

Ki-hong Jung

List of Publications by Year in descending order

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181
papers

10,051
citations

57758

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all docs

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docs citations

191
times ranked

10808
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, .	2.4	3
2	OsSIRH2-23, a rice salt-induced RING finger protein H2-23, contributes to insensitivity to salinity stress. <i>Environmental and Experimental Botany</i> , 2022, 194, 104715.	4.2	2
3	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.	5.6	2
4	Cytokinin increases vegetative growth period by suppressing florigen expression in rice and maize. <i>Plant Journal</i> , 2022, 110, 1619-1635.	5.7	17
5	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.	4.1	15
6	Epitranscriptomics: An Additional Regulatory Layer in Plantsâ€™ Development and Stress Response. <i>Plants</i> , 2022, 11, 1033.	3.5	7
7	Tissue-specific enhancement of OsRNS1 with root-preferred expression is required for the increase of crop yield. <i>Journal of Advanced Research</i> , 2022, , .	9.5	0
8	<i>GORI</i>, encoding the WD40 domain protein, is required for pollen tube germination and elongation in rice. <i>Plant Journal</i> , 2021, 105, 1645-1664.	5.7	31
9	<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.	2.5	4
10	Metabolic Dynamics and Ginsenoside Biosynthesis. <i>Compendium of Plant Genomes</i> , 2021, , 121-141.	0.5	1
11	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.	4.1	19
12	Recurrent mutations promote widespread structural and functional divergence of MULE-derived genes in plants. <i>Nucleic Acids Research</i> , 2021, 49, 11765-11777.	14.5	13
13	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.	4.1	8
14	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.	3.6	11
15	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.	3.6	6
16	Evolution and Application of Genome Editing Techniques for Achieving Food and Nutritional Security. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5585.	4.1	27
17	Advantage of Nanotechnology-Based Genome Editing System and Its Application in Crop Improvement. <i>Frontiers in Plant Science</i> , 2021, 12, 663849.	3.6	71
18	CTP synthase is essential for early endosperm development by regulating nuclei spacing. <i>Plant Biotechnology Journal</i> , 2021, 19, 2177-2191.	8.3	9

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19	OsMTD2-mediated reactive oxygen species (ROS) balance is essential for intact pollen tube elongation in rice. <i>Plant Journal</i> , 2021, 107, 1131-1147.	5.7	17
20	Optimization of Protein Isolation and Label-Free Quantitative Proteomic Analysis in Four Different Tissues of Korean Ginseng. <i>Plants</i> , 2021, 10, 1409.	3.5	7
21	A Systemic View of Carbohydrate Metabolism in Rice to Facilitate Productivity. <i>Plants</i> , 2021, 10, 1690.	3.5	5
22	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.	3.6	5
23	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.	3.6	6
24	Key Genes in the Melatonin Biosynthesis Pathway with Circadian Rhythm Are Associated with Various Abiotic Stresses. <i>Plants</i> , 2021, 10, 129.	3.5	35
25	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.	3.6	6
26	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.	4.8	28
27	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.	5.7	23
28	Emerging concepts of potassium homeostasis in plants. <i>Journal of Experimental Botany</i> , 2020, 71, 608-619.	4.8	81
29	A modified transient gene expression protocol for subcellular protein localization analysis in rice. <i>Plant Biotechnology Reports</i> , 2020, 14, 131-138.	1.5	3
30	Volatile content variation in the petals of cut roses during vase life. <i>Scientia Horticulturae</i> , 2020, 261, 108960.	3.6	9
31	Rice Senescence-Induced Receptor-Like Kinase (OsSRLK) Is Involved in Phytohormone-Mediated Chlorophyll Degradation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 260.	4.1	16
32	Phenylalanine ammonia-lyase family is closely associated with response to phosphate deficiency in rice. <i>Genes and Genomics</i> , 2020, 42, 67-76.	1.4	25
33	CAFRI-Rice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	5.7	26
34	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.	2.1	14
35	Physiological Importance of Pectin Modifying Genes During Rice Pollen Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4840.	4.1	14
36	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.	3.6	16

