

Jiayang Li

List of Publications by Year in descending order

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157
papers

24,948
citations

8732

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149
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163
all docs

163
docs citations

163
times ranked

15957
citing authors

#	ARTICLE	IF	CITATIONS
1	A map of rice genome variation reveals the origin of cultivated rice. <i>Nature</i> , 2012, 490, 497-501.	13.7	1,428
2	Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice. <i>Nature Genetics</i> , 2010, 42, 541-544.	9.4	1,240
3	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
4	Control of tillering in rice. <i>Nature</i> , 2003, 422, 618-621.	13.7	988
5	Natural variation at the DEP1 locus enhances grain yield in rice. <i>Nature Genetics</i> , 2009, 41, 494-497.	9.4	858
6	DWARF 53 acts as a repressor of strigolactone signalling in rice. <i>Nature</i> , 2013, 504, 401-405.	13.7	660
7	Genome-Wide Binding Analysis of the Transcription Activator IDEAL PLANT ARCHITECTURE1 Reveals a Complex Network Regulating Rice Plant Architecture. <i>Plant Cell</i> , 2013, 25, 3743-3759.	3.1	588
8	DWARF27, an Iron-Containing Protein Required for the Biosynthesis of Strigolactones, Regulates Rice Tiller Bud Outgrowth. <i>Plant Cell</i> , 2009, 21, 1512-1525.	3.1	549
9	Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. <i>Nature Genetics</i> , 2015, 47, 834-838.	9.4	527
10	Molecular Basis of Plant Architecture. <i>Annual Review of Plant Biology</i> , 2008, 59, 253-279.	8.6	512
11	Copy number variation at the CL7 locus contributes to grain size diversity in rice. <i>Nature Genetics</i> , 2015, 47, 944-948.	9.4	485
12	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21760-21765.	3.3	469
13	Identification of Trait-Improving Quantitative Trait Loci Alleles From a Wild Rice Relative, <i>Oryza rufipogon</i> . <i>Genetics</i> , 1998, 150, 899-909.	1.2	463
14	Genetic Regulation of Shoot Architecture. <i>Annual Review of Plant Biology</i> , 2018, 69, 437-468.	8.6	454
15	Rare allele of <i>OsPPKL1</i> associated with grain length causes extra-large grain and a significant yield increase in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21534-21539.	3.3	426
16	DWARF14 is a non-canonical hormone receptor for strigolactone. <i>Nature</i> , 2016, 536, 469-473.	13.7	399
17	A phenylalanine in DGAT is a key determinant of oil content and composition in maize. <i>Nature Genetics</i> , 2008, 40, 367-372.	9.4	384
18	BRITTLE CULM1, Which Encodes a COBRA-Like Protein, Affects the Mechanical Properties of Rice Plants. <i>Plant Cell</i> , 2003, 15, 2020-2031.	3.1	369

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19	Molecular Genetic Dissection of Quantitative Trait Loci Regulating Rice Grain Size. <i>Annual Review of Genetics</i> , 2014, 48, 99-118.	3.2	369
20	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	3.8	363
21	Genes from wild rice improve yield. <i>Nature</i> , 1996, 384, 223-224.	13.7	335
22	Strigolactone Signaling in Arabidopsis Regulates Shoot Development by Targeting D53-Like SMXL Repressor Proteins for Ubiquitination and Degradation. <i>Plant Cell</i> , 2015, 27, 3128-3142.	3.1	310
23	Gene replacements and insertions in rice by intron targeting using CRISPR-Cas9. <i>Nature Plants</i> , 2016, 2, 16139.	4.7	303
24	A single transcription factor promotes both yield and immunity in rice. <i>Science</i> , 2018, 361, 1026-1028.	6.0	296
25	Rational design of high-yield and superior-quality rice. <i>Nature Plants</i> , 2017, 3, 17031.	4.7	293
26	Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis. <i>Nature Communications</i> , 2015, 6, 6258.	5.8	292
27	LAZY1 controls rice shoot gravitropism through regulating polar auxin transport. <i>Cell Research</i> , 2007, 17, 402-410.	5.7	288
28	<i>TAC1</i> , a major quantitative trait locus controlling tiller angle in rice. <i>Plant Journal</i> , 2007, 52, 891-898.	2.8	281
29	Activation of <i>Big Grain1</i> significantly improves grain size by regulating auxin transport in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11102-11107.	3.3	265
30	Targeted, random mutagenesis of plant genes with dual cytosine and adenine base editors. <i>Nature Biotechnology</i> , 2020, 38, 875-882.	9.4	259
31	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
32	IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. <i>Cell Research</i> , 2017, 27, 1128-1141.	5.7	229
33	Expression of the Nitrate Transporter Gene <i>OsNRT1.1A/OsNPF6.3</i> Confers High Yield and Early Maturation in Rice. <i>Plant Cell</i> , 2018, 30, 638-651.	3.1	227
34	Crystal structures of two phytohormone signal-transducing $\hat{1}\pm/\hat{1}^2$ hydrolases: karrikin-signaling KAI2 and strigolactone-signaling DWARF14. <i>Cell Research</i> , 2013, 23, 436-439.	5.7	222
35	Deficiency in Fatty Acid Synthase Leads to Premature Cell Death and Dramatic Alterations in Plant Morphology. <i>Plant Cell</i> , 2000, 12, 405-417.	3.1	213
36	Generation of herbicide tolerance traits and a new selectable marker in wheat using base editing. <i>Nature Plants</i> , 2019, 5, 480-485.	4.7	210

