Bing Yang

List of Publications by Year
in descending order

81 papers	11,239 citations	61687 45 h-index	71088 80 g-index
85 all docs	85 docs citations	85 times ranked	9350 citing authors

#	Article	IF	Citations
1	Potential applications of the CRISPR/Cas technology for genetic improvement of yam (<i>Dioscorea</i>) Tj ETQq1 1 0.784314 rgBT /Ov	2.0	8
2	Dissecting the labdaneâ€related diterpenoid biosynthetic gene clusters in rice reveals directional crossâ€cluster phytotoxicity. New Phytologist, 2022, 233, 878-889.	3.5	17
3	<i>OsSWEET11b</i>, a potential sixth leaf blight susceptibility gene involved in sugar transportâ€dependent male fertility. New Phytologist, 2022, 234, 975-989.	3.5	18
4	Rice diterpenoid phytoalexins are involved in defence against parasitic nematodes and shape rhizosphere nematode communities. New Phytologist, 2022, 235, 1231-1245.	3.5	12
5	A CRISPR/Cas9â€based genomeâ€editing system for yam (<i>Dioscorea</i> spp.). Plant Biotechnology Journal, 2021, 19, 645-647.	4.1	31
6	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. Developmental Cell, 2021, 56, 557-568.e6.	3.1	129
7	A (conditional) role for labdaneâ€related diterpenoid natural products in rice stomatal closure. New Phytologist, 2021, 230, 698-709.	3.5	18
8	The Xa7 resistance gene guards the rice susceptibility gene SWEET14 against exploitation by the bacterial blight pathogen. Plant Communications, 2021, 2, 100164.	3.6	30
9	Functional Identification of the Xanthomonas oryzae pv. oryzae Type I-C CRISPR-Cas System and Its Potential in Gene Editing Application. Frontiers in Microbiology, 2021, 12, 686715.	1.5	3
10	High-efficiency plastome base editing in rice with TAL cytosine deaminase. Molecular Plant, 2021, 14, 1412-1414.	3.9	30
11	Interdependent evolution of biosynthetic gene clusters for momilactone production in rice. Plant Cell, 2021, 33, 290-305.	3.1	34
12	Editorial: New Genome Editing Tools and Resources: Enabling Gene Discovery and Functional Genomics. Frontiers in Genome Editing, 2021, 3, 771622.	2.7	1
13	The SUMO ligase MMS21 profoundly influences maize development through its impact on genome activity and stability. PLoS Genetics, 2021, 17, e1009830.	1.5	10
14	Genome editing in grass plants. ABIOTECH, 2020, 1, 41-57.	1.8	11
15	An <i>Agrobacterium</i>â€delivered <scp>CRISPR</scp>/Cas9 system for targeted mutagenesis in sorghum. Plant Biotechnology Journal, 2020, 18, 319-321.	4.1	40
16	The maize heterotrimeric G protein Î² subunit controls shoot meristem development and immune responses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1799-1805.	3.3	77
17	Disruption of miRNA sequences by TALENs and CRISPR/Cas9 induces varied lengths of miRNA production. Plant Biotechnology Journal, 2020, 18, 1526-1536.	4.1	35
18	Differential activities of maize plant elicitor peptides as mediators of immune signaling and herbivore resistance. Plant Journal, 2020, 104, 1582-1602.	2.8	21