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37	A Revolution toward Gene-Editing Technology and Its Application to Crop Improvement. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5665.	4.1	62
38	First Steps in the Successful Fertilization of Rice and Arabidopsis: Pollen Longevity, Adhesion and Hydration. <i>Plants</i> , 2020, 9, 956.	3.5	12
39	High-throughput phenotyping platform for analyzing drought tolerance in rice. <i>Planta</i> , 2020, 252, 38.	3.2	50
40	Global Analysis of Cereal microProteins Suggests Diverse Roles in Crop Development and Environmental Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3709-3717.	1.8	7
41	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.	4.1	8
42	An Abiotic Stress Responsive U-Box E3 Ubiquitin Ligase Is Involved in OsGI-Mediating Diurnal Rhythm Regulating Mechanism. <i>Plants</i> , 2020, 9, 1071.	3.5	7
43	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.	2.3	5
44	Comparative Transcriptome Analysis Reveals Gene Regulatory Mechanism of UDT1 on Anther Development. <i>Journal of Plant Biology</i> , 2020, 63, 289-296.	2.1	16
45	PERSISTENT TAPETAL CELL2 Is Required for Normal Tapetal Programmed Cell Death and Pollen Wall Patterning. <i>Plant Physiology</i> , 2020, 182, 962-976.	4.8	41
46	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.	1.5	31
47	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.	3.6	23
48	NH ₄ ⁺ Suppresses NO ₃ ⁻ -Dependent Lateral Root Growth and Alters Gene Expression and Gravity Response in OsAMT1 RNAi Mutants of Rice (<i>Oryza sativa</i>). <i>Journal of Plant Biology</i> , 2020, 63, 391-407.	2.1	9
49	Rice CaM-binding transcription factor (OsCBT) mediates defense signaling via transcriptional reprogramming. <i>Plant Biotechnology Reports</i> , 2020, 14, 309-321.	1.5	13
50	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.	2.2	16
51	Fast Track to Discover Novel Promoters in Rice. <i>Plants</i> , 2020, 9, 125.	3.5	0
52	OsHLH073 Negatively Regulates Internode Elongation and Plant Height by Modulating GA Homeostasis in Rice. <i>Plants</i> , 2020, 9, 547.	3.5	12
53	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.	4.1	241
54	Homeobox transcription factor OsZHD2 promotes root meristem activity in rice by inducing ethylene biosynthesis. <i>Journal of Experimental Botany</i> , 2020, 71, 5348-5364.	4.8	24

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55	Re-Analysis of 16S Amplicon Sequencing Data Reveals Soil Microbial Population Shifts in Rice Fields under Drought Condition. <i>Rice</i> , 2020, 13, 44.	4.0	17
56	Chromatin interacting factor OsVIL2 increases biomass and rice grain yield. <i>Plant Biotechnology Journal</i> , 2019, 17, 178-187.	8.3	25
57	A Systematic View Exploring the Role of Chloroplasts in Plant Abiotic Stress Responses. <i>BioMed Research International</i> , 2019, 2019, 1-14.	1.9	14
58	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	4.0	21
59	A web-based tool for the prediction of rice transcription factor function. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
60	Transcriptome analysis of rice-seedling roots under soil "salt stress using RNA-Seq method. <i>Plant Biotechnology Reports</i> , 2019, 13, 567-578.	1.5	37
61	A Multiprotein Complex Regulates Interference-Sensitive Crossover Formation in Rice. <i>Plant Physiology</i> , 2019, 181, 221-235.	4.8	20
62	Rice Genome-Scale Network Integration Reveals Transcriptional Regulators of Grass Cell Wall Synthesis. <i>Frontiers in Plant Science</i> , 2019, 10, 1275.	3.6	14
63	Molecular Basis of Pollen Germination in Cereals. <i>Trends in Plant Science</i> , 2019, 24, 1126-1136.	8.8	34
64	Mutations in the microRNA172 binding site of SUPERNUMERARY BRACT (SNB) suppress internode elongation in rice. <i>Rice</i> , 2019, 12, 62.	4.0	19
65	Identification of a module of HAP transcription factors for seed development in rice. <i>Plant Biotechnology Reports</i> , 2019, 13, 389-397.	1.5	0
66	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.	2.1	29
67	Triterpenoid-biosynthetic UDP-glycosyltransferases from plants. <i>Biotechnology Advances</i> , 2019, 37, 107394.	11.7	114
68	Transcriptome Analysis of Diurnal Gene Expression in Chinese Cabbage. <i>Genes</i> , 2019, 10, 130.	2.4	13
69	Rice RHC Encoding a Putative Cellulase is Essential for Normal Root Hair Elongation. <i>Journal of Plant Biology</i> , 2019, 62, 82-91.	2.1	35
70	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.	4.1	15
71	RSL Class II Transcription Factors Guide the Nuclear Localization of RHL1 to Regulate Root Hair Development. <i>Plant Physiology</i> , 2019, 179, 558-568.	4.8	23
72	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.	0.9	12

