

# Ki-hong Jung

## List of Publications by Year in descending order

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181  
papers

10,051  
citations

57758

44  
h-index

40979

93  
g-index

191  
all docs

191  
docs citations

191  
times ranked

10808  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
2	T-DNA insertional mutagenesis for functional genomics in rice. <i>Plant Journal</i> , 2000, 22, 561-570.	5.7	711
3	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
4	Rice Undeveloped Tapetum1 Is a Major Regulator of Early Tapetum Development. <i>Plant Cell</i> , 2005, 17, 2705-2722.	6.6	367
5	Characterization of a Rice Chlorophyll-Deficient Mutant Using the T-DNA Gene-Trap System. <i>Plant and Cell Physiology</i> , 2003, 44, 463-472.	3.1	277
6	Wax-deficient anther1 Is Involved in Cuticle and Wax Production in Rice Anther Walls and Is Required for Pollen Development. <i>Plant Cell</i> , 2006, 18, 3015-3032.	6.6	244
7	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
8	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
9	Towards Establishment of a Rice Stress Response Interactome. <i>PLoS Genetics</i> , 2011, 7, e1002020.	3.5	199
10	The Rice Oligonucleotide Array Database: an atlas of rice gene expression. <i>Rice</i> , 2012, 5, 17.	4.0	192
11	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , 2013, 6, 1.	4.0	186
12	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.	4.8	166
13	Towards a better bowl of rice: assigning function to tens of thousands of rice genes. <i>Nature Reviews Genetics</i> , 2008, 9, 91-101.	16.3	143
14	Stress-inducible OsP5CS2 gene is essential for salt and cold tolerance in rice. <i>Plant Science</i> , 2004, 167, 417-426.	3.6	140
15	Structure, expression, and functional analysis of the hexokinase gene family in rice ( <i>Oryza sativa</i> L.). <i>Planta</i> , 2006, 224, 598-611.	3.2	133
16	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
17	Tissue-Preferential Expression of a Rice $\alpha$ -Tubulin Gene, OsTubA1, Mediated by the First Intron1. <i>Plant Physiology</i> , 2000, 123, 1005-1014.	4.8	124
18	Metabolomic and transcriptomic analysis of the rice response to the bacterial blight pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Metabolomics</i> , 2010, 6, 451-465.	3.0	114

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19	Triterpenoid-biosynthetic UDP-glycosyltransferases from plants. <i>Biotechnology Advances</i> , 2019, 37, 107394.	11.7	114
20	Rice Immature Pollen 1 ( RIP1 ) is a Regulator of Late Pollen Development. <i>Plant and Cell Physiology</i> , 2006, 47, 1457-1472.	3.1	111
21	Isolation and Characterization of a Rice Cysteine Protease Gene, OsCPI1, Using T-DNA Gene-Trap System. <i>Plant Molecular Biology</i> , 2004, 54, 755-765.	3.9	110
22	Construction of a Rice Glycosyltransferase Phylogenomic Database and Identification of Rice-Diverged Glycosyltransferases. <i>Molecular Plant</i> , 2008, 1, 858-877.	8.3	110
23	Refinement of Light-Responsive Transcript Lists Using Rice Oligonucleotide Arrays: Evaluation of Gene-Redundancy. <i>PLoS ONE</i> , 2008, 3, e3337.	2.5	104
24	Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 581-592.	2.1	101
25	Reverse Genetic Approaches for Functional Genomics of Rice. <i>Plant Molecular Biology</i> , 2005, 59, 111-123.	3.9	101
26	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
27	RiceArrayNet: A Database for Correlating Gene Expression from Transcriptome Profiling, and Its Application to the Analysis of Coexpressed Genes in Rice. <i>Plant Physiology</i> , 2009, 151, 16-33.	4.8	91
28	Rice <i>GLYCOSYLTRANSFERASE1</i> Encodes a Glycosyltransferase Essential for Pollen Wall Formation. <i>Plant Physiology</i> , 2013, 161, 663-675.	4.8	88
29	Emerging concepts of potassium homeostasis in plants. <i>Journal of Experimental Botany</i> , 2020, 71, 608-619.	4.8	81
30	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
31	<i>ndeterminate domain 10</i> regulates ammonium-mediated gene expression in rice roots. <i>New Phytologist</i> , 2013, 197, 791-804.	7.3	75
32	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
33	Identification and Functional Analysis of Light-Responsive Unique Genes and Gene Family Members in Rice. <i>PLoS Genetics</i> , 2008, 4, e1000164.	3.5	69
34	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
35	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
36	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