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37	QTL detection for rice grain quality traits using an interspecific backcross population derived from cultivated Asian (<i>O. sativa</i> L.) and African (<i>O. glaberrima</i> S.) rice. <i>Genome</i> , 2004, 47, 697-704.	0.9	208
38	Construction of a Genome-Wide Mutant Library in Rice Using CRISPR/Cas9. <i>Molecular Plant</i> , 2017, 10, 1238-1241.	3.9	208
39	Genomic basis of geographical adaptation to soil nitrogen in rice. <i>Nature</i> , 2021, 590, 600-605.	13.7	204
40	Branching in rice. <i>Current Opinion in Plant Biology</i> , 2011, 14, 94-99.	3.5	200
41	High-efficiency prime editing with optimized, paired pegRNAs in plants. <i>Nature Biotechnology</i> , 2021, 39, 923-927.	9.4	189
42	Transcriptional regulation of strigolactone signalling in <i>Arabidopsis</i> . <i>Nature</i> , 2020, 583, 277-281.	13.7	188
43	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	9.4	184
44	Breeding high-yield superior quality hybrid super rice by rational design. <i>National Science Review</i> , 2016, 3, 283-294.	4.6	179
45	Fine Mapping of a Grain-Weight Quantitative Trait Locus in the Pericentromeric Region of Rice Chromosome 3. <i>Genetics</i> , 2004, 168, 2187-2195.	1.2	178
46	Tryptophan-independent auxin biosynthesis contributes to early embryogenesis in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4821-4826.	3.3	169
47	Degradation of MONOCULM 1 by APC/CTAD1 regulates rice tillering. <i>Nature Communications</i> , 2012, 3, 750.	5.8	168
48	Through the genetic bottleneck: <i>O. rufipogon</i> as a source of trait-enhancing alleles for <i>O. sativa</i> . <i>Euphytica</i> , 2007, 154, 317-339.	0.6	163
49	Critical roles of soluble starch synthase SSIIIa and granule-bound starch synthase Waxy in synthesizing resistant starch in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12844-12849.	3.3	154
50	Destabilization of strigolactone receptor DWARF14 by binding of ligand and E3-ligase signaling effector DWARF3. <i>Cell Research</i> , 2015, 25, 1219-1236.	5.7	152
51	A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice. <i>Nature Communications</i> , 2017, 8, 14789.	5.8	149
52	Increased Expression of MAP KINASE KINASE7 Causes Deficiency in Polar Auxin Transport and Leads to Plant Architectural Abnormality in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2006, 18, 308-320.	3.1	148
53	Structural basis for recognition of diverse transcriptional repressors by the TOPLESS family of corepressors. <i>Science Advances</i> , 2015, 1, e1500107.	4.7	140
54	The Plant Architecture of Rice (<i>Oryza sativa</i>). <i>Plant Molecular Biology</i> , 2005, 59, 75-84.	2.0	139

