated rice leaves reveals UV-induced phytoalexin biosynthetic pathways and their regulatory networks in rice. <i>Phytochemistry</i> , 2013, 96, 57-71.	1.4	65
107	Genome-wide identification and analysis of Japonica and Indica cultivar-preferred transcripts in rice using 983 Affymetrix array data. <i>Rice</i> , 2013, 6, 19.	1.7	28
108	Genome-wide expression analysis of HSP70 family genes in rice and identification of a cytosolic HSP70 gene highly induced under heat stress. <i>Functional and Integrative Genomics</i> , 2013, 13, 391-402.	1.4	65

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109	Functional Characterization of Rice Genes Using a Gene-Indexed T-DNA Insertional Mutant Population. <i>Methods in Molecular Biology</i> , 2013, 956, 57-67.	0.4	7
110	Transcriptome Profiling Analysis Using Rice Oligonucleotide Microarrays. <i>Methods in Molecular Biology</i> , 2013, 956, 95-107.	0.4	1
111	The Rice Oligonucleotide Array Database: an atlas of rice gene expression. <i>Rice</i> , 2012, 5, 17.	1.7	192
112	Application of MapMan and RiceNet drives systematic analyses of the early heat stress transcriptome in rice seedlings. <i>Journal of Plant Biology</i> , 2012, 55, 436-449.	0.9	49
113	Genome-wide identification and analysis of early heat stress responsive genes in rice. <i>Journal of Plant Biology</i> , 2012, 55, 458-468.	0.9	44
114	Genome-Wide Analysis of Genes Induced by <i>Fusarium graminearum</i> Infection in Resistant and Susceptible Wheat Cultivars. <i>Journal of Plant Biology</i> , 2012, 55, 64-72.	0.9	11
115	A Survey of Databases for Analysis of Plant Cell Wall-Related Enzymes. <i>Bioenergy Research</i> , 2010, 3, 108-114.	2.2	6
116	The Submergence Tolerance Regulator <i>Sub1A</i> Mediates Stress-Responsive Expression of <i>AP2</i> / <i>ERF</i> Transcription Factors. <i>Plant Physiology</i> , 2010, 152, 1674-1692.	2.3	166
117	The Rice Kinase Phylogenomics Database: a guide for systematic analysis of the rice kinase super-family. <i>Trends in Plant Science</i> , 2010, 15, 595-599.	4.3	60
118	A two-genome microarray for the rice pathogens <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> and <i>X. oryzae</i> pv. <i>oryzicola</i> and its use in the discovery of a difference in their regulation of <i>hrp</i> genes. <i>BMC Microbiology</i> , 2008, 8, 99.	1.3	40
119	Hierarchical Structures and Dissected Functions of MADS-Box Transcription Factors in Rice Development. <i>Journal of Plant Biology</i> , 0, , 1.	0.9	3