Yanjun Kou

List of Publications by Year
in descending order

23 papers	5,839 citations	516710 16 h-index	642732 23 g-index
26 all docs	26 docs citations	26 times ranked	14686 citing authors

#	Article	IF	Citations
1	Warm temperature compromises JA-regulated basal resistance to enhance Magnaporthe oryzae infection in rice. Molecular Plant, 2022, 15, 723-739.	8.3	31
2	MoWhi2 Mediates Mitophagy to Regulate Conidiation and Pathogenesis in Magnaporthe oryzae. International Journal of Molecular Sciences, 2022, 23, 5311.	4.1	4
3	UvKmt2-Mediated H3K4 Trimethylation Is Required for Pathogenicity and Stress Response in Ustilaginoidea virens. Journal of Fungi (Basel, Switzerland), 2022, 8, 553.	3.5	3
4	MoWhi2 regulates appressorium formation and pathogenicity via the MoTor signalling pathway in <i>Magnaporthe oryzae</i>. Molecular Plant Pathology, 2021, 22, 969-983.	4.2	18
5	Selective Degradation of Mitochondria by Mitophagy in Pathogenic Fungi. American Journal of Molecular Biology, 2021, 11, 15-27.	0.3	1
6	Recent Progress in Rice Broad-Spectrum Disease Resistance. International Journal of Molecular Sciences, 2021, 22, 11658.	4.1	18
7	UvKmt6-mediated H3K27 trimethylation is required for development, pathogenicity, and stress response in <i>Ustilaginoidea virens</i>. Virulence, 2021, 12, 2972-2988.	4.4	16
8	A candidate gene for the determination of rice resistant to rice false smut. Molecular Breeding, 2020, 40, 1.	2.1	10
9	Comparative transcriptomic analysis reveals the mechanistic basis of Pib-mediated broad spectrum resistance against Magnaporthe oryzae. Functional and Integrative Genomics, 2020, 20, 787-799.	3.5	3
10	UvAtg8-Mediated Autophagy Regulates Fungal Growth, Stress Responses, Conidiation, and Pathogenesis in Ustilaginoidea virens. Rice, 2020, 13, 56.	4.0	29
11	Mitochondrial dynamics and mitophagy are necessary for proper invasive growth in rice blast. Molecular Plant Pathology, 2019, 20, 1147-1162.	4.2	21
12	Every Coin Has Two Sides: Reactive Oxygen Species during Riceâ€“Magnaporthe oryzae Interaction. International Journal of Molecular Sciences, 2019, 20, 1191.	4.1	30
13	Label-Free Quantitative Proteomics of Lysine Acetylome Identifies Substrates of Gcn5 in Magnaporthe oryzae Autophagy and Epigenetic Regulation. MSystems, 2018, 3, .	3.8	23
14	Structureâ€“function analyses of the Pth11 receptor reveal an important role for <scp>CFEM</scp> motif and redox regulation in rice blast. New Phytologist, 2017, 214, 330-342.	7.3	91
15	Surface sensing and signaling networks in plant pathogenic fungi. Seminars in Cell and Developmental Biology, 2016, 57, 84-92.	5.0	32
16	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
17	Comparative genomics identifies the <i><scp>M</scp>agnaporthe oryzae</i> avirulence effector <i><scp>A</scp>vr<scp>P</scp>i9</i> that triggers <i><scp>P</scp>i9</i>â€mediated blast resistance in rice. New Phytologist, 2015, 206, 1463-1475.	7.3	169
18	The rice RAD51C gene is required for the meiosis of both female and male gametocytes and the DNA repair of somatic cells. Journal of Experimental Botany, 2012, 63, 5323-5335.	4.8	38

#	Article	IF	Citations
19	Toward an understanding of the molecular basis of quantitative disease resistance in rice. Journal of Biotechnology, 2012, 159, 283-290.	3.8	41
20	OsWRKY45 alleles play different roles in abscisic acid signalling and salt stress tolerance but similar roles in drought and cold tolerance in rice. Journal of Experimental Botany, 2011, 62, 4863-4874.	4.8	228
21	Identification of genes contributing to quantitative disease resistance in rice. Science China Life Sciences, 2010, 53, 1263-1273.	4.9	17
22	Broad-spectrum and durability: understanding of quantitative disease resistance. Current Opinion in Plant Biology, 2010, 13, 181-185.	7.1	273
23	Molecular analyses of the rice tubby-like protein gene family and their response to bacterial infection. Plant Cell Reports, 2009, 28, 113-121.	5.6	31