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55	Natural variation of rice strigolactone biosynthesis is associated with the deletion of two <i>MAX1</i> orthologs. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2379-2384.	3.3	138
56	Silencing of Phosphoethanolamine N-Methyltransferase Results in Temperature-Sensitive Male Sterility and Salt Hypersensitivity in Arabidopsis. Plant Cell, 2002, 14, 2031-2043.	3.1	122
57	Malate transported from chloroplast to mitochondrion triggers production of ROS and PCD in Arabidopsis thaliana. Cell Research, 2018, 28, 448-461.	5.7	122
58	Strigolactones regulate rice tiller angle by attenuating shoot gravitropism through inhibiting auxin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11199-11204.	3.3	121
59	MONOCULM 3, an Ortholog of WUSCHEL in Rice, Is Required for Tiller Bud Formation. Journal of Genetics and Genomics, 2015, 42, 71-78.	1.7	121
60	Strigolactone promotes cytokinin degradation through transcriptional activation of <i>CYTOKININ OXIDASE/DEHYDROGENASE 9</i> in rice. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14319-14324.	3.3	119
61	A Core Regulatory Pathway Controlling Rice Tiller Angle Mediated by the <i>LAZY1</i> -Dependent Asymmetric Distribution of Auxin. Plant Cell, 2018, 30, 1461-1475.	3.1	114
62	Mitogen-Activated Protein Kinase Cascade MKK7-MPK6 Plays Important Roles in Plant Development and Regulates Shoot Branching by Phosphorylating PIN1 in Arabidopsis. PLoS Biology, 2016, 14, e1002550.	2.6	114
63	The Rice Circadian Clock Regulates Tiller Growth and Panicle Development Through Strigolactone Signaling and Sugar Sensing. Plant Cell, 2020, 32, 3124-3138.	3.1	112
64	Signalling and responses to strigolactones and karrikins. Current Opinion in Plant Biology, 2014, 21, 23-29.	3.5	111
65	Designing future crops: challenges and strategies for sustainable agriculture. Plant Journal, 2021, 105, 1165-1178.	2.8	110
66	Targeting a gene regulatory element enhances rice grain yield by decoupling panicle number and size. Nature Biotechnology, 2022, 40, 1403-1411.	9.4	110
67	Towards molecular breeding and improvement of rice in China. Trends in Plant Science, 2005, 10, 610-614.	4.3	108
68	Rice functional genomics: decades' efforts and roads ahead. Science China Life Sciences, 2022, 65, 33-92.	2.3	107
69	SLR1 inhibits MOC1 degradation to coordinate tiller number and plant height in rice. Nature Communications, 2019, 10, 2738.	5.8	103
70	Strigolactone and Karrikin Signaling Pathways Elicit Ubiquitination and Proteolysis of SMXL2 to Regulate Hypocotyl Elongation in Arabidopsis. Plant Cell, 2020, 32, 2251-2270.	3.1	103
71	Tissue-Specific Ubiquitination by IPA1 INTERACTING PROTEIN1 Modulates IPA1 Protein Levels to Regulate Plant Architecture in Rice. Plant Cell, 2017, 29, 697-707.	3.1	102
72	A super pan-genomic landscape of rice. Cell Research, 2022, 32, 878-896.	5.7	99

