

Xiangbing Meng

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

4,083
citations

29
h-index

47
g-index

47
ext. papers

5,533
ext. citations

14.1
avg, IF

5.12
L-index

#	Paper	IF	Citations
44	Targeting a gene regulatory element enhances rice grain yield by decoupling panicle number and size.. <i>Nature Biotechnology</i> , 2022 ,	44.5	2
43	Generating broad-spectrum tolerance to ALS-inhibiting herbicides in rice by base editing. <i>Science China Life Sciences</i> , 2021 , 64, 1624-1633	8.5	18
42	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021 , 184, 1156-1170.e14	56.2	81
41	LAZY2 controls rice tiller angle through regulating starch biosynthesis in gravity-sensing cells. <i>New Phytologist</i> , 2021 , 231, 1073-1087	9.8	3
40	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	14.4	5
39	FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021 , 64, 167-170	8.5	3
38	Expanding the scope of genome editing with SpG and SpRY variants in rice. <i>Science China Life Sciences</i> , 2021 , 64, 1784-1787	8.5	5
37	Regulation of Rice Tillering by RNA-Directed DNA Methylation at Miniature Inverted-Repeat Transposable Elements. <i>Molecular Plant</i> , 2020 , 13, 851-863	14.4	19
36	Targeted, random mutagenesis of plant genes with dual cytosine and adenine base editors. <i>Nature Biotechnology</i> , 2020 , 38, 875-882	44.5	133
35	ScCas9 recognizes NNG protospacer adjacent motif in genome editing of rice. <i>Science China Life Sciences</i> , 2020 , 63, 450-452	8.5	7
34	A Strigolactone Biosynthesis Gene Contributed to the Green Revolution in Rice. <i>Molecular Plant</i> , 2020 , 13, 923-932	14.4	35
33	βCarotene Isomerase Suppresses Tillering in Rice through the Coordinated Biosynthesis of Strigolactone and Abscisic Acid. <i>Molecular Plant</i> , 2020 , 13, 1784-1801	14.4	21
32	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	11.6	22
31	Improving the efficiency of the CRISPR-Cas12a system with tRNA-crRNA arrays. <i>Crop Journal</i> , 2020 , 8, 403-407	4.6	9
30	SLR1 inhibits MOC1 degradation to coordinate tiller number and plant height in rice. <i>Nature Communications</i> , 2019 , 10, 2738	17.4	44
29	Strigolactone promotes cytokinin degradation through transcriptional activation of in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14319-14324	11.5	46
28	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	14.4	36

27	OsBRXL4 Regulates Shoot Gravitropism and Rice Tiller Angle through Affecting LAZY1 Nuclear Localization. <i>Molecular Plant</i> , 2019 , 12, 1143-1156	14.4	29
26	Gene Replacement by Intron Targeting with CRISPR-Cas9. <i>Methods in Molecular Biology</i> , 2019 , 1917, 285-296	11.6	3
25	xCas9 expands the scope of genome editing with reduced efficiency in rice. <i>Plant Biotechnology Journal</i> , 2019 , 17, 709-711	11.6	65
24	Expression of the Nitrate Transporter Gene Confers High Yield and Early Maturation in Rice. <i>Plant Cell</i> , 2018 , 30, 638-651	11.6	145
23	Robust genome editing of CRISPR-Cas9 at NAG PAMs in rice. <i>Science China Life Sciences</i> , 2018 , 61, 122-125	11.6	36
22	Increasing the efficiency of CRISPR-Cas9-VQR precise genome editing in rice. <i>Plant Biotechnology Journal</i> , 2018 , 16, 292-297	11.6	56
21	A Core Regulatory Pathway Controlling Rice Tiller Angle Mediated by the -Dependent Asymmetric Distribution of Auxin. <i>Plant Cell</i> , 2018 , 30, 1461-1475	11.6	55
20	Construction of a Genome-Wide Mutant Library in Rice Using CRISPR/Cas9. <i>Molecular Plant</i> , 2017 , 10, 1238-1241	14.4	127
19	Tissue-Specific Ubiquitination by IPA1 INTERACTING PROTEIN1 Modulates IPA1 Protein Levels to Regulate Plant Architecture in Rice. <i>Plant Cell</i> , 2017 , 29, 697-707	11.6	58
18	IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. <i>Cell Research</i> , 2017 , 27, 1128-1141	24.7	115
17	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	6.2	24
16	Gene replacements and insertions in rice by intron targeting using CRISPR-Cas9. <i>Nature Plants</i> , 2016 , 2, 16139	11.5	221
15	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	11.5	100
14	Copy number variation at the GL7 locus contributes to grain size diversity in rice. <i>Nature Genetics</i> , 2015 , 47, 944-8	36.3	317
13	Strigolactone Signaling in Arabidopsis Regulates Shoot Development by Targeting D53-Like SMXL Repressor Proteins for Ubiquitination and Degradation. <i>Plant Cell</i> , 2015 , 27, 3128-42	11.6	216
12	MONOCULM 3, an ortholog of WUSCHEL in rice, is required for tiller bud formation. <i>Journal of Genetics and Genomics</i> , 2015 , 42, 71-8	4	73
11	Correction for Cardoso et al., Natural variation of rice strigolactone biosynthesis is associated with the deletion of two MAX1 orthologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6528-6528	11.5	78
10	Natural variation of rice strigolactone biosynthesis is associated with the deletion of two MAX1 orthologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2379-84	11.5	96

9	Strigolactones regulate rice tiller angle by attenuating shoot gravitropism through inhibiting auxin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11199-204	11.5	88
8	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, 3743-59	11.6	417
7	DWARF 53 acts as a repressor of strigolactone signalling in rice. <i>Nature</i> , 2013 , 504, 401-5	50.4	475
6	Degradation of MONOCULM 1 by APC/C(TAD1) regulates rice tillering. <i>Nature Communications</i> , 2012 , 3, 750	17.4	110
5	Cloning and Characterization of the DHDP5 Gene Encoding the Lysine Biosynthetic Enzyme Dihydrodipicolinate Synthase from <i>Zizania latifolia</i> (Griseb). <i>Plant Molecular Biology Reporter</i> , 2009 , 27, 199-208	1.7	5
4	Short panicle1 encodes a putative PTR family transporter and determines rice panicle size. <i>Plant Journal</i> , 2009 , 58, 592-605	6.9	157
3	DWARF27, an iron-containing protein required for the biosynthesis of strigolactones, regulates rice tiller bud outgrowth. <i>Plant Cell</i> , 2009 , 21, 1512-25	11.6	431
2	Rice gene OsNAC19 encodes a novel NAC-domain transcription factor and responds to infection by <i>Magnaporthe grisea</i> . <i>Plant Science</i> , 2007 , 172, 120-130	5.3	74
1	Molecular cloning and characterization of a rice gene encoding AP2/EREBP-type transcription factor and its expression in response to infection with blast fungus and abiotic stresses. <i>Physiological and Molecular Plant Pathology</i> , 2007 , 70, 60-68	2.6	21