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19	Functional Analysis of the teosinte branched 1 Gene in the Tetraploid Switchgrass (Panicum virgatum) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	10
20	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. Nature Plants, 2020, 6, 1375-1388.	4.7	52
21	Grand Challenges in Genome Editing in Plants. Frontiers in Genome Editing, 2020, 2, 2.	2.7	17
22	Xa1 Allelic R Genes Activate Rice Blight Resistance Suppressed by Interfering TAL Effectors. Plant Communications, 2020, 1, 100087.	3.6	52
23	CRISPR/Cas9-Based Gene Editing Using Egg Cell-Specific Promoters in Arabidopsis and Soybean. Frontiers in Plant Science, 2020, 11, 800.	1.7	51
24	Achieving Plant Genome Editing While Bypassing Tissue Culture. Trends in Plant Science, 2020, 25, 427-429.	4.3	22
25	Considerations in adapting CRISPR/Cas9 in nongenetic model plant systems. Applications in Plant Sciences, 2020, 8, e11314.	0.8	56
26	An efficient method to clone TAL effector genes from <i>Xanthomonas oryzae</i> using Gibson assembly. Molecular Plant Pathology, 2019, 20, 1453-1462.	2.0	12
27	Can Designer Indels Be Tailored by Gene Editing?. BioEssays, 2019, 41, 1900126.	1.2	3
28	Broad-spectrum resistance to bacterial blight in rice using genome editing. Nature Biotechnology, 2019, 37, 1344-1350.	9.4	470
29	Diagnostic kit for rice blight resistance. Nature Biotechnology, 2019, 37, 1372-1379.	9.4	92
30	Development of an <i>Agrobacterium</i>â€delivered <scp>CRISPR</scp>/Cas9 system for wheat genome editing. Plant Biotechnology Journal, 2019, 17, 1623-1635.	4.1	155
31	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. Nature Plants, 2019, 5, 1043-1056.	4.7	60
32	CRISPR/Cas9 for Mutagenesis in Rice. Methods in Molecular Biology, 2019, 1864, 279-293.	0.4	12
33	An Agrobacterium-Mediated CRISPR/Cas9 Platform for Genome Editing in Maize. Methods in Molecular Biology, 2019, 1917, 121-143.	0.4	8
34	Creating Large Chromosomal Deletions in Rice Using CRISPR/Cas9. Methods in Molecular Biology, 2019, 1917, 47-61.	0.4	17
35	A male-expressed rice embryogenic trigger redirected for asexual propagation through seeds. Nature, 2019, 565, 91-95.	13.7	324
36	Highly Efficient AÂ·T to GÂ·C Base Editing by Cas9n-Guided tRNA Adenosine Deaminase in Rice. Molecular Plant, 2018, 11, 631-634.	3.9	177

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37	Inferring Roles in Defense from Metabolic Allocation of Rice Diterpenoids. Plant Cell, 2018, 30, 1119-1131.	3.1	55
38	Impaired phloem loading in <i>zmsweet13a,b,c</i> sucrose transporter triple knockâ€out mutants in <i>Zea mays</i>. New Phytologist, 2018, 218, 594-603.	3.5	127
39	<scp>SWEET</scp>11 and 15 as key players in seed filling in rice. New Phytologist, 2018, 218, 604-615.	3.5	214
40	Interaction of Rice and Xanthomonas TAL Effectors. , 2018, , 375-391.		3
41	Targeted mutagenesis in tetraploid switchgrass (<i>Panicum virgatum</i> L.) using CRISPR/Cas9. Plant Biotechnology Journal, 2018, 16, 381-393.	4.1	71
42	Sugar flux and signaling in plantâ€“microbe interactions. Plant Journal, 2018, 93, 675-685.	2.8	180
43	Non-TAL Effectors From Xanthomonas oryzae pv. oryzae Suppress Peptidoglycan-Triggered MAPK Activation in Rice. Frontiers in Plant Science, 2018, 9, 1857.	1.7	14
44	Application of CRISPR/Cas9 to <i>Tragopogon</i> (Asteraceae), an evolutionary model for the study of polyploidy. Molecular Ecology Resources, 2018, 18, 1427-1443.	2.2	31
45	New variants of CRISPR RNAâ€guided genome editing enzymes. Plant Biotechnology Journal, 2017, 15, 917-926.	4.1	79
46	Gene Editing With TALEN and CRISPR/Cas in Rice. Progress in Molecular Biology and Translational Science, 2017, 149, 81-98.	0.9	27
47	Translational genomics of grain size regulation in wheat. Theoretical and Applied Genetics, 2017, 130, 1765-1771.	1.8	64
48	An <i>Agrobacterium</i>â€delivered <scp>CRISPR</scp>/Cas9 system for highâ€frequency targeted mutagenesis in maize. Plant Biotechnology Journal, 2017, 15, 257-268.	4.1	300
49	The broadly effective recessive resistance gene <i>xa5</i> of rice is a virulence effectorâ€dependent quantitative trait for bacterial blight. Plant Journal, 2016, 86, 186-194.	2.8	64
50	The Regulatory Status of Genomeâ€edited Crops. Plant Biotechnology Journal, 2016, 14, 510-518.	4.1	223
51	Interfering TAL effectors of Xanthomonas oryzae neutralize R-gene-mediated plant disease resistance. Nature Communications, 2016, 7, 13435.	5.8	139
52	Use of designer nucleases for targeted gene and genome editing in plants. Plant Biotechnology Journal, 2016, 14, 483-495.	4.1	195
53	TALEN-Mediated Homologous Recombination Produces Site-Directed DNA Base Change and Herbicide-Resistant Rice. Journal of Genetics and Genomics, 2016, 43, 297-305.	1.7	72
54	A quick guide to CRISPR sgRNA design tools. GM Crops and Food, 2015, 6, 266-276.	2.0	80

