Meng Yuan

List of Publications by Citations

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49 papers	1,922 citations	17 h-index	43 g-index
55 ext. papers	2,649 ext. citations	9.4 avg, IF	4.78 L-index

#	Paper	IF	Citations
49	Promoter mutations of an essential gene for pollen development result in disease resistance in rice. *Genes and Development*, **2006**, 20, 1250-5	12.6	363
48	The bacterial pathogen Xanthomonas oryzae overcomes rice defenses by regulating host copper redistribution. *Plant Cell*, **2010**, 22, 3164-76	11.6	166
47	A paralog of the MtN3/saliva family recessively confers race-specific resistance to Xanthomonas oryzae in rice. *Plant, Cell and Environment*, **2011**, 34, 1958-69	8.4	155
46	uORF-mediated translation allows engineered plant disease resistance without fitness costs. *Nature*, **2017**, 545, 491-494	50.4	145
45	Rice MtN3/saliva/SWEET family genes and their homologs in cellular organisms. *Molecular Plant*, **2013**, 6, 665-74	14.4	119
44	Molecular and functional analyses of COPT/Ctr-type copper transporter-like gene family in rice. *BMC Plant Biology*, **2011**, 11, 69	5.3	117
43	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E5411-9	11.5	116
42	Improvement of multiple agronomic traits by a disease resistance gene via cell wall reinforcement. *Nature Plants*, **2017**, 3, 17009	11.5	108
41	Pathogen-induced expressional loss of function is the key factor in race-specific bacterial resistance conferred by a recessive R gene xa13 in rice. *Plant and Cell Physiology*, **2009**, 50, 947-55	4.9	73
40	Dual function of rice OsDR8 gene in disease resistance and thiamine accumulation. *Plant Molecular Biology*, **2006**, 60, 437-49	4.6	73
39	A host basal transcription factor is a key component for infection of rice by TALE-carrying bacteria. *ELife*, **2016**, 5,	8.9	72
38	Overexpression of OsSWEET5 in rice causes growth retardation and precocious senescence. *PLoS ONE*, **2014**, 9, e94210	3.7	51
37	Rice MtN3/saliva/SWEET gene family: Evolution, expression profiling, and sugar transport. *Journal of Integrative Plant Biology*, **2014**, 56, 559-70	8.3	46
36	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. *Nature Plants*, **2020**, 6, 1447-1454	11.5	25
35	Translational Regulation of Metabolic Dynamics during Effector-Triggered Immunity. *Molecular Plant*, **2020**, 13, 88-98	14.4	23
34	The versatile functions of OsALDH2B1 provide a genic basis for growth-defense trade-offs in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 3867-3873	11.5	21
33	Multiple Alleles Encoding Atypical NLRs with Unique Central Tandem Repeats in Rice Confer Resistance to pv.. *Plant Communications*, **2020**, 1, 100088	9	17