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73	Peptidyl-prolyl isomerization targets rice Aux/IAAs for proteasomal degradation during auxin signalling. <i>Nature Communications</i> , 2015, 6, 7395.	5.8	95
74	Tiller Bud Formation Regulators MOC1 and MOC3 Cooperatively Promote Tiller Bud Outgrowth by Activating FON1 Expression in Rice. <i>Molecular Plant</i> , 2019, 12, 1090-1102.	3.9	93
75	A Strigolactone Biosynthesis Gene Contributed to the Green Revolution in Rice. <i>Molecular Plant</i> , 2020, 13, 923-932.	3.9	91
76	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018, 5, 78-87.	4.6	90
77	Malate Circulation: Linking Chloroplast Metabolism to Mitochondrial ROS. <i>Trends in Plant Science</i> , 2020, 25, 446-454.	4.3	84
78	Genetic variations in ARE1 mediate grain yield by modulating nitrogen utilization in rice. <i>Nature Communications</i> , 2018, 9, 735.	5.8	82
79	Deficient plastidic fatty acid synthesis triggers cell death by modulating mitochondrial reactive oxygen species. <i>Cell Research</i> , 2015, 25, 621-633.	5.7	80
80	CRISPR-Cas9 expands the scope of genome editing with reduced efficiency in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 709-711.	4.1	79
81	Increasing the efficiency of CRISPR-Cas9/CQR precise genome editing in rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 292-297.	4.1	78
82	Towards a deeper haplotype mining of complex traits in rice with RFG v2.0. <i>Plant Biotechnology Journal</i> , 2020, 18, 14-16.	4.1	78
83	Rice Ferredoxin-Dependent Glutamate Synthase Regulates Nitrogen-Carbon Metabolomes and Is Genetically Differentiated between japonica and indica Subspecies. <i>Molecular Plant</i> , 2016, 9, 1520-1534.	3.9	73
84	OsBRXL4 Regulates Shoot Gravitropism and Rice Tiller Angle through Affecting LAZY1 Nuclear Localization. <i>Molecular Plant</i> , 2019, 12, 1143-1156.	3.9	71
85	Î-Î-Carotene Isomerase Suppresses Tillering in Rice through the Coordinated Biosynthesis of Strigolactone and Abscisic Acid. <i>Molecular Plant</i> , 2020, 13, 1784-1801.	3.9	70
86	An Arabidopsis Secondary Metabolite Directly Targets Expression of the Bacterial Type III Secretion System to Inhibit Bacterial Virulence. <i>Cell Host and Microbe</i> , 2020, 27, 601-613.e7.	5.1	66
87	Karrikin Signaling Acts Parallel to and Additively with Strigolactone Signaling to Regulate Rice Mesocotyl Elongation in Darkness. <i>Plant Cell</i> , 2020, 32, 2780-2805.	3.1	65
88	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , 2017, 3, e1601217.	4.7	64
89	Regulation of Rice Tillering by RNA-Directed DNA Methylation at Miniature Inverted-Repeat Transposable Elements. <i>Molecular Plant</i> , 2020, 13, 851-863.	3.9	63
90	Molecular dissection of complex agronomic traits of rice: a team effort by Chinese scientists in recent years. <i>National Science Review</i> , 2014, 1, 253-276.	4.6	56

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91	FIS1 encodes a GA2-oxidase that regulates fruit firmness in tomato. <i>Nature Communications</i> , 2020, 11, 5844.	5.8	56
92	Transnitrosylation Mediated by the Non-canonical Catalase ROG1 Regulates Nitric Oxide Signaling in Plants. <i>Developmental Cell</i> , 2020, 53, 444-457.e5.	3.1	51
93	Generating broad-spectrum tolerance to ALS-inhibiting herbicides in rice by base editing. <i>Science China Life Sciences</i> , 2021, 64, 1624-1633.	2.3	49
94	Synergistic interplay of ABA and BR signal in regulating plant growth and adaptation. <i>Nature Plants</i> , 2021, 7, 1108-1118.	4.7	49
95	Robust genome editing of CRISPR-Cas9 at NAG PAMs in rice. <i>Science China Life Sciences</i> , 2018, 61, 122-125.	2.3	48
96	The integrated genomics of crop domestication and breeding. <i>Cell</i> , 2022, 185, 2828-2839.	13.5	47
97	Retrospective and perspective of rice breeding in China. <i>Journal of Genetics and Genomics</i> , 2018, 45, 603-612.	1.7	45
98	Glabrous Rice 1, encoding a homeodomain protein, regulates trichome development in rice. <i>Rice</i> , 2012, 5, 32.	1.7	43
99	The <i>Arabidopsis</i> CROWDED NUCLEI genes regulate seed germination by modulating degradation of ABI5 protein. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 669-678.	4.1	41
100	Rice DWARF14 acts as an unconventional hormone receptor for strigolactone. <i>Journal of Experimental Botany</i> , 2018, 69, 2355-2365.	2.4	40
101	Molecular marker-assisted selection for yield-enhancing genes in the progeny of '93111' × 'O. rufipogon' using SSR. <i>Euphytica</i> , 2004, 139, 159-165.	0.6	39
102	DROOPY LEAF1 controls leaf architecture by orchestrating early brassinosteroid signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21766-21774.	3.3	39
103	DWARF14, A Receptor Covalently Linked with the Active Form of Strigolactones, Undergoes Strigolactone-Dependent Degradation in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1935.	1.7	37
104	Witnessing the advance of science and technology in life sciences in the new era. <i>Science China Life Sciences</i> , 2018, 61, 1-1.	2.3	37
105	Validation of DGAT1-2 polymorphisms associated with oil content and development of functional markers for molecular breeding of high-oil maize. <i>Molecular Breeding</i> , 2012, 29, 939-949.	1.0	36
106	Dynamic expression reveals a two-step patterning of WUS and CLV3 during axillary shoot meristem formation in <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2017, 214, 1-6.	1.6	36
107	Identification of chromosome regions conferring dry matter accumulation and photosynthesis in wheat (<i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2010, 171, 145-156.	0.6	33
108	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. <i>Chinese Science Bulletin</i> , 2015, 60, 367-371.	0.4	31