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55	The Application of Synthetic Biology to Elucidation of Plant Mono-, Sesqui-, and Diterpenoid Metabolism. Molecular Plant, 2015, 8, 6-16.	3.9	75
56	XA23 Is an Executor R Protein and Confers Broad-Spectrum Disease Resistance in Rice. Molecular Plant, 2015, 8, 290-302.	3.9	202
57	Heritable siteâ€specific mutagenesis using <scp>TALEN</scp>s in maize. Plant Biotechnology Journal, 2015, 13, 1002-1010.	4.1	110
58	Gene targeting by the <scp>TAL</scp> effector PthXo2 reveals cryptic resistance gene for bacterial blight of rice. Plant Journal, 2015, 82, 632-643.	2.8	409
59	Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport. Nature Genetics, 2015, 47, 1489-1493.	9.4	360
60	Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. PLoS Pathogens, 2014, 10, e1003972.	2.1	137
61	Large chromosomal deletions and heritable small genetic changes induced by CRISPR/Cas9 in rice. Nucleic Acids Research, 2014, 42, 10903-10914.	6.5	547
62	XA23 is an executor R protein and confers broad-spectrum disease resistance in rice. Molecular Plant, 2014, , .	3.9	7
63	TALEN-mediated genome editing: prospects and perspectives. Biochemical Journal, 2014, 462, 15-24.	1.7	109
64	TALEN utilization in rice genome modifications. Methods, 2014, 69, 9-16.	1.9	17
65	The broad bacterial blight resistance of rice line <scp>CBB</scp>23 is triggered by a novel transcription activatorâ€like (<scp>TAL</scp>) effector of <i><scp>X</scp>anthomonas oryzae</i> pv. <i>oryzae</i>. Molecular Plant Pathology, 2014, 15, 333-341.	2.0	39
66	TALE activation of endogenous genes in Chlamydomonas reinhardtii. Algal Research, 2014, 5, 52-60.	2.4	51
67	Efficient CRISPR/Cas9-Mediated Gene Editing in Arabidopsis thaliana and Inheritance of Modified Genes in the T2 and T3 Generations. PLoS ONE, 2014, 9, e99225.	1.1	136
68	Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice. Nucleic Acids Research, 2013, 41, e188-e188.	6.5	1,066
69	Inoculation and Virulence Assay for Bacterial Blight and Bacterial Leaf Streak of Rice. Methods in Molecular Biology, 2013, 956, 249-255.	0.4	42
70	TAL Effector Nuclease (TALEN) Engineering. Methods in Molecular Biology, 2013, 978, 63-72.	0.4	19
71	High-efficiency TALEN-based gene editing produces disease-resistant rice. Nature Biotechnology, 2012, 30, 390-392.	9.4	965
72	Modularly assembled designer TAL effector nucleases for targeted gene knockout and gene replacement in eukaryotes. Nucleic Acids Research, 2011, 39, 6315-6325.	6.5	368

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73	TAL nucleases (TALNs): hybrid proteins composed of TAL effectors and FokI DNA-cleavage domain. Nucleic Acids Research, 2011, 39, 359-372.	6.5	477
74	Mutagenesis of 18 Type III Effectors Reveals Virulence Function of XopZ_{PXO99} in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>. Molecular Plant-Microbe Interactions, 2010, 23, 893-902.	1.4	97
75	Rice <i>xa13</i> Recessive Resistance to Bacterial Blight Is Defeated by Induction of the Disease Susceptibility Gene Os-<i>11N3</i> Â Â. Plant Cell, 2010, 22, 3864-3876.	3.1	401
76	Os8N3 is a host disease-susceptibility gene for bacterial blight of rice. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10503-10508.	3.3	543
77	Avoidance of Host Recognition by Alterations in the Repetitive and C-Terminal Regions of AvrXa7, a Type III Effector of Xanthomonas oryzae pv. oryzae. Molecular Plant-Microbe Interactions, 2005, 18, 142-149.	1.4	74
78	R gene expression induced by a type-III effector triggers disease resistance in rice. Nature, 2005, 435, 1122-1125.	13.7	502
79	Diverse Members of the AvrBs3/PthA Family of Type III Effectors Are Major Virulence Determinants in Bacterial Blight Disease of Rice. Molecular Plant-Microbe Interactions, 2004, 17, 1192-1200.	1.4	183
80	The C Terminus of AvrXa10 Can Be Replaced by the Transcriptional Activation Domain of VP16 from the Herpes Simplex Virus. Plant Cell, 1999, 11, 1665-1674.	3.1	80
81	AvrXa10 Contains an Acidic Transcriptional Activation Domain in the Functionally Conserved C Terminus. Molecular Plant-Microbe Interactions, 1998, 11, 824-832.	1.4	165