32	DgcA, a diguanylate cyclase from Xanthomonas oryzae pv. oryzae regulates bacterial pathogenicity on rice. *Scientific Reports*, **2016**, 6, 25978	4.9	17
31	A Conserved Basal Transcription Factor Is Required for the Function of Diverse TAL Effectors in Multiple Plant Hosts. *Frontiers in Plant Science*, **2017**, 8, 1919	6.2	16
30	Cryo-EM structure of the human mitochondrial translocase TIM22 complex. *Cell Research*, **2021**, 31, 369-372	24.7	16
29	TALE-carrying bacterial pathogens trap host nuclear import receptors for facilitation of infection of rice. *Molecular Plant Pathology*, **2019**, 20, 519-532	5.7	15
28	Dynamic phytohormone profiling of rice upon rice black-streaked dwarf virus invasion. *Journal of Plant Physiology*, **2018**, 228, 92-100	3.6	14
27	pv. Inoculation and Growth Rate on Rice by Leaf Clipping Method. *Bio-protocol*, **2017**, 7, e2568	0.9	14
26	Characterization of a disease susceptibility locus for exploring an efficient way to improve rice resistance against bacterial blight. *Science China Life Sciences*, **2017**, 60, 298-306	8.5	13
25	An update on molecular mechanism of disease resistance genes and their application for genetic improvement of rice. *Molecular Breeding*, **2019**, 39, 1	3.4	12
24	The group I GH3 family genes encoding JA-Ile synthetase act as positive regulator in the resistance of rice to Xanthomonas oryzae pv. oryzae. *Biochemical and Biophysical Research Communications*, **2019**, 508, 1062-1066	3.4	10
23	uORFlight: a vehicle toward uORF-mediated translational regulation mechanisms in eukaryotes. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	9
22	Dominant and Recessive Major Genes Lead to Different Types of Host Cell Death During Resistance to in Rice. *Frontiers in Plant Science*, **2018**, 9, 1711	6.2	9
21	An Oryza-specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. *Science Bulletin*, **2021**, 66, 2369-2369	10.6	8
20	The host basal transcription factor IIA subunits coordinate for facilitating infection of TALEs-carrying bacterial pathogens in rice. *Plant Science*, **2019**, 284, 48-56	5.3	7
19	Xanthomonas TAL effectors hijack host basal transcription factor IIA and subunits for invasion. *Biochemical and Biophysical Research Communications*, **2018**, 496, 608-613	3.4	7
18	Autophagy-Like Cell Death Regulates Hydrogen Peroxide and Calcium Ion Distribution in -Mediated Resistance to pv.. *International Journal of Molecular Sciences*, **2019**, 21,	6.3	7
17	Different Cell Wall-Degradation Ability Leads to Tissue-Specificity between pv and pv. *Pathogens*, **2020**, 9,	4.5	6
16	Natural variations of TFIIA gene and LOB1 promoter contribute to citrus canker disease resistance in Atalantia buxifolia. *PLoS Genetics*, **2021**, 17, e1009316	6	6
15	Update on the Roles of Rice MAPK Cascades. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	5

14	The rice Raf-like MAPKKK OsILA1 confers broad-spectrum resistance to bacterial blight by suppressing the OsMAPKK4-OsMAPK6 cascade. *Journal of Integrative Plant Biology*, **2021**, 63, 1815-1842	8.3	5
13	Knock out of transcription factor WRKY53 thickens sclerenchyma cell walls, confers bacterial blight resistance. *Plant Physiology*, **2021**, 187, 1746-1761	6.6	5
12	The key residues of OsTFIIA/Xa5 protein captured by the arginine-rich TFB domain of TALEs compromising rice susceptibility and bacterial pathogenicity. *Journal of Integrative Agriculture*, **2019**, 18, 1178-1188	3.2	4
11	Towards Engineering Broad-Spectrum Disease-Resistant Crops. *Trends in Plant Science*, **2020**, 25, 424-427	13.1	4
10	Precise Editing Enables Crop Broad-Spectrum Resistance. *Molecular Plant*, **2019**, 12, 1542-1544	14.4	4
9	Structural insight into the SAM-mediated assembly of the mitochondrial TOM core complex. *Science*, **2021**, 373, 1377-1381	33.3	4
8	miR395-regulated sulfate metabolism exploits pathogen sensitivity to sulfate to boost immunity in rice.. *Molecular Plant*, **2021**,	14.4	3
7	Rice group I GH3 gene family, positive regulators of bacterial pathogens. *Plant Signaling and Behavior*, **2019**, 14, e1588659	2.5	2
6	Impaired SWEET-mediated sugar transportation impacts starch metabolism in developing rice seeds. *Crop Journal*, **2021**,	4.6	2
5	Engineering false smut resistance rice via host-induced gene silencing of two chitin synthase genes of Ustilaginoidea virens. *Plant Biotechnology Journal*, **2021**, 19, 2386-2388	11.6	2
4	Development of marker-free rice with stable and high resistance to rice black-streaked dwarf virus disease through RNA interference. *Plant Biotechnology Journal*, **2021**, 19, 212-214	11.6	1
3	Promotes Abscisic Acid Accumulation to Accelerate Leaf Senescence and Inhibit Seed Germination by Downregulating Abscisic Acid Catabolic Genes in Rice.. *Frontiers in Plant Science*, **2021**, 12, 816156	6.2	0
2	An MKP-MAPK protein phosphorylation cascade controls vascular immunity in plants.. *Science Advances*, **2022**, 8, eabg8723	14.3	0
1	In Loving Memory of Professor Shiping Wang. *Molecular Plant*, **2019**, 12, 1171-1172	14.4	