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109	<i>Growing Slowly 1</i> locus encodes a PLS-type PPR protein required for RNA editing and plant development in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 5687-5698.	2.4	31
110	Recent advances in molecular basis for strigolactone action. <i>Science China Life Sciences</i> , 2018, 61, 277-284.	2.3	30
111	Breeding future crops to feed the world through de novo domestication. <i>Nature Communications</i> , 2022, 13, 1171.	5.8	30
112	Molecular basis underlying rice tiller angle: Current progress and future perspectives. <i>Molecular Plant</i> , 2022, 15, 125-137.	3.9	29
113	Identification of microRNAs in rice root in response to nitrate and ammonium. <i>Journal of Genetics and Genomics</i> , 2016, 43, 651-661.	1.7	28
114	Microsatellite markers in rice: abundance, diversity, and applications. , 2008, , 117-135.		27
115	Profiling of RNA ribose methylation in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2021, 49, 4104-4119.	6.5	27
116	<i>LAZY2</i> controls rice tiller angle through regulating starch biosynthesis in gravity-sensing cells. <i>New Phytologist</i> , 2021, 231, 1073-1087.	3.5	27
117	A transgenic wheat with a stilbene synthase gene resistant to powdery mildew obtained by biolistic method. <i>Science Bulletin</i> , 2000, 45, 634-638.	1.7	26
118	Detection of major loci associated with the variation of 18 important agronomic traits between <i>Solanum pimpinellifolium</i> and cultivated tomatoes. <i>Plant Journal</i> , 2018, 95, 312-323.	2.8	26
119	Extensive sequence divergence between the reference genomes of <i>Taraxacum kok-saghyz</i> and <i>Taraxacum mongolicum</i> . <i>Science China Life Sciences</i> , 2022, 65, 515-528.	2.3	26
120	Nitric oxide negatively regulates gibberellin signaling to coordinate growth and salt tolerance in <i>Arabidopsis</i> . <i>Journal of Genetics and Genomics</i> , 2022, 49, 756-765.	1.7	26
121	Identification of Regulatory DNA Elements Using Genome-wide Mapping of DNase I Hypersensitive Sites during Tomato Fruit Development. <i>Molecular Plant</i> , 2016, 9, 1168-1182.	3.9	24
122	Regulation of mitochondrial NAD pool via NAD ⁺ transporter 2 is essential for matrix NADH homeostasis and ROS production in <i>Arabidopsis</i> . <i>Science China Life Sciences</i> , 2019, 62, 991-1002.	2.3	24
123	Deletion of the Initial 45 Residues of ARR18 Induces Cytokinin Response in <i>Arabidopsis</i> . <i>Journal of Genetics and Genomics</i> , 2012, 39, 37-46.	1.7	23
124	Differential expression of triplicate phosphoribosylanthranilate isomerase isogenes in the tryptophan biosynthetic pathway of <i>Arabidopsis thaliana</i> (L.) Heynh.. <i>Planta</i> , 2001, 212, 641-647.	1.6	21
125	Development of gene-tagged molecular markers for starch synthesis-related genes in rice. <i>Science Bulletin</i> , 2010, 55, 3768-3777.	1.7	20
126	Enhancing rice grain production by manipulating the naturally evolved cis-regulatory element-containing inverted repeat sequence of OsREM20. <i>Molecular Plant</i> , 2021, 14, 997-1011.	3.9	19

