Saet-Byul Kim

List of Publications by Year
in descending order

19 papers	1,627 citations	759190 12 h-index	940516 16 g-index
22 all docs	22 docs citations	22 times ranked	1980 citing authors

#	Article	IF	Citations
1	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. Nature Genetics, 2014, 46, 270-278.	21.4	867
2	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. Genome Biology, 2017, 18, 210.	8.8	255
3	Current Understandings of Plant Nonhost Resistance. Molecular Plant-Microbe Interactions, 2017, 30, 5-15.	2.6	122
4	Divergent evolution of multiple virusâ€resistance genes from a progenitor in <i>Capsicum</i> spp.. New Phytologist, 2017, 213, 886-899.	7.3	81
5	Multiple recognition of <scp>RXLR</scp> effectors is associated with nonhost resistance of pepper against <i>Phytophthora infestans</i>. New Phytologist, 2014, 203, 926-938.	7.3	53
6	Genomeâ€wide functional analysis of hot pepper immune receptors reveals an autonomous NLR clade in seed plants. New Phytologist, 2021, 229, 532-547.	7.3	40
7	RNA-Dependent RNA Polymerase (NIb) of the Potyviruses Is an Avirulence Factor for the Broad-Spectrum Resistance Gene Pvr4 in Capsicum annuum cv. CM334. PLoS ONE, 2015, 10, e0119639.	2.5	31
8	The Coiled-Coil and Leucine-Rich Repeat Domain of the Potyvirus Resistance Protein Pvr4 Has a Distinct Role in Signaling and Pathogen Recognition. Molecular Plant-Microbe Interactions, 2018, 31, 906-913.	2.6	30
9	Global gene expression profiling for fruit organs and pathogen infections in the pepper, Capsicum annuum L.. Scientific Data, 2018, 5, 180103.	5.3	29
10	A simple method for screening of plant NBS-LRR genes that confer a hypersensitive response to plant viruses and its application for screening candidate pepper genes against Pepper mottle virus. Journal of Virological Methods, 2014, 201, 57-64.	2.1	27
11	Positive-Selection and Ligation-Independent Cloning Vectors for Large Scale in Planta Expression for Plant Functional Genomics. Molecules and Cells, 2010, 30, 557-562.	2.6	24
12	Analysis of the transcriptomic, metabolomic, and gene regulatory responses to <i>Puccinia sorghi</i> in maize. Molecular Plant Pathology, 2021, 22, 465-479.	4.2	18
13	Use of virusâ€induced gene silencing to characterize genes involved in modulating hypersensitive cell death in maize. Molecular Plant Pathology, 2020, 21, 1662-1676.	4.2	12
14	A maize cytochrome bâ€"c1 complex subunit protein ZmQCR7 controls variation in the hypersensitive response. Planta, 2019, 249, 1477-1485.	3.2	10
15	The maize ZmMIEL1 E3 ligase and ZmMYB83 transcription factor proteins interact and regulate the hypersensitive defence response. Molecular Plant Pathology, 2021, 22, 694-709.	4.2	10
16	Characterization of Brassica rapa S-adenosyl-L-methionine synthetase gene including its roles in biosynthesis pathway. Horticulture Environment and Biotechnology, 2012, 53, 57-65.	2.1	9
17	Maize Plants Chimeric for an Autoactive Resistance Gene Display a Cell-Autonomous Hypersensitive Response but Nonâ€"Cell Autonomous Defense Signaling. Molecular Plant-Microbe Interactions, 2021, 34, 606-616.	2.6	2
18	Multiple insertions of COIN , a novel maize Foldback transposable element, in the Conring gene cause a spontaneous progressive cell death phenotype. Plant Journal, 2020, 104, 581-595.	5.7	0

#	Article	IF	Citations
19	Close encounters in the corn field. Molecular Plant, 2022, , .	8.3	0