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37	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.	8.8	60
38	The protein phosphatase 2C clade A protein OsPP2C51 positively regulates seed germination by directly inactivating OsZIP10. <i>Plant Molecular Biology</i> , 2017, 93, 389-401.	3.9	56
39	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
40	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
41	<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
42	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
43	High-throughput phenotyping platform for analyzing drought tolerance in rice. <i>Planta</i> , 2020, 252, 38.	3.2	50
44	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
45	Genetic and Molecular Insights into the Enhancement of Rice Yield Potential. <i>Journal of Plant Biology</i> , 2011, 54, 1-9.	2.1	48
46	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
47	Comparative phylogenomic analysis provides insights into TCP gene functions in Sorghum. <i>Scientific Reports</i> , 2016, 6, 38488.	3.3	48
48	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
49	Identification of Active Transposon dTok, a Member of the hAT Family, in Rice. <i>Plant and Cell Physiology</i> , 2006, 47, 1473-1483.	3.1	42
50	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
51	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 hrp genes. <i>BMC Microbiology</i> , 2008, 8, 99.	3.3	40
52	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
53	The rice FON1 gene controls vegetative and reproductive development by regulating shoot apical meristem size. <i>Molecules and Cells</i> , 2006, 21, 147-52.	2.6	39
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	2.1	34
62	Molecular insights into the function of ankyrin proteins in plants. <i>Journal of Plant Biology</i> , 2015, 58, 271-284.	2.1	34
63	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
64	Molecular Basis of Pollen Germination in Cereals. <i>Trends in Plant Science</i> , 2019, 24, 1126-1136.	8.8	34
65	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
66	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
67	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
68	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
69	<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.	5.7	31
70	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
71	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
72	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

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73	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
74	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
75	Mitochondria Provide the Main Source of Cytosolic ATP for Activation of Outward-rectifying K <sup>+</sup> Channels in Mesophyll Protoplast of Chlorophyll-deficient Mutant Rice (OsCHLH) Seedlings. <i>Journal of Biological Chemistry</i> , 2004, 279, 6874-6882.	3.4	27
76	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
77	OsABCG9 Is an Important ABC Transporter of Cuticular Wax Deposition in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 960.	3.6	26
78	CAFRI-Rice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	5.7	26
79	Rice Importin Î21 Gene Affects Pollen Tube Elongation. <i>Molecules and Cells</i> , 2011, 31, 523-530.	2.6	25
80	Web Tools for Rice Transcriptome Analyses. <i>Journal of Plant Biology</i> , 2011, 54, 65-80.	2.1	25
81	Rice OsMYB5P improves plant phosphate acquisition by regulation of phosphate transporter. <i>PLoS ONE</i> , 2018, 13, e0194628.	2.5	25
82	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
83	Chromatin interacting factor Os<scp>VIL</scp>2 increases biomass and rice grain yield. <i>Plant Biotechnology Journal</i> , 2019, 17, 178-187.	8.3	25
84	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
85	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
86	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
87	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
88	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
89	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
90	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

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91	Genome-wide analysis of root hair-preferential genes in rice. <i>Rice</i> , 2018, 11, 48.	4.0	21
92	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	4.0	21
93	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
94	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
95	A Multiprotein Complex Regulates Interference-Sensitive Crossover Formation in Rice. <i>Plant Physiology</i> , 2019, 181, 221-235.	4.8	20
96	Mutations in the microRNA172 binding site of SUPERNUMERARY BRACT (SNB) suppress internode elongation in rice. <i>Rice</i> , 2019, 12, 62.	4.0	19
97	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
98	Cross-Family Translational Genomics of Abiotic Stress-Responsive Genes between Arabidopsis and <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2014, 9, e91721.	2.5	19
99	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
100	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
101	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
102	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
103	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
104	Cytokinin increases vegetative growth period by suppressing florigen expression in rice and maize. <i>Plant Journal</i> , 2022, 110, 1619-1635.	5.7	17
105	Genome-Wide Identification and Functional Analysis of Genes Expressed Ubiquitously in Rice. <i>Molecular Plant</i> , 2015, 8, 276-289.	8.3	16
106	A secreted chitinase-like protein (<sc>OsCLP</sc>) supports root growth through calcium signaling in <i>Oryza sativa</i>. <i>Physiologia Plantarum</i> , 2017, 161, 273-284.	5.2	16
107	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
108	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