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127	Resistant starch formation in rice: Genetic regulation and beyond. <i>Plant Communications</i> , 2022, 3, 100329.	3.6	19
128	Short- and long-term challenges in crop breeding. <i>National Science Review</i> , 2021, 8, nwab002.	4.6	17
129	Involvement of a Putative Bipartite Transit Peptide in Targeting Rice Pheophorbide a Oxygenase into Chloroplasts for Chlorophyll Degradation during Leaf Senescence. <i>Journal of Genetics and Genomics</i> , 2016, 43, 145-154.	1.7	16
130	OsMPK4 promotes phosphorylation and degradation of IPA1 in response to salt stress to confer salt tolerance in rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 766-775.	1.7	16
131	The dual effects of ethylene on the negative gravicurvature of arabidopsis inflorescence, an intriguing action model for the plant hormone ethylene. <i>Science Bulletin</i> , 2001, 46, 279-283.	1.7	15
132	Identification of brassinosteroid responsive genes in Arabidopsis by cDNA array. <i>Science in China Series C: Life Sciences</i> , 2001, 44, 637-643.	1.3	15
133	Molecular mechanisms underlying plant architecture and its environmental plasticity in rice. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	15
134	Expanding the scope of genome editing with SpG and SpRY variants in rice. <i>Science China Life Sciences</i> , 2021, 64, 1784-1787.	2.3	15
135	Understanding the Molecular Bases of Agronomic Trait Improvement in Rice. <i>Plant Cell</i> , 2019, 31, 1416-1417.	3.1	12
136	ScCas9 recognizes NNG protospacer adjacent motif in genome editing of rice. <i>Science China Life Sciences</i> , 2020, 63, 450-452.	2.3	12
137	Rice Protein Tagging Project: A Call for International Collaborations on Genome-wide In-Locus Tagging of Rice Proteins. <i>Molecular Plant</i> , 2020, 13, 1663-1665.	3.9	11
138	Advances in the regulation and crosstalks of phytohormones. <i>Science Bulletin</i> , 2009, 54, 4069-4082.	1.7	10
139	Action of Strigolactones in Plants. <i>The Enzymes</i> , 2014, 35, 57-84.	0.7	10
140	Combination of Eight Alleles at Four Quantitative Trait Loci Determines Grain Length in Rice. <i>PLoS ONE</i> , 2016, 11, e0150832.	1.1	9
141	Grain Quality. , 2013, , 237-254.		8
142	FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021, 64, 167-170.	2.3	8
143	Toward a Molecular Understanding of Plant Hormone Actions. <i>Molecular Plant</i> , 2016, 9, 1-3.	3.9	7
144	Strigolactones. , 2017, , 327-359.		7

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145	Rapid and specific isolation of intact mitochondria from Arabidopsis leaves. Journal of Genetics and Genomics, 2020, 47, 65-68.	1.7	6
146	Monitoring gene expression by cDNA array. Science Bulletin, 1999, 44, 441-444.	1.7	5
147	Evolution of Strigolactone Perception by Seeds of Parasitic Plants: Reinventing the Wheel. Molecular Plant, 2016, 9, 493-495.	3.9	5
148	Plant and animal organelles in cell death. Oncotarget, 2015, 6, 13852-13853.	0.8	5
149	Toward understanding the molecular mechanisms governing plant hormone actions: A brief introduction to the major research program "Molecular mechanisms of plant hormone actions" funded by the national natural science foundation of china (NSFC). Science Bulletin, 2010, 55, 2197-2197.	1.7	4
150	Rice Plant Architecture: Molecular Basis and Application in Breeding. , 2018, , 129-154.		4
151	Combination of twelve alleles at six quantitative trait loci determines grain weight in rice. PLoS ONE, 2017, 12, e0181588.	1.1	4
152	Fine-mapping of an Arabidopsis cell death mutation locus. Science in China Series C: Life Sciences, 2000, 43, 138-145.	1.3	3
153	Mapping and characterization of a tiller-spreading mutant lazy-2 in rice. Science Bulletin, 2003, 48, 2715-2717.	1.7	2
154	Rice geographic adaption to poor soil: novel insights for sustainable agriculture. Molecular Plant, 2021, 14, 369-371.	3.9	1
155	Expression of Arabidopsis tryptophan biosynthetic pathway genes: effect of the 5' coding region of phosphoribosylanthranilate isomerase gene. Science in China Series C: Life Sciences, 1999, 42, 274-280.	1.3	0
156	Advances in Arabidopsis research in China from 2006 to 2007. Science Bulletin, 2007, 52, 1729-1733.	1.7	0
157	Immunopurification of Mitochondria from Arabidopsis. Current Protocols, 2021, 1, e34.	1.3	0