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73	Defense Response to Pathogens Through Epigenetic Regulation in Rice. <i>Journal of Plant Biology</i> , 2018, 61, 1-10.	2.1	9
74	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.	3.5	16
75	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.	2.1	8
76	Circadian rhythm gene expression and daily melatonin levels vary in athletes and sedentary males. <i>Biological Rhythm Research</i> , 2018, 49, 237-245.	0.9	6
77	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.	3.9	4
78	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.	3.5	6
79	Genome-wide analysis of root hair-preferential genes in rice. <i>Rice</i> , 2018, 11, 48.	4.0	21
80	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.	3.6	13
81	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.	4.0	32
82	OsABCG9 Is an Important ABC Transporter of Cuticular Wax Deposition in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 960.	3.6	26
83	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.	2.1	14
84	Rice OsMYB5P improves plant phosphate acquisition by regulation of phosphate transporter. <i>PLoS ONE</i> , 2018, 13, e0194628.	2.5	25
85	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.	1.5	25
86	Effective Strategies for Enhancing Tolerance to High-Temperature Stress in Rice during the Reproductive and Ripening Stages. <i>Plant Breeding and Biotechnology</i> , 2018, 6, 1-18.	0.9	30
87	A secreted chitinase-like protein (OsCLP) supports root growth through calcium signaling in <i>Oryza sativa</i> . <i>Physiologia Plantarum</i> , 2017, 161, 273-284.	5.2	16
88	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.	2.1	15
89	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.	3.9	56
90	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.	1.8	6

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91	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.	3.3	15
92	Construction and application of functional gene modules to regulatory pathways in rice. <i>Journal of Plant Biology</i> , 2017, 60, 358-379.	2.1	2
93	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.	4.0	20
94	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.	1.5	4
95	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.	3.6	56
96	Genome-Wide Identification and Analysis of Genes, Conserved between japonica and indica Rice Cultivars, that Respond to Low-Temperature Stress at the Vegetative Growth Stage. <i>Frontiers in Plant Science</i> , 2017, 8, 1120.	3.6	34
97	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.	3.6	36
98	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.	3.9	32
99	Comparative phylogenomic analysis provides insights into TCP gene functions in Sorghum. <i>Scientific Reports</i> , 2016, 6, 38488.	3.3	48
100	Genome-wide identification and analysis of rice genes to elucidate morphological agronomic traits. <i>Journal of Plant Biology</i> , 2016, 59, 639-647.	2.1	5
101	Application of rice microspore-preferred promoters to manipulate early pollen development in Arabidopsis: a heterologous system. <i>Plant Reproduction</i> , 2016, 29, 291-300.	2.2	1
102	Updated Rice Kinase Database RKD 2.0: enabling transcriptome and functional analysis of rice kinase genes. <i>Rice</i> , 2016, 9, 40.	4.0	20
103	Comparison of rice flowering-time genes under paddy conditions. <i>Journal of Plant Biology</i> , 2016, 59, 238-246.	2.1	6
104	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.	3.5	33
105	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.	4.0	17
106	The effects of rice seed dressing with <i>Paenibacillus yonginensis</i> and silicon on crop development on South Korea's reclaimed tidal land. <i>Field Crops Research</i> , 2016, 188, 121-132.	5.1	12
107	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.	2.1	18
108	<i>Loose Plant Architecture1</i> (<i>LPA1</i>) determines lamina joint bending by suppressing auxin signalling that interacts with C-22-hydroxylated and 6-deoxo brassinosteroids in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 1883-1895.	4.8	51