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109	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
110	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
111	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
112	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
113	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
114	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
115	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
116	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
117	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
118	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
119	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
120	Physiological Importance of Pectin Modifying Genes During Rice Pollen Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4840.	4.1	14
121	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
122	Transcriptome Analysis of Diurnal Gene Expression in Chinese Cabbage. <i>Genes</i> , 2019, 10, 130.	2.4	13
123	Rice CaM-binding transcription factor (OsCBT) mediates defense signaling via transcriptional reprogramming. <i>Plant Biotechnology Reports</i> , 2020, 14, 309-321.	1.5	13
124	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
125	Phylogenomics databases for facilitating functional genomics in rice. <i>Rice</i> , 2015, 8, 60.	4.0	12
126	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



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127	First Steps in the Successful Fertilization of Rice and Arabidopsis: Pollen Longevity, Adhesion and Hydration. <i>Plants</i> , 2020, 9, 956.	3.5	12
128	OsBHLH073 Negatively Regulates Internode Elongation and Plant Height by Modulating GA Homeostasis in Rice. <i>Plants</i> , 2020, 9, 547.	3.5	12
129	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
130	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
131	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
132	Assessing probe-specific dye and slide biases in two-color microarray data. <i>BMC Bioinformatics</i> , 2008, 9, 314.	2.6	10
133	Defense Response to Pathogens Through Epigenetic Regulation in Rice. <i>Journal of Plant Biology</i> , 2018, 61, 1-10.	2.1	9
134	Volatile content variation in the petals of cut roses during vase life. <i>Scientia Horticulturae</i> , 2020, 261, 108960.	3.6	9
135	NH <sub>4</sub> <sup>+</sup> Suppresses NO <sub>3</sub> <sup>-</sup> -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
136	CTP synthase is essential for early endosperm development by regulating nuclei spacing. <i>Plant Biotechnology Journal</i> , 2021, 19, 2177-2191.	8.3	9
137	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
138	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
139	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
140	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
141	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
142	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
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	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
146	Epitranscriptomics: An Additional Regulatory Layer in Plantsâ€™ Development and Stress Response. <i>Plants</i> , 2022, 11, 1033.	3.5	7
147	Characterization of a cold-responsive gene, OsPTR1, isolated from the screening of Î²-Glucuronidase (GUS) gene-trapped rice. <i>Journal of Plant Biology</i> , 2004, 47, 133-141.	2.1	6
148	A Survey of Databases for Analysis of Plant Cell Wall-Related Enzymes. <i>Bioenergy Research</i> , 2010, 3, 108-114.	3.9	6
149	Integrating omics analysis of salt stress-responsive genes in rice. <i>Genes and Genomics</i> , 2015, 37, 645-655.	1.4	6
150	Comparison of rice flowering-time genes under paddy conditions. <i>Journal of Plant Biology</i> , 2016, 59, 238-246.	2.1	6
151	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
152	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
153	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
154	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
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156	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
157	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
158	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
159	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
160	A Systemic View of Carbohydrate Metabolism in Rice to Facilitate Productivity. <i>Plants</i> , 2021, 10, 1690.	3.5	5
161	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
162	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

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163	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
164	<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
165	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
166	Hierarchical Structures and Dissected Functions of MADS-Box Transcription Factors in Rice Development. <i>Journal of Plant Biology</i> , 0, , 1.	2.1	3
167	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
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173	Rice Immature Pollen 1 (RIP1) is a Regulator of Late Pollen Development. <i>Plant and Cell Physiology</i> , 2006, 48, 204-204.	3.1	1
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