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109	Defective Tapetum Cell Death 1 (DTC1) Regulates ROS Levels by Binding to Metallothionein during Tapetum Degeneration. <i>Plant Physiology</i> , 2016, 170, 1611-1623.	4.8	126
110	Genome-Wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2015, 8, 276-289.	8.3	16
111	Phylogenomics databases for facilitating functional genomics in rice. <i>Rice</i> , 2015, 8, 60.	4.0	12
112	Integrating omics analysis of salt stress-responsive genes in rice. <i>Genes and Genomics</i> , 2015, 37, 645-655.	1.4	6
113	Genome-wide identification and analysis of <i>Catharanthus roseus</i> RLK1-like kinases in rice. <i>Planta</i> , 2015, 241, 603-613.	3.2	55
114	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.	2.1	22
115	Rice tissue-specific promoters and condition-dependent promoters for effective translational application. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 913-924.	8.5	35
116	Genome-wide transcriptome comparison of flag leaves among japonica and indica varieties. <i>Journal of Plant Biology</i> , 2015, 58, 333-343.	2.1	2
117	Molecular insights into the function of ankyrin proteins in plants. <i>Journal of Plant Biology</i> , 2015, 58, 271-284.	2.1	34
118	Expression analysis of two rice pollen-specific promoters using homologous and heterologous systems. <i>Plant Biotechnology Reports</i> , 2015, 9, 297-306.	1.5	5
119	A systematic view of the rice calcineurin B-like protein interacting protein kinase family. <i>Genes and Genomics</i> , 2015, 37, 55-68.	1.4	7
120	Development of Defense Signaling Pathways Against Bacterial Blight Disease in Rice Using Genome-Wide Transcriptome Data. <i>Journal of Agricultural Science</i> , 2014, 6, .	0.2	2
121	Genome-wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2014, , .	8.3	0
122	Quantitative Trait Locus Mapping and Candidate Gene Analysis for Plant Architecture Traits Using Whole Genome Re-Sequencing in Rice. <i>Molecules and Cells</i> , 2014, 37, 149-160.	2.6	50
123	Evaluation of rice promoters conferring pollen-specific expression in a heterologous system, <i>Arabidopsis</i> . <i>Plant Reproduction</i> , 2014, 27, 47-58.	2.2	21
124	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	2.1	34
125	Overexpression of <i>PYL5</i> in rice enhances drought tolerance, inhibits growth, and modulates gene expression. <i>Journal of Experimental Botany</i> , 2014, 65, 453-464.	4.8	204
126	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.	7.1	406

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127	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.	3.5	95
128	Cross-Family Translational Genomics of Abiotic Stress-Responsive Genes between <i>Arabidopsis</i> and <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2014, 9, e91721.	2.5	19
129	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014, 30, 343-354.	1.7	40
130	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , 2013, 6, 1.	4.0	186
131	Analysis of the early-flowering mechanisms and generation of T-DNA tagging lines in Kitaake, a model rice cultivar. <i>Journal of Experimental Botany</i> , 2013, 64, 4169-4182.	4.8	48
132	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.	2.9	65
133	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.	4.0	28
134	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.	3.5	65
135	Functional Characterization of Rice Genes Using a Gene-Indexed T-DNA Insertional Mutant Population. <i>Methods in Molecular Biology</i> , 2013, 956, 57-67.	0.9	7
136	Transcriptome Profiling Analysis Using Rice Oligonucleotide Microarrays. <i>Methods in Molecular Biology</i> , 2013, 956, 95-107.	0.9	1
137	A systematic view of rice heat shock transcription factor family using phylogenomic analysis. <i>Journal of Plant Physiology</i> , 2013, 170, 321-329.	3.5	30
138	<i>N</i>-determinate domain 10</i> regulates ammonium-mediated gene expression in rice roots. <i>New Phytologist</i> , 2013, 197, 791-804.	7.3	75
139	Genome-wide expression analysis of rice aquaporin genes and development of a functional gene network mediated by aquaporin expression in roots. <i>Planta</i> , 2013, 238, 669-681.	3.2	76
140	Rice <i>GLYCOSYLTRANSFERASE1</i> Encodes a Glycosyltransferase Essential for Pollen Wall Formation. <i>Plant Physiology</i> , 2013, 161, 663-675.	4.8	88
141	Construction of a rice glycoside hydrolase phylogenomic database and identification of targets for biofuel research. <i>Frontiers in Plant Science</i> , 2013, 4, 330.	3.6	35
142	The Rice Oligonucleotide Array Database: an atlas of rice gene expression. <i>Rice</i> , 2012, 5, 17.	4.0	192
143	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.	2.1	49
144	Genome-wide identification and analysis of early heat stress responsive genes in rice. <i>Journal of Plant Biology</i> , 2012, 55, 458-468.	2.1	44

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145	The rice gene <i>DEFECTIVE TAPETUM AND MEIOCYTES 1</i> (<i>DTM1</i>) is required for early tapetum development and meiosis. <i>Plant Journal</i> , 2012, 70, 256-270.	5.7	38
146	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.	2.1	11
147	Transcriptional dynamics during cell wall removal and regeneration reveals key genes involved in cell wall development in rice. <i>Plant Molecular Biology</i> , 2011, 77, 391-406.	3.9	17
148	Rice Importin $\beta 1$ Gene Affects Pollen Tube Elongation. <i>Molecules and Cells</i> , 2011, 31, 523-530.	2.6	25
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